Chapter 4
Epidemic Models with Switching

In this chapter, the methods developed thus far are applied to a variety of infectious disease models with different physiological and epidemiological assumptions. Many of the previous results are immediately applicable, thanks to the flexibility of the simple techniques used here. However, some complicating modeling assumptions lead to a need for different switched systems techniques and results not present in the previous chapter. First, the so-called SIS model is considered, followed by incorporation of media coverage, network epidemic models with interconnected cities (or patches), and diseases spread by vector agents (e.g., mosquitoes) which are modeled using time delays. Straightforward extensions of eradication results are given for models with vertical transmission, disease-induced mortality, waning immunity, passive immunity, and a model with general compartments.

4.1 Absence of Conferred Natural Immunity: The SIS Model

Consider the set-up of a two-compartment disease model where the infected, once recovered, immediately return to the susceptible class (i.e., only the susceptible, S, and the infected, I, are considered). Implicitly, the assumption of conferred natural immunity in the switched SIR model (3.8) is being discarded. Invoking the other assumptions of Sects. 3.1 and 3.3 yield the switched SIS model:

$$\begin{aligned} \dot{S}(t) &= \mu - \beta_\sigma S(t)I(t) + gI(t) - \mu S(t), \\ \dot{I}(t) &= \beta_\sigma S(t)I(t) - (g+\mu)I(t), \\ (S(0), I(0)) &= (S_0, I_0), \end{aligned} \tag{4.1}$$

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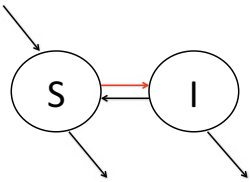

Fig. 4.1 Flow diagram of the switched SIS system (4.1). The *red line* represents horizontal transmission of the disease

where $\sigma \in \mathscr{S}_{\text{dwell}}$ designates a switching rule; $\sigma(t) \in \mathscr{M} \equiv \{1, \ldots, m\}$ and $\beta_{\sigma(t)} \in \{\beta_1, \ldots, \beta_m\}$ for each t. Again, the variables have been normalized by the constant total population and $(S_0, I_0) \in D_{(4.1)} \equiv \{(S, I) \in \mathbb{R}^2_+ : S + I = 1\}$, the meaningful domain which is positively invariant to (4.1);

$$\{\dot{S} + \dot{I}\}|_{S+I=1} = 0, \quad \dot{S}|_{S=0} = \mu + gI > 0, \quad \dot{I}|_{I=0} = 0.$$

The flow of (4.1) is outlined in Fig. 4.1. Since the domain is positively invariant and the switched system has continuously differentiable functions on the right-hand side in each mode, the model is well-posed, biologically and mathematically.

The disease-free solution of (4.1) is $Q^{(4.1)}_{\text{DFS}} \equiv (1, 0)$. There exist m endemic equilibria, each associated with a mode of (4.1), given by

$$Q^{(4.1),i}_{\text{ES}} \equiv \left(\frac{\mu + g}{\beta_i}, 1 - \frac{\mu + g}{\beta_i} \right). \tag{4.2}$$

Since $S + I = 1$ is an invariant to (4.1), the differential equation for S may be omitted:

$$\begin{aligned} \dot{I}(t) &= -\beta_\sigma I^2(t) + (\beta_\sigma - g - \mu) I(t), \\ I(0) &= I_0. \end{aligned} \tag{4.3}$$

For any $i \in \mathscr{M}$,

$$\dot{I}(t) = -\beta_i I^2(t) + (\beta_i - g - \mu) I(t),$$

is a Bernoulli switched differential equation. With this in mind for the piecewise switching case, the SIS model (4.1) admits the following solution (adopted from [63]):

$$I(t) \equiv \begin{cases} \frac{I(t_{k-1}) \exp(\lambda_{i_k}(t - t_{k-1}))}{I(t_{k-1})\beta_{i_k}(\exp(\lambda_{i_k}(t - t_{k-1})) - 1)/\lambda_{i_k} + 1}, & \text{if } \lambda_{i_k} \neq 0, \\ \frac{I(t_{k-1})}{I(t_{k-1})\beta_{i_k}(t - t_{k-1}) + 1}, & \text{if } \lambda_{i_k} = 0, \end{cases}$$

for all $t \in [t_{k-1}, t_k)$, where $\lambda_i \equiv \beta_i - g - \mu$ for each $i \in \mathscr{M}$. The solution can be given in a closed-form expression, as a function of parameters (i.e., initial condition and switching rule) and t: if $\lambda_{i_1} \neq 0$, then

$$I(t_1) = \frac{I_0 \exp(\lambda_{i_1}(t_1))}{I_0 \beta_{i_1}(\exp(\lambda_{i_1}(t_1)) - 1)/\lambda_{i_1} + 1}.$$

If $\lambda_{i_2} \neq 0$, then

$$\begin{aligned} I(t_2) &= \frac{I(t_1)\exp(\lambda_{i_2}(t_2-t_1))}{I(t_1)\beta_{i_2}(\exp(\lambda_{i_2}(t_2-t_1))-1)/\lambda_{i_2}+1}, \\ &= \frac{I_0\exp(\lambda_{i_1}(t_1)+\lambda_{i_2}(t_2-t_1))}{\left(\frac{I_0\beta_{i_2}\exp(\lambda_{i_1}(t_1))(\exp(\lambda_{i_2}(t_2-t_1))-1)}{\lambda_{i_2}}\right)+\left(\frac{I_0\beta_{i_1}(\exp(\lambda_{i_1}(t_1))-1)}{\lambda_{i_1}}\right)+1}. \end{aligned}$$

Assuming that $\lambda_{i_k} \neq 0$ for each k, then the solution is given by

$$I(t) \equiv \frac{I_0\exp\left(\sum_{j=1}^{k-1}\lambda_{i_j}(t_j-t_{j-1})+\lambda_{i_k}(t-t_{k-1})\right)}{I_0\left(\beta_{i_k}B_{i_k}(t)+\sum_{j=1}^{k-1}\beta_{i_j}A_{i_j}\right)+1}, \quad \forall t\in[t_{k-1},t_k), \tag{4.4}$$

where

$$\begin{aligned} B_{i_k}(t) &\equiv \exp\left(\sum_{j=1}^{k-1}\lambda_{i_j}(t_j-t_{j-1})+\lambda_{i_k}(t-t_{k-1})\right)\frac{\exp(\lambda_{i_k}(t-t_{k-1}))-1}{\lambda_{i_k}}, \\ A_{i_j} &\equiv \widehat{A}_{i_j}\exp(\lambda_{i_1}(t_1)+\ldots+\lambda_{i_{j-1}}(t_{j-1}-t_{j-2})), \end{aligned}$$

and,

$$\widehat{A}_{i_j} \equiv \begin{cases} \frac{\exp(\lambda_{i_j}(t_j-t_{j-1}))-1}{\lambda_{i_j}}, & \text{if } \lambda_{i_j}\neq 0, \\ t_j-t_{j-1}, & \text{if } \lambda_{i_j}=0. \end{cases}$$

Compare this result to the time-constant contact rate SIS model:

$$\begin{aligned} \dot{S}(t) &= \mu-\beta S(t)I(t)-\mu S(t)+gI(t), \\ \dot{I}(t) &= \beta S(t)I(t)-(g+\mu)I(t), \end{aligned} \tag{4.5}$$

which has basic reproduction number

$$\mathrm{R}_0^{(4.5)} \equiv \frac{\beta}{\mu+g}, \tag{4.6}$$

and, after eliminating the equation for S via the invariant $S+I=1$, simplifies to the Bernoulli differential equation

$$\begin{aligned} \dot{I}(t) &= -\beta I^2(t)+(\beta-g-\mu)I(t), \\ I(0) &= I_0>0. \end{aligned} \tag{4.7}$$

Equation (4.7) has two equilibria: $Q_{\mathrm{DFS}}^{(4.7)} \equiv 0$ and $Q_{\mathrm{ES}}^{(4.7)} \equiv 1 - 1/\mathrm{R}_0^{(4.5)}$, corresponding to the disease-free solution and endemic solution of (4.5), respectively. Equation (4.7) admits a unique solution [63] which can be found analytically. The details are explored to draw comparisons with the switched contact rate case outlined above. Letting $\lambda \equiv \beta - \mu - g$,

$$\dot{I}(t) - \lambda I(t) = -\beta I^2(t),$$

if $\mathrm{R}_0^{(4.5)} \neq 1$ (i.e., $\lambda \neq 0$). In this case,

$$\frac{\dot{I}}{I^2} - \frac{\lambda}{I} = -\beta.$$

The substitution $y \equiv I^{-1}$, which is valid for $I \neq 0$, yields

$$\dot{y} = -\frac{\dot{I}}{I^2}.$$

Hence,

$$\begin{aligned} \dot{y}(t) &= -\lambda y(t) + \beta, \\ y(0) &= I_0 > 0, \end{aligned}$$

(where $I_0 > 0$ has been assumed to make the problem interest) which admits a unique solution given by

$$y(t) \equiv \left(I_0 - \frac{\beta}{\lambda}\right) \exp(-\lambda t) + \frac{\beta}{\lambda}, \quad \forall t \in \mathbb{R}_+.$$

Consequently, the unique solution is

$$\begin{aligned} I(t) &\equiv \frac{1}{\left(I_0 - \frac{\beta}{\lambda}\right) \exp(-\lambda t) + \frac{\beta}{\lambda}}, \\ &= \frac{\exp((\mu + g)(\mathrm{R}_0^{(4.5)} - 1)t)}{\mathrm{R}_0^{(4.5)}(\exp((\mu + g)(\mathrm{R}_0^{(4.5)} - 1)t) - 1)/(\mathrm{R}_0^{(4.5)} - 1) + 1/I_0}, \quad \forall t \in \mathbb{R}_+. \end{aligned}$$

In the case that $\mathrm{R}_0^{(4.5)} = 1$, $\dot{I}(t) = -\beta I^2(t)$ which is readily solved to get the unique solution

$$I(t) \equiv \frac{1}{\beta t + \frac{1}{I_0}}, \quad \forall t \in \mathbb{R}_+.$$

Combining the cases,

$$I(t) \equiv \begin{cases} \frac{\exp((\mu+g)(\mathrm{R}_0^{(4.5)}-1)t)}{\mathrm{R}_0^{(4.5)}(\exp((\mu+g)(\mathrm{R}_0^{(4.5)}-1)t)-1)/(\mathrm{R}_0^{(4.5)}-1)+1/I_0}, & \text{if } \mathrm{R}_0^{(4.5)} \neq 1, \\ \frac{1}{\beta t+1/I_0}, & \text{if } \mathrm{R}_0^{(4.5)} = 1. \end{cases} \tag{4.8}$$

As $\lambda = 0$ is equivalent to $\mathrm{R}_0^{(4.5)} = 1$, notice that (4.4) reduces to (4.8) when $\beta_\sigma = \beta$. By inspection, if $\mathrm{R}_0^{(4.5)} \leq 1$, it follows that

$$\lim_{t\to\infty} I(t) = 0,$$

and $Q_{\mathrm{DFS}}^{(4.7)}$ is asymptotically stable in the meaningful domain. If $\mathrm{R}_0^{(4.5)} > 1$ then

$$\lim_{t\to\infty} I(t) = 1 - 1/\mathrm{R}_0^{(4.5)} > 0$$

and $Q_{\mathrm{ES}}^{(4.7)}$ is asymptotically stable in the meaningful domain. The basic reproduction number completely determines the long-term behavior of (4.7) (and therefore (4.5)).

In light of these findings, let us return to (4.3) in order to study its qualitative behavior.

Theorem 4.1 *If* $\sigma \in \mathscr{S}_{\mathrm{periodic}}(\omega)$ *and*

$$\mathrm{R}_0^{(4.1)} \equiv \frac{\sum_{i=1}^m \beta_i \tau_i}{\omega(\mu+g)} < 1,$$

then the disease-free solution $Q_{\mathrm{DFS}}^{(4.1)} \equiv (1,0)$ *of the switched SIS model* (4.1) *is globally asymptotically stable in the meaningful domain* $D_{(4.1)}$.

Proof Since $A_i > 0$ for each $i \in \mathscr{M}$ and $B_i(t) > 0$ for each $i \in \mathscr{M}$ and $t \in \mathbb{R}_+$, Eq. (4.4) implies that

$$I(t) \leq I_0 \exp\left(\sum_{j=1}^{k-1} \lambda_{i_j}(t_j - t_{j-1}) + \lambda_{i_k}(t - t_{k-1})\right), \quad \forall t \in [t_{k-1}, t_k), \tag{4.9}$$

and, from $\sigma \in \mathscr{S}_{\mathrm{periodic}}$,

$$I(\omega) \leq I_0 \exp\left(\sum_{i=1}^m \lambda_i \tau_i\right),$$

where $\sum_{i=1}^m \lambda_i \tau_i < 0$ since $\mathrm{R}_0^{(4.1)} < 1$. Letting

$$\eta \equiv \exp\left(\sum_{i=1}^m \lambda_i \tau_i\right) < 1,$$

$I(h\omega) \leq I_0\eta^h$ for any $h \in \mathbb{N}$ and the sequence $\{I(h\omega)\}$ is monotonically decreasing and converges to zero, and, similarly to the proof of Theorem 3.1, $\lim_{t\to\infty} I(t) = 0$. Moreover, (4.9) gives that $I(t) \leq I_0 M \equiv I_{\max}$ for all $t \in \mathbb{R}_+$ where

$$M \equiv \exp\left(\sum_{i\in\mathscr{M}^+} \lambda_i \tau_i\right),$$

with $\mathscr{M}^+ \equiv \{i \in \mathscr{M} : \lambda_i > 0\}$. The result follows from the fact that $S = 1 - I$.

From the proof of Theorem 4.1, an approximation of the epidemic severity is given as

$$I_{\max} \equiv I_0 \exp\left(\sum_{i\in\mathscr{M}^+} \lambda_i \tau_i\right),$$

which is greater than I_0 but may not be achieved. Importantly, a small amount of initial infected cases results in a small number of infections in time and the disease is eventually eradicated. However, in the case that the basic reproduction number $\mathrm{R}_0^{(4.1)}$ is greater than one, a result on the persistence of the disease can be established along the lines of the proof of Theorem 3.3 in [83] and Lemma 4.1 and Theorem 4.1 in [68]. If weak uniform persistence does not hold, then for any $\epsilon > 0$,

$$\limsup_{t\to\infty} I(t) < \epsilon.$$

In this case,

$$\dot{S}(t) = \mu - \beta_k S(t)I(t) + gI(t) - \mu S(t) > \mu - \beta_{\max}\epsilon - \mu S(t), \quad \forall t \in [t_{k-1}, t_k),$$

where $\beta_{\max} \equiv \max\{\beta_1, \ldots, \beta_m\}$. The comparison ODE system

$$\begin{aligned} \dot{S}_m(t) &= \mu - \beta_{\max}\epsilon - \mu S_m(t), \\ S_m(0) &= S_0, \end{aligned} \tag{4.10}$$

has a unique solution converging to $S^* \equiv 1 - \beta_{\max}\epsilon/\mu$. Hence, there exists a time $t^* > 0$ for which $S(t) \geq 1 - \beta_{\max}\epsilon/\mu - \epsilon$ for all $t \geq t^*$ and, for any $k \in \mathbb{N}$ satisfying $t^* < t_{k-1} < t \leq t_k$,

$$\dot{I}(t) = \beta_k S(t)I(t) - (g + \mu)I(t) \geq (\beta_k - g - \mu - \epsilon(1 + \beta_{\max}/\mu)\beta_k)I(t).$$

For $t \in [t^* + (k-1)\omega, t^* + k\omega)$,

$$
\begin{aligned}
I(t) &\geq I(t^*)\exp\left(\int_{t^*}^{t}(\beta_{\sigma(s)}-g-\mu-\epsilon(1+\beta_{\max}/\mu)\beta_{\sigma(s)})\mathrm{d}s\right),\\
&= I(t^*)\exp\left(\int_{t^*}^{t^*+(k-1)\omega}(\beta_{\sigma(s)}-g-\mu-\epsilon(1+\beta_{\max}/\mu)\beta_{\sigma(s)})\mathrm{d}s\right)\\
&\quad\times\exp\left(\int_{t^*+(k-1)\omega}^{t}(\beta_{\sigma(s)}-g-\mu-\epsilon(1+\beta_{\max}/\mu)\beta_{\sigma(s)})\mathrm{d}s\right),\\
&\geq M\exp\left\{(k-1)\left[\int_0^{\omega}(\beta_{\sigma(s)}-g-\mu)\mathrm{d}s-\epsilon\omega\beta_{\max}(1+\beta_{\max}/\mu)\right]\right\},
\end{aligned}
$$

where $M\equiv I(t^*)\exp(-\omega(g+\mu)-\epsilon\omega\beta_{\max}(1+\beta_{\max}/\mu))$. Choosing ϵ to satisfy

$$
0<\epsilon\leq\frac{\int_0^{\omega}(\beta_{\sigma(s)}-g-\mu)ds}{2\omega\beta_{\max}\left(1+\frac{\beta_{\max}}{\mu}\right)},
$$

$$
\phi(\epsilon)\equiv\left(\int_0^{\omega}(\beta_{\sigma(s)}-g-\mu)ds-\epsilon\omega\beta_{\max}(1+\beta_{\max}/\mu)\right)>0,
$$

and $I(t)\geq M\exp((k-1)\phi(\epsilon))$, which contradicts the boundedness of I; there exists a time $t^1>t^*$ such that $I(t^1)\geq\eta$. Uniform persistence is then shown along the lines of the proof of Theorem 3.4 to give the following result.

Theorem 4.2 *If* $\sigma\in\mathscr{S}_{\text{periodic}}(\omega)$ *and* $\mathrm{R}_0^{(4.1)}>1$, *then the disease persists uniformly in* (4.1).

A permanence result (see [148] for the original definition, also see [49]) can be derived in terms of the endemic equilibria associated with each mode of (4.1), i.e., $Q_{\text{ES}}^{(4.1),i}$ as outlined in (4.2).

Definition 4.1 The disease is said to be permanent in (4.1) if there exists a compact set $\Omega\subset\text{int}(D_{(4.1)})$ such that for every initial condition in $D_{(4.1)}$, $I(t)$ eventually enters and remains in Ω.

Note that permanence implies persistence. Periodicity of the switching rule is not required in this case.

Theorem 4.3 *If* $\sigma\in\mathscr{S}_{\text{dwell}}$ *and* $\min\{\mathrm{R}_0^{(4.1),i}:i\in\mathscr{M}\}>1$, *then the disease is permanent in* (4.1); $I(t)$ *converges to* $\text{conv}\{Q_{\text{ES}}^{(4.1),1},\ldots,Q_{\text{ES}}^{(4.1),m}\}$.

