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On time-discretized versions of the stochastic SIS epidemic model: A comparative analysis

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Abstract In this paper, the interest is in the use of time-discretized models as approximations to the continuous-time birth-death (BD) process $\mathcal{I} = \{I(t) : t \geq 0\}$ describing the number $I(t)$ of infective hosts at time t in the stochastic $susceptible \to infective \to susceptible$ (SIS) epidemic model under the assumption of an additional source of infection from the environment. We illustrate some simple techniques for analyzing discrete-time versions of the continuous-time BD process $\mathcal{I}$, and we show the similarities and differences between the discrete-time BD process $\widetilde{\mathcal{I}}$ of Allen and Burgin (2000), which is inspired from the infinitesimal transition probabilities of $\mathcal{I}$, and an alternative discrete-time Markov chain $\bar{\mathcal{I}}$, which is defined in terms of the number $I(\tau_n)$ of infective hosts at a sequence $\{\tau_n : n \in \mathbb{N}_0\}$ of *inspection* times. Processes $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$ can be thought of as a uniformized version and the discrete skele-

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ton of process $\mathcal{I}$, respectively, and are commonly used to derive, in the more general setting of Markov chains, theorems about a continuous-time Markov chain by applying known theorems for discrete-time Markov chains. We shall demonstrate here that the continuous-time BD process $\mathcal{I}$ and its discrete-time counterparts $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$ behave asymptotically the same in the limit of large time index, while the processes $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$ differ from the continuous-time BD process $\mathcal{I}$ in terms of the random length of an outbreak, or when considering their dynamics during a predetermined time interval $[0, t']$. To compare the dynamics of process $\mathcal{I}$ with those of the discrete-time processes $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$ during $[0, t']$, we consider extreme values (i.e., maximum and minimum number of infectives simultaneously observed during $[0, t']$) in these three processes. Finally, we illustrate our analytical results by means of a number of numerical examples, where we use the Hellinger distance between two probability distributions to quantify the similarity between the resulting extreme value distributions of either $\mathcal{I}$ and $\widetilde{\mathcal{I}}$, or $\mathcal{I}$ and $\bar{\mathcal{I}}$.

Keywords SIS epidemic model · Extreme values · Finite birth-death process · Cayley-Hamilton approach · Hellinger distance

Mathematics Subject Classification (2000) 60J28 · 92B05

1 Introduction

The *susceptible* $\rightarrow$ *infective* $\rightarrow$ *susceptible* (SIS) epidemic model can be seen as a special case of the deterministic Verhulst logistic model (Verhulst 1838), and it has become a routinely used tool to describe the dynamics of a disease that does not lead to immunity. Its stochastic formulation yields a birth-death (BD) process $\mathcal{I}$ with discrete state space and continuous time, which is first studied by Feller (1939), Bartlett (1957), and Weiss and Dishon (1971). The book by Allen (2003) provides much of the basic theory and methodology when considering deterministic or stochastic SIS-models either in continuous or discrete time; see also the expository paper by Allen (2008). A detailed study of the extinction and quasi-stationary dynamics of the stochastic SIS-model can be found in the monograph by Nåsell (2011).

Discrete-time epidemic models have been widely used in the literature to represent epidemic processes that do typically occur in reality in continuous-time, and thus it is relevant to study how similar these processes are when looking at particular summary statistics of interest, and when focusing both on the short-term and long-term dynamics. There are different approaches to model the dynamics of a disease in discrete time, including chain binomial epidemic models (Abbey 1952; Greenwood 1931), discrete-time Markov chain models (Allen and Burgin 2000; Chalub and Souza 2014), branching processes (Allen and van den Driessche 2013), arbitrarily distributed disease stages (Hernández-Cerón et al. 2013a, 2013b, 2015; Hernández-Cerón 2015), the next-generation approach (Allen and van den Driessche 2008; van den Driessche and Yakubu 2019), and linear and nonlinear difference equations

which are usually derived either by making use of the dynamics of the disease (Allen et al. 1991; Castillo-Chávez and Yakubu 2001; De Jong et al. 1994; Zhou et al. 2004) or by discretizing the continuous-time model (Ma et al. 2013) by using, for example, Euler techniques (Enatsu et al. 2010; Hu et al. 2012; Sekiguchi 2010), among others. For related work, see e.g. the papers by Allen (1994), Brauer et al. (2010), Lewis et al. (2006), Longini (1986), Pellis et al. (2008), and Zhang and Jin (2009).

In the setting of discrete-time Markov chain models, Allen and Burgin (2000) formulate and analyze three stochastic epidemic models in discrete time –more concretely, the SIS-model with constant population size, the SIS-model with variable population size, and the SIR-model with constant population size– as discrete-time Markov chains which may be seen as approximations to the continuous-time Markov jump processes describing the state of the population at time t. Specifically, it is assumed that the time step is sufficiently small so that, consequently, only one event at most can occur during this time step. In the case of the SIS-model with constant population size $N < \infty$, Allen and Burgin (2000) present a discrete-time BD process $\widetilde{\mathcal{I}}$, which is inherently linked to the infinitesimal transition probabilities of process $\mathcal{I}$ for a sufficiently small time step τ, and demonstrate that the behavior of $\widetilde{\mathcal{I}}$ agrees with that of the continuous-time BD process $\mathcal{I}$ in terms of a certain random walk as the population size N is sufficiently large, and the expected length of an outbreak. More recently, Chalub and Souza (2014) revisit the discrete-time BD process $\widetilde{\mathcal{I}}$ and a related deterministic model by introducing a continuous model, which is based on a partial differential equation, and derive a diffusion-drift approximation to the probability density of process $\widetilde{\mathcal{I}}$.

In this paper, we complement the work of Allen and Burgin (2000) by focusing on the discrete-time BD process $\widetilde{\mathcal{I}}$ and an alternative discrete-time Markov chain $\bar{\mathcal{I}}$, which is defined by inspecting the number of infective hosts in the original continuous-time Markov chain model at a sequence $\{\tau_n : n \in \mathbb{N}_0\}$ of inspection times with $\tau_n = n\tau$. The aim is to study the similarities and differences between the continuous-time process $\mathcal{I}$, and the discrete-time processes $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$, in three different ways. The first way is related to the limiting distributions of $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$, which shall be compared with the limiting distribution of process $\mathcal{I}$ as the time index tends to infinite. In the second way, the interest is in the end of the epidemic –in terms of $\mathcal{I}$, the first visit to state 0– in the SIS-model, and the *scaled* versions derived from the random number of steps before the first visit of processes $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$ to state 0. The third way, which is common among statistical modelers, leads us to replace the dynamics of process $\mathcal{I}$ by its discrete-time versions $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$ during a predetermined time interval of length $t' > 0$, where the aim is then to compare how the dynamics of processes $\mathcal{I}$, $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$, differ during $[0, t']$, in terms of a couple of summary statistics related to extreme values.

It is important to stress that the SIS epidemic model studied here differs from the well-known SIS-model with transmission rate $\beta i s N^{-1}$ and recovery rate γi, where $s = N - i$ and i denote the number of susceptible and infective

hosts, and N is the population size. More concretely, the SIS epidemic model in this manuscript includes an additional source of infection from the environment of rate β', which yields the transmission rate $(\beta i + \beta')sN^{-1}$.

The paper is organized as follows. In Section 2, we show that, in terms of long-term epidemic dynamics, processes $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$ are equivalent to each other and amount to process $\mathcal{I}$ as the time index tends to infinity, whereas they differ from process $\mathcal{I}$ in terms of the random length of an outbreak. In Section 3, the aim is to analytically compare the dynamics of the number $I(t)$ of infective hosts at time t over times $t \in [0, t']$ with those given by the number $\bar{I}_n = I(\tau_n)$ of infective hosts at equidistant times $\tau_n = n\tau$ with time step $\tau = m^{-1}t'$, for $n \in \{0, 1, ..., m\}$ and a predetermined time length $t' > 0$. Although it appears to be analytically intractable, the problem is closely related to the distribution of the total area between the sample paths of infective hosts in the continuous-time BD process $\mathcal{I}$ and its discrete-time counterpart $\bar{\mathcal{I}}$. In Section 4, the interest is in the minimum and maximum number $(I_{\min}(t'), I_{\max}(t'))$ of hosts which are simultaneously infective at any time $t \in [0, t']$ in the SIS-model, and its counterparts $(\widetilde{I}_{\min}(m), \widetilde{I}_{\max}(m))$ and $(\bar{I}_{\min}(m), \bar{I}_{\max}(m))$ in the discrete-time processes $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$, respectively. The joint probability mass functions of the random vectors $(I_{\min}(t'), I_{\max}(t'))$, $(\widetilde{I}_{\min}(m), \widetilde{I}_{\max}(m))$ and $(\bar{I}_{\min}(m), \bar{I}_{\max}(m))$ are used in Section 5 in order to study the different behaviours of processes $\mathcal{I}$, $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$ during $[0, t']$, depending on the number $m = \tau^{-1}t'$ of inspection times and the infection and recovery rates. We do this by using the Hellinger distance between these probability mass functions. In Section 5, we also present numerical results when focusing on the expected length of an outbreak and the probability of not detecting the end of the outbreak within process $\bar{\mathcal{I}}$. Finally, we give some concluding remarks in Section 6.

2 The continuous-time SIS-model and related discrete-time processes

2.1 Model definition

In the SIS-model, the interest is in a homogeneously well-mixed and finite population of hosts, with constant population size N, where each susceptible (S) host can become infective (I) after some time, becoming again susceptible (S) after recovery, thus allowing for a bidirectional transition between the two possible states. Specifically, a typical infective host makes infectious contacts at random points of a Poisson process with rate $\beta > 0$ during its infectious period, which follows an exponentially distributed recovery time with expected value γ^{-1}, in such a way that the newly infective hosts at successive contacts are selected independently and uniformly from the subpopulation of susceptible hosts; additional to this, we consider an exogenous Poisson stream of infection of rate $\beta' > 0$, to represent potential external sources of infection not directly related to contacts (e.g., environmental sources). Further, all in-

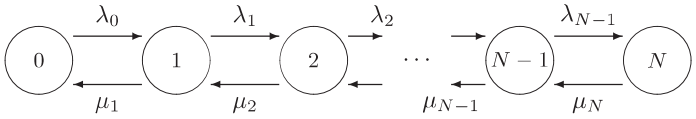

Fig. 1 State space and transitions in the continuous-time BD process $\mathcal{I}$ with birth rates $\{\lambda_i : i \in \{0, ..., N-1\}\}$ and death rates $\{\mu_i : i \in \{1, ..., N\}\}$.

fectious periods, and internal and exogenous contact processes are assumed to be mutually independent.

This description results in a finite continuous-time BD process $\mathcal{I} = \{I(t) : t \geq 0\}$ where $I(t)$ is the number of infective hosts at time t (Figure 1), and its infinitesimal transition probabilities are given by

$$P\left(I(t+dt) = j \,|I(t) = i\,\right) = \begin{cases} \lambda_i dt + o(dt), & \text{if } j = i+1, \\ 1 - (\lambda_i + \mu_i)dt + o(dt), & \text{if } j = i, \\ \mu_i dt + o(dt), & \text{if } j = i-1, \\ o(dt), & \text{otherwise,} \end{cases} \tag{1}$$

for integers $i, j \in \{0, 1, ..., N\}$, with $o(dt)/dt \to 0$ as $dt \to 0$; more concretely, the birth and death parameters in (1) are specified by $\lambda_i = N^{-1}(\beta i + \beta')(N - i)$ and $\mu_i = \gamma i$ representing, respectively, infection and recovery events.

