Chapter 7
Spatial Structure: Patch Models

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Abstract Discrete spatial heterogenity is introduced into disease transmission models, resulting in large systems of ordinary differential equations. Such metapopulation models describe disease spread on a number of spatial patches. In the first model considered, there is no explicit movement of individuals; rather infectives can pass the disease to susceptibles in other patches. The second type of model explicitly includes rates of travel between patches and also takes account of the resident patch as well as the current patch of individuals. A formula for and useful bounds on the basic reproduction number of the system are determined. Brief descriptions of application of this type of metapopulation model are given to investigate the spread of bovine tuberculosis and the effect of quarantine on the spread of influenza.

7.1 Introduction

Basic deterministic models assume no spatial variation. However, since both the environment and any population are spatially heterogeneous, it is obviously desirable to include spatial structure into an epidemic model. Demographic and disease parameters may vary spatially, and a human population may live in cities or be scattered in rural areas. Populations travel, animals and people by foot, birds and mosquitoes (reservoir and vector for West Nile virus) by wing. In addition, people travel by air between cities, so diseases can be spread quickly between very distant places (as was the case with the SARS outbreak in 2003).

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Spatial structure can be included in either a continuous or discrete way. If time is assumed continuous, then continuous space yields reaction-diffusion equations, which are discussed in the chapter by Wu [15], whereas discrete space yields coupled patch models. These models, which are the focus of this chapter, are called metapopulation models . They usually consist of a system (often a large system) of ordinary differential equations with the dynamics of each patch coupled to that of other patches by travel. A patch can be a city, community, or some other geographical region. If time is assumed discrete, then continuous space yields integrodifference equation models, whereas discrete space yields coupled lattice or cellular automata models [8, page 268].

Four different types of metapopulation models from the literature are considered in this chapter. The first two models are fairly general and are formulated and discussed in detail, whereas the last two, which deal with influenza and with tuberculosis in possums, are described in less detail. But since these metapopulation models can be complicated, readers are asked to consult the references for more background and details.

7.2 Spatial Heterogeneity

Consider a basic susceptible, exposed, infective, recovered (SEIR) compartmental model such as is frequently used for childhood diseases; see, for example, [1], [13, Sect. 2.2 with $p = q = 0$]. To incorporate spatial effects, Lloyd and May [9] divide the population into connected subpopulations. Let S_i, E_i, I_i, R_i denote respectively the number of susceptible, exposed, infective and recovered individuals in patch i for $i = 1, ..., n$. The total population of patch i is $N_i = S_i + E_i + I_i + R_i$. The birth and natural death rate constant d is assumed to be the same in each patch, so that the total population of each patch remains constant. The average latent period $1/\epsilon$ and the average infectious period $1/\gamma$ are assumed to be the same in each patch. This spatial model can be written for $i = 1, ..., n$ as

$$\begin{aligned} S_i' &= dN_i - dS_i - \lambda_i S_i \\ E_i' &= \lambda_i S_i - (d+\epsilon)E_i \\ I_i' &= \epsilon E_i - (d+\gamma)I_i \\ R_i' &= \gamma I_i - dR_i; \end{aligned} \tag{7.1}$$

with the force of infection in patch i given by a mass action type of incidence

$$\lambda_i = \sum_{j=1}^{n} \beta_{ij} I_j.$$

Thus infective individuals in one patch can infect susceptible individuals in another patch, but there is no explicit movement of individuals in this model. If the exposed period tends to zero, corresponding to $\epsilon \to \infty$, then this reduces to an SIR model; which is now analyzed. Please consult [9] for analysis of the SEIR model.

For the SIR model, the equations are

$$\begin{aligned} S_i' &= dN_i - dS_i - \lambda_i S_i \\ I_i' &= \sum_{j=1}^{n} \beta_{ij} I_j S_i - (d+\gamma) I_i \end{aligned} \tag{7.2}$$

and the disease-free equilibrium is $S_i = N_i,\ I_i = R_i = 0$. Using the next generation matrix method [14], the basic reproduction number $\mathcal{R}_0$ can be calculated from (7.2) as $\mathcal{R}_0 = \rho(FV^{-1})$ where the i, j entry of FV^{-1} is $\beta_{ij} N_i/(d+\gamma)$.

