A COMPARATIVE ANALYSIS BETWEEN TWO TIME-DISCRETIZED VERSIONS OF SIS EPIDEMIC MODELS

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The talk is based on the paper

“On time-discretized versions of SIS epidemic models: A comparative analysis”

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Organization

1. Motivating comments

- The SIS-model as a birth-and-death process
- A discrete-time SIS-model [Allen & Burgin (2000)]

The SIS-model as a birth-and-death process

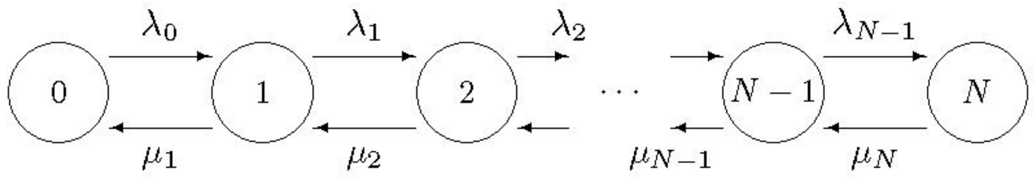
- A homogeneously mixing population of N hosts.
- Each host passes from being ***SUSCEPTIBLE*** to turning ***INFECTIVE***, to becoming again ***SUSCEPTIBLE***.

(Bidirectional transition between states: $S \to I \to S$)

- Infectious contacts generated by a Poisson process with rate $\beta > 0$ during the infectious period.
- Exponentially distributed recovery times with expected length γ^{-1}.
- Exogenous Poisson stream of infection of rate $\beta' > 0$.

A ***birth-and-death (BD) process***

$$I = \{I(t): t \geq 0\},$$



where $I(t)$ is the ***number of infective hosts*** at time t with birth rates $\lambda_i = N^{-1}(\beta i + \beta')(N - i)$ and death rates $\mu_i = \gamma i$.

The birth-and-death process I is an irreducible time-homogeneous continuous-time Markov chain taking values on a finite state space $\{0, \ldots, N\}$. As a result,

- $\exists \lim_{t\to\infty} P_{i_0,i}(t)$, for any state $\mathrm{i} \in \{0, \ldots, N\}$, where $P_{i_0,i}(t) = P(I(t) = i \,|I(0) = i_0)$.
- Its stationary vector $\boldsymbol{p} = (p_i = \lim_{t\to\infty} P_{i_0,i}(t) \colon \mathrm{i} \in \{0, \ldots, N\})$ is the unique solution to $\boldsymbol{pQ} = \boldsymbol{0_{N+1}}$ and $\boldsymbol{p1_{N+1}} = 1$, i.e.,

$$p_i = \begin{cases} S^{-1} \dfrac{\lambda_0 \ldots \lambda_{i-1}}{\mu_1 \ldots \mu_i}, & if\ i \in \{1, \ldots, N\}, \\ S^{-1}, & if\ i = 0, \end{cases}$$

where $S = 1 + \sum_{i=1}^{N} \frac{\lambda_0 \ldots \lambda_{i-1}}{\mu_1 \ldots \mu_i}$, with $\lambda_i = N^{-1}(\beta i + \beta')(N - i)$ and $\mu_i = \gamma i$.

- Regarding to the random length T of an ***outbreak***, $T \sim PH\,(\boldsymbol{e}_N(i),\ \boldsymbol{T}'(0))$ of order N under the assumption of i initially infective hosts, with $\mathrm{i} \in \{1, \dots, N\}$, where

$$\boldsymbol{T}'(0) = \begin{pmatrix} -(\lambda_1+\mu_1) & \lambda_1 & & & \\ \mu_{\boldsymbol{2}} & -(\lambda_2+\mu_2) & \lambda_2 & & \\ & \ddots & \ddots & \ddots & \\ & & \mu_{\boldsymbol{N-1}} & -(\lambda_{N-1}+\mu_{N-1}) & \lambda_{N-1} \\ & & & \mu_{\boldsymbol{N}} & -\mu_{\boldsymbol{N}} \end{pmatrix}.$$

- Moments of T are given by $E[T^k \middle| I(0)=i] = k!\,(\boldsymbol{e}_N(i)(-\boldsymbol{T}'(0))^{-1})^k \boldsymbol{1}_N$, for $k \geq 1$.

A discrete-time SIS-model [Allen & Burgin (2000)]

The infinitesimal transition probabilities of I are given by

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

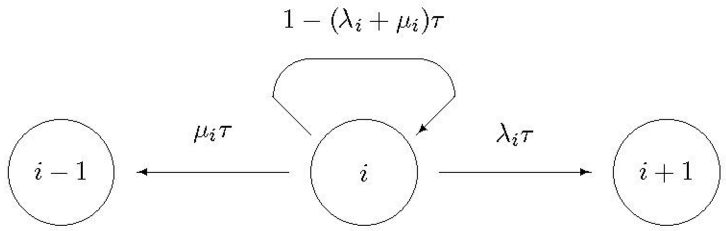
for integers $i, j \in \{0, \dots, N\}$, with $^{o(dt)}/_{dt} \to 0$ as $dt \to 0$.