For later use, we briefly discuss two simple but revealing properties of process $\mathcal{I}$. First, it is routinely seen (see e.g. page 292 in the book of Kulkarni (1995)) that, irrespectively of $I(0) = i \in \{0, 1, ..., N\}$, the limiting distribution of the number of infective hosts is specified by

$$\lim_{t\to\infty} P(I(t) = j | I(0) = i) = \Lambda^{-1} \frac{\lambda_0 \cdots \lambda_{j-1}}{\mu_1 \cdots \mu_j}, \quad j \in \{0, 1, ..., N\},$$

where $\Lambda = \sum_{j=0}^{N} \frac{\lambda_0 \cdots \lambda_{j-1}}{\mu_1 \cdots \mu_j}$ and $\frac{\lambda_0 \cdots \lambda_{j-1}}{\mu_1 \cdots \mu_j} \equiv 1$ if $j = 0$. Second, we point out that, under the assumption of $i \in \{1, 2, ..., N\}$ initially infective hosts, the random length $T = \inf\{t > 0 : I(t) = 0\}$ of an outbreak can be seen as a continuous phase-type random variable (see e.g. Chapter 2 in the book of Latouche and Ramaswami (1999)) of order N with representation $(\mathbf{e}_N(i), \mathbf{Q}^*)$, where $\mathbf{e}_a(b)$ denotes a row null vector of order a with a single 1 in its bth entry, and $\mathbf{Q}^*$ records infinitesimal rates associated with jumps of $\mathcal{I}$ between states in $\{1, 2, ..., N\}$; see also Section 7.3.2 of the book by Allen (2003). For practical use, moments of T can be evaluated (Artalejo et al. 2012; Norden 1982) from the iterative relation

$$E\left[T^k \,|I(0) = i\right] = k \sum_{j=0}^{i-1} d_j \sum_{i'=j+1}^{N} \frac{1}{\lambda_{i'} d_{i'}} E\left[T^{k-1} \,|I(0) = i'\right], \quad k \in \mathbb{N},$$

where $d_j = 1$ if $j = 0$, and $\frac{\mu_1 \cdots \mu_j}{\lambda_1 \cdots \lambda_j}$ if $j \in \{1, 2, ..., N\}$, and $E[T^0 | I(0) = i] = 1$, for states $i \in \{0, 1, ..., N\}$.

2.2 A discrete-time BD process

Equation (1) is used in Section 2.2.1 of (Allen and Burgin 2000) (see also Section 1.1 of the paper by Chalub and Souza (2014)) to define, for a predetermined value τ verifying

$$0 < \tau < \min\{\lambda_0^{-1}, (\lambda_i + \mu_i)^{-1}, \mu_N^{-1} : i \in \{1, 2, ..., N-1\}\}, \tag{2}$$

a discrete-time BD process $\widetilde{\mathcal{I}} = \{\widetilde{I}_n : n \in \mathbb{N}_0\}$ from the one-step transition probabilities

$$P\left(\widetilde{I}_{n+1} = j \,\middle|\, \widetilde{I}_n = i\right) = \begin{cases} \lambda_i\tau, & \text{if } j = i+1, \\ 1-(\lambda_i+\mu_i)\tau, & \text{if } j = i, \\ \mu_i\tau, & \text{if } j = i-1, \\ 0, & \text{otherwise,} \end{cases} \tag{3}$$

for integers $i, j \in \{0, 1, ..., N\}$. The one-step transition probabilities $P(\widetilde{I}_{n+1} = j|\widetilde{I}_n = i)$ of $\widetilde{\mathcal{I}}$ are inspired from the infinitesimal behavior in (1) and can be thus seen as approximations of $P(I(t+\tau) = j|I(t) = i)$ at *time steps* $t = \tau_n$ with $\tau_n = n\tau$, for $n \in \mathbb{N}_0$, when τ is sufficiently small. We note that (2) is just a technical condition so that the probabilities in (3) are all non-negative and, consequently, the process $\widetilde{\mathcal{I}}$ is well defined. Moreover, the minimum in (2) can be interpreted as the smallest mean holding time in any state of the process.

By denoting the infinitesimal generator of $\mathcal{I}$ and the one-step transition probability matrix of $\widetilde{\mathcal{I}}$ by $\mathbf{Q}$ and $\widetilde{\mathbf{P}}(\tau)$, respectively, we may express Eq. (3) in matrix form as $\widetilde{\mathbf{P}}(\tau) = \mathbf{I}_{N+1} + \tau\mathbf{Q}$, where $\mathbf{I}_a$ denotes the identity matrix of order a, and notice that $\widetilde{\mathcal{I}}$ is a uniformised version of $\mathcal{I}$. This means that the random variable $I(t)$ is identically distributed to $\widetilde{I}_{N(t)}$, where $\mathcal{N} = \{N(t) : t \geq 0\}$ is a Poisson process of rate τ^{-1}, and $\mathcal{N}$ and $\widetilde{\mathcal{I}}$ are assumed to be independent; for details on uniformization techniques, see e.g. the expository presentation of van Dijk et al. (2018). This relation enables us to express the transition function $\mathbf{P}(t) = (P_{i,j}(t) : i, j \in \{0, 1, ..., N\})$ of process $\mathcal{I}$ in terms of

$$\mathbf{P}(t) = \sum_{n=0}^{\infty} e^{\tau^{-1}t} \frac{(\tau^{-1}t)^n}{n!} \widetilde{\mathbf{P}}^n(\tau),$$

and if we are interested in approximating $\mathbf{P}(t)$ within $\varepsilon > 0$, then we may approximate $\mathbf{P}(t)$ by the finite sum

$$\sum_{n=n_0}^{n_1} e^{-\tau^{-1}t} \frac{(\tau^{-1}t)^n}{n!} \widetilde{\mathbf{P}}^n(\tau),$$

with $\sum_{n=0}^{n_0-1} e^{-\tau^{-1}t} \frac{(\tau^{-1}t)^n}{n!} + \sum_{n=n_1+1}^{\infty} e^{-\tau^{-1}t} \frac{(\tau^{-1}t)^n}{n!} < \varepsilon$; see e.g. the paper by Fox an Glynn (1988) for a method to find the truncation integers n_0 and n_1 given a predefined ε, and values τ and t.

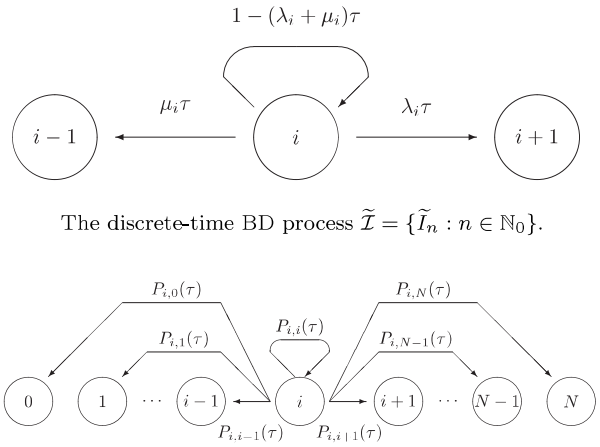

Fig. 2 A graphical comparison between the discrete-time BD process $\widetilde{\mathcal{I}}$ of Allen and Burgin (2000) and the continuous-time BD process $\mathcal{I}$ in terms of the one-step transition probabilities $P(\widetilde{I}_{n+1}=j|\widetilde{I}_n=i)$ in Eq. (3), for integers $j\in\{i-1,i,i+1\}$, and the time-dependent probabilities $P_{i,j}(\tau)$, for integers $j\in\{0,1,...,N\}$, respectively, for any number $i\in\{0,1,...,N\}$ of initially infective hosts.

It is worth noting that, unlike the continuous-time BD process $\mathcal{I}$ in (1) where multiple events can occur with strictly positive probability $P_{i,j}(\tau)=P(I(t+\tau)=j|I(t)=i)$ at any time interval $[t,t+\tau)$ and integers $i,j\in\{0,1,...,N\}$, in the discrete-time BD process $\widetilde{\mathcal{I}}$ it is assumed that at most one event occurs in the time period τ, either a new infection or the recovery of an infective host, which depends only on the state variables at the current time; see Figure 2.

Despite the fact that the discrete-time BD process $\widetilde{\mathcal{I}}$ is inherently linked to the time step τ verifying Eq. (2), it possesses two interesting properties that remain valid regardless of the concrete specification of τ. For a proof of Lemma 1, see Appendix A.

Lemma 1 *For any number $i\in\{0,1,...,N\}$ of initially infective hosts and time step τ satisfying condition (2), it is seen that*

(i) The limiting distribution of $\widetilde{\mathcal{I}}$ satisfies

$$\lim_{n\to\infty} P\left(\widetilde{I}_n=j\,\middle|\,\widetilde{I}_0=i\right)=\lim_{t\to\infty} P\left(I(t)=j|I(0)=i\right), \tag{4}$$

for integers $j\in\{0,1,...,N\}$.

(ii) The random number $\widetilde{T}=\inf\{n\in\mathbb{N}_0 : \widetilde{I}_n=0\}$ of steps before the first visit of process $\widetilde{\mathcal{I}}$ to state 0 is a discrete phase-type random variable of order N and representation $(\mathbf{e}_N(i),\widetilde{\mathbf{P}}^*(\tau))$, where $\widetilde{\mathbf{P}}^*(\tau)$ consists of one-step transition probabilities for states in $\{1,2,...,N\}$. It is also found that

$$\tau E[\widetilde{T}|\widetilde{I}_0=i]=E[T|I(0)=i], \tag{5}$$

and $Var(\tau\widetilde{T}|\widetilde{I}_0 = i) > Var(T|I(0) = i)$.

We note however that the random variables T and $\tau\widetilde{T}$ are not identically distributed – in fact, the former is a continuous phase-type random variable and the latter is a discrete one –, but a striking property is that their expectations (not higher moments) are identical, regardless of the particular choice of τ. As the reader may verify, the equality $\tau E[\widetilde{T}|\widetilde{I}_0 = i] = E[T|I(0) = i]$ amounts to Eq. (9) in the paper by Allen and Burgin (2000) for the expected duration of the epidemic beginning with i infective hosts in the continuous-time BD process $\mathcal{I}$ and its discrete-time counterpart $\widetilde{\mathcal{I}}$. We shall return to the discrete-time BD process $\widetilde{\mathcal{I}}$ – and the underlying selection of a sufficiently small value $\tau > 0$ – in Sections 4.2 and 4.3.

2.3 An alternative discrete-time Markov chain model

By assuming that time steps $\tau_n = n\tau$, for $n \in \mathbb{N}_0$, represent *inspection* times in $\mathcal{I}$, we may define the time-discretized process $\bar{\mathcal{I}} = \{\bar{I}_n = I(\tau_n) : n \in \mathbb{N}_0\}$, which is a discrete-time Markov chain having state space $\{0, 1, ..., N\}$ and one-step transition probability matrix $\bar{\mathbf{P}}(\tau) = (P_{i,j}(\tau) : i, j \in \{0, 1, ..., N\})$, where $P_{i,j}(\tau)$ are the transient probabilities of the original continuous-time BD process $\mathcal{I}$.

In this setting, the value $\tau > 0$ is not subject to (2) or any other condition, and one-step transition probabilities $P_{i,j}(\tau)$ are all strictly positive for every strictly positive rates β, β' and γ. The sequence of numbers $\bar{I}_n = I(\tau_n)$ of infective hosts, for $n \in \mathbb{N}_0$, results in a summary of the continuous-time BD process $\mathcal{I}$ in such a way that, with the exception of states $\bar{I}_n = I(\tau_n)$ and $\bar{I}_{n+1} = I(\tau_{n+1})$, states visited by $\mathcal{I}$ in any inter-inspection interval (τ_n, τ_{n+1}) are ignored.

In the general framework of Markov chains (see e.g. Chapter 5 in the book by Anderson (1991)), the time-discretized process $\bar{\mathcal{I}}$ is called the τ-*skeleton* of process $\mathcal{I}$ and can be used to derive some properties of the continuous-time BD process $\mathcal{I}$, such as the division of the state space into communicating classes and the limiting behavior as $t \to \infty$, from the corresponding properties of the discrete skeleton. More particularly, the proof of Lemma 2.(i) is based on Theorem 2 of Kingman (1963), from which the limiting results for a continuous function $f(t)$, as $t \to \infty$, can be deduced from the limiting behavior of the sequences $\{f(n\tau) : n \in \mathbb{N}_0\}$, as $n \to \infty$, for different values of τ. For a detailed proof of Lemma 2, see Appendix B.

