Mathematical Statistics
Stockholm University

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Research Report 2010:1

ISSN 1650-0377

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Research Report **2010:1**,
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We study an open population stochastic epidemic model from the time of introduction of the disease, through a possible outbreak and to extinction. The model describes an SIS (susceptible-infective-susceptible) epidemic where all individuals, including infectious ones, reproduce at a given rate. An approximate expression for the outbreak probability is derived using a coupling argument. Further, we analyse the behaviour of the model close to quasi-stationarity, and the time to disease extinction, with the aid of a diffusion approximation. In this situation the number of susceptibles and infectives behaves as an Ornstein-Uhlenbeck process, centred around the stationary point, for an exponentially distributed time before going extinct.

Key words: stochastic epidemic model, quasi stationarity, sis model, coupling, Ornstein-Uhlenbeck, diffusion approximation, outbreak probability

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December 21, 2009

Abstract

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1 Introduction

Stochastic epidemic models have been studied intensely over the past decades, trying to capture the behaviour of a real epidemic spreading in a population, may it be human or bacterial (see e.g. [3] and [4]). Over time more general models have been analysed such as multitype epidemics models, and models allowing for individual heterogeneities and demographics in the monitored population. We focus on the last of these generalisations.

More specifically, we analyse an SIS (susceptible → infectious → susceptible) stochastic epidemic model with demography. The model aims at capturing the behaviour of the

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process of infectious individuals introduced into a population where both susceptible and infectious individuals reproduce and die. We determine the probability of an outbreak, analyse the dynamics of the process close to quasi-stationarity i.e. the endemic state, and derive results concerning the time to disease extinction given that the process is started in the quasi-stationary state. That is, the complete dynamics from introduction to extinction.

Similar models have been analysed by e.g. [9] and [5]. In the first, it is assumed that only susceptibles reproduce and no recovery from infection is possible, in the latter, immigration is assumed instead of, as in our model, reproduction from within the process itself. Both [8] and [2] address the question of time to disease extinction, but where [8] is concerned with an open population model with immigration whereas [2] studies a closed population model. In the present paper the time to extinction is analysed using the same methods as used in [8].

In the model we make some standard, albeit unrealistic, assumptions regarding the spread of the disease. These include the assumption of homogeneous mixing, i.e. that all pairs of individuals have the same probability of meeting and infecting each other. A thorough treatment of stochastic epidemic models and the standard assumptions can be found in [1].

The rest of the paper is organised as follows: Section 2 describes the model and the assumptions made in detail. In Section 3 the basic reproduction number is derived. In Section 4 an approximation of the probability of an outbreak is calculated under the assumption that the number of susceptibles is large compared to the number of infectives at the early stages of the epidemic. This is done via coupling arguments. In Section 5 the endemic phase is studied, i.e. when the number of infectives has reached a level that is stable for a longer period of time. A diffusion approximation is derived which provides insights into the dynamics of the disease. Section 6 is devoted to calculating the distribution of the time to extinction given that the process is started in quasi- stationarity. Following [8] we show that it is exponentially distributed and provide an approximate formula for its expected value. In Section 7 the paper is concluded by a discussion of the results obtained.

2 Model

We will consider a two-dimensional Markov process $\{(S(t), I(t)), t \geq 0\}$, where $S(t)$ and $I(t)$ represent the number of susceptibles and infectives respectively, at time t. The process $\{(S(t), I(t)), t \geq 0\}$ makes transitions in continuous time according to the transition rates given in Table 1. The parameter ν is a scaling parameter and will be proportional to the initial population size and intuitively also to the inhabited area. We analyse the behaviour of the model for large populations, i.e. when $\nu \to \infty$. Infected individuals make infectious contacts according to independent processes with intensities $\frac{\beta}{\nu}S(t)$ until recovery or death. The parameter $\frac{\beta}{\nu}$ is thus interpreted as the rate of *infectious* contacts per unit of area. This definition of the contact intensity guarantees that the process is a so called density dependent process. Intuitively it means that the dynamics are the same

Event	Transition	Transition rate
Infection of susceptible	$(x, y) \to (x-1, y+1)$	$\frac{\beta}{\nu} xy$
Birth of susceptible	$(x, y) \to (x+1, y)$	$\mu(x+y)$
Death of susceptible	$(x, y) \to (x-1, x)$	δx
Death of infective	$(x, y) \to (x, y-1)$	$(\delta+\eta)y$
Recovery of infective	$(x, y) \to (x+1, y-1)$	γy

Table 1: Transitions rates of the epidemic process at t with $\{(S(t), I(t)) = (x, y)\}$, where all parameters are larger than 0.

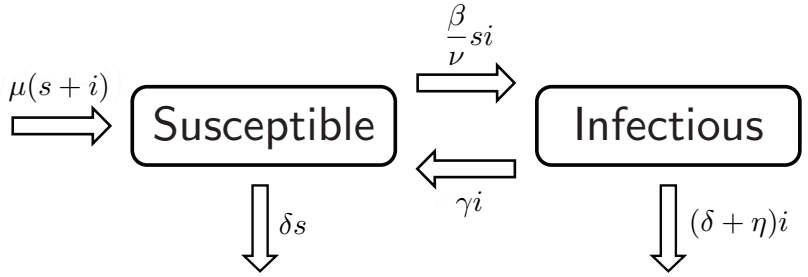

Figure 1: Transition diagram.

in a large population on a larger area as within a small population on a smaller area, i.e. the dynamics is scale invariant. Our process being density dependent is crucial for the diffusion approximation in Section 5.2.

