



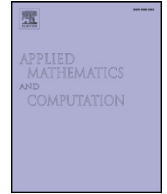
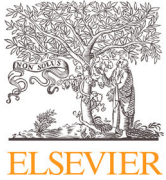
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SDE SIS epidemic model with demographic stochasticity and varying population size



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ABSTRACT

In this paper we look at the two dimensional stochastic differential equation (SDE) susceptible-infected-susceptible (SIS) epidemic model with demographic stochasticity where births and deaths are regarded as stochastic processes with per capita disease contact rate depending on the population size. First we look at the SDE model for the total population size and show that there exists a unique non-negative solution. Then we look at the two dimensional SDE SIS model and show that there exists a unique non-negative solution which is bounded above given the total population size. Furthermore we show that the number of infecteds and the number of susceptibles become extinct in finite time almost surely. Lastly, we support our analytical results with numerical simulations using theoretical and realistic disease parameter values.

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1. Introduction

One of the simplest possible models for how diseases spread amongst a population is the susceptible-infected-susceptible (SIS) epidemic model. In this model a typical individual starts off susceptible, at some stage catches the disease and after a short infectious period becomes susceptible again. Such a model is appropriate for a bacterial disease such as pneumococcus or sexually transmitted diseases such as gonorrhoea. It is sometimes used as an approximate model for tuberculosis and can also be used to model the common cold [1–3]. The SIS model is strictly speaking not applicable for tuberculosis as infection provides partial immunity to re-infection but it can be used as an approximate model [4].

If $S(t)$ denotes the number of susceptibles at time t and $I(t)$ denotes the number of infecteds at time t then the spread of the disease is described by the pair of differential equations

$$\frac{dS}{dt} = \mu N - \beta S(t)I(t) + \gamma I(t) - \mu S(t), \quad (1.1)$$

$$\frac{dI}{dt} = \beta S(t)I(t) - (\mu + \gamma)I(t) \quad (1.2)$$

with appropriate starting values $S(0)$ and $I(0)$ with $S(0) + I(0) = N$. In these equations μ is the rate at which a single individual dies and γ is the per capita rate at which a single individual recovers. Hence assuming that the infectious period follows an

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exponential distribution the average infectious period is $1/\gamma$. β is the rate at which a single infected individual makes contact with and infects each susceptible individual, so that $\beta = \lambda/N$, where λ is the per capita disease contact rate of a single infected individual.

A key concept in mathematical epidemiology is the idea of the basic reproduction number R_0 . This is defined as the expected number of secondary cases produced by a single newly infected individual entering a disease-free population at equilibrium [5]. We find that

$$R_0 = \frac{\beta N}{\mu + \gamma}.$$

If a single newly infected individual enters a disease free population then this person dies at rate μ and becomes susceptible at rate γ and stays in this state for time $1/(\mu + \gamma)$. During this time he or she makes potentially infectious contacts with the susceptible individuals present each at rate β and if N is large there are approximately N of them. So the average number of infections made during the infectious period is $\beta N/(\mu + \gamma)$ which is thus R_0 as stated above.

This model is discussed by Hethcote [6] and Brauer in Brauer et al. [5]. It is equivalent to the well-known logistic equation for population growth and has a solution given by

$$I(t) = \begin{cases} \left[\frac{\beta}{\beta N - \mu - \gamma} (1 - e^{-(\beta N - \mu - \gamma)t}) + \frac{1}{I_0} e^{-(\beta N - \mu - \gamma)t} \right]^{-1}, & \text{if } R_0 \neq 1, \\ \left[\beta t + \frac{1}{I_0} \right]^{-1}, & \text{if } R_0 = 1, \end{cases} \tag{1.3}$$

[7]. Hence if $R_0 \leq 1, I(t) \rightarrow 0$ as $t \rightarrow \infty$ whereas if $R_0 > 1, I(t) \rightarrow N(1 - \frac{1}{R_0})$ as $t \rightarrow \infty$.

Hethcote and Yorke [8] outline a series of mathematical models for gonorrhoea. One of the simplest ones uses the above SIS model with births and deaths included to model the spread of gonorrhoea in a homogeneous homosexual population. This is suitable as a very simple approximation to reality as it assumes that all individuals are the same whereas in reality there is a great deal of heterogeneity in sexual behaviour and rates of sexual contact. The latter issue is discussed by Lajmanovich and Yorke [9] and Nold [10] who introduce heterogeneity into this simple SIS epidemic model for gonorrhoea.

Another situation where SIS models can be used is for pneumococcus amongst young schoolchildren. Pneumococcus is a bacterial disease which does not cause permanent immunity hence SIS models are appropriate although there are several strains or serotypes. Lipsitch [11] models vaccination against pneumococcus and his work is based on an SIS model. In a series of three papers Greenhalgh et al. [12,13] and Lamb et al. [14] study SIS mathematical epidemic models for pneumococcus transmission where transmission depends on serotype and genetic multilocus sequence type (which is genetic material within the serotype), and the Ph.D. theses of Lamb [15] and Weir [16] are based on SIS models for pneumococcus.

Another disease which can be modelled by using the SIS model is the common cold [1–3]. The common cold (rhinovirus) is a viral infectious disease of the upper respiratory tract which has symptoms such as sneezing and sore throat [17]. Rhinovirus is the predominant cause of common cold, it is responsible for around 30–50% of colds each year [17] with over 100 known serotypes, thus making it impossible to produce a unifying vaccine [17,18]. Most importantly, exposure to one rhinovirus does not confer significant immunity against other serotypes [19]. Consequently, there have been papers that suggest that an SIS model would be suitable in analysing the behaviour of the common cold (e.g. [1–3]).

While most commonly studied epidemic models are deterministic, real life must take account of random effects to account for phenomena such as diseases dying out by chance. One way to do this is outlined by Bailey [20]. The simplest deterministic epidemic model assumes that the population size is constant so that when an infected individual dies he or she is replaced by another susceptible individual. If we make the same assumption in a stochastic model then if

$$p_i(t) = \mathbb{P}(\text{There are exactly } i \text{ infected individuals at time } t)$$

assuming that all events in the stochastic model occur according to a Markov process with rate the same as the corresponding rate in the deterministic model we can derive the differential equations satisfied by the probabilities $p_i(t)$ as

$$\frac{dp_0}{dt} = (\mu + \gamma)p_1(t), \tag{1.4}$$

$$\frac{dp_i}{dt} = \beta(i - 1)(N - i + 1)p_{i-1} - \beta i(N - i)p_i + (\mu + \gamma)(i + 1)p_{i+1} - (\mu + \gamma)ip_i, \tag{1.5}$$

$$1 \leq i \leq N - 1,$$

$$\frac{dp_N}{dt} = \beta(N - 1)p_{N-1} - (\mu + \gamma)Np_N, \tag{1.6}$$

[20]. We could then numerically solve these equations, however this is difficult if the number of equations involved is large.