Lemma 2 *For a fixed time step* $\tau > 0$ *and any number* $i \in \{0, 1, ..., N\}$ *of initially infective hosts, it is seen that*

(i) The limiting probabilities of $\bar{\mathcal{I}}$ *satisfy*

$$\lim_{n\to\infty} P\left(\bar{I}_n = j \,\middle|\, \bar{I}_0 = i\right) = \lim_{t\to\infty} P\left(I(t) = j | I(0) = i\right), \quad j \in \{0, 1, ..., N\}.$$

(ii) The random number $\bar{T} = \inf\{n \in \mathbb{N}_0 : \bar{I}_n = 0\}$ *of steps before the first visit of process* $\bar{\mathcal{I}}$ *to state* 0 *can be thought of as a discrete phase-type random variable of order* N *with representation* $(\mathbf{e}_N(i), \bar{\mathbf{P}}^*(\tau))$*, where* $\bar{\mathbf{P}}^*(\tau) = (P_{i,j}(\tau) : i, j \in \{1, 2, ..., N\})$*, and it is seen that* $T \leq_{st} \tau\bar{T}$ *in the usual stochastic order.*

In replacing the continuous-time BD process $\mathcal{I}$ in the SIS-model by a time-discretized version, Lemmas 1 and 2 allow us to establish a first comparison between the discrete-time BD process $\widetilde{\mathcal{I}}$ of Allen and Burgin (2000) and the discrete-time Markov chain $\bar{\mathcal{I}}$. In terms of long-term epidemic dynamics, processes $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$ are seen to become equivalent as the time index tends to infinity in the sense that they yield the same description of the number of infective hosts; i.e., $\lim_{n\to\infty} P(\widetilde{I}_n = j|\widetilde{I}_0 = i) = \lim_{n\to\infty} P(\bar{I}_n = j|\bar{I}_0 = i) = \lim_{t\to\infty} P(I(t) = j|I(0) = i)$, for integers $i, j \in \{0, 1, ..., N\}$. Roughly speaking, it is seen that the effect of the time step $\tau > 0$ on $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$ becomes negligible in the long term, as long as the discrete-time BD process $\widetilde{\mathcal{I}}$ is well defined (i.e., τ satisfies the additional condition (2)).

When the focus is on the random length T of an outbreak, $\widetilde{\mathcal{I}}$ leads to an exact description of the outbreak in terms of its expectation (see (5)), but the *scaled* length $\tau\widetilde{T}$ of the outbreak in $\widetilde{\mathcal{I}}$ is neither stochastically greater than, less than nor equal to the random length T of the outbreak in the SIS-model. On the contrary, the discrete-time Markov chain $\bar{\mathcal{I}}$ yields the stochastic ordering $T \leq_{st} \tau\bar{T}$, from which it follows that $E[T|I(0) = i] \leq \tau E[\bar{T}|\bar{I}_0 = i]$, for any number $i \in \{1, 2, ..., N\}$ of initially infective hosts.

3 Discrete-time versions on a time interval $[0, t']$

Let us now examine the dynamics of process $\mathcal{I}$ and those of its discrete-time versions $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$ from another angle. For a fixed time $t' > 0$ and an arbitrary integer $m \in \mathbb{N}$, we may focus on a finite sequence of inspection times $\tau_0 = 0 < \tau_1 < ... < \tau_{m-1} < \tau_m = t'$ with $\tau_n = n\tau$ and $\tau = m^{-1}t'$, yielding a decomposition of the interval $[0, t')$ into m sub-intervals $[\tau_{n-1}, \tau_n)$, for $n \in \{1, 2, ..., m\}$, of length τ. The question is if, for a suitably selected number $m \equiv m(t')$ of inspection times –and the corresponding time step τ– the summary of either numbers $\widetilde{\mathcal{I}}^{(m)} = \{\widetilde{I}_n : n \in \{0, 1, ..., m\}\}$ or numbers $\bar{\mathcal{I}}^{(m)} = \{\bar{I}_n : n \in \{0, 1, ..., m\}\}$ of infective hosts results in an accurate description of the continuous-time BD process $\mathcal{I}$ evolving over the predetermined time interval $[0, t')$.

At first sight, the following lemma plays a crucial role when, for a fixed time t', we formally intend to approximate the process $\mathcal{I}(t') = \{I(t) : t \in [0, t']\}$ by a time-discretized process $\bar{\mathcal{I}}^{(m)}$, for a sufficiently large m. The reader is alerted to the fact that random variables in $\mathcal{I}(t')$ and $\bar{\mathcal{I}}^{(m)}$ are not necessarily defined on a common probability space, whence a similar asymptotic result for $\widetilde{\mathcal{I}}^{(m)}$ does not seem to be plausible.

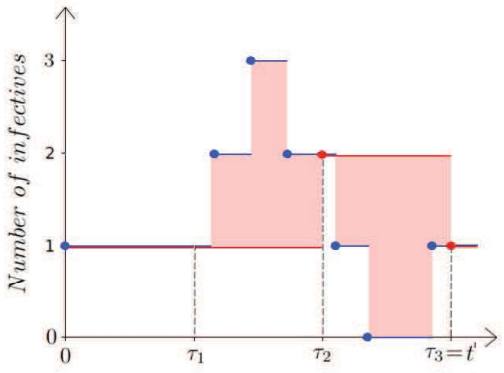

Fig. 3 A sample path of the continuous-time BD process $\mathcal{I}(t')$ (blue) versus the resulting sample path of $\bar{\mathcal{I}}^{(m)}$ (red) in the case $m = 3$, with $\bar{I}_0 = \bar{I}_1 = 1$, $\bar{I}_2 = 2$ and $\bar{I}_3 = 1$.

Lemma 3 *For a fixed time length $t' > 0$ and an arbitrary integer $m \in \mathbb{N}$, let Z_m be the total area between the sample paths of infectives in the processes $\mathcal{I}(t')$ and $\bar{\mathcal{I}}^{(m)}$; see Figure 3. Then, the sequence $\{Z_m : m \in \mathbb{N}\}$ of random variables converges almost surely to 0 as $m \to \infty$.*

Proof: Assume that, for times $t \in [0, t']$, the random numbers $I(t)$ of infective hosts are defined on a common probability space $(\Omega, \mathcal{A}, P)$. Under the exponential assumption for infectious periods, and exogenous and internal infectious contacts, it is clear that there exists a set $A(t') \in \mathcal{A}$ with $P(A(t')) = 1$ verifying $M(t'; \omega) < \infty$ for every $\omega \in A(t')$, where $M(t'; \omega)$ is the number of jumps of the sample path $I(.; \omega) : t \to I(t; \omega)$ for times $t \in [0, t']$; note that, for every fixed $\omega \in \Omega$, the mapping $I(.; \omega) : t \to I(t; \omega)$ is defined on the measure space $([0, t'], \mathcal{A}'[0, t'], \lambda)$, where $\mathcal{A}'[0, t']$ denotes the Borel σ-algebra on $[0, t']$ and λ is the Lebesgue measure. Furthermore, for each realization $\omega \in A(t')$, we may evaluate the smallest inter-jump time $l(t'; \omega)$, thus satisfying $l(t'; \omega) \leq M^{-1}(t'; \omega)t'$.

In giving a formal definition for Z_m, we formulate the time-discretized process $\bar{\mathcal{I}}^{(m)}$ as the continuous-time process $\mathcal{I}^{(m)}(t') = \{I^{(m)}(t) : t \in [0, t']\}$ with

$$I^{(m)}(t) = \sum_{n=1}^{m} I(\tau_{n-1}) 1_{[\tau_{n-1}, \tau_n)}(t), \quad t \in [0, t'],$$

where $1_B(t) = 1$ if $t \in B$, and 0 otherwise, which allows us to define the random variable Z_m in terms of the mapping $Z_m(.) : \omega \to \int_{[0,t']} Y_m(t; \omega) d\lambda$, where $Y_m(t; \omega) = |I(t; \omega) - I^{(m)}(t; \omega)|$ and $\int_B Y_m(t; \omega) d\lambda$ is the Lebesgue integral of $Y_m(t; \omega)$ on the set $B \in \mathcal{A}'[0, t']$. Then, the result follows by observing that $A(t') \subset \{\omega \in \Omega : \lim_{m \to \infty} Z_m(\omega) = 0\}$ since the sample paths of $\mathcal{I}(t')$ coincide with those of $\mathcal{I}^{(m)}(t')$ [1] in the case $m \geq M_0(t'; \omega)$, for a sufficiently

[1] For pairs $(t, \omega) \in [0, t'] \times A(t')$, it is seen that $I(t; \omega) = I^{(m)}(t; \omega)$.

large integer $M_0(t';\omega) > M(t';\omega)$. $\square$

Figure 3 illustrates, at the level of the underlying sample paths of processes $\mathcal{I}$ and $\bar{\mathcal{I}}$, why one would expect the relation $E[T|I(0)=i] \leq \tau E[\bar{T}|\bar{I}_0 = i]$ to hold, for any number $i \in \{1,2,...,N\}$ of initially infective hosts and time step $\tau > 0$. In a more general setting, we remark that $E[g(T)] \leq E[g(\tau\bar{T})]$ for any nondecreasing function g, since $T \leq_{st} \tau\bar{T}$ from Lemma 2.

Remark 1 By appealing to Theorem 6.14 in the book by Çinlar (2010), it is readily seen that

$$E[Z_m] = \int_{[0,t']} E[Y_m(t,.)]d\lambda,$$

since $\int_{[0,t']\times\Omega} Y_m(.,.)d(\lambda\otimes P) = \int_{[0,t']}\int_{\Omega} Y_m(t,.)dPd\lambda = \int_{\Omega}\int_{[0,t']} Y_m(t,\omega)d\lambda dP$, where $\lambda \otimes P$ is the *product* measure of λ and P on the measurable space $([0,t'] \times \Omega, \mathcal{A}'[0,t'] \otimes \mathcal{A})$.

Although it is straightforward to derive the limit result for Z_m in Lemma 3, computing the probability law of Z_m is not immediate. As a result, a direct comparison between the dynamics of processes $\mathcal{I}$ and $\bar{\mathcal{I}}$ during $[0,t']$ in terms of the probability law of Z_m does not seem to be feasible for practical use. In Section 4, we shall suggest the alternative of using extreme values, and estimating the approximating error in terms of the Hellinger distance between two probability distributions.

4 Extreme values

It is the purpose of this section to study extreme values in the continuous-time BD process $\mathcal{I}(t')$ for a fixed time length $t' > 0$ (Section 4.1), and the finite sequences $\widetilde{\mathcal{I}}^{(m)}$ and $\bar{\mathcal{I}}^{(m)}$, for an arbitrary integer $m \in \mathbb{N}$ and the resulting time step $\tau = m^{-1}t'$ (Section 4.2). The Hellinger distance between two probability distributions is then used to quantify the similarity between the resulting extreme value distributions (Section 4.3).

4.1 Extreme values in the continuous-time BD process $\mathcal{I}(t')$

For a fixed time length $t' > 0$, we let $I_{\min}(t')$ and $I_{\max}(t')$ denote the minimum and maximum number of hosts which are simultaneously infective during $[0,t']$, respectively, in the SIS-model, which can be expressed as

$$I_{\min}(t') = \min\{I(t):\ t \in [0,t']\} \quad \text{and} \quad I_{\max}(t') = \max\{I(t):\ t \in [0,t']\}.$$

The random variables $I_{\min}(t')$ and $I_{\max}(t')$ are related to the continuous-time BD process $\mathcal{I}(t')$ and, for a fixed number $i \in \{0,1,...,N\}$ of initially infective hosts, their joint probability law can be characterized by the conditional

probabilities

$$Q_i(t';y,y') = P\left(y \le I_{\min}(t'), I_{\max}(t') \le y' | I(0)=i\right),$$

for integers $0 \le y \le i \le y' \le N$. Note that the special choices $y=0$ and $y'=N$ yield the marginal probability laws of $I_{\max}(t')$ and $I_{\min}(t')$, respectively, in terms of $P(I_{\max}(t') \le y' | I(0)=i)$ and $1-P(I_{\min}(t') \le y-1 | I(0)=i)$.