Proof Note that $\min\{\mathrm{R}_0^{(4.1),i}:i\in\mathscr{M}\}>1$ implies that

$$
\frac{\beta_{\min}}{\mu+g}>1,
$$

where $\beta_{\min} \equiv \min\{\beta_i : i \in \mathscr{M}\}$. Let $\Lambda \equiv \text{conv}\{Q_{\text{ES}}^{(4.1),1}, \ldots, Q_{\text{ES}}^{(4.1),m}\}$ and $\lambda_i \equiv \beta_i - \mu - g$ for each $i \in \mathscr{M}$. For each $i \in \mathscr{M}$, $Q_{\text{ES}}^{(4.1),i} = (S_i^*, I_i^*, R_i^*)$ where $I_i^* \equiv \lambda_i/\beta_i$. Then

$$\Lambda = \{(S, I) \in \mathbb{R}_+^2 : I_{\min}^* \le I \le I_{\max}^*, S = 1 - I\},$$

where $I_{\min} \equiv \min\{I_1^*, \ldots, I_m^*\}$ and $I_{\max} \equiv \max\{I_1^*, \ldots, I_m^*\}$. For any $i \in \mathscr{M}$,

$$\dot{I}|_{I=I_{\min}^*} = -\beta_i \left(\frac{\lambda_{\min}}{\beta_{\min}}\right)^2 + \lambda_i \frac{\lambda_{\min}}{\beta_{\min}} = \frac{\lambda_{\min}}{\beta_{\min}} \beta_i \left(\frac{\lambda_i}{\beta_i} - \frac{\lambda_{\min}}{\beta_{\min}}\right) \ge 0,$$

since $\min\{\text{R}_0^{(4.1),i} : i \in \mathscr{M}\} > 1$. Similarly, for any $i \in \mathscr{M}$,

$$\dot{I}|_{I=I_{\max}^*} = -\beta_i \left(\frac{\lambda_{\max}}{\beta_{\max}}\right)^2 + \lambda_i \frac{\lambda_{\max}}{\beta_{\max}} = \frac{\lambda_{\max}}{\beta_{\max}} \beta_i \left(\frac{\lambda_i}{\beta_i} - \frac{\lambda_{\max}}{\beta_{\max}}\right) \le 0.$$

The invariance of $S + I = 1$ immediately implies that Λ is positively invariant to (4.1); if $I_0 \in \Lambda$, $\{I(t) : t \in \mathbb{R}_+\} \subset \Lambda$. If $0 < I_0 < \lambda_{\min}/\beta_{\min}$, then

$$\dot{I}(t) = -\beta_\sigma I^2(t) + \lambda_\sigma I(t) = \beta_\sigma I(t) \left(\frac{\lambda_\sigma}{\beta_\sigma} - I(t)\right) > 0, \quad \forall t \in \mathbb{R}_+,$$

implying that either $I(t) \in \Lambda$ in finite time or $\lim_{t\to\infty} I(t) = I_{\min}^* \in \Lambda$. Similar arguments can be used for the case $\lambda_{\max}/\beta_{\max} < I_0 \le 1$.

Example 4.1 Consider the switched SIS model (4.1) with switching in all model parameters:

$$\begin{aligned} \dot{S}(t) &= \mu_\sigma - \beta_\sigma S(t) I(t) + g_\sigma I(t) - \mu_\sigma S(t), \\ \dot{I}(t) &= \beta_\sigma S(t) I(t) - (g_\sigma + \mu_\sigma) I(t), \\ (S(0), I(0)) &= (S_0, I_0), \end{aligned} \tag{4.11}$$

where $\mathscr{M} = \{1, 2\}$ and σ is defined by the seasonal switching rule (3.37) (which is periodic with $\tau_1 = 0.25$, $\tau_2 = 0.75$ and $\omega = 1$). Letting $\beta_1 = 1/4$, $\beta_2 = 1/12$, $g_1 = 1/10$, $g_2 = 1/8$, $\mu_1 = 1/70$, and $\mu_2 = 1/60$ (motivated by the parameter values in [173]), there is an increase in the contact rate and decrease in the recovery rate in the winter seasons and the birth rate increases during the summer months. The basic reproduction number is calculated as

$$\text{R}_0^{(4.11)} = \frac{\sum_{i=1}^2 \beta_i \tau_i}{\sum_{i=1}^2 (\mu_i + g_i) \tau_i} = 0.927$$

and, by a straightforward extension of Theorem 4.1 (see Theorem 2.1 in [98]), the disease-free solution is globally asymptotically stable in the meaningful domain.

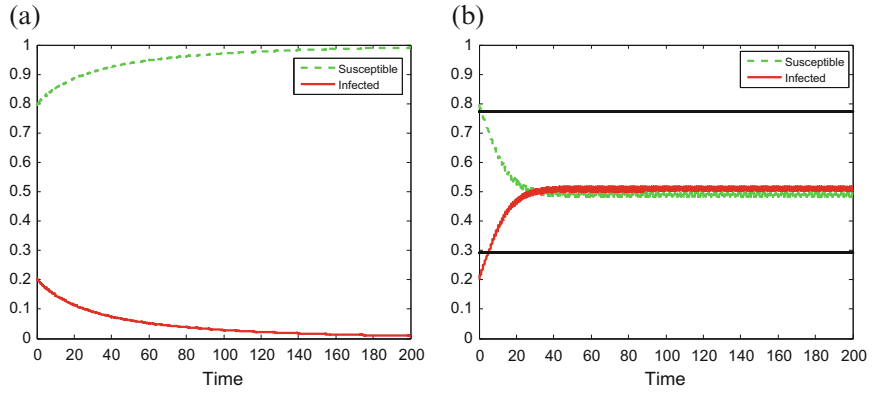

Fig. 4.2 Simulation of Example 4.1. (**a**) $\mathrm{R}_0^{(4.11)} = 0.927$. (**b**) $\min\{\mathrm{R}_0^{(4.11),i} : i \in \mathscr{M}\} = 1.41$; the *black lines* are $I^*_{\min}$ and $I^*_{\max}$

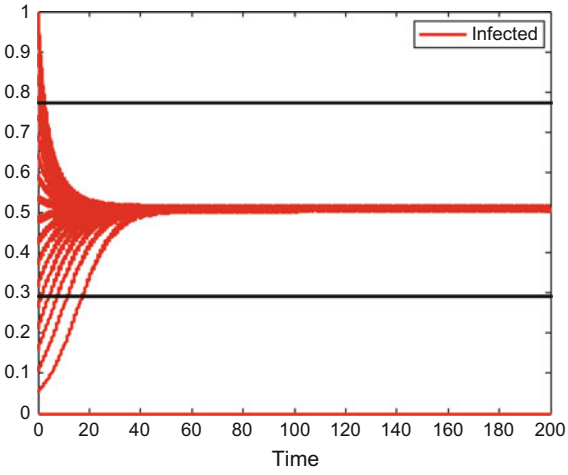

Fig. 4.3 Simulations of Example 4.1 with different initial conditions. The solution eventually satisfies $I(t) \in [I^*_{\min}, I^*_{\max}]$ unless $I_0 = 0$

If instead $\beta_1 = 1/2$, $\beta_2 = 1/5$, $g_1 = 1/10$, $g_2 = 1/8$, $\mu_1 = 1/70$, and $\mu_2 = 1/60$, then $\mathrm{R}_0^{(4.11)} = 2.04$ and the disease persists according to an extension of Theorem 4.2 (Theorem 2.3 in [98]). In fact, $\min\{\mathrm{R}_0^{(4.1),1}, \mathrm{R}_0^{(4.1),2}\} = 1.41$ and the solution converges to the convex hull of the endemic equilibria according to an extension of Theorem 4.3 (Theorem 2.4 in [98]). See Fig. 4.2 for an illustration with $(S_0, I_0) = (0.8, 0.2)$ and Fig. 4.3 for simulations with different initial conditions.

The spread of an infectious disease in a population depends crucially on two factors: (1) properties of its transmission mechanisms; and (2) the behavior of the host population. These two items are manifested in the infectious disease models via incidence rate constructions. In this part, we consider the following two generalizations of the standard incidence rate studied thus far: first, the standard incidence rate as

$$(S, I) \mapsto \beta(S + I)^{\alpha-1} SI = \beta N^{\alpha} \frac{SI}{N},$$

where $\alpha \in [0, 1]$ represents the pattern of daily encounters by individuals in the population $N = S + I$ ($\alpha = 0$ corresponds to the standard incidence rate) and the variables are non-normalized here. According to studies [171], $\alpha \approx 0.05 \pm 0.02$, justifying the choice of using the standard incidence rate thus far compared to the mass-action incidence rate (which corresponds to $\alpha = 1$). To see the effect of α on the switched SIS model, we proceed in this part with $\alpha \in [0, 1]$. Second, the host population's psychological behavior is taken into account by considering media coverage of an epidemic. The authors Li and Cui [83] considered the incidence rate

$$(S, I) \mapsto \left(\beta - \gamma \frac{I}{b + I}\right) SI,$$

where the variables are normalized, $\beta \equiv \rho c_1$, $\gamma \equiv \rho c_2$, $\rho > 0$ is the transmission probability if a contact is made between individuals, $c_1 > 0$ is the average number of contacts, and $c_2 > 0$ is the reduction in average number of contacts due to media coverage. Knowledge of an impending severe epidemic in a population via increased media coverage shifts the population behavior. Here $\beta \geq \gamma > 0$ is assumed to hold (the average number of new cases per unit time cannot become negative). The term $I/(b + I)$, $b > 0$, captures the relationship between the media coverage and psychological behavior of the susceptible population. This motivates the following switched incidence rate form:

$$(t, S, I) \mapsto \left(\beta_\sigma - \gamma_\sigma \frac{I}{b + I}\right) (S + I)^{\alpha-1} SI,$$

where $\beta_i \geq \gamma_i > 0$ for each $i \in \mathscr{M}$, and the corresponding switched SIS model:

$$\begin{aligned}
\dot{S}(t) &= A - \left(\beta_\sigma - \frac{\gamma_\sigma I}{b + I}\right) (S(t) + I(t))^{\alpha-1} S(t) I(t) + gI(t) - \mu S(t), \\
\dot{I}(t) &= \left(\beta_\sigma - \frac{\gamma_\sigma I(t)}{b + I(t)}\right) (S(t) + I(t))^{\alpha-1} S(t) I(t) - (g + \mu) I(t), \\
(S(0), I(0)) &= (S_0, I_0),
\end{aligned} \tag{4.12}$$

where the emigration rate $A > 0$ satisfies $0 < S_0 + I_0 \leq A/\mu$. Note that

$$\dot{N}(t) = \dot{S}(t) + \dot{I}(t) = A - \mu N(t)$$

and S and I are not fractions here as they have been up to this point; the meaningful physical domain is given by

$$D_{(4.12)} \equiv \{(S, I) \in \mathbb{R}^2_+ : S + I \leq A/\mu\},$$

whose positive invariance to (4.12) follows from

$$\{\dot{S} + \dot{I}\}|_{S+I=1} = 0, \quad \dot{S}|_{S=0} = A + gI > 0, \quad \dot{I}|_{I=0} = 0.$$

Here the disease-free equilibria is given by $Q_{\text{DFS}}^{(4.12)} \equiv (A/\mu, 0)$, whose stability can be shown by incorporating the comparison theorem into the methods previously outlined.

Theorem 4.4 *If* $\sigma \in \mathscr{S}_{\text{periodic}}$ *and*

$$\mathrm{R}_0^{(4.12)} \equiv \left(\frac{A}{\mu}\right)^{\alpha} \left(\frac{\sum_{i=1}^{m} \beta_i \tau_i}{\omega(\mu + g)}\right) < 1$$

then the disease is eradicated; the solution of the switched SIS system (4.12) *converges to the disease-free solution* $Q_{\text{DFS}}^{(4.12)}$. *If*

$$\widehat{\mathrm{R}_0}^{(4.12)} \equiv \left(\frac{A}{\mu}\right)^{\alpha} \left(\frac{\beta_{\max}}{\mu + g}\right) < 1$$

then the disease-free solution $Q_{\text{DFS}}^{(4.12)}$ *is globally asymptotically stable in the meaningful domain* $D_{(4.12)}$.

With the techniques of the previous chapter, combined with the intrinsic one-dimensionality of the model, global asymptotic stability of $Q_{\text{DFS}}^{(4.12)}$ in the meaningful domain is shown.

Proof The differential equation for I satisfies

$$\begin{aligned}
\dot{I}(t) &= \left(\beta_k - \frac{\gamma_k I(t)}{b + I(t)}\right)(S(t) + I(t))^{\alpha - 1} S(t) I(t) - (g + \mu) I(t), \\
&\leq \beta_k (A/\mu)^{\alpha - 1} (A/\mu) I(t) - (g + \mu) I(t), \\
&= \beta_k (A/\mu)^{\alpha} I(t) - (g + \mu) I(t), \\
&= \lambda_k I(t), \quad \forall t \in [t_{k-1}, t_k),
\end{aligned}$$

where $\lambda_i \equiv \beta_i (A/\mu)^{\alpha} - g - \mu$ for all $i \in \mathscr{M}$. It follows that

$$I(t) \leq I(t_{k-1}) \exp(\lambda_k (t - t_{k-1})), \quad \forall t \in [t_{k-1}, t_k), \tag{4.13}$$

which gives that

$$I(h\omega) \leq I_0 \exp\left(h \left(\sum_{i=1}^{m} \lambda_i \tau_i\right)\right), \quad \forall h \in \mathbb{N}. \tag{4.14}$$

Hence, $\{I(h\omega)\}$ is a monotonically decreasing sequence that converges to zero and, by the arguments in the proof of Theorem 3.1, $\lim_{t \to \infty} I(t) = 0$. The differential equation for the total population $\dot{N}(t) = A - \mu N(t)$ implies that

$$S(t) + I(t) = (S_0 + I_0 - A/\mu)\exp(-\mu t) + A/\mu, \quad \forall t \in \mathbb{R}_+,$$

so that $\lim_{t\to\infty} S(t) = A/\mu$. More than that, the solution can be given an upper bound in terms of the initial condition and a constant:

$$I(t) \le I_0 \exp\left(\sum_{i\in\mathscr{M}^+} \lambda_i \tau_i\right), \quad \forall t \ge 0,$$

where $\mathscr{M}^+ \equiv \{i \in \mathscr{M} : \lambda_i \ge 0\}$; for any $\epsilon > 0$ choose $\delta = 0.5\epsilon \exp\left(-\sum_{i\in\mathscr{M}^+} \lambda_i \tau_i\right)$, then

$$|(S(t), I(t)) - (1, 0)| \le |S(t) - 1| + |I(t)| = 2I(t) < \epsilon.$$

Using the Generalized Binomial Theorem, a persistence result can be established for the endemic case.

Theorem 4.5 *If* $\sigma \in \mathscr{S}_{\text{periodic}}(\omega)$ *and* $\mathrm{R}_0^{(4.12)} > 1$, *then the disease persists uniformly; there exists* $\eta > 0$ *such that* $\liminf_{t\to\infty} I(t) \ge \eta$.

Proof If $I(t) < \epsilon$ for $t \in [t_e, +\infty)$ for some $t_e > 0$ then $\dot{S}(t) > A - \beta_{\max}(A/\mu)^{\alpha-1}(A/\mu)\epsilon - \mu S(t)$ for all $t \in [t_e, +\infty)$. The ODE system

$$\begin{aligned} \dot{S}_m(t) &= \left(A - \epsilon\beta_{\max}\left(\frac{A}{\mu}\right)^{\alpha}\right) - \mu S_m(t), \\ S_m(t_e) &= S_0, \end{aligned} \tag{4.15}$$

has a unique solution S_m on $[t_e, +\infty)$ which satisfies

$$\lim_{t\to\infty} S_m(t) = \frac{A}{\mu} - \frac{\epsilon\beta_{\max}A^{\alpha}}{\mu^{\alpha+1}}.$$

The existence of $t^* \ge t_e$ follows such that

$$S(t) \ge \frac{A}{\mu} - \frac{\epsilon\beta_{\max}A^{\alpha}}{\mu^{\alpha+1}} - \epsilon, \quad \forall t \ge t^*.$$

For $k \in \mathbb{N}$ satisfying $t^* < t_{k-1} < t \le t_k$,

$$\begin{aligned} \dot{I}(t) &= \left(\beta_k - \frac{\gamma_k I(t)}{b + I(t)}\right)(S(t) + I(t))^{\alpha-1} S(t) I(t) - (g + \mu) I(t), \\ &\ge \left(\beta_k - \frac{\gamma_{\max}\epsilon}{b + \epsilon}\right)\left(\frac{A}{\mu} - \frac{\epsilon\beta_{\max}A^{\alpha}}{\mu^{\alpha+1}} - \epsilon\right)^{\alpha} I(t) - (g + \mu) I(t), \end{aligned}$$

where $\gamma_{\max} \equiv \max\{\gamma_i : i \in \mathscr{M}\}$. Defining

$$B \equiv \frac{\beta^* A^\alpha}{\mu^{\alpha+1}} + 1,$$

$A/\mu > B\epsilon$ implies that $(A/\mu - B\epsilon)^\alpha$ can be expanded using the Generalized Binomial Theorem:

$$\begin{aligned}\left(\frac{A}{\mu} - B\epsilon\right)^\alpha &= \sum_{k=0}^{\infty} \binom{\alpha}{k} \left(\frac{A}{\mu}\right)^{\alpha-k} (-B\epsilon)^k, \\ &= \left(\frac{A}{\mu}\right)^\alpha - \epsilon\alpha B \left(\frac{A}{\mu}\right)^{\alpha-1} + \sum_{k=2}^{\infty} \binom{\alpha}{k} \left(\frac{A}{\mu}\right)^{\alpha-k} (-B\epsilon)^k.\end{aligned}$$

Then, if $A/\mu > B\epsilon$ and $\epsilon < 1$,

$$\begin{aligned}\sum_{k=2}^{\infty} \binom{\alpha}{k} \left(\frac{A}{\mu}\right)^{\alpha-k} (-B\epsilon)^k &= \left(\frac{A}{\mu}\right)^\alpha \sum_{k=2}^{\infty} \binom{\alpha}{k} \left(\frac{-\epsilon B\mu}{A}\right)^k, \\ &\geq \frac{-\alpha(\alpha-1)}{2} \left(\frac{B\mu}{A}\right).\end{aligned}$$

