Mathematical Biosciences Institute Lecture Series 1.3
Stochastics in Biological Systems

Linda J. S. Allen

Stochastic Population and Epidemic Models

Persistence and Extinction

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Stochasticity is fundamental to biological systems. In some situations the system can be treated as a large number of similar agents interacting in a homogeneously mixing environment, and so the dynamics are well-captured by deterministic ordinary differential equations. However, in many situations, the system can be driven by a small number of agents or strongly influenced by an environment fluctuating in space and time. For example, fluctuations are critical in the early stages of an epidemic; a small number of molecules may determine the direction of cellular processes; changing climate may alter the balance among competing populations. Spatial models may be required when agents are distributed in space and interactions between agents are local. Systems can evolve to become more robust or co-evolve in response to competitive or host-pathogen interactions. Consequently, models must allow agents to change and interact in complex ways. Stochasticity increases the complexity of models in some ways, but may also simplify and smooth results in other ways.

Volume 1 provides a series of lectures by internationally well-known authors based on the year on Stochastics in Biological Systems which took place at the MBI in 2011–2012.

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Mathematical Biosciences Institute Lecture Series
Volume 1: Stochastics in Biological Systems

Stochastic Population and Epidemic Models
Linda J. S. Allen

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Preface

The intent of this monograph is to introduce graduate students to branching process applications of populations and epidemics. Deterministic models of populations and epidemics are well known in the scientific literature and they provide useful information on the dynamics when population and epidemic sizes are large. However, when sizes are not large, stochastic models and theory are required, for example, to estimate the probability of extinction. The stochastic theory of branching processes has a long history and can be used as a tool in understanding extinction in many situations. In the mid 19th century, Galton and Watson introduced branching processes to explain the extinction of family names. Whittle applied the theory in 1955 to an SIR epidemic to estimate the probability of a major outbreak. In this brief monograph, a summary is presented of single-type and multi-type branching process theory. This theory is used to estimate the probability of ultimate extinction in some classic population and epidemic models such as SEIR epidemic and logistic growth, and some new applications of species invasions and spatial spread of disease. Some MatLaB programs of stochastic simulations are provided in the Appendix, and some references are given to additional applications of branching processes to populations and epidemics.

I thank Rick Durrett and Mike Reed for the invitation to develop these lecture notes as part of the Mathematical Biosciences Institute Graduate Lecture Series, Volume 1: Stochastics in Biological Systems. In addition, I thank Edward Allen, Texas Tech University, who provided valuable feedback on Chapter 4, and an anonymous reviewer who provided suggestions and corrections on Chapters 1–4. I especially thank the editorial and production staff at Springer.

Lubbock, TX, USA Linda J.S. Allen

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Continuous-Time and Discrete-State Branching Processes

1.1 Introduction

The study of branching processes began in the mid 19th century with the work of Bienaymé, Galton, and Watson [10, 23, 39]. Galton and Watson's original problem was to study the extinction of family surnames. They formalized the problem using probability generating functions. This first application employed discrete-time branching processes. Continuous-time branching process theory is closely related to discrete-time theory. In this chapter, we summarize the basic theory for continuous-time and discrete-state branching processes for single-type and multi-type processes. This theory is used to estimate population extinction (absorption) in two examples, a birth-death model and a birth-death-dispersal model. In later chapters, the branching process theory, developed in this chapter, is applied to some classic population and epidemic models to predict species invasions or outbreaks in more complex settings. Further mathematical details about the theory and additional biological examples can be found in the references (e.g., [7, 14, 20, 23, 24, 32]).

1.2 Single-Type Branching Processes

Let $\{X(t)|t \in [0,\infty)\}$ be a collection of a discrete random variables that takes values in the set of nonnegative integers $\{0,1,2,\ldots\}$ and has the Markov property. The Markov assumption makes the time between events exponentially distributed. The process is a continuous-time Markov chain (CTMC). Assume for simplicity that the process is time-homogeneous. Let $p_{ij}(\Delta t)$ denote a transition probability from state i to state j during a time period Δt:

$$p_{ij}(\Delta t) = \mathbb{P}(X(t+\Delta t) = j|X(t) = i\}.$$

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The process is assumed to be nonexplosive, that is, sample paths do not approach infinity for finite time t. The state space can consist of number of animals, plants, cells, genes, etc., and therefore, we refer to the elements as the number of "individuals."

A continuous-time branching process puts restrictions on the birth and death process. Four important assumptions distinguish a continuous-time branching process from other CTMCs.

(i) For any time $t > 0$, each individual gives "birth" to Y "offspring" of the same type. The random variable Y is discrete with values in the set $\{0,1,2\ldots\}$. Probabilities associated with Y are

$$p_j = \mathbb{P}\{Y = j\}, \quad j = 0,1,2,\ldots.$$

(ii) Each individual gives birth independently of all other individuals.
(iii) The same birth probabilities apply to all individuals, referred to as a "single-type process," meaning all individuals are of the same type.
(iv) The transition probabilities satisfy

$$\sum_{j=0}^{\infty} p_{ij}(t)s^j = \left(\sum_{j=0}^{\infty} p_{1j}(t)s^j\right)^i, \quad s \in [0,1]. \tag{1.1}$$

The terms birth and offspring in assumption (i) are used in a general sense. For example, in an epidemic outbreak, the number of infected individuals represents the states of the branching process and a birth means a new infection and offspring means the number of new infections produced. Also, in assumptions (i)–(iv), there is no mention of death. Generally, in branching processes, the birth of offspring implies death of the parent. That is, the parent is replaced by the offspring. In the continuous-time process, the birth of offspring may or may not be accompanied by the death of the parent. If the parent gives birth to j offspring, then dies, the number of new offspring is j with corresponding probability p_j. However, if the parent gives birth to j offspring and survives, then the number of new offspring, counting the surviving parent, is $j+1$ with corresponding probability p_{j+1}. This latter assumption can be thought of as a death of the parent and replacement by an "identical substitute" [14]. Such an assumption is reasonable in an epidemic outbreak, where the infected parent continues to spread infection until death or recovery.

The mathematical assumption (iv) implies that the process is additive. That is, the process beginning from state $X(0) = i$ is equivalent to the sum of i independent processes beginning from state $X(0) = 1$. The identity in (iv) means if $X(0) = \sum_{l=1}^{i} X_l(0)$ where $X_l(0) = 1$, then the probability generating function (pgf) of $X(t)$ satisfies

$$\mathscr{P}(s,t) = \mathbb{E}\left(s^{X(t)}\right) = \prod_{l=1}^{i} \mathbb{E}\left(s^{X_l(t)}\right).$$

Therefore, there is no loss of generality to assume $X(0) = 1$.

An additional assumption is made in regard to the offspring probabilities:

$$0 < p_0 < 1. \tag{1.2}$$

Assumption (1.2) implies there is a positive probability of extinction at each generation $p_0 > 0$ and that there is at least one offspring, $p_j > 0$ for some $j \geq 1$. The zero state (extinction) is an absorbing state of the Markov chain: $X(\tau) = 0$ implies $X(t+\tau) = 0$ for $t > 0$.

Let $\lambda > 0$ denote the parameter in the exponential distribution for the lifetime of one individual, i.e., $\lambda e^{-\lambda t}$ is the probability density function. In particular,

$$p_{ij}(\Delta t) = \begin{cases} \lambda i p_{j-i+1}\Delta t + o(\Delta t), & j \geq i-1, j \neq i \\ 1 - \lambda i \Delta t + o(\Delta t), & j = i \\ o(\Delta t), & j < i-1. \end{cases}$$

The transition probabilities associated with $X(t)$ satisfy the following forward and backward Kolmogorov differential equations, respectively,

$$\frac{dp_{ji}(t)}{dt} = -\lambda i p_{ji}(t) + \lambda \sum_{k=1}^{i+1} k p_{jk}(t) p_{i-k+1} \tag{1.3}$$

$$\frac{dp_{ij}(t)}{dt} = -\lambda i p_{ij}(t) + \lambda i \sum_{k=i-1}^{\infty} p_{kj}(t) p_{k-i+1} \tag{1.4}$$

with initial conditions for both equations given by $p_{ij}(0) = \delta_{ij}$, where $\delta_{ij} = 0$, $i \neq j$, and $\delta_{ii} = 1$. The terms in the summation in (1.3) represent the probability of a transition from state j to state k in time t followed by a jump from state k to state i at rate $\lambda k p_{i-k+1}$. The terms in the summation in (1.4) represent a jump from state i to state k at rate $\lambda i p_{k-i+1}$ followed by a transition from state k to state j in time t.

Let $f(s)$ denote the probability generating function (pgf) of the offspring random variable Y, i.e.,

$$f(s) = \sum_{j=0}^{\infty} p_j s^j, \quad s \in [0,1].$$

We assume that f is well defined, continuous, and differentiable on $[0,1]$, with $f(0) > 0$ and $f(1) = 1$. Several properties of the pgf are $f(0) = p_0$, $f(1) = 1$ and

$$f'(1) = \sum_{j=0}^{\infty} j p_j$$

is the mean number of offspring.

Let $\mathscr{P}(s,t)$ denote the pgf of $X(t)$. Formally, $\mathscr{P}(s,t) = \mathbb{E}(s^{X(t)})$. Expressed in terms of the transition probabilities,

$$\mathscr{P}(s,t) = \sum_{j=0}^{\infty} p_{1j}(t) s^j, \quad t \in [0,\infty), \quad s \in [0,1],$$

where $\mathscr{P}(s,0) = s$, and $X(0) = 1$.

From assumption (iv), it can be shown that the pgf $\mathscr{P}(s,t)$ is a solution of the backward equations (1.4). Since $X(0)=1$, let $i=1$. Multiplying the backward equations (1.4) by s^j, summing from $j=0$ to ∞ and interchanging summations on the second term, leads to

$$\frac{d[\sum_{j=0}^{\infty} p_{1j}(t)]}{dt} = -\lambda \sum_{j=0}^{\infty} p_{1j}(t)s^j + \lambda \sum_{k=0}^{\infty} p_k \sum_{j=0}^{\infty} p_{kj}(t)s^j.$$

Applying property (iv) to the last term in the preceding equation yields the following expression for the double sum:

$$\sum_k p_k [\mathscr{P}(s,t)]^k = f(\mathscr{P}(s,t)).$$

Thus, the backward Kolmogorov differential equations lead to the following differential equation for the pgf $\mathscr{P}(s,t)$, given $X(0)=1$,

$$\frac{\partial \mathscr{P}(s,t)}{\partial t} = -\lambda [\mathscr{P}(s,t) - f(\mathscr{P}(s,t))] \tag{1.5}$$

with initial condition $\mathscr{P}(s,0)=s$. For our purposes, it is important to note that the probability of extinction, $\mathscr{P}(0,t)=p_{j0}(t)=q(t)$, also satisfies the differential equation (1.5). That is,

$$\frac{dq(t)}{dt} = -\lambda[q(t)-f(q(t))] = F(q(t)), \;\; q(0)=0. \tag{1.6}$$

The differential equation for $q(t)=p_{j0}(t)$ can also be derived directly from the backward equation (1.4).

Our goal is to compute the **probability of ultimate extinction**,

$$\lim_{t\to\infty} \mathbb{P}(X(t)=0|X(0)=1) = q^*.$$

A simple proof verifies that the probability q^* is the minimal fixed point of f on $[0,1]$; a solution of

$$f(s)=s, \;\; s\in(0,1].$$

In fact, it can also be verified that q^* is the unique fixed point on $(0,1)$ if $f'(1)>1$ [3, 20].

Theorem 1.1. *The probability of ultimate extinction of $X(t)$ given $X(0)=1$ is the smallest fixed point q^* of the offspring pgf f on $(0,1]$.*

Proof. Since the differential equation (1.6) is autonomous, $F(q)=-\lambda[q-f(q)]$ and the solution q is bounded, $q\in[0,1]$ ($F(0)=\lambda f(0)>0$ and $F(1)=-\lambda[1-f(1)]=0$), the asymptotic dynamics of $q(t)$ as a function of t are determined by a phase line diagram (Figure 1.1). That is, the dynamics of $q(t)$ are determined by the graph of $F(q)$ and whether the direction of flow is increasing or decreasing along

the q axis. Since $q(0) = 0$ and $F(0) > 0$, $q(t)$ is increasing. The limiting value of $q(t)$ as $t \to \infty$ is the minimal stationary solution of $F(q) = 0$ on $(0, 1]$ or equivalently, the minimal fixed point of f on $(0, 1]$. □

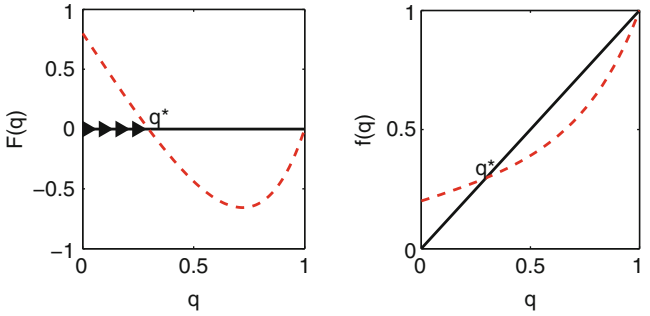

Fig. 1.1 Phase line diagram of the dynamics of q with graph of $F(q)$ and the graph of $f(q)$ showing the fixed point q^*.