For integers $1 \le y \le i \le y' \le N-1$, we observe that the probability $Q_i(t';y,y')$ equals the conditional probability that, starting from state $i \in \{y, y+1, ..., y'\}$, the continuous-time BD process $\mathcal{I}$ does not leave the sub-set $\{y, y+1, ..., y'\}$ of states before time t'. This conditional probability can be derived by studying the non-absorption probability in an absorbing process $\mathcal{J}(y,y') = \{J(t) : t \ge 0\}$ having two absorbing states $(y-1)^*$ and $(y'+1)^*$, and a class $\{y, y+1, ..., y'\}$ of transient states. The infinitesimal generator of $\mathcal{J}(y,y')$ has the block-structured form

$$\mathbf{Q}(y,y') = \begin{pmatrix} 0 & \mathbf{0}_{y'-y+1}^T & 0 \\ \mu_y \mathbf{e}_{y'-y+1}(1) & \mathbf{S}(y,y') & \lambda_{y'} \mathbf{e}_{y'-y+1}(y'-y+1) \\ 0 & \mathbf{0}_{y'-y+1}^T & 0 \end{pmatrix},$$

where the sub-matrix $\mathbf{S}(y,y')$ is given by

$$\mathbf{S}(y,y') = \begin{pmatrix} -(\lambda_y+\mu_y) & \lambda_y & & & \\ \mu_{y+1} & -(\lambda_{y+1}+\mu_{y+1}) & \lambda_{y+1} & & \\ & \ddots & \ddots & \ddots & \\ & & \mu_{y'-1} & -(\lambda_{y'-1}+\mu_{y'-1}) & \lambda_{y'-1} \\ & & & \mu_{y'} & -(\lambda_{y'}+\mu_{y'}) \end{pmatrix}.$$

In terms of process $\mathcal{J}(y,y')$, we have $Q_i(t';y,y') = 1 - P(J(t') \in \{(y-1)^*, (y'+1)^*\} | J(0)=i)$, for integers $1 \le y \le i \le y' \le N-1$, and a simple computation using the transition function of $\mathcal{J}(y,y')$ shows that

$$Q_i(t';y,y') = \mathbf{e}_{y'-y+1}(i-y+1) \exp\{\mathbf{S}(y,y')t'\} \mathbf{1}_{y'-y+1}. \tag{6}$$

Equation (6) is closely related to the solution of Krinik and Mortensen (2007) for the transient probability function of a finite continuous-time BD process (with or without catastrophes), which can be derived by using a recursive, Cayley-Hamilton approach, leading to Theorem 1.

Theorem 1 *For any time length $t' > 0$ and integers $1 \le y \le i \le y' \le N-1$, the conditional probability $Q_i(t';y,y')$ can be expressed as*

$$Q_i(t';y,y') = \sum_{l=y}^{y'} e^{z_l(y,y')t'} \sum_{k=y}^{y'} c_{i,k}^{(l)}(y,y'), \tag{7}$$

where $\{z_l(y,y') : l \in \{y, y+1, ..., y'\}\}$ are the eigenvalues of $\mathbf{S}(y,y')$, which are all strictly negative real numbers and satisfy $-2\max\{\lambda_k+\mu_k : k \in \{y, y+1, ..., y'\}\} \le z_y(y,y') < z_{y+1}(y,y') < ... < z_{y'}(y,y')$. For integers $k \in \{y, y+$

$1, ..., y'\}$, *coefficients* $\{c_{i,k}^{(l)}(y, y') : l \in \{y, y+1, ..., y'\}\}$ *in Eq.* (7) *satisfy a Vandermonde system of linear equations and are evaluated from*

$$\begin{pmatrix} c_{i,k}^{(y)}(y,y') \\ c_{i,k}^{(y+1)}(y,y') \\ \vdots \\ c_{i,k}^{(y')}(y,y') \end{pmatrix} = \mathbf{C}^{-1}(y,y') \begin{pmatrix} (\mathbf{S}(y,y'))_{i,k} \\ (\mathbf{S}^2(y,y'))_{i,k} \\ \vdots \\ (\mathbf{S}^{y'-y+1}(y,y'))_{i,k} \end{pmatrix},$$

where

$$\mathbf{C}(y,y') = \begin{pmatrix} z_y(y,y') & z_{y+1}(y,y') & \cdots & z_{y'}(y,y') \\ z_y^2(y,y') & z_{y+1}^2(y,y') & \cdots & z_{y'}^2(y,y') \\ \vdots & \vdots & & \vdots \\ z_y^{y'-y+1}(y,y') & z_{y+1}^{y'-y+1}(y,y') & \cdots & z_{y'}^{y'-y+1}(y,y') \end{pmatrix}. \quad (8)$$

Proof: The analytical treatment of Krinik and Mortensen (2007) for transient probability functions of finite continuous-time BD processes can be appropriately adapted to time-dependent probabilities of continuous-time Markov chains with a taboo subset of states, which is our case in process $\mathcal{J}(y, y')$. More particularly, it is found that the (i, k)th entry of the matrix exponential $\exp\{\mathbf{S}(y, y')t'\}$ in Eq. (6) has the form

$$(\exp\{\mathbf{S}(y,y')t'\})_{i,k} = \delta_{i,k} - \sum_{l=y}^{y'} c_{i,k}^{(l)}(y,y') \left(1 - e^{z_l(y,y')t'}\right),$$

for integers $i, k \in \{y, y+1, ..., y'\}$, where $\delta_{a,b}$ denotes the Kronecker's delta. To derive this expression, it is first seen that $\mathbf{S}(y, y')$ is non-singular and, consequently, the eigenvalues $\{z_l(y, y') : l \in \{y, y+1, ..., y'\}\}$ of $\mathbf{S}(y, y')$ are strictly negative with $-2\max\{\lambda_k + \mu_k : k \in \{y, y+1, ..., y'\}\} \leq z_y(y, y') < z_{y+1}(y, y') < ... < z_{y'}(y, y')$, since these eigenvalues are all real and distinct; see e.g. the book by Noble and Daniel (1988).

Equation (7) is then obtained by using the equality

$$\delta_{i,k} = \sum_{l=y}^{y'} c_{i,k}^{(l)}(y,y'),$$

which is derived by observing that the absorption of process $\mathcal{J}(y, y')$ into the subset $\{(y-1)^*, (y'+1)^*\}$ of absorbing states occurs almost surely in a finite time; i.e., $\lim_{t' \to \infty} P(J(t') = k | J(0) = i) = 0$, for transient states $i, k \in \{y, y+1, ..., y'\}$. This completes the proof. □

The following results summarize the marginal laws of $I_{\min}(t')$ and $I_{\max}(t')$, which are derived by adapting our preceding arguments to suitably defined absorbing processes $\mathcal{J}(y, N)$ and $\mathcal{J}(0, y')$ taking values in $\{(y)^*\} \cup \{y+1, y+2, ..., N\}$ and $\{0, 1, ..., y'\} \cup \{(y'+1)^*\}$, respectively.

Theorem 2 *For a fixed time length $t' > 0$ and integer $i \in \{0, 1, ..., N\}$, it is seen that*

(i) The conditional probabilities $P_i^{min}(t'; y) = P(I_{\min}(t') \leq y | I(0) = i)$ are given by

$$P_i^{min}(t'; y) = \begin{cases} 1, & if\ i \leq y \leq N, \\ 1 - \sum_{l=y+1}^{N} e^{z_l'(y+1)t'} \sum_{k=y+1}^{N} b_{i,k}^{(l)}(y+1), & if\ 0 \leq y \leq i-1, \end{cases} \tag{9}$$

where $\{z_l'(y+1) : l \in \{y+1, y+2, ..., N\}\}$ are the eigenvalues of sub-matrix $\mathbf{S}(y+1, N)$, which is defined in Theorem 1 with $\lambda_N \equiv 0$. These eigenvalues are all strictly negative real numbers and satisfy $-2\max\{\lambda_k + \mu_k, \mu_N : k \in \{y+1, y+2, ..., N-1\}\} \leq z_{y+1}'(y+1) < z_{y+2}'(y+1) < ... < z_N'(y+1)$. For integers $k \in \{y+1, y+2, ..., N\}$, coefficients $\{b_{i,k}^{(l)}(y+1) : l \in \{y+1, y+2, ..., N\}\}$ are specified from

$$\begin{pmatrix} b_{i,k}^{(y+1)}(y+1) \\ b_{i,k}^{(y+2)}(y+1) \\ \vdots \\ b_{i,k}^{(N)}(y+1) \end{pmatrix} = \mathbf{B}^{-1}(y+1) \begin{pmatrix} (\mathbf{S}(y+1, N))_{i,k} \\ (\mathbf{S}^2(y+1, N))_{i,k} \\ \vdots \\ (\mathbf{S}^{N-y}(y+1, N))_{i,k} \end{pmatrix},$$

where matrix $\mathbf{B}(y+1)$ has the form of $\mathbf{C}(y+1, N)$ in (8) with eigenvalues $z_l(y+1, N)$ replaced by $z_l'(y+1)$, for integers $l \in \{y+1, y+2, ..., N\}$.

(ii) The conditional probabilities $P_i^{max}(t'; y') = P(I_{\max}(t') \leq y' | I(0) = i)$ are given by

$$P_i^{max}(t'; y') = \begin{cases} 0, & if\ 0 \leq y' \leq i-1, \\ \sum_{l=0}^{y'} e^{z_l''(y')t'} \sum_{k=0}^{y'} d_{i,k}^{(l)}(y'), & if\ i \leq y' \leq N-1, \\ 1, & if\ y' = N, \end{cases} \tag{10}$$

where $\{z_l''(y') : l \in \{0, 1, ..., y'\}\}$ are the eigenvalues of sub-matrix $\mathbf{S}(0, y')$, which is defined in Theorem 1 with $\mu_0 \equiv 0$. These eigenvalues are all strictly negative real numbers and satisfy $-2\max\{\lambda_0, \lambda_k + \mu_k : k \in \{1, 2, ..., y'\}\} \leq z_0''(y') < z_1''(y') < ... < z_{y'}''(y')$. For integers $k \in \{0, 1, ..., y'\}$, coefficients $\{d_{i,k}^{(l)}(y') : l \in \{0, 1, ..., y'\}\}$ are specified from

$$\begin{pmatrix} d_{i,k}^{(0)}(y') \\ d_{i,k}^{(1)}(y') \\ \vdots \\ b_{i,k}^{(y')}(y') \end{pmatrix} = \mathbf{D}^{-1}(y') \begin{pmatrix} (\mathbf{S}(0, y'))_{i,k} \\ (\mathbf{S}^2(0, y'))_{i,k} \\ \vdots \\ (\mathbf{S}^{y'+1}(0, y'))_{i,k} \end{pmatrix},$$

where matrix $\mathbf{D}(y')$ has the form of $\mathbf{C}(0, y')$ in (8) with eigenvalues $z_l(0, y')$ replaced by $z_l''(y')$, for integers $l \in \{0, 1, ..., y'\}$.

As a last remark, we point out that the marginal mass functions of $I_{\min}(t')$ and $I_{\max}(t')$, and the joint mass function of $(I_{\min}(t'), I_{\max}(t'))$ can be routinely determined from Theorems 1-2 (Appendix C), leading to the probability laws

$$\begin{aligned}\mathcal{P}_i^{min}(t') &= \{p_i^{min}(t';y) : y \in \{0,1,...,i\}\},\\ \mathcal{P}_i^{max}(t') &= \{p_i^{max}(t';y') : y' \in \{i,i+1,...,N\}\},\\ \mathcal{Q}_i(t') &= \{q_i(t';y,y') : 0 \le y \le i \le y' \le N\},\end{aligned}$$

where $p_i^{min}(t';y) = P(I_{\min}(t') = y|I(0) = i)$, $p_i^{max}(t';y') = P(I_{\max}(t') = y'|I(0) = i)$ and $q_i(t';y,y') = P(I_{\min}(t') = y, I_{\max}(t') = y'|I(0) = i)$.

4.2 Extreme values in the discrete-time processes $\widetilde{\mathcal{I}}^{(m)}$ and $\bar{\mathcal{I}}^{(m)}$

Next, we turn to extreme values in the finite sequences $\widetilde{\mathcal{I}}^{(m)}$ and $\bar{\mathcal{I}}^{(m)}$. For the sake of brevity, we focus on $\bar{\mathcal{I}}^{(m)}$ and briefly comment on appropriate results for $\widetilde{\mathcal{I}}^{(m)}$.