For the case that each patch has the same population (i.e., $N_i = N$) and β_{ij} are such that the endemic equilibrium values of S_i, I_i, and λ_i are independent of i, then the endemic equilibrium is given explicitly for $\mathcal{R}_0 > 1$ by

$$S_{i\infty} = S_\infty = \frac{N}{\mathcal{R}_0}, \quad I_{i\infty} = I_\infty = \frac{dN}{d+\gamma}(1 - \frac{1}{\mathcal{R}_0}), \quad R_{i\infty} = R_\infty = \frac{\gamma I_\infty}{d}, \tag{7.3}$$

with $\lambda_{i\infty} = \lambda_\infty = d(\mathcal{R}_0 - 1)$.

As an example of a symmetric situation that satisfies the above requirements, assume that $\beta_{ij} = \beta$ if $i = j$ and $\beta_{ij} = p\beta$ with $p < 1$ if $i \neq j$. Thus the contact rate is the same within each patch and has a smaller value between each pair of different patches. Then matrix $B = [\beta_{ij}] = \beta(pJ_{n\times n} + (1-p)I_{n\times n})$ where $J_{n\times n}$ is the matrix of all ones and $I_{n\times n}$ is the identity matrix. The eigenvalues of B are $\beta[pn + (1-p)]$, which is simple, and $\beta(1-p)$ with multiplicity $n-1$. Thus

$$\mathcal{R}_0 = \frac{\beta N[pn + (1-p)]}{(d+\gamma)},$$

which depends on the number of patches n and the coupling strength p.

Linearizing about the endemic equilibrium and assuming solutions are proportional to $\exp(zt)$ yields a characteristic equation that can be written in the form $\det(B - \Gamma I_{n\times n}) = 0$ with

$$\Gamma = (z + d + \lambda_\infty)\frac{(z+d+\gamma)}{(z+d)S_\infty}.$$

Thus Γ takes values that are the eigenvalues of B. The simple eigenvalue of B gives rise to the quadratic

$$z^2 + d\mathcal{R}_0 z + d(d+\gamma)(\mathcal{R}_0 - 1) = 0.$$

Following [1], the authors [9] set $d\mathcal{R}_0 = 1/A$ where A is the average age of first infection, and $1/\tau = d + \gamma \approx \gamma$ where τ is the average infective period. As $A >> \tau$, the quadratic can be approximated by

$$z^2 + z/A + 1/(A\tau) = 0,$$

which gives $z \approx -1/(2A) \pm i/\sqrt{A\tau}$. This represents a weakly damped oscillation about and towards the endemic equilibrium, with the period of oscillation shorter than the damping time. The number of individuals in each compartment in all patches oscillate in phase. The repeated eigenvalue (of multiplicity $n-1$) of B gives rise to internal modes that are strongly damped. Thus, for all but the smallest values of p, the oscillations quickly become phase locked. This result is based on a linear stability analysis, but the authors [9] believe that the endemic equilibrium is globally attracting for $\mathcal{R}_0 > 1$.

Simulation results for a two patch model ($n = 2$) for the above example are presented [9, Sect. 4]. Parameters are chosen to model measles epidemics in a population of $N_1 = N_2 = 10^6$, with $d = 0.02$ year^{-1}. The average infective period is taken as five days ($\tau = 5$) giving $\gamma = 73.0$ year^{-1}, with $\beta = 0.0010107$ year^{-1} infective^{-1}. When $p = 0$, these parameters give $\mathcal{R}_0 \approx 13.8$, with $A \approx 3.6$ years. Rapid phase locking occurs for p larger than about 0.002. For $p = 0.01$, numerical simulations show I_1 and I_2 synchronized by about five years as they approach I_∞ given by (7.3) with damped oscillations. A stochastic formulation of this SIR model is also shown numerically to give synchronization, although a slightly larger value of p is required. Assuming that the within-patch contact rate is seasonally forced, in-phase and out of phase biennial oscillations are seen with chaotic solutions possible for some parameter values (illustrated in [9, Fig. 3] with $p = 10^{-3}$). As found in other metapopulation models, with larger p values (i.e., stronger between patch coupling) the system effectively behaves more like that of a single patch.

7.3 Geographic Spread

Sattenspiel and Dietz [11] introduced a metapopulation epidemic model in which individuals are labeled with their city of residence as well as the city in which they are present at a given time. This model explicitly includes rates of travel between n patches, which can be cities or geographical regions. A susceptible-infective-recovered (SIR) model incorporating this spatial heterogeneity is formulated [11, Sect. 2], and the same spatial heterogeneity is incorporated in a susceptible- infective-susceptible (SIS) model formulated by Arino and van den Driessche [2]. The notation of [2] is used here.