Both susceptible and infective individuals give birth at the rate μ, whereas infective individuals die a higher rate $\delta + \nu$ than susceptibles which die at the rate δ. We assume that all parameters are strictly positive and that $\delta < \mu < \delta + \eta$. The latter assumption is crucial since it ensures the existence of a quasi-stationarity state of the process. This can be seen heuristically as follows: Should, violating the assumption, $\mu < \delta$ the birth rate of the total population would be smaller than the average death rate and the population would go extinct. If the second inequality is violated and $\delta + \eta < \mu$ the birth rate of the total population would be larger than the average death rate making the total population process supercritical and thereby excluding the possibility of a quasi-stationary state.

Infective individuals leaves the infective state with intensity $\delta + \eta + \gamma$, thus implying an exponentially distributed infectious period with mean $1/(\delta + \eta + \gamma)$. Furthermore, the probability of dying of the disease when infected is $\eta/(\delta + \eta + \gamma)$.

3 The basic reproduction number

The basic reproduction number, commonly denoted R_0, is the mean offspring of an individual in a branching process. When used in epidemic modeling R_0 is interpreted as the mean number of infections caused by an infective. In the latter case R_0 is calculated assuming that the vast majority of the population is susceptible, i.e. during the initial

stages of an epidemic when a branching process approximation of the process of infectives is valid. Since we are analysing an open population model we also need to worry about the susceptible population fluctuating. Thus R_0 calculated for our model is not necessarily valid as the mean number of infections caused by an infective, for as long as in the corresponding fixed population model, since the conditions change more rapidly. We derive R_0 as follows:

The first infective is introduced into a population of ν susceptibles where ν is large. The first infectives spread the disease according to a process with intensity $\frac{\beta}{\nu}S(t) \approx \frac{\beta}{\nu}\nu = \beta$, during the infectious period, for small t. That is, when there are approximately ν susceptibles, and few infectives compared to susceptibles. Let $\{\xi(t), t \geq 0\}$ be a Poisson process with intensity β and let Y be the infectious period of an infective individual, where ξ and Y are independent. Then

$$R_0 = E[E[\xi(Y)|Y]] = E[\beta Y] = \frac{\beta}{\gamma + \delta + \eta}, \tag{3.1}$$

since $\xi([0,t])$ is Poisson distributed with mean βt and the infectious period Y is exponentially distributed with mean $\frac{1}{\gamma+\delta+\eta}$.

4 Outbreak probability

The aim of the present section is to approximate, the probability that a large outbreak occurs, p, when a single infected individual is introduced into a large susceptible population. We will show that our process can be approximated arbitrarily well by the process analysed in [10], here denoted $\{(\tilde{S}, \tilde{I})\}$, for which the outbreak probability is known. This process describes the spread of an epidemic in a open population, different to ours in that no recovery or reproduction is allowed in the infective state. The process $\{(\tilde{S}, \tilde{I})\}$ is governed by the transition rates in Table 2.

Transition	Transition rate
$(x,y,u,v) \to (x-1, y+1, u, v)$	$\frac{\beta}{\nu}xy$
$(x,y,u,v) \to (x-1, y, u, v)$	δx
$(x,y,u,v) \to (x+1, y, u, v)$	μx
$(x,y,u,v) \to (x, y-1, u, v)$	$(\delta+\eta)y$
$(x,y,u,v) \to (x, y-1, u+1, v)$	γy
$(x,y,u,v) \to (x, y, u+1, v)$	$\mu(y+u+v)$
$(x,y,u,v) \to (x, y, u-1, v)$	δu
$(x,y,u,v) \to (x-y, i, u, v+1)$	$\frac{\beta}{\nu}xv$
$(x,y,u,v) \to (x, y, u-1, v+1)$	$\frac{\beta}{\nu}u(y+v)$
$(x,y,u,v) \to (x, y, u, v-1)$	$(\delta+\eta)v$

Table 2: Transitions rates of the process $\{(\tilde{S}(t), \tilde{I}(t)), S_G(t), I_G(t)\}$ at $\{x, y, u, v\}$.

That the approximation of (S, I) by $(\tilde{S}, \tilde{I})$ is valid will be verified by the following coupling argument. Let $\tilde{S}(0) = \nu$, $\tilde{I}(0) = 1$, $S_G(0) = I_G(0) = 0$, $S \equiv \tilde{S} + S_G$ and

$I \equiv \tilde{I} + I_G$. We think of S_G and I_G as ghost susceptibles and ghost infectives respectively from the point of view of the approximating process $\{(\tilde{S}, \tilde{I})\}$, since they are a product of the process $\{(\tilde{S}, \tilde{I})\}$ but does not affect it. It follows readily that the transition rates of our process $\{(S, I)\}$ in Table 2 are the same as those in Table 1. The number of infectives $\tilde{I}$ in the approximating model are the same as the number of infectives in our model, I, as long as there are no ghost infectives I_G. Thus the coupling of I and $\tilde{I}$ breaks down at $T = \inf\{t : I_G(t) > 0\}$. The idea behind the coupling is that, in the initial phase, there are relatively few recovered and children of infectives in the population, compared to the total number of susceptibles. More specifically we want to prove that $P(T > t) \to 1$ as $\nu \to \infty$ for all $t > 0$. To this end we define the counting process $N(t) = \{\#$ jumps from S_G into I_G in $[0, t]\}$ and exploit that $P(T > t) = P(N(t) = 0)$. Furthermore, for $t < T$ it holds that $N(t) \mid \{S_G(s)\}_{s \le t}, \{\tilde{I}(s)\}_{s \le t}$ is Poisson distributed with mean $\int_0^t \frac{\beta}{\nu} S_G(s)\tilde{I}(s)ds$. Thus

