Journal of Computational and Applied Mathematics 233 (2010) 2563–2574

Contents lists available at ScienceDirect

Journal of Computational and Applied Mathematics

journal homepage: www.elsevier.com/locate/cam

The maximum number of infected individuals in SIS epidemic models: Computational techniques and quasi-stationary distributions

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ARTICLE INFO

Article history:
Received 27 August 2009
Received in revised form 28 October 2009

Keywords:
Stochastic SIS epidemic model
Maximum number of infected individuals
Extinction time
Transient distribution
Quasi-stationary distribution
Absorption probabilities

ABSTRACT

We study the maximum number of infected individuals observed during an epidemic for a Susceptible–Infected–Susceptible (SIS) model which corresponds to a birth–death process with an absorbing state. We develop computational schemes for the corresponding distributions in a transient regime and till absorption. Moreover, we study the distribution of the current number of infected individuals given that the maximum number during the epidemic has not exceeded a given threshold. In this sense, some quasi-stationary distributions of a related process are also discussed.

1. Introduction

Several models have been proposed for the quantitative analysis of an epidemic. The most classical among them are the Susceptible–Infected (SI), Susceptible–Infected–Susceptible (SIS) and Susceptible–Infected–Removed (SIR) models. All of them model the outbreak and spread of contagious diseases under different assumptions (e.g. according to whether an infected individual remains for ever infected, recovers becoming again susceptible or is removed due to immunity/death/quarantine). The textbooks and monographs of Bailey [1], Daley and Gani [2], Diekmann and Heesterbeek [3] and Allen [4] give a recent account of the main results in this area, with many examples.

For the study of the spread of an epidemic in a large population, investigators use primarily deterministic models. Recent studies deal with refinements of the SI, SIS and SIR models using ordinary and partial differential equations; see e.g. the papers of Moghadas and Gumel [5], Wei and Zou [6], Song, Ma and Takeuchi [7] and Yoshida and Hara [8]. On the other hand, stochastic methods complement the deterministic approach and are particularly useful for the study of epidemics in small populations. However, the dynamics of the underlying processes yield intractable models, even in the simplest cases of the SIS and SIR models. For this reason interest is still focused on various aspects of the fundamental SIS and SIR Markovian models and some variants; see e.g. the papers of Clancy [9], Coolen-Schrijner and van Doorn [10], Xu, Allen and Perelson [11], Ball and Neal [12], Lindholm [13], Stone, Wilkinson-Herbots and Isham [14].

The study of the maximum number of infected individuals (MNI) during an epidemic is of great importance for assessing its impact and the possibilities of intervention for controlling it. In this paper we study the MNI in the framework of a generalized SIS model. This epidemic is modeled as a birth–death process that counts the number of infected individuals in a finite population. State 0 is the unique absorbing state that corresponds to the end of the epidemic; all other states are

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doi:10.1016/j.cam.2009.11.003

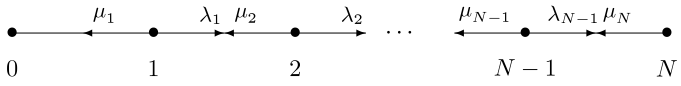

Fig. 1. States and transitions in the SIS epidemic model.

transient. Therefore, the stationary distribution of the model is degenerate and the main measures of the system behavior concern the so-called quasi-stationary distribution and some transient distributions associated with its evolution. The importance of the quasi-stationary distributions of Markov chains in the study of biological problems has been shown in a series of papers; see e.g. [15,16].

As a related work, we mention [14], where the distribution of the MNI within an individual outbreak of an SIS model with immigration is studied. Similar questions have been studied in the framework of queueing theory, where the maximum number of customers during a busy period has been used for assessing the level of congestion. Neuts [17] studied the maximum number of customers during a busy period in a basic queueing model, while Serfozo [18] introduced an asymptotic approach for the study of the extreme values of a birth–death process. These works have been further generalized and extended for certain structured multidimensional Markov chains (see e.g. [19–21]).

The paper is organized as follows. In Section 2, we introduce the dynamics of the SIS epidemic model and present its mathematical formulation. In Section 3, we present an efficient algorithm for computing the transient distribution of the MNI. The corresponding distribution till absorption time is also derived in closed form. In Section 4, we study the relation of the MNI with quasi-stationary distributions of the model. Finally, in Section 5, we present several numerical results that illustrate the applicability of the proposed methods and shed light on various aspects of the stochastic SIS model.

2. The stochastic SIS epidemic model

An SIS epidemic model in continuous time is a closed population model of N individuals, in which the population consists only of susceptible and infected individuals. Thus, an infected individual does not acquire immunity after a recovery but becomes susceptible again, and so on. The evolution of such a model can be described by a birth–death process $\{I(t) : t \geq 0\}$ with state space $S = \{0, 1, \ldots, N\}$, where $I(t)$ records the number of infected individuals at time t. The birth rates, corresponding to infections, are denoted by λ_i, and the death rates, corresponding to recoveries, are denoted by μ_i, $i = 0, 1, \ldots, N$. The infections are supposed to occur because of a contagious disease. Therefore, when there are no infected individuals, the process stays there for ever. The other states are assumed transient. More specifically, we assume that $\lambda_0 = \lambda_N = \mu_0 = 0$, while $\mu_1, \mu_2, \ldots, \mu_N > 0$ and $\lambda_1, \lambda_2, \ldots, \lambda_{N-1} > 0$. In the classical SIS model, it is assumed that $\lambda_i = \beta i(N - i)/N$ and $\mu_i = \gamma i$, where β is the contact rate and γ is the recovery rate per customer. However, in the present paper, we will present the results for general birth and death rates. Indeed, in several biological systems the data do not support the above classical rates. The transitions among states are represented in Fig. 1.

3. Distributions in the transient regime and till absorption of the MNI

In this section, we are interested in studying the MNI $M(t)$, defined as

$$M(t) = \max(I(s) : 0 \leq s \leq t). \tag{1}$$

The augmented process $\{(I(t), M(t)) : t \geq 0\}$ is a continuous time Markov chain. In Fig. 2 we show a typical transition diagram (for the case where the population size is $N = 6$ and the initial MNI observed is $k_0 = 3$).

We will first derive an algorithmic scheme for computing its transient probabilities. Let $I(0) = i_0$ be the number of infected individuals at the beginning of the observation period and $M(0) = k_0$ be the maximum number observed till that time, for $0 < i_0 \leq k_0$. We are interested in computing the transient distribution

$$p_{i,k}(t) = \Pr[I(t) = i, M(t) = k | I(0) = i_0, M(0) = k_0], \quad k_0 \leq k \leq N,\ 0 \leq i \leq k. \tag{2}$$

We will now present a stable algorithmic scheme for computing the Laplace transforms

$$\tilde{p}_{i,k}(s) = \int_0^\infty \mathrm{e}^{-st} p_{i,k}(t)\mathrm{d}t, \quad k_0 \leq k \leq N,\ 0 \leq i \leq k. \tag{3}$$

Then, the corresponding transient probabilities $p_{i,k}(t)$ can be computed by numerically inverting the Laplace transforms using any standard numerical algorithm (see e.g. [22]).