As can be seen from the graph of f in Figure 1.1, $f(0) = p_0 > 1$, $f(1) = 1$, and f is increasing and convex. A fixed point other than one exists if the mean number of offspring is greater than one, $f'(1) > 1$. If $f'(1) \leq 1$, then the only fixed point of f on $(0, 1]$ is one, so that $q^* = 1$. In general, if $f'(1) < 1$, the branching process is said to be **subcritical**, if $f'(1) = 1$, it is **critical**, and if $f'(1) > 1$, it is **supercritical**. As a consequence of the branching process assumptions, if $X(0) = i$, the probability of extinction is $(q^*)^i$ and probability of persistence is $1 - (q^*)^i$. We summarize this latter result in the following corollary.

Corollary 1.1. *The probability of ultimate extinction of the branching process $X(t)$ given $X(0) = i$ is $(q^*)^i$, where q^* is the smallest fixed point of f on $(0, 1]$.*

The two properties from branching process theory, extinction with probability $(q^*)^i$ and persistence with probability $1 - (q^*)^i$, are applied to other CTMC processes, where the branching process provides a good approximation when the population or epidemic sizes are small so that assumptions (i)–(iii) are biologically reasonable.

1.2.1 Birth-Death

A simple birth and death process is a single-type branching process, a Markov chain model with linear transition rates. The transition probabilities for a simple birth and death process define the probability of a birth or a death in a short period of time Δt:

$$p_{ij}(\Delta t) = \begin{cases} bi\Delta t + o(\Delta t), & j = i+1 \\ di\Delta t + o(\Delta t), & j = i-1 \\ 1-(bi+di)\Delta t + o(\Delta t), & j = i \\ o(\Delta t), & j \neq i-1, i, i+1. \end{cases} \tag{1.7}$$

The parameter λ, defined in the previous section, for the exponential distribution of the lifetime of an individual is $\lambda = b + d$.

The analogous deterministic model for a simple birth and death process is exponential growth, which can be expressed as the differential equation,

$$\frac{dn(t)}{dt} = (b-d)n(t), \;\; n(0) = n_0$$

with solution $n(t) = n_0 \exp((b-d)t)$. The deterministic solution only provides information about the expected population size of the Markov chain model [3]. If $b < d$, the expected population size approaches zero, extinction, which agrees with the behavior of the Markov chain model; the probability of extinction is one. However, if $b > d$, the expected population size approaches infinity, but as demonstrated below, there is still a positive probability of extinction in the Markov chain model due to the variability in the stochastic process.

Two methods for formulating the offspring pgfs for a stochastic simple birth and death process are discussed by Dorman et al. [14]. These methods are referred to as the budding model and the bursting model. In the budding model, an individual "dies and is replaced by an identical substitute" but in the bursting model, the individual "collects its offspring and holds them for release until death." In the first case, the parent reproduces offspring and survives and in the second case, the parent reproduces offspring and dies.

In the first method, p_0 is the probability of dying and p_i, $i = 2, 3, \ldots$ is the probability of giving birth to $i-1$ individuals with the parent being included as part of the new offspring [14]. Given the assumptions concerning the transition probabilities, the probability of death is $d/(b+d)$. Also, the probability of reproduction of one offspring is $b/(b+d)$ but with survival of the parent (an identical substitute), there are two offspring. These assumptions agree with the transition probabilities in (1.7). Such types of models are applicable to cell reproduction, where cell division results in two identical daughter cells [24]. The budding model is also reasonable for epidemic outbreaks when an infectious individual passes infection to another individual but remains infectious. To formulate the branching process, we assume that each individual has the same probabilities of a birth or a death (assumption (iii)). Therefore, the offspring pgf has the following form:

$$f(s) = \frac{d}{b+d} + \frac{b}{b+d}s^2. \tag{1.8}$$

The probability of more than two offspring or one offspring is zero, $p_j = 0$ for $j = 1$ and $j > 2$. The mean number of offspring is $f'(1) = 2b/(b+d)$. The condition for

supercriticality, $f'(1) > 1$, is equivalent to $2b/(b+d) > 1$ or $b > d$. The fixed point of f or probability of extinction can be easily shown to be equal to

$$q^* = \begin{cases} \frac{d}{b}, & b > d \\ 1, & b \leq d. \end{cases} \tag{1.9}$$

The transition probabilities in (1.7) correspond to the budding model assumptions, where $\lambda = b+d$ is the parameter in the lifetime distribution.

Alternately, in the second method, if we assume a parent individual dies at the same time as giving birth, we assume a geometric birth function to ensure the Markov property is preserved [14]. The offspring pgf has the form:

$$f(s) = \frac{d}{b+d} \sum_{j=0}^{\infty} \left(\frac{bs}{b+d} \right)^j = \frac{d}{d+b(1-s)}. \tag{1.10}$$

An individual dies with no offspring with probability $p_0 = d/(b+d)$ or has one offspring then dies with probability $p_1 = db/(b+d)^2$ or has 2 offspring then dies with probability $p_2 = db^2/(b+d)^3$, etc. The parent holds the offspring until its death and releases them in one big burst [14]. The value of $f'(1) = b/d$ is the mean number of births during the lifetime of an individual. The lifetime distribution for the bursting model differs from the budding model (1.8). The parameter $\lambda = d$ in the bursting model but $\lambda = b+d$ in the budding model. It is interesting that although the assumptions are different in the budding and bursting model, the fixed point of (1.10) is the same as for (1.8). The probability of ultimate extinction, given the initial population size $X(0) = n_0$, is

$$\mathbb{P}_0(n_0) = (d/b)^{n_0}.$$

Four sample paths of the CTMC applying the transition probabilities in (1.7) are graphed in Figure 1.2. The MatLaB program that generated the four sample paths is given in Appendix A.1. It is clear that the graphs of the sample paths provide a more realistic picture of the growth of a population when population sizes are small than the deterministic solution.

1.3 Multi-Type Branching Processes

In a multi-type branching process, there are n different types, such as n stages. Let $\mathbf{X}(t) = (X_1(t), \ldots, X_n(t))$ be a discrete random vector of the n types. The discrete random variable $X_i(t)$ represents the ith type which has the Markov property and takes values in the set $\{0, 1, 2, \ldots\}$. The transition probabilities for the multi-type process are

$$p_{\mathbf{j},\mathbf{i}}(\Delta t) = \mathbb{P}(\mathbf{X}(t+\Delta t) = \mathbf{i} | \mathbf{X}(t) = \mathbf{j}).$$

The zero state (extinction) is an absorbing state.

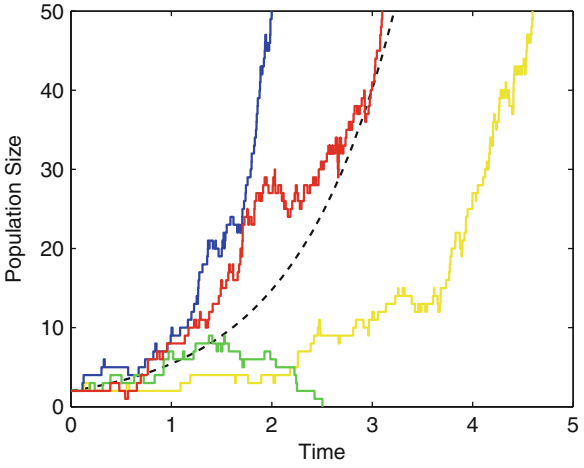

Fig. 1.2 The exponential solution (black dashed curve) and four sample paths of the branching process for parameter values $b = 2$, $d = 1$, and $n_0 = 2$. The probability of extinction is $\mathbb{P}_0(2) = (0.5)^2 = 0.25$.

Similar assumptions (i)–(iv) apply to each of the i types. Let Y_{ik} denote the discrete random variable for the number of offspring of type k from a "parent" of type i. Let $\mathbb{P}_i(\mathbf{k}) = \mathbb{P}(Y_{i1} = k_1, Y_{i2} = k_2, \ldots, Y_{in} = k_n)$, where $k_j \in \{0, 1, \ldots\}$, $j = 1, \ldots, n$ be the probability parent type i has k_1 offspring of type 1, k_2 offspring of type 2, etc. Each individual of type i gives birth independently of others and has the same offspring probabilities for all time. We assume $X_i(0) = 1$ and $X_j(0) = 0$ for $j \neq i$ in defining the ith offspring pgf:

$$f_i(\mathbf{s}) = \sum_{\mathbf{k}} \mathbb{P}_i(\mathbf{k})\mathbf{s}^{\mathbf{k}} = \sum_{k_1=0}^{\infty} \cdots \sum_{k_n=1}^{\infty} \mathbb{P}_i(k_1, \ldots, k_n) s_1^{k_1} \cdots s_n^{k_n}$$

for $i = 1, \ldots, n$. An assumption similar to (1.2) is required to ensure that the asymptotic probability of extinction can be computed. Assume that not all of the functions f_i satisfy: $f_i(\mathbf{0}) = 0$ and f_i is a linear function of the s_j (known as simple functions). That is, not all of the pgfs are simple functions. If, for example, all of the pgfs $f_i(\mathbf{0}) = 0$, then the probability of extinction is zero.

Because of the Markov property, the time between events for type i has an exponential distribution with parameter λ_i. Forward and backward Kolmogorov differential equations can be written in terms of the transition probabilities for the multi-type process. Let $\mathscr{P}(\mathbf{s}, t) = (\mathscr{P}_1(\mathbf{s}, t), \ldots, \mathscr{P}_n(\mathbf{s}, t))$ denote the vector of pgfs for $\mathbf{X}(t)$, where formally, $\mathscr{P}(\mathbf{s}, t) = \mathbb{E}(\mathbf{s}^{\mathbf{X}(t)})$. Each $\mathscr{P}_i$ is a solution of the backward differential equation,

$$\frac{\partial \mathscr{P}_i(\mathbf{s}, t)}{\partial t} = -\lambda_i[\mathscr{P}_i(\mathbf{s}, t) - f_i(\mathscr{P}(\mathbf{s}, t))], \quad i = 1, \ldots, n,$$

with $\mathscr{P}_i(\mathbf{s},0) = s_i$. Also, as in the case of the single-type branching process, the probability of extinction by time t, $\mathbf{q}(t) = (q_1(t),\ldots,q_n(t))$ for the multi-type process is a solution of the backward differential equations:

$$\frac{dq_i(t)}{dt} = -\lambda_i[q_i(t) - f_i(\mathbf{q}(t))] = F_i(\mathbf{q}(t)), \;\; q_i(0) = 0, \;\; i = 1,\ldots,n. \tag{1.11}$$

The main difference between the probability of extinction for the multi-type case and the single-type case is that there is a vector $\mathbf{q}^*$ of probabilities that determine extinction. The vector $\mathbf{q}^*$ is the large time limit of $\mathbf{q}(t)$.

The mean number of offspring of type k from a parent of type i is computed from the partial derivative of f_i evaluated when the s_j are all equal to one: $\partial f_i/\partial s_j|\mathbf{s} = \mathbf{1}$. The $n \times n$ matrix

$$M = [\partial f_i/\partial s_j]|_{\mathbf{s}=\mathbf{1}}$$

is called the expectation matrix. We make the additional assumption that M is irreducible. The matrix M is the multi-type generalization of $f'(1)$. Matrix $J = \Lambda[M-I]$ is the Jacobian matrix of system (1.11) evaluated when the s_j equal one, where $\Lambda = \text{diag}(\lambda_1,\ldots,\lambda_n)$ and I is the $n \times n$ identity matrix. The spectral abscissa of J, denoted $s(J)$ (maximum real part of the eigenvalues of J), determines whether the multi-type process is subcritical, $s(J) < 0$, critical, $s(J) = 0$ or supercritical $s(J) > 0$. Alternately, criticality can be expressed in terms of the spectral radius of M, denoted $\rho(M)$ (maximum absolute value of the eigenvalues of M) [6]. That is,

$$s(J) < 0\,(=0,\,>0) \;\text{ if and only if }\; \rho(M) < 1\,(=1,\,>1).$$

The analogous theorem for the multi-type process on probability of extinction is stated below without proof. The proof in the case that matrix M is regular (M^k is a positive matrix for some positive integer k) is verified by Harris [20] and in the case that M is irreducible and the pgfs are not all simple is summarized in Pénisson [32].

Theorem 1.2. *The probability of ultimate extinction of the continuous-time branching process* $\mathbf{X}(t)$ *given* $X_i(0) = 1$ *and* $X_j(0) = 0$, $j \neq i$ *is the smallest fixed point* $\mathbf{q} = (q_1^*,\ldots,q_n^*)$ *of the system of pgfs* f_i, *where* $q_i^* \in [0,1]$. *The probability of ultimate extinction for* $\mathbf{X}(t)$ *given* $X_i(0) = k_i$ *for* $i = 1,\ldots,n$ *is*

$$\mathbb{P}_0(k_1,\ldots,k_n) = (q_1^*)^{k_1}\cdots(q_n^*)^{k_n}.$$

The term smallest means the smallest value for each coordinate of $\mathbf{q}$. In the case that $\rho(M) > 1$ (supercritical), $\mathbf{q}$ is the unique solution in $[0,1)^n$ [20, 32]. The next example illustrates extinction in a birth-death-dispersal branching process with two types, where the types are distinguished by their location.

1.3.1 Birth-Death-Dispersal

We consider a simple example of a population inhabiting two patches, 1 and 2, with dispersal between the two patches. Let $X_i(t)$ be the random variable for the

population size in patch i, $i = 1,2$, at time t, $\Delta X_i(t) = X_i(t+\Delta t) - X_i(t)$, and $\mathbf{X}(t) = (X_1(t), X_2(t))$. In addition, let b_i and d_i be constant per capita birth and death rates, and m_i be the per capita movement rate out of patch i and into patch j, $i \neq j$, $i, j = 1,2$. All parameters are positive. The transition rates, summarized in Table 1.1, are linear functions of the population size X_i.