Thus,

$$\begin{aligned}\left(\frac{A}{\mu} - B\epsilon\right)^\alpha &\geq \left(\frac{A}{\mu}\right)^\alpha - \epsilon \left(\frac{A}{\mu}\right)^\alpha \left(\frac{B\mu}{A} + \frac{\alpha(\alpha-1)B\mu}{2A}\right), \\ &= \left(\frac{A}{\mu}\right)^\alpha - \epsilon B \left(\frac{A}{\mu}\right)^{\alpha-1} \left(1 + \frac{\alpha(\alpha-1)}{2}\right),\end{aligned}$$

which yields that

$$\begin{aligned}I(t) &\geq I(t^*) \exp\left(\int_{t^*}^t \left\{\left[\beta_{\sigma(s)} - \frac{\gamma_{\max}\epsilon}{b+\epsilon}\right]\left[\frac{A}{\mu} - B\epsilon\right]^\alpha - (g+\mu)\right\} \mathrm{d}s\right), \\ &\geq I(t^*) \exp\left(\int_{t^*}^t \left\{\left[\beta_{\sigma(s)} - \frac{\gamma_{\max}\epsilon}{b+\epsilon}\right]\left(\frac{A}{\mu}\right)^\alpha\right\} \mathrm{d}s\right) \\ &\quad \times \exp\left[-\int_{t^*}^t \left\{\left[\beta_{\sigma(s)} - \frac{\gamma_{\max}\epsilon}{b+\epsilon}\right]\left[\epsilon B \left(\frac{A}{\mu}\right)^{\alpha-1}\left[1 + \frac{\alpha(\alpha-1)}{2}\right]\right]\right\} \mathrm{d}s\right] \\ &\quad \times \exp\left[-\int_{t^*}^t (g+\mu)\mathrm{d}s\right], \\ &= I(t^*) \exp\left[\int_{t^*}^t \left(\beta_{\sigma(s)}\left(\frac{A}{\mu}\right)^\alpha - g - \mu + G(\epsilon)\right) \mathrm{d}s\right],\end{aligned}$$

for all $t \in [t^* + (k-1)\omega, t^* + k\omega)$, where

$$G(\epsilon) \equiv -\frac{\gamma_{\max}\epsilon}{a+\epsilon}\left[\left(\frac{A}{\mu}\right)^{\alpha} + \epsilon B\left(\frac{A}{\mu}\right)^{\alpha-1}\left[1 + \frac{\alpha(\alpha-1)}{2}\right]\right]$$
$$- \epsilon\beta_{\max}B\left(\frac{A}{\mu}\right)^{\alpha-1}\left[1 + \frac{\alpha(\alpha-1)}{2}\right].$$

It follows that

$$I(t) \geq I(t^*)\exp\left\{\int_{t^*}^{t^*+(k-1)\omega}(\beta_{\sigma(s)}(A/\mu)^{\alpha} - g - \mu + G(\epsilon))\mathrm{d}s\right\}$$
$$\times \exp\left\{\int_{t^*+(k-1)\omega}^{t}(\beta_{\sigma(s)}(A/\mu)^{\alpha} - g - \mu + G(\epsilon))\mathrm{d}s\right\},$$
$$\geq M\exp\left\{(k-1)\left[\int_0^{\omega}(\beta_{\sigma(s)}(A/\mu)^{\alpha} - g - \mu)\mathrm{d}s + \omega G(\epsilon)\right]\right\},$$

where $M \equiv I(t^*)\exp(-\omega(g+\mu) + \omega G(\epsilon))$. $\mathrm{R}_0^{(4.12)} > 1$ implies the existence of $\epsilon_1 > 0$ such that

$$\phi(\epsilon_1) \equiv \left((A/\mu)^{\alpha}\sum_{i=1}^{m}\beta_i\tau_i - \omega(g+\mu) + \omega G(\epsilon_1)\right) > 0.$$

Choosing $\epsilon \equiv 0.5\min\{\epsilon_1, A/(\mu B), 1\}$ yields that $I(t) \geq M\exp((k-1)\phi(\epsilon))$, a contradiction. There must exist a time $t^1 > t^*$ for which $I(t^1) \geq \eta$; weak uniform persistence of I holds. Uniform persistence can then be shown by observing that $\dot{I}(t) \geq -(g+\mu)(t)$ and using similar arguments as in the proof of Theorem 3.4.

From a practical point of view, it can be difficult to approximate the basic reproduction number, and even more so when it is changing over time. Moreover, the switching rule may not always be exactly periodic. Defining the mode basic reproduction numbers

$$\mathrm{R}_0^{(4.12),i} \equiv \left(\frac{A}{\mu}\right)^{\alpha}\left(\frac{\sum_{i=1}^{m}\beta_i\tau_i}{\omega(\mu+g)}\right),$$

the results in Sect. 3.4 are easily mirrored (i.e., Theorems 3.2 and 3.3) via the bound (4.13). Namely, $\mathcal{Q}_{\mathrm{DFS}}^{(4.12)}$ is globally attractive and exponentially I-stable in the physically meaningful domain $D_{(4.12)}$ if either of the following conditions hold:

(1) $\sigma \in \mathscr{S}_{\mathrm{dwell}}$ and

$$\left\langle \mathrm{R}_0^{(4.12)} \right\rangle \equiv \sup_{t\geq h}\sum_{i=1}^{m}\mathrm{R}_0^{(4.12),i}T_i(t) < 1,$$

for some $h > 0$;

(2) $\sigma \in \mathscr{S}_{\text{dwell}}$ satisfies $T^+ \le N_0 + qT^-(t)$ for some $q \in (0,1)$ and $N_0 \ge 0$ such that

$$\mathrm{R}_0^{(4.12),-} - 1 < q(\mathrm{R}_0^{(4.12),+} - 1),$$

where $\mathrm{R}_0^{(3.8),-} \equiv \max\{\mathrm{R}_0^{(3.8),i} : i \in \mathscr{M}^-\}$ and $\mathrm{R}_0^{(3.8),+} \equiv \max\{\mathrm{R}_0^{(3.8),i} : i \in \mathscr{M}^+\}$ and

$$T^+(t) \equiv |\{t \in [0,t] : \sigma(t) \in \mathscr{M}^+\}|,$$
$$T^-(t) \equiv |\{t \in [0,t] : \sigma(t) \in \mathscr{M}^-\}|.$$

Example 4.2 Consider the switched SIS model with media coverage incidence rate (4.12) and assume that $\mathscr{M} = \{1,2\}$ follows the switching rule

$$\sigma(t) \equiv \begin{cases} 1, & \text{if } t \in [2k, 2k+2), \quad k = 0,1,2,\ldots, \\ 2, & \text{if } t \in [2k+2, 2k+4), \end{cases} \tag{4.16}$$

which is periodic with $\tau_1 = 2$, $\tau_2 = 2$ and $\omega = 4$. Motivated by the parameter values of [171], let $A = 3000$, $\beta_1 = 1/10$, $\beta_2 = 1/5$, $\gamma_1 = 1/30$, $\gamma_2 = 1/7$, $g = 1/5$, $\mu = 1/10$, $b = 0.5$, and $\alpha = 0.07$. The contact rate varies every 2 years and, accordingly, there is an increase in media coverage (and hence reduction in the real, media-adjusted contact rate). Let $(S_0, I_0) = (12,000, 2000)$ (i.e., $N_0 = 14,000$) and $\alpha = 0.07$ to reflect the daily contact patterns of individuals. Then $\mathrm{R}_0^{(4.12)} = 3.50$ and the disease persists by Theorem 4.5 (see Fig. 4.4a). If instead, $A = 300$, $\beta_1 = 1/10$, $\beta_2 = 1/5$, $\gamma_1 = 1/20$, $\gamma_2 = 1/10$, $g_1 = 9/10$, $g_2 = 2/5$, (i.e., switching recovery rates) $\mu = 1/10$, $b = 0.5$, and $\alpha = 0.5$, then $\mathrm{R}_0^{(4.12)} = 11.0$ and the disease persists by an extension of Theorem 4.5 (Theorem 3.2 in [98]). Here $\alpha = 0.5$ reflects the influence of the smaller community size on daily encounters. Given the initial conditions $(S_0, I_0) = (1800, 15)$, see Fig. 4.4b for an illustration.

4.2 Multi-City Epidemics: Modeling Traveling Infections

Travel has created an easy way for many infectious diseases to be transmitted from one region to another. The SARS outbreak in 2003 is a clear example of the effects of travel on the spread of a disease as it initially began in only one area of China and eventually spread to most of the country as well as other cities in the world due to travel of infected individuals [100]. A second example can be seen in the outbreak of measles in Iceland due, in part, to infected individuals traveling to the country [147]. More recently, in April 2009, the H1N1 influenza virus appeared in Mexico, and soon spread to other countries all over the world [167]. In many developing

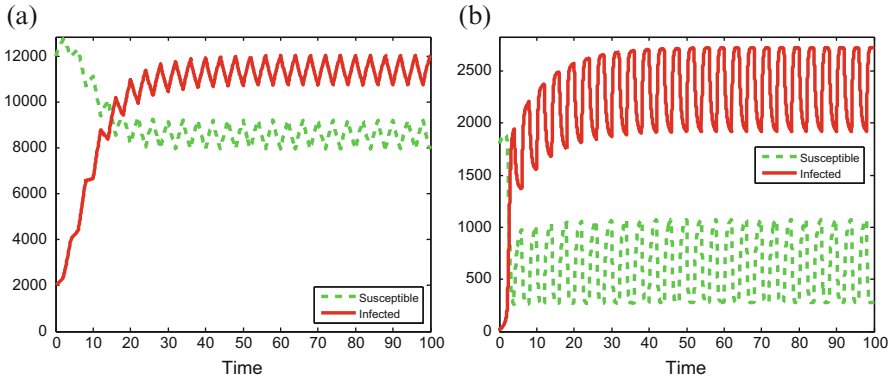

Fig. 4.4 Simulations of Example 4.2. (**a**) $\mathrm{R}_0^{(4.12)} = 3.50$. (**b**) $\mathrm{R}_0^{(4.12)} = 11.0$

countries, poor traveling conditions in mass transit, such as limited sanitation, leads to an increase in the spread of diseases due to infected individuals using transit [146].

Consider complicating the switched SIS system (4.1) by adding geographic factors. To begin, suppose that there are two cities (or patches) and the susceptible population is permitted to travel at a per capita rate $\alpha > 0$ (called the dispersal rate) between the cities. With the other modeling assumptions of the switched SIS system (4.1), the multi-city model is given as

$$\begin{aligned}
\dot{S}^{(1)}(t) &= \mu N^{(1)}(t) - \beta_\sigma \frac{S^{(1)}(t)I^{(1)}(t)}{N^{(1)}(t)} - \mu S^{(1)}(t) \\
&\quad + gI^{(1)}(t) - \alpha S^{(1)}(t) + \alpha S^{(2)}(t), \\
\dot{I}^{(1)}(t) &= \beta_\sigma \frac{S^{(1)}(t)I^{(1)}(t)}{N^{(1)}(t)} - gI^{(1)}(t) - \mu I^{(1)}(t), \\
\dot{S}^{(2)}(t) &= \mu N^{(2)}(t) - \frac{S^{(2)}(t)I^{(2)}(t)}{N^{(2)}(t)} - \mu S^{(2)}(t) \\
&\quad + gI^{(2)}(t) - \alpha S^{(2)}(t) + \alpha S^{(1)}(t), \\
\dot{I}^{(2)}(t) &= \beta_\sigma \frac{S^{(2)}(t)I^{(2)}(t)}{N^{(2)}(t)} - gI^{(2)}(t) - \mu I^{(2)}(t), \\
(S^{(j)}(0), I^{(j)}(0)) &= (S_0^{(j)}, I_0^{(j)}), \quad \forall j \in \{1, 2\},
\end{aligned} \tag{4.17}$$

where $N^{(1)} \equiv S^{(1)} + I^{(1)}$ and $N^{(2)} \equiv S^{(2)} + I^{(2)}$. In this way, homogeneity of the population mixing has been changed; the groups $S^{(1)}$ and $S^{(2)}$ interact with the infected group $I^{(1)}$ in vastly different ways. The flow of the model can be seen in Fig. 4.5.

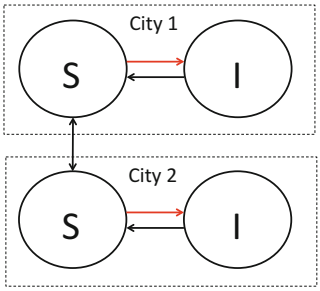

Fig. 4.5 Flow diagram of the Multi-city SIS model (4.17)

Next, suppose that infected individuals also travel and, due to dense crowds on mass transportation (which may have relatively poor sanitary conditions in developing countries [146]), the disease is transmitted between traveling individuals. More specifically, assume that the disease is transmitted at a contact rate $\gamma > 0$ during travel. The traveling incidence rate therefore takes the form

$$\gamma \frac{(\alpha S^{(j)})(\alpha I^{(j)})}{\alpha N^{(j)}} = \gamma \frac{(\alpha S^{(j)})(\alpha I^{(j)})}{(\alpha S^{(j)}) + (\alpha I^{(j)})} = \gamma \alpha \frac{S^{(j)} I^{(j)}}{S^{(j)} + I^{(j)}}.$$

This leads to the following model:

$$\begin{aligned}
\dot{S}^{(1)}(t) &= \mu N^{(1)}(t) - \beta_\sigma \frac{S^{(1)}(t) I^{(1)}(t)}{N^{(1)}(t)} - \mu S^{(1)}(t) + g I^{(1)}(t) \\
&\quad - \alpha S^{(1)}(t) + \alpha S^{(2)}(t) - \alpha \gamma \frac{S^{(2)}(t) I^{(2)}(t)}{N^{(2)}(t)}, \\
\dot{I}^{(1)}(t) &= \beta_\sigma \frac{S^{(1)}(t) I^{(1)}(t)}{N^{(1)}(t)} - g I^{(1)}(t) - \mu I^{(1)}(t) - \alpha I^{(1)}(t) \\
&\quad + \alpha I^{(2)}(t) + \alpha \gamma \frac{S^{(2)}(t) I^{(2)}(t)}{N^{(2)}(t)}, \\
\dot{S}^{(2)}(t) &= \mu N^{(2)}(t) - \frac{S^{(2)}(t) I^{(2)}(t)}{N^{(2)}(t)} - \mu S^{(2)}(t) + g I^{(2)}(t) \\
&\quad - \alpha S^{(2)}(t) + \alpha S^{(1)}(t) - \alpha \gamma \frac{S_{c_1(t)} I^{(1)}(t)}{N^{(1)}(t)}, \\
\dot{I}^{(2)}(t) &= \beta_\sigma \frac{S^{(2)}(t) I^{(2)}(t)}{N^{(2)}(t)} - g I^{(2)}(t) - \mu I^{(2)}(t) - \alpha I^{(2)}(t) \\
&\quad + \alpha I^{(1)}(t) + \alpha \gamma \frac{S^{(1)}(t) I^{(1)}(t)}{N^{(1)}(t)}, \\
(S^{(j)}(0), I^{(j)}(0)) &= (S_0^{(j)}, I_0^{(j)}), \quad \forall j \in \{1, 2\}.
\end{aligned} \tag{4.18}$$

The total population, $N \equiv N^{(1)} + N^{(2)}$, satisfies

$$\dot{N}(t) = \dot{S}^{(1)}(t) + \dot{I}^{(1)}(t) + \dot{S}^{(2)}(t) + \dot{I}^{(2)}(t) = 0,$$

though $N^{(1)}$ and $N^{(2)}$ need not be constant (the system is closed when considering both cities together).

The meaningful physical domain of (4.18) is given by

$$D_{(4.18)} \equiv \{(S^{(1)}, S^{(2)}, I^{(1)}, I^{(2)}) \in \mathbb{R}^4_+ : S^{(1)} + I^{(1)} + S^{(2)} + I^{(2)} = N\},$$

which is positively invariant to (4.18). Observe that

$$\alpha S^{(j)} - \alpha\gamma \frac{S^{(j)} I^{(j)}}{S^{(j)} + I^{(j)}} \geq 0, \quad \forall j \in \{1, 2\},$$

as long as $(S^{(j)}, I^{(j)}) \in \mathbb{R}^2_+$; the difference between the number of susceptible individuals traveling from city j and those being infected while traveling from city j is nonnegative. From this, invariance of $D_{(4.18)}$ to (4.18) is shown as follows:

$$\{\dot{S}^{(1)} + \dot{I}^{(1)} + \dot{S}^{(2)} + \dot{I}^{(2)}\}|_{S^{(1)}+I^{(1)}+S^{(2)}+I^{(2)}=N} = 0,$$

$$\dot{S}^{(1)}|_{S^{(1)}=0} = (\mu + g)I^{(1)} + \alpha S^{(2)} - \alpha\gamma \frac{S^{(2)} I^{(2)}}{N^{(2)}} \geq 0, \quad \dot{I}^{(1)}|_{I^{(1)}=0} = \alpha I^{(2)} + \alpha\gamma \frac{S^{(2)} I^{(2)}}{N^{(2)}} \geq 0,$$

$$\dot{S}^{(2)}|_{S^{(2)}=0} = (\mu + g)I^{(2)} + \alpha S^{(1)} - \alpha\gamma \frac{S^{(1)} I^{(1)}}{N^{(1)}} \geq 0,$$

$$\dot{I}^{(2)}|_{I^{(2)}=0} = \alpha I^{(1)} + \alpha\gamma \frac{S^{(1)} I^{(1)}}{N^{(1)}} \geq 0.$$

If $\sigma \in \mathscr{S}_{\text{periodic}}(\omega)$ and the basic reproduction number

$$\mathrm{R}_0^{(4.18)} \equiv \frac{\left(\sum_{i=1}^m \beta_i \tau_i\right) + \omega\alpha\gamma}{\omega(\mu + g)} < 1$$

then $Q_{\text{DFS}}^{(4.18)} \equiv (N/2, 0, N/2, 0)$ is attractive in the meaningful domain $D_{(4.12)}$. A more precise characterization is that $Q_{\text{DFS}}^{(4.18)}$ is exponentially $(I^{(1)}, I^{(2)})$-stable in $D_{(4.12)}$, which can be shown using the techniques detailed thus far:

$$\frac{\mathrm{d}(I^{(1)} + I^{(2)})}{\mathrm{d}t}(t) = \beta_\sigma \left(\frac{S^{(1)}(t) I^{(1)}(t)}{S^{(1)}(t) + I^{(1)}(t)} + \frac{S^{(2)}(t) I^{(2)}(t)}{S^{(2)}(t) + I^{(2)}(t)} \right) - (g + \mu)(I^{(1)}(t) + I^{(2)}(t))$$

$$
\begin{aligned}
&+ \alpha\gamma \left(\frac{S^{(1)}(t)I^{(1)}(t)}{S^{(1)}(t) + I^{(1)}(t)} + \frac{S^{(2)}(t)I^{(2)}(t)}{S^{(2)}(t) + I^{(2)}(t)} \right), \\
&\leq (\beta_\sigma + \alpha\gamma - g - \mu)(I^{(1)}(t) + I^{(2)}(t)), \\
&= \lambda_\sigma (I^{(1)}(t) + I^{(2)}(t)),
\end{aligned} \tag{4.19}
$$

where $\lambda_i \equiv \beta_i + \alpha\gamma - g - \mu$ for each $i \in \mathscr{M}$. It is straightforward to show that the 1-norm satisfies

$$
|(I^{(1)}(t), I^{(2)}(t))|_1 = I^{(1)}(t) + I^{(2)}(t) \leq (I_0^{(1)} + I_0^{(2)}) \exp(-ct)
$$

for some $c > 0$. The limiting equations for $S^{(1)}$ and $S^{(2)}$ are given by the system

$$
\begin{aligned}
\dot{S}^{(1)}(t) &= -\alpha S^{(1)}(t) + \alpha S^{(2)}(t), \\
\dot{S}^{(2)}(t) &= -\alpha S^{(2)}(t) + \alpha S^{(1)}(t).
\end{aligned} \tag{4.20}
$$

$S^{(1)} + S^{(2)} = N$ is an invariant of (4.20), from which it follows that

$$
\lim_{t\to\infty} S^{(1)}(t) = \lim_{t\to\infty} S^{(2)}(t) = N/2.
$$

Note that traveling infected can cause the disease to become endemic in both cities while eradication would be the outcome in either city if travel were to be restricted (i.e., $\alpha = 0$). This can be observed in the basic reproduction number via the $\alpha\gamma$ term and motivates the notion of limiting the spread of a disease by restricting travel and screening individuals (this idea will be revisited in Chap. 5).