This is used by Allen & Burgin (2000) to define, for a sufficiently small value $dt > 0$, a discrete-time BD process $\tilde{I} = \{\widetilde{I_n}: n \in N_0\}$ from the one-step transition probabilities

$$P\left(\widetilde{I_{n+1}}=j\,|\widetilde{I_n}=i\right) = \begin{cases} \lambda_i dt, & if\ j=i+1, \\ 1-(\lambda_i+\mu_i)dt, & if\ j=i, \\ \mu_i dt, & if\ j=i-1, \\ 0, & otherwise. \end{cases}$$

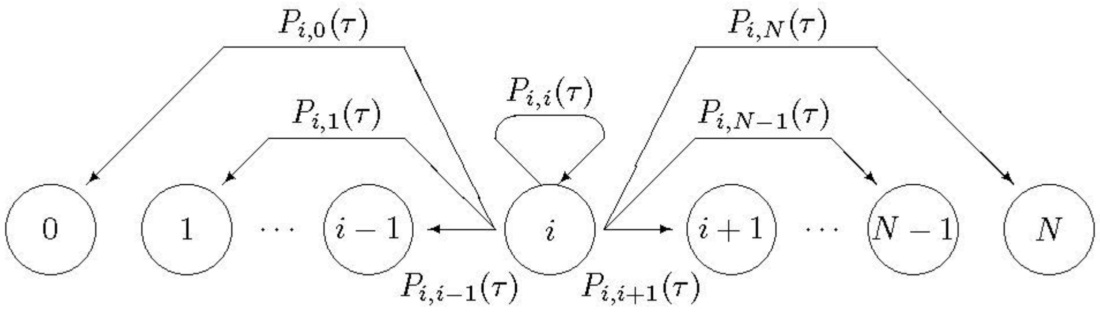
Transition probabilities $P(I(t+dt)=j\,|I(t)=i)$ are approximated at time steps $t \in \{0, dt, 2dt, \dots\}$.

In the discrete-time BD model of Allen & Burgin (2000),



under the assumption that $1-(\lambda_i+\mu_i)\tau>0$, for a sufficiently small value $\tau=dt>0$.

Jumps in the original BD process $I=\{I(t): t\geq 0\}$ are given by



regardless of the time step $\tau=dt$, where $P_{i,j}(\tau)>0$ for any pair (i,j) of states.

A major drawback: The discrete-time BD process $\tilde{I} = \{\widetilde{I_n}: n \in N_0\}$ of Allen & Burgin (2000) is well defined only when $1 - (\lambda_i + \mu_i)\tau > 0$, for a sufficiently small time step $\tau = dt > 0$.

When can we say that the time step is sufficiently small?

Two interesting properties:

Stationary probabilities of the discrete-time BD process $\tilde{I} = \{\widetilde{I_n}: n \in N_0\}$ and ***limiting probabilities*** of the original BP process $I = \{I(t): t \geq 0\}$ are identical; i.e.,

$$\lim_{n\to\infty} P\left(\widetilde{I_n} = i \,\middle|\, \widetilde{I_0} = i_0\right) = \lim_{t\to\infty} P(I(t) = i \,|I(0) = i_0).$$

The *scaled* expected length of an ***outbreak*** in the discrete-time BD process $\tilde{I} = \{\widetilde{I_n}: n \in N_0\}$ and its counterpart in the original BP process $I = \{I(t): t \geq 0\}$ are identical; i.e.,

$$\tau\, E\left[\tilde{T} \,|\, \widetilde{I_0} = i_0\right] = \boldsymbol{e}_N(i_0)\left(-\boldsymbol{T}'(0)\right)^{-1}\boldsymbol{1}_N = E[T \,|\, I(0) = i_0].$$

2. A time-discretized version of the SIS-model

- Statement of the problem
- Area between the sample paths of infective hosts

Statement of the problem

For a fixed time $t' > 0$ and an arbitrary integer $m \in N$, a finite sequence of inspection times

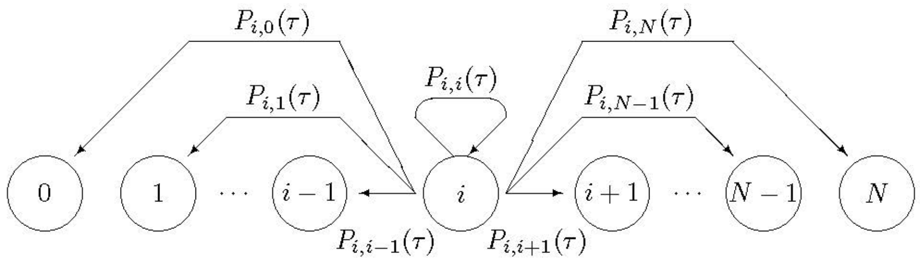
$$\tau_0 = 0 < \tau_1 < \cdots < \tau_{m-1} < \tau_m = t'$$

with $\tau_n = n\tau$ and $\tau = m^{-1}t'$, allows us to decompose the interval $[0, t')$ into m sub-intervals $[0, \tau_1) \cup [\tau_1, \tau_2) \ldots \cup [\tau_{m-1}, t')$ of length τ.