Allen [21] and Allen [22] outline an alternative approach, namely to consider possible changes Δi in a small time interval Δt and then find the mean change $E((\Delta i)^2)$ for the time interval Δt and define

$$\mu(t, i) = \frac{E(\Delta i)}{\Delta t}, \quad V(t, i) = \frac{E(\Delta i)^2}{\Delta t} \text{ and } B(t, i) = \sqrt{V(t, i)}.$$

Then an SDE is inferred for this process by similarities in the forward Kolmogorov equations between the discrete and continuous stochastic processes [22]

$$dI = (\beta I(N - I) - (\mu + \gamma)I)dt + \sqrt{\beta I(N - I) + (\mu + \gamma)I} dW. \quad (1.7)$$

We have changed Allen's β to βN for consistency of notation. McCormack and Allen [23] construct an SDE approximation similar to an SIS multihost epidemic model and explore the deterministic and stochastic models numerically. We shall explore the solution to this SDE in a separate paper.

However this is a direct analogue of the SIS epidemic model in that it retains the (unrealistic) assumption that population size remains constant and that infected individuals who die are immediately replaced by susceptible individuals. A more realistic (but more complicated) stochastic analogue of the deterministic SIS epidemic model can be obtained by following a similar procedure but assuming that births and deaths of individuals are independent. This is what we shall study in this paper.

Note that this implies that whereas in the deterministic model the population size remains constant, in the stochastic model the population size may vary. Most deterministic models for infectious diseases assume that the population size remains constant but there has been some work done on epidemic models with variable population size. This is usually for a different reason, because either there is disease-related mortality so infected individuals die at an increased rate compared to susceptible ones or there is some sort of population density dependence in either the birth rate or the death rate, due for example to competition for scarce resources.

There has been much work already done on the stochastic aspects of the SIS epidemic model. For example, Norden [24] described the stochastic SIS model as a logistic population model and investigated the distribution of the extinction times both numerically and theoretically, while Cavender [25] treated the SIS model as a birth and death process. Kryscio and Lefèvre [26] extended and combined the results mentioned in [24] and [25], by working with the stochastic SIS logistic model. There are many more papers that deal with the stochastic SIS model obtaining useful results (e.g. [27–33]).

Most of the classical work on epidemiological models has assumed that the population size remains constant (e.g. [6,20,34]). Such an assumption is appropriate if the disease spreads rapidly in a short period of time and that disease-related deaths are insignificant in terms of their effect on the whole population [35].

In the past humans have experienced many diseases that have caused a dramatic impact on the size of populations resulting in disease-related mortality. For example, in the fourteenth century, the Black Death wiped out about 25% of the whole population of Europe, killing 25 million people [20]. In 1520 smallpox killed half of the Aztec population. These diseases were in the past but even now some countries are under constant threat from diseases with a high mortality rate such as malaria and HIV/AIDS for which the assumption of a constant population size is not appropriate [36,37]. As a result it would no longer be reasonable to consider the population size as a constant. Another example of a mathematical model in which the population size is not a constant is given by Derrick and van den Driessche [38].

Quite a bit of previous work has been done on SIS epidemic models with varying population sizes. For example in Hethcote and van den Driessche's paper [39] they looked at an SIS epidemic model with varying population size and a time delay. The model contained an exponential demographic structure, disease-related deaths and a delay corresponding to the infectious period. Lahrouz and Settati [37] looked at the asymptotic properties of an SDE SIS epidemic model with standard incidence and variable population size where white vector noise and telegraph noise modelled by Markovian switching are included. Busenberg et al. [40] focused on analysing the SIS model of a vertically transmitted disease with varying population size. They also performed a complete global stability analysis of their model. Apart from the SIS epidemic model with varying population size work has been done on SIR and SIRS models.

Busenberg and van den Driessche [36] analysed global stability for an SIRS epidemic model with vital dynamics in a varying size population. Li et al. [41] gave a detailed analysis of the global stability of a unique equilibrium for the fractions of susceptibles, exposed, infected and removed and the global dynamics of an SEIR model with varying population size.

There are many ways in which stochasticity can be introduced into an epidemic model. Dalal et al. [42] introduced environmental stochasticity into the disease transmission term in a model for AIDS and condom use with two distinct states. In a second paper Dalal et al. [43] introduce stochasticity into a deterministic model of internal HIV viral dynamics via the same technique of parameter perturbation into the death rate of healthy cells, infected cells and virus particles. Gray et al. [7] also study the SIS epidemic model with environmental stochasticity introduced into the disease transmission parameter. Another way to introduce stochasticity into deterministic models is telegraph noise where the parameters switch from one set to another according to a Markov switching process [44]. However in this paper we focus on demographic stochasticity which is a different way of approximating the differential equations which describe the spread of the disease.

We shall be looking at the two dimensional SDE SIS model system (S, I) with demographic stochasticity introduced into both birth and death processes, replacing the unrealistic assumption that the population size remains constant. We model births and deaths of individuals independently and it is no longer the case that an infected individual who dies is immediately replaced by a susceptible individual and thus the population size will vary with respect to time. However the reader might argue that the SIS epidemic model given by (1.1) and (1.2) with transmission term $\beta S(t)I(t)$, corresponding to per capita disease contact rate $\lambda = \beta N$, might not be realistic when analysing models where population size is allowed to change as the transmission rate β may not remain constant especially when N is large. The transmission term $\beta S(t)I(t)$ is more suitable for describing diseases in a closely packed community such as school or a large city where doubling the population size could arguably double the number of contacts [35,45]. However, there are many diseases such as gonorrhoea and AIDS, where doubling the population size would not realistically have a significant effect on the number of contacts, and thus β should vary with respect to the population size