$$\begin{aligned} P(T > t) &= E[P(N(t) = 0) \mid \{S_G(s)\}_{s \le t}\{\tilde{I}(s)\}_{s \le t}] \\ &= E\Big[\exp\Big\{-\int_0^t \frac{\beta}{\nu} S_G(s)\tilde{I}(s)ds\Big\}\Big] \\ &\ge \exp\Big\{-\frac{\beta}{\nu} E\Big[\int_0^t S_G(s)\tilde{I}(s)ds\Big]\Big\} \\ &\ge \exp\Big\{-\frac{\beta}{\nu}\int_0^t \sqrt{E[S_G^2(s)]E[\tilde{I}^2(s)]}ds\Big\} \end{aligned} \tag{4.1}$$

where the second to last inequality follows from Jensen's inequality and the last from the Cauchy-Schwarz inequality. In order to show that (4.1) $\to 1$ we introduce birth (-death) processes that are stochastically larger than S_G and $\tilde{I}$ on $[0, t]$. Take $\epsilon > 0,\ t < T$ and let the processes z, z', w, w' make transitions according to Table 3.

Transition	Transition rate
$z(s) \to z(s) + 1$	$\beta \exp\{(\mu - \delta)s\}z(s)$
$z(s) \to z(s) - 1$	$(\delta + \eta + \gamma)z(s)$
$z'(s) \to z'(s) + 1$	$\beta \exp\{(\mu - \delta)t\}z'(s)$
$w(s) \to w(s) + 1$	$(z'(s) + \epsilon)(\gamma + \mu) + \mu w(s)$
$w'(s) \to w'(s) + 1$	$(z'(t) + \epsilon)(\gamma + 2\mu)w'(s)$

Table 3: Transition rates of birth (-death) processes larger than S_G and $\tilde{I}$ on $[0, t]$, with $z(0) = z'(0) = w(0) = w'(0) = 1$,.

By Theorem 3.2 in [10] there exists ν' such that $\tilde{I}^{(\nu)}(\omega, s) \le z(\omega, s) + \epsilon$ a.s. for all $\nu \ge \nu'$. For $s \le t$ and $\nu \ge \nu'$ we therefore have that $\tilde{I}^{(\nu)}(s) \le^D z(s) + \epsilon \le^D z'(s) + \epsilon \le z'(t) + \epsilon$, where the second inequality is by the construction of the processes z and z' and the last follows from that $z'(s)$ is non-decreasing. Furthermore, for $\nu \ge \nu'$ and $s \le t < T$ we have that $S_G^{(\nu)}(s) \le^D w(s)$ since the the birth rate of w is $(z'(s) + \epsilon)(\gamma + \mu) + \mu w(s) \ge$

$(\mu+\gamma)\tilde{I}(s)+\mu w(s)$. Hence, for $\nu > \nu'$,

$$\begin{aligned}\int_0^t \sqrt{E[S_G^2(s)]E[\tilde{I}^2(s)]}ds &\leq \int_0^t \sqrt{E[(z'(s)+\epsilon)^2]E[(w^2(s)]}ds \\ &\leq tE[(z'(t)+\epsilon)^2]E[w^2(t)] \\ &\leq t(1+\epsilon)^2E[z'(t)^2]E[E((w^{'}(t))^2 \mid z'(t))],\end{aligned}$$

where $z^{'}$ and $w^{'}|z^{'}$ are Yule processes. The second inequality holds since $z', w \geq 1$ and z', w are non decreasing, and the third since $w \leq^D w'|z'$. This last fact follows since the birth intensity of w' is larger than that of w, which is seen by examining the last two lines of Table 3.

According to [12] p. 377 it holds that $z^{'}$ and $w^{'}|z^{'}(t)$ are geometrically distributed with second moments $\frac{2-q_1}{q_1^2}$ and $\frac{2-q_2}{q_2^2}$ respectively, where $q_1 := \beta\exp\{-\exp\{(\mu-\delta)t\}t\}$ and $q_2 := (z^{'}+\epsilon)(\gamma+2\mu)t$. Thus

$$\begin{aligned}E[z'(t)^2]E[E((w^{'}(t))^2 \mid z'(t))] &= \frac{2-q_1}{q_1^2}E[(2-q_2)/q_2] \\ &\leq \frac{2}{q_1^2}E[\frac{2}{q_2}] \\ &\leq \frac{2\exp\{2\exp\{(\mu-\delta)t\}t\}}{\beta^2(1+\epsilon)(\gamma+2\mu)t} < \infty \ \forall t, \qquad (4.2)\end{aligned}$$

where the last inequality holds since $z' \geq 1$. Hence $\int_0^t E[S_G^2(s)]E[\tilde{I}^2(s)]ds$ is bounded for all $t > 0$ and $\exp\Big\{-E\Big[\int_0^t \beta y(s)w(s)ds\Big]/\nu\Big\} \to 1$ as $\nu \to \infty \ \forall\ t > 0$.