Theorem 1. *The Laplace transforms $\tilde{p}_{i,k}(s)$, $k_0 \leq k \leq N,\ 0 \leq i \leq k$, are computed by the equations*

$$\tilde{p}_{k_0,k_0}(s) = \frac{(s + g_{k_0-1} + \lambda_{k_0-1})\delta_{k_0,i_0} + \lambda_{k_0-1} D_{k_0-1}}{(s + \lambda_{k_0})(s + g_{k_0-1}) + (s + \lambda_{k_0})\lambda_{k_0-1} + (s + g_{k_0-1})\mu_{k_0}}, \tag{4}$$

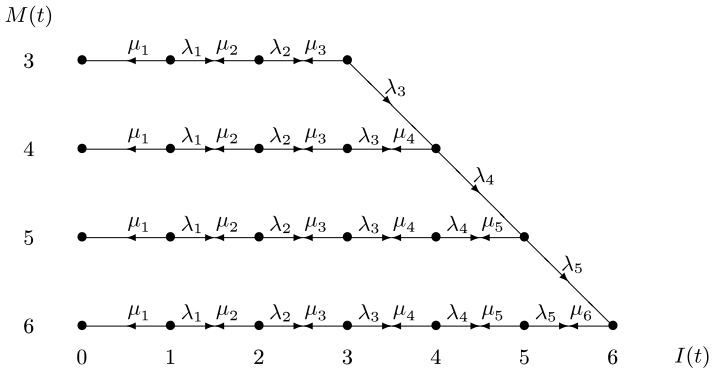

Fig. 2. States and transitions of the process $\{(I(t), M(t))\}$ for $N = 6$, $k_0 = 3$.

$$\tilde{p}_{i,k_0}(s) = \sum_{j=i}^{k_0-1} \frac{D_j}{\mu_{j+1}} \prod_{n=i}^{j} \frac{\mu_{n+1}}{s+g_n+\lambda_n} + \tilde{p}_{k_0,k_0}(s) \prod_{j=i}^{k_0-1} \frac{\mu_{j+1}}{s+g_j+\lambda_j}, \quad 0 \le i \le k_0-1, \tag{5}$$

$$\tilde{p}_{k,k}(s) = \frac{(s+g_{k-1}+\lambda_{k-1})\lambda_{k-1}\tilde{p}_{k-1,k-1}(s)}{(s+\lambda_k)(s+g_{k-1})+(s+\lambda_k)\lambda_{k-1}+(s+g_{k-1})\mu_k}, \quad k_0+1 \le k \le N, \tag{6}$$

$$\tilde{p}_{i,k}(s) = \tilde{p}_{k,k}(s) \prod_{j=i}^{k-1} \frac{\mu_{j+1}}{s+g_j+\lambda_j}, \quad k_0+1 \le k \le N,\ 0 \le i \le k-1, \tag{7}$$

where the coefficients g_i, for $0 \le i \le N-1$, and D_i, for $0 \le i \le k_0-1$, are given by the recursive scheme

$$g_0 = 0, \tag{8}$$

$$g_i = \mu_i \frac{s+g_{i-1}}{s+g_{i-1}+\lambda_{i-1}}, \quad 1 \le i \le N-1, \tag{9}$$

$$D_i = \delta_{i,i_0}, \quad 0 \le i \le i_0, \tag{10}$$

$$D_i = \prod_{j=i_0}^{i-1} \frac{\lambda_j}{s+g_j+\lambda_j}, \quad i_0+1 \le i \le k_0-1, \tag{11}$$

with $\delta_{i,k}$ being Kronecker's 0-1 *function.*

Proof. The forward Kolmogorov differential equations for the process $\{(I(t), M(t)) : t \ge 0\}$ assume the form

$$\begin{aligned} \frac{\mathrm{d}}{\mathrm{d}t}p_{i,k}(t) = {} & -(\lambda_i+\mu_i)p_{i,k}(t) + (1-\delta_{i,0})\lambda_{i-1}p_{i-1,k}(t) + (1-\delta_{i,k})(1-\delta_{i,N})\mu_{i+1}p_{i+1,k}(t) \\ & + (1-\delta_{k,k_0})\delta_{i,k}\lambda_{i-1}p_{i-1,k-1}(t), \quad k_0 \le k \le N,\ 0 \le i \le k, \end{aligned} \tag{12}$$

with initial conditions

$$p_{i,k}(0) = \delta_{i,i_0}\delta_{k,k_0}, \quad k_0 \le k \le N,\ 0 \le i \le k. \tag{13}$$

By employing Laplace transforms, the system of equations (12)–(13) yields the linear system

$$\begin{aligned} s\tilde{p}_{i,k}(s) = {} & \delta_{i,i_0}\delta_{k,k_0} - (\lambda_i+\mu_i)\tilde{p}_{i,k}(s) + (1-\delta_{i,0})\lambda_{i-1}\tilde{p}_{i-1,k}(s) + (1-\delta_{i,k})(1-\delta_{i,N})\mu_{i+1}\tilde{p}_{i+1,k}(s) \\ & + (1-\delta_{k,k_0})\delta_{i,k}\lambda_{i-1}\tilde{p}_{i-1,k-1}(s), \quad k_0 \le k \le N,\ 0 \le i \le k. \end{aligned} \tag{14}$$

For every fixed k with $k_0 \le k \le N$, the system (14) has the tridiagonal form

$$\beta_i\tilde{p}_{i-1,k}(s) + \gamma_i\tilde{p}_{i,k}(s) + \alpha_i\tilde{p}_{i+1,k}(s) = \delta_i, \quad 0 \le i \le k-1, \tag{15}$$

where $\beta_0 = 0$, $\beta_i = -\lambda_{i-1}$, for $1 \le i \le k-1$, $\gamma_i = s+\lambda_i+\mu_i$, for $0 \le i \le k-1$, $\alpha_i = -\mu_{i+1}$, for $0 \le i \le k-1$, and $\delta_i = \delta_{i,i_0}\delta_{k,k_0}$, for $0 \le i \le k-1$.