In the case of the finite sequence $\bar{\mathcal{I}}^{(m)}$, the joint distribution of the random vector $(\bar{I}_{\min}(m), \bar{I}_{\max}(m))$, with $\bar{I}_{\min}(m) = \min\{\bar{I}_0, \bar{I}_1, ..., \bar{I}_m\}$ and $\bar{I}_{\max}(m) = \max\{\bar{I}_0, \bar{I}_1, ..., \bar{I}_m\}$, can be determined from the conditional probabilities

$$\bar{Q}_i(m;y,y') = P\left(y \le \bar{I}_{\min}(m), \bar{I}_{\max}(m) \le y' \,\middle|\, \bar{I}_0 = i\right), \quad 0 \le y \le i \le y' \le N,$$

for $i \in \{0,1,...,N\}$, with $\bar{Q}_i(m;0,y') = P(\bar{I}_{\max}(m) \le y'|\bar{I}_0 = i)$ and $1 - \bar{Q}_i(m;y,N) = P(\bar{I}_{\min} \le y-1|\bar{I}_0 = i)$.

One can repeat the arguments yielding Theorems 1-2 to show that, for integers $1 \le y \le i \le y' \le N-1$, it is possible to write down

$$\bar{Q}_i(m;y,y') = \mathbf{e}_{y'-y+1}(i-y+1)\bar{\mathbf{P}}^m(\tau;y,y')\mathbf{1}_{y'-y+1}, \tag{11}$$

with $\bar{\mathbf{P}}(\tau;y,y') = (P_{i,j}(\tau) : i,j \in \{y,y+1,...,y'\})$ and $\tau = m^{-1}t'$. More particularly, Eq. (11) is derived as the non-absorption probability before step m of an absorbing discrete-time process $\bar{\mathcal{J}}(y,y')$ taking values in $\{(y-1)^*\} \cup \{y,y+1,...,y'\} \cup \{(y'+1)^*\}$, where $\{(y-1)^*\}$ and $\{(y'+1)^*\}$ are absorbing states, and one-step transition probabilities between transient states $\{y,y+1,...,y'\}$ are given by $P_{i,j}(\tau)$, for $i,j \in \{y,y+1,...,y'\}$. One can also determine the conditional probabilities $\bar{P}_i^{min}(m;y) = 1 - P(\bar{I}_{\min}(m) \ge y+1|\bar{I}_0 = i)$ in terms of $P(\bar{I}_{\min}(m) \ge y|\bar{I}_0 = i) = 1$ if $y = 0$, and $\mathbf{e}_{N-y+1}(i-y+1)\bar{\mathbf{P}}^m(\tau;y,N)\mathbf{1}_{N-y+1}$ if $y \in \{1,2,...,i\}$; in a similar manner, the conditional probabilities $\bar{P}_i^{max}(m;y') = P(\bar{I}_{\max}(m) \le y'|\bar{I}_0 = i)$ are given by $P(\bar{I}_{\max}(m) \le y|\bar{I}_0 = i) = \mathbf{e}_{y'+1}(i+1)\bar{\mathbf{P}}^m(\tau;0,y')\mathbf{1}_{y'+1}$ if $y' \in \{i,i+1,...,N-1\}$, and 1, if $y' = N$.

The marginal mass functions

$$\begin{aligned}\bar{\mathcal{P}}_i^{min}(m) &= \{\bar{p}_i^{min}(m;y) : y \in \{0,1,...,i\}\},\\ \bar{\mathcal{P}}_i^{max}(m) &= \{\bar{p}_i^{max}(m;y') : y \in \{i,i+1,...,N\}\},\end{aligned}$$

with $\bar{p}_i^{min}(m;y) = P(\bar{I}_{\min}(m) = y|\bar{I}_0 = i)$ and $\bar{p}_i^{max}(m;y') = P(\bar{I}_{\max}(m) = y'|\bar{I}_0 = i)$, and the joint mass function

$$\bar{\mathcal{Q}}_i(m) = \{\bar{q}_i(m;y,y') : 0 \le y \le i \le y' \le N\},$$

with $\bar{q}_i(m;y,y') = P(\bar{I}_{\min}(m) = y, \bar{I}_{\max}(m) = y'|\bar{I}_0 = i)$, can be then easily evaluated (Appendix C) from the probabilities $\bar{Q}_i(m;y,y')$ in (11).

Turning to the extreme values $\widetilde{I}_{\min}(m) = \min\{\widetilde{I}_0, \widetilde{I}_1, ..., \widetilde{I}_m\}$ and $\widetilde{I}_{\max}(m) = \max\{\widetilde{I}_0, \widetilde{I}_1, ..., \widetilde{I}_m\}$ in the finite sequence $\widetilde{\mathcal{I}}^{(m)}$, we can replace $\bar{\mathbf{P}}(\tau;y,y')$ in the preceding arguments by the sub-matrix $\widetilde{\mathbf{P}}(\tau;y,y') = (P(\widetilde{I}_1 = j|\widetilde{I}_0 = i) : i,j \in \{y, y+1, ..., y'\})$ with $\tau = m^{-1}t'$ into (11) to derive the probabilities

$$\begin{aligned}
\widetilde{Q}_i(m;y,y') &= P(y \le \widetilde{I}_{\min}(m), \widetilde{I}_{\max}(m) \le y'|\widetilde{I}_0 = i),\ 0 \le y \le i \le y' \le N,\\
\widetilde{P}_i^{min}(m;y) &= P(\widetilde{I}_{\min}(m) \le y|\widetilde{I}_0 = i),\ y \in \{0,1,...,i\},\\
\widetilde{P}_i^{max}(m;y') &= P(\widetilde{I}_{\max}(m) \le y'|\widetilde{I}_0 = i),\ y' \in \{i, i+1, ..., N\}.
\end{aligned}$$

Finally, we note that the joint mass function

$$\widetilde{\mathcal{Q}}_i(m) = \{\widetilde{q}_i(m;y,y') : 0 \le y \le i \le y' \le N\}$$

of $(\widetilde{I}_{\min}(m), \widetilde{I}_{\max}(m))$, where $\widetilde{q}_i(m;y,y') = P(\widetilde{I}_{\min}(m) = y, \widetilde{I}_{\max}(m) = y'|\widetilde{I}_0 = i)$, and the marginal mass functions

$$\begin{aligned}
\widetilde{\mathcal{P}}_i^{min}(m) &= \{\widetilde{p}_i^{min}(m;y) : y \in \{0,1,...,i\}\},\\
\widetilde{\mathcal{P}}_i^{max}(m) &= \{\widetilde{p}_i^{max}(m;y') : y \in \{i, i+1, ..., N\}\}
\end{aligned}$$

of $\widetilde{I}_{\min}(m)$ and $\widetilde{I}_{\max}(m)$, where $\widetilde{p}_i^{min}(m;y) = P(\widetilde{I}_{\min}(m) = y|\widetilde{I}_0 = i)$ and $\widetilde{p}_i^{max}(m;y') = P(\widetilde{I}_{\max}(m) = y'|\widetilde{I}_0 = i)$, can be routinely evaluated (Appendix C) from the joint probabilities $\widetilde{Q}_i(m;y,y')$.

4.3 Discretization of continuous-time dynamics

When focusing on a predetermined time interval $[0,t']$, we can compare the dynamics of the process $\mathcal{I}(t')$ with those of the approximative discretized versions $\widetilde{\mathcal{I}}^{(m)}$ and $\bar{\mathcal{I}}^{(m)}$, in terms of the extreme value distributions analysed above and by means of the Hellinger distance (Pardo 2006). To this end, we point out that, for discrete random variables X and Y taking values on a common set $\mathcal{D}$, the Hellinger distance between the mass functions $\mathcal{P}_X = \{p_X(u) = P(X = u) : u \in \mathcal{D}\}$ and $\mathcal{P}_Y = \{p_Y(u) = P(Y = u) : u \in \mathcal{D}\}$ is defined by

$$H(\mathcal{P}_X, \mathcal{P}_Y) = \frac{1}{\sqrt{2}}\sqrt{\sum_{u\in\mathcal{D}}\left(\sqrt{p_X(u)} - \sqrt{p_Y(u)}\right)^2},$$

which amounts to the Euclidean norm of difference of square root vectors; i.e., $H(\mathcal{P}_X, \mathcal{P}_Y) = (\sqrt{2})^{-1}||\sqrt{\mathcal{P}_X} - \sqrt{\mathcal{P}_Y}||_2$ with $0 \le H(\mathcal{P}_X, \mathcal{P}_Y) \le 1$. The Hellinger

distance is closely related to the Bhattacharyya distance, and it measures the closeness of the probability distributions $\mathcal{P}_X$ and $\mathcal{P}_Y$ of two random variables X and Y. It was first defined in terms of the Hellinger integral, and it can be seen as a type of f-divergence satisfying the property

$$H^2(\mathcal{P}_X, \mathcal{P}_Y) \ \leq \ \delta(\mathcal{P}_X, \mathcal{P}_Y) \ \leq \ \sqrt{2} H(\mathcal{P}_X, \mathcal{P}_Y),$$

where $\delta(\mathcal{P}_X, \mathcal{P}_Y)$ denotes the total variation distance between $\mathcal{P}_X$ and $\mathcal{P}_Y$.

In Section 5 we demonstrate, using the Hellinger distance between $\mathcal{Q}_i(t')$ and $\bar{\mathcal{Q}}_i(m)$, and between $\mathcal{Q}_i(t')$ and $\widetilde{\mathcal{Q}}_i(m)$, that approximations of properties of process $\mathcal{I}(t')$, for a fixed time length $t' > 0$, by the corresponding properties of processes $\bar{\mathcal{I}}^{(m)}$ and $\widetilde{\mathcal{I}}^{(m)}$ –for a suitably chosen integer $m \in \mathbb{N}$ and resulting time step $\tau = m^{-1}t'$– are often very accurate.

5 Numerical experiments and discussion

In what follows, we illustrate how the dynamics of the continuous-time BD process $\mathcal{I}(t')$ can be significantly different from those of the finite sequences $\widetilde{\mathcal{I}}^{(m)}$ and $\bar{\mathcal{I}}^{(m)}$, and how these differences can depend on certain model parameters, the choice of m (equivalently, τ), as well as on the particular summary statistic of interest. In our numerical examples, we consider a population consisting of $N = 20$ hosts, and set $\gamma^{-1} = 1.0$ in such a way that time is measured in terms of the average recovery time of an infective host. To better appreciate relevant behaviors in our examples, a log scale is used in the x-axes of Figures 4-6.

In Figure 4, differences between the descriptor $I_{\min}(t')$ and the discrete-time versions $\widetilde{I}_{\min}(m)$ and $\bar{I}_{\min}(m)$ are measured in terms of the Hellinger distances $H(\mathcal{P}_i^{min}(t'), \widetilde{\mathcal{P}}_i^{min}(m))$ and $H(\mathcal{P}_i^{min}(t'), \bar{\mathcal{P}}_i^{min}(m))$, for time steps τ verifying $\tau = m^{-1}t'$ with $t' \in \{5.0, 10.0\}$, $\beta' \in \{1.0, 10.0\}$ and under the assumption of $I(0) = i$ initially infective hosts with $i = 10$. When focusing on the discrete-time process $\bar{I}_{\min}(m)$ (bottom row of sub-plots in Figure 4), it is seen that, as intuition tells us, the Hellinger distance behaves as a decreasing function of the integer m, irrespectively of other parameter values. Larger values of m are needed to reach a predetermined value of the Hellinger distance with increasing values of the time length t'. In Figure 4 it is also observed that larger values of the contact-related infection rate β lead to a more significant effort (i.e., larger integers m) needed for the finite sequence $\bar{\mathcal{I}}^{(m)}$ to mimic the continuous-time BD process $\mathcal{I}(t')$, in terms of the stochastic descriptor $I_{\min}(t')$. This could be explained by noting that larger values of β yield more events occurring during the time interval $[0, t']$, so that there are higher chances of *missing* relevant events during the discretization process. For a similar reason, increasing values of the exogenous infection rate β' lead to larger differences between $\mathcal{I}(t')$ and the discrete-time sequence $\bar{\mathcal{I}}^{(m)}$, and these differences are seen to increase with increasing values of the time length t'.