The analogous deterministic model for birth-death-dispersal has the form:

Table 1.1 The six events and corresponding transition rates $r_i(t)$ associated with the MC birth-death-dispersal model, where the transition probabilities are $r_i(t)\Delta t + o(\Delta t)$.

Event	$\Delta\mathbf{X}(t)$	Rate, $r_i(t)$
1	$(1,0)$	$b_1 X_1(t)$
2	$(0,1)$	$b_2 X_2(t)$
3	$(-1,0)$	$d_1 X_1(t)$
4	$(0,-1)$	$d_2 X_2(t)$
5	$(-1,1)$	$m_1 X_1(t)$
6	$(1,-1)$	$m_2 X_2(t)$

$$\begin{aligned} \frac{dn_1(t)}{dt} &= (b_1 - d_1)n_1(t) - m_1 n_1(t) + m_2 n_2(t) \\ \frac{dn_2(t)}{dt} &= (b_2 - d_2)n_2(t) - m_2 n_2(t) + m_1 n_1(t). \end{aligned} \tag{1.12}$$

If $b_i > d_i$, $i = 1,2$, then each population grows exponentially. The rate of dispersal from patch 1 to 2 is m_1 and from patch 2 to 1 is m_2. Because the transition rates are linear in the X_i (Table 1.1) it follows that the solution (n_1, n_2) of the deterministic model is the expected population size of the MC model [3].

A two-type branching process $\mathbf{X}(t) = (X_1(t), X_2(t))$ can be formulated for the MC birth-death-dispersal model, similar to the simple birth and death process. The parameter λ_i for the exponential lifetime distribution for type i is $\lambda_i = d_i + b_i + m_i$. One individual of type i dies with probability $d_i/(d_i + b_i + m_i)$, gives birth to individuals of the same type but does not die with probability $b_i/(d_i + b_i + m_i)$ (or equivalently dies and is replaced with an identical substitute), or disperses to a different patch with probability $m_i/(d_i + b_i + m_i)$. The offspring pgfs for populations 1 and 2 in each patch are

$$\begin{aligned} f_1(s_1, s_2) &= \frac{d_1 + b_1 s_1^2 + m_1 s_2}{d_1 + b_1 + m_1} \\ f_2(s_1, s_2) &= \frac{d_2 + b_2 s_2^2 + m_2 s_1}{d_2 + b_2 + m_2}. \end{aligned}$$

The expectation matrix M of the offspring pgfs and the Jacobian matrix $J = \Lambda(M - I)$ of the backward Kolmogorov differential equations are

$$M = \begin{bmatrix} \dfrac{2b_1}{d_1 + b_1 + m_1} & \dfrac{m_1}{d_1 + b_1 + m_1} \\ \dfrac{m_2}{d_2 + b_2 + m_2} & \dfrac{2b_2}{d_2 + b_2 + m_2} \end{bmatrix} \tag{1.13}$$

and

$$J = \begin{bmatrix} b_1 - d_1 - m_1 & m_1 \\ m_2 & b_2 - d_2 - m_2 \end{bmatrix}. \tag{1.14}$$

Both matrices are irreducible. Note that the transpose of the Jacobian matrix J agrees with the Jacobian matrix of the deterministic model (1.12).

We cannot obtain an explicit expression for the probability of extinction in the supercritical case ($s(J) > 0$ or $\rho(M) > 1$), but the dynamics in special cases will be illustrated. It is straightforward to check that a necessary condition for survival is $b_i > d_i$ for some i. If $b_i < d_i$ for $i = 1,2$, then the process is subcritical ($s(J) < 0$ or $\rho(M) < 1$); extinction occurs with probability one. For example, if the birth and death rates are the same, $b_1 = b_2 = b$, $d_1 = d_2 = d$, and $b > d$, then $q_1^* = q_2^* = d/b$, a result similar to the simple birth-death process. In this case, dispersal between the patches does not influence survival. Another interesting case is if $b_1 > d_1$ and $b_2 < d_2$, then dispersal can rescue patch 2 from extinction. For example, in the case $b_1 = d_2$, $d_1 = b_2$, with $b_1 > d_1$, then it is easy to show that the process is supercritical, provided $m_1 < m_2 + b_1 - d_1$. Dispersal into the exponentially declining patch 2 from the exponentially growing patch 1 rescues patch 2 from extinction. On the other hand, if $m_1 > m_2 + b_1 - d_1$, the process is subcritical and regardless of the magnitude of dispersal, extinction occurs.

In the supercritical case with $m_1 < m_2 + b_1 - d_1$, Figure 1.3 illustrates two sample paths with persistence of the population in both patches. Figure 1.4 plots the probability of extinction q_1^* and q_2^* as a function of m_1 for the case $b_1 = 2 = d_2$, $d_1 = 1 = b_2$ and $m_2 = 1$. The fixed points (q_1^*, q_2^*) are computed numerically.

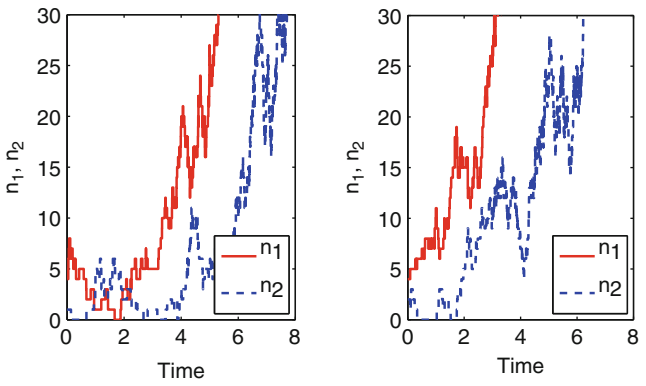

Fig. 1.3 Two sample paths of the branching process for the two-patch birth-death-dispersal model with parameter values $b_1 = 2 = d_2$, $d_1 = 1 = b_1$, $m_1 = 0.5$ and $m_2 = 1$ and $X_1(0) = 5$ and $X_2(0) = 1$. The probability of extinction is $\mathbb{P}_0(5,1) \approx (0.6347)^5(0.8315) = 0.0857$.

Alternately, defining births as in a bursting model (birth followed by death), where births follow a geometric distribution, then the offspring pgfs for the branching process are

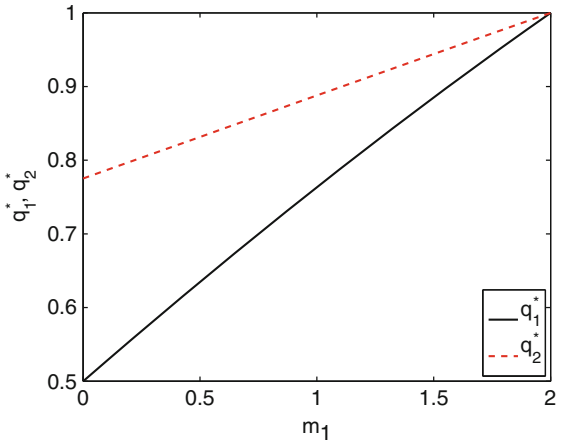

Fig. 1.4 Graphs of the probability of extinction for the birth-death-dispersal model as a function of dispersal parameter m_1. Other parameters are $b_1 = 2 = d_2$, $d_1 = 1 = b_1$, and $m_2 = 1$.

$$f_1(s_1,s_2) = \frac{d_1 + m_1 s_2}{b_1 + d_1 + m_1} \sum_{j=0}^{\infty} \left(\frac{b_1 s_1}{b_1 + d_1 + m_1} \right)^j = \frac{d_1 + m_1 s_2}{d_1 + m_1 + b_1(1 - s_1)}$$

$$f_2(s_1,s_2) = \frac{d_2 + m_2 s_1}{b_2 + d_2 + m_2} \sum_{j=0}^{\infty} \left(\frac{b_2 s_2}{b_2 + d_2 + m_2} \right)^j = \frac{d_2 + m_2 s_1}{d_2 + m_2 + b_2(1 - s_2)}.$$

Although the expectation matrix M' for this set of pgfs differs from M defined in (1.13), matrix $J' = \Lambda'(M' - I)$ with $\Lambda' = \text{diag}(d_1 + m_1, d_2 + m_2)$ equals matrix J defined in (1.14). In addition, it can be shown that the solution for the fixed points of the pgfs is the same as defined above.

1.4 Summary

Continuous-time Markov chains realistically model the discrete changes that occur in the birth-death-dispersal process. The solution of the underlying deterministic model for the linear birth-death-dispersal model only predicts the mean of the stochastic process; it cannot predict the extinction behavior for small population sizes. Continuous-time and discrete-state branching process theory is shown to be a useful method to predict population extinction, absorption into the zero state for the CTMC birth-death-dispersal process.

The basic theory of single- and multi-type branching processes is well known in the stochastic literature [20, 23, 30], but it is not as widely known or applied in the population or epidemic literature. In the following two chapters, several applications of branching process theory are presented to illustrate the insight obtained from this theory in the study of species invasions or of epidemic outbreaks. Additional applications of branching process theory that include immigration, environmental variation, or catastrophes can be found in the references (e.g., [7, 8, 21, 23, 34]).

Chapter 2
Applications of Single-Type Branching Processes

2.1 Introduction

Two applications of single-type branching process theory to population and epidemic processes are presented. The first application is to an epidemic model with susceptible, infectious, and recovered individuals in which there is only temporary immunity to reinfection. In the branching process approximation, the infectious stage is modeled by a birth and death process. Branching process theory provides an estimate for the probability of a major outbreak. Whittle in 1955 was the first to apply this theory in an epidemic setting [38]. The second application is to a classic competition model for two species. In this application, one species is native and the other species is nonnative and invasive. Invasive species pose a serious threat to the survival of many native species [35]. An important problem in conservation theory is how to prevent this invasive process. Branching process theory is used to investigate this problem, through analysis of a competition model between the native and the invasive species.

2.2 SIRS Epidemic

Introduction of infectious individuals into a susceptible population may result in an outbreak, causing a large increase in the number of infectious individuals. Whether an outbreak occurs depends on the rates of transmission, recovery, death, and the size of the susceptible population. In the SIR epidemic model, the population is divided into susceptible, infectious, and recovered individuals, S, I, and R, respectively. Let the parameters β and γ denote the transmission and the recovery rates, respectively. In the case of a serious disease, infection may result in disease mortality at rate α. In addition, if recovered individuals have only temporary immunity to reinfection, with a waning immunity rate δ, then recovered individuals return to

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being susceptible. With waning immunity, there is a potential for a second outbreak. The model with waning immunity is referred to as an SIRS epidemic model.

For the SIRS epidemic model, the ratio $\beta/(\gamma+\alpha)$ is known as the basic reproduction number, denoted as $\mathscr{R}_0$, an important parameter in epidemic theory. It is often defined as the number of secondary infections caused by introduction of one infectious individual into an entirely susceptible population. Therefore, if the magnitude of $\mathscr{R}_0$ is greater than one, the number of cases increases, an epidemic situation. For different infectious diseases, there have been a wide range of estimates for $\mathscr{R}_0$ that depend on many factors, including the infectious agent, the time, and the location [13].

Let the three random variables for the states (S,I,R) in the CTMC epidemic model be denoted as $(X_1X_2,X_3)=\mathbf{X}$ with $N=\sum_{i=1}^{3}X_i$ equal to the random variable for the total population size. The transition rates in the CTMC model are given in Table 2.1. For example, event 1 in Table 2.1 is a new infection. The transition probability for event 1 is

$$\mathbb{P}(\Delta\mathbf{X}(t)=(-1,1,0)|\mathbf{X}(t))=\beta\frac{X_1(t)}{N(t)}X_2(t)\Delta t+o(\Delta t),$$

where $\Delta\mathbf{X}(t)=\mathbf{X}(t+\Delta t)-\mathbf{X}(t)$ and the MC Rate $\beta\dfrac{X_1(t)}{N(t)}X_2(t)$ is nonlinear.

Table 2.1 Transition rates for the CTMC SIRS epidemic model (MC Rates) and for the approximating branching process for infectious individuals, $X_2(t)$ (BP Rates). In the branching process approximation, event 1 corresponds to a birth of an infective and events 2 and 3 correspond to a death of an infective.

Event	$\Delta\mathbf{X}(t)$	MC Rates	BP Rates
1	$(-1,1,0)$	$\beta\dfrac{X_1(t)}{N(t)}X_2(t)$	$\beta X_2(t)$
2	$(0,-1,1)$	$\gamma X_2(t)$	$\gamma X_2(t)$
3	$(0,-1,0)$	$\alpha X_2(t)$	$\alpha X_2(t)$
4	$(1,0,-1)$	$\delta X_3(t)$	—

The deterministic SIRS model corresponding to the CTMC model described above can be expressed as the following system of ordinary differential equations (ODEs):

$$\begin{aligned}\frac{dS(t)}{dt}&=-\beta\frac{S(t)}{N(t)}S(t)I(t)+\delta R(t)\\ \frac{dI(t)}{dt}&=\beta\frac{S(t)}{N(t)}S(t)I(t)-\gamma I(t)-\alpha I(t)\\ \frac{dR(t)}{dt}&=\gamma I(t)-\delta R(t),\end{aligned}\tag{2.1}$$

where $S(0)>0, I(0)>0, R(0)=0$, and $S(t)+I(t)+R(t)=N(t)$. In this model, $N(t)$ is not random. Because of the nonlinearity in the state variables, the solution

$(S(t),I(t),R(t))$ corresponding to the SIRS model (2.1) is not the expectation of the random variables in the CTMC model,

$$(S(t),I(t),R(t)) \neq (\mathbb{E}(X_1(t)),\mathbb{E}(X_2(t)),\mathbb{E}(X_3(t))).$$

As will be clear from the examples, at the initiation of an outbreak and end of the outbreak, the CTMC model with discrete random variables provides a more realistic description of the disease dynamics than the ODE model. However, during an outbreak, if the population size is large, then the dynamics of the CTMC and ODE models are close. Kurtz [26–28] showed in a series of papers in the 1970s that the large population limit of a Markov chain model is a system of ODEs. In particular, the SIRS ODE model is the large population limit of the SIRS CTMC model.