In words, the probability that I and $\tilde{I}$ are the same on any given time interval tends to 1 as the initial number of susceptibles tends to infinity. Hence we may for large ν approximate the probability of an epidemic outbreak p in our model with the probability of an epidemic outbreak p' in the approximating model. The outbreak probability is

$$p' = (I+1)^{-1} \qquad (4.3)$$

$$I = \int_0^\infty (\delta+\eta+\gamma)\exp\Big\{(\delta+\eta+\gamma)s + \frac{\beta}{\mu-\delta}(1-\exp\{(\mu-\delta)s\})\Big\}ds \qquad (4.4)$$

(see [10] p. 456). For $\mu = \delta$ we instead have

$$p' = (\int_0^\infty (\delta+\eta+\gamma)\exp\{(\delta+\gamma+\eta-\beta)s\}ds + 1)^{-1} = 1 - 1/R_0$$

which equals the outbreak probability equals the corresponding one for a SIR model with closed, homogeneously mixing, population. In the present and the following section we study the model for the parameter values: $\delta = 1, \eta = 5, \gamma = 2, \beta = 10$ and $\mu = 2$. The parameters are chosen so that the demography and disease related dynamics of the process are of the same magnitude and on the same time-scale. In Figure 2 it is seen that the probability of an outbreak is increasing in R_0, which is intuitive from the the definition of

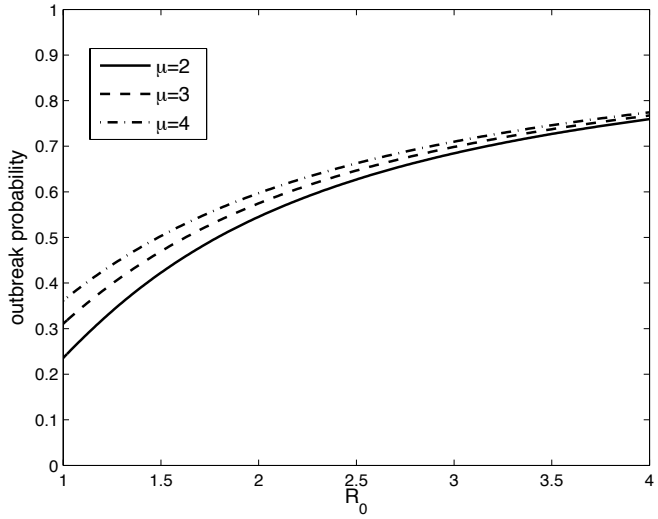

Figure 2: Outbreak probability as function of R_0 for different values of μ, where $\beta = 10, \gamma = 2, \eta = 5$ and $\delta = 1$.

R_0 as the expected number of infections caused by a single infective in an otherwise disease free population. Furthermore we note that the outbreak probability increases as $\mu - \delta$ increases. It is also seen that an approximation by the simple expression $p' = 1 - 1/R_0$ is good when R_0 is large. We also want to compare the result with estimates from simulations of the epidemic. In Table 4 we see estimates and 95%-confidence intervalls, based on 1000 simulations of the epidemic, for different initial population sizes. To be classified as an outbreak we require that at least $\sqrt(\nu)$ is infected. Assuming that the simulations producing an estimate are iid geometrically distributed, we use a normal approximation to derive the confidence intervalls.

ν	$\hat{p}$	95%-CI
100	0.374	(0.344 , 0.404)
500	0.336	(0.307 , 0.365)
1000	0.338	(0.309 , 0.367)
2000	0.335	(0.306 , 0.364)
4000	0.338	(0.309 , 0.367)
10000	0.314	(0.285 , 0.343)
20000	0.331	(0.302 , 0.360)

Table 4: Estimates of the outbreak probability p from 1000 simulations, where the theoretical estimate is 0.338

We see that the theoretical approximation is inside the 95% confidence intervalls for this choice of parameters and initial population sizes. We also note that the estimate 0.338 is substantially better than the crude estimate $p = 1 - 1/R_0 = 0.2$.

5 Endemic phase

Once an outbreak has occurred the branching process approximation in the previous section breaks down. To be able to study the behaviour of the process after the outbreak, in the endemic phase, we instead rely on a Gaussian diffusion approximation. The scaling parameter will as before be ν, i.e. we will let the inhabited area of the model grow large. To emphasise the dependence on ν we will denote the process $\{(S(t), I(t)), t \geq 0\}$ with parameter ν by $\{(S^{(\nu)}(t), I^{(\nu)}(t)), t \geq 0\}$. We will rely on the results in [7] and in particular Theorems 8.1 and 8.2 therein.

5.1 Law of large numbers

Our approximations will depend on the fact that $(S^{(\nu)}(t), I^{(\nu)}(t))$ is a so called density dependent Markov process, i.e. the transition rates depend on the current state of the process only through the *density* of susceptibles and infectives. The notion of density dependence is formalised by denoting the transition intensities in Table 1 by $q^{(\nu)}((x,y),(x,y)+l)$ and noting that

$$q^{(\nu)}((x,y),(x,y)+l) = \nu f((x,y)/\nu, l),$$

for $l \in \{(-1,0),(-1,1),(1,-1),(1,0),(0,-1))\}$, i.e. all possible jumps and f given by Table 5. As ν increases, we begin by considering the sequence of density processes

Event	l	$f((x,y),l)$	$\nu f((x,y)/\nu, l)$
Death of susceptible	$(-1,0)$	$(\delta x\nu)/\nu$	δx
Recovery of infective	$(1,-1)$	$(\gamma y\nu)/\nu$	γy
Birth of susceptible	$(1,0)$	$(\mu(x\nu + y\nu))/\nu$	$\mu(x+y)$
Death of infective	$(0,-1)$	$((\delta+\eta)y\nu)/\nu$	$(\delta+\eta)y$
Infection of susceptible	$(-1,1)$	$(\beta x\nu y\nu)/\nu$	$\beta xy/\nu$,

Table 5: Transition rates.