To formulate the demographic model with travel, let $N_{ij}(t)$ be the number of residents of patch i who are present in patch j at a time t. Residents of patch i leave this patch at a per capita rate $g_i \geq 0$ per unit time, with a fraction $m_{ji} \geq 0$ going to patch j, thus $g_i m_{ji}$ is the travel rate from patch i to patch j. Here $m_{ii} = 0$ and $\sum_{j=1}^{n} m_{ij} = 1$. Residents of patch i who are in patch j return home to patch i with a per capita rate of $r_{ij} \geq 0$ with $r_{ii} = 0$. It is natural to assume that $g_i m_{ji} > 0$ if and only if $r_{ij} > 0$. These travel rates determine a directed graph with patches as vertices and arcs between vertices if the travel rates between them are positive. It is assumed that the travel rates are such that this directed graph is strongly connected.

Assume that birth occurs in the home patch at a per capita rate $d > 0$, and death occurs in any patch with this same rate. Then the population numbers satisfy the equations

$$N'_{ii} = \sum_{k=1}^{n} r_{ik} N_{ik} - g_i N_{ii} + d\Big(\sum_{k=1}^{n} N_{ik} - N_{ii}\Big) \tag{7.4}$$

$$N'_{ij} = g_i m_{ji} N_{ii} - r_{ij} N_{ij} - d N_{ij} \text{ for } i \neq j. \tag{7.5}$$

These equations describe the evolution of the number of residents in patch i who are currently in patch i (7.4) and those who are currently in patch $j \neq i$ (7.5). The number of residents of patch i, namely $N_i^r = \sum_{j=1}^{n} N_{ij}$ is constant, as is the total population of the n patch system. With initial conditions $N_{ij}(0) > 0$, the system (7.4)–(7.5) has an asymptotically stable equilibrium $\hat{N}_{ij}$.

An epidemic model is now formulated in each of the n patches, with $S_{ij}(t)$ and $I_{ij}(t)$ denoting the number of susceptible and infective individuals resident in patch i who are present in patch j at time t. Taking an SIS model with standard incidence [2], equations for the evolution of the number of susceptibles and infectives resident in patch i (with $i = 1, ..., n$) are

$$S'_{ii} = \sum_{k=1}^{n} r_{ik} S_{ik} - g_i S_{ii} - \sum_{k=1}^{n} \kappa_i \beta_{iki} \frac{S_{ii} I_{ki}}{N_i^p} + d\Big(\sum_{k=1}^{n} N_{ik} - S_{ii}\Big) + \gamma I_{ii} \tag{7.6}$$

$$I'_{ii} = \sum_{k=1}^{n} r_{ik} I_{ik} - g_i I_{ii} + \sum_{k=1}^{n} \kappa_i \beta_{iki} \frac{S_{ii} I_{ki}}{N_i^p} - (\gamma + d) I_{ii} \tag{7.7}$$

and for $j \neq i$

$$S'_{ij} = g_i m_{ji} S_{ii} - r_{ij} S_{ij} - \sum_{k=1}^{n} \kappa_j \beta_{ikj} \frac{S_{ij} I_{kj}}{N_j^p} - d S_{ij} + \gamma I_{ij} \tag{7.8}$$

$$I'_{ij} = g_i m_{ji} I_{ii} - r_{ij} I_{ij} + \sum_{k=1}^{n} \kappa_j \beta_{ikj} \frac{S_{ij} I_{kj}}{N_j^p} - (\gamma + d) I_{ij} \tag{7.9}$$

with $N_i^p = \sum_{j=1}^n N_{ji}$, the number present in patch i. Here $\beta_{ikj} > 0$ is the proportion of adequate contacts in patch j between a susceptible from patch i and an infective from patch k that results in disease transmission, $\kappa_j > 0$ is the average number of such contacts in patch j per unit time, and $\gamma > 0$ is the recovery rate of infectives (assumed the same in each patch). Note that the disease is assumed to be sufficiently mild so that it does not cause death and does not inhibit travel, and individuals do not change disease status during travel. Equations (7.6)–(7.9) together with nonnegative initial conditions constitute the SIS metapopulation model. It can be shown that the nonnegative orthant $R_+^{2n^2}$ is positively invariant under the flow and solutions are bounded.

The disease-free equilibrium is given by $S_{ij} = \hat{N}_{ij}, I_{ij} = 0$ for all $i, j = 1, ..., n$. If the system is at an equilibrium and one patch is at the disease-free equilibrium, then all patches are at the disease-free equilibrium; whereas if one patch is at an endemic disease level, then all patches are at an endemic level. These results hold based on the assumption that the directed graph determined by the travel rates is strongly connected. If this is not the case, then the results apply to patches within a strongly connected component.

