



# Applications of the fundamental matrix to mean absorption and conditional mean absorption problems

Evan Milliken

School of Mathematical and Statistical Sciences, Arizona State University, United States



## ARTICLE INFO

*Article history:*

Received 2 October 2018

Received in revised form 6 February 2019

Accepted 1 April 2019

Available online 12 April 2019

*Keywords:*

Continuous time Markov chain

Discrete time Markov chain

Finite Markov chain

Fundamental matrix

## ABSTRACT

A proof of a general theorem for the calculation of conditional mean duration of a finite absorbing discrete time Markov chain is presented. In the simplest case, this result is equivalent to one suggested in the book of Kemeny and Snell (1976). In addition, we prove that the mean duration and mean conditional duration of a finite absorbing continuous time Markov chain can be calculated via the fundamental matrix of the embedded discrete time chain. These results are also extended to certain non-absorbing Markov chains. Applications are presented to illustrate the utility of these results.

© 2019 Elsevier B.V. All rights reserved.

## 1. Introduction

A discrete time Markov chain (DTMC)  $X_n$  on a finite state space with homogeneous transition probabilities is characterized by its probability transition matrix  $P$ . The state space of  $X_n$  can be partitioned into equivalence classes by the equivalence relation of communication. If it is impossible to leave an equivalence class once it has been entered, it is called closed. The states in an equivalence class which is not closed are called transient. Suppose that  $X_n$  admits more than one closed equivalence class with at least one class comprised of transient states. In this case, by reindexing the state space and exchanging rows and columns of  $P$ , we obtain its canonical form

$$P = \begin{bmatrix} S & 0 \\ R & Q \end{bmatrix}, \tag{1}$$

where  $S$  is a block diagonal matrix. The rows and columns of a block submatrix of  $S$  are associated to the states which form a closed equivalence class. This describes the one-to-one correspondence between the blocks of  $S$  and the closed equivalence classes of the underlying state space. In the case of an absorbing chain, all closed classes are singletons and  $S = I$ , the identity matrix, so that

$$P = \begin{bmatrix} I & 0 \\ R & Q \end{bmatrix}, \tag{2}$$

where the dimension  $n$  of the identity matrix  $I$  is determined by the number of absorbing states.

The fundamental matrix of  $X_n$  is given by

$$N = (I - Q)^{-1}, \tag{3}$$

where the dimension  $m$  of the identity matrix  $I$  is determined by the number of transient states. The book of [Kemeny and Snell \(1976\)](#) contains many well-known results involving the analysis of finite absorbing DTMCs via the fundamental

E-mail address: [Evan.Milliken@asu.edu](mailto:Evan.Milliken@asu.edu).

matrix. In this article, we will be focused the probability of absorption and the mean time to absorption. At the end of Chapter 3 (Kemeny and Snell, 1976), the authors elude to the calculation of mean time to absorption conditioned on the fact that absorption takes place in a specific state. In Section 2, we prove a general theorem regarding the calculation of the mean time to absorption conditioned on absorption in any subset  $\mathcal{I}$  of absorbing states. This result is equivalent to the one eluded to in Kemeny and Snell (1976) in the case that  $\mathcal{I}$  is a singleton.

If  $X_t$  is a time homogeneous continuous time Markov chain (CTMC), then there exists a DTMC  $Y_n$  associated to  $X_t$ , formed by conditioning on the fact that a transition has taken place, and called the embedded chain. If  $X_t$  is a finite absorbing CTMC, then  $Y_n$  will be a finite absorbing DTMC. In Section 3, we develop techniques to calculate mean absorption and conditional mean absorption times for a CTMC via the fundamental matrix of the embedded DTMC. The general theory of both continuous and discrete time Markov chains can be found in Allen (2003), Karlin and Taylor (1963) and Norris (1997).

Consider a general time homogeneous CTMC on a countable state space with initial distribution  $\pi$ . In Milliken (2019), it is proven that if  $\pi$  is supported on a finite subset of the state space, then the evolution of  $\pi$  according to the CTMC can be approximated locally in time and space by a finite state space absorbing CTMC. It follows that, in addition to the analysis of finite absorbing CTMCs, the results in Section 3 are applicable to analysis of local properties of CTMCs on a countable state space. This local analysis is frequently useful in mathematical models of the spread of infectious disease (Arino et al., 2019; Milliken, 2019).

If the homogeneous DTMC chain  $X_n$  has a finite state space,  $\mathcal{S}$ , which, when partition by the equivalence relation of communication, has at least one equivalence class comprised of transient states and  $m > 1$  closed equivalence classes, then the probability transition matrix  $P$  of  $X_n$  has canonical form (1), where the submatrix  $S$  has  $m$  blocks on the diagonal. Let  $C_i$ , for  $i = 1, \dots, m$ , be the closed equivalence classes of  $\mathcal{S}$ . Then, regardless of where the process starts, the probability that  $X_n \in \bigcup_{i=1}^m C_i$  tends to 1 as  $n$  tends to infinity. As a result of the properties of the equivalence relation of communication and the memoryless property of Markov chains, if  $X_n \in C_i$  for some  $i$  and  $n$ , then the long-term behavior of  $X_n$  is determined by the theory of finite irreducible Markov chains. This theory can be found in many books including Allen (2003), Karlin and Taylor (1963), Kemeny and Snell (1976) and Norris (1997) and is not the focus of this article. However, in Section 4, we will extend the results of Section 2 to finite DTMCs with at least one equivalence class comprised of transient states and more than one closed equivalence class. As noted below, the results of Section 4 can be extended to CTMCs in a manner similar to the results given in Section 3. Since such extension is so similar to Section 3 as to be redundant, it is omitted.