Near the disease-free state, $(X_1(0),X_2(0),X_3(0)) \approx (N(0)-i_0,i_0,0)$. If $N(0)$ is large and i_0 is small, then the transition rates are approximately linear. The CTMC infectious population can be approximated by a continuous-time branching process. Either the Markov chain hits zero, an absorbing state, or grows exponentially away from zero, a disease outbreak. The probability of hitting zero can be estimated from the branching process approximation.

The transition rates corresponding to a branching process approximation of the infectious population $X_2(t)$ are given in Table 2.1 (BP Rates). For example, event 1 in the branching process approximation is

$$\mathbb{P}(\Delta X_2(t) = 1 | X_2(t)) = \beta X_2(t)\Delta t + o(\Delta t),$$

a "birth" of an infectious individual. The branching process rate βX_2 is linear in X_2.

The infectious population X_2 in the CTMC epidemic model has a per capita birth rate equal to $b = \beta$ and a per capita death rate equal to $d = \gamma + \alpha$ (Table 2.1). It follows from the branching process formula in Chapter 1 that the probability of extinction is equal to $q^* = d/b$ when $b > d$ (supercritical case). Expressed in terms of the basic reproduction number,

$$q^* = \begin{cases} \dfrac{1}{\mathscr{R}_0}, & \mathscr{R}_0 > 1 \\ 1, & \mathscr{R}_0 \leq 1. \end{cases}$$

The preceding estimate was first described by Whittle in 1955 [38] for the simpler SIR epidemic model with no disease-related mortality ($\alpha = 0$) and no waning immunity ($\delta = 0$). Given $X_2(0) = i_0$ initial infectious individuals introduced into an entirely susceptible population, the probability of no major outbreak is

$$\mathbb{P}_0(i_0) \approx (1/\mathscr{R}_0)^{i_0}.$$

The probability of a major outbreak is $1-(1/\mathscr{R}_0)^{i_0}$. As noted above, this result depends on the fact that $X_1(0) \approx N(0)$ is sufficiently large and i_0 is small.

The graphs in Figure 2.1 illustrate the dynamics in two cases: $N(0) = 100$ and $N(0) = 500$. The branching process is supercritical, $\mathscr{R}_0 > 1$. For the ODE model, the disease becomes endemic. However, in Figure 2.1 (a) and (c), the disease in the stochastic model does not become endemic and generally ends after a single outbreak. For the larger population size of 500, in Figure 2.1 (c), the first outbreak is followed by one of smaller magnitude, where the maximum outbreak size is about 30. A single major outbreak may be followed by one or more minor ones, if there is a sufficient number of susceptible individuals after the first outbreak. It is apparent in Figure 2.1 that the stochastic sample paths are closer to the deterministic ODE solution in Figure 2.1 (c) than in Figure 2.1 (a) because of the much large population size in 2.1 (c). The MatLaB program that generated the sample paths in Figure 2.1 is given in Appendix A.2.

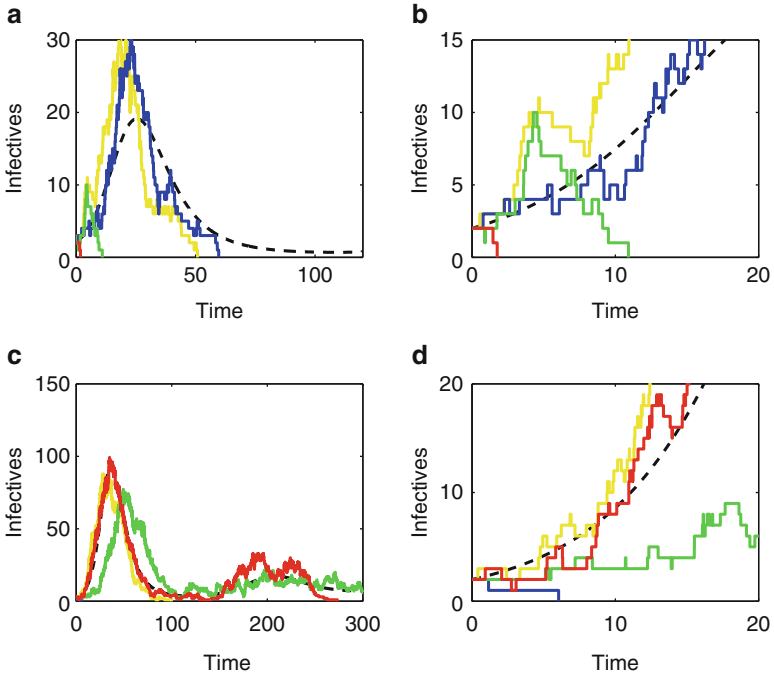

Fig. 2.1 Four sample paths of the CTMC SIRS epidemic model and the corresponding ODE solution (dashed curve). Parameter values for the SIRS epidemic model $\beta = 0.3$, $\gamma = 0.1$, $\alpha = 0.05$, $\delta = 0.01$, $I(0) = 2$, $S(0) = N(0) - 2$. In (a) and (b), $N(0) = 100$ and in (c) and (d), $N(0) = 500$. The shorter time scale in (b) and (d) illustrates the growth phase in the branching process approximation. The probability of a major outbreak is $1 - \mathbb{P}_0(2) = 1 - (1/2)^2 = 3/4$.

2.3 Species Invasion

According to the NOAA website [31], "An invasive species is an organism that causes ecological or economic harm in a new environment where it is not native." Charles Elton's book *The Ecology of Invasions by Animals and Plants* published in 1958 was the first to call attention to the environmental impact of invasions by nonnative species [15]. Many nonnative invasive species from amphibians and ants to water hyacinths and zebra mussels are documented in [35]. An important question in conservation theory is how to prevent and control invasive species. Models and branching processes can help address these questions and inform public policy decisions.

Four stages are generally identified in the invasion process: arrival, establishment, integration, and spread [37]. The first two stages of the invasion process may be modeled by competition between two species with one being the native species and the other, the nonnative species. The invader may arrive many times but each time it only has a small chance of success unless several propagules are introduced simultaneously.

We model competition between two species via the well-known Lotka-Volterra competition model. Let n_1 be the native species and n_2 the invader in a deterministic model for competition:

$$\begin{aligned}\frac{dn_1(t)}{dt} &= r_1 n_1(t)\left(1-\frac{n_1(t)}{K_1}\right) - c_{12}n_1(t)n_2(t)\\ &= n_1(t)\left(r_1 - r_1\frac{n_1(t)}{K_1} - c_{12}n_2(t)\right)\\ \frac{dn_2(t)}{dt} &= r_2 n_2(t)\left(1-\frac{n_2(t)}{K_2}\right) - c_{21}n_2(t)n_1(t)\\ &= n_2(t)\left(r_2 - r_2\frac{n_2(t)}{K_2} - c_{21}n_1(t)\right).\end{aligned} \tag{2.2}$$

All parameters are positive. Each species in the absence of the other grows logistically to their respective carrying capacity, K_i, $i = 1,2$. The terms c_{ij} are interspecies competition coefficients. It is well known that a stable coexistence equilibrium exists if $K_i < r_j/c_{ji}$, where $i, j = 1,2$, $i \neq j$. However, if $K_1 < r_2/c_{21}$ and $K_2 > r_1/c_{12}$, then species 2 outcompetes species 1; species 1 goes extinct and species 2 approaches carrying capacity K_2.

To formulate a CTMC model for the invasion process, we use the particular form from the Lotka-Volterra competition model (2.2) to formulate the birth and death rates. Let $\mathbf{X}(t) = (X_1(t), X_2(t))$ denote the random vector for species 1 and 2 and $\Delta\mathbf{X}(t) = \mathbf{X}(t+\Delta t) - \mathbf{X}(t)$. Assume birth and death rates for species i, respectively, are dependent on both population sizes, competition within and between species. That is, let the birth rate be

$$b_i(t) = b_{i1}X_i(t) - b_{i2}X_i^2(t), \quad X_i(t) \leq b_{i1}/b_{i2} \tag{2.3}$$

and the death rate be

$$d_i(t) = d_{i1}X_i(t) + d_{i2}X_i^2(t) + c_{ij}X_i(t)X_j(t), \quad i \neq j, \tag{2.4}$$

where $b_{i1} > 0$, $d_{i1} > 0$, $b_{i2} \geq 0$, and $d_{i2} \geq 0$. If $X_i(t) > b_{i1}/b_{i2}$, then $b_i(t) = 0$. The competition term $c_{ij}n_i(t)n_j(t)$ is assumed to contribute to the death rate. Because the dynamics of the ODE and CTMC are nonlinear in the state variables, the deterministic solution does not correspond to the mean of the stochastic model.

To compare the CTMC dynamics to those of the ODE model, assume that $r_i = b_{i1} - d_{i1} > 0$ and $b_{i2} + d_{i2} = r_i/K_i$. (See Table 2.2.) Even though the deterministic model predicts invader success, this is not the case in the stochastic model. If the invader population is not sufficiently large, then it cannot become established.

Table 2.2 Transition rates for the CTMC competition model (MC Rates) and for the continuous-time branching process approximation (BP Rates). Rates $b_i(t)$ and $d_i(t)$ are defined in (2.3) and (2.4).

Event	$\Delta\mathbf{X}(t)$	MC Rates	BP Rates
1	$(1,0)$	$b_1(t)$	–
2	$(0,1)$	$b_2(t)$	$b_{21}X_2(t)$
3	$(-1,0)$	$d_1(t)$	–
4	$(0,-1)$	$d_2(t)$	$(d_{21} + c_{21}K_1)X_2(t)$

Theory from branching process can be applied when $X_1(0) = K_1$ is sufficiently large and $X_2(0) = n_{20}$ is small. To estimate the probability of species 2 invasion success, the rates for the branching process (BP Rates) for X_2 are applied from Table 2.2. The corresponding linear approximation for the ODE model for $n_2(t)$ is

$$\frac{dn_2(t)}{dt} \approx (b_{21} - d_{21} - c_{21}K_1)\, n_2(t).$$

The zero state for species 2 (or species 1) is an absorbing state. It follows that the branching process approximation for the invader $X_2(t)$ will have per capita birth and death rates, $b = b_{21}$ and $d = d_{21} + c_{21}K_1$, respectively. Thus, species 2 can invade species 1 iff $b > d$ iff $b_{21} > d_{21} + c_{21}K_1$ (supercritical case). This latter inequality is equivalent to the inequality $K_1 < r_2/c_{21}$. Therefore, from branching process theory, if $K_1 < r_2/c_{21}$, the probability of extinction or an unsuccessful invasion of species 2 is approximately

$$\mathbb{P}_0(n_{20}) = \left(\frac{d_{21} + c_{21}K_1}{b_{21}}\right)^{n_{20}}$$

and the probability of a successful invasion is $1 - \mathbb{P}_0(n_{20})$, where n_{20} is the initial population size of the invader.

If the interspecies competitive effect of species 1 on species 2 is relatively small, that is, $c_{21}K_1$ is small compared to b_{21}, then species 2 has a competitive advantage

and a greater chance of invasion. The stochastic model also shows that invasion success depends on the population size of the invader, n_{20}. If the invasion is successful, the outcome of the competition, either coexistence of both species or dominance by species 2, can be predicted by the ODE model. This outcome may be representative of the third stage of invasion, integration. Which of these two outcomes occurs depends on the relation of b_{11} to $d_{11}+c_{12}K_2$. If species 2 is a better competitor, $b_{11} < d_{11}+c_{12}K_2$, then species 2 will replace species 1.

An example of the CTMC species invasion model is simulated with parameter values chosen so that species 2 dominates after it successfully invades. Parameter values are $K_1 = 100$, $K_2 = 200$, and $K_1 > r_2/c_{21}$ in Figure 2.2. The four sample paths of the CTMC competition model illustrate four invasion attempts, but only one is successful.