(e.g. [8]). As a result, it is reasonable to assume that the per capita disease contact rate λ depends on the population size N [35,45,46]. Inspired by this, we obtain the following alternative SIS epidemic model with transmission term $\frac{\lambda(N)}{N}S(t)I(t)$:

$$\frac{dS}{dt} = \mu N - \frac{\lambda(N)}{N}S(t)I(t) + \gamma I(t) - \mu S(t), \tag{1.8}$$

$$\frac{dI}{dt} = \frac{\lambda(N)}{N}S(t)I(t) - (\mu + \gamma)I(t). \tag{1.9}$$

There are various choices for $\lambda(N)$, for example Anderson and May [47] assume that $\lambda(N)$ is linearly proportional to N for small population size while Busenberg and van den Driessche [36] assume that $\lambda(N)$ does not depend on N . One important conclusion that Anderson [48] obtained is that the dependence of $\lambda(N)$ on N decreases for sufficiently large $N(t)$, which further highlights the fact that the previous SIS epidemic model with transmission term $\beta S(t)I(t)$ might not be realistic if $N(t)$ continues to increase in size with respect to time. The assumption we make for $\lambda(N)$ in this paper aims to take into consideration both of the extreme population sizes and we will show that the SIS epidemic model (1.1) and (1.2) could be derived from (1.8) and (1.9) for when $N(t)$ is sufficiently small.

To the best of our knowledge there has not been any work done previously on the resulting two dimensional SDE system. Consequently in this paper we hope to fill the gap by providing a thorough analysis of the behaviour of this model. The one dimensional SDE SIS epidemic model retaining the assumption that the population size remains constant has been discussed above (1.7).

The paper is organised as follows: In Section 2 we will discuss the formulation of our two dimensional SDE SIS epidemic model and the assumptions we imposed on the contact rate $\lambda(N)$. In Section 3, we will focus on analysing the behaviour of the SDE model for the total population size $N(t) = S(t) + I(t)$. The existence and uniqueness of a non-negative non-explosive solution is also shown. In Section 4 we shall look at the existence of a unique non-negative solution $(S(t, \omega), I(t, \omega))$ to the two dimensional SDE SIS epidemic model. In Section 5 we examine the conditions for our solution to the two dimensional SDE SIS model to go extinct in finite time. Lastly numerical simulations with theoretical parameter values and realistic parameter values for pneumococcus and the common cold are given in Sections 6 and 7 respectively.

2. Demographic stochasticity for the two dimensional SDE SIS epidemic model

Throughout this paper, we let $(\Omega, \mathcal{F}, \{\mathcal{F}_t\}_{t \geq 0}, \mathbb{P})$ be a complete probability space with filtration $\{\mathcal{F}_t\}_{t \geq 0}$ satisfying the usual conditions (i.e., it is increasing and right continuous while \mathcal{F}_0 contains all \mathbb{P} -null sets). Let us consider the deterministic SIS model (1.8) and (1.9) where $\lambda(N)$ has the following properties:

- (i) $\lambda(N)$ is a continuous function of $N \geq 0$ and continuously differentiable in $N > 0$,
- (ii) $\lambda(N)$ is a monotone increasing function of N ,
- (iii) $\lambda(N) > 0$ if $N(t) > 0$.

Let us also define $\lambda(0) = \lim_{N \rightarrow 0} \lambda(N)$, where it is biologically reasonable to assume that it represents a small population.

We follow the model of Allen [21] outlined above. For this model, since the births and deaths are introduced independently we have five possible interactions that could occur in the overall population. These changes and their probabilities to the first order in Δt are given in Table 1 with $\mathbf{x} = (S, I)$, $\mathbf{x}(0) = (S(0), I(0))^T$.

We use the notation

$$\boldsymbol{\mu} = \frac{E(\Delta \mathbf{x})}{\Delta t} = \begin{bmatrix} -\frac{\lambda(N)SI}{N} + (\mu + \gamma)I \\ \frac{\lambda(N)SI}{N} - (\mu + \gamma)I \end{bmatrix},$$

$$\mathbf{V} = \frac{E[(\Delta \mathbf{x})(\Delta \mathbf{x})^T]}{\Delta t} = \begin{bmatrix} a & b \\ b & c \end{bmatrix},$$

$$\mathbf{B} = \mathbf{V}^{\frac{1}{2}} = \frac{1}{d} \begin{bmatrix} a + w & b \\ b & c + w \end{bmatrix},$$

where $a = \frac{\lambda(N)SI}{N} + (\mu + \gamma)I + 2\mu S$, $b = -\frac{\lambda(N)SI}{N} - \gamma I$, $c = \frac{\lambda(N)SI}{N} + (\mu + \gamma)I$, $w = \sqrt{ac - b^2}$ and $d = \sqrt{a + c + 2w}$. Then following Allen [21] and Allen [22], the SDE SIS model with demographic stochasticity for the dynamics of two interacting populations takes the form

$$dS(t) = \left[-\frac{\lambda(N)SI}{N} + (\mu + \gamma)I \right] dt + \frac{a + w}{d} dW_1 + \frac{b}{d} dW_2, \tag{2.1}$$

$$dI(t) = \left[\frac{\lambda(N)SI}{N} - (\mu + \gamma)I \right] dt + \frac{b}{d} dW_1 + \frac{c + w}{d} dW_2, \tag{2.2}$$

Table 1
Possible changes in $\mathbf{x} = (S, I)$ and their probabilities.

Change	Probability
$\Delta \mathbf{x}^{(1)} [-1 \ 0]^T$	$\mu S \Delta t$
$\Delta \mathbf{x}^{(2)} [0 \ -1]^T$	$\mu I \Delta t$
$\Delta \mathbf{x}^{(3)} [1 \ 0]^T$	$\mu(S + I) \Delta t$
$\Delta \mathbf{x}^{(4)} [1 \ -1]^T$	$\gamma I \Delta t$
$\Delta \mathbf{x}^{(5)} [-1 \ 1]^T$	$\frac{\lambda(N)SI}{N} \Delta t$

where $W(t) = (W_1, W_2)^T$ is a two-dimensional Brownian motion. Let us integrate (2.1) to get

$$S(t) = \int_0^t \left[-\frac{\lambda(N)S(s)I(s)}{N(s)} + (\mu + \gamma)I(s) \right] ds + \int_0^t \frac{a(s) + w(s)}{d(s)} dW_1(s) + \int_0^t \frac{b(s)}{d(s)} dW_2(s). \tag{2.3}$$

Now we define

$$M(t) = \int_0^t \frac{a(s) + w(s)}{d(s)} dW_1(s) + \int_0^t \frac{b(s)}{d(s)} dW_2(s). \tag{2.4}$$