One common application of CTMC models is the population dynamics of the spread of an infectious disease. A key question in all models of population dynamics is that of persistence: what are the conditions under which the population will persist or go extinct. In the context of stochastic models, persistence can be measured by either the probability of extinction or mean time to extinction (Keeling and Ross, 2008). In the specific setting of epidemic models, emergence of the disease can lead to minor epidemics characterized by fluctuations of low numbers of infected individuals leading to extinction or major epidemics characterized by fluctuations about the solution to a companion deterministic model with a positive epidemic equilibrium (Arino et al., 2019; Tritch and Allen, 2018). In this case, the mean duration of a minor epidemic is a feature of interest for public health authorities and is a variant of the mean time to extinction problem. CTMC models of population dynamics may have a state random variable which accounts for many individual types leading to high dimensionality and often the state space is countable, rather than finite. Techniques to approximate the probability of extinction and mean time to extinction have been an area of interest dating back to the work of Whittle (1955) and continues to be an area of active research today (Arino et al., 2019; Allen and Lahodny, 2012; Billings and Forgoston, 2018; Borchering and McKinley, 2018; Milliken, 2017; Ovaskainen and Meerson, 2010; Tritch and Allen, 2018).

Commonly used techniques include branching processes, diffusion approximation and the WKB method of asymptotic analysis. Branching process approximation (including GWbp and multitype) is a linearization technique leading to potential error in the approximation (Milliken, 2017). Diffusion approximation, also known as Fokker–Planck approximation, is a second order approximation and can fail for very large or very small populations (Borchering and McKinley, 2018; Ovaskainen and Meerson, 2010). The WKB method has shown promising accuracy, but along with the diffusion approximation, it can be difficult to implement for high dimensional state space models (Ovaskainen and Meerson, 2010). The results presented below can be coupled together with a technique known as local approximation in time and space (LATS) (Milliken, 2019) to form a useful addition to the existing approximation tools mentioned above. Essentially, LATS combines taking a neighborhood of a set of initial states in the state space (with respect to graph distance in the induced graph) and the theory of collapsed Markov chains to form finite absorbing Markov chains which capture all local features of the original model. LATS approximates a CTMC with an absorbing DTMC on a finite state space. One of the well known results presented by Kemeny and Snell (1976) is that the matrix of absorption probabilities of an absorbing finite state space DMTC

$$B = NR \tag{4}$$

is the product of its fundamental matrix given by (3) and a submatrix of the probability transition matrix (2). In Milliken (2019), a combination of LATS and this result is used to calculate absorption probabilities related extinction of an emerging disease outbreak in a single population model of Infectious Salmon Anemia and in a two population Susceptible–Infected–Susceptible (SIS) metapopulation model. We extend these results by calculating the mean duration of a minor epidemic when the disease is introduced into the population or into the environment in Section 5. Also in Section 5, we apply LATS in together with Corollary 2 to form a fast and accurate approximation tool with which we analyze and validate the results and conclusions of Tritch and Allen (2018).

**2. Mean absorption times in the discrete time setting**

Consider the DTMC  $X_n$  on a finite state space,  $\mathcal{S}$ , with stationary transition probability matrix,  $P$ , given by (2). Suppose that  $\mathcal{S} = \mathcal{C} \cup \mathcal{T}$  where  $\mathcal{C}$  and  $\mathcal{T}$  are non-empty disjoint sets comprised of the absorbing and transient states of  $\mathcal{S}$ , respectively. Let  $N = (I - Q)^{-1}$  be the fundamental matrix of  $X_n$  and let  $\xi$  be a column vector with 1 in every entry. The following result is a combination of results in Chapter 3 of [Kemeny and Snell \(1976\)](#).

**Theorem 2.1.** *Let  $X_n$  be as above. Then the matrix  $B$  given by (4) contains the probability of absorption in absorbing state  $s_j$  from transient state  $s_i$  in the entry  $(B)_{ij}$ . Furthermore,  $\tau = N\xi$  contains the mean time to absorption into some absorbing state from the transient state  $s_i$  in entry  $\omega_i$ .*

In addition to the above assumptions on  $X_n$ , now assume that  $\mathcal{I}$  is a non-empty, proper subset of  $\mathcal{C}$ . The next theorem is the main result for in this Section.

**Theorem 2.2.** *Let  $X_n$  be as above. Then the mean time to absorption in the set of states  $\mathcal{I}$  from the transient state  $s_i$  is the  $i$ th entry of the vector*

$$\alpha = D_{b_{\mathcal{I}}}^{-1} N D_{b_{\mathcal{I}}} \xi, \tag{5}$$

where  $D_{b_{\mathcal{I}}}$  is the diagonal matrix whose diagonal entries are the entries of  $b_{\mathcal{I}} = \sum_{\ell \in \mathcal{I}} b_{\ell}$  with  $b_{\ell}$  the  $\ell^{\text{th}}$  column of  $B = NR$ .

**Proof.** The well-known formula  $\omega = N\xi$  is derived from the one-step analysis

$$\omega_i = 1 + \sum_{k \in \mathcal{T}} p_{ik} \omega_k \tag{6}$$

where  $\omega_i$  is the mean time to absorption in the set  $\mathcal{C}$  from the transient state  $s_i$ . This equation can be rewritten

$$\omega_i = \sum_{j \in \mathcal{C}} p_{ij} 1 + \sum_{k \in \mathcal{T}} p_{ik} (1 + \omega_k) \tag{7}$$