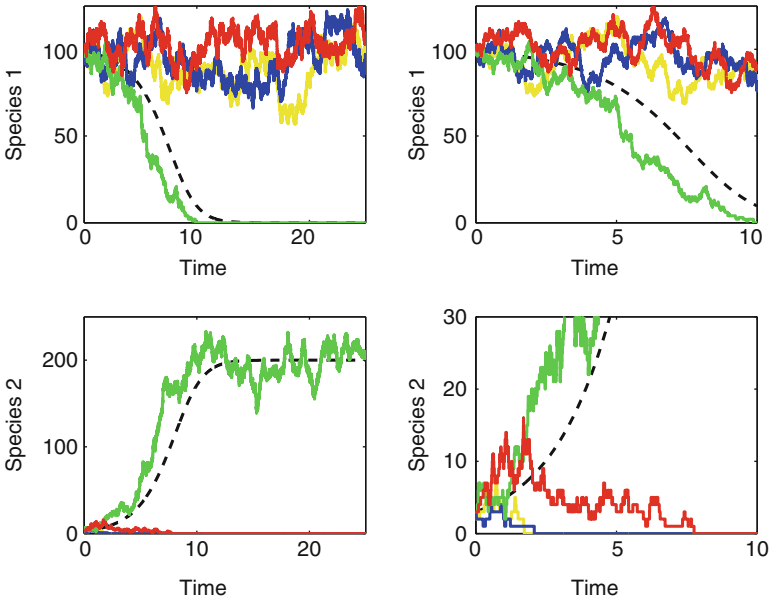

Fig. 2.2 Four sample paths of the two species CTMC competition model and the solution of the ODE model (2.2) with parameter values $r_1 = 1$, $r_2 = 2$, $b_{11} = 2$, $d_{11} = 1 = d_{21}$, $b_{21} = 3$, $d_{i2} = 0$, $i = 1,2$, $c_{12} = 0.01 = c_{21} = 0.01$, $K_1 = 100$, and $K_2 = 200$. Initial conditions are $X_1(0) = 100$ and $X_2(0) = 3$. The graphs on the left are for the time interval $[0,25]$, whereas the graphs on the right are for the time interval $[0,10]$. The shorter time scale illustrates the initial exponential growth of species 2 invasion. The probability that species 2 invades species 1 at equilibrium is $1-\mathbb{P}_0(3) = 1-(2.5/3)^3 \approx 0.421$.

2.4 Summary

Continuous-time and discrete-state branching process theory from Chapter 1 is applied to two problems. One problem is to estimate the probability of a major outbreak in an SIRS epidemic with temporary immunity and the second problem is to estimate the probability of species invasion when a native species competes with a nonnative species. Additional applications of branching process theory involving multiple species and multiple sites in the study of species invasions and epidemic outbreaks can be found in the references (e.g., [5, 6, 29, 34]).

Chapter 3
Applications of Multi-Type Branching Processes

3.1 Introduction

Two applications of multi-type branching processes to epidemic models are presented. The first application is to an SEIR epidemic model and the second application is to the same epidemic model but with dispersal. The SEIR epidemic is modeled as a two-type branching process. Occurrence of an outbreak depends on the number of exposed and infectious individuals. It is shown that the offspring pgfs for the exposed and infectious populations lead to an explicit formula for the probability of an outbreak. In the SEIR model with dispersal, the case of two regions with different healthcare situations are considered. One region has poor healthcare versus another region with excellent healthcare. It is shown that the rate and the direction of movement have a large impact on the occurrence of an outbreak. Branching process theory is used to investigate the probability of an outbreak when the movement rates differ between the two regions.

Although the SIR and SEIR epidemic models are simple, they are often used as a first approximation during or after disease outbreaks to provide estimates of the potential spread of the disease or to understand the pattern of spread. For example, SIR and SEIR epidemic models in conjunction with data provided useful information about the spread of the 2002–2003 SARS (Severe Acute Respiratory Syndrome) pandemic which began in China, the 2009–2010 H1N1 influenza pandemic which began in Mexico, and the 2014 Ebola outbreak in Africa [11, 22, 33].

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3.2 SEIR Epidemic

Consider an SEIR epidemic model, where S, E, I, and R are the susceptible, exposed, infectious, and recovered individuals, respectively. With disease-related mortality rate α, the population size is not constant, $S(t)+E(t)+I(t)+R(t)=N(t)$. The deterministic SEIR ODE model has the form:

$$\begin{aligned}
\frac{dS(t)}{dt} &= -\beta\frac{S(t)}{N(t)}I(t)\\
\frac{dE(t)}{dt} &= \beta\frac{S(t)}{N(t)}I(t)-\delta E(t)\\
\frac{dI(t)}{dt} &= \delta E(t)-\gamma I(t)-\alpha I(t)\\
\frac{dR(t)}{dt} &= \gamma I(t).
\end{aligned} \tag{3.1}$$

Births, deaths, and temporary immunity are not included in this model. However, the basic reproduction number near the disease-free state has the same form as in the SIRS model considered in Chapter 2 [36]:

$$\mathscr{R}_0=\frac{\beta}{\gamma+\alpha}. \tag{3.2}$$

For the CTMC SEIR epidemic model, let $\mathbf{X}(t)=(X_1(t),X_2(t),X_3(t),X_4(t))$ denote the discrete random variables for the four states, $(S(t),E(t),I(t),R(t))$. The transition rates for the CTMC SEIR epidemic model (MC Rates) and those for the corresponding branching process approximation (BP rates) for exposed and infectious populations, X_2 and X_3 are given in Table 3.1. Because the rates are nonlinear, the solution of the deterministic model does not represent the mean of the stochastic model. Note that event 1 has a nonlinear transition rate in the MC model but a linear rate in the branching process approximation.

Table 3.1 Transition rates for the CTMC SEIR epidemic model (MC Rates) and for the corresponding branching process approximation for exposed and infectious individuals (BP Rates).

Event	$\Delta\mathbf{X}(t)$	MC Rates	BP Rates
1	$(-1,1,0,0)$	$\beta\frac{X_1(t)}{N(t)}I(t)$	$\beta I(t)$
2	$(0,-1,1,0)$	$\delta X_2(t)$	$\delta X_2(t)$
3	$(0,0,-1,1)$	$\gamma X_3(t)$	$\gamma X_3(t)$
4	$(0,0,-1,0)$	$\alpha X_3(t)$	$\alpha X_3(t)$

To compute the probability of epidemic extinction for the multi-type branching process, the pgfs for the random variables, X_2 and X_3, are defined. Applying the transition rates from Table 3.1, the pgfs for X_2 and X_3 are

$$f_1(s_1,s_2) = \frac{\delta s_2}{\delta}$$
$$f_2(s_1,s_2) = \frac{\beta s_1 s_2 + \gamma + \alpha}{\beta+\gamma+\alpha}.$$

Although f_1 is a simple function, f_2 is not. The expectation matrix of the pgfs is

$$M = \begin{bmatrix} 0 & 1 \\ \dfrac{\beta}{\beta+\gamma+\alpha} & \dfrac{\beta}{\beta+\gamma+\alpha} \end{bmatrix}.$$

Matrix $J = \Lambda(M-I)$ is

$$J = \begin{bmatrix} -\delta & \delta \\ \beta & -\gamma-\alpha \end{bmatrix},$$

where $\Lambda = \text{diag}(\delta, \beta+\gamma+\alpha)$. Both matrices are irreducible. It is clear that if $\mathscr{R}_0 > 1$, the branching process is supercritical. In particular, if $\mathscr{R}_0 > 1$, the unique fixed point of the pgfs is $(q_1^*, q_2^*) \in (0,1)^2$, where $q_i^* = 1/\mathscr{R}_0$ (Whittle's result). The difference between the SIR and SEIR CTMC models is that the exposed period increases the time until extinction and the presence of both exposed and infectious individuals increases the probability of an outbreak. This latter result can be seen in the probability of extinction (no major outbreak) for the CTMC SEIR epidemic model, which is given by

$$\mathbb{P}_0(e_0, i_0) \approx (1/\mathscr{R}_0)^{e_0+i_0}.$$

A numerical example of the SEIR CTMC model along with the deterministic solution is given in Figure 3.1. Three of the four sample paths represent an outbreak, whereas in one there is no outbreak. The probability of a major outbreak is $1 - \mathbb{P}_0(1,0) = 0.625$.

If additional mortality occurs during the exposed period at rate $\varepsilon X_2(t)$, then the pgf for X_2 is

$$f_1(s_1,s_2) = \frac{\delta s_2 + \varepsilon}{\delta+\varepsilon}.$$

The basic reproduction number for the ODE model with mortality during the exposed period differs from (3.2) and is equal to

$$\mathscr{R}_0 = \frac{\beta\delta}{(\delta+\varepsilon)(\gamma+\alpha)}. \tag{3.3}$$

If $\mathscr{R}_0 > 1$, then the fixed point can be explicitly determined,

$$q_1^* = \frac{\delta}{\delta+\varepsilon}\frac{1}{\mathscr{R}_0} + \frac{\varepsilon}{\delta+\varepsilon}$$
$$q_2^* = \frac{1}{\mathscr{R}_0}.$$

A model with natural births and deaths in all stages yields a similar result [4]. The value for the probability of extinction is greater in the exposed period than in the infectious period, $q_1^* > q_2^*$. This is a reasonable result since in the exposed period, individuals may die with probability $\varepsilon/(\delta+\varepsilon)$ before becoming infectious or become infectious but not transmit the disease with probability $\delta/[(\delta+\varepsilon)\mathscr{R}_0]$.

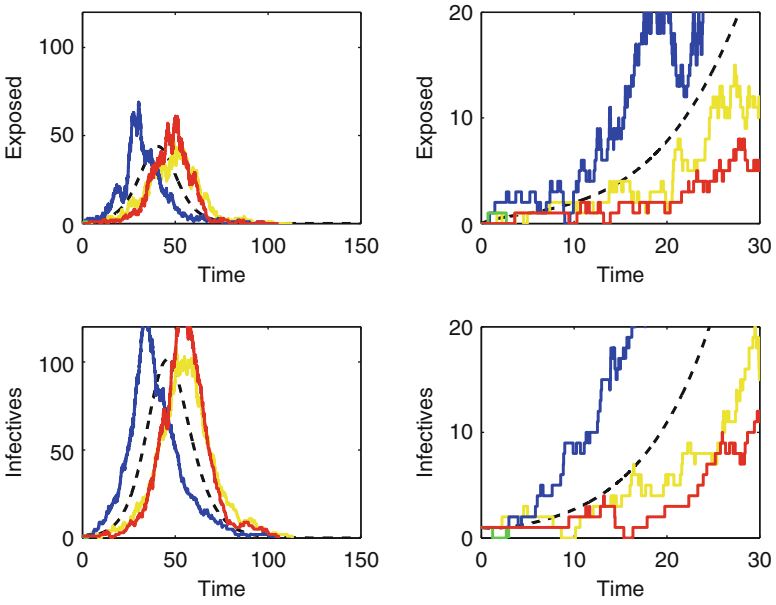

Fig. 3.1 Four sample paths of the CTMC SEIR epidemic model along with the deterministic solution (dashed curve). Parameter values are $\beta = 0.4$, $\delta = 0.4$, $\gamma = 0.1$, $\alpha = 0.05$, and $\varepsilon = 0$. Initial values are $S(0) = 499$, $E(0) = 1$, $I(0) = 0 = R(0)$. The basic reproduction number $\mathscr{R}_0 = 2.67$. The probability of a major outbreak is $1 - \mathbb{P}_0(1,0) = 0.625$.

3.3 Epidemic Dispersal

Suppose disease is spread between two populations each occupying different regions or patches and modeled by the SEIR epidemic equations within each patch. In population 1, poor healthcare facilities result in frequent disease outbreaks. In population 2, better healthcare facilities and reduced mortality and recovery rates result in no major outbreaks. For population 1, the basic reproduction number is greater than one but for population 2, the basic reproduction number is less than one. With dispersal between these two populations, the outcome changes depending on the direction and the rate of dispersal.

Let the disease parameters for each of these populations be denoted as β_i, δ_i, γ_i, and ε_i, $i = 1,2$. The rate of dispersal from population 1 to 2 is m_1 and the rate from

population 2 to 1 is m_2. For simplicity, the model assumes that all individuals within each stage, S, E, I, or R, disperse at the same rates, i.e., with rates m_1 and m_2. The disease is spread by the movement of exposed or infectious individuals between these two populations. The deterministic model for population 1 with dispersal is

$$\begin{aligned}
\frac{dS_1(t)}{dt} &= -\beta_1 \frac{S_1(t)}{N_1(t)} I_1(t) - m_1 S_1(t) + m_2 S_2(t) \\
\frac{dE_1(t)}{dt} &= \beta_1 \frac{S_1(t)}{N_1(t)} I_1(t) - \delta_1 E_1(t) - \varepsilon_1 E_1(t) - m_1 E_1(t) + m_2 E_2(t) \\
\frac{dI_1(t)}{dt} &= \delta_1 E_1(t) - \gamma_1 I_1(t) - \alpha_1 I_1(t) - m_1 I_1(t) + m_2 I_2(t) \\
\frac{dR_1(t)}{dt} &= \gamma_1 I_1(t) - m_1 R_1(t) + m_2 R_2(t).
\end{aligned} \tag{3.4}$$

A similar system holds for population 2. Without dispersal, $m_i = 0$, the basic reproduction number $\mathscr{R}_{0i}$, $i = 1,2$, for each population is given by formula (3.3), where the parameters for population 1 or 2 have subscripts 1 or 2, respectively. We assume $\mathscr{R}_{01} > 1$ and $\mathscr{R}_{02} < 1$.

A branching process approximation for the corresponding CTMC SEIR model for two patches can be applied if the population size is large but the exposed and infectious population sizes are small. For the branching process, we are only interested in the exposed and infectious stages. The direction and the rate of movement of individuals in these disease stages have a large impact on the probability of an outbreak.