This is a martingale with respect to the filtration [49]. Hence its quadratic variation is given by

$$\begin{aligned} \langle M(t) \rangle &= \int_0^t \frac{(a(s) + w(s))^2}{d(s)^2} ds + \int_0^t \frac{b(s)^2}{d(s)^2} ds, \\ &= \int_0^t \left(\frac{\lambda(N)S(s)I(s)}{N(s)} + (\mu + \gamma)I(s) + 2\mu S(s) \right) ds. \end{aligned} \tag{2.5}$$

By the Martingale Representation Theorem in terms of Brownian motion, Eq. (2.5) could be written as an Itô integral (e.g. [49]). Hence \exists a Brownian motion W_3 such that

$$M(t) = \int_0^t \sqrt{\frac{\lambda(N)S(s)I(s)}{N(s)} + (\mu + \gamma)I(s) + 2\mu S(s)} dW_3(s). \tag{2.6}$$

As a result, Eq. (2.3) becomes

$$S(t) = \int_0^t \left[-\frac{\lambda(N)S(s)I(s)}{N(s)} + (\mu + \gamma)I(s) \right] ds + \int_0^t \sqrt{\frac{\lambda(N)S(s)I(s)}{N(s)} + (\mu + \gamma)I(s) + 2\mu S(s)} dW_3(s), \tag{2.7}$$

and thus, Eq. (2.1) could be written as

$$dS(t) = \left[-\frac{\lambda(N)SI}{N} + (\mu + \gamma)I \right] dt + \sqrt{\frac{\lambda(N)SI}{N} + (\mu + \gamma)I + 2\mu S} dW_3. \tag{2.8}$$

Similarly, the same procedure could be applied to Eq. (2.2) to get

$$dI(t) = \left[\frac{\lambda(N)SI}{N} - (\mu + \gamma)I \right] dt + \sqrt{\frac{\lambda(N)SI}{N} + (\mu + \gamma)I} dW_4, \tag{2.9}$$

where W_4 is also a Brownian motion.

By using (2.1) and (2.2) and the fact that $S + I = N$, we have constructed the following SDE model illustrating the behaviour for N :

$$dN(t) = \frac{a + b + w}{d} dW_1 + \frac{b + c + w}{d} dW_2. \tag{2.10}$$

Again, by using the same technique as we have done to obtain Eqs. (2.8) and (2.9), Eq. (2.10) could be simplified to get

$$dN(t) = \sqrt{2\mu N(t)} dW_5 \tag{2.11}$$

where W_5 is also a Brownian motion. Note that we could have derived this equation directly using the method outlined above.

By letting $u = \log_e(N)$ and applying Itô's formula to (2.11) we get that $N(t)$ satisfies the implicit equation

$$N(t) = N_0 \exp \left[\int_0^t \left(-\frac{\mu}{N} \right) ds + \int_0^t \sqrt{\frac{2\mu}{N}} dW \right].$$

Eq. (2.11) is a very specialised case (with $k = 0$) of the mean-reverting square root process or Cox–Ingersoll–Ross model [49,50]. This equation is meant to model instantaneous interest rates and has applications in financial markets. The equation can be written as

$$dr = k(\theta - r)dt + \sigma \sqrt{r} dW.$$

The density function of $r(s)$ at time s conditional on its value at time t is given by

$$f(r(s), s; r(t), t) = ce^{-u-v} \left(\frac{v}{u}\right)^{\frac{q}{2}} I_q(2(uv)^{\frac{1}{2}}),$$

where

$$\begin{aligned} c &= \frac{2k}{\sigma^2(1 - e^{-k(s-t)})}, \\ u &= cr(t)e^{-k(s-t)}, \\ v &= cr(s), \\ q &= \frac{2k\theta}{\sigma^2} - 1, \end{aligned}$$

and $I_q(\cdot)$ is the modified Bessel function of the first kind of order q . This is the non-central chi-square distribution $\chi^2[2cr(s); 2q + 2, 2u]$. The non-centrality parameter is $2u$ proportional to the present interest rate.

The mean and variance of $r(s)$, the interest rate at time s , are

$$\begin{aligned} E(r(s)|r(t)) &= r(t)e^{-k(s-t)} + \theta(1 - e^{-k(s-t)}), \\ \text{Var}(r(s)|r(t)) &= r(t) \left(\frac{\sigma^2}{k}\right) (e^{-k(s-t)} - e^{-2k(s-t)}) + \theta \left(\frac{\sigma^2}{2k}\right) (1 - e^{-k(s-t)})^2. \end{aligned}$$

As k becomes small (relevant to our model) the conditional mean goes to $r(t)$ and the variance to $\sigma^2 r(t)(s - t)$.

Hence the system of SDEs

$$\begin{aligned} dS(t) &= \left[-\frac{\lambda(N)SI}{N} + (\mu + \gamma)I \right] dt + \sqrt{\frac{\lambda(N)SI}{N} + (\mu + \gamma)I + 2\mu S} dW_3, \\ \text{and } dI(t) &= \left[\frac{\lambda(N)SI}{N} - (\mu + \gamma)I \right] dt + \sqrt{\frac{\lambda(N)SI}{N} + (\mu + \gamma)I} dW_4, \end{aligned}$$

describe how the number of susceptible and infected individuals change with time for $N(t) > 0$. However the same system can be more simply described by the SDEs

$$dI(t) = \left[\frac{\lambda(N)}{N} I(N - I) - (\mu + \gamma)I \right] dt + \sqrt{\frac{\lambda(N)}{N} I(N - I) + (\mu + \gamma)I} dW_4, \tag{2.12}$$

$$\text{and } dN(t) = \sqrt{2\mu N(t)} dW_5, \tag{2.13}$$

where $N(t) = S(t) + I(t) > 0$. In the remainder of the paper we shall focus on showing existence, uniqueness, boundedness, extinction and persistence of the system of Eqs. (2.12) and (2.13). In the next section we focus solely on the second of these equations (2.13). Throughout this paper, unless stated otherwise, we shall assume that the unit of time is one day, and the population sizes are measured in units of one million.

3. Existence of a unique nonnegative solution for the total number of individuals

Before we begin illustrating some of the important theorems for our two-dimensional SDE SIS model, it is important we understand the behaviour of the solution for our SDE for $N(t)$ (2.13). Let $a \wedge n$ represent the minimum of $\{a, n\}$ and $a \vee n$ represent the maximum of $\{a, n\}$. For $a < N_0 < n$ define

$$\begin{aligned} \tau_a &= \inf\{t \geq 0 : N(t) \leq a\}, \\ \tau_n &= \inf\{t \geq 0 : N(t) \geq n\}, \end{aligned}$$

where $\tau_0 = \lim_{a \downarrow 0} \tau_a$, $\tau_\infty = \lim_{n \uparrow \infty} \tau_n$ and $\tau = \tau_0 \wedge \tau_\infty$.