Now, by a forward elimination procedure, the tridiagonal system (15) reduces to the didiagonal system

$$G_i\tilde{p}_{i,k}(s) + \alpha_i\tilde{p}_{i+1,k}(s) = D_i, \quad 0 \le i \le k-1, \tag{16}$$

where

$$G_0 = \gamma_0 = s, \tag{17}$$

$$G_i = \gamma_i - \frac{\beta_i \alpha_{i-1}}{G_{i-1}} = s + \lambda_i + \mu_i - \frac{\lambda_{i-1}\mu_i}{G_{i-1}}, \quad 1 \le i \le k-1, \tag{18}$$

$$D_0 = \delta_0 = 0, \tag{19}$$

$$D_i = \delta_i - \frac{\beta_i D_{i-1}}{G_{i-1}} = \delta_{i,i_0}\delta_{k,k_0} + \frac{\lambda_{i-1}D_{i-1}}{G_{i-1}}, \quad 1 \le i \le k-1. \tag{20}$$

To avoid subtractions so that we obtain a stable scheme, we introduce the new variables $g_i = G_i - s - \lambda_i$, for $0 \le i \le k-1$. Then, the Eqs. (17)–(20) assume the form

$$g_0 = 0, \tag{21}$$

$$g_i = \mu_i \frac{s + g_{i-1}}{s + g_{i-1} + \lambda_{i-1}}, \quad 1 \le i \le k-1, \tag{22}$$

$$D_0 = 0, \tag{23}$$

$$D_i = \delta_{i,i_0}\delta_{k,k_0} + \frac{\lambda_{i-1}D_{i-1}}{s + g_{i-1} + \lambda_{i-1}}, \quad 1 \le i \le k-1. \tag{24}$$

Then, we can obtain $\tilde{p}_{i,k}(s)$ using the backward substitution procedure implied by (16):

$$\tilde{p}_{i,k}(s) = \frac{D_i - \alpha_i \tilde{p}_{i+1,k}(s)}{G_i} = \frac{D_i + \mu_{i+1}\tilde{p}_{i+1,k}(s)}{s + g_i + \lambda_i}, \quad 0 \le i \le k-1. \tag{25}$$

Iterating (25) yields

$$\tilde{p}_{i,k}(s) = \sum_{j=i}^{k-1} \frac{D_j}{\mu_{j+1}} \prod_{n=i}^{j} \frac{\mu_{n+1}}{s + g_n + \lambda_n} + \tilde{p}_{k,k}(s) \prod_{j=i}^{k-1} \frac{\mu_{j+1}}{s + g_j + \lambda_j}, \quad 0 \le i \le k-1. \tag{26}$$

Now, using (14) for $i = k > 0$ and substituting $\tilde{p}_{k-1,k}$ by (25), we get that

$$\tilde{p}_{k,k}(s) = \frac{(s + g_{k-1} + \lambda_{k-1})(\delta_{k,i_0}\delta_{k,k_0} + (1 - \delta_{k,k_0})\lambda_{k-1}\tilde{p}_{k-1,k-1}(s)) + \lambda_{k-1}D_{k-1}}{(s + \lambda_k)(s + g_{k-1}) + (s + \lambda_k)\lambda_{k-1} + (s + g_{k-1})\mu_k}. \tag{27}$$

For $k = k_0$, the recursive scheme (23)–(24) yields $D_i = 0$, for $0 \le i \le i_0 - 1$, $D_{i_0} = 1$, and $D_i = \frac{\lambda_{i-1}D_{i-1}}{s+g_{i-1}+\lambda_{i-1}}$, for $i_0 + 1 \le i \le k_0 - 1$, which gives (10)–(11). Moreover, for $k = k_0$, (27) and (26) reduce to (4) and (5), respectively. On the other hand, for $k_0 + 1 \le k \le N$, the recursive scheme (23)–(24) yields $D_i = 0$, for $0 \le i \le k-1$. So, in this case (27) simplifies to (6) and (26) to (7). ■

Once the Laplace transforms $\tilde{p}_{i,k}(s)$ have been computed, the marginal distribution $p_{\cdot,k}(t) = \Pr[M(t) = k]$, for $k_0 \le k \le N$, can be easily obtained by inverting numerically the sum $\sum_{i=0}^{k} \tilde{p}_{i,k}(s)$. This allows us to compute the transient moments

$$E[M^n(t)] = \sum_{k=k_0}^{N} k^n p_{\cdot,k}(t), \quad n \ge 1,$$

and, in particular, the expectation $E[M(t)]$ and the standard deviation $\sigma(M(t)) = \left(E[M^2(t)] - E^2[M(t)]\right)^{1/2}$ (see Section 5).

Let now M denote the MNI till absorption. We are interested in the distribution of M, given that $(I(0), M(0)) = (i, k)$. We set $y_{i,k,m} = \Pr[M = m | I(0) = i, M(0) = k]$, $0 \le i \le k \le m \le N$. These probabilities can be obtained easily in closed form, as stated in the following theorem.

Theorem 2. *The probabilities $y_{i,k,m} = \Pr[M = m | I(0) = i, M(0) = k]$, $0 \le i \le k \le m \le N$, are given by the formulas*

$$y_{i,k,m} = \frac{\rho_{i-1}}{\rho_{m-1}} - \frac{\rho_{i-1}}{\rho_m}, \quad 1 \le i \le k \le m-1,\ 1 \le m \le N-1, \tag{28}$$

$$y_{i,m,m} = 1 - \frac{\rho_{i-1}}{\rho_m}, \quad 1 \le i \le m \le N-1, \tag{29}$$

$$y_{i,k,N} = \frac{\rho_{i-1}}{\rho_{N-1}}, \quad 1 \le i \le k \le N-1, \tag{30}$$

$$y_{i,N,N} = 1, \quad 1 \le i \le N, \tag{31}$$

where

$$\rho_0 = 1, \qquad \rho_i = \sum_{s=0}^{i} \prod_{j=1}^{s} \frac{\mu_j}{\lambda_j}, \quad 1 \le i \le N-1. \tag{32}$$

Proof. By conditioning on the first transition out of the initial state for the process $\{(I(t), M(t)) : t \ge 0\}$ (first-step analysis), we obtain the linear system

$$y_{0,k,m} = \delta_{k,m}, \quad 0 \le k \le m \le N, \tag{33}$$

$$y_{i,k,m} = \frac{\mu_i}{\lambda_i + \mu_i} y_{i-1,k,m} + \frac{\lambda_i}{\lambda_i + \mu_i} y_{i+1,k,m}, \quad 2 \le k \le m \le N,\ 1 \le i \le k-1, \tag{34}$$

$$y_{k,k,m} = \frac{\mu_k}{\lambda_k + \mu_k} y_{k-1,k,m} + \frac{(1-\delta_{k,m})\lambda_k}{\lambda_k + \mu_k} y_{k+1,k+1,m}, \quad 1 \le k \le m \le N. \tag{35}$$

For any fixed pair (k, m), the system (33)–(35) is tridiagonal with respect to $y_{i,k,m}$, for $0 \le i \le k$, and can be solved explicitly. Indeed, note that for fixed pair (k, m), (34) can be written as

$$\begin{aligned} y_{i+1,k,m} - y_{i,k,m} &= (y_{i,k,m} - y_{i-1,k,m}) \frac{\mu_i}{\lambda_i} \\ &= (y_{1,k,m} - y_{0,k,m}) \prod_{j=1}^{i} \frac{\mu_j}{\lambda_j}, \quad 1 \le i \le k-1. \end{aligned} \tag{36}$$

Then, using repeatedly (36) and taking also into account (33) yields

$$\begin{aligned} y_{i,k,m} &= y_{0,k,m} + \sum_{s=0}^{i-1} (y_{s+1,k,m} - y_{s,k,m}) \\ &= \delta_{k,m} + (y_{1,k,m} - \delta_{k,m}) \sum_{s=0}^{i-1} \prod_{j=1}^{s} \frac{\mu_j}{\lambda_j} \\ &= \delta_{k,m} + \rho_{i-1}(y_{1,k,m} - \delta_{k,m}), \quad 1 \le i \le k \le m \le N. \end{aligned} \tag{37}$$

So, we need to compute $y_{1,k,m}$, for $1 \le k \le m \le N$, and then we can obtain $y_{i,k,m}$, for $1 \le i \le k \le m \le N$, using (37). Plugging (37) in (35) for $k = m$ and solving the resulting equation for $y_{1,m,m}$ yields after some straightforward manipulations that

$$y_{1,m,m} = 1 - \rho_m^{-1}, \quad 1 \le m \le N-1, \tag{38}$$

$$y_{1,N,N} = 1. \tag{39}$$

Now, combining (38) and (39) with (37), we obtain respectively (29) and (31).