Now let  $\alpha_i$  be the mean time to absorption in some absorbing state in  $\mathcal{I}$  from  $s_i$  and  $\beta_i$  be the mean time to absorption in some absorbing state in  $\mathcal{C} \setminus \mathcal{I}$ . Let  $(b_{\mathcal{I}})_i$  be the  $i$ th entry of  $b_{\mathcal{I}} = \sum_{\ell \in \mathcal{I}} b_{\ell}$ . Then

$$\omega_i = (b_{\mathcal{I}})_i \alpha_i + (1 - (b_{\mathcal{I}})_i) \beta_i \tag{8}$$

and

$$(b_{\mathcal{I}})_i \alpha_i + (1 - (b_{\mathcal{I}})_i) \beta_i = \sum_{\ell \in \mathcal{I}} p_{i\ell} 1 + \sum_{k \in \mathcal{T}} p_{ik} (b_{\mathcal{I}})_k (1 + \alpha_k) + \sum_{j \in \mathcal{C} \setminus \mathcal{I}} p_{ij} 1 + \sum_{k \in \mathcal{T}} p_{ik} (1 - (b_{\mathcal{I}})_k) (1 + \beta_k). \tag{9}$$

Since absorption in  $\mathcal{I}$  and absorption in  $\mathcal{C} \setminus \mathcal{I}$  are independent events, we can restrict our consideration to

$$(b_{\mathcal{I}})_i \alpha_i = \sum_{\ell \in \mathcal{I}} p_{i\ell} 1 + \sum_{k \in \mathcal{T}} p_{ik} (b_{\mathcal{I}})_k (1 + \alpha_k). \tag{10}$$

Let  $D_{r_{\mathcal{I}}}$  be the diagonal matrix whose diagonal entries are the entries of  $r_{\mathcal{I}} = \sum_{\ell \in \mathcal{I}} r_{\ell}$ , where  $r_{\ell}$  is the  $\ell^{\text{th}}$  column of  $R$ . Written as a matrix equation, (10) becomes

$$D_{b_{\mathcal{I}}} \alpha = D_{r_{\mathcal{I}}} \xi + Q D_{b_{\mathcal{I}}} (\xi + \alpha) \tag{11}$$

$$(I - Q) D_{b_{\mathcal{I}}} \alpha = (D_{r_{\mathcal{I}}} + Q D_{b_{\mathcal{I}}}) \xi \tag{12}$$

$$\alpha = D_{b_{\mathcal{I}}}^{-1} (I - Q)^{-1} (D_{r_{\mathcal{I}}} + Q D_{b_{\mathcal{I}}}) \xi \tag{13}$$

The result follows from the fact that  $N = (I - Q)^{-1} = \sum_{k=0}^{\infty} Q^k$  and

$$R + QB = R + QNR = IR + Q \left( \sum_{k=0}^{\infty} Q^k \right) R = \left( \sum_{k=0}^{\infty} Q^k \right) R = NR = B. \quad \square \tag{14}$$

**3. Mean absorption times in the continuous time case**

Let  $X_t$  be a finite absorbing homogeneous CTMC with jump times  $J_k, k = 0, 1, 2, \dots$ , and embedded DTMC  $Y_n$  such that

$$X_{J_n} = Y_n, \quad n = 0, 1, 2, \dots \tag{15}$$

The waiting times (also called holding times or residence times)  $W_k = J_k - J_{k-1}$  are the random variables representing the time spent in state  $X_{J_{k-1}}$  before transitioning to a different state. Therefore,  $W_k$  are random variables that depend only on the current state. The waiting time, and hence mean waiting time, for transition out of an absorbing state  $s_j$  is infinite. However, the mean waiting times for transition out of a transient state are strictly positive and finite. Let  $\eta$  be the vector such that  $\eta_i$  is the mean waiting time for the transition out of the transient state  $s_i$ . The following is a Corollary to [Theorem 2.1](#).

**Corollary 1.** *Let  $X_t$  be a finite absorbing homogeneous CTMC with embedded chain  $Y_n$ . Then the probability transition matrix  $P$  for  $Y_n$  is of the form (2) and the mean time to absorption in the set of absorbing states is*

$$\omega = N\eta, \tag{16}$$

where  $N = (I - Q)^{-1}$  and  $\eta$  are as described above.

**Proof.** Let  $\mathcal{T}$  be the set of transient states and  $\mathcal{C}$  be the set of absorbing states. Let  $\omega_i$  be the mean time to absorption in  $\mathcal{C}$  from  $s_i \in \mathcal{T}$ . In this case, the one-step analysis equation becomes

$$\omega_i = \eta_i + \sum_{k \in \mathcal{T}} p_{ik} \omega_k. \tag{17}$$

In matrix form we have

$$\omega = \eta + Q\omega \tag{18}$$

$$(I - Q)\omega = \eta \tag{19}$$

$$\omega = (I - Q)^{-1}\eta \quad \square \tag{20}$$

Similarly, by substituting  $\eta_i$  for 1 in (7), we may extend [Theorem 2.2](#) to finite absorbing homogeneous CTMCs. Let  $\mathcal{S}$  be the state space of  $X_t$  and let  $\mathcal{T}$  the set of transient states and  $\mathcal{C}$  the set of absorbing states. Let  $\mathcal{I}$  be a nonempty proper subset of  $\mathcal{C}$ .

**Corollary 2.** *Let  $X_t, Y_n, P,$  and  $\eta$  be as in the previous Corollary. Let  $\mathcal{S}, \mathcal{T}, \mathcal{C}$  and  $\mathcal{I}$  be as above. Then the mean time to absorption in the set  $\mathcal{I}$  is*

$$\alpha = D_{b_{\mathcal{I}}}^{-1} N D_{b_{\mathcal{I}}} \eta, \tag{21}$$

where  $D_{b_{\mathcal{I}}}$  is as in [Theorem 2.2](#).