Theorem 3.1. For any given initial value $N(0) = N_0$, the probability that the SDE (2.13) has a unique and nonnegative solution $N(t)$ for all $t \geq 0$ is one, i.e., $N(t) \geq 0$ a.s. for all $t \geq 0$ and that the solution is non explosive.

Proof. It is easy to see that our SDE (2.13) is a special case of the SDE considered in the ‘‘Mean reverting square root process’’ mentioned by Mao [49] with parameters $\bar{\lambda} = \bar{\mu} = 0$ and $\bar{\sigma} = \sqrt{2\mu}$. Thus, it is easy to see that $N(t) \geq 0$ for all $t \geq 0$ a.s. Furthermore, since $\bar{\sigma}^2 > 2\bar{\lambda}\bar{\mu}$, we could conclude from [49] that $\sup_{0 \leq t < \tau} N(t) < \infty$ a.s. where τ is defined as above. Our SDE (2.13) also satisfies the localised version of Theorem 3.2 and condition (2.18) mentioned in Chapter IV of [51] which represent the uniqueness theorem and the sufficient condition for non-explosion of solutions respectively. As a result, we have reached our desired result that there exists a unique, nonnegative and non-explosive solution to the SDE (2.13). \square

As a result, this completes our proof on the properties for the SDE (2.13), and that we have shown there exists a unique and nonnegative solution $N(t)$ for the SDE (2.13).

4. Existence of a unique nonnegative solution for the two-dimensional SDE SIS model

In this section, we will focus on proving that there exists a unique and nonnegative solution for our two-dimensional SDE SIS model (2.12) and (2.13). The existence, uniqueness and non-explosivity of a solution to the SDE (2.13) was discussed above. We refer to Ikeda and Watanabe [51] as it is a classic work on this topic. The existence theorem mentioned in [51] (Theorem 2.2 in Chapter IV) holds for a d -dimensional stochastic process, as a result the existence of a (possibly explosive) solution for our two-dimensional SDE SIS model (2.12) and (2.13) (or (2.8) and (2.9)) follows directly. However, the uniqueness theorem mentioned in [51] (Theorem 3.2, Chapter IV) cannot be applied directly to our model as (i) it applies only for a one-dimensional process and (ii) the coefficients $b(x) : \mathbb{R} \rightarrow \mathbb{R}$ and $\sigma(x) : \mathbb{R} \rightarrow \mathbb{R}$ of the SDE mentioned in this theorem are purely deterministic functions not time dependent stochastic functions. Consequently we will construct a localised version of the uniqueness proof mentioned in [51] and show that it can be extended to a one-dimensional SDE where the coefficients $b(x, t, \omega) : \mathbb{R} \times \mathbb{R}^+ \times \Omega \rightarrow \mathbb{R}$ and $\sigma(x, t, \omega) : \mathbb{R} \times \mathbb{R}^+ \times \Omega \rightarrow \mathbb{R}$ are time-dependent stochastic functions. For the purposes of the uniqueness theorem proof we will consider the one-dimensional SDE SIS model (2.12) with $N(t, \omega)$ as a given stochastic function $\mathbb{R} \times \Omega \rightarrow \mathbb{R}$ (which is the unique nonnegative non-explosive solution to (2.13)). We will then prove that the solution to the SDE SIS model (2.12) has a unique solution, hence as S is given by $N - I$ the solution for S is also unique.

Note that the derivation of the SDE SIS model (2.12) and (2.13) is valid only for $I(t, \omega) \in [0, N(t, \omega)(1 + \frac{\mu+\gamma}{\lambda(N)})]$, as otherwise the term under the square root is negative. Furthermore, as $N \rightarrow 0$, $\lambda(N) \rightarrow \lambda(0)$. As mentioned before, all biologically reasonable disease contact rates increase at most linearly with the number of individuals when the population size is small (e.g. [47,48]). In Section 2, we have also assumed that $\lambda(N)$ is a continuously differentiable monotone increasing function of N . Therefore, if $\lambda(0) = 0$, then it is also biologically reasonable to assume that $\lambda'(0) > 0$. We have the following two cases:

- (i) **Case A.** If $\lambda(0) > 0$ then $\lambda(N) = \lambda(0) + o(1)$ in a neighbourhood of $N = 0$, or
- (ii) **Case B.** If $\lambda(0) = 0$ and $\lambda'(0) > 0$, then $\lambda(N) = \lambda'(0)N + o(N)$ in a neighbourhood of $N = 0$.

Suppose that n is a given nonnegative integer with $n > |N(0)|$. We now extend the domain of (2.12) and (2.13) into the whole domain by defining $\lambda_n(x, t, \omega), \sigma_n(x, t, \omega) : \mathbb{R} \times \mathbb{R}^+ \times \Omega \rightarrow \mathbb{R}$ by

$$\lambda_n(x, t, \omega) = \begin{cases} 0, & \text{for } x < 0, \\ \frac{\lambda(N)x}{N}(N(t \wedge \tau_n, \omega) - x) - (\mu + \gamma)x, & \text{for } 0 \leq x \leq N(t \wedge \tau_n, \omega)\left(1 + \frac{\mu + \gamma}{\lambda(N)}\right), \\ \lambda_n\left(N(t \wedge \tau_n, \omega)\left(1 + \frac{\mu + \gamma}{\lambda(N)}\right), t, \omega\right), & \text{for } x > N(t \wedge \tau_n, \omega)\left(1 + \frac{\mu + \gamma}{\lambda(N)}\right), \end{cases} \tag{4.1}$$

and

$$\sigma_n(x, t, \omega) = \begin{cases} 0, & \text{for } x < 0, \\ \sqrt{\frac{\lambda(N)x}{N}(N(t \wedge \tau_n, \omega) - x) + (\mu + \gamma)x}, & \text{for } 0 \leq x \leq N(t \wedge \tau_n, \omega)\left(1 + \frac{\mu + \gamma}{\lambda(N)}\right), \\ 0, & \text{for } x > N(t \wedge \tau_n, \omega)\left(1 + \frac{\mu + \gamma}{\lambda(N)}\right), \end{cases} \tag{4.2}$$