Similarly, plugging (37) in (35), for $1 \le k \le m-1$, yields

$$y_{1,k,m} = \rho_k^{-1} y_{k+1,k+1,m}, \quad 1 \le k \le m-1. \tag{40}$$

Finally, using (40) repeatedly in combination with (29) and (31) gives respectively (28) and (30). ■

4. Quasi-stationarity and MNI

The continuous time Markov chain $\{(I(t), M(t)) : t \ge 0\}$ given that $(I(0), M(0)) = (i_0, k_0)$ is absorbing. Indeed, with probability 1, the chain will be absorbed in some state in $A = \{(0, k_0), (0, k_0 + 1), \ldots, (0, N)\}$, while the other states in $S = \{(i, k) : k_0 \le k \le N, 1 \le i \le k\}$ are transient. Therefore, its stationary and limiting distributions give positive probabilities only to states in A. These probabilities have been computed in Theorem 2. However, to quantify the behavior of the process, it is important to study what happens given that the absorption has not yet occurred; that is, as long as the process remains in S. To this end, we will use the notion of quasi-stationarity.

For the sake of self-completeness, we summarize the main definitions and results here. Consider a continuous time Markov chain $\{X(t) : t \ge 0\}$ on a finite state space $\{0\} \cup S$ consisting of an absorbing state 0 and the set of transient states $S = \{1, 2, \ldots, n\}$. The generator of $\{X(t) : t \ge 0\}$ can be written in the form

$$\begin{pmatrix} 0 & \underline{0} \\ -A_Q \underline{1}^T & A_Q \end{pmatrix}, \tag{41}$$

where $\underline{0}$ and $\underline{1}$ are row vectors of zeros and ones respectively and the superscript T denotes transposition. For a distribution $\underline{w} = (w_1, w_2, \ldots, w_n)$ over S, let $\Pr_{\underline{w}}(\cdot)$ be the probability measure of the process when $X(0)$ is distributed according to $\underline{w}$. Let also $T = \sup\{t \geq 0 : X(t) \in S\}$ be the absorption time of $X(t)$. A distribution $\underline{q} = (q_1, q_2, \ldots, q_n)$ on S is said to be a quasi-stationary distribution of the process $\{X(t)\}$, if $\Pr_{\underline{q}}[X(t) = j | T > t] = q_j,\ j \in S, t \geq 0$; that is, if $X(0)$ is initially distributed as $\underline{q}$ then the conditional distribution of $X(t)$ given that the absorption has not yet occurred is constant over t. The problem of the determination of the quasi-stationary distributions in the case where S is irreducible (i.e. it constitutes a single communicating class) has been studied by several authors.

We summarize the main findings for the Quasi-Stationarity Irreducible (QSI) case in the following series of statements that are based on the recent paper of [16] (see also [23,15]):

(QSI-i) The matrix A_Q has a unique eigenvalue $-\alpha$ with maximal real part. α is real and positive.

(QSI-ii) The eigenvalue $-\alpha$ of A_Q has geometric multiplicity 1. In particular, there exists a unique row vector $\underline{q} = (q_1, q_2, \ldots, q_n)$ such that $\underline{q}A_Q = -\alpha\underline{q}$ and $\underline{q}\underline{1}^T = 1$.

(QSI-iii) The vector $\underline{q}$ is pointwise positive.

(QSI-iv) $\Pr_{\underline{q}}[T > t + s | T > t] = \mathrm{e}^{-\alpha s},\ t, s \geq 0$.

(QSI-v) $\Pr_{\underline{q}}[X(t) = j | T > t] = q_j,\ j \in S,\ t \geq 0$. The distribution $\underline{q}$ is the unique distribution with this property; that is, it is the unique quasi-stationary distribution of $\{X(t) : t \geq 0\}$.

(QSI-vi) If $\underline{w}$ is any distribution concentrated on S, then

$$\lim_{t\to\infty} \Pr_{\underline{w}}[T > t + s | T > t] = \mathrm{e}^{-\alpha s}, \quad s \geq 0.$$

(QSI-vii) If $\underline{w}$ is any distribution concentrated on S, then

$$\lim_{t\to\infty} \Pr_{\underline{w}}[X(t) = j | T > t] = q_j, \quad j \in S.$$

Thus, in the case of an irreducible set of transient states, we have that there exists a unique quasi-stationary distribution which coincides with the normalized left eigenvector corresponding to the unique eigenvalue of the matrix A_Q with maximal real part. Moreover, starting with any initial distribution and given that absorption has not yet occurred, the limiting distribution of the remaining time till the absorption is exponential and the limiting distribution of the state of the process is the quasi-stationary distribution itself.

van Doorn and Pollett [16] have recently studied various results concerning the quasi-stationarity issue for absorbing continuous time Markov chains with a finite state of transient states S which is reducible. Their results generalize the previously reported results that we presented above concerning the case where S is irreducible. The general framework of [16] is indispensable for our study since the set of transient states of the process of interest $\{(I(t), M(t)) : t \geq 0\}$ of our model is reducible. We summarize below the results of [16] for the Quasi-Stationarity Reducible (QSR) case.

Consider a continuous time Markov chain $\{X(t) : t \geq 0\}$ on a finite state space $\{0\} \cup S$ consisting of an absorbing state 0 and the set of transient states $S = \{1, 2, \ldots, n\}$ with transition rate matrix given by (41). We suppose that the set S is reducible and we denote by $S_1, S_2, \ldots, S_L$ its L communicating classes and by $A_{Q_1}, A_{Q_2}, \ldots, A_{Q_L}$ the corresponding submatrices of A_Q for the transitions within the classes. Moreover, we suppose that the classes have been numbered so that S_i is accessible from S_j implies that $i \leq j$. Under such a numbering (which is always possible), the matrix A_Q is lower block triangular and the following statements hold:

(QSR–i) The matrices $A_{Q_k},\ k = 1, 2, \ldots, L$ have all the properties (QSI-i)–(QSI-vii) with T being the sojourn time in class S_k. The matrix A_Q has an eigenvalue $-\alpha$ with maximal real part. α is real and positive. We have that $\alpha = \min\{\alpha_k : k = 1, 2, \ldots, L\}$, where $-\alpha_k$ is the unique maximal eigenvalue of the matrix $A_{Q_k},\ k = 1, 2, \ldots, L$. We set $I(\alpha) = \{k : \alpha_k = \alpha\}$, the set of indices of the communicating classes S_k whose maximal eigenvalues coincide with the maximal eigenvalue of the matrix A_Q. Moreover, we set $a(\alpha) = \min I(\alpha)$ and $b(\alpha) = \max I(\alpha)$.