Extending the model to $n \in \mathbb{N}$ cities or patches is natural at this point: let $S^{(j)}$, $I^{(j)}$, $R^{(j)}$, and $N^{(j)}$ denote the susceptible, infected, recovered, and total population in city $j \in \mathscr{N} \equiv \{1, \ldots, n\}$, respectively. Motivated by the analysis of (3.29), consider a general switched incidence rate for its flexibility in modeling a term-time forcing contact rate or a change in the fundamental structure of the disease spread. Assume that, in city $j \in \mathscr{N}$, the birth/death rate is given by $\mu^{(j)} > 0$ and the recovery rate by $g^{(j)} > 0$. Individuals do not die, recover, or give birth while traveling between cities. The per capita dispersal rate from city $l \in \mathscr{N}$ to city $j \in \mathscr{N} \setminus \{l\}$ is given by $\alpha^{(l,j)} \geq 0$. Let $-\alpha^{(j,j)} \geq 0$ denote the emigration rate from city j to all other cities. The general switched incidence rate in city $j \in \mathscr{N}$ is denoted by the function

$$
(t, S^{(j)}, I^{(j)}) \mapsto f_\sigma^{(j)}(S^{(j)}, I^{(j)})
$$

(only individuals in city j affect the spread of the disease there), where $\sigma \in \mathscr{S}_{\text{dwell}}$ is a switching rule, and dependence on $N^{(j)}$ is not explicitly stated but is understood. The generalized traveling incidence rate from city $l \in \mathscr{N}$ to city $j \in \mathscr{N} \setminus \{l\}$ is denoted by the function

$$
(t, S^{(l)}, I^{(l)}) \mapsto h_\sigma^{(l,j)}(S^{(l)}, I^{(l)}).
$$

Omitting the arguments for the switched incidence rate functions, the model is thus formulated as the following ODE system:

$$\begin{aligned}
\dot{S}^{(j)}(t) &= \mu^{(j)}N^{(j)}(t) - f_\sigma^{(j)} - \mu^{(j)}S^{(j)}(t) \\
&\quad + \sum_{l\in\mathscr{N}} \alpha^{(l,j)}S^{(l)}(t) - \sum_{l\in\mathscr{N}\setminus\{j\}} \alpha^{(l,j)}h_\sigma^{(l,j)}, \quad \forall j \in \mathscr{N} \\
\dot{I}^{(j)}(t) &= f_\sigma^{(j)} - g^{(j)}I^{(j)}(t) - \mu^{(j)}I^{(j)}(t) \\
&\quad + \sum_{l\in\mathscr{N}} \alpha^{(l,j)}I^{(l)}(t) + \sum_{l\in\mathscr{N}\setminus\{j\}} \alpha^{(l,j)}h_\sigma^{(l,j)}, \quad \forall j \in \mathscr{N}, \\
\dot{R}^{(j)}(t) &= g^{(j)}I^{(j)}(t) - \mu^{(j)}R^{(j)}(t) + \sum_{l\in\mathscr{N}} \alpha^{(l,j)}R^{(l)}(t), \quad \forall j \in \mathscr{N}, \\
(S^{(j)}(0), I^{(j)}(0), R^{(j)}(0)) &= (S_0^{(j)}, I_0^{(j)}, R_0^{(j)}), \quad \forall j \in \mathscr{N}.
\end{aligned} \tag{4.21}$$

The following observations are made (some of which are extended from [146, 167]):

1. $h_i^{(l,j)}(S^{(l)}, I^{(l)}) = h_i^{(j,l)}(S^{(l)}, I^{(l)})$ for each $l, j \in \mathscr{N}$; the transportation method between cities l and j is identical in either direction.
2. $S^{(j)}(t) + I^{(j)}(t) + R^{(j)}(t) = N^{(j)}(t)$ for all t and $\sum_{j\in\mathscr{N}} N^{(j)} \equiv N \in \mathbb{R}_+$.
3. Most often it is assumed that $S_0^{(j)} > 0$ for all $j \in \mathscr{N}$ (all cities begin with some number of susceptible) and $I_0^{(j^*)} > 0$ for some $j^* \in \mathscr{N}$ (at least one city begins with some infected).
4. The meaningful domain is positively invariant and given by

$$D_{(4.21)} \equiv \left\{ (S, I, R) \in \mathbb{R}_+^{3n} : N = \sum_{j\in\mathscr{N}} S^{(j)} + I^{(j)} + R^{(j)} \right\},$$

   where the notation

$$(S, I, R) \equiv (S^{(1)}, S^{(2)}, \ldots, S^{(n)}, I^{(1)}, I^{(2)}, \ldots, I^{(n)}, R^{(1)}, R^{(2)}, \ldots, R^{(n)})$$

   is adopted for the rest of this section.
5. $\sum_{l\in\mathscr{N}} \alpha^{(l,j)} = 0$ for each $j \in \mathscr{N}$ (sum of immigration must equal emigration);
6. The matrix formed with entries $(\alpha^{(l,j)})_{1\le l,j\le n}$ in row l and column j is irreducible (the n cities cannot be separated into two groups of cities such that there is no immigration from one group of cities to the other).
7. For each $l \in \mathscr{N}, j \in \mathscr{N} \setminus \{l\}, i \in \mathscr{M}$, the traveling condition

$$\alpha^{(l,j)}S^{(j)} - \alpha^{(l,j)}h_i^{(l,j)}(S^{(l)}, I^{(l)}) \ge 0, \tag{4.22}$$

holds (the number of susceptible individuals traveling to city $j \in \mathscr{N}$ must enter city j as either susceptible or infected);

8. The function $f_i^{(j)}$ is assumed to be smooth for each $j \in \mathscr{N}$ and each $i \in \mathscr{M}$ and satisfies physically reasonable restrictions; i.e.,

$$f_i^{(j)}(S^{(j)}, I^{(j)}) > 0,$$

and

$$f_i^{(j)}(S^{(j)}, 0) = 0,$$

for physically realizable values of $(S^{(j)}, I^{(j)})$.

9. The function $h_i^{(j,l)}$ is assumed to be smooth for each $l \in \mathscr{N}$, $j \in \mathscr{N} \setminus \{l\}$, and $i \in \mathscr{M}$ and satisfies similar physically reasonable restrictions.

Figure 4.6 illustrates the flow diagram of (4.21). Observe that $D_{(4.21)}$ is positively invariant to (4.21) under the above assumptions:

$$\left(\sum_{j \in \mathscr{N}} \dot{S}^{(j)} + \dot{I}^{(j)} + \dot{R}^{(j)} \right) |_{\sum_{j \in \mathscr{N}} S^{(j)} + I^{(j)} + R^{(j)} = N} = 0,$$

$\dot{S}^{(j)}|_{S^{(j)}=0} \geq 0$, $\dot{I}^{(j)}|_{I^{(j)}=0} \geq 0$, and $\dot{R}^{(j)}|_{R^{(j)}=0} \geq 0$. The flow of (4.21) is detailed in Fig. 4.6.

We detail the basic reproduction number of (4.21) by working from a simplified version of the model (i.e., restricted travel and time-invariant incidence rates) up to the full model.

1. *Restricted travel and time-invariant incidence rates*: When $\alpha^{(l,j)} = 0$ for all $i, j \in \mathscr{N}$ and $f_\sigma^{(j)}(S^{(j)}, I^{(j)}) \equiv f^{(j)}(S^{(j)}, I^{(j)})$ for all $j \in \mathscr{N}$, $i \in \mathscr{M}$, the switched multi-city system (4.21) models n closed cities which do not interact. The basic reproduction number of each city is given by the closed-form expression [73]:

$$\mathrm{R}_0^{(4.21),(j)} = \frac{1}{\mu + g} \left(\frac{\partial f^{(j)}}{\partial I^{(j)}}(N^{(j)}, 0) \right), \quad \forall j \in \mathscr{N},$$

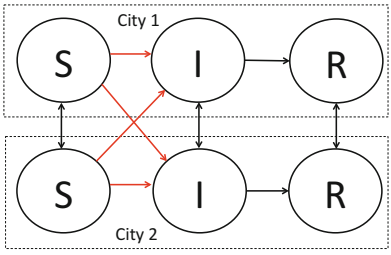

Fig. 4.6 Flow of multi-city SIR model (4.21) for $n = 2$. The *red lines* represent new infections

where $N^{(j)}$ is constant in this case since

$$\dot{N}^{(j)}(t) = \dot{S}^{(j)}(t) + \dot{I}^{(j)}(t) + \dot{R}^{(j)}(t) = 0, \quad \forall t.$$

As expected, the long-term behavior is dictated by $\mathrm{R}_0^{(4.21),(j)}$ as follows: $\mathrm{R}_0^{(4.21),(j)} < 1$ yields global asymptotic stability of $(N^{(j)}, 0)$ in each city, while $\mathrm{R}_0^{(4.21),(j)} > 1$ yields global asymptotic stability of an endemic equilibrium (the results of [73] are applicable to each city individually).

2. *Restricted travel and switching incidence rates*: If $\sigma \in \mathscr{S}_{\text{periodic}}(\omega)$, then the basic reproduction number of each city in the switched multi-city model (4.21) is given by [11]:

$$\mathrm{R}_0^{(4.21),(j)} = \sum_{i=1}^{m} \frac{\partial f^{(j)}}{\partial I^{(j)}}(N^{(j)}, 0)\tau_i \frac{1}{\omega(\mu + g)}, \quad \forall j \in \mathscr{N},$$

where $N^{(j)}$ is constant, as above, and has the usual physical interpretation; $\mathrm{R}_0^{(4.21),(j)}$ is the average number of secondary infections resulting from the introduction of an infected individual into city j with a wholly susceptible population.

3. *Unrestricted travel and time-invariant incidence rates*: The basic reproduction number of the multi-city model (4.21) in this case is the spectral radius of its next-generation matrix [152]:

$$\mathrm{R}_0^{(4.21)} = \rho(FV^{-1}),$$

where

$$F \equiv \begin{bmatrix} \frac{\partial f^{(1)}}{\partial I^{(1)}} & \alpha^{(2,1)}\frac{\partial h^{(2,1)}}{\partial I^{(2)}} & \cdots & \alpha^{(n,1)}\frac{\partial h^{(n,1)}}{\partial I^{(n)}} \\ \alpha^{(1,2)}\frac{\partial h^{(1,2)}}{\partial I^{(2)}} & \frac{\partial f^{(2)}}{\partial I^{(2)}} & \cdots & \alpha^{(n,2)}\frac{\partial h^{(n,1)}}{\partial I^{(n)}} \\ \vdots & & \ddots & \vdots \\ \alpha^{(1,n)}\frac{\partial h^{(1,n)}}{\partial I^{(2)}} & \cdots & \alpha^{(n-1,n)}\frac{\partial h^{(n-1,n)}}{\partial I^{(n-1)}} & \frac{\partial f^{(n)}}{\partial I^{(n)}} \end{bmatrix},$$

and

$$V \equiv \begin{bmatrix} \mu^{(1)} + g^{(1)} + \alpha^{(1,1)} & -\alpha^{(2,1)} & \cdots & -\alpha^{(n,1)} \\ -\alpha^{(1,2)} & \mu^{(2)} + g^{(2)} + \alpha^{(2,2)} & \cdots & -\alpha^{(n,2)} \\ \vdots & & \ddots & \vdots \\ -\alpha^{(1,n)} & \cdots & -\alpha^{(n-1,n)} & \mu^{(n)} + g^{(n)} + \alpha^{(n,n)} \end{bmatrix},$$

where the argument of $h^{(l,j)}$ in the matrix F is $(\widetilde{S}^{(l)}, 0)$ (the disease-free solution, whose existence is guaranteed from the irreducibility and cooperativeness of the matrix A but whose full form is omitted; see [170] for details).

Here, the (i,j) entry of F represents the rate of new infections in city $j \in \mathscr{N}$ caused by infected individuals in city $i \in \mathscr{N}$ and the (i,j) entry of V^{-1} represents the average period of time spent in city $j \in \mathscr{N}$ during an average lifetime (assuming the population remains near the disease-free solution) [152].

4. *Unrestricted travel and switching incidence rates*: The basic reproduction number is complicated by multiple infected compartments flowing into one another and can only be implicitly defined as the spectral radius of its next-generation integral operator, $\mathrm{R}_0^{(4.21)} = \rho(L)$. However, the disease is eradicated in each city under a threshold condition on the model parameters, which may be interpreted as an approximation of the basic reproduction number.

Theorem 4.6 *Assume that $\sigma \in \mathscr{S}_{\text{periodic}}(\omega)$ and there exist $\beta_i, \gamma_i > 0$ such that $f_i^{(j)}(S^{(j)}, I^{(j)}, N^{(j)}) \leq \beta_i S^{(j)} I^{(j)}/N^{(j)}$ and $h_i^{(l,j)}(S^{(l)}, I^{(l)}, N^{(l)}) \leq \gamma_i S^{(l)} I^{(l)}/N^{(l)}$ for each $j \in \mathscr{N}$, $l \in \mathscr{N}$, $i \in \mathscr{M}$. If*

$$\widehat{\mathrm{R}_0}^{(4.21)} \equiv \frac{\sum_{i=1}^m (\beta_i + (n-1)\alpha_{\max}\gamma_i)\tau_i}{\omega(\mu_{\min} + g_{\min})} < 1, \tag{4.23}$$

where $\alpha_{\max} \equiv \max\{\alpha^{(l,j)} : l \in \mathscr{N}, j \in \mathscr{N} \setminus \{l\}\}$, $\mu_{\min} \equiv \min\{\mu^{(j)} : j \in \mathscr{N}\}$, and $g_{\min} \equiv \min\{g^{(j)} : j \in \mathscr{N}\}$, then the solution of the switched multi-city (4.21) satisfies

$$\lim_{t\to\infty} I(t) = \lim_{t\to\infty} (I^{(1)}(t), \ldots, I^{(n)}(t)) = 0;$$

the disease is eradicated in each city.

Proof Let $I \equiv \sum_{j\in\mathscr{N}} I^{(j)}$. Then

$$\begin{aligned}
\dot{I}(t) &= \sum_{j\in\mathscr{N}} \left(f_\sigma^{(j)}(S^{(j)}(t), I^{(j)}(t), N^{(j)}(t)) - (g^{(j)} + \mu^{(j)})I^{(j)}(t)\right) \qquad (4.24)\\
&\quad + \sum_{l\in\mathscr{N}\setminus\{j\}} \alpha^{(l,j)} h_\sigma^{(l,j)}(S^{(l)}(t), I^{(l)}(t), N^{(l)}(t)),\\
&\leq \sum_{j\in\mathscr{N}} \left((\beta_\sigma - g_{\min} - \mu_{\min})I^{(j)}(t) + \sum_{l\in\mathscr{N}\setminus\{j\}} \alpha^{(l,j)}\gamma_\sigma I^{(l)}(t)\right),\\
&\leq (\beta_\sigma - g_{\min} - \mu_{\min} + (n-1)\alpha_{\max}\gamma_\sigma) \sum_{j\in\mathscr{N}} I^{(j)}(t),\\
&= \lambda_\sigma I(t), \qquad (4.25)
\end{aligned}$$

where $\lambda_i \equiv \beta_i + (n-1)\alpha_{\max}\gamma_i - g_{\min} - \mu_{\min}$ for each $i \in \mathscr{M}$. Successive applications of Eq. (4.25) on each subinterval $[t_{k-1}, t_k)$, $k \in \mathbb{N}$, and noting that (4.23) implies $\sum_{i=1}^m \lambda_i\tau_i < 0$ yield

$$I(\omega) \leq \left(\sum_{j \in \mathscr{N}} I_0^{(j)} \right) \exp\left(\sum_{i=1}^{m} \lambda_i \tau_i \right). \tag{4.26}$$

The usual approach can thus be applied (i.e., the proof of Theorem 3.1) to conclude that $\{\sum_{j=1}^{n} I^{(j)}(h\omega)\}_{h=0}^{\infty}$ converges to zero and, moreover,

$$\lim_{t \to \infty} I^{(j)}(t) = 0, \quad \forall j \in \mathscr{N}.$$

Example 4.3 Consider the multi-city SIR system (4.21) with $n = 2$ cities. Suppose that the dynamics in city 1 are governed by the following switched system:

$$\begin{aligned}
\dot{S}^{(1)}(t) &= \mu^{(1)} \left(1 + \delta \exp\left(\frac{t}{L}\right)\right) N^{(1)}(t) - f_\sigma^{(1)} - \mu^{(1)} \left(1 + \delta \exp\left(\frac{t}{L}\right)\right) S^{(1)}(t) \\
&\quad + \alpha^{(1,1)} S^{(1)}(t) + \alpha^{(2,1)} S^{(2)}(t) - \alpha^{(2,1)} \gamma \frac{S^{(2)}(t) I^{(2)}(t)}{N^{(2)}(t)}, \\
\dot{I}^{(1)}(t) &= f_\sigma^{(1)} - g^{(1)} \left(1 - \zeta \exp\left(\frac{t}{L}\right)\right) I^{(1)}(t) - \mu^{(1)} \left(1 + \delta \exp\left(\frac{t}{L}\right)\right) I^{(1)}(t) \\
&\quad + \alpha^{(1,1)} I^{(1)}(t) + \alpha^{(2,1)} I^{(2)}(t) + \alpha^{(2,1)} \gamma \frac{S^{(2)}(t) I^{(2)}(t)}{N^{(2)}(t)}, \\
\dot{R}^{(1)}(t) &= g^{(1)} \left(1 - \zeta \exp\left(\frac{t}{L}\right)\right) I^{(1)}(t) - \mu^{(1)} \left(1 + \delta \exp\left(\frac{t}{L}\right)\right) R^{(1)}(t) \\
&\quad + \alpha^{(1,1)} R^{(1)}(t) + \alpha^{(2,1)} R^{(2)}(t),
\end{aligned} \tag{4.27}$$

and, in city 2,

$$\begin{aligned}
\dot{S}^{(2)}(t) &= \mu^{(2)} N^{(2)}(t) - f_\sigma^{(2)} - \mu^{(2)} S^{(2)}(t) \\
&\quad + \alpha^{(2,2)} S^{(2)}(t) + \alpha^{(1,2)} S^{(1)}(t) - \alpha^{(1,2)} \gamma \frac{S^{(1)}(t) I^{(1)}(t)}{N^{(1)}(t)}, \\
\dot{I}^{(2)}(t) &= f_\sigma^{(2)} - g^{(2)} I^{(2)}(t) - \mu^{(2)} I^{(2)}(t) \\
&\quad + \alpha^{(1,2)} I^{(1)}(t) + \alpha^{(2,2)} I^{(2)}(t) + \alpha^{(1,2)} \gamma \frac{S^{(1)}(t) I^{(1)}(t)}{N^{(1)}(t)}, \\
\dot{R}^{(2)}(t) &= g^{(2)} I^{(2)}(t) - \mu^{(2)} R^{(2)}(t) \\
&\quad + \alpha^{(2,2)} R^{(2)}(t) + \alpha^{(1,2)} R^{(1)}(t).
\end{aligned} \tag{4.28}$$