in Case A, or in Case B if $N > 0$. In Case A, if $N = 0$ and $x \geq 0$ we interpret $\lambda_n(x, t, \omega)$ as zero, and if $N = x = 0$ we interpret $\sigma_n(x, t, \omega)$ as zero. It is easy to see from (4.1) and (4.2) that in Case A then as $N \rightarrow 0$, then $\lambda_n(x, t, \omega) \rightarrow 0$ and $\sigma_n(x, t, \omega) \rightarrow 0, \forall x, t, \omega$. In Case B then in the limit as $N \rightarrow 0$, (4.1) and (4.2) become

$$\lambda_n(x, t, \omega) = \begin{cases} 0, & \text{for } x < 0, \\ -\lambda'(0)x^2 - (\mu + \gamma)x, & \text{for } 0 \leq x \leq \frac{\mu + \gamma}{\lambda'(0)}, \\ \frac{-2(\mu + \gamma)^2}{\lambda'(0)}, & \text{for } x > \frac{\mu + \gamma}{\lambda'(0)}, \end{cases} \tag{4.3}$$

and

$$\sigma_n(x, t, \omega) = \begin{cases} 0, & \text{for } x < 0, \\ \sqrt{x\{(\mu + \gamma) - \lambda'(0)x\}}, & \text{for } 0 \leq x \leq \frac{\mu + \gamma}{\lambda'(0)}, \\ 0, & \text{for } x > \frac{\mu + \gamma}{\lambda'(0)}. \end{cases} \tag{4.4}$$

Hence here we take (4.3) and (4.4) as the definitions of $\lambda_n(x, t, \omega)$ and $\sigma_n(x, t, \omega)$ at $N = 0$. Note that Eqs. (4.3) and (4.4) also represent the case with disease transmission term βSI as $N \rightarrow 0$. Throughout the rest of the paper in Case B for $N = 0$ we interpret $N(1 + \frac{\mu+\gamma}{\lambda(N)})$ as $\frac{\mu+\gamma}{\lambda'(0)}$.

Also if $m \geq n, \tau_m \geq \tau_n$ and

$$\lambda_n(x, t, \omega) = \lambda_m(x, t, \omega) \text{ and } \sigma_n(x, t, \omega) = \sigma_m(x, t, \omega)$$

for $t \leq \tau_n$. Moreover if we define functions $\lambda(x, t, \omega)$ and $\sigma(x, t, \omega) : \mathbb{R} \times \mathbb{R}^+ \times \Omega \rightarrow \mathbb{R}$ by

$$\lambda(x, t, \omega) = \begin{cases} 0, & \text{for } x < 0, \\ \frac{\lambda(N)x}{N} (N(t, \omega) - x) - (\mu + \gamma)x, & \text{for } 0 \leq x \leq N(t, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)}\right), \\ \lambda \left(N(t, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)}\right), t, \omega\right), & \text{for } x > N(t, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)}\right), \end{cases} \tag{4.5}$$

and

$$\sigma(x, t, \omega) = \begin{cases} 0, & \text{for } x < 0, \\ \sqrt{\frac{\lambda(N)x}{N} (N(t, \omega) - x) + (\mu + \gamma)x}, & \text{for } 0 \leq x \leq N(t, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)}\right), \\ 0, & \text{for } x > N(t, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)}\right), \end{cases} \tag{4.6}$$

then $\lambda_n(x, t, \omega) = \lambda(x, t, \omega)$ and $\sigma_n(x, t, \omega) = \sigma(x, t, \omega)$, for $t \leq \tau_n$.

The following is the localised version of the uniqueness theorem mentioned in [51]:

Theorem 4.1 (Localised version of Uniqueness Theorem). *Suppose that $x : \mathbb{R}^+ \times \Omega \rightarrow \mathbb{R}$. Consider the SDE*

$$dx(t) = \lambda_n(x, t, \omega)dt + \sigma_n(x, t, \omega) dW(t), \tag{4.7}$$

with given initial condition $x_n(0)$, for $t \leq \tau_n$, and note that $\lambda_n(x, t, \omega)$ and $\sigma_n(x, t, \omega)$ are bounded. Then there exists a unique strong pathwise solution $x_n(t, \omega)$ to the SDE (4.7) for $t \leq \tau_n$ if for each nonnegative integer $M \geq 1$

- (i) $|\lambda_n(x, t, \omega) - \lambda_n(y, t, \omega)| \leq \kappa_{n,M}(|x - y|)$, where $\kappa_{n,M} : [0, M] \rightarrow \mathbb{R}$ is a strictly increasing and concave function on $[0, M]$ such that $\kappa_{n,M}(0) = 0$ and $\int_{0+}^M \kappa_{n,M}^{-1}(u)du = \infty$ for all x, y with $|x| \vee |y| \leq M, \forall t \in \mathbb{R}^+, \omega \in \Omega$,
- (ii) $|\sigma_n(x, t, \omega) - \sigma_n(y, t, \omega)| \leq \rho_{n,M}(|x - y|)$, where $\rho_{n,M} : [0, M] \rightarrow \mathbb{R}$ is a strictly increasing function on $[0, M]$ such that $\rho_{n,M}(0) = 0$ and $\int_{0+}^M \rho_{n,M}^{-2}(u)du = \infty$ for all x, y with $|x| \vee |y| \leq M, \forall t \in \mathbb{R}^+, \omega \in \Omega$.

Proof. This is a straightforward modification of the proof of Theorem 3.2 in Chapter IV of [51]. \square

The next stage is to show that our SDE SIS model (2.12) satisfies the conditions mentioned in Theorem 4.1, in other words the functions $\kappa_{n,M}$ and $\rho_{n,M}$ exist for each n, M .

Lemma 4.2. $\lambda_n(x, t, \omega)$ and $\sigma_n(x, t, \omega)$ defined by (4.1) and (4.2) satisfy conditions (i) and (ii) of Theorem 4.1.

Proof.