(QSR–ii) The eigenvalue $-\alpha$ of A_Q has algebraic multiplicity equal to the number of elements of $I(\alpha)$. Its geometric multiplicity is 1 if and only if the family $\{S_k : k \in I(\alpha)\}$ is linearly ordered (i.e. S_i is accessible from S_j if and only if $i \leq j$). In the latter case, we have in particular that there exists a unique row vector $\underline{q} = (q_1, q_2, \ldots, q_n)$ such that $\underline{q}A_Q = -\alpha\underline{q}$ and $\underline{q}\underline{1}^T = 1$.

(QSR–iii) If $-\alpha$ has geometric multiplicity 1, then the vector $\underline{q}$ is pointwise non-negative. Moreover, $q_j > 0$ if and only if j is accessible from $S_{a(\alpha)}$.

(QSR–iv) If $-\alpha$ has geometric multiplicity 1 and $\underline{q}$ is the vector in (QSR-ii), then

$$\Pr_{\underline{q}}[T > t + s | T > t] = \mathrm{e}^{-\alpha s}, \quad t, s \geq 0.$$

(QSR–v) If $-\alpha$ has geometric multiplicity 1 and $\underline{q}$ is the vector in (QSR-ii), then

$$\Pr_{\underline{q}}[X(t) = j | T > t] = q_j, \quad j \in S,\ t \geq 0.$$

The distribution $\underline{q}$ is the unique distribution with this property, among all distributions under which the subset $S_a(\alpha)$ is accessible; that is, it is the unique quasi-stationary distribution of $\{X(t) : t \geq 0\}$ within the class of distributions under which $S_a(\alpha)$ is accessible.

(QSR–vi) If $-\alpha$ has geometric multiplicity 1, $\underline{q}$ is the vector in (QSR-ii) and $\underline{w}$ is any distribution concentrated on S such that the set $S_a(\alpha)$ is accessible, then

$$\lim_{t\to\infty} \Pr_{\underline{w}}[T > t+s | T > t] = \mathrm{e}^{-\alpha s}, \quad s \geq 0.$$

(QSR–vii) If $-\alpha$ has geometric multiplicity 1 and $\underline{q}$ is the vector in (QSR-ii) and $\underline{w}$ is any distribution concentrated on S such that the set $S_a(\alpha)$ is accessible, then

$$\lim_{t\to\infty} \Pr_{\underline{w}}[X(t) = j | T > t] = q_j, \quad j \in S.$$

We are now studying our process of interest $\{(I(t), M(t)) : t \geq 0\}$. Observe that the subset of transient states in our case consists of $N - k_0 + 1$ communicating classes: $S_j = \{(i, N-j+1) : 1 \leq i \leq N-j+1\}, j = 1, 2, \ldots, N-k_0+1$. Note that with this ordering we have that S_j is accessible from $S_{j'}$ if and only if $j \leq j'$. The submatrix A_Q corresponding to the transient states in S, under the ordering $\{(1,N), (2,N), \ldots, (N,N), (1,N-1), (2,N-1), \ldots, (N-1,N-1), \ldots, (1,k_0), (2,k_0), \ldots, (k_0,k_0)\}$, is lower block didiagonal, of the form

$$A_Q = \begin{pmatrix} B_N & 0 & 0 & \cdots & 0 & 0 & 0 \\ C_{N-1} & B_{N-1} & 0 & \cdots & 0 & 0 & 0 \\ 0 & C_{N-2} & B_{N-2} & \cdots & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \cdots & C_{k_0-1} & B_{k_0-1} & 0 \\ 0 & 0 & 0 & \cdots & 0 & C_{k_0} & B_{k_0} \end{pmatrix}. \tag{42}$$

The $k \times k$ diagonal block B_k corresponding to transitions within the set $\{(1,k), (2,k), \ldots, (k,k)\}$ is tridiagonal and it is identical to the corresponding submatrix of the transition rate matrix of $\{I(t) : t \geq 0\}$. More specifically, we have that

$$B_k = \begin{pmatrix} -(\lambda_1+\mu_1) & \lambda_1 & 0 & \cdots & 0 & 0 \\ \mu_2 & -(\lambda_2+\mu_2) & \lambda_2 & \cdots & 0 & 0 \\ 0 & \mu_3 & -(\lambda_3+\mu_3) & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots \\ 0 & 0 & 0 & \cdots & -(\lambda_{k-1}+\mu_{k-1}) & \lambda_{k-1} \\ 0 & 0 & 0 & \cdots & \mu_k & -(\lambda_k+\mu_k) \end{pmatrix}. \tag{43}$$

The $k \times (k+1)$ subdiagonal block C_k corresponding to transitions from $\{(1,k), (2,k), \ldots, (k,k)\}$ to $\{(1,k+1), (2,k+1), \ldots, (k+1,k+1)\}$ has only one non-zero entry, the entry $(k, k+1)$ with value λ_k.

We are now ready to apply the results of [16] to conclude with the study of the SIS model. We have the following theorem.

Theorem 3. *Consider the submatrix B_N of the transition rate matrix of $\{I(t) : t \geq 0\}$ corresponding to the transient states and let $-\alpha < 0$ be its unique maximal eigenvalue and $(q_1, q_2, \ldots, q_N)$ the corresponding unique left eigenvector (i.e. the quasi-stationary distribution of $\{I(t) : t \geq 0\}$). We also define the absorption time*

$$T = \sup\{t \geq 0 : I(t) \neq 0\}. \tag{44}$$

Then

1. *The maximal eigenvalue of the submatrix A_Q of the transition rate matrix of $\{(I(t), M(t)) : t \geq 0\}$ corresponding to the transient states is $-\alpha$.*
2. *There exists a unique row vector $\underline{q} = \left(q_{1,N}, q_{2,N}, \ldots, q_{N,N}, \ldots, q_{1,k_0}, q_{2,k_0}, \ldots, q_{k_0,k_0}\right)$, such that $\underline{q} \geq \underline{0}$, $\underline{q}A_Q = -\alpha\underline{q}$ and $\underline{q}\underline{1}^T = 1$. The only non-zero entries of $\underline{q}$ correspond to the states in S_1. The vector $(q_{1,N}, q_{2,N}, \ldots, q_{N,N})$ is exactly the quasi-stationary distribution of $\{I(t) : t \geq 0\}$. We have*

$$\Pr_{\underline{q}}[T > t+s | T > t] = \mathrm{e}^{-\alpha s}, \quad s \geq 0, \tag{45}$$

$$\Pr_{\underline{q}}[(I(t), M(t)) = (i,k) | T > t] = \delta_{k,N} q_i, \quad 1 \leq i \leq k, \ t \geq 0. \tag{46}$$