This results in a time-discretized version $\overline{I^{(m)}} = \{\overline{I_n} = I(\tau_n + 0): n \in \{0, \ldots m\}\}$ we may use to approximate the original BD process $I = \{I(t): t \geq 0\}$, for a sufficiently large integer m.

The time-discretized process $\bar{I} = \{\overline{I_n} = I(\tau_n + 0): n \in N_0\}$ is a DTMC with transition matrix

$$P(\tau) = \begin{pmatrix} P_{0,0}(\tau) & P_{0,1}(\tau) & \cdots & P_{0,N}(\tau) \\ P_{1,0}(\tau) & P_{1,1}(\tau) & \cdots & P_{1,N}(\tau) \\ \vdots & \vdots & \ddots & \vdots \\ P_{N,0}(\tau) & P_{N,1}(\tau) & \cdots & P_{N,N}(\tau) \end{pmatrix}.$$

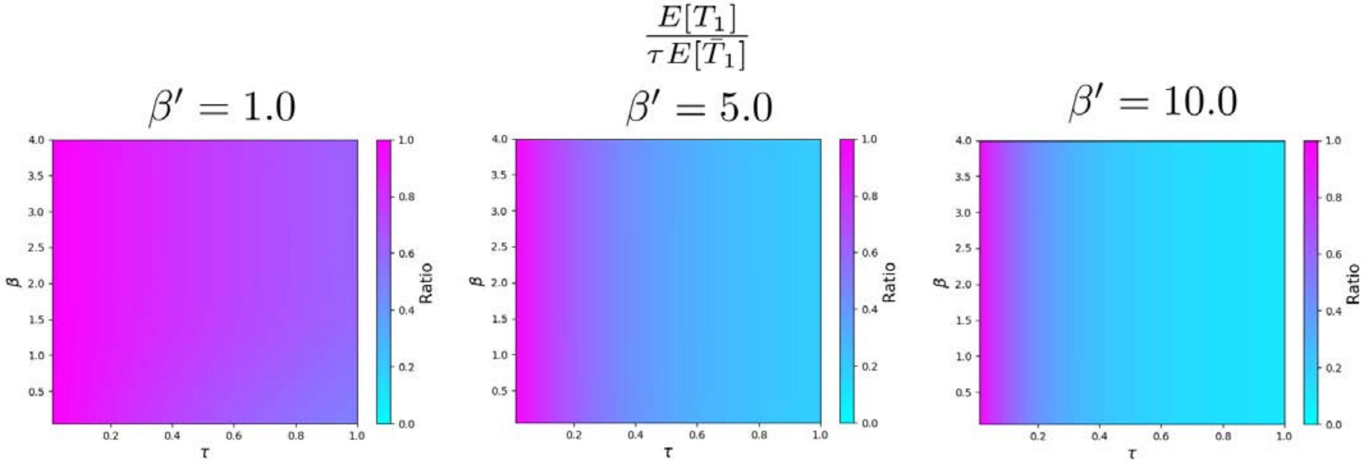


Two interesting properties:

Stationary probabilities of the time-discretized process $\bar{I} = \{\overline{I_n} = I(\tau_n + 0): n \in N_0\}$ and ***limiting probabilities*** of the original BP process $I = \{I(t): t \geq 0\}$ are identical; i.e.,

$$\lim_{n\to\infty} P(\overline{I_n} = i \mid \overline{I_0} = i_0) = \lim_{t\to\infty} P(I(t) = i \mid I(0) = i_0).$$

The scaled random length $\bar{T}$ of an outbreak in the time-discretized process $\bar{I} = \{\overline{I_n} = I(\tau_n + 0): n \in N_0\}$ is stochastically larger than the random length T of an ***outbreak*** in the original BP process $I = \{I(t): t \geq 0\}$ are identical; i.e., $T \leq_{st} \tau\, \bar{T}$.