When focusing on the discrete-time counterpart $\widetilde{\mathcal{I}}^{(m)}$ in Figure 4 (top row), we recall that restrictions are put on the time step τ (i.e., on m) to ensure

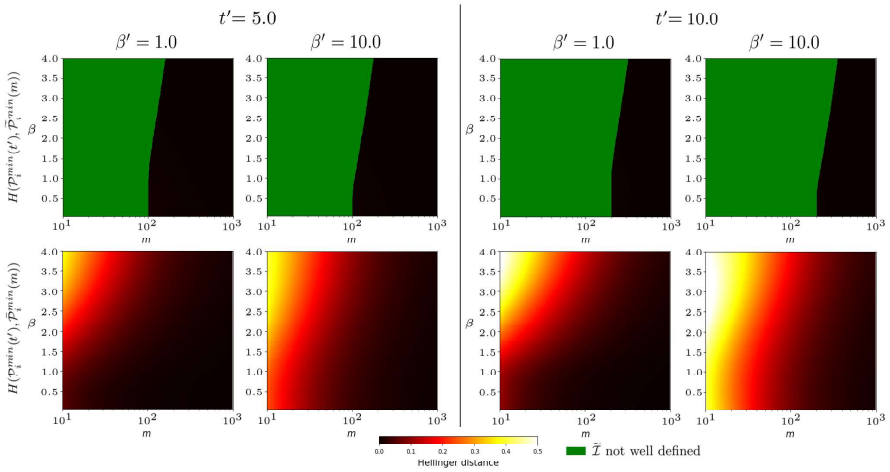

Fig. 4 Hellinger distances $H(\mathcal{P}_i^{min}(t'), \widetilde{\mathcal{P}}_i^{min}(m))$ and $H(\mathcal{P}_i^{min}(t'), \bar{\mathcal{P}}_i^{min}(m))$ between the mass function of $I_{\min}(t')$ and the mass functions of $\widetilde{I}_{\min}(m)$ and $\bar{I}_{\min}(m)$, respectively, versus parameters (m, β), for values $\beta' \in \{1.0, 10.0\}$, $N = 20$, $\gamma^{-1} = 1.0$ and time step τ verifying $\tau = m^{-1}t'$ with $t' \in \{5.0, 10.0\}$. $I(0) = \widetilde{I}_0 = \bar{I}_0 = 10$ initially infective hosts. The green region is related to pairs (m, β) for which the discrete-time BD process $\widetilde{\mathcal{I}}$ is not well defined, due to condition (2).

that the finite sequences $\widetilde{\mathcal{I}}^{(m)}$ give true transition probabilities in (3), whereas $\bar{\mathcal{I}}^{(m)}$ is always well defined for any selection of parameters (m, β). Thus, green regions in Figure 4 represent parameter regimes and values of τ (i.e., m) for which the process $\widetilde{\mathcal{I}}$ is not well defined. Still, it is remarkable to note that any selection of (m, β) yielding a well-defined sequence $\widetilde{\mathcal{I}}^{(m)}$ is enough to guarantee a good approximation of process $\mathcal{I}(t')$ in terms of the Hellinger distance $H(\mathcal{P}_i^{min}(t'), \widetilde{\mathcal{P}}_i^{min}(m))$, regardless of the exogenous infection rate β', the contact-related transmission rate β, and the time length t', even if the selected pair (m, β) is close to the border of the green region in Figure 4. In fact, for selections of (m, β) yielding well-defined sequences $\widetilde{\mathcal{I}}^{(m)}$, it is always verified that $H(\mathcal{P}_i^{min}(t'), \widetilde{\mathcal{P}}_i^{min}(m)) \leq H(\mathcal{P}_i^{min}(t'), \bar{\mathcal{P}}_i^{min}(m))$ in our examples, which shows a stronger similarity (in terms of the summary statistic $I_{\min}(t')$) between the continuous-time BD process $\mathcal{I}(t')$ and the finite sequence $\widetilde{\mathcal{I}}^{(m)}$ of Allen and Burgin (2000) than between process $\mathcal{I}(t')$ and the finite sequence $\bar{\mathcal{I}}^{(m)}$ defined by inspection (at least for large enough values of m so that $\widetilde{\mathcal{I}}^{(m)}$ is well defined). On the other hand, we can note that green regions are significantly wider for $t = 10'$, which shows how the discretization effort in terms of m needs to increase for process $\widetilde{\mathcal{I}}$ to be well defined, when looking into the dynamics over longer time intervals $[0, t']$. This effort also depends on some model parameters such as β, with larger values of β leading to larger intervals in green (i.e., larger values of m for which this discrete-time process is not properly defined). This indicates that the discretization effort (in terms of m)

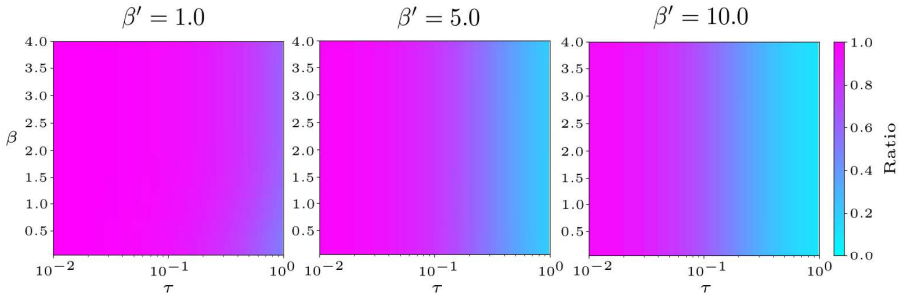

Fig. 5 Ratio ρ_i between the expected length of the outbreak in process $\mathcal{I}$ and its scaled version in process $\bar{\mathcal{I}}$, provided that $I(0) = \bar{I}_0 = 1$, versus parameters (τ, β), for values $\beta' \in \{1.0, 5.0, 10.0\}$, $N = 20$ and $\gamma^{-1} = 1.0$.

does not only depend on the length t' of the time interval of interest, but also on the parameter values for the particular population and infectious disease under study. It is at the same time striking how the alternative discrete-time process $\bar{\mathcal{I}}^{(m)}$ is able to approximate relatively well the dynamics of process $\mathcal{I}(t')$ –in terms of the summary statistic $I_{\min}(t')$– even in parameter regions leading to these green areas for process $\widetilde{\mathcal{I}}$. That is, process $\bar{\mathcal{I}}^{(m)}$ can relatively well approximate the continuous-time process even in parameter regimes for which $\widetilde{\mathcal{I}}$ is not even properly defined. Finally, we point out that very similar comments can be made to the alternative descriptor $I_{\max}(t')$, which has been omitted in this section for the sake of brevity.

In Figures 5-6 we focus on the discrete-time Markov chain $\bar{\mathcal{I}}$. Given that $E[T|I(0) = i] \leq \tau E[\bar{T}|\bar{I}_0 = i]$ from statement (ii) of Lemma 2, we explore in Figure 5 the value of the ratio $\rho_i = (\tau E[\bar{T}|\bar{I}_0 = i])^{-1} E[T|I(0) = i]$ between the expected length of an outbreak in process $\mathcal{I}$ and the scaled average in process $\bar{\mathcal{I}}$, under the assumption of $I(0) = \bar{I}_0 = i$ initially infective hosts with $i = 1$. We note that because we are focusing in Figure 5 on the length of an outbreak, rather than observing a fixed time interval $[0, t']$, it does not make sense here to consider a number of sub-intervals m, and thus we plot results in Figure 5 just as a function of the time step τ. We also note that the inequality $E[T|I(0) = i] \leq \tau E[\bar{T}|\bar{I}_0 = i]$ can be intuitively explained as follows: in some sample paths, the continuous-time process $\mathcal{I}$ may enter into state 0, and leave this state, between two consecutive inspection instants τ_n and τ_{n+1}, leading to a *non-detection* of the end of an outbreak for the time-discretized version $\bar{\mathcal{I}}$. The plots in Figure 5 suggest that, for fixed infection rates β and β', the scaled average $\tau E[\bar{T}|\bar{I}_0 = i]$ converges to the true expectation $E[T|I(0) = i]$ with decreasing values of the time step τ, complementing the statement (ii) of Lemma 2. This allows us to conclude that, in terms of the expected length of an outbreak, the time-discretized process $\bar{\mathcal{I}}$ becomes a more suitable approximation of the continuous-time BD process $\mathcal{I}$ with increasing values of the number m of inspection times, in such a way that better approximations are derived with decreasing values of the exogenous infection rate β'. On the

contrary, the convergence rate of $\tau E[\bar{T}|\bar{I}_0 = i]$ towards the expected length $E[T|I(0) = i]$ of an outbreak in the SIS-model is not affected significantly by the internal infection rate β, for a fixed rate β'. This is to be expected, since the probability of missing a visit to state 0 (i.e., missing the end of the outbreak) should mainly depend on the rate λ_0 for the process leaving this state, which depends on parameter β' but not on β. Note that an analogue to the behavior of the ratio ρ_i as a function of β' is not necessarily observed in terms of the Hellinger distance for extreme values; for example, numerical results not reported here show that smaller values of β' do not lead necessarily to small values of the Hellinger distance between $\mathcal{P}_i^{max}(t')$ and $\mathcal{P}_i^{max}(m)$ if m is small or moderate (e.g. $m < 50$ in Figure 4).

Some of the behaviors observed in Figures 4-5 and discussed above are directly related to the idea of missing events when looking at the discretized version $\bar{\mathcal{I}}$. For example, for a fixed time interval $[0, t']$ and when focusing on a visit to state 0 (i.e., the end of an outbreak), one can define the conditional probability $\delta_i(t')$ that the end of the outbreak is not observed by the finite sequence $\bar{\mathcal{I}}^{(m)}$ (i.e., $\bar{I}_n \neq 0$ for steps $n \in \{0, 1, ..., m\}$), provided that the end of an outbreak in the SIS-model occurs before time t' (i.e., $I(u) = 0$ for some $u < t'$) and $I(0) = \bar{I}_0 = i$ with $i \in \{1, 2, ..., N\}$. We note that the end of an outbreak in process $\mathcal{I}$ (respectively, process $\bar{\mathcal{I}}$) occurring before time t' (respectively, step m) can be readily identified with the event $\{I^{\{0\}}(t') = 0\}$ (respectively, $\{\bar{I}_m^{\{0\}} = 0\}$) in an auxiliary process $\{I^{\{0\}}(t) : t \geq 0\}$ (respectively, $\{\bar{I}_n^{\{0\}} : n \in \mathbb{N}_0\}$) which is described as the original process with $\lambda_0 = 0$; i.e., state 0 in process $\mathcal{I}$ (respectively, $\bar{\mathcal{I}}$) becomes an absorbing state in process $\{I^{\{0\}}(t) : t \geq 0\}$ (respectively, $\{\bar{I}_n^{\{0\}} : n \in \mathbb{N}_0\}$). Thus, the probability $\delta_i(t')$ of missing the end of an outbreak can be written as

$$\delta_i(t') = P\left(I^{\{0\}}(t') = 0 \,\middle|\, I^{\{0\}}(0) = i\right) - P\left(\bar{I}_m^{\{0\}} = 0 \,\middle|\, \bar{I}_0^{\{0\}} = i\right),$$

for integers $i \in \{1, 2, ..., N\}$, and

$$P\left(I^{\{0\}}(t') = 0 \,\middle|\, I^{\{0\}}(0) = i\right) = \sum_{k=1}^{N} \sum_{l=1}^{N} c_{i,k}^{(l)}(1, N) \left(1 - e^{z_l(1,N)t'}\right),$$

$$P\left(\bar{I}_m^{\{0\}} = 0 \,\middle|\, \bar{I}_0^{\{0\}} = i\right) = 1 - \mathbf{e}_N(i+1) \left(\bar{\mathbf{P}}^*(\tau)\right)^m \mathbf{1}_N,$$

where eigenvalues $\{z_l(1, N) : l \in \{1, 2, ..., N\}\}$ of matrix $\mathbf{S}(1, N)$ and coefficients $\{c_{i,k}^{(l)}(1, N) : l \in \{1, 2, ..., N\}\}$, for integers $k \in \{1, 2, ..., N\}$, are specified in Theorem 1, and the one-step transition probability sub-matrix $\bar{\mathbf{P}}^*(\tau)$ is described in Lemma 2.