For the n-patch connected model, the next generation matrix [6,14] can be determined from (7.7) and (7.9), leading to a formula for the basic reproduction number $\mathcal{R}_0$. To keep the notation simple, the formula for $n = 2$ patches is explicitly given here, thus $m_{12} = m_{21} = 1$, and g_1, g_2, r_{12}, r_{21} are assumed positive. For the general n case see [2, page 185]. Ordering the infective variables as $I_{11}, I_{12}, I_{21}, I_{22}$, the matrix of new infections at the disease-free equilibrium F is a block matrix with 4 blocks, in which each block F_{ij} is the 2×2 diagonal matrix

$$F_{ij} = diag\Big(\kappa_1 \beta_{ij1} \frac{\hat{N}_{i1}}{\hat{N}_1^p}, \quad \kappa_2 \beta_{ij2} \frac{\hat{N}_{i2}}{\hat{N}_2^p}\Big).$$

Matrix V, accounting for transfer between infective compartments, can be written as $V = V_1 \oplus V_2$, where $\oplus$ denotes the direct sum, and

$$V_1 = \begin{bmatrix} g_1 + \gamma + d & -r_{12} \\ -g_1 & r_{12} + \gamma + d \end{bmatrix}, \qquad V_2 = \begin{bmatrix} r_{21} + \gamma + d & -g_2 \\ -r_{21} & g_2 + \gamma + d \end{bmatrix}.$$

Matrices V_1 and V_2 are irreducible nonsingular M-matrices (for definition and properties of M-matrices see [4]) thus their inverses are positive, and $V^{-1} = V_1^{-1} \oplus V_2^{-1}$. Using these blocks, $\mathcal{R}_0$ can easily be computed for a given set of parameter values as $\mathcal{R}_0 = \rho(FV^{-1})$, where ρ denotes the spectral radius. For n patches, a similar formula is obtained, with FV^{-1} being an $n^2 \times n^2$ positive matrix. It is apparent that $\mathcal{R}_0$ depends on the travel rates as well as the epidemic parameters. If $\mathcal{R}_0 < 1$, then the disease-free equilibrium is locally asymptotically stable; whereas if $\mathcal{R}_0 > 1$, then it is unstable.

Assume that the disease transmission coefficients are equal for all populations present in a patch, i.e., $\beta_{ijk} = \beta_k$ for $i, j = 1, ..., n$. With this assumption, the following bounds can be found for $\mathcal{R}_0$ for n patches:

$$\min_{i=1,...,n} \mathcal{R}_0^{(i)} \leq \mathcal{R}_0 \leq \max_{i=1,...,n} \mathcal{R}_0^{(i)} \tag{7.10}$$

where $\mathcal{R}_0^{(i)} = \kappa_i \beta_i / (d + \gamma)$ is the basic reproduction number of patch i in isolation. Thus if $\mathcal{R}_0^{(i)} < 1$ for all i, the disease dies out; whereas if $\mathcal{R}_0^{(i)} > 1$ for all i, then the disease-free equilibrium is unstable.

Numerical simulations presented in [2] with $n = 3$ patches show that (for parameter values relevant for gonorrhea) when $\mathcal{R}_0 > 1$, the number of infectives in each subpopulation goes to an endemic value. Further numerical investigations for $n = 2$ patches focus on a case in which in isolation the disease would be absent in patch 1 but endemic in patch 2 (i.e., $\mathcal{R}_0^{(1)} < 1$, $\mathcal{R}_0^{(2)} > 1$). The bounds in (7.10) give $\mathcal{R}_0 \in [\mathcal{R}_0^{(1)}, \mathcal{R}_0^{(2)}]$. Parameter values are chosen to be relevant for a disease like gonorrhea: $\gamma = 1/25$, $d = 1/(75 \times 365)$ with the time unit of one day. Suppose that $N_1^r = N_2^r = 1500$, $\kappa_1 = \kappa_2 = 1$, $r_{12} = r_{21} = 0.05$, $\beta_1 = 0.016$ giving $\mathcal{R}_0^{(1)} = 0.4$, and $\beta_2 = 0.048$ giving $\mathcal{R}_0^{(2)} = 1.2$. A change in travel rates g_1, g_2 can induce a bifurcation from $\mathcal{R}_0 < 1$ to $\mathcal{R}_0 > 1$ or vice versa, see [2, Fig. 3a]. Another view of this case is presented in Fig. 7.1 in which $g_1 = g_2$ and $\mathcal{R}_0$ is plotted as a function of $g_1 = g_2$, with $\mathcal{R}_0 = 1$ shown as a broken horizontal line. Thus travel can stabilize (small travel rates) or destabilize (larger travel rates) the disease-free equilibrium. These numerical results support the claim that for $\mathcal{R}_0 > 1$, the endemic equilibrium is unique and that $\mathcal{R}_0$ acts as a sharp threshold between extinction and invasion of the disease.