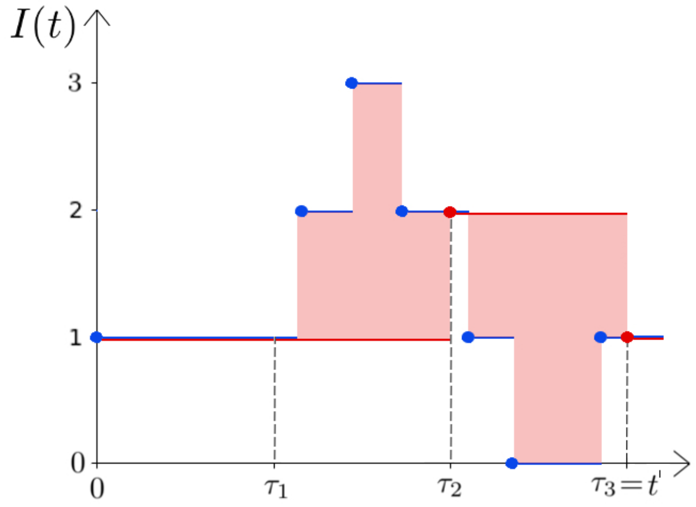
Ratio between expected lengths of an outbreak, for $N = 20$, $\gamma = 1.0$, and $I(0) = 1$.

A major drawback:

How to select the smallest number $m = m(t')$ of sub-intervals in such a way that the summary of numbers $\overline{I_n} = I(\tau_n + 0)$ of infective hosts, for $n \in \{0, \dots, m\}$, results in an appropriate description of the original BD process $I = \{I(t): t \geq 0\}$ evolving over the time interval $[0, t')$?

Area between the sample paths of infective hosts

For a fixed time interval $[0, t')$, a sample path of the process $I(t') = \{I(t): t \in [0, t')\}$ (blue) versus the resulting sample path of the time-discretized version $\overline{I^{(m)}} = \{\overline{I_n} = I(\tau_n + 0): n \in \{0, \dots m\}\}$ (red) in the case $m = 3$ with $\overline{I_0} = \overline{I_1} = 1$, $\overline{I_2} = 2$ and $\overline{I_3} = 1$.



With $Y_m(t;\omega) = |I(t;\omega) - I^{(m)}(t;\omega)|$ and

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

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

where λ is the Lebesgue measure on $[0, \infty)$.

Lemma 1 For a fixed length $t' > 0$ and an arbitrary integer $m \in N$, let Z_m be the total area between the sample paths of infectives in the processes $I(t')$ and $\overline{I^{(m)}}$. Then, the sequence $\{Z_m: m \in N\}$ of random variables converges almost surely to 0 as $m \to \infty$.

3. Non-detection of an outbreak

Non-detection of an outbreak

For a fixed number $i \epsilon \{1, \dots, N\}$ of initially infective hosts, we may define

$\delta_i(t)$: Conditional probability that, starting from i initially infective hosts, the sequence of inspection times does not allow us to detect the end of an outbreak, provided that an outbreak occurs within the time interval $[0, t]$.

It is readily seen that

$$\delta_i(t) = P(I(t) = 0 \mid I(0) = i) - P\left(\widetilde{I_m} = 0 \mid \widetilde{I_0} = i\right), \qquad i \in \{1, \dots, N\},$$

where $\{I(t): t \geq 0\}$ is a modified version of the BD process with $\lambda_0 = 0$, and $\{\widetilde{I_m}: m \in N_0\}$ is defined as an absorbing discrete-time BD process on $\{0, \dots, N\}$ with one-step transition probability matrix