3. *For any initial distribution $\underline{w}$ of $(I(0), M(0))$, where absorption has not yet occurred (i.e. there is zero probability on states with $I(0) = 0$), we have*

$$\lim_{t\to\infty} \Pr_{\underline{w}}[T > t+s | T > t] = \mathrm{e}^{-\alpha s}, \quad s \geq 0, \tag{47}$$

$$\lim_{t\to\infty} \Pr_{\underline{w}}[(I(t), M(t)) = (i,k) | T > t] = \delta_{k,N} q_i, \quad 1 \leq i \leq k. \tag{48}$$

Proof. Since A_Q is block triangular, its eigenvalues are given as the union of the eigenvalues of the matrices $B_N, B_{N-1}, \ldots, B_{k_0}$. Moreover, the matrix B_k is the part of B_N corresponding to its left-upper $k \times k$ submatrix and B_N is a real tridiagonal matrix. We have also that the product of any two corresponding elements of the subdiagonal and the superdiagonal is strictly positive, so the eigenstructure of B_k is well known. More specifically, we can apply the so-called Given's theorem (see [24] Theorem 6.2–2) and we immediately conclude that the matrix B_k has k distinct real eigenvalues for every k with $k_0 \leq k \leq N$. Moreover, the k eigenvalues of B_k separate the $k+1$ eigenvalues of B_{k+1}, for every k with $k_0 \leq k \leq N-1$. As a corollary, we have in particular that the maximal eigenvalue of A_Q is given as the maximal eigenvalue of B_N and has algebraic multiplicity 1.

Using the above facts, we can now apply the results of [16] reported in the statements (QSR-i)–(QSR-vii). Note that in our case the maximal eigenvalue $-\alpha$ has algebraic and hence geometric multiplicity 1, because of Given's theorem. Moreover, we have that the $N - k_0 + 1$ communicating classes S_j are linearly ordered. Indeed, this is an obvious consequence of the block didiagonal form of the matrix A_Q given by (42).

Statements (QSR-ii) and (QSR-iii) show that there exists a unique row vector $\underline{q}$ such that $\underline{q} \geq \underline{0}, \underline{q}A_Q = -\alpha\underline{q}$ and $\underline{q}\underline{1}^T = 1$. The only non-zero entries of $\underline{q}$ correspond to the states in $S_1 = \{(1, N), (2, N), \ldots, (N, N)\}$, because this is the set $S_{a(\alpha)}$ of (QSR-iii) for the present model. The application of (QSR-iv)–(QSR-vii) yields immediately (45)–(48). ■

The above theorem assures that, for $t \to \infty$ and given that the absorption has not yet occurred, it is certain that the MNI has reached N, and then the process $\{I(t) : t \geq 0\}$ resides in state i with probability q_i.

Similar results can be derived regarding the corresponding quasi-stationarity of the process, given that the epidemic has not yet finished nor has exceeded a given threshold m for the number of infected individuals. Thus, we have a quantification of the behavior of the process $\{(I(t), M(t)) : t \geq 0\}$, given that it keeps evolving in the subset $\{1, 2, \ldots, m\}$. Then, starting from a state $(I(0), M(0)) = (i_0, k_0)$, the process stays in the subset $S_{\leq m} = \{(i, k) : k_0 \leq k \leq m, \quad 1 \leq i \leq k\}$ till absorption to some state in $\{(0, k_0), (0, k_0+1), \ldots, (0, m)\} \cup \{(m+1, m+1)\}$. Let $A_Q^{(m)}$ be the corresponding subset of transient states, which is now given as

$$A_Q^{(m)} = \begin{pmatrix} B_m & 0 & 0 & \cdots & 0 & 0 & 0 \\ C_{m-1} & B_{m-1} & 0 & \cdots & 0 & 0 & 0 \\ 0 & C_{m-2} & B_{m-2} & \cdots & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & \cdots & C_{k_0-1} & B_{k_0-1} & 0 \\ 0 & 0 & 0 & \cdots & 0 & C_{k_0} & B_{k_0} \end{pmatrix}. \tag{49}$$

The analysis goes along the same lines of Theorem 3, so we state the results but we omit the proof.

Theorem 4. *Consider the submatrix B_m of the transition rate matrix of $\{I(t) : t \geq 0\}$ corresponding to the subset $\{1, 2, \ldots, m\}$ of transient states and let $-\alpha^{(m)} < 0$ be its unique maximal eigenvalue and $(q_1^{(m)}, q_2^{(m)}, \ldots, q_m^{(m)})$ the corresponding unique left eigenvector. We also define*

$$T^{(m)} = \sup\{t \geq 0 : I(t) \neq 0, \ M(t) \leq m\}. \tag{50}$$

Then

1. *The maximal eigenvalue of $A_Q^{(m)}$ is $-\alpha^{(m)}$.*
2. *There exists a unique row vector $\underline{q}^{(m)} = \left(q_{1,m}^{(m)}, q_{2,m}^{(m)}, \ldots, q_{m,m}^{(m)}, \ldots, q_{1,k_0}^{(m)}, q_{2,k_0}^{(m)}, \ldots, q_{k_0,k_0}^{(m)}\right)$, such that $\underline{q}^{(m)} \geq \underline{0}$, $\underline{q}^{(m)}A_Q^{(m)} = -\alpha^{(m)}\underline{q}^{(m)}$ and $\underline{q}^{(m)}\underline{1}^T = 1$. The only non-zero entries of $\underline{q}^{(m)}$ correspond to the states in the subset $\{(1, m), (2, m), \ldots, (m, m)\}$. The vector $(q_{1,m}^{(m)}, q_{2,m}^{(m)}, \ldots, q_{m,m}^{(m)})$ is exactly the quasi-stationary distribution $(q_1^{(m)}, q_2^{(m)}, \ldots, q_m^{(m)})$ of $\{I(t) : t \geq 0\}$ till absorption to $\{0, m+1\}$. We have*

$$\Pr_{\underline{q}^{(m)}}[T^{(m)} > t + s | T^{(m)} > t] = \mathrm{e}^{-\alpha^{(m)}s}, \quad s \geq 0, \tag{51}$$

$$\Pr_{\underline{q}^{(m)}}[(I(t), M(t)) = (i, k) | T^{(m)} > t] = \delta_{k,m} q_i^{(m)}, \quad 1 \leq i \leq k, \ t \geq 0. \tag{52}$$

3. *For any initial distribution $\underline{w}$ of $(I(0), M(0))$, where absorption has not yet occurred, we have*

$$\lim_{t\to\infty} \Pr_{\underline{w}}[T^{(m)} > t + s | T^{(m)} > t] = \mathrm{e}^{-\alpha^{(m)}s}, \quad s \geq 0, \tag{53}$$

$$\lim_{t\to\infty} \Pr_{\underline{w}}[(I(t), M(t)) = (i, k) | T^{(m)} > t] = \delta_{k,m} q_i^{(m)}, \quad 1 \leq i \leq k. \tag{54}$$

The above theorem assures that, for $t \to \infty$, and given that the time $T^{(m)}$ has not yet expired, it is certain that the MNI has reached the level m. Then the process $\{I(t) : t \geq 0\}$ resides in state i with probability $q_i^{(m)}$; that is, the quasi-stationary probability of $I(t)$ at state i given that the process has not yet visited the subset $\{0, m+1\}$.