**Proof.** Substituting  $\eta_i$  in (7) and following the arguments in the proof of [Theorem 2.2](#) yields the result.  $\square$

#### 4. Mean time to absorption in a closed communication class

In this Section, we turn our attention to discrete and continuous Markov chains with a finite state space  $\mathcal{S}$ , which when partitioned into equivalence classes, consists of more than one closed class and at least one class containing transient states. If  $Y_n$  is a homogeneous DTMC on  $\mathcal{S}$ , then its transition probability matrix has the form (1). The assumption on  $\mathcal{S}$  implies that the submatrix  $S$  of  $P$  is block diagonal with at least two blocks. Each block corresponds to one of the closed equivalence classes. A closed class, as a set, behaves in manner similar to an absorbing state, in that once the process enters a closed class it remains there with probability 1. Also, regardless of where the process starts, its distribution is eventually supported on the states of the closed equivalence classes. Together, these facts mean that the chain eventually behaves like an irreducible chain. Irreducible (or regular) chains are covered in many sources including [Allen \(2003\)](#), [Karlin and Taylor \(1963\)](#), [Kemeny and Snell \(1976\)](#) and [Norris \(1997\)](#), but are not the focus here. Instead we will focus on the mean time to absorption in the set of closed equivalence classes and the conditional mean time to absorption in one or more closed classes.

To study the Markov chains described above, we will make use of the theory of collapsed Markov chains ([Burke and Rosenblatt, 1958](#); [Dey and Mukherjea, 2014](#); [Hachigian, 1963](#); [Milliken, 2019](#)), called lumpable chains in [Kemeny and Snell \(1976\)](#). The basic definitions and results below are given for DTMCs, but hold for CTMCs as well.

**Definition 4.1.** Let  $X_n$  be a DTMC on a finite state space  $S = \{1, 2, \dots, m\}$ . Let  $S_1, S_2, \dots, S_r$  be  $r, 1 \leq r < m$ , pairwise disjoint subsets of  $S$  containing more than one state so that  $S = S_1 \cup S_2 \cup \dots \cup S_r \cup A$ , where  $A = S \setminus \bigcup_{i=1}^r S_i$ . Then the partition of  $S$ , given by  $S_1, S_2, \dots, S_r$  and the singletons of  $A$  defines a collapsed chain  $Y_n$  given by

$$Y_n = i \text{ if and only if } X_n \in S_i \text{ and } Y_n = u \text{ if and only if } X_n = u,$$

where  $n \geq 0, 1 \leq i \leq r$ , and  $u \in A$ .

A collapsed chain is a stochastic process, but may not be a Markov process. The main obstacle is that the probability of transition out of a state  $i$ , the result of collapsing  $S_i$ , may depend the manner in which the original chain entered  $S_i$ , and its evolution in  $S_i$ , before leaving. This violates the memoryless property of a Markov chain. We are able to avoid this problem and refer to the following theorem and corollary from Milliken (2019).

**Theorem 4.2.** Let  $X_n$  be a homogeneous DTMC on a countable state space  $S$ . Let  $C \subset S$  be a proper subset of the state space which is closed with respect to communication. Let  $f$  be a many to one function given by

$$f(s) = \begin{cases} s & \text{if } s \in S \setminus C \\ c & \text{if } s \in C. \end{cases}$$

Then  $Y_n = f(X_n)$  is a Markov chain.

Corollary 3 is crucial to the application of collapsed chains in the results that follow. However, before we proceed we must establish the following definition, also from Milliken (2019).

**Definition 4.3.** For a DTMC  $X_n$  on a state space  $S$ , the probability of first hitting a state  $y$  from another state  $x$  in exactly  $m$  steps is denoted

$$h_{(y;x)}^{(m)}(x) = P(X_m = y | X_0 = x \cap X_i \neq y \forall i = 1, \dots, m - 1).$$

The probability of first hitting  $y$  from  $x$  is given by

$$h_{(y;x)}(x) = \sum_{m=0}^{\infty} h_{(y;x)}^{(m)}(x) = \lim_{N \rightarrow \infty} \sum_{m=0}^N h_{(y;x)}^{(m)}(x). \tag{22}$$

**Corollary 3.** Let  $X_n$  be a homogeneous DTMC on a countable state space  $S$ . Let  $Y_n$  be the collapsed chain formed by collapsing  $X_n$  along disjoint subsets which are closed with respect to communication. Then  $Y_n$  has the Markov property. Following the notation in Definition 4.1, whenever  $x \in A$  for all  $1 \leq i$ ,

$$h_{(S_i;x)}(x) = h_{(i;y)}(x),$$

where  $h_{(S_i;x)}(x)$  is the probability of first hitting the set  $S_i$  from state  $x$  with respect to chain  $X_n$  and  $h_{(i;y)}(x)$  is the probability of first hitting state  $i$  from  $x$  with respect to  $Y_n$ .

Consider the homogeneous DTMC,  $X_n$ , on the finite state space  $S$ . Suppose that  $S$  has at least one equivalence class comprised of transient states and  $m > 1$  closed equivalence classes. Let  $Y_n$  be the chain formed by collapsing the closed equivalence classes of  $X_n$ . If  $P$  is the probability transition matrix of  $X_n$ , then it has canonical form (1). If there are  $j$  transient states in  $S$ , then  $Q$  is a  $j \times j$  matrix. Let  $k_0 = 0$  and let  $k_1, \dots, k_m$  be defined such that  $k_i - k_{i-1}$  is the number of states in the  $i$ th closed class of  $S$ . Then  $S$  is a  $k_m \times k_m$  matrix and  $R$  is a  $j \times k_m$  matrix. Let  $K$  be the  $k_m \times m$  matrix such that the  $i$ th column of  $K$  is 1 in the  $k_{i-1} + 1, \dots, k_i$  entries and 0 in the remaining entries. Let  $\tilde{P}$  be the probability transition matrix of  $Y_n$ . Then

$$\tilde{P} = \begin{bmatrix} I & 0 \\ R & Q \end{bmatrix}, \tag{23}$$

where  $I$  is the  $m \times m$  identity matrix and  $\tilde{R} = RK$ .