$(S^{(\nu)}(t)/\nu, I^{(\nu)}(t)/\nu)$. Towards stating a Law of Large Numbers we introduce the functions $s(t)$ and $i(t)$ defined as the solution to the system of ODEs:

$$\frac{ds}{dt} = \mu(s+i) + \gamma i - s\delta - \beta si,\ s(0) = s_0, \tag{5.1}$$

$$\frac{di}{dt} = \beta si - i(\gamma + \delta + \eta),\ i(0) = i_0. \tag{5.2}$$

We also introduce the drift vector of this system by F, i.e $F = \sum_l q_l(\cdot)$, where $q_l((x,y)) \equiv q^{(1)}((x,y),(x,y)+l)$. Now, given the conditions

(i) $\sum_l |l| \sup_{(x,y)\in K} f((x,y),l) < \infty,\ \forall$ compact $K \subset \mathbb{R}^2$,

(ii) $\exists\ M_K > 0\ s.t.\ |F((x,y)) - F((x',y'))| \leq M_K|(x,y)-(x',y')|,\ \forall\ (x,y),(x',y') \in K$,

(iii) $\lim_{\nu\to\infty}(S^{(\nu)}(0)/\nu, I^{(\nu)}(0)/\nu) = (s_0, i_0)$,

we get by Theorem 8.1 in [7] that

$$\lim_{\nu\to\infty}\sup_{t\leq s}|(S^{(\nu)}(t)/\nu, I^{(\nu)}(t)/\nu) - (s(t), i(t))| = 0 \ a.s. \ \forall \ s > 0.$$

The first condition is clear since $f(\cdot,\cdot)$ is continuous in the first variable and therefore bounded over a compact set. The second condition follows from F being C^1 on any compact K, thus locally Lipschitz.

Having obtained a Law of Large Numbers it is of interest to investigate the implications of this, that is to investigate $(s(t), i(t))$. The system (5.1), (5.2) does not admit an explicit solution. However, since we are primarily interested in the endemic state, that is the properties of the process after a long time with the infection present, we investigate the asymptotic properties of the solutions. Of immediate interest is then the stationary point, $(s^\star, i^\star)$, of the system of ODEs, i.e. the solutions to the equations $\frac{ds}{dt} = 0$ and $\frac{di}{dt} = 0$. Easy calculations show that the only positive solutions to these equations, given the previously stated restrictions on the parameters, are

$$s^\star = \frac{\gamma+\delta+\eta}{\beta} = \frac{1}{R_0}, \tag{5.3}$$

$$i^\star = \frac{s^\star(\mu-\delta)}{s^\star\beta - \mu - \gamma}. \tag{5.4}$$

The asymptotics of $s(t)$ and $i(t)$ are to a large extent determined by the stability of the ODE system. We say that the system is stable in the stationary point if the Jacobian matrix evaluated in the stationary point is stable, i.e. if

$$\partial F(s,i) = \begin{pmatrix} \mu-\delta-\beta i & \mu+\gamma-\beta s \\ \beta i & \beta s-\gamma-\delta-\eta \end{pmatrix}, \tag{5.5}$$

evaluated in the stationary point

$$\partial F(s^\star, i^\star) = \begin{pmatrix} \frac{-(\mu-\delta)(\mu+\gamma)}{\delta+\eta-\mu} & -\delta-\eta+\mu \\ \frac{(\mu-\delta)(\gamma+\delta+\eta)}{\delta+\eta-\mu} & 0 \end{pmatrix},$$

is stable. Denote the elements of this matrix by $\partial F(s^\star, i^\star) \equiv \{F_{ij}\}$. The matrix is stable if both eigenvalues have negative real parts, i.e. if the roots of the characteristic polynomial $\lambda^2 - \lambda F_{11} - F_{12}F_{21}$ all have negative real parts. By the Routh Hurwitz conditions this is true precisely if $-F_{11} > 0$ and $-F_{11}(-F_{12}F_{21}) > 0$. We see that $-F_{11} > 0$ since, by assumption, all parameters are positive and $\delta < \mu$. Further we have that

$$\begin{aligned} -F_{11}(-F_{12}F_{21}) &= \frac{(\mu-\delta)(\mu+\gamma)}{\delta+\eta-\mu}(\delta+\eta-\mu)\frac{(\mu-\delta)(\gamma+\delta+\eta)}{\delta+\eta-\mu} \\ &= \frac{(\mu-\delta)^2(\delta+\eta+\gamma)}{\delta+\eta-\mu} > 0, \end{aligned}$$

since we have assumed that $\mu < \delta+\eta$. This allows us to conclude that the local asymptotic stability of the stationary point, i.e. given that (s_0, i_0) is close enough to $(s^\star, i^\star)$, we have that

$$\lim_{t\to\infty}(s(t), i(t)) = (s^\star, i^\star).$$

We therefore conclude that after having an outbreak the epidemic is likely to reach the endemic level, given by the stationary point.