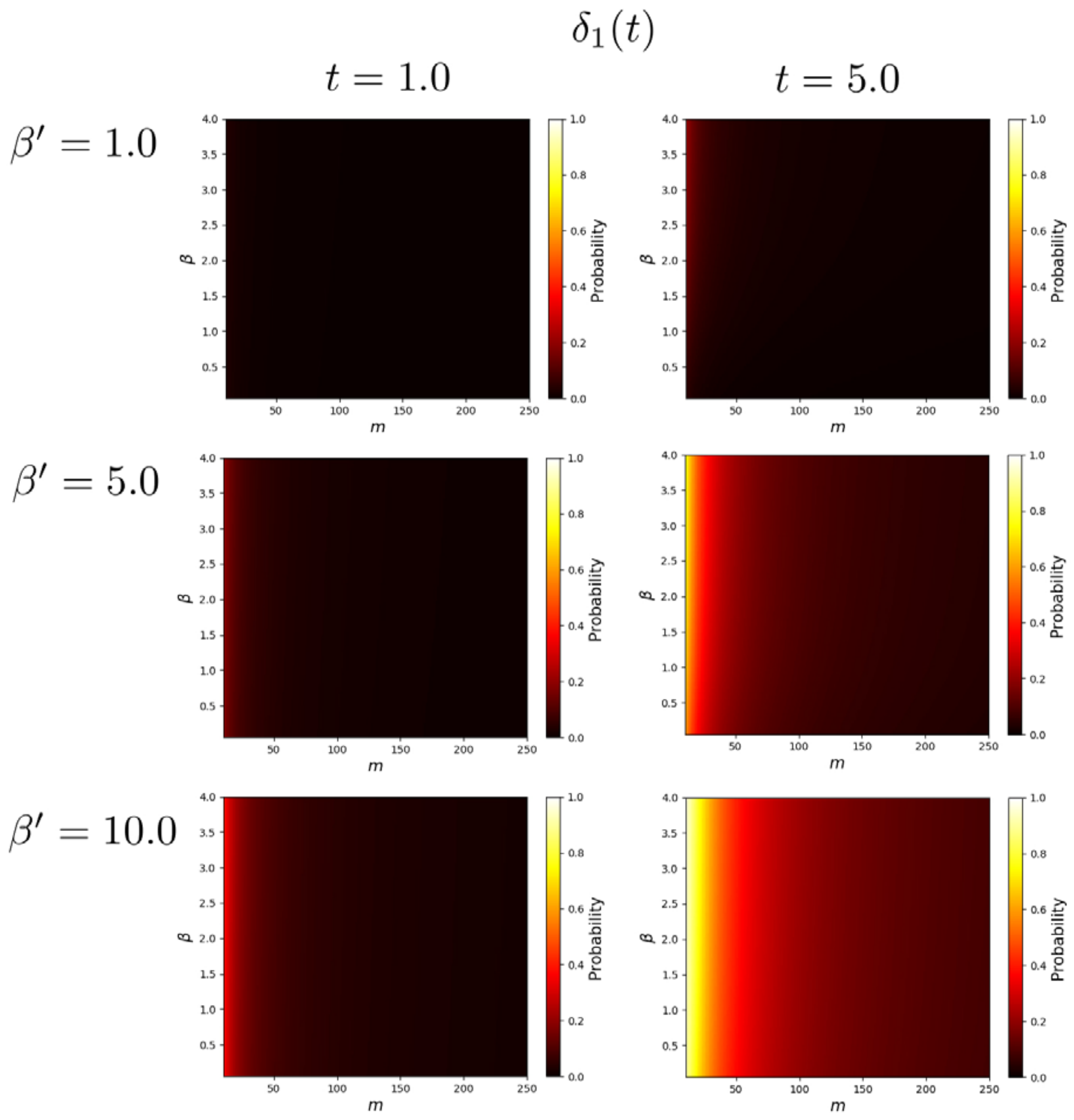
$$P^*(\tau) = \begin{pmatrix} 1 & 0 & \cdots & 0 \\ P_{1,0}(\tau) & P_{1,1}(\tau) & \cdots & P_{1,N}(\tau) \\ \vdots & \vdots & \ddots & \vdots \\ P_{N,0}(\tau) & P_{N,1}(\tau) & \cdots & P_{N,N}(\tau) \end{pmatrix} = \begin{pmatrix} 1 & 0_N^T \\ p_0^*(\tau) & \overline{P^*}(\tau) \end{pmatrix},$$

from which it follows that $P\left(\widetilde{I_m} = 0 \mid \widetilde{I_0} = i\right) = 1 - \left((\overline{P^*}(\tau))^m \mathbf{1}_N\right)_{1+i}$.

Probability of missing an outbreak

$N = 20, \gamma = 1.0$, and $I(0) = 1$

Time step $\tau = {}^{t}/_{m}$.



4. Extreme values during an outbreak

- Maximum number of infective hosts
- Minimum number of infective hosts
- An approximating model based on the Hellinger distance between extreme values

Maximum and minimum numbers of infective hosts

For a fixed number $i \in \{0, \dots, N\}$ and a predetermined time $t' > 0$, let us define

$I_{min}(t')$: minimum number of hosts which are simultaneously infective at any time of $[0, t']$,

$I_{max}(t')$: maximum number of hosts which are simultaneously infective at any time of $[0, t']$.

The aim is to determined the joint distribution of $(I_{min}(t'), I_{max}(t'))$ by means of

$$Q_i(y; y') = P(y \leq I_{min}(t'), I_{max}(t') \leq y' \,|\, I(0) = i), \qquad 0 \leq y \leq i \leq y' \leq N,$$

with

$$Q_i(0; y') = P(I_{max}(t') \leq y' \,|\, I(0) = i), \;\; 0 \leq i \leq y' \leq N,$$

$$Q_i(y; N) = P(y \leq I_{min}(t') \,|\, I(0) = i), \;\; 0 \leq y \leq i \leq N.$$