Let σ be defined as the periodic switching rule,

$$\sigma(t) \equiv \begin{cases} 1, & \text{if } t \in [k, k+0.25), \quad k = 0, 1, 2, 3, 4, \\ 2, & \text{if } t \in [k+0.25, k+1), \quad k = 0, 1, 2, 3, 4, \\ 3, & \text{if } t \in [k, k+0.25), \quad k = 5, 6, 7, 8, \ldots, \\ 4, & \text{if } t \in [k+0.25, k+1), \quad k = 5, 6, 7, 8, \ldots. \end{cases}$$

Let

$$f_1^{(j)} \equiv f_1^{(j)}(S^{(j)}, I^{(j)}, N^{(j)}) \equiv \beta_1 \frac{S^{(j)} I^{(j)}}{N^{(j)}}, \quad j = 1, 2,$$

$$f_2^{(j)} \equiv f_2^{(j)}(S^{(j)}, I^{(j)}, N^{(j)}) \equiv \beta_2 \frac{S^{(j)} I^{(j)}}{N^{(j)}}, \quad j = 1, 2,$$

$$f_3^{(j)} \equiv f_3^{(j)}(S^{(j)}, I^{(j)}, N^{(j)}) \equiv \beta_1 \frac{S^{(j)} I^{(j)}}{N^{(j)}}, \quad j = 1, 2,$$

$$f_4^{(j)} \equiv f_4^{(j)}(S^{(j)}, I^{(j)}, N^{(j)}) \equiv \beta_2 \frac{S^{(j)} I^{(j)} (1 - I^{(j)})}{N^{(j)}}, \quad j = 1, 2,$$

with $\beta_1 > \beta_2 > 0$. Here $f_1^{(j)}, f_2^{(j)}, f_3^{(j)}$ are standard incidence rates with term-time forced contact rates while $f_4^{(j)}$ takes psychological effects into account. For $t \in [0, 5]$, the disease is transmitted by standard incidence rate with seasonal variations in both cities. After $t = 5$, city 2 exhibits a shift in population behavior (e.g., due to media coverage resulting in widespread aversion). The traveling incidence rates $h^{(l,j)}(S^{(l)}, I^{(l)}, N^{(l)} = \gamma \frac{S^{(l)} I^{(l)}}{N^{(l)}}$ satisfy (4.22) if $\gamma \in [0, 1]$ and it follows from the derivation in [146]:

$$\gamma \frac{(\alpha^{(l,j)} S^{(l)})(\alpha^{(l,j)} I^{(l)})}{\alpha^{(l,j)} N^{(l)}} = \gamma \alpha^{(l,j)} \frac{S^{(l)} I^{(l)}}{N^{(l)}}.$$

Let $(S_0^{(1)}, I_0^{(1)}, R_0^{(1)}) = (0.5, 0, 0)$ and $(S_0^{(2)}, I_0^{(2)}, R_0^{(2)}) = (0.3, 0.2, 0)$ (i.e., the epidemic begins in city 2), and model parameters $\beta_1 = 2$, $\beta_2 = 0.5$, $g^{(1)} = 1.5$, $g^{(2)} = 2$, $\gamma = 0.8$, $\mu^{(1)} = 0.125$, $\mu^{(2)} = 0.1$, $-\alpha^{(1,1)} = \alpha^{(1,2)} = 0.6$, $-\alpha^{(2,2)} = \alpha^{(2,1)} = 0.3$, $\zeta = 0.2$, $\delta = 0.5$, and $L = 10$. These model parameters can be interpreted as follows:

1. In city 2, individuals recover faster from the disease and the death rate is less.
2. The dispersal rate indicates that individuals in the population favor traveling from city 1 to city 2.
3. The birth rate, death rate, and infectious period decrease over time in city 1 (i.e., socioeconomic advancements).

Let $\alpha = \max\{\alpha^{(1,2)}, \alpha^{(2,1)}\}$, $g = \min\{\inf\{g_1(1 - \zeta e^{-t/L}) : t \geq 0\}, g_2\} = g_2$, $\mu = \min\{\inf\{\mu_1(1 + \delta e^{-t/L}) : t \geq 0\}, \mu_2\} = \mu_2$. The value

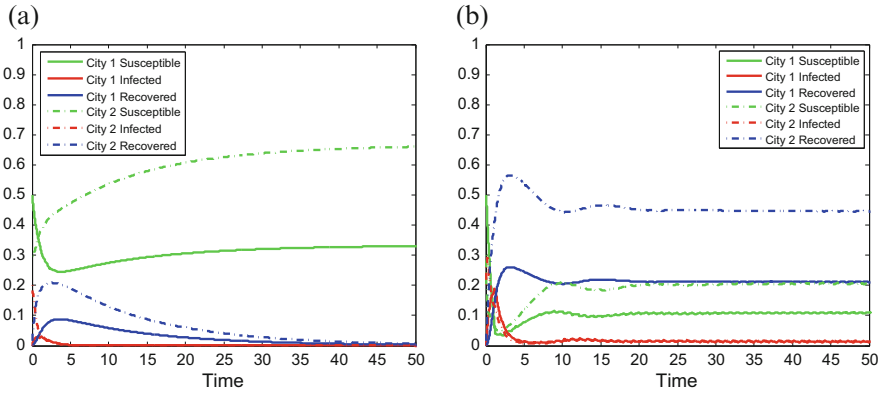

Fig. 4.7 Simulations of Example 4.3. (**a**) $\left\langle \mathrm{R}_0^{(4.21)} \right\rangle = 0.955$. (**b**) $\left\langle \mathrm{R}_0^{(4.21)} \right\rangle > 3.7$

$$\left\langle \mathrm{R}_0^{(4.21)} \right\rangle \equiv \sup_{t \geq 2.25} \frac{\int_0^t \beta_\sigma \mathrm{d}s + \alpha\gamma t}{(g+\mu)t} = 0.955$$

ensures eradication of the disease across both cities by a straightforward extension of Theorem 3.2 to the multi-city case (see Theorem 2.1 in [97]). If $\beta_1 = 10$, $\beta_2 = 4$, then $\left\langle \mathrm{R}_0^{(4.21)} \right\rangle > 3.7$ for any value of h and the disease persists in both cities. The two cases are illustrated in Fig. 4.7.

4.3 Vector-Borne Diseases with Seasonality

The assumption of horizontal transmission of infections between members of the population is reconsidered here. More specifically, vector agents which are outside the host population transmit the disease (e.g., via mosquito–human interactions). By considering fast and slow timescales of the dynamics involved, and seasonal variations in transmission, infectious disease dynamics are modeled using switched delay differential equations. We begin by considering a host population (e.g., humans) modeled using an SIR compartmental model (with compartments denoted by $S^{(H)}$, $I^{(H)}$, and $R^{(H)}$, respectively). Assume that the vector population (e.g., mosquitoes) is split into two groups: the susceptible, denoted by $S^{(M)}$, and the infected, denoted by $I^{(M)}$. The following demographic and epidemiological assumptions are made [16, 145]:

1. The host population birth rate $\mu^{(H)} > 0$ is equal to the host population natural death rate.
2. The vector population birth rate $\mu^{(M)} > 0$ is equal to the vector population natural death rate.

3. The average number of contacts sufficient for disease transmission between susceptible host individuals and infected vector agents is given by $\beta^{(H)} > 0$.
4. The average number of contacts sufficient for disease transmission between susceptible vector agents and infected host individuals is given by $\beta^{(M)} > 0$.
5. Infected individuals in the host population recover at a per unit time rate $g^{(H)} > 0$ and, once infected, a vector agent remains infected until death.
6. At the time of infection, a susceptible vector agent exhibits a periodic of incubation, denoted by $u > 0$, before becoming infectious.
7. The timescale of the vector agent vital dynamics is much faster than that of the host population.

Some conclusions can be drawn from these assumptions: the total host and vector populations, denoted by $N^{(H)} \equiv S^{(H)} + I^{(H)} + R^{(H)}$ and $N^{(M)} \equiv S^{(M)} + I^{(M)}$, respectively, are constant in time. The ratio $\epsilon \equiv N^{(H)}/N^{(M)} \ll 1$, implying that $\mu^{(M)} \gg \mu^{(H)}$. The corresponding ODE system is written as follows:

$$\begin{aligned}
\dot{S}^{(H)}(t) &= \mu^{(H)}(N^{(H)} - S^{(H)}(t)) - \beta^{(H)} S^{(H)}(t) I^{(M)}(t), \\
\dot{I}^{(H)}(t) &= \beta^{(H)} S^{(H)}(t) I^{(M)}(t) - (g^{(H)} + \mu^{(H)}) I^{(H)}(t), \\
\dot{R}^{(H)}(t) &= g^{(H)} I(t) - \mu^{(H)} R(t), \\
\dot{S}^{(M)}(t) &= \mu^{(M)} N^{(M)} - \beta^{(M)} \exp(-\mu^{(M)} u) I^{(H)}(t-u) S^{(M)}(t-u) - \mu^{(M)} S^{(M)}(t), \\
\dot{I}^{(M)}(t) &= \beta^{(M)} \exp(-\mu^{(M)} u) I^{(H)}(t-u) S^{(M)}(t-u) - \mu^{(M)} I^{(M)}(t), \\
(S^{(H)}(0), I^{(H)}(0), R^{(H)}(0), S^{(M)}(0), I^{(M)}(0)) &= (S_0^{(H)}, I_0^{(H)}, R_0^{(H)}, S_0^{(M)}, I_0^{(M)}).
\end{aligned} \tag{4.29}$$

There exist two dimensionless timescales: a slow timescale, corresponding to the dynamics of the host population ($t^{(H)}(t) \equiv \beta^{(M)} N^{(H)} t$), and a fast timescale, corresponding to the dynamics of the vector population ($t^{(M)}(t) \equiv \beta^{(M)} N^{(M)} t$). The flow diagram is shown in Fig. 4.8.

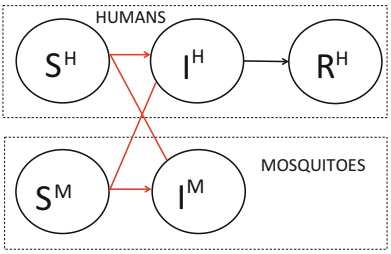

Fig. 4.8 Flow of the vector-borne model (4.29). The *red lines* represent human–mosquito interactions leading to new infections; an infected mosquito must interact with a susceptible human or an infected human with a susceptible mosquito to produce a new infection. The population dynamics are omitted here

Consideration of the dynamics on the slower timescale yields an equivalent DDE system (see [145] for the details): introduce the dimensionless variables $s^{(H)} \equiv S^{(H)}/N^{(H)}$, $i^{(H)} \equiv I^{(H)}/N^{(H)}$, $r^{(H)} \equiv R^{(H)}/N^{(H)}$, $s^{(M)} \equiv S^{(M)}/N^{(M)}$, $i^{(M)} \equiv I^{(M)}/N^{(M)}$. On the fast timescale, the differential equations corresponding to $s^{(M)}$ and $i^{(M)}$ can be rewritten as

$$\begin{aligned} \frac{\mathrm{d}s^{(M)}}{\mathrm{d}t^{(M)}}(t) &= -\frac{\mathrm{d}i^{(M)}}{\mathrm{d}t^{(M)}}(t), \\ \frac{\mathrm{d}i^{(M)}}{\mathrm{d}t^{(M)}}(t) &= \epsilon \left(\exp(-\mu^{(M)}u) i^{(H)}(t-u) s^{(M)}(t-u) - \frac{\mu^{(M)}}{\beta^{(M)} N^{(H)}} i^{(M)}(t) \right), \end{aligned} \tag{4.30}$$

where $s^{(M)}(t) + i^{(M)}(t) = 1$ and $s^{(H)}(t) + i^{(H)}(t) + r^{(H)}(t) = 1$ hold for all t. Equation (4.30) yields that

$$-\frac{\epsilon \mu^{(M)}}{\beta^{(M)} N^{(H)}} \leq \frac{\mathrm{d}i^{(M)}}{\mathrm{d}t^{(M)}}(t) \leq \epsilon \exp(-\mu^{(M)}u), \quad \forall t. \tag{4.31}$$

and, as $\epsilon \to 0$,

$$\frac{\mathrm{d}s^{(M)}}{\mathrm{d}t^{(M)}}(t) = -\frac{\mathrm{d}i^{(M)}}{\mathrm{d}t^{(M)}}(t) = 0$$

so that $i^{(M)}$ and $i^{(S)}$ approach their equilibria values:

$$\begin{aligned} i^{(M)}(t) &= \frac{\beta^{(M)} N^{(H)}}{\mu^{(M)}} \exp(-\mu^{(M)}u) i^{(H)}(t-u) s^{(M)}(t-u), \\ s^{(M)}(t) &= 1 - i^{(M)}(t). \end{aligned} \tag{4.32}$$

From this it is apparent that the vector agent variables $s^{(H)}$ and $i^{(H)}$ approach their equilibria since $i^{(H)}(t-u)$ is approximately equal to a constant on the fast timescale. If

$$\frac{\beta^{(M)} N^{(H)}}{\mu^{(M)}} \exp(-\mu^{(M)}u) \ll 1,$$

then $s^{(M)}(t) \approx 1$. Hence,

$$i^{(M)}(t) \approx \frac{\beta^{(M)} N^{(H)}}{\mu^{(M)}} \exp(-\mu^{(M)}u) i^{(H)}(t-u)$$

so that $S^{(M)}(t) \approx N^{(H)}$ and

$$I^{(M)}(t) \approx \frac{\beta^{(M)} N^{(M)} \exp(-\mu^{(M)}u)}{\mu^{(M)}} I^{(H)}(t-u)$$

where $I^{(H)}(t-u)$ evolves on the slow timescale (and thus constant in this setting).

Omitting $S^{(M)}$ and $I^{(M)}$ (which no longer appear in the equations for the host population) and normalizing the host population variables by $N^{(H)}$ (and dropping their superscripts) leads to the slow timescale reformulation of the epidemic model (4.29) as the following DDE system:

$$\begin{aligned} \dot{S}(t) &= \mu(1 - S(t)) - \beta S(t) I(t-u), \\ \dot{I}(t) &= \beta S(t) I(t-u) - (g+\mu) I(t), \\ \dot{R}(t) &= g I(t) - \mu R(t), \\ (S(s), I(s), R(s)) &= (S_0, I_0(s), R_0), \quad \forall s \in [-u, 0], \end{aligned} \tag{4.33}$$

where $S_0 \in \mathbb{R}_+$, $R_0 \in \mathbb{R}_+$, and the function $I_0 \in \mathrm{PC}([-u, 0], \mathbb{R}_+)$, and where

$$\beta \equiv \frac{\beta^{(H)} N^{(M)} \exp(-\mu^{(M)} u)}{\mu^{(M)}}, \quad g \equiv \frac{g^{(H)}}{\beta_M^{(M)} N}, \quad \mu = \frac{\mu_H}{\beta_M N}.$$

A more realistic assumption is that the period of incubation, u, follows a distribution: $u \in [0, d]$ for some $d > 0$ (i.e., the upper bound for the incubation time) [145]. After u units of time, it is assumed that a fraction $f(u)$ of the vector population becomes infectious; the force of infection is given by

$$\beta S(t) \int_0^d f(u) I(t-u) \mathrm{d}u.$$

Here, f is assumed to satisfy the following conditions:

(a) f is a nonnegative, square integrable function on $[0, d]$ (the force of infection is positive and the distribution is well-defined);
(b) $\int_0^d f(u)\mathrm{d}u = 1$ (the distrubtion is normalized);
(c) $\int_0^d u f(u)\mathrm{d}u < +\infty$ (finite average incubation time until vector agents become infectious after adequate contact).

The vector-borne disease model is a system of integro-differential equations:

$$\begin{aligned} \dot{S}(t) &= \mu(1 - S(t)) - \beta S(t) \int_0^d f(u) I(t-u) \mathrm{d}u, \\ \dot{I}(t) &= \beta S(t) \int_0^d f(u) I(t-u) \mathrm{d}u - (g+\mu) I(t), \\ \dot{R}(t) &= g I(t) - \mu R(t), \\ (S(s), I(s), R(s)) &= (S_0, I_0(s), R_0), \quad \forall s \in [-d, 0], \end{aligned} \tag{4.34}$$

Considering seasonal variations in the contact rate pattern between host and vector populations leads to the following dynamic system:

$$\begin{aligned}
\dot{S}(t) &= \mu(1 - S(t)) - \beta_\sigma S(t) \int_0^d f(u) I(t-u) \mathrm{d}u, \\
\dot{I}(t) &= \beta_\sigma S(t) \int_0^d f(u) I(t-u) \mathrm{d}u - (g + \mu) I(t), \\
\dot{R}(t) &= gI(t) - \mu R(t), \\
(S(s), I(s), R(s)) &= (S_0, I_0(s), R_0), \quad \forall s \in [-d, 0].
\end{aligned} \tag{4.35}$$

A detailed stability analysis of (4.35) is presented in Part III under a number of control strategies (switching control in Sect. 5.5 and impulsive control in Sect. 6.1.7).

4.4 Other Epidemiological Considerations

In this part, other physiological and epidemiological assumptions are considered, leading to complications in the infectious disease models. Straightforward variations in the switched systems techniques used thus far overcome the difficulties and lead to appropriate eradication results. That is, once the assumption is properly incorporated into the model, the methods of the previous sections become applicable. The new transmission or population behaviors play a role in the spread of a disease and manifest themselves in the basic reproduction number of the models. The following complications are considered here:

1. Vertical transmission of infections, in addition to horizontal transmission.
2. Varying total population sizes (i.e., a model with disease-induced mortality).
3. Waning immunity (i.e., an SIRS model).
4. The introduction of a passively immune class (i.e., an MSIR model).
5. A model with general compartments.