Let $\mathbf{X}(t) = (X_1(t), X_2(t), X_3(t), X_4(t))$ denote the four discrete random variables for stages E_1, I_1, E_2, and I_2, respectively. The four probability generating functions of the approximating branching process are

$$\begin{aligned}
f_1(s_1,s_2,s_3,s_4) &= \frac{\delta_1 s_2 + \varepsilon_1 + m_1 s_3}{\delta_1 + m_1 + \varepsilon_1} \\
f_2(s_1,s_2,s_3,s_4) &= \frac{\beta_1 s_1 s_2 + \gamma_1 + \alpha_1 + m_1 s_4}{\beta_1 + \gamma_1 + \alpha_1 + m_1} \\
f_3(s_1,s_2,s_3,s_4) &= \frac{\delta_2 s_4 + \varepsilon_2 + m_2 s_1}{\delta_2 + \varepsilon_2 + m_2} \\
f_4(s_1,s_2,s_3,s_4) &= \frac{\beta_2 s_3 s_4 + \gamma_2 + \alpha_2 + m_2 s_2}{\beta_2 + \gamma_2 + \alpha_2 + m_2}.
\end{aligned} \tag{3.5}$$

If the spectral radius of the expectation matrix $\rho(M) > 1$, then the process is supercritical. A formula for the minimal fixed point of (3.5), $(q_1^*, q_2^*, q_3^*, q_4^*)$ can be computed numerically. In the supercritical case, the probability of no major outbreak is approximately

$$\mathbb{P}_0(e_{10}, i_{10}, e_{20}, i_{20}) = (q_1^*)^{e_{10}} (q_2^*)^{i_{10}} (q_3^*)^{e_{20}} (q_4^*)^{i_{20}},$$

where e_{j0} and i_{j0} are the initial number of exposed and infectious individuals in patch j, respectively. The probability of a major outbreak is $1 - \mathbb{P}_0(e_{10}, i_{10}, e_{20}, i_{20})$.

An example with equal dispersal rates for the two populations, $m_1 = m_2$, results in outbreaks in both populations. The probability of an outbreak increases in population 1 but decreases in population 2. In Figure 3.2, population 1 has $\mathscr{R}_{01} = 2.67$ but in population 2 there is lower transmission, higher recovery, and lower mortality, so that $\mathscr{R}_{02} = 0.89$. One infectious individual introduced into population 1 gives a probability for no major outbreak, $\mathbb{P}_0(0,0,0,1) = 0.751$.

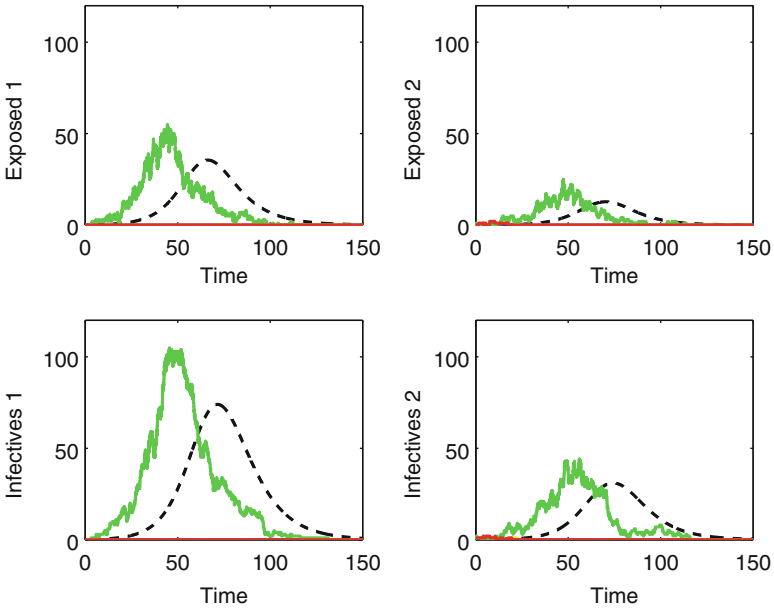

Fig. 3.2 Four sample paths of the SEIR CTMC model with dispersal along with the ODE solution (dashed curve). Parameter values are $\beta_1 = 0.4$, $\beta_2 = 0.2$, $\delta_1 = 0.4 = \delta_2$, $\gamma = 0.1$, $\gamma_2 = 0.05$, $\alpha_1 = 0.05$, $\alpha_2 = 0.025$, $\varepsilon_1 = 0 = \varepsilon_2$, and $m_1 = 0.05 = m_2$. Initial values are $S_1(0) = 500$, $S_2(0) = 499$, $E_1(0) = 0 = E_2(0)$, $I_1(0) = 1$, and $R_1(0) = 0 = R_2(0)$. The basic reproduction numbers for each population are $\mathscr{R}_{10} = 2.67$ and $\mathscr{R}_{02} = 0.89$. Probability of no major outbreak is $\mathbb{P}_0(0,0,0,1) = 0.751$.

With unequal dispersal between the two populations, the probability of an outbreak depends on the direction and magnitude of the dispersal rates (as in the birth-death-dispersal model in Chapter 1). In Figure 3.3, the fixed points $(q_1^*, q_2^*, q_3^*, q_4^*)$ of the pgfs in (3.5) are computed numerically given both m_1 and m_2 lie in the range $[0, 0.2]$. If dispersal is greater toward the population with good healthcare facilities it is possible to eradicate disease in both populations, that is, no major outbreaks occur. Allowing movement out of the poor healthcare region but restricting movement into the region (bottom left graph in Figure 3.3) is a good strategy for disease control, but restricting movement out of the poor healthcare strategy but allowing movement into that region (bottom right graph in Figure 3.3) is a poor strategy.

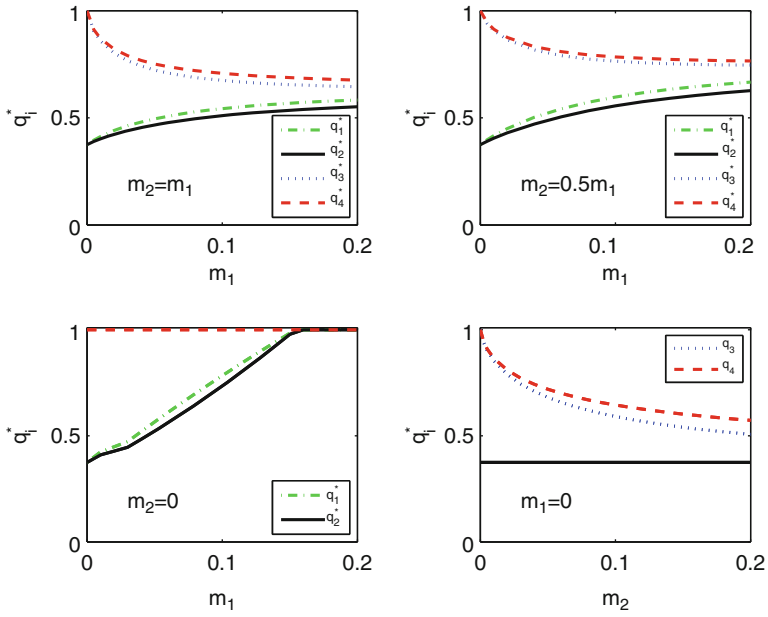

Fig. 3.3 Probability of no major outbreak for a CTMC SEIR epidemic model with dispersal between two populations as estimated by the fixed points q_i^*. Dispersal from population 1 to 2 is m_1 and from population 2 to 1 is m_2. Parameter values are the same as in Figure 3.2, except for the dispersal parameters: $\beta_1 = 0.4$, $\beta_2 = 0.2$, $\delta_1 = 0.4 = \delta_2$, $\gamma = 0.1$, $\gamma_2 = 0.05$, $\alpha_1 = 0.05$, $\alpha_2 = 0.025$, $\varepsilon_1 = 0 = \varepsilon_2$.

3.4 Summary

The multi-type branching process application to an SEIR epidemic with dispersal illustrates the importance of controlling movement into and out of particular regions to prevent an outbreak. Although prevention and control measures are more complex in real epidemic or pandemic situations, the basic SIR and SEIR models are often used in conjunction with data to help estimate the potential spread of the disease, e.g., SARS, influenza, and Ebola [11, 22, 33]. The control measures in pandemic situations often include travel restrictions, quarantine, isolation, and drugs such as antiviral medication to prevent infection. Other specific applications of branching processes to infectious disease models include vector-transmitted diseases [4, 6, 9, 18], HIV infection, [12] and bovine respiratory syncytial virus [19].

Chapter 4
Continuous-Time and Continuous-State Branching Processes

4.1 Introduction

For the continuous-time and continuous-state branching process, the probability of extinction differs from that of the continuous-time and discrete-state branching process considered in the preceding chapters. One obvious difference is, in the continuous-state process, the random variable $X(t) \in [0,\infty)$ as opposed to $X(t) \in \{0,1,2\ldots\}$. Another major difference is that the estimate for probability of extinction in the continuous-state branching process is an upper bound for the corresponding discrete-state process. That is, the probability of extinction is always greater for the continuous-state branching process. Although the estimates differ, it is also shown that the two branching process estimates for probability of extinction are close when the maximum population size is large and the birth to death ratio is small. Therefore, the continuous-state branching process provides a reasonable alternative to estimating population or epidemic persistence or extinction. Certainly, when computing the probability of extinction for biological processes that are continuous-valued rather than discrete-valued, the continuous-state process should be applied. Furthermore, continuous-time and continuous-state branching process models have an advantage of being easily formulated and computationally simulated for complex biological systems with demographic and environmental variability.

In this chapter, an analytical formula for the probability of extinction is obtained for the single-type, continuous-state, birth-death branching process through solution of the backward Kolmogorov differential equation. This extinction formula is compared to the corresponding estimate from the discrete-state branching process. Two applications are used to illustrate the extinction estimate for the continuous-state branching approximation, logistic growth and an SIR epidemic.

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4.2 Single-Type Branching Processes

A continuous-time and continuous-state branching process $\{X(t)|t \in [0,\infty)\}$ is a Markov process with nonnegative state space $X(t) = x \in [0,\infty)$. The branching property depends on the probability measure of $X(t)$. Briefly, $P(t,x,E)$ is the transition probability measure of $X(t)$. Given $X(0) = x$, the probability measure of a transition to a state in E is $P(t,x,E)$, where E is a Borel measurable subset of $[0,\infty)$. For example, the probability of extinction at time t beginning from state x is $P(t,x,\{0\})$. The transition probability measure satisfies the following branching property [7]:

$$P(t,x+y,E) = \int_0^\infty P(t,x,E-u)P(t,y,du). \tag{4.1}$$

Equation (4.1) implies the process is additive, similar to the assumption (1.1) in Chapter 1. The preceding relation means the probability of reaching state E at time t beginning from $x+y$ is the sum of two independent processes, one beginning at x and the other at y. Other properties of the branching process can be derived from condition (4.1). The first and second moments satisfy

$$\lim_{\Delta t\to 0^+} \frac{\mathbb{E}[\Delta X(t)|X(t)=x]}{\Delta t} = a_1 x, \quad \lim_{\Delta t\to 0^+} \frac{\mathbb{E}[(\Delta X(t))^2|X(t)=x]}{\Delta t} = a_2 x, \tag{4.2}$$

properties that define a diffusion process. These two moments lead to the derivation of the backward Kolmogorov differential equation (e.g., [3]):

$$\frac{\partial P(t,x,y)}{\partial t} = a_1 x \frac{\partial P(t,x,y)}{\partial x} + \frac{1}{2} a_2 x \frac{\partial^2 P(t,x,y)}{\partial x^2}, \tag{4.3}$$

where the first term on the right is known as the drift and the second term as the diffusion. Similarly a forward Kolmogorov differential equation can be derived:

$$\frac{\partial P(t,x,y)}{\partial t} = -\frac{\partial (a_1 y P(t,x,y))}{\partial y} + \frac{1}{2}\frac{\partial^2 (a_2 y P(t,x,y))}{\partial y^2}. \tag{4.4}$$

The continuous-state process is related to the MC branching process. In the MC branching process, $\Delta X(t) = +1$ with probability $bX(t)\Delta t + o(\Delta t)$ and $\Delta X(t) = -1$ with probability $dX(t)\Delta t + o(\Delta t)$. With these assumptions, the mean and variance given in (4.2) are $a_1 x = (b-d)x$ and $a_2 x = (b+d)x$. The forward Kolmogorov differential equations lead to an Itô stochastic differential equation (SDE) for the continuous-state branching process $X(t)$ [1, 2, 27]:

$$\begin{aligned} dX(t) &= a_1 X(t)dt + \sqrt{a_2 X(t)}\, dW(t) \\ &= (b-d)X(t)\, dt + \sqrt{(b+d)X(t)}\, dW(t), \end{aligned} \tag{4.5}$$

where $W(t)$ is a Wiener process, $\Delta W(t) = W(t+\Delta t) - W(t) \sim Normal(0,\Delta t)$, normally distributed with mean zero and variance Δt.

Numerical solutions of the Itô SDE (4.5) are graphed in Figure 4.1. The MatLaB program that generated these four sample paths is given in Appendix A.3. These sample paths are comparable to the sample paths of the birth-death process in Figure 1.2.

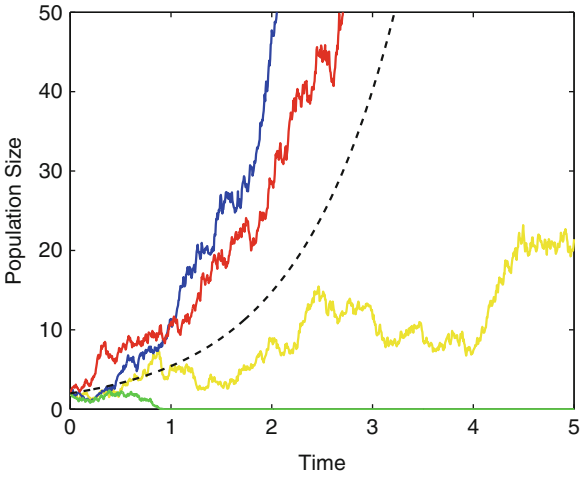

Fig. 4.1 The exponential growth model $n(t) = n_0 e^{(b-d)t}$ (dashed curve) and four sample paths of the continuous-state branching process for $b = 2$, $d = 1$, and $x = n_0 = 2$. One sample path hits zero. Compare with Figure 1.2. The probability of extinction for the continuous-state branching process is $\mathbb{P}_0(n_0) = \exp(-2n_0(b-d)/(b+d)) = \exp(-4/3) \approx 0.2636$.