**Remark 1.** The final two results deal with DTMCs. There exist extensions to the CTMC case as described in Section 3. Since these extensions and their reasoning are so similar to the results of Section 3, they are omitted.

**Corollary 4.** Let  $X_n$  be as described above. The probability of absorption in the  $i$ th closed equivalence class from the transient state  $s_j$  is the  $ij^{\text{th}}$  entry of  $\tilde{B} = \tilde{N}\tilde{R}$ . Furthermore, the mean time to absorption into the closed equivalence classes is  $\tau = N\xi$ .

**Proof.** The calculation of  $\tilde{B}$  and  $\tau$  are the result of application of Theorem 2.1 to the collapsed chain  $Y_n$ . The statement follows from Corollary 3.  $\square$

Let  $C_1, \dots, C_m$  be the  $m > 1$  closed equivalence classes of  $X_n$ . If  $\mathcal{I}^*$  is a proper subset of  $\{1, \dots, m\}$ , then let

$$\bigcup_{i \in \mathcal{I}^*} C_i = \bigcup_{i \in \mathcal{I}^*} \{k_{i-1} + 1, \dots, k_i\} = \mathcal{I}. \tag{24}$$

**Corollary 5.** Let  $X_n$  be as described above. The mean time to absorption in any of the closed equivalence classes of  $S$  with index in  $\mathcal{I}^*$  from the transient state  $s_i$  is the  $i$ th entry of the vector

$$v = D_{b_{\mathcal{I}}}^{-1} N D_{b_{\mathcal{I}}} \xi, \tag{25}$$

where  $N$  and  $D_{b_{\mathcal{I}}}$  are as in [Theorem 2.2](#) and  $\mathcal{I} = \bigcup_{i \in \mathcal{I}^*} \mathcal{C}_i$ .

**Proof.** Applying [Theorem 2.2](#) to the collapsed chain  $Y_n$  suggests that  $v = D_{b_{\mathcal{I}^*}}^{-1} N D_{b_{\mathcal{I}^*}} \xi$ , where  $\tilde{b}_{\mathcal{I}}^* = \sum_{\ell \in \mathcal{I}^*} \tilde{b}_{\ell}$  with  $\tilde{b}_{\ell}$  the  $\ell^{\text{th}}$  column of  $\tilde{B}$ . So, it suffices to show that  $\tilde{b}_{\mathcal{I}}^* = b_{\mathcal{I}}$ . For a set  $A$ , let

$$\delta_A(i) = \begin{cases} = 1 & \text{if } i \in A \\ = 0 & \text{otherwise.} \end{cases} \tag{26}$$

Let  $\iota(\mathcal{I})$  be the  $k_m \times 1$  vector with  $\delta_{\mathcal{I}}(i)$  in the  $i$ th entry and  $\iota(\mathcal{I}^*)$  be the corresponding  $m \times 1$  vector formed using  $\delta_{\mathcal{I}^*}$ . Since  $\tilde{B} = NR = NRK = BK$ ,

$$b_{\mathcal{I}}^* = \tilde{B} \iota(\mathcal{I}^*) = BK \iota(\mathcal{I}^*) = B \iota(\mathcal{I}) = b_{\mathcal{I}}. \quad \square \tag{27}$$

### 5. Applications

In this Section, two applications are presented to illustrate the utility of the results presented above. In the first application we consider a Susceptible–Infected–Virus model of Infectious Salmon Anemia. This model has two infectious compartments. It has been shown the multitype branching process approximation fails to adequately capture the probability of extinction of very small populations, while approximation with LATS together with (4) matches the probability estimated by analysis of repeated numerical simulation ([Milliken, 2019](#)). We extend these results by applying [Corollary 2](#) to calculate the duration of a minor epidemic when the disease is introduced into the population by a single infected individual or into the environment by an infectious dose of virus. In the second application, we consider a simple Susceptible–Infected–Susceptible (SIS) model which can be reduced to a one dimensional birth–death process. This model is studied by numerous authors (cf [Borchering and McKinley, 2018](#); [Ovaskainen and Meerson, 2010](#)), but we will compare directly to the recent work of [Tritch and Allen \(2018\)](#). We illustrate the accuracy of our techniques, validate the results of [Tritch and Allen \(2018\)](#) and provide new insight into the behavior of the model near the critical value  $\mathcal{R}_0 = 1$ .

#### 5.1. Accuracy for very small populations

In [Milliken \(2019\)](#), a Susceptible–Infected–Virus model of Infectious Salmon Anemia is presented. Parameters are chosen compare and contrast numerical approximation, multitype branching process approximation and the combination of LATS with (4) to approximate the probability of extinction in a very small population. This CTMC is related to the scaled system of differential equations

$$\begin{aligned} \dot{S} &= S(\beta - \mu S) - S(I + V) \\ \dot{I} &= S(I + V) - \alpha I \\ \dot{V} &= -\omega V + \delta I. \end{aligned} \tag{28}$$

The state variables  $S$  and  $I$  represent number of infected finfish, while the state variable  $V$  represents the number of infectious doses of viral pathogen in the environment. The parameters  $\beta, \mu, \alpha, \omega, \delta$  are the net birth rate of susceptible fish, density dependent death rate of susceptible fish, disease induced mortality for infected fish, viral clearance rate and viral shedding rate, respectively. We consider the CTMC  $X(t) = (S(t), I(t), V(t))$  characterized by the infinitesimal transition probabilities

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

where the transition rates are given in [Table 1](#).