Since the switched systems techniques already established are applied in a straightforward way to these model variations, the eradication results are reserved for the end of this section (see Sect. 4.4.6). In some cases, model parameters yielding persistence and permanence are also easily found.

4.4.1 Vertical Transmission

One complication to the SIS model (4.1) is to consider both horizontal and vertical transmission, which is the direct transmission of communicable diseases by an infected mother to her newborn or unborn child. A typical vertical incidence term in a deterministic model is the product of the probability of transmission per birth,

the birth rate and the number of infected women [64]. Assume that $0 \leq \rho \leq 1$ is the probability that a mother with the disease does not transmit it transplacentally, then $(1-\rho)$ is the probability that a child gains the infection transplacentally. This vertical transmission is incorporated into the model then by assuming that a flux $\mu(1-\rho)I$ enters the infected group through birth and the remaining births from infected mothers which are not infected, $\mu\rho I$, enters the susceptible group as normal. The switched SIS model with vertical transmission then is

$$\begin{aligned} \dot{S}(t) &= \mu(S(t)+\rho I(t)) - \beta_\sigma S(t)I(t) - \mu S(t) + gI(t), \\ \dot{I}(t) &= \mu(1-\rho)I(t) + \beta_\sigma SI - (g+\mu)I(t), \\ (S(0), I(0), R(0)) &= (S_0, I_0, R_0). \end{aligned} \tag{4.36}$$

As in the switched SIS model (4.1), the meaningful domain, which is positively invariant, is given by

$$D_{(4.36)} \equiv \{(S,I) \in \mathbb{R}^2_+ : S+I=1\} = D_{(4.1)},$$

with initial conditions satisfying $(S_0, I_0) \in D_{(4.36)}$. In the limit $\rho \to 1$, the model (4.36) becomes the SIS model (4.1), and in the limit $\rho \to 0$, all infected pass on the infection to offspring. For each mode, the basic reproduction number (from the time-invariant case, e.g., [102]) is given as

$$\mathrm{R}_0^{(4.36),i} \equiv \frac{\beta_i}{\rho\mu + g}, \quad \forall i \in \mathscr{M}, \tag{4.37}$$

which biologically represent the average number of secondary infections produced by a single infected individual. Notice that these reproduction numbers are greater than when there is only horizontal transmission (i.e., the mode basic reproduction numbers of (4.1)).

$$\mathrm{R}_0^{(4.1),i} = \frac{\beta_i}{\mu+g} \leq \frac{\beta_i}{\rho(\mu+g)} = \mathrm{R}_0^{(4.36),i}, \quad \forall i \in \mathscr{M}.$$

This makes sense biologically, as there are now infected individuals being recruited through birth. Figure 4.9 shows the flow diagram of (4.36).

There is a single disease-free equilibrium point $\mathcal{Q}_{\mathrm{DFS}}^{(4.36)} \equiv (1,0)$ that is common to all modes and each mode also has endemic equilibrium

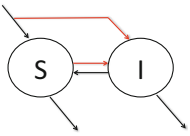

Fig. 4.9 Flow of the SIS model (4.36). The *red lines* represent new infections (some newborns are born infected)

$$Q_{\mathrm{ES}}^{(4.36),i} \equiv \left(\frac{1}{\mathrm{R}_0^{(4.36),i}}, 1 - \frac{1}{\mathrm{R}_0^{(4.36),i}} \right), \quad \forall i \in \mathscr{M}, \tag{4.38}$$

which exists in the meaningful domain if $\mathrm{R}_0^{(4.36),i} \geq 1$. Again, since $S + I = 1$, the system is intrinsically one-dimensional. In the case that

$$\mathrm{R}_0^{(4.36),1}, \ldots, \mathrm{R}_0^{(4.36),m} \leq 1,$$

then $\dot{I}(t) < 0$ in the domain $D_{(4.36)}$ for $I \neq 0$, and since $S + I = 1$, the disease-free equilibrium $Q_{\mathrm{DFS}}^{(4.36)}$ is asymptotically stable in the meaningful domain. From (4.36),

$$\dot{I}(t) = \beta_\sigma S(t) I(t) - gI(t) - \rho\mu I(t) \leq (\beta_\sigma - \rho\mu - g) I(t) = \lambda_\sigma I(t), \tag{4.39}$$

where $\lambda_i \equiv \beta_i - \rho\mu - g$ for all $i \in \mathscr{M}$; the eradication and persistence results from Sect. 4.1 are applicable to (4.36) (see Sect. 4.4.6).

Example 4.4 Consider (4.36) with $\mathscr{M} = \{1, 2\}$, σ defined as in (3.37), $\beta_1 = 0.8$, $\beta_2 = 0.2$, $\rho = 0.4$, $\mu = 0.07$ and $g = 0.3$ (from [102]). In this case, $\mathrm{R}_0^{(4.36)} = 1.067$ and the disease persists. If instead $\rho = 0$, then the disease is eradicated; the vertical transmission is driving persistence of the disease. See Fig. 4.10 for a simulation.

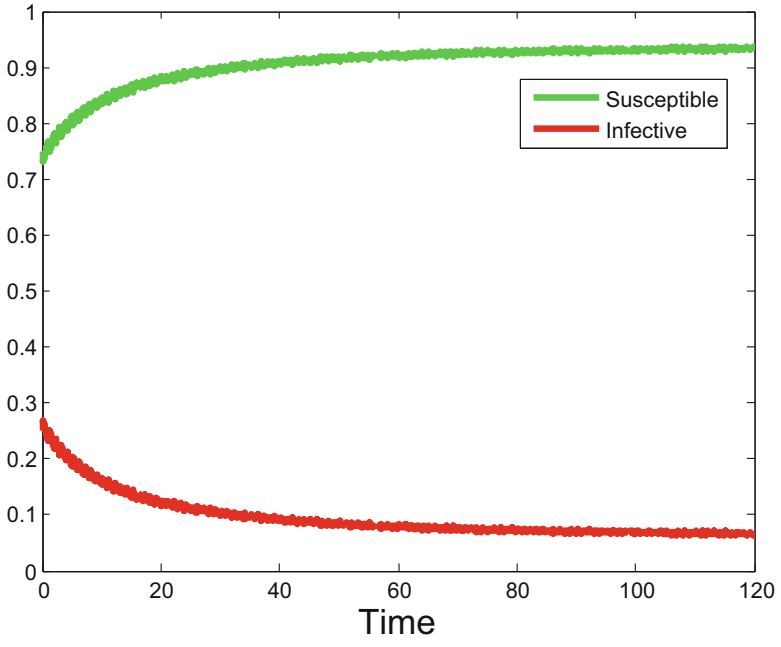

Fig. 4.10 Simulation of Example 4.4

4.4.2 Disease-Induced Mortality: Varying Population Size

In this section, two different population demographic structures are investigated here. First, we revisit the assumption that the natural birth and death rates are equal. Assume a simple birth–death demographic structure for the total population N based on the differential equation

$$\dot{N}(t) = (b-d)N(t), \tag{4.40}$$

where bN are births and dN are the natural deaths. In the absence of births and deaths, i.e. $b = d = 0$, the model is suitable for describing an epidemic in a short time period, for example less than 1 year [64]. This leads to models without population dynamics, such as the classical epidemic model (3.4) studied earlier. If $b = d \neq 0$, then there is an inflow of susceptibles from births, but the population size is a constant because of the corresponding deaths. This is the demographic structure that is most often assumed in the literature and has been assumed up until this point. If $b - d \neq 0$, then the population is exponentially growing or decaying. Applied to the switched SIS model (4.1),

$$\begin{aligned} \dot{S}_c(t) &= bN(t) - \frac{\beta_\sigma S_c(t) I_c(t)}{N(t)} + gI_c(t) - dS_c(t), \\ \dot{I}_c(t) &= \frac{\beta_\sigma S_c(t) I_c(t)}{N(t)} - gI_c(t) - dI_c(t), \end{aligned} \tag{4.41}$$

where S_c, I_c are the number of infected and susceptible individuals (i.e., not fractions), and the total population is $N \equiv S_c + I_c$, which is not necessarily constant and satisfies the differential equation (4.40). The flow associated with (4.41) is shown in Fig. 4.11.

Normalizing the equations using $I \equiv I_c/N$ and $S \equiv S_c/N$ gives $S + I = 1$,

$$\dot{S}(t) = \frac{\dot{S}_c(t)}{N(t)} - S(t)\frac{\dot{N}(t)}{N(t)},$$

and

$$\dot{I}(t) = \frac{\dot{I}_c(t)}{N(t)} - I(t)\frac{\dot{N}(t)}{N(t)}.$$

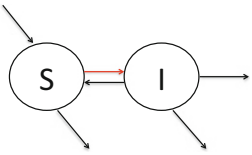

Fig. 4.11 Flow of the SIS model (4.41). New infections are represented by the *red line*

Hence, the switched model is rewritten as

$$\begin{aligned} \dot{S}(t) &= b - \beta_\sigma S(t)I(t) + gI(t) - dS(t), \\ \dot{I}(t) &= \beta_\sigma S(t)I(t) - gI(t) - dI(t), \\ (S(0), I(0)) &= (S_0, I_0), \end{aligned} \tag{4.42}$$

with initial conditions $(S_0, I_0) \in D_{(4.42)} \equiv \{(S, I) \in \mathbb{R}^2_+ : S + I = 1\}$, the positively invariant meaningful domain. The mode basic reproduction numbers are thus given by

$$\mathrm{R}_0^{(4.42),i} \equiv \frac{\beta_i}{b+g}, \quad \forall i \in \mathscr{M}. \tag{4.43}$$

Equation (4.42) admits a single disease-free equilibrium point $Q_{\mathrm{DFS}}^{(4.42)} \equiv (1, 0)$ common to all modes. Each mode also has an endemic equilibrium

$$Q_{\mathrm{ES}}^{(4.42),i} \equiv \left(\frac{1}{\mathrm{R}_0^{(4.42),i}}, 1 - \frac{1}{\mathrm{R}_0^{(4.42),i}} \right), \quad \forall i \in \mathscr{M}. \tag{4.44}$$

Again, since $S + I = 1$ is an invariant to (4.42), the system (4.42) is intrinsically one-dimensional. In the case that

$$\max\{\mathrm{R}_0^{(4.42),i} : i \in \mathscr{M}\} \leq 1,$$

then $\dot{I}(t) < 0$ for all t and $(S, I) \in D_{(4.42)} \setminus \{(S, I) : I = 0\}$; the disease-free solution $Q_{\mathrm{DFS}}^{(4.42)}$ is thus globally asymptotically stable in the meaningful domain. Notice that system (4.42) is identical to the switched SIS model (4.1) if b is replaced by μ. Therefore, the theorems in Sect. 4.1 apply to this system, with the following caveat: the fraction I converges to zero, but it does not necessarily mean the total infected individuals, $I_c \equiv I/N$, converge to zero since the population is not constant, and possibly growing without bound. From $I_c \equiv IN$, $S_c \equiv SN$, if $b = d$ it follows that the population N is constant, and the results for the switched SIS model (4.1) are recovered. If $b < d$, then the total population N converges to zero exponentially, and so $\lim_{t\to\infty} I(t) = 0$ implies that $\lim_{t\to\infty} I_c(t) = 0$. In the final case when $b > d$, the population is growing exponentially but, since $S \to 1$ as $t \to \infty$, it is apparent that $\lim_{t\to\infty} S_c(t) = \lim_{t\to\infty} N(t)$ and hence $\lim_{t\to\infty} I_c(t) = 0$ since $N \equiv S_c + I_c$.

Next, we consider a population demographic structure which includes a disease-induced mortality rate, $\alpha > 0$. In this setting, the population satisfies the differential equation

$$\dot{N}(t) = (b - d)N(t) - \alpha I_c(t). \tag{4.45}$$

The epidemic model is given as

$$\begin{aligned}\dot{S}_c(t) &= bN(t) - \frac{\beta_\sigma S_c(t) I_c(t)}{N(t)} - dS_c(t) + gI_c(t),\\ \dot{I}_c(t) &= \frac{\beta_\sigma S_c(t) I_c(t)}{N(t)} - gI_c(t) - dI_c(t) - \alpha I_c(t),\end{aligned} \tag{4.46}$$

where S_c, I_c are the number of infected and susceptible individuals, respectively, and $N \equiv S_c + I_c$. Again normalizing the equations using $I \equiv I_c/N$ and $S \equiv S_c/N$ leads to

$$\begin{aligned}\dot{S}(t) &= b - \beta_\sigma S(t) I(t) - bS(t) + gI(t) + \alpha S(t) I(t),\\ \dot{I}(t) &= \beta_\sigma S(t) I(t) - gI(t) - bI(t) - \alpha I(t) + \alpha I^2(t),\\ (S(0), I(0)) &= (S_0, I_0).\end{aligned} \tag{4.47}$$

The meaningful domain is the same as (4.42). The αSI and αI^2 terms are nonlinear positive feedbacks induced by the disease-related death rate α: At any time that individuals die from the disease, the population size N decreases resulting in the fraction of individuals in each group increasing [103]. Define the mode basic reproduction numbers as

$$\mathrm{R}_0^{(4.47),i} \equiv \frac{\beta_i}{b + g + \alpha}, \quad \forall i \in \mathscr{M}, \tag{4.48}$$

the disease-free solution $Q_{\mathrm{DFS}}^{(4.47)} \equiv (1, 0)$ and mode-dependent endemic equilibria:

$$Q_{\mathrm{ES}}^{(4.47),i} \equiv (S_i^*, I_i^*) \equiv \left(\frac{b + g}{\beta_i - \alpha}, \frac{b + g + \alpha}{\beta_i - \alpha} (\mathrm{R}_0^{(4.47),i} - 1) \right), \quad \forall i \in \mathscr{M}, \tag{4.49}$$

which are in the meaningful domain only when $\mathrm{R}_0^{(4.47),i} \geq 1$. (Again, since $S+I = 1$, the system is intrinsically one-dimensional.)

Linearizing (4.47) about the disease-free solution gives the following system:

$$\begin{aligned}\dot{S}_L(t) &= -\beta_\sigma I_L(t) - bS_L(t) + gI_L(t) + \alpha I_L(t),\\ \dot{I}_L(t) &= \beta_\sigma I_L(t) - gI_L(t) - bI_L(t) - \alpha I_L(t),\\ (S_L(0), I_L(0)) &= (S_0, I_0).\end{aligned} \tag{4.50}$$

Therefore,

$$\dot{I}_L(t) = (\beta_\sigma - g - b - \alpha) I_L(t) = \lambda_\sigma I_L(t), \tag{4.51}$$

where $\lambda_i \equiv \beta_i - g - b - \alpha$ for all $i \in \mathscr{M}$. Applying the previous switching techniques implies similar eradication thresholds but are local in nature. For example,

$$\mathrm{R}_0^{(4.47)} \equiv \frac{1}{\omega}\sum_{i=1}^{m} \mathrm{R}_0^{(4.47),i}\tau_i < 1$$

implies local asymptotic stability of $Q_{\mathrm{DFS}}^{(4.47)}$ if $\sigma \in \mathscr{S}_{\mathrm{periodic}}(\omega)$. Global results can be achieved under stronger conditions, i.e., if

$$\frac{\sum_{i=1}^{m}\beta_i\tau_i}{\omega(\mu+g)} = \mathrm{R}_0^{(4.1)} < \mathrm{R}_0^{(4.47)} < 1.$$

This follows from the observation that

$$\dot{I}_L(t) = \beta_\sigma S(t) I_L(t) - gI_L(t) - bI_L(t) - \alpha I_L(t) + \alpha I^2(t) \le (\beta_\sigma - b - g) I_L(t).$$

As before, such eradication results only establish that the fractions of infected individuals in the population $I \to 0$ as $t \to \infty$, but not necessarily that the actual number of infected individuals, I_c, go to zero. Recall that the infected fraction is $I \equiv I_c/N$ so that $I_c \equiv IN$, but if $I \to 0$ and $N \to \infty$, it is not immediately clear what will happen to the actual infected number of individuals. The different cases must be investigated: Recalling the equation for the population dynamics (4.45), $b < d$ implies that the total population is going to zero, and hence $I \to 0$ implies $I_c \to 0$. The case $b = d$ gives $\dot{N}(t) = -\alpha I(t)N(t) \le 0$, from which it follows that the total population approaches a constant value since $I \to 0$. Hence, $I_c \to 0$ in this case. Finally, if $b > d$, then the total population grows without bound since $I \to 0$. In this case, since $S \to 1$, $S_c \equiv SN$ gives $S_c \to N$ and then $N \equiv S_c + I_c$ implies $I_c \to 0$.

Lastly, permanence of the disease can be established once again by simply adjusting the switching system techniques as in Theorem 4.3: If $\sigma \in \mathscr{S}_{\mathrm{dwell}}$ and

$$\min\{\mathrm{R}_0^{(4.47),i} : i \in \mathscr{M}\} > 1,$$

then the solution of the SIS system with disease-induced deaths (4.47) converges to the convex hull of the set of endemic points $\{Q_{\mathrm{ES}}^{(4.47),1}, \ldots, Q_{\mathrm{ES}}^{(4.47),m}\}$ (i.e., the disease is permanent). The endemic equilibria,

$$I_i^* \equiv (\beta_i - g - b - \alpha)/(\beta_i - \alpha), \quad \forall i \in \mathscr{M},$$

imply that

$$\mathrm{conv}\{Q_{\mathrm{ES}}^{(4.47),1}, \ldots, Q_{\mathrm{ES}}^{(4.47),m}\} = \{(S,I) \in \mathbb{R}_+^2 : I_{\min}^* \le I \le I_{\max}^*, S = 1 - I\},$$

where

$$I_{\min}^* \equiv \min\{I_i^* : i \in \mathscr{M}\} = \frac{\beta_{\min} - g - b - \alpha}{\beta_{\min} - \alpha},$$

and

$$I^*_{\max} \equiv \max\{I^*_i : i \in \mathscr{M}\} = \frac{\beta_{\max} - g - b - \alpha}{\beta_{\max} - \alpha}.$$

Moreover, the differential equation for I can be rewritten as

$$\dot{I}(t) = (\beta_\sigma - g - b - \alpha)I(t) - (\beta_\sigma - \alpha)I^2(t),$$

so that at $I = I^*_{\min}$,

$$\begin{aligned}
\dot{I}|_{I=I^*_{\min}} &= (\beta_i - g - b - \alpha)I^*_{\min} - (\beta_i - \alpha)(I^*_{\min})^2, \\
&= I^*_{\min}\left(\beta_i - g - b - \alpha - (\beta_i - \alpha)\frac{\beta_{\min} - g - b - \alpha}{\beta_{\min} - \alpha}\right), \\
&= (\beta_i - \alpha)I^*_{\min}\left[\frac{\beta_i - g - b - \alpha}{\beta_i - \alpha} - \frac{\beta_{\min} - g - b - \alpha}{\beta_{\min} - \alpha}\right] \geq 0.
\end{aligned}$$

For any i, at $I = I^*_{\max}$:

$$\begin{aligned}
\dot{I}|_{I=I^*_{\max}} &= (\beta_i - g - b - \alpha)I^*_{\max} - (\beta_i - \alpha)(I^*_{\max})^2, \\
&= I^*_{\max}\left(\beta_i - g - b - \alpha - (\beta_i - \alpha)\frac{\beta_{\max} - g - b - \alpha}{\beta_{\max} - \alpha}\right), \\
&= (\beta_i - \alpha)I^*_{\max}\left[\frac{\beta_i - g - b - \alpha}{\beta_i - \alpha} - \frac{\beta_{\max} - g - b - \alpha}{\beta_{\max} - \alpha}\right] \leq 0.
\end{aligned}$$

Since $S = 1 - I$,

$$I_0 \in \operatorname{conv}\{Q_{\mathrm{ES}}^{(4.47),1}, \ldots, Q_{\mathrm{ES}}^{(4.47),m}\}$$

implies that I remains in the set for all $t \in \mathbb{R}_+$, regardless of the switching rule. If $0 < I_0 < I^*_{\min}$,

$$\begin{aligned}
\dot{I}(t) &= (\beta_\sigma - g - b - \alpha)I(t) - (\beta_\sigma - \alpha)I^2(t), \\
&= (\beta_\sigma - \alpha)\left[\frac{\beta_\sigma - g - b - \alpha}{\beta_\sigma - \alpha} - I(t)\right]I(t) > 0, \quad \forall t \in \mathbb{R}_+,
\end{aligned}$$

and the rest of the argument follows similarly as in the proof of Theorem 4.3.