In deriving $Q_i(y;y') = P(y \le I_{min}(t'), I_{max}(t') \le y' |\, I(0) = i)$, for $1 \le y \le i \le y' \le N-1$,

$$Q_i(y;y') = 1 - P\big(J_{y,y'}(t') \in \{(y-1)^*, (y'+1)^*\} \,\big|\, I(0) = i\big),$$

where $J_{y,y'} = \{J_{y,y'}(t): t \ge 0\}$ is an absorbing BD process on the state space

$$S(y;y') = \{(y-1)^*\} \cup \{y, y+1, \dots, y'-1, y'\} \cup \{(y'+1)^*\},$$

with infinitesimal generator

$$Q(y;y') = \begin{pmatrix} 0 & 0_{y'-y+1} & 0 \\ s_{(y-1)^*}(y;y') & S(y;y') & s_{(y'+1)^*}(y;y') \\ 0 & 0_{y'-y+1} & 0 \end{pmatrix},$$

where

$$S(y;y') = \begin{pmatrix} -(\lambda_y + \mu_y) & \lambda_y & & & \\ \mu_{y+1} & -(\lambda_{y+1} + \mu_{y+1}) & \lambda_{y+1} & & \\ & \ddots & \ddots & \ddots & \\ & & \mu_{y'-1} & -(\lambda_{y'-1} + \mu_{y'-1}) & \lambda_{y'-1} \\ & & & \mu_{y'} & -(\lambda_{y'} + \mu_{y'}) \end{pmatrix}, \quad s_{(y-1)^*}(y;y') = \begin{pmatrix} \mu_y \\ 0 \\ \vdots \\ 0 \end{pmatrix}, s_{(y'+1)^*}(y;y') = \begin{pmatrix} 0 \\ \vdots \\ 0 \\ \lambda_{y'} \end{pmatrix}.$$

As a result,

$$Q_i(y;y') = \boldsymbol{e}^T_{y'-y+1} exp\{S(y;y')t'\}\mathbf{1}_{y'-y+1}, \qquad 1 \le y \le i \le y' \le N-1.$$

By using a **Cayley-Hamilton approach,**

$$Q_i(y;y') = \sum_{l=y}^{y\prime} e^{u_l(y,y')t\prime} \sum_{k=y}^{y\prime} c_{i,k}^{(l)}(y,y'), \qquad 1 \le y \le i \le y' \le N-1,$$

where $u_y(y,y') < u_{y+1}(y,y') < \cdots < u_{y\prime}(y,y')$ are the eigenvalues of $S(y;y')$ and

$$\begin{pmatrix} c_{i,k}^{(y)}(y,y') \\ \vdots \\ c_{i,k}^{(y\prime)}(y,y') \end{pmatrix} = \begin{pmatrix} u_y(y,y') & \cdots & u_{y\prime}(y,y') \\ \vdots & & \vdots \\ (u_y(y,y'))^{y'-y+1} & \cdots & (u_y(y,y'))^{y'-y+1} \end{pmatrix}^{-1} \begin{pmatrix} (S(y;y'))_{i,k} \\ \vdots \\ (S^{y'-y+1}(y;y'))_{i,k} \end{pmatrix}.$$

Indeed, $-2\max\{(\lambda_k + \mu_k)\colon \mathrm{y} \le k \le y'\} \le u_y(y,y') < u_{y+1}(y,y') < \cdots < u_{y'}(y,y') < 0.$

An approximating model based on the Hellinger distance between extreme values

For a fixed initial number $i \in \{0, \dots, N\}$ and a predetermined time $t' > 0$, we may derive

- for the original BD process $I = \{I(t): t \in [0, t']\}$, the mass function $P(i; t') = \{q_i(y, y'): 0 \le y \le i \le y' \le N\}$, where $q_i(y, y') = P(I_{min}(t') = y, I_{max}(t') = y' \mid I(0) = i)$.

- for the time-discretized version $\overline{I^{(m)}} = \{\overline{I_n} = I(\tau_n + 0): n \in \{0, \dots m\}\}$, the mass function $\bar{P}(i; t') = \{\bar{q}_i(y, y'): 0 \le y \le i \le y' \le N\}$, where $\bar{q}_i(y, y') = P(\overline{I_{min}}(m) = y, \overline{I_{max}}(m) = y' \mid \overline{I_0} = i)$ and the time step is given by $\tau = m^{-1} t'$.