Assuming that the number of Susceptible fish is fixed at the disease-free quasistationary distribution  $S(t) = \bar{S} = \frac{\beta}{\mu}$  and that all transitions are independent, we can use branching process approximation ([Allen and Lahodny, 2012](#); [Milliken, 2019](#); [Harris, 1963](#)) to estimate the probability of extinction by

$$\mathbb{P}_{\text{ext}} = q_1^i q_2^j, \tag{29}$$

where  $I(0) = i_1$  and  $V(0) = i_2$  and  $(q_1, q_2)$  is the minimal fixed point of the offspring probability generating function (pgf) for the multitype branching process given by

$$F(u_1, u_2) = (f_1(u_1, u_2), f_2(u_1, u_2)) = \left( \frac{\alpha + \delta u_1 u_2 + \bar{S} u_1^2}{\alpha + \delta + \bar{S}}, \frac{\omega + \bar{S} u_1 u_2}{\omega + \bar{S}} \right). \tag{30}$$

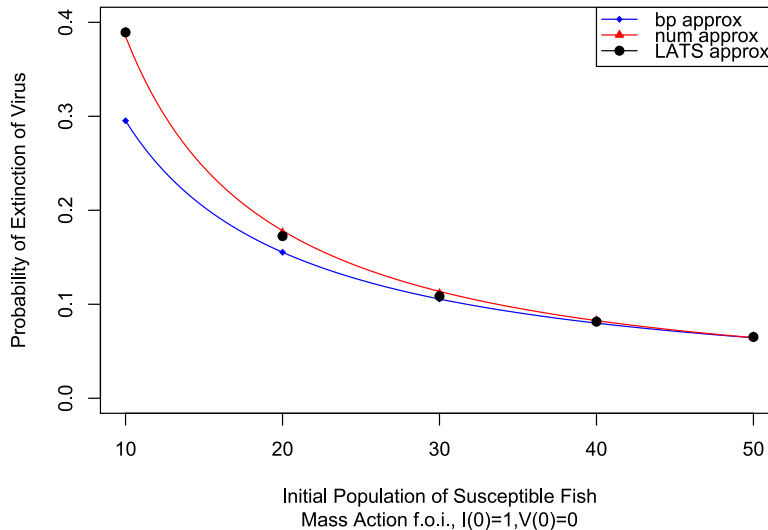
**Table 1**  
Transition rates for the CTMC  $X(t) = (S(t), I(t), V(t))$ .

$i$	$j$	$\sigma_{ij}$
$(S, I, V)$	$(S + 1, I, V)$	$\beta S$
$(S, I, V)$	$(S - 1, I, V)$	$\mu S^2$
$(S, I, V)$	$(S - 1, I + 1, V)$	$S(I + V)$
$(S, I, V)$	$(S, I - 1, V)$	$\alpha I$
$(S, I, V)$	$(S, I, V + 1)$	$\delta I$
$(S, I, V)$	$(S, I, V - 1)$	$\omega V$

**Table 2**  
Duration of a minor epidemic when the disease is introduced into the population ( $S(0) = 10, I(0) = 1, V(0) = 0$ ) or into the environment ( $S(0) = 10, I(0) = 0, V(0) = 1$ ) with parameters  $\beta = 10, \mu = 1, \alpha = 3.3, \delta = 1.3, \omega = 4$  calculated via numerical simulation (Mean) and LATS with Corollary 2 (MTE).

Initial State	Mean	MTE
$(10, 1, 0)$	0.2857	0.2851
$(10, 0, 1)$	0.2544	0.2542

**BP Approximation vs Numerical Simulation**



**Fig. 1.** The size of the susceptible population at the disease-free quasistationary distribution is given by  $\frac{\beta}{\mu}$ .  $\beta$  is the independent variable, while  $\mu = 1, \alpha = 3.3, \delta = 1.3, \omega = 4$  are fixed. The probability of extinction is approximated using branching process approximation (blue), numerical simulation via Gillespie algorithm (red) and LATS (black). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

Source: Modified from Milliken (2019)

Fig. 1 compares using numerical simulation, multitype branching process approximation and LATS together with (4) to approximate the true probability of extinction for a particular set of parameters. Likewise, in Table 2 we present the duration of a minor epidemic calculated using numerical simulation in column Mean and using LATS with Corollary 2 in column MTE when the disease is introduced into the population (i.e.  $(S(0) = \bar{S}, I(0) = 1, V(0) = 0)$ ) or in the environment (i.e.  $(S(0) = \bar{S}, I(0) = 1, V(0) = 0)$ ).

5.2. Mean duration of minor epidemic near  $\mathcal{R}_0 = 1$

The basic reproduction number of an epidemic,  $\mathcal{R}_0$ , is defined as the average number of secondary infections generated by a single infectious individual in a totally susceptible population in its lifetime. The threshold  $\mathcal{R}_0 = 1$  is a well known threshold separating persistence ( $\mathcal{R}_0 > 1$ ) and extinction of the disease ( $\mathcal{R}_0 \leq 1$ ) in many deterministic epidemic models. It has also been shown to be a threshold in branching process models separating  $\mathbb{P}\{\text{extinction}\} < 1$  ( $\mathcal{R}_0 > 1$ ) and