Example 4.5 Consider (4.47) with $\mathscr{M} = \{1, 2\}$, σ defined as in (3.37), $\beta_1 = 1.5$, $\beta_2 = 1$, $b = 0.07$, $d = 0.01$, $\alpha = 1$, $g = 0.3$. From this, $\mathrm{R}_0^{(4.47)} = 0.821$. If $\alpha = 0$ and $b = d = \mu = 0.07$ then the disease persists; disease-induced mortality helps in achieving eradication of the disease. See Fig. 4.12 for a simulation.

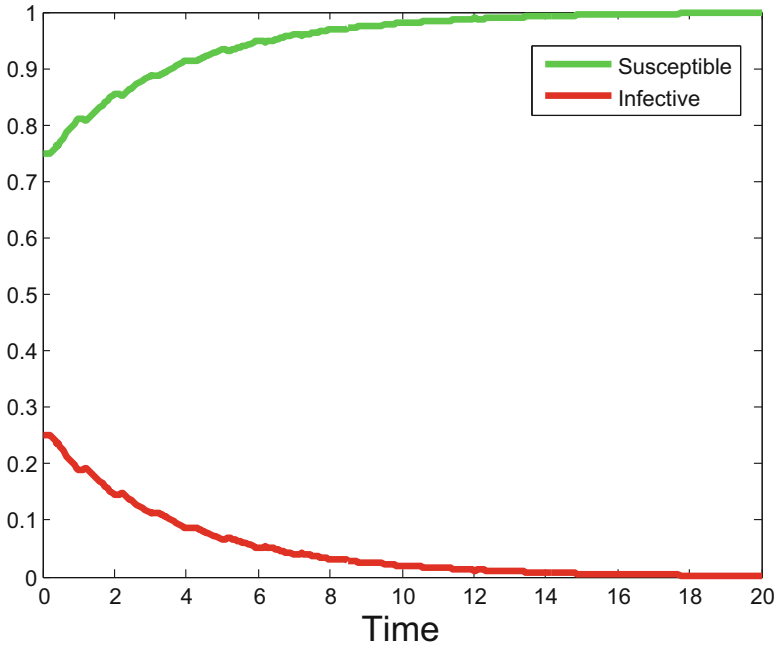

Fig. 4.12 Simulation of Example 4.5

4.4.3 Waning Immunity: The Switched SIRS Model

Individuals that recover from infection and lose immunity over time is reconsidered here. More precisely, assume that individuals lose immunity at rate $\theta > 0$ (thus giving an average period of immunity by $1/\theta$). Along with the other assumptions of the switched SIR model (3.8), the model is given as

$$\begin{aligned} \dot{S}(t) &= \mu - \beta_\sigma S(t)I(t) - \mu S(t) + \theta R(t), \\ \dot{I}(t) &= \beta_\sigma S(t)I(t) - gI(t) - \mu I(t), \\ \dot{R}(t) &= gI(t) - \mu R(t) - \theta R(t), \\ (S(0), I(0), R(0)) &= (S_0, I_0, R_0), \end{aligned} \tag{4.52}$$

The flow of this model is now given by $S \to I \to R \to S$. The mode basic reproduction numbers are the same as from the SIR model (i.e., the mode reproduction numbers $\mathrm{R}_0^{(3.8),i}$ in (3.12)):

$$\mathrm{R}_0^{(4.52),i} \equiv \frac{\beta_i}{\mu + g} = \mathrm{R}_0^{(3.8),i}, \quad \forall i \in \mathscr{M}. \tag{4.53}$$

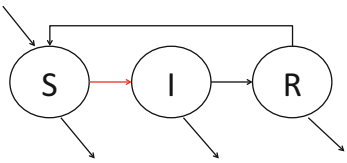

Fig. 4.13 Flow of the SIRS model (4.52). New infections are represented by the *red line*

Fundamentally, the disease spreads at the same rate in the switched SIR and SIRS models, whether the immunity is temporary or permanent. If there is no immunity at all (switched SIS model (4.1)), the basic reproduction rate still does not change. Furthermore, the meaningful domain is the same as the switched SIR model (3.8), i.e., $D_{(4.52)} \equiv \{(S, I, R) \in \mathbb{R}^3_+ : S + I + R = 1\}$, and remains positively invariant: $\{\dot{S} + \dot{I} + \dot{R}\}|_{S+I+R=1} = 0$, $\dot{S}|_{S=0} = \mu + \theta R > 0$, $\dot{I}|_{I=0} = 0$ and $\dot{R}|_{R=0} = gI \geq 0$. Note that the SIS model (4.1) can be regarded as the limiting case of the SIRS model as $1/\theta \to 0$ (i.e., the average immunity period goes to zero). Figure 4.13 shows the flow diagram of (4.52).

Because of these observations, the eradication conditions for (4.52) are the same as those outlined for (3.8) (i.e., Theorems 3.1 and 3.4). For example, it is straightforward to show that if $\sigma \in \mathscr{S}_{\text{periodic}}(\omega)$ and

$$\mathrm{R}_0^{(4.52)} \equiv \frac{\sum_{i=1}^{m} \beta_i \tau_i}{\omega(\mu + g)} < 1,$$

then the solution of (4.52) satisfies $\lim_{t\to\infty}(S(t), I(t), R(t)) = (1, 0, 0) \equiv Q_{\text{DFS}}^{(4.52)}$ (the disease-free solution) and global asymptotic I-stability in the meaningful domain, while if $\mathrm{R}_0^{(4.52)} > 1$ then the disease persists uniformly in (4.52).

One important difference between these models arises from the waning immunity rate θ: as the waning immunity is increased (and hence the immunity period $1/\theta$ is reduced), the prevalence of disease at the endemic equilibria increases and the period of the damped oscillations decreases [69]. Observe that in this case,

$$\begin{aligned} Q_{\text{ES}}^{(4.52),i} &\equiv (S_i^*, I_i^*, R_i^*), \\ &\equiv \left(\frac{1}{\mathrm{R}_0^{(4.52),i}}, \frac{\mu + \theta}{\mu + \theta + g}\left(1 - \frac{1}{\mathrm{R}_0^{(4.52),i}}\right), \frac{g}{\mu + \theta + g}\left(1 - \frac{1}{\mathrm{R}_0^{(4.52),i}}\right)\right), \end{aligned}$$

for all $i \in \mathscr{M}$. Indeed, when the disease is persistent, the endemic points I_i^* are greater than the corresponding endemic points in the switched SIR model with permanent immunity (i.e., $Q_{\text{ES}}^{(3.8),i}$ in (3.13)). This is reasonable biologically, because the loss of immunity should result in more individuals being infected when the disease is persistent. Moreover, the expected rate of convergence to equilibria are different in the SIR and SIRS models. This is because the removed class is being sent back into the susceptible class, because of the temporary immunity. As a result of this, the infectives have more susceptibles to infect.

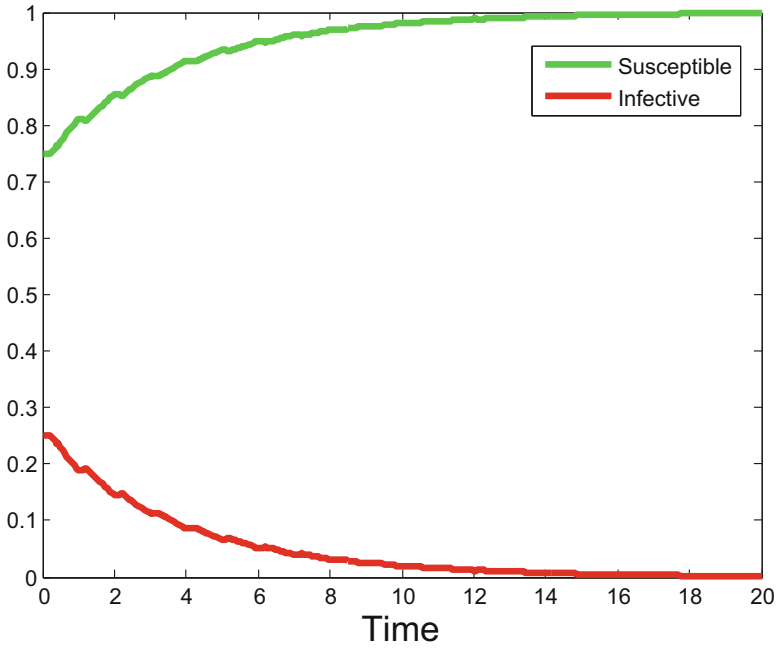

Fig. 4.14 Simulation of Example 4.5

Example 4.6 Consider (4.52) with $\mathscr{M} = \{1, 2\}$, σ defined as in (3.37). Let $\beta_1 = 3$, $\beta_2 = 0.2$, $g = 1$, $\mu = 0.02$, and $\theta = 1$ so that $\mathrm{R}_0^{(4.52)} = 0.882$. See Fig. 4.14 for an illustration with initial conditions $S_0 = 0.75$, $I_0 = 0.25$, $R_0 = 0$. Compared to the SIR case, it takes longer for the disease to become eradicated (even though the susceptible population converges to one more quickly). As the recovered class filters back into the susceptible class from the temporary immunity, the pool of susceptibles becomes larger for the infected to come into contact with.

4.4.4 Passive Immunity: The Switched MSIR Model

Suppose that all mothers who are infected (infected class) or have been infected in the past (recovered/removed class) give birth to children with temporary passive immunity, denoted by the passively immune class M. Assume that individuals born into the passively immune class lose immunity at a rate $\delta > 0$ (hence an average passive immunity period of $1/\delta$). Introducing these assumptions into the switched SIR model (3.8) gives the following epidemic model:

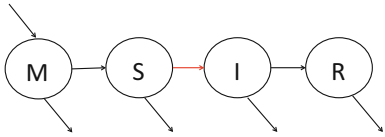

Fig. 4.15 Flow of the MSIR model (4.54). New infections are represented by the *red line*

$$\begin{aligned}
\dot{M}(t) &= \mu(M(t) + I(t) + R(t)) - \delta M(t) - \mu M(t),\\
\dot{S}(t) &= \mu S(t) - \beta_\sigma S(t) I(t) - \mu S(t) + \delta M(t),\\
\dot{I}(t) &= \beta_\sigma S(t) I(t) - g I(t) - \mu I(t),\\
\dot{R}(t) &= g I(t) - \mu R(t),\\
(M(0), S(0), I(0), R(0)) &= (M_0, S_0, I_0, R_0).
\end{aligned} \tag{4.54}$$

Here, the positively invariant meaningful domain is given as

$$D_{(4.54)} \equiv \{(M, S, I, R) \in \mathbb{R}^4_+ : M + S + I + R = 1\} \ni (M_0, S_0, I_0, R_0),$$

and the total population is constant (variables have been normalized). Notice that $\{\dot{M} + \dot{S} + \dot{I} + \dot{R}\}|_{M+S+I+R=1} = 0$, $\dot{S}|_{S=0} = \delta M \geq 0$, $\dot{I}|_{I=0} = 0$, $\dot{R}|_{R=0} = gI \geq 0$ and $\dot{M}|_{M=0} = \mu I + \mu R \geq 0$. Illustrated in Fig. 4.15 is the flow of (4.54).

For this model, again define the mode basic reproduction numbers according to

$$\mathrm{R}_0^{(4.54),i} \equiv \frac{\beta_i}{\mu + g}, \quad \forall i \in \mathscr{M},$$

which are the same as the switched SIS model, switched SIR model, and switched SIRS model. Hence, the addition of the M class does not alter the spread of the disease physically but there are differences here. There is a single common disease-free equilibrium point $Q_{\mathrm{DFS}}^{(4.54)} \equiv (0, 1, 0, 0)$ and each mode also has an endemic equilibrium $Q_{\mathrm{ES}}^{(4.54),i} \equiv (M_i^*, S_i^*, I_i^*, R_i^*)$ with

$$\begin{aligned}
M_i^* &\equiv \frac{\mu}{\delta + \mu}\left(1 - 1/\mathrm{R}_0^{(4.54),i}\right),\\
S_i^* &\equiv \frac{1}{\mathrm{R}_0^{(4.54),i}},\\
I_i^* &\equiv \frac{\delta}{\delta + \mu}\frac{\mu}{\mu + g}\left(1 - 1/\mathrm{R}_0^{(4.54),i}\right),\\
R_i^* &\equiv \frac{g}{\delta + \mu}\frac{\mu}{\mu + g}\left(1 - 1/\mathrm{R}_0^{(4.54),i}\right).
\end{aligned}$$

The endemic equilibria points are again different from the SIR and SIRS cases. From the differential equation for I, it is apparent that if

$$\max\{\mathrm{R}_0^{(4.54),i} : i \in \mathscr{M}\} \leq 1$$

then $\dot{I}(t) < 0$ in the physical domain unless $I = 0$ or $S = 1$. Hence the disease will be eradicated. Inspection of the system (4.54) with an absence of infection, $I(t) \equiv 0$, gives that R converges to zero, from which it follows that M converges to zero. By constant total population then, S converges to one and the reduced system converges to the disease-free solution. Hence, the eradication results of the switched SIR model (3.8) may be applied. For example, if $\sigma \in \mathscr{S}_{\text{periodic}}(\omega)$ and

$$\mathrm{R}_0^{(4.54)} \equiv \frac{\sum_{i=1}^{m} \beta_i \tau_i}{\omega(\mu + g)} < 1,$$

then the solution of (4.54) satisfies $\lim_{t\to\infty}(M(t), S(t), I(t), R(t)) = (0, 1, 0, 0) = \mathcal{Q}_{\text{DFS}}^{(4.54)}$.

4.4.5 Infectious Disease Model with General Compartments

As highlighted in the previous sections, there are a number of compartments and interactions that can be considered in an epidemic model, based on the population behavior and the disease dynamics. Here, we consider an epidemic model with general compartments with the following assumptions:

1. There is a susceptible and infected compartment, labeled by S and I, respectively.
2. Individuals in the susceptible group move to the infected class with switched incidence rate $(t, S, I) \mapsto h_\sigma(I)S$, where $\{h_i : i \in \mathscr{M}\}$ is a family of forces of infection with appropriate assumptions. Namely, the forces of infection h_i are assumed to be sufficiently smooth functions satisfying $h_i(t, I) > 0$ for $I > 0$ and $h_i(t, 0) = 0$ for $t \geq 0$ and $i \in \mathscr{M}$ from physical considerations.
3. The birth rate is given by the switched constant $\mu_\sigma > 0$, which is equal to the death rate.
4. There are n_Y other epidemiological compartments $Y^{(1)}, Y^{(2)}, \ldots, Y^{(n_Y)}$, representing various other stages in the progression of the disease.
5. It is possible for said n_Y compartments to filter back into the susceptible class (e.g., due to waning immunity) at a switched rate $\theta_\sigma^{(j)} \geq 0$ for each $j \in \{1, 2, \ldots, n_Y\}$.
6. The infected class moves to the $Y^{(j)}$ compartments (e.g., due to natural recovery) via a switched function $(t, I, Y) \mapsto \Psi_\sigma(I, Y)$, where $Y \equiv (Y^{(1)}, Y^{(2)}, \ldots, Y^{(n_Y)})$.
7. The progression of the disease in compartment $Y^{(j)}$ is governed by a switched vector function $(t, S, I, Y) \mapsto \Upsilon_\sigma(S, I, Y)$.

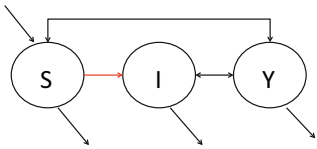

Fig. 4.16 Flow of the epidemic model with general compartments (4.55). The *red line* represents horizontal transmission

Putting together these modeling assumptions, the switched system is given by

$$\begin{aligned}
\dot{S}(t) &= \mu_\sigma - h_\sigma(I(t))S(t) - \mu_\sigma S(t) + \sum_{j=1}^{n_Y} \theta_\sigma^{(j)} Y^{(j)}(t), \\
\dot{I}(t) &= h_\sigma(I(t))S(t) - \mu_\sigma I + \Psi_\sigma(I(t), Y(t)), \\
\dot{Y}(t) &= \Upsilon_\sigma(S(t), I(t), Y(t)), \\
(S(0), I(0), Y(0)) &= (S_0, I_0, Y_0),
\end{aligned} \tag{4.55}$$

with $S_0, I_0 \in \mathbb{R}_+$ and $Y_0 \in \mathbb{R}_+^{n_Y}$. The flow between the general compartments is shown in Fig. 4.16. The variables have been normalized by the total population so that

$$S(t) + I(t) + \sum_{j=1}^{n_Y} Y^{(j)}(t) = 1, \quad \forall t.$$

Assume that $\Upsilon_i \equiv (\Upsilon_i^{(1)}, \Upsilon_i^{(2)}, \ldots, \Upsilon_i^{(n_Y)})$ is a sufficiently smooth vector function satisfying $\Upsilon_i^{(j)}(S, I, 0) \geq 0$ for each $i \in \mathscr{M}$ and $j \in \{1, \ldots, n_Y\}$ and

$$\begin{aligned}
&(\Upsilon_i^{(1)}(S, 0, Y), \ldots, \Upsilon_i^{(n_Y)}(S, 0, Y)) \\
&\quad = -(\phi_i^{(1)}(S, Y), \ldots, \phi_i^{(n_Y)}(S, Y)), \\
&\quad = -\phi_i(S, Y), \quad \forall (S, I, Y) \in D_{(4.55)}, \quad \forall i \in \mathscr{M}, \quad \forall j \in \{1, \ldots, n_Y\}, \quad \forall t \in \mathbb{R}_+,
\end{aligned}$$

where

$$D_{(4.55)} \equiv \{(S, I, Y) \in \mathbb{R}_+^{2+n_Y} : S + I + \sum_{j=1}^{n_Y} Y^{(j)} = 1\},$$

$\phi_i^{(j)}(S, Y) \geq 0$ are sufficiently smooth functions. Assume that $\Psi_i : \mathbb{R}^{n_Y+1} \to \mathbb{R}_+$ is a sufficiently smooth scalar function satisfying $\Psi_i(0, Y) = 0$ for suitable Y and all $i \in \mathscr{M}$. Lastly, assume that $\theta_i^{(j)} \geq 0$ for each $i \in \mathscr{M}$ and $j \in \{1, \ldots, n_Y\}$. The normalization of the variables implies that the functions satisfy

$$\mu_i - \mu_i(S(t) + I(t)) + \sum_{j=1}^{n_Y} \Upsilon_i^{(j)}(t) + \Psi_i(I(t), Y(t)) + \sum_{j=1}^{n_Y} \theta_i^{(j)} Y^{(j)}(t) = 0$$

for all $i \in \mathscr{M}$, $j \in \{1, \ldots, n_Y\}$, and $t \in \mathbb{R}_+$. Along with the conditions on the functions outlined above, this implies the meaningful domain is invariant to system (4.55), and hence the model is mathematically and physically well-posed. System (4.55) admits a disease-free equilibrium

$$\mathcal{Q}_{\text{DFS}}^{(4.55)} \equiv (1, 0, \underbrace{0, \ldots, 0}_{n_Y}).$$

Even in this general setting, the previously outlined switching systems methods can be applied to give eradication results based on the model parameters. One such result is highlighted in detail.