The behavior of the probability $\delta_i(t')$ is shown in Figure 6 for time length $t' = 10.0$. It is seen that $\delta_i(t')$ increases with increasing values of β', where smaller values of β' are linked to shorter outbreaks in our examples. On the other hand, and by noting that the expected recovery time of the initially infective host is equal to one, the value $\beta' = 10.0$ leads to a major outbreak in our examples, and shows how a large integer m is necessary for the finite

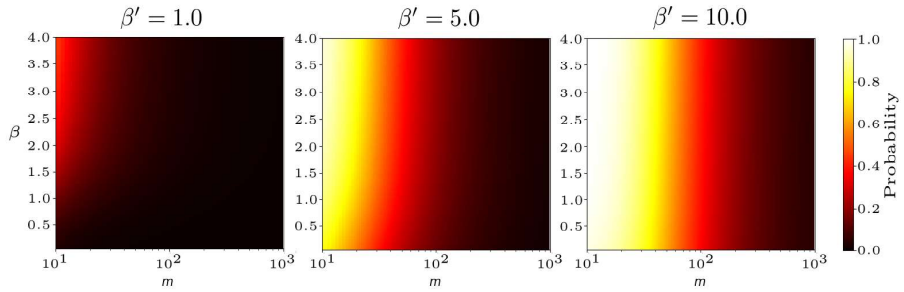

Fig. 6 Conditional probability $\delta_i(t')$ of missing the end of an outbreak in process $\bar{\mathcal{I}}$ during the time interval $[0, t']$ with $t' = 10.0$, provided that $I(0) = \bar{I}_0 = i$ with $i = 1$, versus parameters (m, β), for values $\beta' \in \{1.0, 5.0, 10.0\}$, $N = 20$, $\gamma^{-1} = 1.0$ and time step τ verifying $\tau = m^{-1}t'$.

sequence $\bar{\mathcal{I}}^{(m)}$ to record the end of an outbreak. We also note that the increasing behavior of $\delta_i(t')$ with increasing values of β' is to be expected, since parameter β' represents the external infection rate, which is the parameter allowing the process to escape from state 0. Thus, large values of β' can lead to missing the end of the outbreak, if an exogenous infection happens quickly enough relative to the number of inspection instants. In terms of $\delta_i(t')$, the influence of the contact rate β on the number m of inspection times is seen to be less relevant in Figure 6 due to the magnitudes of parameters γ and β', and the time length t'. We can still appreciate that larger values of β lead to slightly larger probabilities of missing the end of the outbreak. This is likely because once the process has escaped state 0 due to rate β', the chances of the process going back to 0 before the next inspection instant (and so that the end of the outbreak would be captured by the discrete-time process $\bar{\mathcal{I}}^{(m)}$) depend on the parameter β, with larger values of β moving the process towards state 2 rather than 0.

6 Conclusions

We have studied analytically and numerically two discrete-time versions of the continuous-time BD process $\mathcal{I}$ recording the number $I(t)$ of infective hosts at time t in the stochastic SIS epidemic model. The first version corresponds to the discrete-time BD process $\widetilde{\mathcal{I}} = \{\widetilde{I}_n : n \in \mathbb{N}_0\}$ of Allen and Burgin (2000) (see also the paper by Chalub and Souza (2014)), which is defined in Eq. (3) by approximating the transition probabilities $P(I(t+\tau) = j | I(t) = i)$ at time steps $t = n\tau$ with $n \in \mathbb{N}_0$, for a sufficiently small value $\tau > 0$ and states $j \in \{i-1, i, i+1\}$ with $i, j \in \{0, 1, ..., N\}$. We have revisited the discrete-time BD process $\widetilde{\mathcal{I}}$ of Allen and Burgin (2000) by showing here that processes $\mathcal{I}$ and $\widetilde{\mathcal{I}}$ become equivalent as the time index tends to infinity (Lemma 1, statement (i)), and that the length T of an outbreak in process $\mathcal{I}$ and its counterpart $\tau\widetilde{T}$ in process $\widetilde{\mathcal{I}}$ are identical in terms of their expectations (Lemma 1, statement

(ii)). In deriving the second approximation, the number $I(t)$ of infectives is collected at a sequence $\{\tau_n : n \in \mathbb{N}_0\}$ of inspection times with $\tau_n = n\tau$, for $n \in \mathbb{N}_0$ and a predetermined value $\tau > 0$. Although the resulting process $\bar{\mathcal{I}} = \{\bar{I}_n = I(\tau_n) : n \in \mathbb{N}_0\}$ is a discrete-time Markov chain with strictly positive one-step transition probabilities $P(I(t+\tau) = j | I(t) = i)$ for any states $i, j \in \{0, 1, ..., N\}$ and times $t = \tau_n$, we have verified that, in a similar manner to the discrete-time BD process $\widetilde{\mathcal{I}}$, processes $\mathcal{I}$ and $\bar{\mathcal{I}}$ are equivalent to each other with increasing values of the time index (Lemma 2, statement (i)), and that the scaled length $\tau\bar{T}$ of an outbreak in $\bar{\mathcal{I}}$ satisfies $T \leq_{st} \tau\bar{T}$ in the usual stochastic order (Lemma 2, statement (ii)).

It is worthwhile to note that the asymptotic property shown in statement (i) of Lemma 1 for $\mathcal{I}$ and $\widetilde{\mathcal{I}}$ is a well-known result (see e.g. Result 3.1 in the paper by van Dijk et al. (2018)) in the more general framework of a continuous-time Markov chain and its uniformized version, whereas statement (i) of Lemma 2 for $\mathcal{I}$ and $\bar{\mathcal{I}}$ has easily been deduced from the classical approach of Kingman (1963) to derive the limiting result for the transition function $P_{i,j}(t)$ as $t \to \infty$ by applying known results for discrete-time processes to the discrete skeleton of scale τ. This means that similar results could be readily derived for the continuous-time process arising in other epidemic models –based on Markov chains– and the corresponding uniformized version and discrete skeleton of scale τ. There is clearly future work to be done on the extension of statement (ii) of Lemmas 1 and 2 about the random lengths T, $\tau\widetilde{T}$ and $\tau\bar{T}$ of an outbreak in processes $\mathcal{I}$, $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$ to other epidemic models and, more interestingly, to first-passage times of a continuous-time Markov chain and its discrete counterparts in the uniformized version and the skeleton of scale τ.

Our arguments for the total area Z_m between the sample paths of infectives in the processes $\mathcal{I}(t')$ and $\bar{\mathcal{I}}^{(m)}$ in Lemma 3 are inherently linked to the fact that the time step τ decreases with increasing values of m, for every fixed length $t' > 0$, since $\tau = m^{-1}t'$. A more difficult problem is the study of whether or not an analogue of Lemma 3 holds for $t' = \infty$, since other different conditions on the variation of τ as a function of m should be required. In analyzing the limit of Z_m as $m \to \infty$, the problem for $t' = \infty$ does not seem to be immediate and, to the best of our knowledge, has not been previously addressed in the more general setting of a continuous-time Markov chain and its discrete skeleton of scale τ, which makes it an interesting open problem.

In an attempt to compare the dynamics of process $\mathcal{I}$ evolving over a time interval $[0, t']$ and those of its discrete-time versions $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$, we have first studied extreme values in the continuous-time BD process $\mathcal{I}(t') = \{I(t) : t \in [0, t']\}$ (Section 4.1), and the finite discrete-time sequences $\widetilde{\mathcal{I}}^{(m)} = \{\widetilde{I}_n : n \in \{0, 1, ..., m\}\}$ and $\bar{\mathcal{I}}^{(m)} = \{\bar{I}_n : n \in \{0, 1, ..., m\}\}$ (Section 4.2) for an arbitrary integer $m \in \mathbb{N}$ and the time step $\tau = m^{-1}t'$. Then, we have used the Hellinger distance (Section 4.3) between the resulting extreme value distributions to obtain global error control when, for a fixed time interval of length t', the continuous-time BD process $\mathcal{I}(t')$ is summarized in terms of either the

discrete-time model $\widetilde{\mathcal{I}}^{(m)}$ of Allen and Burgin (2000) or the time-discretized version $\bar{\mathcal{I}}^{(m)}$. Observe that, as a consequence of Eq. (11), the approach described in Section 4 for $\widetilde{\mathcal{I}}^{(m)}$ and $\bar{\mathcal{I}}^{(m)}$ applies to other finite discrete-time sequences, provided they can be formulated as a discrete-time Markov chain, and it complements the limit result for the total area between the sample paths of infectives in the processes $\mathcal{I}(t')$ and $\bar{\mathcal{I}}^{(m)}$ (Section 3), as m tends to infinity.

A particularly appealing feature of our approach in Section 4.1 is related to the analytical treatment of the exponential of certain matrices $\mathbf{S}(y, y')$, for integers $0 \leq y \leq y' \leq N$, using techniques of Cayley-Hamilton type, which is inspired from the solution of Krinik and Mortensen (2007) for transient probabilities of finite continuous-time BD process with or without catastrophes. The solution in Theorems 1-2 is given in terms of the eigenvalues of $\mathbf{S}(y, y')$ and a related system of linear equations, regardless of the time length t'; see the paper by Moler and Van Loan (2003) for a review of ways to compute the exponential of a matrix, including splitting methods (Gómez-Corral and López-García 2013). In our approach, the nature of the time-dependent solution contrasts however with the simplicity to derive extreme values during a *regenerative* cycle, such as an outbreak in epidemic models of SIS type (Economou et al. 2015) and multi-type epidemic models (Amador et al. 2019; Gómez-Corral and López-García 2018), an extinction cycle in two-species competition processes (Gómez-Corral and López-García 2012), and maximum clonal sizes for a naive T cell clonotype (Artalejo et al. 2017).

In terms of computational times, there is no clear relationship between the process $\mathcal{I}$ and its discrete-time versions $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$. In this sense, we remark here that, in a similar manner to Theorems 1 and 2, the solution in Eq. (11) can be reduced to the computation of the eigenvalues and eigenvectors of $\widetilde{\mathbf{P}}(\tau; y, y')$ and $\bar{\mathbf{P}}(\tau; y, y')$, respectively, by using the method of eigenvalues; see e.g. Kulkarni (1995, Section 2.4.2). A similar remark can be made for $P(T \leq t | I(0) = i)$ and the computation of matrix powers arising in $P(\tau\widetilde{T} \leq t | \widetilde{I}_0 = i)$ and $P(\tau\bar{T} \leq t | \bar{I}_0 = i)$, for any time t. Therefore, the advantages and disadvantages that the continuous-time BD process $\mathcal{I}$ could have —compared to either the discrete-time BD process $\widetilde{\mathcal{I}}$ of Allen and Burgin (2000) or the discrete-time Markov chain $\bar{\mathcal{I}}$— should be more related to the ease of collecting data from one or other model.

In presenting the numerical experiments in Section 5, our intention has been to emphasize the fact that the simplifying assumption yielding $\widetilde{\mathcal{I}}$ –based on restricting jumps in $\mathcal{I}$ to neighboring states– on the one hand, and to describe the disease using the Markov chain model $\bar{\mathcal{I}}$ –by inspecting the continuous-time BD process $\mathcal{I}$– on the other hand, are two distinct issues and a comparative study, while being recommended, is somewhat ignored in early presentations of discrete-time epidemic models in the literature. For this reason, we have illustrated how the dynamics of the continuous-time BD process $\mathcal{I}(t')$ can be similar to (or different from) those of the discrete-time sequences $\widetilde{\mathcal{I}}^{(m)}$ and $\bar{\mathcal{I}}^{(m)}$, and how these similarities (or differences) can depend on the

selection of the underlying time step τ and other model rates. To do this, the focus has been on the Hellinger distance between $\mathcal{Q}_i(t')$ and $\widetilde{\mathcal{Q}}_i(m)$, and between $\mathcal{Q}_i(t')$ and $\bar{\mathcal{Q}}_i(m)$, and their marginal probability laws. A particularly striking behaviour observed in our numerical exploration, and when focusing on the discrete-time BD process $\widetilde{\mathcal{I}}^{(m)}$, is that the dynamics of this process can accurately mimic those of the continuous-time BD process $\mathcal{I}(t')$ when focusing on some particular summary statistics (e.g. extreme values in Figure 4), even when the discretization step τ is relatively large, as long as it leads to a well-defined process $\widetilde{\mathcal{I}}^{(m)}$ according to Eq. (2). It should be pointed out that a similar approach for the random lengths T, $\tau\widetilde{T}$ and $\tau\bar{T}$ of an outbreak in processes $\mathcal{I}$, $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$, respectively, cannot be addressed in terms of the Hellinger distance between the probability laws of T and $\tau\widetilde{T}$, and between the probability laws of T and $\tau\bar{T}$, since T is a continuous random variable, and $\tau\widetilde{T}$ and $\tau\bar{T}$ are discrete. We stress here that it is necessary that the probability measures $\mathcal{P}_X$ and $\mathcal{P}_Y$ of two random variables X and Y are absolutely continuous with respect to a third probability measure for the Hellinger distance between $\mathcal{P}_X$ and $\mathcal{P}_Y$ to be defined.