5.2 Diffusion approximation

While the Law of Large Numbers is interesting in its own right it is a poor approximation of the process $(S(t), I(t))$ since it does not tell us anything about the fluctuations we expect around the endemic level. To get a more accurate approximation we therefore need to consider a diffusion approximation. For ease of notation let us define the scaled process

$$Z^{(\nu)}(t) \equiv \sqrt{\nu}((S^{(\nu)}(t), I^{(\nu)}(t))/\nu - (s(t), i(t))),$$

that is, the original process with its mean subtracted and scaled by $1/\sqrt{\nu}$. We note here that the scaling parameter is a multiple of the population size in equilibrium. Now, Theorem 8.2 in [7] ensures that $Z^{(\nu)}(\cdot)$ converges weakly to $Z(\cdot)$ where $Z(t)$ is the solution to the linear SDE

$$dZ = \partial F(s(t), i(t))Z dt + \sqrt{G(s(t), i(t))} dW, \tag{5.6}$$

where W is a 2-dimensional Wiener process and $G(x, y) = \sum_l ll^T q_l(x, y)$, if the following conditions are satisfied:

(i) $\sum_l |l|^2 \sup_{(x,y)} f((x, y), l) < \infty$,

(ii) $\partial F(x, y)$ is bounded and continuous,

(iii) $\lim_{\nu\to\infty} \sqrt{\nu}|(S^{(\nu)}(0), I^{(\nu)}(0)) - (s(t), i(t))| = 0$,

By the asymptotic stability of the stationary point, the trajectory of $(s(t), i(t))$ is contained in some compact set and the restriction of f and ∂F to a compact set is bounded, which implies the first and second condition.

As $t \to \infty$ we get that $\partial F(s(t), i(t)) \to \partial F(s^\star, i^\star) \equiv \partial F^\star$ and $G(s(t), i(t)) \to G(s^\star, i^\star) \equiv G^\star$ so that $Z(t)$ approaches a stationary Ornstein-Uhlenbeck process given as the solution to

$$dZ = \partial F^\star Z dt + \sqrt{G^\star} dW. \tag{5.7}$$

The stationary distribution of Z is multivariate normal with mean $(s^\star, i^\star)$ and covariance matrix Σ satisfying

$$\partial F^\star \Sigma + \Sigma \partial F^\star = -G^\star. \tag{5.8}$$

The definition of $G(\xi)$ implies that $z^T G z > 0 \ \forall x \in \mathbb{R}^2$, i.e $G(\xi)$ is positive definite. This together with the stability of ∂F guarantees the existence of unique positive definite symmetric Σ that solves the above equation, thereby ensuring the interpretation as a covariance matrix. Using this it is also possible to calculate the covariance function of Z according to

$$\rho(t) = \Sigma e^{t(\partial F^\star)^T} \tag{5.9}$$

(see e.g. [6] Theorem 5.6.7).

5.3 Dynamics in the limit

Using the results in the above section we are able to draw conclusions concerning the dynamics of the system when ν is large. It is possible to obtain an explicit solution to Eq. (5.8). We note in particular that the covariance between the number of susceptibles and infectives $\sigma_{S,I} = -\sqrt{\nu}R$ and since $R > 0$ the correlation is negative for all choices of parameters. There also exists explicit expressions for the variance of the number of susceptible and infective but these are more involved and are therefore omitted. We also get that $(S(t), I(t)) \sim N((\nu s^\star, \nu i^\star), \nu\Sigma)$ in quasi-stationarity. In Figure 3 we plot the level curves of this distribution together with a trajectory simulated from Table 1, using the parameter values from Section 4. We start the simulation in $(s^\star, i^\star)$ and discard the first 10^6 transitions ensuring that we are indeed in quasi-stationarity. The simulated trajectory seem to fit well with the approximate distribution.

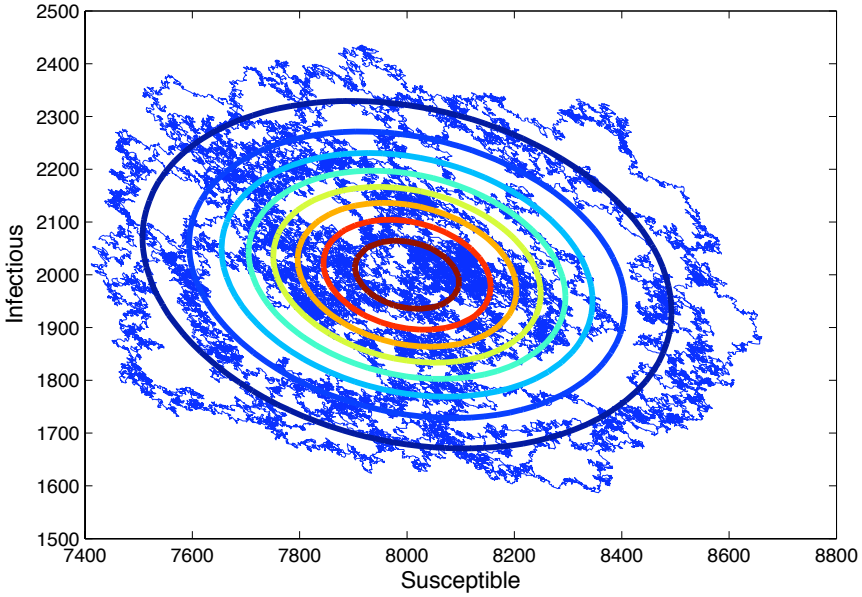

Figure 3: Level curves of the approximating distribution together with a simulated trajectory.

We may also, from Eq. (5.9), calculate the autocorrelation of the number of susceptibles and infectives, respectively. We plot these functions in Figure 4, showing an oscillatory behaviour with a period of about 2 years. These oscillations are easily seen when plotting the marginals of the above trajectory against time, as in Figure 5.