Feller computed the probability of extinction for the continuous-state branching process [16]. The probability of ultimate extinction $\mathbb{P}_0(x)$, where x is the initial state, can be obtained directly from equation (4.3) by computing the stationary solution with appropriate boundary conditions. That is, $\mathbb{P}_0(x)$ is the solution $u(x)$ of the boundary value problem:

$$0 = (b-d)u'(x) + \frac{(b+d)}{2}u''(x), \quad u(0) = 1, \quad u(\infty) = 0,$$

where $x \in (0, \infty)$ is the initial population size. The solution of this boundary value problem is easily obtained as

$$u(x) = \mathbb{P}_0(x) = \exp\left(-2x\frac{(b-d)}{(b+d)}\right) = \exp\left(-2x\frac{(b/d-1)}{(b/d+1)}\right). \tag{4.6}$$

It is interesting to note that a lower bound for probability of extinction is e^{-2x}, e.g.,

$$\lim_{(b/d)\to\infty} \mathbb{P}_0(x) = e^{-2x}.$$

This is in contrast to the MC model, where the probability of extinction $\mathbb{P}_0(x) = (d/b)^x$ approaches zero as $b/d \to \infty$. A graph comparing the probability of extinction as a function of b/d is plotted in Figure 4.2.

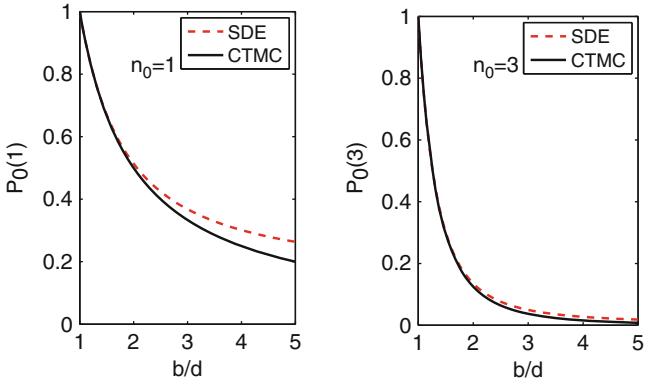

Fig. 4.2 The probability of extinction $\mathbb{P}_0(x)$ for the continuous-state (SDE) versus the discrete state (CTMC) branching processes are graphed as a function of b/d and $x = n_0$.

4.3 Applications

Two applications are presented. The first application is to the logistic growth model and the second application is to the SIR epidemic model.

4.3.1 Logistic Growth

The formulation of a stochastic logistic growth model depends on assumptions regarding birth and death rates, $b(t)$ and $d(t)$. A general form for a stochastic logistic model that includes variability due to births and deaths is similar to (4.5):

$$dX(t) = (b(t) - d(t))X(t)\,dt + \sqrt{(b(t) + d(t))X(t)}\,dW(t).$$

The birth and death rates can be related to the well-known form for births and deaths in the logistic growth model $dn(t)/dt = rn(t)(1 - n(t)/K)$. If

$$b(t) = b_1 n(t) - b_2 n^2(t)$$

and

$$d(t) = d_1 n(t) + d_2 n^2(t),$$

where b_1, b_2, d_2, and d_2 are nonnegative $b_1 - d_1 = r$ and $b_2 - d_2 = r/K$, then $b(t) - d(t)$ agrees with the growth rate in the logistic growth model. That is,

$$b(t) - d(t) = rn(t)\left(1 - \frac{n(t)}{K}\right).$$

Unfortunately, there is an infinite number of possible choices for the coefficients b_i and d_i for the birth and the death rates.

The nonlinear logistic model is approximated by the continuous-state branching process in (4.5) if the nonlinear terms are dropped in the birth and death rates. The branching approximation can be applied when the population size is small and the carrying capacity K is large.

As an example, let $r = 1$ with $b_1 = 2$, d_1=1, b_2=$r/(cK)$, and $d_2 = (c-1)r/(cK)$, $c \geq 1$. With these parameter values, the nonlinear logistic SDE model is

$$dX(t) = rX(t)(1 - X(t)/K)\,dt + \sqrt{X(t)(3 + X(t)/K)}\,dW(t), \tag{4.7}$$

with $r = 1$. If the carrying capacity K is large and $X(0)$ is small, then the approximation of the nonlinear logistic SDE model (4.7) by the branching process SDE model (4.5) takes the form:

$$dX(t) = X(t)\,dt + \sqrt{3X(t)}\,dW(t).$$

Applying formula (4.6) with $b - d = b_1 - d_1 = 1$ and $b + d = b_1 + d_1 = 3$ and $x = n_0 = 2$, the probability of extinction is approximately $\mathbb{P}_0(x) = \exp(-4/3)$. Four sample paths are plotted in Figure 4.3. (See Appendix A.3.)

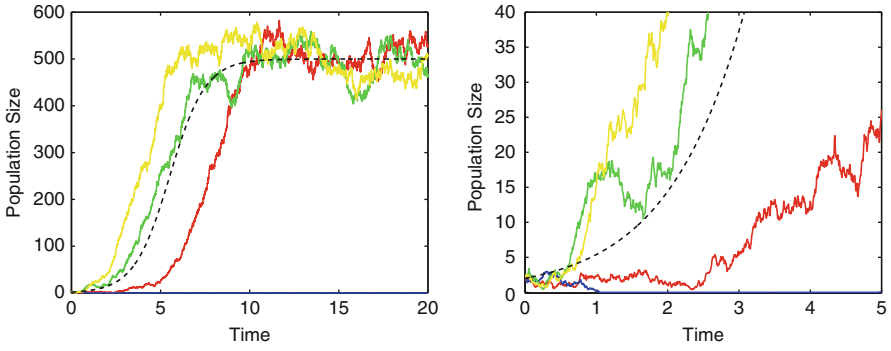

Fig. 4.3 Four sample paths of the stochastic logistic growth model (4.7) and the solution of the deterministic logistic growth model (dashed curve). Parameter values are $r = 1$, $K = 1$, $b_1 = 2$, $d_1 = 1$, $b_2 = r/(cK)$, and $d_2 = r(c-1)/(cK)$ with $c \geq 1$. Initial condition $X(0) = n_0 = 2$. Three sample paths persist and one hits zero. Probability of extinction is approximately $\mathbb{P}_0(n_0) \approx \exp(-4/3) \approx 0.2636$.

4.3.2 SIR Epidemic

In the second application, consider an SDE SIR epidemic model. As in Chapters 2 and 3, the infectious population size is approximated by a branching process when the population size is large but the infectious population size is small. One form for the full nonlinear SDE SIR epidemic model that is consistent with the CTMC model is [1, 2]:

$$\begin{aligned} dS(t) &= -\beta I(t)\frac{S(t)}{N(t)}\,dt - \sqrt{\beta I(t)\frac{S(t)}{N(t)}}\,dW_1(t) \\ dI(t) &= \left[\beta I(t)\frac{S(t)}{N(t)} - (\gamma+\alpha)I(t)\right]dt + \sqrt{\beta I(t)\frac{S(t)}{N(t)}}\,dW_1(t) \\ &\quad -\sqrt{\gamma I(t)}\,dW_2(t) + \sqrt{\alpha I(t)}dW_3(t) \\ dR(t) &= \gamma I(t)\,dt + \sqrt{\gamma I(t)}dW_2(t), \end{aligned}$$

where $W_i(t)$, $i = 1,2,3$ are three independent Wiener processes. The total population size is $S(t)+I(t)+R(t) = N(t)$. In the case that $S(0) \approx N(0)$ and $N(0)$ is large, then $S(t)/N(t) \approx 1$, initially. Setting $S(t)/N(t) = 1$ in the SDE for $I(t)$ yields the SDE:

$$dI(t) = (\beta-\gamma-\alpha)I(t)\,dt + \sqrt{\beta I(t)}\,dW_1(t) - \sqrt{\gamma I(t)}\,dW_2(t) + \sqrt{\alpha I(t)}dW_3(t).$$

The SDE for $I(t)$ does not depend on the variables $S(t)$ or $R(t)$. Since the terms $\Delta W_i(t)$ are normally distributed and independent, their sum is also normally distributed. In particular, an equivalent SDE approximation for $I(t)$ is

$$dI(t) = (\beta-\gamma-\alpha)I(t)\,dt + \sqrt{(\beta+\gamma+\alpha)I(t)}\,dW(t), \;\; I(0) = i0.$$

Hence, $I(t)$ can be approximated by the SDE branching process model (4.5) with $b = \beta$ and $d = \gamma+\alpha$. Such a branching process appears obvious if b and d are identified as in the SIRS model as $b = \beta$ and as $d = \gamma+\alpha$. Estimates for the probability of epidemic extinction are given by the formula in (4.6), provided $S(0)$ is close to $N(0)$, $N(0)$ is sufficiently large, and i_0 is small.

4.4 Summary

For the single-type, continuous-state branching process, an explicit formula for probability of extinction is computed as the solution of the backward Kolmogorov differential equation. The continuous-state branching process estimate for probability of extinction is greater than the corresponding one for the discrete-state process:

$$\left(\frac{d}{b}\right)^x \le \exp\left(-2x\frac{b-d}{b+d}\right), \;\; b \ge d, \;\; x > 0.$$

However, the two approximations are close if the ratio b/d is small.

For the multi-type continuous-state branching process an explicit formula is difficult to obtain because the probability of extinction is the solution of more complex backward Kolmogorov differential equations. However, an estimate for the probability of extinction can be obtained by numerically approximating the solution of these equations with appropriate boundary and initial conditions. Applications to more general SDE epidemic and population models can be found in the references (e.g., [1–3, 5]).

Appendix A
MatLaB Programs

A.1 MatLaB Programs: Chapter 1

The Gillespie algorithm is used to generate sample paths for the birth and death continuous-time branching process [17]. Four sample paths are plotted with the MatLaB code.

```
%  Birth and Death Process
clear all
n0=2; b=2; d=1; % Initial value and parameters
t=[0:.1:5];
y=n0*exp((b-d).*t);% Deterministic solution
plot(t,y,'k--','Linewidth',2);
axis([0,5,0,50]);
hold on
for k=1:4 % Four Sample Paths, Gillespie algorithm
  clear t x
  t(1)=0; x(1)=n0;
  j=1;
  while x(j)>0 & x(j)<50 % Stop hits zero or reaches size=50
    u1=rand; u2=rand; % Two uniform random numbers
    t(j+1)=-log(u1)/(b*x(j)+d*x(j))+t(j); %Time to next event
    if u2<b/(b+d)
      x(j+1)=x(j)+1; % Birth
    else
      x(j+1)=x(j)-1; % Death
    end
    j=j+1;
  end
  if k==1
    stairs(t,x,'y-','Linewidth',2);
  end
```


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```
    if k==2
      stairs(t,x,'b-','Linewidth',2);
    end
    if k==3
      stairs(t,x,'g-','Linewidth',2);
    end
    if k==4
      stairs(t,x,'r-','Linewidth',2);
    end
  end
  xlabel('Time');
  ylabel('Population Size');
  hold off
```

A.2 MatLaB Programs: Chapter 2

The Gillespie algorithm is used to generate sample paths for the SIRS Markov chain model [17]. To compare the branching process formula $(1/\mathscr{R}_0)^{i_0}$ for the probability of extinction to the extinction probability for the nonlinear Markov chain in the SIRS epidemic model, ten thousand sample paths are simulated for the Markov chain model. If the cumulative number of cases hits a predetermined outbreak size *outb*, it is counted as an outbreak, whereas if the number of cases hits zero, it is counted as an extinction event. An estimate for probability of extinction is the proportion of extinction events out of the ten thousand sample paths. It should be noted that the predetermined outbreak size depends on the population size. Here it is set to the minimum of 25 and $0.25N(0)$ which for initial population sizes greater than 100 equals 25. For larger population sizes there is better agreement between the branching process formula and the probability of extinction estimate of the Markov chain model.