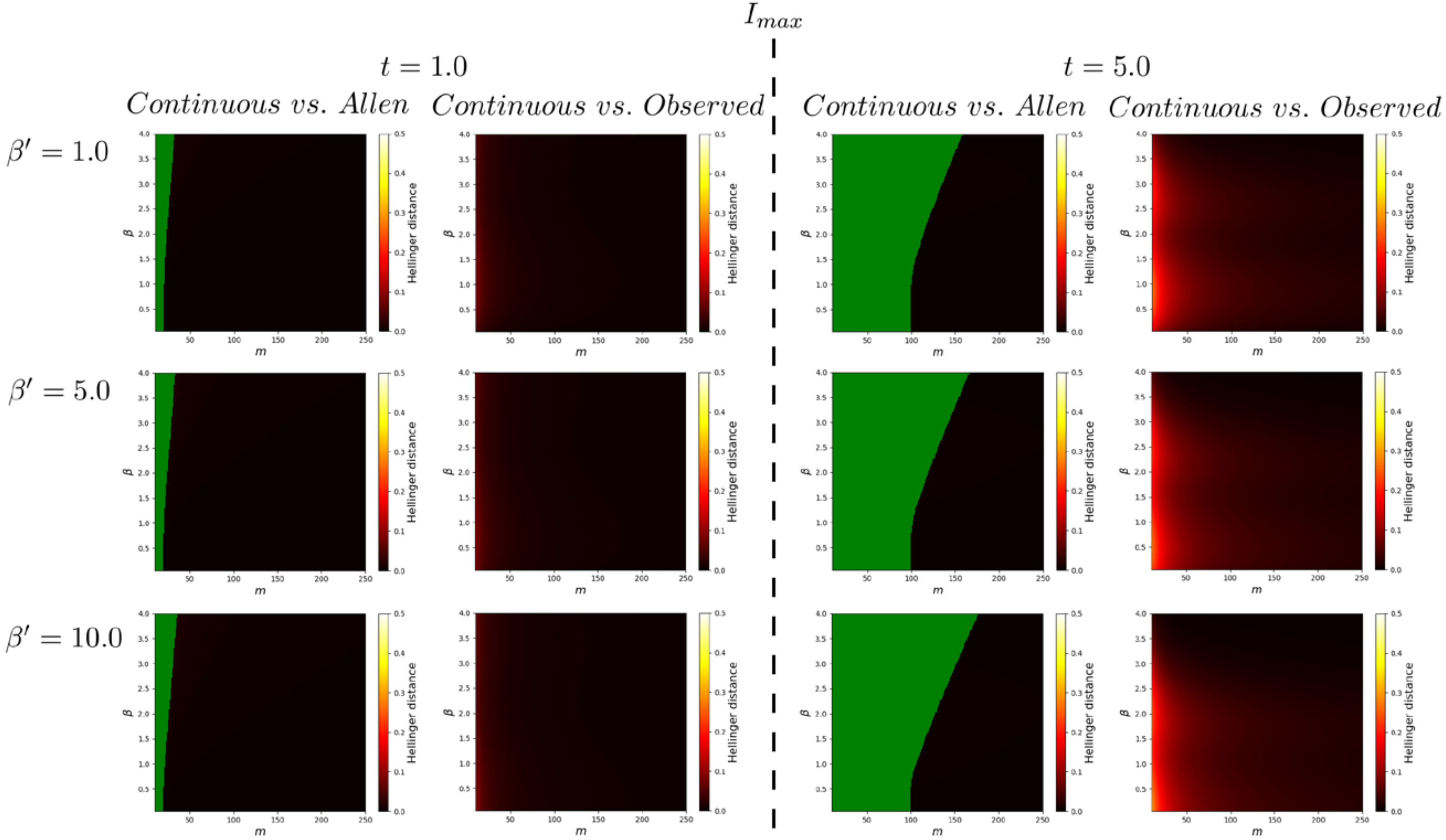
Based on the Hellinger distance between $P(i; t')$ and $\bar{P}(i; t')$,

$$\mathrm{H}\big(P(i; t'), \bar{P}(i; t')\big) = \frac{1}{\sqrt{2}} \sqrt{\sum_{(y, y')} \left(\sqrt{q_i(y, y')} - \sqrt{\bar{q}_i(y, y')}\right)^2},$$

we suggest to select the smallest integer m verifying $\mathrm{H}\big(P(i; t'), \bar{P}(i; t')\big) < \varepsilon$, for an arbitrary small $\varepsilon > 0$.

Hellinger distances: Maximum number of simultaneously infective hosts

$N = 20, \gamma = 1.0$, and $I(0) = 1$.
Time step $\tau = {}^{t}/_{m}$.