6 Time to extinction

We would like to find an approximation for the distribution of the time to extinction from quasi-stationarity, τ_q. Following [8] we write the forward equation in the state

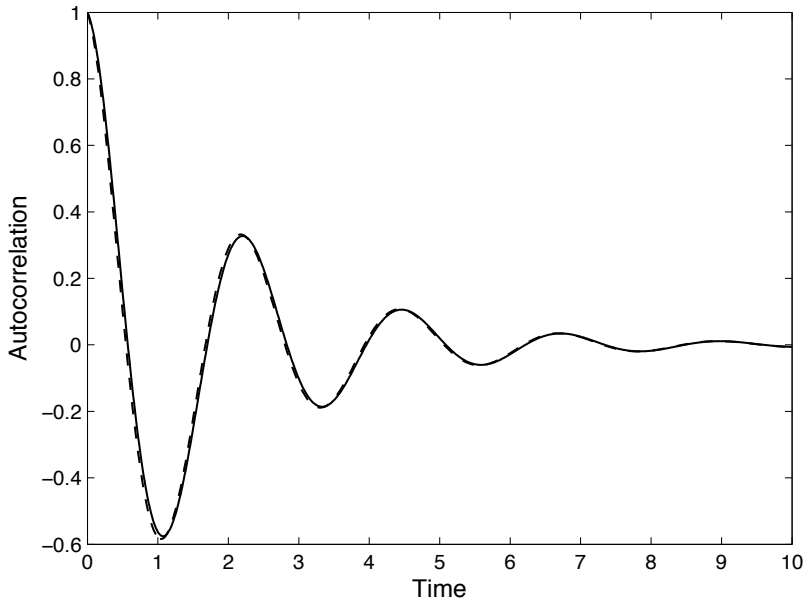

Figure 4: Plot of the autocorrelation function for the number of susceptible (solid) and infectious (dashed).

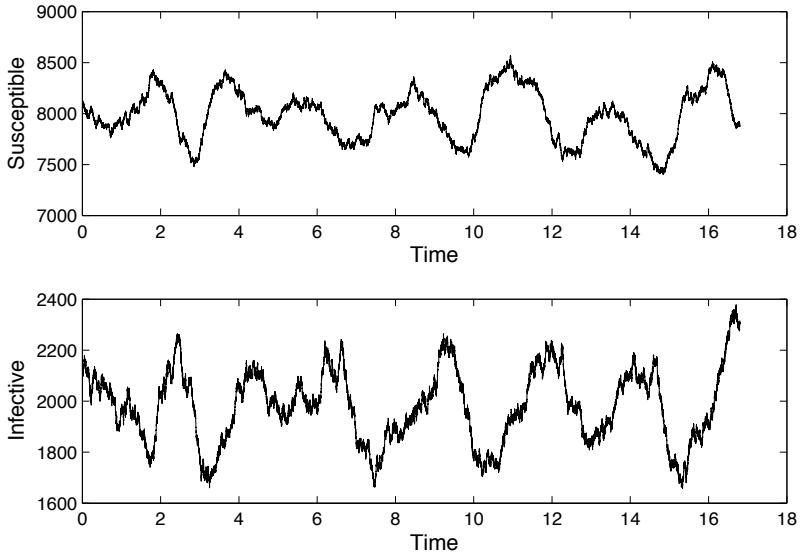

Figure 5: Simulated marginal trajectory.

$(S(t), I(t)) = (s, 0)$

$$p'_{s,0}(t) = p_{s-1,0}(t)\mu(s-1) + p_{s+1,0}(t)\delta(s+1) + p_{s,1}(t)(\delta+\eta) + p_{s-1,1}(t)\gamma - p_{s,0}(t)(\mu s + \delta s).$$

We also define

$$p'_{\cdot,0}(t) \equiv \sum_{s=0}^{\infty} p'_{s,0}(t) = p_{\cdot,1}(t)(\delta+\eta+\gamma). \tag{6.1}$$

We define the quasi-stationary distribution, $q_{s,i}(t)$ as the stationary distribution, conditioned on not being extinct, i.e.

$$q_{s,i}(t) \equiv P(S(t)=s, I(t)=i | I(t)\neq 0) = \frac{p_{s,i}(t)}{1-p_{\cdot,0}(t)}.$$

Differentiating this we obtain

$$\begin{aligned} q'_{s,i}(t) &= \frac{p'_{s,i}(t)}{1-p_{\cdot,0}(t)} + \frac{p_{s,i}(t)}{1-p_{\cdot,0}(t)}\frac{p'_{\cdot,0}(t)}{1-p_{\cdot,0}(t)} \\ &= \frac{p'_{s,i}(t)}{1-p_{\cdot,0}(t)} + \frac{p_{s,i}(t)}{1-p_{\cdot,0}(t)}\frac{p_{\cdot,1}(t)}{1-p_{\cdot,0}(t)}(\delta+\eta+\gamma) \\ &= \frac{p'_{s,i}(t)}{1-p_{\cdot,0}(t)} + \frac{p_{s,i}(t)}{1-p_{\cdot,0}(t)} q_{\cdot,1}(t)(\delta+\eta+\gamma). \end{aligned}$$

Now, in stationarity we should have $q'_{s,i}(t)=0$, giving us the differential equation

$$p'_{s,i}(t) = -(\delta+\eta+\gamma)q_{\cdot,1}p_{s,i}(t),\ p_{s,i}(0)=q_{s,i},$$

with the solution

$$p_{s,i}(t) = q_{s,i}e^{-(\delta+\eta+\gamma)q_{\cdot,1}t}.$$

Summing over s, we get

$$p_{\cdot,i}(t) = q_{\cdot,i}e^{-(\delta+\eta+\gamma)q_{\cdot,1}t},$$

which we insert in (6.1) to get

$$p'_{\cdot,0}(t) = p_{\cdot,1}(t)(\delta+\eta+\gamma) = q_{\cdot,1}(\delta+\eta+\gamma)e^{-(\delta+\eta+\gamma)q_{\cdot,1}t}.$$