We have developed our arguments on the assumption of birth rates $\lambda_i > 0$, for $i \in \{0, ..., N-1\}$, and death rates $\mu_i > 0$, for $i \in \{1, ..., N\}$, in the continuous-time BD process $\mathcal{I}$, and not making use of the model parameters (i.e., rates β, β' and γ that determine rates λ_i and μ_i as a function of the state variable) in an explicit way. Therefore, analytical expressions in Sections 2-4 are valid for any continuous-time BD process $\mathcal{I}$ –with strictly positive birth and death rates– and the uniformized version $\widetilde{\mathcal{I}}$ and the discrete skeleton $\bar{\mathcal{I}}$ of scale τ. Although the standard SIS-model, which is related to the limiting case $\beta' = 0$, leads to the birth rate $\lambda_0 = 0$, it can also be treated analytically by using the approach of Sections 2-4 with obvious modifications. More concretely, the continuous-time BD process $\mathcal{I}$, and the discrete-time processes $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$ in the case $\beta' = 0$ are defined on a reducible state space with the absorbing state 0 and the class of transient states $\{1, ..., N\}$. This implies that, in a similar manner to statement (i) of Lemmas 1-2, it is found that

$$\begin{aligned}\lim_{t\to\infty} P(I(t) = j | I(0) = i) &= \lim_{n\to\infty} P\left(\widetilde{I}_n = j | \widetilde{I}_0 = i\right) \\ &= \lim_{n\to\infty} P\left(\bar{I}_n = j | \bar{I}_0 = i\right), \quad j \in \{0, ..., N\},\end{aligned}$$

with $\lim_{t\to\infty} P(I(t) = j | I(0) = i) = \delta_{0,j}$, irrespectively of the initial number $i \in \{0, ..., N\}$ of infective hosts. By the same argument as Section 2.1, it is also seen that the random lengths T, $\tau\widetilde{T}$ and $\tau\bar{T}$ of an outbreak in processes $\mathcal{I}$, $\widetilde{\mathcal{I}}$ and $\bar{\mathcal{I}}$, respectively, for $\beta' = 0$ are phase-type random variables satisfying statement (ii) of Lemmas 1-2; the only precaution that one should take is that sub-matrices $\mathbf{Q}^*$, $\widetilde{\mathbf{P}}^*(\tau)$ and $\bar{\mathbf{P}}^*(\tau)$ should be computed with $\lambda_i = N^{-1}\beta i(N-i)$, instead of $\lambda_i = N^{-1}(\beta i + \beta')(N-i)$. Extreme values in the case $\beta' = 0$ may also be analyzed by repeating almost verbatim the argument of Sections 4.1-4.2. Nevertheless, we remark here that, although the argument is based newly on the use of auxiliary absorbing processes and the

Cayley-Hamilton approach, the resulting expressions for $\mathcal{Q}_i(t')$, $\widetilde{\mathcal{Q}}_i(m)$ and $\bar{\mathcal{Q}}_i(m)$ –and the marginal probability laws $\mathcal{P}_i^{max}(t')$, $\widetilde{\mathcal{P}}_i^{max}(m)$ and $\bar{\mathcal{P}}_i^{max}(m)$, as well as $\mathcal{P}_i^{min}(t')$, $\widetilde{\mathcal{P}}_i^{min}(m)$ and $\bar{\mathcal{P}}_i^{min}(m)$– cannot be obtained directly from the analytical expressions in Theorems 1-2 by taking $\beta' = 0$.

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Appendix A: Proof of Lemma 1

Statement (i) of Lemma 1 is derived by noting that the row vectors $\mathbf{p} = (\lim_{t\to\infty} P(I(t) = j|I(0) = i) : j \in \{0, 1, ..., N\})$ and $\widetilde{\pi} = (\lim_{n\to\infty} P(\widetilde{I}_n = j|\widetilde{I}_0 = i) : j \in \{0, 1, ..., N\})$ are the unique solution, up to normalization, of the balance equations for the continuous-time BD process $\mathcal{I}$ and the discrete-time BD process $\widetilde{\mathcal{I}}$, which are given by $\mathbf{pQ} = \mathbf{0}_{N+1}^T$ and $\widetilde{\pi} = \widetilde{\pi}\widetilde{\mathbf{P}}(\tau)$, respectively, where $\mathbf{0}_a$ denotes the column null vector of order a. The details can be found, for example, in Result 3.1 of (van Dijk et al. 2018).

In proving the equality $\tau E[\widetilde{T}|\widetilde{I}_0 = i] = E[T|I(0) = i]$ in statement (ii) of Lemma 1, we notice that $\widetilde{T}$ is a discrete phase-type random variable of order N and representation $(\mathbf{e}_N(i), \widetilde{\mathbf{P}}^*(\tau))$. Then, the equality $\tau E[\widetilde{T}|\widetilde{I}_0 = i] = E[T|I(0) = i]$ is derived from the general-purpose expression $E[\widetilde{T}|\widetilde{I}_0 = i] = \mathbf{e}_N(i)(\mathbf{I}_N - \widetilde{\mathbf{P}}^*(\tau))^{-1}\mathbf{1}_N$ for the expected value of a discrete phase-type random variable, where $\mathbf{1}_a$ denotes the column unit vector of order a, and the fact that $\mathbf{I}_N - \widetilde{\mathbf{P}}^*(\tau) = -\tau\mathbf{Q}^*$. In a similar manner, the inequality $Var(\tau\widetilde{T}|\widetilde{I}_0 = i) > Var(T|I(0) = i)$ is derived by noting that $E[(\tau\widetilde{T})^2|\widetilde{I}_0 = i] = E[T^2|I(0) = i] + 3\tau E[T|I(0) = i]$. This completes the proof. □

Appendix B: Proof of Lemma 2

The proof of statement (i) of Lemma 2 is based on the fact that $\bar{\mathcal{I}}$ is the discrete skeleton of scale τ of $\mathcal{I}$ and mostly repeats the arguments in Section 3 of (Kingman 1963). To be concrete, we first recall that the continuous-time BD process $\mathcal{I}$ is irreducible and positive recurrent, whence the limit of $P(I(t) = j|I(0) = i)$ as $t \to \infty$ exists and does not depend on i. In a similar manner, we have that, for any value $\tau > 0$, the resulting time-discretized process $\bar{\mathcal{I}}$ is irreducible, aperiodic and positive recurrent so that the limit of $P(\bar{I}_n = j|\bar{I}_0 = i)$ as $n \to \infty$ exists and does not depend on i. Then, statement (i) of Lemma 2 follows immediately from Theorem 2 of (Kingman 1963) since $P(\bar{I}_n = j|\bar{I}_0 = i) = P(I(n\tau) = j|I(0) = i)$.

The random variable $\bar{T}$ is the first-passage time of process $\bar{\mathcal{I}}$ to state 0, which clearly indicates (see e.g. Section 2.5 of (Latouche and Ramaswami 1999)) that we are dealing with a discrete phase-type distribution of order N and representation $(\mathbf{e}_N(i), \bar{\mathbf{P}}^*(\tau))$. In order to prove the stochastic ordering $T \leq_{st} \tau\bar{T}$, we observe that the underlying condition $P(T > t) \leq P(\tau\bar{T} > t)$, for all $t \in \mathbb{R}$, reduces to the inequality $\mathbf{e}_N(i)e^{\mathbf{Q}^*t}\mathbf{1}_N \leq \mathbf{e}_N(i)(\bar{\mathbf{P}}^*(\tau))^{[\tau^{-1}t]}\mathbf{1}_N$, for $t > 0$, where $[x]$ denotes the integer part of x, since T and $\tau\bar{T}$ are non-negative. To prove this inequality, we first derive the relation $\mathbf{e}_N(i)e^{\mathbf{Q}^*t}\mathbf{1}_N \leq \mathbf{e}_N(i)e^{\mathbf{Q}^*[\tau^{-1}t]\tau}\mathbf{1}_N$, for $t > 0$, by noting that $\mathbf{e}_N(i)e^{\mathbf{Q}^*u}\mathbf{1}_N$ records the conditional probability that, starting from state i, the process $\mathcal{I}$ remains in states of $\{1, ..., N\}$ for the time interval $[0, u]$ and values $u \in \{[\tau^{-1}t]\tau, t\}$ with $[\tau^{-1}t]\tau \leq t$. Then, the remainder of the proof follows by observing that $e^{\mathbf{Q}^*\tau} \leq \bar{\mathbf{P}}^*(\tau)$. This last relation is found by noting that the (i, j)-th entry of $e^{\mathbf{Q}^*\tau}$ is the conditional probability that, starting from state i, the process $\mathcal{I}$ visits state j at time τ under the taboo of the subset $\{0\}$, whereas the (i, j)-th entry of matrix $\bar{\mathbf{P}}^*(\tau)$ is the conditional probability that $\mathcal{I}$ visits state j at time τ, provided that the intial state is i. □

Appendix C: Marginal and joint mass functions

The marginal mass functions $\mathcal{P}_i^{min}(t')$ and $\mathcal{P}_i^{max}(t')$ of $I_{\min}(t')$ and $I_{\max}(t')$, respectively, can be obtained from the probabilities

$$p_i^{min}(t';y) = \begin{cases} P_i^{min}(t';0), & if\ y=0, \\ P_i^{min}(t';y) - P_i^{min}(t';y-1), & if\ y \in \{1,2,...,i-1\}, \\ 1 - P_i^{min}(t';i-1), & if\ y=i, \end{cases}$$

$$p_i^{max}(t';y') = \begin{cases} P_i^{max}(t';i), & if\ y'=i, \\ P_i^{max}(t';y') - P_i^{max}(t';y'-1), & if\ y' \in \{i+1,i+2,...,N-1\}, \\ 1 - P_i^{max}(t';N-1), & if\ y'=N. \end{cases}$$

Furthermore, the joint mass function $\mathcal{Q}_i(t')$ of $(I_{\min}(t'), I_{\max}(t'))$ is specified as follows:

(i) In the case $i \in \{0, N\}$, we have $q_0(t';0,y') = p_0^{max}(t';y')$ and $q_N(t';y,N) = p_N^{min}(t';y')$, for integers $y, y' \in \{0,1,...,N\}$.

(ii) For a number of $i \in \{1,2,...,N-1\}$ initially infective hosts, it is seen that $q_i(t';i,y') = Q_i(t';i,i)$ if $y'=i$, and $Q_i(t';i,y') - Q_i(t';i,y'-1)$ if $y' \in \{i+1,i+2,...,N\}$; and $q_i(t';y,y') = Q_i(t';y,i) - Q_i(t';y+1,i)$ if $y'=i$, and $Q_i(t';y,y') - Q_i(t';y+1,y') - Q_i(t';y,y'-1) - Q_i(t';y+1,y'-1)$ if $y' \in \{i+1,i+2,...,N\}$, for integers $y \in \{0,1,...,i-1\}$.

The joint mass function of $(\bar{I}_{min}(m), \bar{I}_{max}(m))$ and the marginal mass functions of $\bar{I}_{min}(m)$ and $\bar{I}_{max}(m)$ can be also evaluated from the above expressions by using probabilities $\bar{Q}_i(m;y,y')$, $\bar{P}_i^{min}(m;y)$ and $\bar{P}_i^{max}(m;y')$ instead of $Q_i(t';y,y')$, $P_i^{min}(t';y)$ and $P_i^{max}(t';y')$, respectively; in a similar manner, the replacement by $\widetilde{Q}_i(m;y,y')$, $\widetilde{P}_i^{min}(m;y)$ and $\widetilde{P}_i^{max}(m;y')$ yields the probability laws of $(\widetilde{I}_{min}(m), \widetilde{I}_{max}(m))$, $\widetilde{I}_{min}(m)$ and $\widetilde{I}_{max}(m)$.

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