Hellinger distances: Minimum number of simultaneously infective hosts

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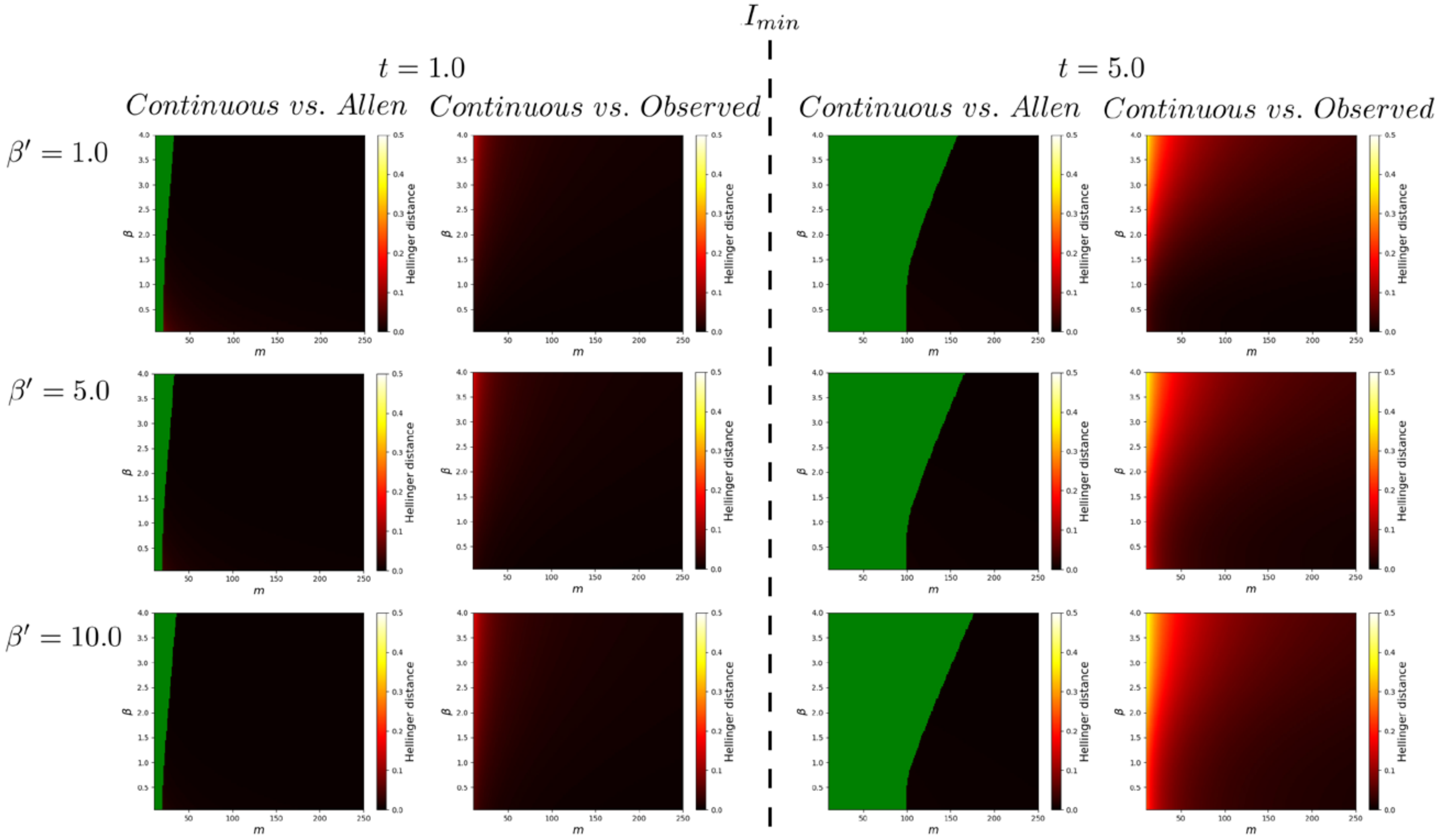

5. Conclusions and references

Conclusions

- Proposal of a probabilistic criterion that allows us to summarize appropriately the dynamics of the number of infective hosts in the stochastic SIS model in terms of discrete-time models.

- Construction of a time-discretized version of the SIS model by recording the number of infective hosts at a finite sequence of m inspection times in the time interval $[0, t']$, with the inter-inspection time or time slot $\tau = {t'}/{m}$.

- Comparison between our time-discretized version and the time-discrete model of Allen & Burgin (2000).

- Key descriptor based on extreme values: minimum/maximum number of simultaneously infective hosts.

- Mathematical tools:

  - Continuous- and discrete-time BR processes (***modelling***)
  - Discrete-time Markov chains (***modelling***)
  - Eigenvalues and related properties (***Cayley-Hamilton approach***)
  - Hellinger distance (***criterion***)

- The continuous-time BD process $I = \{I(t): t \geq 0\}$, the discrete-time BD process $\tilde{I} = \left\{\widetilde{I_n}: n \in N_0\right\}$ of Allen & Burgin (2000), and our time-discretized model are IDENTICAL in the ***long term***:

$$\lim_{n\to\infty} P\left(\widetilde{I_n} = i \,\middle|\, \widetilde{I_0} = i_0\right) = \lim_{t\to\infty} P(I(t) = i \,|I(0) = i_0) = \lim_{n\to\infty} P(\overline{I_n} = i \,|\overline{I_0} = i_0).$$

- In the setting of an ***outbreak***,

    - In the time-discrete BD process of Allen & Burgin (2000),

$$\tau\, E\left[\tilde{T} \mid \widetilde{I_0} = i_0\right] = E[T \mid I(0) = i_0].$$

    - In the discretized model,

$$T \ \leq_{stoch} \tau\, \bar{T}.$$

The selection of the number m of inspection times in the ***time interval*** $[\mathbf{0}, \boldsymbol{t'}]$ to define the time-discretized version, and equivalently the time step $\tau = t'/m$ to deal with the discrete-time BD process of Allen & Burgin (2000), is based on the use of the HELLINGER DISTANCE:

    - Hellinger distance between $P(i; t')$ and $\bar{P}(i; t')$.
    - Hellinger distance between $P(i; t')$ and $\tilde{P}(i; t')$.

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Thank you for your attention!

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