Theorem 4.7 *Suppose that there exist $\beta_i \geq 0$ and $\alpha_i \geq 0$ such that $h_i(I) \leq \beta_i I$ and $\Psi_i(I, Y) \leq -\alpha_i I$ for $i \in \mathscr{M}$. If either of the following conditions hold:*

(i) $\sigma \in \mathscr{S}_{\text{dwell}}$ and

$$\left\langle \mathrm{R}_0^{(4.55)} \right\rangle \equiv \sup_{t \geq h} \sum_{i=1}^{m} T_i(t) \frac{\beta_i}{\mu_i + \alpha_i} < 1,$$

(ii) $\sigma \in \mathscr{S}_{\text{periodic}}(\omega)$ and

$$\widehat{\mathrm{R}_0}^{(4.55)} \equiv \sum_{i=1}^{m} \tau_i \frac{\beta_i}{\mu_i + \alpha_i} < 1,$$

then the solution of (4.55) converges to the disease-free solution $\mathcal{Q}_{\text{DFS}}^{(4.55)}$.

Proof First we prove case (i). From the system (4.55), let i_k follow a switching rule $\sigma \in \mathscr{S}$, then for $t \in [t_{k-1}, t_k)$,

$$\begin{aligned} \dot{I}(t) &= h_\sigma(I(t))S(t) - \mu_\sigma I(t) + \Psi_\sigma(I(t), Y(t)), \\ &\leq (\beta_\sigma - \mu_\sigma - \alpha_\sigma)I(t), \\ &= \lambda_\sigma I(t), \end{aligned} \tag{4.56}$$

where $\lambda_i \equiv \beta_i - \mu_i - \alpha_i$ for each $i \in \mathscr{M}$. Equation (4.56) and the proof of Theorem 3.2 gives that $\lim_{t\to\infty} I(t) = 0$. Since $\Upsilon_i(S, 0, Y) = -\phi_i(S, Y)$, it is clear that the variables $Y_1, \ldots, Y_k$ converge to zero. Finally, $S = 1 - I - \sum_{j=1}^{n_Y} Y^{(j)}$ implies that S converges to one. Hence, the solution converges to the disease-free equilibrium. Case (ii) follows from Eq. (4.56) and the proof of Theorem 3.1.

4.4.6 Summary of Mode Basic Reproduction Numbers and Eradication Results

One consistently revisited theme of this chapter is the ease of application of the switched systems techniques to epidemic models with different epidemiological and physiological assumptions. The main reason for this flexibility is the focus on global attractivity and partial I-stability or that the models involved are intrinsically of dimension one (strengthening the results to global stability). In either case, establishable differential equation bounds of the form

$$\dot{I}(t) \leq \lambda_\sigma I(t),$$

where λ_i is defined different for each model, makes the following results possible.

Theorem 4.8 *Consider the epidemic models with vertical transmission, varying population size, and disease-induced mortality ((4.36), (4.42), and (4.47), respectively) and their corresponding mode basic reproduction numbers* $\mathrm{R}_0^{(*),i}$ *and disease-free solutions* $Q_{\mathrm{DFS}}^{(*)}$*. Then the following statements hold:*

(i) If $\sigma \in \mathscr{S}_{\mathrm{periodic}}(\omega)$ *and*

$$\mathrm{R}_0^{(*)} \equiv \frac{1}{\omega} \sum_{i=1}^{m} \mathrm{R}_0^{(*),i} \tau_i < 1,$$

then the disease-free solution $Q_{\mathrm{DFS}}^{(*)}$ *is globally asymptotically stable in the meaningful domain* $D_{(*)}$ *(locally asymptotically stable if* $(*) = (4.47)$*).*

(ii) If $\sigma \in \mathscr{S}_{\mathrm{dwell}}$ *and*

$$\left\langle \mathrm{R}_0^{(*)} \right\rangle \equiv \sup_{t \geq h} \frac{1}{t} \sum_{i=1}^{m} \mathrm{R}_0^{(*),i} T_i(t) < 1, \tag{4.57}$$

for some $h > 0$*, then the disease-free solution* $Q_{\mathrm{DFS}}^{(*)}$ *is globally exponentially stable in the domain* $D_{(*)}$ *(locally exponentially stable if* $(*) = (4.47)$*).*

(iii) If $\sigma \in \mathscr{S}_{\mathrm{dwell}}$ *satisfies* $T^+ \leq N_0 + qT^-(t)$ *for some* $q \in (0, 1)$ *and* $N_0 \geq 0$ *such that*

$$\mathrm{R}_0^{(*),-} - 1 < q(\mathrm{R}_0^{(*),+} - 1),$$

where $\mathrm{R}_0^{(*),-} \equiv \max\{\mathrm{R}_0^{(*),i} : i \in \mathscr{M}^-\}$, $\mathrm{R}_0^{(*),+} \equiv \max\{\mathrm{R}_0^{(*),i} : i \in \mathscr{M}^+\}$, $\mathscr{M}^- \equiv \{i \in \mathscr{M} : \mathrm{R}_0^{(*),i} < 1\}$, $\mathscr{M}^+ \equiv \{i \in \mathscr{M} : \mathrm{R}_0^{(*),i} \geq 1\}$, *and*

$$T^+(t) \equiv |\{t \in [0, t] : \sigma(t) \in \mathscr{M}^+\}|,$$
$$T^-(t) \equiv |\{t \in [0, t] : \sigma(t) \in \mathscr{M}^-\}|,$$

then the disease-free solution $Q^{(*)}_{\mathrm{DFS}}$ *is globally exponentially stable in the domain* $D_{(*)}$ *(locally exponentially stable if* $(*) = (4.47)$*).*

(iv) If $\sigma \in \mathscr{S}_{dwell}$ *and* $\min\{\mathrm{R}_0^{(*),i} : i \in \mathscr{M}\} > 1$*, then the disease is permanent in (*);* $I(t)$ *converges to conv*$\{Q_{\mathrm{ES}}^{(*),1}, \ldots, Q_{\mathrm{ES}}^{(*),m}\}$.

Similarly for the epidemic models of intrinsic dimension greater than or equal to two, the following theorem is given.

Theorem 4.9 *Consider the epidemic models with waning immunity, passive immunity, and general compartments ((4.52), (4.54), and (4.55), respectively) and their corresponding mode basic reproduction numbers* $\mathrm{R}_0^{(*),i}$ *and disease-free solutions* $Q^{(*)}_{\mathrm{DFS}}$*. Then the following statements hold:*

(i) If $\sigma \in \mathscr{S}_{\mathrm{periodic}}(\omega)$ *and*

$$\mathrm{R}_0^{(*)} \equiv \frac{1}{\omega} \sum_{i=1}^{m} \mathrm{R}_0^{(*),i} \tau_i < 1,$$

then the disease-free solution $Q^{(*)}_{\mathrm{DFS}}$ *is globally attractive and asymptotically I-stable in the meaningful domain* $D_{(*)}$.

(ii) If $\sigma \in \mathscr{S}_{\mathrm{dwell}}$ *and*

$$\left\langle \mathrm{R}_0^{(*)} \right\rangle \equiv \sup_{t \geq h} \frac{1}{t} \sum_{i=1}^{m} \mathrm{R}_0^{(*),i} T_i(t) < 1, \tag{4.58}$$

for some $h > 0$*, then the disease-free solution* $Q^{(*)}_{\mathrm{DFS}}$ *is globally attractive and exponentially I-stable in the meaningful domain* $D_{(*)}$.

(iii) If $\sigma \in \mathscr{S}_{\mathrm{dwell}}$ *satisfies* $T^+ \leq N_0 + qT^-(t)$ *for some* $q \in (0, 1)$ *and* $N_0 \geq 0$ *such that*

$$\mathrm{R}_0^{(*),-} - 1 < q(\mathrm{R}_0^{(*),+} - 1),$$

where $\mathrm{R}_0^{(*),-} \equiv \max\{\mathrm{R}_0^{(*),i} : i \in \mathscr{M}^-\}$, $\mathrm{R}_0^{(*),+} \equiv \max\{\mathrm{R}_0^{(*),i} : i \in \mathscr{M}^+\}$*, then the disease-free solution* $Q^{(*)}_{\mathrm{DFS}}$ *is globally attractive and exponentially I-stable in the meaningful domain* $D_{(*)}$.

The results are summarized in Table 4.1. It should be noted that although some epidemic models share the same mode basic reproduction numbers, they may possess differing qualitative behaviors (i.e., via different mode-dependent endemic equilibria and therefore different permanence sets in Theorem 4.8 (iv), for example).

Table 4.1 Mode basic reproduction numbers of the outlined disease models

Epidemiological assumption	Disease model	Mode basic reproduction numbers	DFS stability
Vertical transmission (SIS)	(4.36)	$\beta_i/(\rho\mu + g)$	Global
Varying population size (SIS)	(4.42)	$\beta_i/(b + g)$	Global
Disease-induced mortality (SIS)	(4.47)	$\beta_i/(b + g + \alpha)$	Local
Waning immunity (SIRS)	(4.52)	$\beta_i/(\mu + g)$	GA and PS
Passive immunity (MSIR)	(4.54)	$\beta_i/(\mu + g)$	GA and PS
General compartments	(4.55)	$\beta_i/(\mu_i + \alpha_i)$	GA and PS

The stability results obtained for $Q_{\mathrm{DFS}}^{(*)}$ in the meaningful domain are global (i.e., global asymptotic or exponential stability), local (i.e., local asymptotic stability), or GA and PS (global attractivity and partial stability)

4.5 Discussions

The SIS model (4.1) with time-constant contact rate has been analyzed extensively in the literature [63, 67, 69, 73, 116]. In Sect. 4.1, an SIS model with term-time forced parameters is analyzed and the analytic solution is explicitly provided. Results on persistence of the disease in the endemic case are given, including some criteria guaranteeing the convergence of the solution to the convex hull of the endemic equilibria. A term-time forced SIS model is also studied that considers an incidence rate which takes media coverage and the pattern of daily encounters in a local community into account. This investigation contributes to the existing literature by extending the studies in [83, 171] through the switching incidence rates and term-time forced seasonal variations, and is based on the work in [98]. The persistence result derived in Theorem 4.2 is established along the lines of the proof of Theorem 3.3 in [83] and Lemma 4.1 and Theorem 4.1 in [68]. The authors Li and Cui [83] considered the incidence rate

$$(S, I) \mapsto \left(\beta - \gamma \frac{I}{b + I}\right) SI,$$

and therefore the autonomous (non-switched) version of (4.12).

As mentioned, infectious diseases like influenza (e.g., the subtype H1N1 in 2009) and SARS are easily transmitted from one geographic region to another due to population dispersal from individuals traveling; the effect of travel on the spread of a disease should be considered [156]. The compartmental epidemic model literature contains formulations and studies of epidemic models with population dispersal;

for example, Sattenspiel and Dietz [132] studied the transmission of measles in the Caribbean island of Dominica using a multi-city SIR model with travel between populations. Arino and van den Driessche [5] developed and studied a multi-city SIS model to study the spatial spread of a disease. A multi-city SIS model with a general nonlinear birth-rate term was studied by Wang and Zhao in [157]. Wang and Mulone explored a two-city SIS model with population dispersal in [156]. Wang and Zhao studied a multi-city SIS model with age structure and time delay in [158]. A two-city SIS model with transport-related infection has been studied by Cui et al. in [146] and some results were extended by Takeuchi et al. in [147]. Wan and Cui analyzed a two-city SEIS model in [155], and Liu and Zhou studied a two-city SIRS model in [88], both with transport-related infection.

There are few reports analyzing multi-city models with seasonality in the literature; Zhang and Zhao studied a multi-city SIS model with general nonlinear birth-rate and periodic model parameters, including the contact rate, in [170]. The multi-city SIR model, suitable for modeling infections such as hepatitis B, measles, influenza, and chickenpox [88, 101], is extended to switched seasonal variations and general incidence rates in (4.21), which is inspired by the work in [97]. The analysis of multi-city epidemic models in Sect. 4.2 naturally leads to age group considerations, which are not presently considered but the interested reader is referred to [65, 82, 107, 129, 130, 137]. The authors Röst and Wu [130] considered age-dependent mixing and provided global asymptotic stability of the disease-free equilibrium. In [107], McCluskey resolved the endemic case and showed global asymptotic stability of the endemic equilibrium, using a Lyapunov functional, whenever the basic reproduction number is greater than one. In the paper [129], Röst analyzed an SEI (susceptible-exposed-infected) model with distributed delays and a death rate for the infected class that depends on the age of infection. A heterogeneous host population can be divided into homogeneous groups according to transmission characteristics (modes of transmission, contact patterns, geographic distributions, etc.) [82]. Motivated by this, a multi-group SEIR (susceptible-exposed-infected-recovered) model with unbounded delay was studied in [82] by Li et al. to model within-group and inter-group interactions separately. The authors found global asymptotic stability results for the disease-free equilibrium and endemic equilibrium based on the spectral radius of the next-generation matrix using Lyapunov functionals. These results were extended by Shu et al. in [137] to model generalized nonlinear transmission rates. Lyapunov functionals were used to give sufficient conditions for global asymptotic stability of the disease-free equilibrium and endemic equilibrium based on the basic reproduction number.

In Sect. 4.3, infectious diseases which spread by vector agents are detailed, motivated by the work in [143]. In particular, those diseases which display a finite incubation time before vector agents become infectious (see, e.g., [16, 17, 19, 27, 50, 104, 108, 145]). Chikungunya virus is usually transmitted via *Aedes aegypti*, however, in recent outbreaks transmission has been observed via *Aedes albopictus* (e.g., in Réunion [114]). Capable of transmitting diseases such as dengue (see the studies [165, 166] for mathematical models of dengue), *Aedes aegypti* is a tropical and subtropic species but *Aedes albopictus* has recently been observed adapting

to non-tropic regions in Southeast Asia, islands in the Pacific and Indian oceans, China, Europe, USA, and Australia [41, 113, 114]. Italy experienced an outbreak in 2007 [127]; globalization of vector-borne disease is of great interest at present, pronounced by recent outbreaks of Zika virus. The author Cooke [27] first proposed a version of the vector-borne disease model (4.34) for study. Beretta and Takeuchi [16, 17] analyzed the stability of the disease-free equilibrium of vector-borne disease models similar to (4.34). Takeuchi et al. [145] and Beretta et al. [19] extended these works to the endemic case. Ma et al. [104] analyzed the permanence of (4.34). Gao et al. [50] investigated a vaccination scheme for an SIR vector-borne disease model with distributed delays. The work on stability of the endemic equilibrium of (4.34), with birth rate unequal to death rate, was completed by McCluskey in [108].

The vector agent population, and thus interactions between host and vector populations, is absent in (4.35); the qualitative behavior of the disease with respect to the host population is the main focus. This is in contrast with the case study in Chap. 7, where the full dynamics between host and vector populations are modeled. The drawback to this omission is the introduction of time delays (leading to theoretical complications) and the exclusion of the vector population for vector-focused control measures (e.g., destruction of breeding sites cannot be adequately modeled in (4.35)). On the other hand, integro-differential equations, as appearing in Sect. 4.3, arise frequently in modeling physical and biological phenomena. Examples are found in [24, 78]: biological population models, predator–prey models with a past hereditary influence, grazing systems, chemical oscillations, nuclear reactors, and heat flow problems [24, 78].

A number of different epidemic models are presented and examined in Sect. 4.4. First, vertical transmission was incorporated into the model in Sect. 4.4.1, which is an important transmission mechanism in a variety of diseases like hepatitis and AIDS [37]. The switched SIS model (4.1) and switched SIS model with vertical transmission (4.36) made the common assumption that births and deaths are equal (leading to a population balance) [73], which is reasonable when considering the often shorter time scales involved in the epidemics when compared to the population dynamics. However, infectious diseases like measles, chickenpox, and pertussis display the characteristic that the susceptible class is mostly composed of younger individuals whose rate of natural mortality does not necessarily coincide with that of the rest of the population [73]. Non-constant population size has been displayed in a number of real-world examples, motivating the analysis of the SIS model with non-constant population (4.42).

In the case of infectious diseases like AIDS, disease-related deaths should be taken into account by modifying the constant-population assumption [140]. As disease-related deaths and persistence of a disease can have the effect of reversing a naturally growing population into a stable or decaying population [64], the switched SIS model with disease-induced mortality (4.47) is investigated. When there is natural recovery from the disease for a non-negligible amount of time yet the immunity wanes in time, the SIRS model is appropriate (see [69, 73]). The modeling assumptions of the SIR model (3.9) are taken with the distinction that individuals recovering from the disease do so temporarily. Examples include the

herpes simplex virus, which tends to relapse after recovery [140]. This has also been demonstrated in a number of sexually transmitted diseases (e.g., gonorrhea and chlamydia) [46]. The switched SIRS model (4.52) is the focus of Sect. 4.4.3 to address these concerns. Diseases in which antibodies are transferred from an infected mother to unborn child (e.g., chickenpox) [65] are modeled according to the so-called switched MSIR model (4.54). Lastly, the seasonally varying epidemic model with generalized compartments in Sect. 4.4.5 was motivated by the time-invariant epidemic model studied in [36].