5. Applicability and numerical analysis of the MNI

In this section, we give some biological insight on the application of the MNI. To this end, in Section 5.1 we comment on the applicability of the MNI to the control of infectious diseases. On the other hand, the influence of the various parameters in the behavioral characteristics of the SIS epidemic model is illustrated in Section 5.2.

5.1. On the applicability of the MNI

One of the important reasons to study epidemiological models is to provide tools for controlling infectious diseases. Several forms of control exist, including vaccination, quarantine and culling. In many situations, in addition to a basic set of control measures, there also exist alternative control actions. For instance, not all individuals need to be vaccinated in order to eradicate an epidemic, so at the early stage only a certain proportion is immunized. However, when the number of infective individuals reaches a critical level, the vaccination policy should be extended to cover a higher proportion of the population.

As a natural measure of the epidemic size at any time, the MNI provides a potential tool for designing the control strategy. In conjunction with empirical observations, statistical methods and simulation permit one to fit the basic parameters of the stochastic epidemiological model (see e.g. [25]). An initial control policy is assumed, but it might be changed if the infected population is over a critical threshold, we say M_c, at a certain inspection time t_i. Obtaining such information can be a very difficult, or even impossible, task in practice. However, the MNI of the epidemiological stochastic model provides a helpful tool to determine the probability involved in

$$P\{M(t_i) \geq M_c\} \geq p_c, \tag{55}$$

where p_c denotes a certain critical p-value. If the inequality in (55) holds, then a more effective control should be applied to shorten the outbreak and avoid the dramatic implications of a massive infection.

The following examples give support to the use of the above control policy based on the MNI.

Example 1. Head lice infections.

Head lice infections are an important health problem among children worldwide (see e.g. [14]). Since this infection is extremely contagious, it is important to observe any outbreak promptly, and to reduce the transmission rate. Control actions at the early stage of the epidemic include avoiding head-to-head contact, not sharing combs and other personal hygiene objects and mechanical removal. Periodical inspections are programmed for monitoring the infection spread. In practice, only a random sample of schools and children can be checked, but the MNI can be used to calculate the key probability in (55). If it is needed, school administrations and parents should coordinate the use of topical insecticides and the isolation of the most affected pupils.

Example 2. Livestock diseases.

Control of livestock diseases provides a scenario in which economical considerations play an important role (see e.g. [26]). A cost–profit analysis may lead to choosing a weak cheap control at the beginning of the outbreak. Such a low-quality control may lead to a prolonged epidemic. However, if the epidemic were to become established it could persist for a long time. In such a case, the public-health authorities may order closure of the farm. Using the MNI, it is possible to determine when a more expensive but more effective control should be adopted to shorten the outbreak.

Example 3. Computer viruses.

In the two last decades, computer networks have become an essential tool for daily life. As a result, computer viruses started to be a major threat (see e.g. [27]). Inspired by epidemiological models, many studies try to acquire a better understanding of computer viruses spreading dynamics. Most virus-cleaning processes consist of a computer program which acts in isolation just limited to a single infected node. This provides a first simple control strategy. However, a rapid propagation of the virus may cause the collapse of the whole network. At this point, the MNI can actually help in fighting against the virus spreading. When the maximum number of infected nodes within, say, the next 72 h reaches the critical threshold determined by (55), a more sophisticated but more effective control strategy can be followed. The connectivity of the network must be exploited. Analyzing where the virus comes from and tracing where it goes, it is possible to treat all the nodes integrated in a subnet simultaneously.

5.2. Behavior analysis of the MNI

In Section 5.1, we showed how the MNI can be applied to control the spread of an epidemic. As a preliminary step, a statistical study is needed to estimate the contact and the recovery rates, but such a study is not the subject matter of this paper. In contrast, in this section, we present some numerical results for an instance of the classical SIS model with population size N; that is, birth rates $\lambda_i = \beta i(N - i)/N$ and death rates $\mu_i = \gamma i$, for $i = 0, \ldots, N$. We also comment on the biological insights that one can gain from performing such numerical analysis.

Table 1
Expected MNI versus β and γ.

$E[M(t)]$	$\beta = 0.05$	$\beta = 0.5$	$\beta = 1.0$	$\beta = 5.0$	$\beta = 10.0$
$\gamma = 0.5$	20.062795	20.956955	22.645022	40.089593	47.856359
	20.063830	21.489649	29.415663	49.226208	49.998893
	20.063830	21.563272	36.631472	49.996687	49.999999
$\gamma = 1.0$	20.030921	20.418540	21.191152	36.118887	45.940009
	20.030928	20.428938	21.530456	46.481532	49.638600
	20.030928	20.428938	21.564466	48.511584	49.999990
$\gamma = 2.0$	20.015228	20.176475	20.427863	29.376866	41.744306
	20.015228	20.176487	20.428938	39.183956	47.290524
	20.015228	20.176487	20.428938	42.803358	48.888843
$\gamma = 5.0$	20.006036	20.063830	20.136371	21.489649	29.415663
	20.006036	20.063830	20.136371	21.563272	36.631472
	20.006036	20.063830	20.136371	21.564490	40.174717

Table 2
Standard deviation of the MNI versus β and γ.

$\sigma(M(t))$	$\beta = 0.05$	$\beta = 0.5$	$\beta = 1.0$	$\beta = 5.0$	$\beta = 10.0$
$\gamma = 0.5$	0.257239	1.205551	2.166914	3.412318	1.511667
	0.259989	1.730322	4.068534	0.705220	0.032878
	0.259989	1.776646	2.257760	0.057244	0.000000
$\gamma = 1.0$	0.178338	0.751302	1.443921	3.923044	2.051675
	0.178361	0.767435	1.758792	1.299111	0.507037
	0.178361	0.767435	1.777283	0.715998	0.000000
$\gamma = 2.0$	0.124259	0.452524	0.765874	4.141422	2.902465
	0.124259	0.452547	0.767435	2.255775	1.043320
	0.124258	0.452547	0.767435	1.323395	0.630043
$\gamma = 5.0$	0.077885	0.259989	0.391637	1.730322	4.068534
	0.077885	0.259989	0.391637	1.776646	2.257760
	0.077885	0.259989	0.391637	1.777297	1.512237

Tables 1 and 2 display, respectively, the expected value and standard deviation for the MNI observed till time t. We consider contact rates $\beta \in \{0.05, 0.5, 1.0, 5.0, 10.0\}$ and recovery rates per individual $\gamma \in \{0.5, 1.0, 2.0, 5.0\}$. We observe a population of $N = 50$ individuals and assume that initially there exist $i_0 = 20$ infectives. For three different epochs, $t = 0.5, 5.0$ and 50.0, in each cell we provide, from top to bottom, the corresponding measure of the MNI.