With the initial condition $p_{\cdot,0}(0)=0$ we get the solution

$$p_{\cdot,0}(t) = 1 - e^{-(\delta+\eta+\gamma)q_{\cdot,1}t}.$$

That is the time to extinction is exponentially distributed with expectation

$$E[\tau_Q] = \frac{1}{(\delta+\eta+\gamma)q_{\cdot,1}}$$

Using our diffusion approximation we know that the number of infectives in stationarity has an approximately normal distribution with mean $\bar{I}=\nu i^\star$ and standard deviation $\sigma_I=\sqrt{\nu\Sigma_{22}}$. Since we necessarily have a non-negative number of infectives we condition the above normal distribution on being non-negative and obtain, employing continuity correction,

$$q_{\cdot i} = \frac{P(I=i)}{P(I>0)} \approx \frac{P(I=i)}{P(I>1/2)} \approx \frac{1}{\sigma_I}\frac{\phi((\bar{I}-i)/\sigma_I)}{\Phi((\bar{I}-0.5)/\sigma_I)}. \tag{6.2}$$

We therefore get that

$$\mathbb{E}[\tau_q] = \frac{1}{(\delta+\eta+\gamma)q_{\cdot 1}} \approx \frac{\sigma_I}{\delta+\eta+\gamma}\frac{\Phi((\bar{I}-0.5)/\sigma_I)}{\phi((\bar{I}-1)/\sigma_I)}. \tag{6.3}$$

We think of this as the inverse of the probability of being in the state with a single infected times the intensity by which this infective becomes susceptible or deceased.

To emphasise the dependence on the parameters and in particular the coefficient of variation of the number of susceptibles $c_v = \sigma_I/\bar{I}$, we use the approximation

$$\Phi(x) \approx 1 - \frac{1}{x\sqrt{2\pi}}e^{-\frac{x^2}{2}},$$

which is good for large x, see e.g. p. 450 of [13]. We then get that

$$E[\tau_Q] \approx c_v\frac{\nu(\mu-\delta)}{\beta(\delta+\eta-\mu)}\frac{\Phi(1/c_v)}{\phi(1/c_v)} \approx c_v\frac{\nu(\mu-\delta)}{\beta(\delta+\eta-\mu)}(\sqrt{2\pi}e^{1/2c^2} - c_v). \tag{6.4}$$

The main conclusion being the exponentially increasing time to extinction as the coefficient of variation decreases.

We may also simulate the time to extinction for different values of ν. We are restricted to fairly small ν to keep the simulation times reasonably short. The same parameter values as before are used, except for $\eta = 2$, this to shorten the simulation times. To ensure quasi-stationarity we discard the 50% shortest extinction times and restart the clock. Plotting the results together with the two approximations in Figure 6 we see that both approximations agree well with the simulations.

7 Discussion

In this paper we analyse an open population SIS epidemic model. We were able to derive good approximations for the initial outbreak of the disease following introduction through a coupling argument. We also determined the behaviour of the epidemic process when it reaches the endemic state. In this phase it behaves as a two-dimensional Ornstein-Uhlenbeck process, fluctuating around the stationary point of susceptibles and infectives, for which we where able to derive the drift and covariance matrices. These matrices determines the dynamics of the limiting process and work as a good approximation for the dynamics of the epidemic process in a large but finite population. Finally we derived the exponential distribution of the time to extinction of the disease given that the process is started in quasi-stationarity.

Further generalisations can be made by including more complex individual heterogeneities and mixing patterns. Another interesting continuation of this work might be to calibrate the model, i.e. estimate the model parameters for some known disease.

Acknowledgements

We thank Mikael Andersson for fruitfull discussions and insights into epidemic modeling. We also thank Tom Britton and Mathias Lindholm for comments on the manuscript.

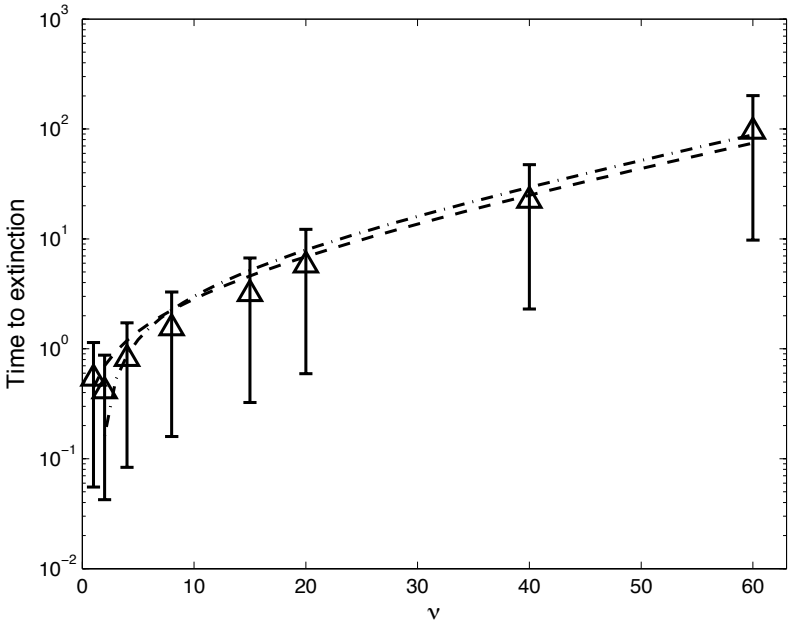

Figure 6: Time to extinction from quasi-stationarity, simulated with 95% confidence interval approximation (6.3) $(- - -)$ and approximation (6.4) $(- \cdot -)$.

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