Similar conclusions are drawn for the more general SEIRS model [3], for which an explicit formula for $\mathcal{R}_0$ is derived. Sattenspiel and Dietz [11] suggested an application of their metapopulation SIR model to the spread of measles in the 1984 epidemic in Dominica. Travel rates of infants, school-age children and adults are assumed to be different, thus making the model system highly complex and requiring knowledge of more data for simulation. Sattenspiel and coworkers; see [10] and references therein, have since used this modeling approach for studying other infectious diseases in the historical archives; one such example is discussed further in the next section.

7.4 Effect of Quarantine on Spread of 1918–1919 Influenza in Central Canada

Work by Sattenspiel and Herring focuses on the spread of the 1918–1919 influenza epidemic in three communities in central Manitoba, Canada. The effect of quarantine on the spread of this epidemic is discussed by Sattenspiel

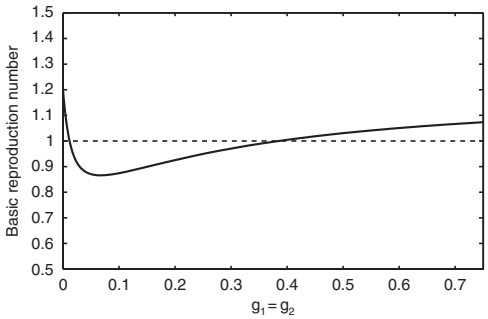

Fig. 7.1 The basic reproduction number as a function of travel rates for the two patch model. For parameter values, see text. Figure by Mahin Salmani

and Herring [12], which is a good source of references to their work. The three communities, all of which are former Hudson's Bay Company fur trade posts, are Norway House (population 746), Oxford House (population 322) and God's Lake (population 299). Many of the inhabitants were fur trappers and Norway House was on a main trading route. Oxford House was in direct contact with Norway House, and God's Lake was connected to the other posts by less travelled routes.

The influenza epidemic occurred in this region during the late fall of 1918 and the following winter. There were 107 deaths among residents of Norway House in a period of a year beginning in July 1918, with most of these probably from influenza. The time taken in winter to travel between Norway House and Oxford House was six days, a factor that slowed the spread of the disease, especially since influenza has a period of communicability of 3–5 days from clinical onset in adults [5, page 272]. Sattenspiel and Herring [12] used a fascinating mix of mathematical modeling and estimation of model parameters, both epidemiological parameters for influenza and anthropological parameters relating to population numbers and travel, to investigate the impact of attempts to limit travel during this influenza epidemic. Norway House was quarantined during December 1918 and January 1919, and this control measure is investigated. Quarantining here means the limit of travel of any individual regardless of disease status. The SIR model formulated for n patches [12, Sect. 3] is similar to the SIS model described in Sect. 7.3

above, except that birth and death are ignored (i.e., $d = 0$). Using the notation of Sect. 7.3, and letting $R_{ij}(t)$ denote the number of recovered individuals resident in patch i who are present in patch j at time t, the system of equations for individuals residing in patch i (with $i = 1, ...n$) is

$$\begin{aligned}
S'_{ii} &= \sum_{k=1}^{n} r_{ik} S_{ik} - g_i S_{ii} - \sum_{k=1}^{n} \kappa_i \beta_{iki} \frac{S_{ii} I_{ki}}{N_i^p} \\
I'_{ii} &= \sum_{k=1}^{n} r_{ik} I_{ik} - g_i I_{ii} + \sum_{k=1}^{n} \kappa_i \beta_{iki} \frac{S_{ii} I_{ki}}{N_i^p} - \gamma I_{ii} \\
R'_{ii} &= \sum_{k=1}^{n} r_{ik} R_{ik} - g_i R_{ii} + \gamma I_{ii}
\end{aligned}$$

and for $j \neq i$

$$\begin{aligned}
S'_{ij} &= g_i m_{ji} S_{ii} - r_{ij} S_{ij} - \sum_{k=1}^{n} \kappa_j \beta_{ikj} \frac{S_{ij} I_{kj}}{N_j^p} \\
I'_{ij} &= g_i m_{ji} I_{ii} - r_{ij} I_{ij} + \sum_{k=1}^{n} \kappa_j \beta_{ikj} \frac{S_{ij} I_{kj}}{N_j^p} - \gamma I_{ij} \\
R'_{ij} &= g_i m_{ji} R_{ii} - r_{ij} R_{ij} + \gamma I_{ij}.
\end{aligned}$$