```
% SIRS Epidemic Model
clear all
for kk=1:2:3
gam=0.1;alpha=.05;delta=.01; beta=0.3; i0=2; % Parameters
if kk==1
    N=100
    time=120;
else
    N=500
    time=300;
end
%Euler's method for solving ODE
dt=.05;  tim=time/dt;
i(1)=i0; s(1)=N-i0;r(1)=0; % Initial values
```

```
ssum=0;
for tt=1:tim
    nn=s(tt)+i(tt)+r(tt);
    i(tt+1)=i(tt)+dt*((beta/nn)*i(tt)*s(tt)-gam*i(tt)
      -alpha*i(tt));
    s(tt+1)=s(tt)+dt*(-(beta/nn)*i(tt)*s(tt)+delta*r(tt));
    r(tt+1)=r(tt)+dt*(gam*i(tt)-delta*r(tt));
    ssum=ssum+dt*(beta/nn)*i(tt)*s(tt);
end
TotalCases=round(ssum)+i0 % Cumm Cases up to time
subplot(2,2,kk)
plot([0:dt:time],i,'k--','linewidth',2);
xlabel('Time');
ylabel('Infectives');
axis([0,time,0,.3*N])
hold on
subplot(2,2,kk+1)
plot([0:dt:time],i,'k--','linewidth',2);
xlabel('Time');
ylabel('Infectives');
axis([0,20,0,20]);
hold on

for k=1:4 % Sample paths for MC, Gillespie algorithm
    clear  t s i r
    t(1)=0; i(1)=i0; s(1)=N-i0;r(1)=0;
    j=1;
    while i(j)>0 & t(j)<time % Stop hits zero or at time
       nn=s(j)+i(j)+r(j);
   u1=rand;u2=rand;
       den=((beta/nn)*i(j)*s(j)+gam*i(j)+alpha*i(j)
         +delta*r(j));
       t(j+1)=-log(u1)/den+t(j) % Time to next event
       e1=(beta/nn)*s(j)*i(j)/den;
       e2=e1+gam*i(j)/den;
       e3=e2+alpha*i(j)/den;
       e4=e3+delta*r(j)/den;
   if (u2<=e1)
          s(j+1)=s(j)-1;
  i(j+1)=i(j)+1;
          r(j+1)=r(j);
       elseif (u2>e1 & u2<=e2)
          s(j+1)=s(j);
  i(j+1)=i(j)-1;
  r(j+1)=r(j)+1;
```

```
        elseif (u2>e2 & u2<=e3)
           s(j+1)=s(j);
           i(j+1)=i(j)-1;
           r(j+1)=r(j);
        else
           s(j+1)=s(j)+1;
           i(j+1)=i(j);
           r(j+1)=r(j)-1;
        end
        j=j+1;
      end
   if k==1
      subplot(2,2,kk)
      stairs(t,i,'y-','linewidth',2);
      hold on
      subplot(2,2,kk+1)
      stairs(t,i,'y-','linewidth',2);
      hold on
   end
   if k==2
      subplot(2,2,kk)
      stairs(t,i,'b-','linewidth',2);
      hold on
      subplot(2,2,kk+1)
      stairs(t,i,'b-','linewidth',2);
      hold on
   end
   if k==3
      subplot(2,2,kk)
      stairs(t,i,'g-','linewidth',2);
      hold on
      subplot(2,2,kk+1)
      stairs(t,i,'g-','linewidth',2);
      hold on
   end
   if k==4
      subplot(2,2,kk)
      stairs(t,i,'r-','linewidth',2);
      hold off
      subplot(2,2,kk+1)
      stairs(t,i,'r-','linewidth',2);
      hold off
   end
end
```

```
% Estimate Probability of Epidemic Extinction
count=0;tots=10000;
for k=1:tots % Number of sample paths
    clear  t s i r
    i=i0; s=N-i0; r=0;
    j=1;
    outb=min(25,.25*N);
    sumi=i0;
    while i>0 & sumi<outb %Stop hits zero or cumm cases=outb
       u1=rand; u2=rand;
       nn=s+i+r;
       den=((beta/nn)*i*s+gam*i+alpha*i+delta*r);
       e1=(beta/nn)*s*i/den;
       e2=e1+gam*i/den;
       e3=e2+alpha*i/den;
       e4=e3+delta*r/den;
       if (u2<=e1)
          i=i+1;
          s=s-1;
          r=r;
          sumi=sumi+1;
       elseif (u2>e1 & u2<=e2)
          s=s;
          i=i-1;
          r=r+1;
       elseif (u2>e2 & u2<=e3)
          s=s;
          i=i-1;
          r=r;
       else
          s=s+1;
          i=i;
          r=r-1;
       end
       j=j+1;
    end
  if i==0
     count=count+1;
  end
end
probextSP=count/tots % Ext Approx from Sample Paths
probextBP=((gam+alpha)/beta)^(i0) % Ext Est from BP
end
```

A.3 MatLaB Programs: Chapter 4

The Euler-Maruyama numerical method is used to numerically solve the SDEs [25]. A sample path of an Itô SDE such as $dX(t) = f(X(t))\,dt + g(X(t))\,dW(t)$ is approximated by the Euler-Maruyama method as follows:

$$X(t+\Delta t) = X(t) + f(X(t))\Delta t + g(X(t))\eta\sqrt{\Delta t},$$

where $\eta \sim Normal(0,1)$ and $\eta\sqrt{\Delta t} \sim Normal(0,\Delta t)$. The MatLaB command *randn(sim,1)* generates a vector of length *sim* of standard normal random numbers. Multiplication by $\sqrt{\Delta t}$ yields a vector of normal random numbers with mean 0 and variance Δt. The following MatLaB program for Figure 4.1 applies the Euler-Maruyama method to generate ten thousand sample paths up to time 10, then graphs the first four sample paths. The proportion of sample paths that hit zero prior to time 10 gives an estimate of the probability of extinction which can be compared to the exact probability of extinction, given by formula (4.6).

```
% SDE exponential growth and extinction, Figure 4.1
clear all
b=2; d=1; n0=2; % Parameter and initial values
dt=0.005;tim=10/dt; sdt=sqrt(dt); sim=10000;
x=zeros(sim,1)+n0;
for t=1:tim % Euler-Maruyama
    rn=randn(sim,1);
    x(:,t+1)=x(:,t)+(b-d)*x(:,t)*dt+sqrt((b+d)*x(:,t)).
      *rn*sdt;
    pos=x(:,t+1)>0;
    x(:,t+1)=x(:,t+1).*pos; % Nonnegative sample paths
end
ze=sum(x(:,tim+1)==0);
approxext=sum(ze)/sim  % Approximate Prob Ext
ext=exp(-2*(b-d)*n0/(b+d)) % Exact Prob Ext
% Graph four sample paths
tt=[0:dt:10];
plot(tt,x(1,:),'r-',tt,x(2,:),'b-',tt,x(3,:),'g-',tt,x(4,:),
  'y-',...
     tt,2*exp((b-d).*tt),'k--','linewidth',2)
xlabel('Time');
ylabel('Population Size')
axis([0,5,0,50])
```

For Figure 4.3, the stochastic logistic growth model (4.7) is solved using the Euler-Maruyama method. The *for* loop in MatLaB code of the preceding program is replaced by the code below. In the plot, four sample paths of the stochastic logistic model are graphed along with the solution of the deterministic logistic model:

$$n(t) = \frac{n_0 K}{n_0 + (K - N_0)e^{-rt}}.$$

```
for t=1:tim
    rn=randn(sim,1);
    f=r*x(:,t).*(1-x(:,t)/K);
    g=sqrt(x(:,t).*(b1+d1+r*x(:,t)/K));
    x(:,t+1)=x(:,t)+f*dt+g.*rn*sdt; % Euler-Maruyama
    pos=x(:,t+1)>0;
    x(:,t+1)=x(:,t+1).*pos;
end
LG=n0*K./(n0+(K-n0)*exp(-r*tt)); %  Logistic growth
```

References

1. E. Allen. 2007. *Modeling with Ito Stochastic Differential Equations*, Springer, Dordrecht, The Netherlands.
2. E. Allen, L. J. S. Allen, A. Arciniega, and C. Greenwood. 2008. Construction of equivalent stochastic differential equation models. *Stoch. Anal. and Appl*. 26: 274–297.
3. L. J. S. Allen. 2010. *An Introduction to Stochastic Processes with Applications to Biology.* 2nd Ed. CRC Press, Boca Raton, Fl.
4. L. J. S. Allen and G. E. Lahodny Jr. 2012. Extinction thresholds in deterministic and stochastic epidemic models. J. Biol. Dyn. 6: 590–611.
5. L. J. S. Allen and V. A. Bokil. 2012. Stochastic models for competing species with a shared pathogen. *Math. Biosci. Eng*. 9: 461–485.
6. L. J. S. Allen and P. van den Driessche. 2013. Relations between deterministic and stochastic thresholds for disease extinction in continuous- and discrete-time infectious disease models. *Math. Biosci.* 243: 99–108.
7. K. B. Athreya, P. E. Ney. 1972. *Branching Processes*. Springer-Verlag, New York.
8. B. Bansaye, J. C. Pardo Millan, and C. Smadi. 2013. On the extinction of continuous state branching processes with catastrophes. *Electron J. Probab* 18: 1–31.
9. M. S. Bartlett. 1964. The relevance of stochastic models for large-scale epidemiological phenomena. *J. Roy. Stat. Soc., Series C* 13: 2–8.
10. I. J. Bienaymé. 1845. De la loi de multiplication et de la durée des familles. *Soc. Philomat. Paris* 5: 37–39.
11. G. Chowell, C. Castillo-Chavez, P. W. Fenimore, C. M. Kribs-Zaleta, L. Arriola and J. M. Hyman. 2004. Model parameters and outbreak control for SARS. *Emerging Infectious Diseases* 10: 1258–1263.
12. J. M. Conway, B. P. Konrad, and D. Coombs. 2013. Stochastic analysis of pre- and postexposure prophylaxis against HIV infection. *SIAM J. Appl. Math.* 73: 904–928.
13. K. Dietz. 1993. The estimation of the basic reproduction number for infectious diseases *Stat. Methods Med. Res.* 2: 23–41.
14. K. S. Dorman, J. S. Sinsheimer, K. Lange. 2004. In the garden of branching processes. *SIAM Review* 46: 202–229.
15. C. S. Elton. 2000. *The Ecology of Invasions by Animals and Plants*. Univ. Chicago Press (republication of 1958 edition).
16. W. Feller. 1951. Diffusion processes in genetics. In: *Proceedings of the Second Berkeley Symposium on Mathematical Statistics and Probability*. Univ. Calif. Press, Berkeley, pp. 227–246.
17. D. T. Gillespie. 1977. Exact stochastic simulation of coupled chemical reactions. *J. Chemical Physics* 81: 2340–2361.

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18. D. A. Griffiths. 1972. A bivariate birth-death process which approximates to the spread of a disease involving a vector. *J. Applied Prob.* 9: 65–75.
19. M. Griffiths and D. Greenhalgh. 2011. The probability of extinction in a bovine respiratory syncytial virus epidemic model. *Math. Biosci.* 231: 144–158.
20. T. E. Harris. 1963. *The Theory of Branching Processes*. Springer-Verlag, Berlin.
21. P. Haccou, P. Jagers, and V. A. Vatutin. 2005. *Branching Processes: Variation, Growth, and Extinction of Populations.* Cambridge Studies in Adaptive Dynamics. Cambridge Univ. Press, Cambridge, UK.
22. Y.-H. Hsieh Y-H, S. Ma, J. X. Velasco Hernandez, V. J. Lee, W. Y. Lim. 2011. Early outbreak of 2009 influenza A (H1N1) in Mexico prior to identification of pH1N1 virus. *PLoS ONE* 6(8): e23853. doi: 10.1371/journal.pone.0023853
23. P. Jagers. 1975. *Branching Processes with Biological Applications*. John Wiley & Sons, London and New York.
24. M. Kimmel and D. E. Axelrod. 2002. *Branching Processes in Biology.* Springer, New York, Berlin.
25. P. E. Kloeden, E. Platen, and H. Schurz. 1997. *Numerical Solution of SDE through Computer Experiments.* Springer-Verlag, Berlin.
26. T. G. Kurtz. 1970. Solutions of ordinary differential equations as limits of pure jump Markov processes. *J. Appl. Prob.* 7: 49–58.
27. T. G. Kurtz. 1971. Limit theorems for sequences of jump Markov processes approximating ordinary differential processes. *J. Appl. Prob.* 8: 344–356.
28. T. G. Kurtz. 1972. The relationship between stochastic and deterministic models for chemical reactions *J. Chem. Physics* 57: 2976–2978.
29. G. E. Lahodny, Jr. and L. J. S. Allen. 2013. Probability of a disease outbreak in stochastic multi-patch epidemic models. *Bull. Math. Biol*. 75:1157–1180.
30. C. J. Mode. 1971. *Multitype Branching Processes Theory and Applications*. Elsevier, New York.
31. National Oceanic and Atmospheric Administration. US Dept. of Commerce Website: `http://oceanservice.noaa.gov/facts/invasive.html` (accessed: 12/31/2014).
32. S. Pénisson. 2010. Conditional limit theorems for multitype branching processes and illustration in epidemiological risk analysis, Ph.D. diss., Institut für Mathematik der Unversität Potsdam, Germany.
33. C. M. Rivers, E. T. Lofgren, M. Marathe, S. Eubank, and B. L. Lewis. 2014. Modeling the Impact of Interventions on an epidemic of Ebola in Sierra Leone and Liberia. *PLOS Currents Outbreaks.* 2014 Nov 6. Edition 2. doi: 10.1371/currents.outbreaks.4d41fe5d6c05e9df30ddce33c66d084c.
34. S. J. Schreiber and J. O. Lloyd-Smith. 2009. Invasion dynamics in spatially heterogeneous environments. *Am. Nat.* 174: 490–505.
35. D. Simberloff and M. Rejmanek (Eds.) 2011. *Encyclopedia of Biological Invasions*. Univ. Calif. Press, Berkeley and Los Angeles, CA.
36. P. van den Driessche and J. Watmough. 2002. Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Math. Biosci.* 180: 29–48.
37. G. J. Vermeij. 1996. An agenda for invasion biology. *Biol. Conserv.* 78: 3–9.
38. P. Whittle. 1955. The outcome of a stochastic epidemic: A note on Bailey's paper. *Biometrika* 42: 116–122.
39. H. W. Watson and F. Galton. 1875. On the probability of the extinction of families. *J. Anthropol. Inst.* 4: 138–144.

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