$\mathbb{P}\{\text{extinction}\} = 1$  ( $\mathcal{R}_0 \leq 1$ ) (Allen and Lahodny, 2012). The deterministic SIS model with transmission rate  $\beta$ , recovery rate  $\gamma$ , total population  $N$  and having  $\mathcal{R}_0 = \frac{\beta}{\gamma}$  is given by the differential equation

$$\dot{S} = -\beta \frac{SI}{N} + \gamma I, \tag{31}$$

$$\dot{I} = \beta \frac{SI}{N} - \gamma I. \tag{32}$$

This model is conservative ( $S(t) + I(t) = N$ ) and can therefore be reduced to

$$\dot{I} = \frac{\beta}{N}(N - I)I - \gamma I. \tag{33}$$

This reduced model is related to the birth–death CTMC  $I(t)$  characterized by the transition probabilities

$$p_{i,i+1}(\Delta t) = \mathbb{P}(I(t + \Delta t) = i + 1 | I(t) = i) = \frac{\beta}{N}(N - i)i\Delta t + o(\Delta t) \tag{34a}$$

$$p_{i,i-1}(\Delta t) = \mathbb{P}(I(t + \Delta t) = i - 1 | I(t) = i) = \gamma i\Delta t + o(\Delta t) \tag{34b}$$

$$p_{i,i}(\Delta t) = \mathbb{P}(I(t + \Delta t) = i | I(t) = i) = 1 - \frac{\beta}{N}(N - i)i\Delta t + \gamma i\Delta t + o(\Delta t). \tag{34c}$$

In Tritch and Allen (2018), Tritch and Allen approximate the process  $I(t)$  given by (34) by a simple birth–death process  $X(t)$  with mean given by the exponential growth model

$$\dot{m} = (\beta - \gamma)m. \tag{35}$$

According to the well known result of Whittle (1955), the probability of extinction for this simple birth–death process given initial  $i$  individuals is

$$\mathbb{P}_{\text{ext}} = \left(\frac{\gamma}{\beta}\right)^i. \tag{36}$$

In addition, Tritch and Allen (2018) derive the mean time to extinction for the simple birth–death process. Let  $T_i$  be the extinction time when  $X(0) = i$ . Suppose that  $\gamma = 1$ . Then, from Tritch and Allen (2018)

$$\mathbb{E}(T_i | T_i < \infty) = \begin{cases} -\ln\left(1 - \frac{1}{\beta}\right) \sum_{k=1}^i \beta^{k-1} + \sum_{k=1}^{i-1} H_k \beta^{k-1}, & \beta > 1 \\ -\ln(1 - \beta) \sum_{k=1}^i \beta^{k-1-i} + \sum_{k=1}^{i-1} H_k \beta^{k-i}, & \beta < 1, \end{cases} \tag{37}$$

where  $H_k = \sum_{n=1}^k \frac{1}{n}$  are the harmonic numbers.

Numerical simulation of the CTMC (34) eventually leads to extinction almost surely. To recover statistics like the probability of extinction and the mean duration of a minor epidemic from repeated numerical simulations, it is necessary to introduce a stopping criterion associated to a full-blown epidemic. A natural choice for this stopping criterion is that the number of infected individuals reaches the level of the epidemic equilibrium of the related deterministic model (33). However, it has been shown that the relevant behavior of a minor epidemic can be captured by choosing an upper threshold number of cases that is less than the equilibrium value of the deterministic model (Arino et al., 2019). In Tritch and Allen (2018), the authors compare the results of Eq. (37) with statistics from  $10^6$  numerical simulations of (34) with the added stopping criterion equivalent to making  $i = 30$  an absorbing state. The LATS approximation of (34) with the assumption that  $i = 30$  is an absorbing state is equivalent to a version of the Gambler’s Ruin problem with two absorbing states and is a finite absorbing Markov chain. Following Tritch and Allen (2018), we assume for illustration that  $\gamma = 1$ ,  $N = 2000$ , making  $\mathcal{R}_0 = \beta$ , which we allow to vary. In Table 3, the mean duration of a minor epidemic as approximated by (37) in column  $\mu$ , the associated statistic calculated from  $10^6$  numerical simulations with  $i = 30$  an absorbing state in column Mean, and the same statistic calculated using (21) from Corollary 2 applied to the related LATS approximation in column MTE are presented for various values of  $\beta = \mathcal{R}_0$ .

From Table 3, we see that the accuracy conditional duration calculated using (21) is confirmed by numerical simulation. It should be noted that  $10^6$  numerical simulations run in parallel on 8 computing cores takes 2–4 h to run, while preparing the matrices and calculating MTE takes 1–2 min. Even though the behavior of a minor epidemic can be captured by choosing an upper threshold number of cases less than the equilibrium number of infected individuals predicted by the deterministic model (31), the choice of threshold depends on  $\mathcal{R}_0$  (Arino et al., 2019). Let  $i_T$  be the upper threshold and let  $\bar{I}$  be the number of cases predicted by the positive equilibrium of the differential equation (33). Let  $\mathbb{P}_{i_T}\{\text{extinction}\}$  be the probability of extinction using of the CTMC with  $i_T$  absorbing and let  $\mathbb{P}_{\bar{I}}\{\text{extinction}\}$  be the probability of extinction of the CTMC with  $\bar{I}$  absorbing. For our purposes we will choose the upper threshold  $i_T$  so  $|\mathbb{P}_{i_T}\{\text{extinction}\} - \mathbb{P}_{\bar{I}}\{\text{extinction}\}| = O(10^{-5})$ . Table 4 presents  $\mu$ , MTE calculated by assuming  $i_T$  is absorbing,  $i_T$  and  $\bar{I}$  for



**Table 3**

The mean duration of a minor epidemic for an SIS model (34) with  $\gamma = 1$ ,  $N = 2000$ , for various values of  $\beta$  calculated using (37) ( $\mu$ ),  $10^6$  numerical simulations with  $i = 30$  absorbing (Mean), and using (21) assuming  $i = 30$  is absorbing (MTE).