The basic reproduction number $\mathcal{R}_0$ is calculated as in Sect. 5.3 with $d = 0$.

Quarantine is incorporated by adjusting the rates of travel between patches, thus g_i and r_{ij} are multiplied by a factor q_i when patch i is quarantined. The parameter q_i lies in the range $0 < q_i < 1$, where 1 would correspond to no quarantine and 0 would correspond to perfect quarantine. The quarantine (control) reproduction number is calculated as for $\mathcal{R}_0$, but including the factor q_i.

Sattenspiel and Herring [12, Sect. 4] estimated model parameters needed for the above system with $n = 3$, for Norway House (NH), Oxford House (OH) and God's Lake (GL). They set $\gamma = 0.2$ (average influenza infective period 5 days), $\beta_{ikj} = \beta = 0.5$ (50% of all contacts result in infection) for all communities, and $\kappa_{NH} = 1$, $\kappa_{OH} = \kappa_{GL} = 0.5$ (twice as many contacts at NH). Estimates of g_i, m_{ji} and r_{ij} were made from records kept by the Hudson Bay Company of arrivals at and departures from each community, and population numbers were determined from census data. Quarantine at NH was incorporated by multiplying g_{NH}, $r_{NH,OH}$ and $r_{NH,GL}$ by a factor q_{NH}.

Simulation results of the above system [12, Sect. 5] show that quarantine causes a slight delay in the arrival of the epidemic peak, with an increase in the peak number of infectives at NH and a decrease in those at OH and GL. Quarantine is found to be most effective if started well before an epidemic peaks, but not right at the start of an epidemic. However, starting

quarantining after an epidemic peaks, has little effect. The authors [12] conclude that when travel rates are low (as between these communities), quarantine must be highly effective before it significantly alters disease patterns.

7.5 Tuberculosis in Possums

An SEI metapopulation model for the spread of bovine tuberculosis (*Mycobacterium bovis*) in the common brushtail possum (*Trichosurus vulpecula*) in New Zealand is formulated and analyzed by Fulford et al. [7]. This is now described very briefly to demonstrate the use of a complex metapopulation model; please consult the original paper for full details.

Tuberculosis has a significant latent period and is a fatal disease in possums, thus an SEI model is appropriate. A two-age class model is formulated with juveniles and adults, with susceptible and exposed (but not infective) juveniles migrating as they mature (1 to 2 years old). In addition pseudovertical transmission is included, accounting for disease transmission between mothers to young in their pouch. For n patches, a system of $6n$ equations describes the dynamics. For a two patch model ($n = 2$), the authors determine the disease-free equilibrium numerically, provide a methodology for computing $\mathcal{R}_0$ by using the next generation matrix [6], and show how this can be generalized to n patches.

Parameters appropriate for tuberculosis in possums are taken for simulations and for a two patch model prevalence shows damped oscillations towards an endemic state with $\mathcal{R}_0 \in [1.55, 1.67]$. Possums are thought to spread tuberculosis to farmland, thus the model is applied to evaluate control (culling) strategies to reduce the control reproduction number below one [7, Sect. 6]. Several spatial configurations are considered and critical culling rates (giving the control reproduction number equal to one) are calculated.

7.6 Concluding Remarks

The metapopulation models discussed in the previous sections demonstrate that such spatial models are usually high dimensional and contain many parameters. However, extended models can be formulated, including biological realism such as age structure and control measures such as restriction of travel. Using the next generation matrix, the basic reproduction number $\mathcal{R}_0$ can be computed for estimated parameters. Simulations can easily be performed with parameters relevant for a particular disease with given demography and spatial structure. These models assume that the population of each patch is sufficiently large so that a deterministic model is appropriate and there is homogeneous mixing within each patch. As noted in [12],

stochastic effects may be significant when patch populations are small, such as in the three communities modeled by [12] and discussed in Sect. 7.4 above.

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