$E[M(t)]$ is non-decreasing as a function of t. Moreover, for $\beta < \gamma$ the function $E[M(t)]$ is nearly constant, while for $\beta > \gamma$ we observe a drastically increasing behavior. For a fixed t, we see that the greater contact rates provide the larger expected MNI, while longer recovery rates imply smaller expected MNI. In general, the standard deviation shows no monotonicity with respect to either the contact rate β, the recovery rate γ or the time. We can observe that for $\beta < \gamma$ the function $\sigma(M(t))$ is also nearly a constant.

The results of Tables 1 and 2 allow one to gain several qualitative and quantitative insights regarding the evolution and variability of the MNI in an SIS epidemic. For example, we observe that for small values of β, e.g. $\beta = 0.05$ and 0.5, the MNI evolves very slowly. Indeed, the first two columns of Table 1 show that, for $t = 0.5, 5.0$ and 50.0, the expected MNI is practically constant. Therefore, there is no need to take preventive measures or to try to upgrade the available facilities in hospitals to accommodate a 'wave' of new infected individuals. Such a sudden outbreak is practically impossible. The small standard deviation of the MNI in the corresponding columns of Table 2 supports further this conclusion. In fact, the small values of $\sigma(M(t))$ show that the expected MNI gives very precise information about the future behavior of the MNI, which evolves almost deterministically. Thus, a long-run scheduling for the administration of the epidemic is possible.

On the other hand, for the intermediate value of $\beta = 1.0$ and $\gamma = 0.5$, the entries in Table 1 show that, as time passes, it is reasonable to expect that we will need more beds in hospitals or other facilities to accommodate an increased number of MNI. Thus, in 4.5 time units (from $t = 0.5$ to $t = 5.0$), the expected MNI increases by almost 7 units. Then, in another 45.0 time units (from $t = 5.0$ to $t = 50.0$), we expect the MNI to increase by 7 more units. However, we see that in the first interval the increase is quite acute, so it seems quite urgent to upgrade the existing facilities, while in the second interval there is enough time to react. Moreover, we see that the corresponding values of the standard deviation in Table 2 are rather high, so the expected MNI does not give precise information about the actual realization of the process of the MNI. A short-term administration of the epidemic seems more plausible.

Tables 1 and 2 can also shed light to the effect of various control actions that may be available for controlling an epidemic. A campaign that urges for hygiene measures may result in a change of the infection contact rate β by halving it. By comparing the second and the third columns of Table 1 for $E[M(t)]$, we see that the result of such a campaign is substantial for the value of $\beta = 1.0$ in the long run. Indeed, such an effort results to an important reduction of the expected MNI from 36.63 to 21.56, for $t = 50.0$. On the other hand, for $\beta = 10.0$, the effect of such measures seems very limited.

Table 3
Expected MNI versus N and i_0.

$E[M(t)]$	$N = 10$	$N = 20$	$N = 30$	$N = 40$	$N = 50$
$i_0 = 5$	7.134617	10.070926	12.043397	13.482362	14.585406
	8.987827	16.814988	24.182266	31.280565	38.216775
	9.237412	18.551945	26.881004	34.676432	42.220449
$i_0 = 15$	–	16.327641	19.840540	23.174986	26.130630
	–	17.638716	24.890314	32.049226	39.070083
	–	19.018756	27.340162	35.189088	42.797624
$i_0 = 25$	–	–	25.748022	28.583930	32.054981
	–	–	26.125879	32.366523	39.304997
	–	–	27.428478	35.205761	42.809281
$i_0 = 35$	–	–	–	35.472585	37.468612
	–	–	–	35.516236	39.844222
	–	–	–	35.851441	42.838609
$i_0 = 45$	–	–	–	–	45.339883
	–	–	–	–	45.342871
	–	–	–	–	45.368125

Table 4
Measures for the conditional quasi-stationary distribution.

m	$\beta = 0.1$	$\beta = 0.2$	$\beta = 1.0$	$\beta = 5.0$	$\beta = 10.0$
10	1	1	1	8	9
	1.107855	1.239391	3.412634	5.761486	5.832030
	0.344832	0.541456	2.191976	2.780049	2.824738
20	1	1	1	18	19
	1.107855	1.239396	4.932547	12.546369	12.370331
	0.344832	0.541453	3.474479	5.444038	5.573498
30	1	1	1	28	29
	1.107855	1.239396	5.070632	21.850379	20.807261
	0.344832	0.541453	3.624925	7.242479	7.843053
40	1	1	1	37	39
	1.107855	1.239396	5.070916	36.174436	33.510247
	0.344832	0.541453	3.625353	2.557275	7.717007
49	1	1	1	40	45
	1.107855	1.239396	5.070916	39.736214	44.753540
	0.344832	0.541453	3.625353	3.212165	2.219021
50	1	1	1	40	45
	1.107855	1.239396	5.070916	39.740001	44.885754
	0.344832	0.541453	3.625353	3.214392	2.264504

In Table 3, we present numerical results for $E[M(t)]$ when varying the population size, N, and the initial number of infectives, i_0. In fact, we consider $N \in \{10, 20, 30, 40, 50\}$ and $i_0 \in \{5, 15, 25, 35, 45\}$. We fixed a contact rate $\beta = 5.0$, an individual recovery rate of $\gamma = 2.0$ and we observed the system at $t = 0.5, 5.0$ and 50.0 time units. The table provides in each cell, from top to bottom, the corresponding expected MNI up to time t. As a function of t, the expected MNI shows an increasing behavior. At a fixed t, we observe larger expected MNI for larger population sizes and also an increasing behavior with regard to the initial number of infectives.

The results in Table 3 can help one to quantify the effect of isolation measures on the control of an epidemic. Indeed, isolation measures result in the reduction of the initial number of infective individuals i_0. Table 3 also shows the effect of a reduction of i_0 on the expected MNI as time passes, for various values of N.

Finally, each cell in Table 4 displays, from top to bottom, the mode, mean and standard deviation of the quasi-stationary distribution of the number of infectives, given that the epidemic has neither yet finished nor has exceeded a fixed threshold m for the number of infected individuals. We considered a population of $N = 50$ individuals and fixed the individual recovery rate as $\gamma = 1.0$ time units. The contact rate varies as $\beta \in \{0.1, 0.2, 1.0, 5.0, 10.0\}$. Results are listed for the threshold levels $m \in \{10, 20, 30, 40, 49, 50\}$.

It can be observed that, when m increases, all measures tend to their analogous ones in the model having no restriction on the maximum number of infectives (i.e., the case $m = 50$). In particular, the convergence is faster for small values of the contact rate β. For a fixed threshold level m, we have a single mode showing an increasing behavior for increasing contact rates.

Acknowledgements

The authors were supported by the Government of Spain (Department of Science and Innovation) and the European Commission through project MTM 2008-01121.

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