$\mathcal{R}_0$	$\mu$	Mean	MTE
0.70	3.50	3.49	3.50
0.90	5.66	5.22	5.22
0.95	7.28	5.67	5.67
1.05	7.02	5.50	5.50
1.10	5.29	4.94	4.94
1.50	1.97	2.23	2.23

**Table 4**

The mean duration of a minor epidemic for an SIS model (34) with  $\gamma = 1$ ,  $N = 2000$ , for various values of  $\beta$  calculated using (37) ( $\mu$ ),  $10^6$  numerical simulations with  $i = 30$  absorbing (Mean), and using (21) assuming  $i = 30$  is absorbing (MTE).

$\mathcal{R}_0$	$\mu$	MTE	$i_T$	$\bar{i}$
0.70	3.50	3.50	30	0
0.90	5.66	5.59	70	0
0.95	7.28	7.03	100	0
1.05	7.02	8.45	95	95
1.10	5.29	5.83	170	182
1.50	1.97	2.23	25	667

various values of  $\beta = \mathcal{R}_0$  when  $\gamma = 1$  and  $N = 2000$ . Results from the table confirm the conclusion of [Tritch and Allen \(2018\)](#) that the mean duration of a minor epidemic increases as  $\mathcal{R}_0$  approaches the critical threshold  $\mathcal{R}_0 = 1$ .

From [Tritch and Allen \(2018\)](#), it is not clear how sample paths are changing, just that the change leads to a longer mean duration of a minor epidemic. It is not clear whether the sample paths remain close to the disease-free quasistationary distribution but fluctuate more or if typical paths make long sojourns away from that distribution. In contrast, our technique provides insight via the upper threshold  $i_T$ . As  $\mathcal{R}_0$  approaches 1 from above or below, the upper threshold number of cases that is needed to make  $|\mathbb{P}_T\{\text{extinction}\} - \mathbb{P}_{i_T}\{\text{extinction}\}|$  sufficiently small becomes large relative to  $\mathcal{R}_0$  values away from 1. This indicates that the probability of long sojourns away from the disease-free distribution which ultimately lead to extinction is higher near  $\mathcal{R}_0 = 1$ . Analyzing the CTMC via the embedded DTMC gives fast, accurate results that capture the underlying behavior of the CTMC.

**6. Discussion**

In this article, we present extensions of a result of [Kemeny and Snell \(1976\)](#) which allow for the calculation of conditional mean duration with respect to a CTMC by analysis of the embedded DTMC. When combined with LATS ([Milliken, 2019](#)), the results presented here form an accurate and robust technique for calculating mean first passage times like the mean time to extinction and the mean duration of a minor epidemic. First passage problems such as these are the topic of recent and ongoing research. There are existing techniques used to approximate first passage problems including branching process approximation (broadly speaking), diffusion approximation and WKB approximation. Branching processes and the diffusion approximation can fail to accurately approximate the meant time to extinction in some cases. WKB approximation combined with small population approximations can be accurate, but can be difficult to implement for models with a large number of population types. The method presented here combining LATS with analysis of the CTMC via the embedded DTMC is accurate and suitable for models with multiple population types. This method is a useful addition to the tools available for studying a wide variety of first passage problems.

**Acknowledgments**

The author would like to thank Dr. Julien Arino for introducing him to the book of [Kemeny and Snell](#). Thanks also to Dr. Arino and Dr. Linda J. S. Allen for their helpful comments. Finally, thanks to the anonymous reviewer for their helpful comments.

**References**

Allen, L.J.S., 2003. *An Introduction to Stochastic Processes with Applications to Biology*. Pearson, Upper Saddle River, NJ.  
 Allen, L.J.S., Lahodny, G.E., 2012. Extinction thresholds in deterministic and stochastic epidemic models. *J. Biol. Dyn.* 6 (2), 590–611.  
 Arino, J., Milliken, E., Rose, J., 2019. Effect of Movement on the Early Phase of an Epidemic. submitted for publication.  
 Billings, L., Forgoston, E., 2018. Seasonal forcing in stochastic epidemiology models. *Ric. Mat.* 67 (1), 27–47.

- Borchering, R., McKinley, S., 2018. Continuum approximation of invasion probabilities. *Multiscale Model. Simul.* 16 (2), 551–582.
- Burke, C.J., Rosenblatt, M., 1958. A Markovian function of a Markov chain. *A. Math. Statist.* 29 (4), 1112–1122.
- Dey, Agnish, Mukherjee, Arunava, 2014. Collapsing of non-homogeneous Markov chains. *Statist. Probab. Lett.* 84 (1), 140–148.
- Hachigian, Jack, 1963. Collapsed Markov chains and the Chapman–Kolmogorov equation. *A. Math. Statist.* 34 (1), 233–237.
- Harris, T.E., 1963. *The Theory of Branching Processes*. Springer-Verlag, Berlin.
- Karlin, S., Taylor, H.M., 1963. *A First Course in Stochastic Processes*, second ed. Academic Press.
- Keeling, M.J., Ross, J.V., 2008. On methods for studying stochastic disease dynamics. *J. R. Soc. Interface* 5 (19), 171–181.
- Kemeny, J.G., Snell, J.L., 1976. *Finite Markov Chains*, volume 356. Springer Verlag.
- Milliken, E., 2017. The probability of extinction of ISAV in one and two patches. *Bull. Math. Biol.* 79, 2887–2904.
- Milliken, E., 2019. Local approximation of Markov chains in time and space. *J. Biol. Dyn.* 1–23.
- Norris, J.R., 1997. *Markov Chains*. Cambridge University Press.
- Ovaskainen, O., Meerson, B., 2010. Stochastic models of population extinction. *Trends Ecol. Evol.* 25 (11), 643–652.
- Tritch, W., Allen, L.J.S., 2018. Duration of a minor epidemic. *Infect. Dis. Model.* 3, 60–73.
- Whittle, P., 1955. The outcome of a stochastic epidemic- A note on Bailey's paper. *Biometrika* 42, 116–122.