- (i) We shall show that there exists a constant K_n such that

$$\frac{|\lambda_n(x, t, \omega) - \lambda_n(y, t, \omega)|}{|x - y|} \leq K_n$$

for $|x| \vee |y| \leq M$, where K_n is independent of ω, x, y and M . Note that the first partial derivative of (4.1) is given as

$$\lambda_{n,x}(x, t, \omega) = \begin{cases} 0, & \text{for } x < 0, \\ \lambda(N) - \frac{2\lambda(N)x}{N} - \mu - \gamma, & \text{for } 0 < x < N(t) \left(1 + \frac{\mu + \gamma}{\lambda(N)}\right), \\ 0, & \text{for } x > N(t) \left(1 + \frac{\mu + \gamma}{\lambda(N)}\right), \end{cases} \tag{4.8}$$

for $N(t) > 0$ and $\lambda_{n,x} = 0$ for $\forall x, t, \omega$ at $N = 0$ in Case A. For $0 < x(t, \omega) < y(t, \omega) < N(t \wedge \tau_n, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)}\right)$, by the Mean Value Theorem we have that for some $\xi(t, \omega) \in (x, y) \subset [0, N(t \wedge \tau_n, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)}\right)]$

$$\frac{|\lambda_n(x, t, \omega) - \lambda_n(y, t, \omega)|}{|x(t, \omega) - y(t, \omega)|} = |\lambda_{n,x}(\xi, t, \omega)|.$$

Moreover, since $\lambda(N)$ is a monotone increasing function, we have that

$$\begin{aligned} |\lambda_{n,x}(\xi, t, \omega)| &\leq \sup_{N \in [0, n]} \max(|\lambda(N) - (\mu + \gamma)|, |\lambda(N) + 3(\mu + \gamma)|), \\ &\leq \max(|\lambda(0) - \mu - \gamma|, |\lambda(n) - \mu - \gamma|, |\lambda(n) + 3(\mu + \gamma)|), \\ &= K_n. \end{aligned}$$

Letting $x \rightarrow 0^+, y \rightarrow (N(t \wedge \tau_n, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)}\right))^-$, we deduce that the same result is true if $x, y \in [0, N(t \wedge \tau_n, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)}\right)]$. It is easy to see that the result follows for $(x, y) \in \mathbb{R}^2$ in Case A. By applying a similar method, we can show that the condition is also satisfied for Case B. Therefore, condition (i) is satisfied for all $N(t \wedge \tau_n) \geq 0$ in both cases with $\kappa_{n,M}(u) = K_n u$ for some constant K_n for all x, y with $|x| \vee |y| \leq M, \forall t \in \mathbb{R}^+, \omega \in \Omega$.

(ii) In order to prove the second condition, we only need to consider the case where $x, y \in [0, N(t \wedge \tau_n, \omega)(1 + \frac{\mu + \gamma}{\lambda(N)})]$, as the rest will follow. Therefore, if there exists a constant L_n independent of ω, x, y and M such that

$$\frac{|\sigma_n(x, t, \omega) - \sigma_n(y, t, \omega)|}{\sqrt{|x(t, \omega) - y(t, \omega)|}} \leq L_n, \tag{4.9}$$

for $x(t, \omega), y(t, \omega) \in [0, N(t \wedge \tau_n, \omega)(1 + \frac{\mu + \gamma}{\lambda(N)})]$, then the proof is complete. By choosing

$\varepsilon = \frac{1}{4}N(t \wedge \tau_n, \omega)(1 + \frac{\mu + \gamma}{\lambda(N)})$ we then consider separately the regions

- (a) $\varepsilon \leq x, y \leq N(t \wedge \tau_n, \omega)(1 + \frac{\mu + \gamma}{\lambda(N)}) - \varepsilon,$
- (b) $0 < x, y \leq \varepsilon,$
- (c) $N(t \wedge \tau_n, \omega)(1 + \frac{\mu + \gamma}{\lambda(N)}) - \varepsilon \leq x, y \leq N(t \wedge \tau_n, \omega)(1 + \frac{\mu + \gamma}{\lambda(N)}),$
- (d) $N(t \wedge \tau_n, \omega)(1 + \frac{\mu + \gamma}{\lambda(N)}) - \varepsilon < x \leq N(t \wedge \tau_n, \omega)(1 + \frac{\mu + \gamma}{\lambda(N)}), 0 < y < \varepsilon,$ and
- (e) $0 < x < \varepsilon, N(t \wedge \tau_n, \omega)(1 + \frac{\mu + \gamma}{\lambda(N)}) - \varepsilon < y \leq N(t \wedge \tau_n, \omega)(1 + \frac{\mu + \gamma}{\lambda(N)}),$

it is straightforward to show that (4.9) holds $\forall N \geq 0$ in both cases. For (a) similarly to above we find an upper bound for the derivative of $\sigma_n(t, x, \omega)$ in $[\varepsilon, N(t \wedge \tau_n)(1 + \frac{\mu + \gamma}{\lambda(N)}) - \varepsilon]$. Case B where $N = 0$ needs a separate argument but follows the same basic idea. For (b) we multiply the top and bottom of (4.9) by $|\sigma_n(t, x, \omega) + \sigma_n(t, y, \omega)|$ and proceed to find the upper bound L_n that way. (c) follows from (b) by making the transformation

$$\xi = N\left(1 + \frac{\mu + \gamma}{\lambda(N)}\right) - x, \quad \eta = N\left(1 + \frac{\mu + \gamma}{\lambda(N)}\right) - y.$$

For (d) and (e) we note that in these ranges $|\sigma_n(x, t, \omega) - \sigma_n(t, y, \omega)|$ is bounded above, and $\sqrt{|x(t, \omega) - y(t, \omega)|}$ is bounded below by a strictly positive lower bound, and the ratio of these depends only on n . As a result, condition (ii) is satisfied with $\rho_{n,M}(u) = L_n\sqrt{u}$ for some constant L_n independent of ω, x, y and M for all x, y with $|x| \vee |y| \leq M, \forall t \in \mathbb{R}^+, \omega \in \Omega$. This completes the proof of Lemma 4.2. \square

We wish to extend the localised uniqueness Theorem 4.1 to show that there exists a unique strong pathwise non-explosive solution to the SDE

$$dx(t) = \lambda(x, t, \omega)dt + \sigma(x, t, \omega) dW_4$$

with given initial condition $x(0)$. However before we can do this we need to show non-explosivity of the solution to (2.12). We cannot use Theorem 2.4 in Chapter IV of [51] directly to do this as the solution does not satisfy condition (2.18) there. However the result is still true in our case.

For any strictly nonnegative integer $p > |I(0)|$ define the stopping time for $I(t)$

$$\nu_p = \inf\{t \geq 0 : |I(t)| \geq p\}. \tag{4.10}$$

Our next step is to show that given $N(t, \omega) : t \in \mathbb{R}^+, \omega \in \Omega$, the solution of the localised version of Eq. (2.12) is nonnegative and bounded. We can then deduce non-explosivity of the SDEs (2.12) and (2.13) as a corollary.

Theorem 4.3. For any given initial value $I(0) = I_0 \in (0, N(0))$ and any nonnegative integer $p > |I(0)|$,

$$0 \leq I(t \wedge \nu_p) \leq N(t \wedge \nu_p)\left(1 + \frac{\mu + \gamma}{\lambda(N)}\right), \quad \text{a.s.} \tag{4.11}$$

for all $t \geq 0$.

Note that the result (4.11) differs from what one might expect on biological considerations, namely $I(t \wedge \nu_p) \in (0, N(t \wedge \nu_p))$. However, this is caused by the method we adopted using the idea illustrated in [21] to introduce stochasticity into our two-dimensional process (I, N) given by (2.12) and (2.13). This is a well-established technique for developing an SDE approximation to an infinite system of differential equations. The resulting SDE system is much easier to handle than the original version so it is important to study the properties of the solution to the SDE approximation. We performed several simulations with realistic parameter values (discussed later in the paper) and although it is theoretically possible for $I(t)$ to exceed $N(t)$, in practice this was not observed for realistic parameter values. Furthermore, the result (4.11) in Case B applies to the important special case where the disease transmission term is $\beta S(t)I(t)$.

Proof. Note that as we are dealing with the localised version for any fixed nonnegative integers n and p by Theorem 4.1, Eq. (2.12) has a unique non-explosive solution in $[0, T \wedge \tau_n \wedge \nu_p]$. The proof for Theorem 4.3 is established based on a similar mechanism as the ‘‘Square root process’’ mentioned in [49]. In order to clarify the proof, we will recall this mechanism. Let $a_0 = 1$ and $a_k = e^{-k(k+1)/2}$ for every integer $k \geq 1$, where

$$\int_{a_k}^{a_{k-1}} \frac{du}{u} = k.$$

Let $\Psi_k(u)$ be a continuous function such that its support is contained in the interval (a_k, a_{k-1}) where

$$0 \leq \Psi_k(u) \leq \frac{2}{ku},$$

and $\Psi_k(a_{k-1}) = \Psi_k(a_k) = 0$

$$\int_{a_k}^{a_{k-1}} \Psi_k(u) du = 1.$$

It can be shown that such a function exists. Define $\varphi_k(x) = 0$ for $x \geq 0$ and

$$\varphi_k(x) = \int_0^{-x} dy \int_0^y \Psi_k(u) du, \quad \text{for } x < 0. \tag{4.12}$$

It is easy to see that $\varphi_k \in C^2(\mathbb{R}, \mathbb{R})$. As in [49]

$$-1 \leq \varphi'_k(x) \leq 0 \text{ if } -\infty < x < -a_k \text{ or otherwise } \varphi'_k(x) = 0; \tag{4.13}$$

$$|\varphi''_k(x)| \leq \frac{2}{k|x|} \text{ if } -a_{k-1} < x < -a_k \text{ or otherwise } \varphi''_k(x) = 0; \tag{4.14}$$

$$\text{and } x^- - a_{k-1} \leq \varphi_k(x) \leq x^- \text{ for all } x \in \mathbb{R}, \tag{4.15}$$

where we define $x^- = -x$ if $x < 0$ or otherwise $x^- = 0$. Now that we have set up this framework, we can proceed to show the bounds for $I(t \wedge \nu_p)$ given by (4.11). We shall first show that the left hand side of expression (4.11) in Theorem 4.3 holds. By using Itô's formula, we obtain that for any $t > 0$

$$\begin{aligned} \varphi_k(I(t \wedge \tau_n \wedge \nu_p)) &= \varphi_k(I_0) + \int_0^{t \wedge \tau_n \wedge \nu_p} \left[\lambda_n(I(s), s, \omega) \varphi'_k(I(s, \omega)) + \frac{\sigma_n(I(s), s, \omega)^2}{2} \varphi''_k(I(s, \omega)) \right] ds \\ &\quad + \int_0^{t \wedge \tau_n \wedge \nu_p} \sigma_n(I(s), s, \omega) \varphi'_k(I(s, \omega)) dW(s). \end{aligned} \tag{4.16}$$

Now from results (4.13) and (4.14), we know that for $I(t \wedge \tau_n \wedge \nu_p) \geq 0$, $\varphi'_k(I(t \wedge \tau_n \wedge \nu_p)) = 0$ and $\varphi''_k(I(t \wedge \tau_n \wedge \nu_p)) = 0$, thus for all $N \geq 0$ in both cases, (4.16) yields

$$\varphi_k(I(t \wedge \tau_n \wedge \nu_p)) \leq \int_0^{t \wedge \tau_n \wedge \nu_p} \sigma_n(I(s), s, \omega) \varphi'_k(I(s, \omega)) dW(s). \tag{4.17}$$

Then by taking the expectations of both sides, we have that

$$\mathbb{E} \varphi_k(I(t \wedge \tau_n \wedge \nu_p)) \leq 0. \tag{4.18}$$

Thus,

$$\mathbb{E} I^-(t \wedge \tau_n \wedge \nu_p) - a_{k-1} \leq \mathbb{E} \varphi_k(I(t \wedge \tau_n \wedge \nu_p)) \leq 0. \tag{4.19}$$

As $k \rightarrow \infty$, we get that

$$\mathbb{E} I^-(t \wedge \tau_n \wedge \nu_p) \leq 0. \tag{4.20}$$

Noting that $I^-(t \wedge \tau_n \wedge \nu_p) \geq 0$, we have that $\mathbb{E} I^-(t \wedge \tau_n \wedge \nu_p) \geq 0$,

$$\mathbb{E} I^-(t \wedge \tau_n \wedge \nu_p) = 0. \tag{4.21}$$

By using proof by contradiction and Eq. (4.21), it is easy to see that for all $t \geq 0$

$$\mathbb{P}(I(t \wedge \tau_n \wedge \nu_p) < 0) = 0$$

which implies that $\mathbb{P}(I(t \wedge \tau_n \wedge \nu_p) \geq 0) = 1$. As a result, $I(t \wedge \tau_n \wedge \nu_p) \geq 0$ a.s. But we have shown in Theorem 3.1 that $\tau_n \rightarrow \infty$ as $n \rightarrow \infty$ a.s. Hence the left hand side of (4.11) holds for all t where $N(t \wedge \nu_p) \geq 0$.

By using the same framework and a similar technique as we did previously, we will now complete the boundedness proof by proving that $I(t \wedge \tau_n \wedge \nu_p) \leq N(t \wedge \tau_n \wedge \nu_p) \left(1 + \frac{\mu + \gamma}{\lambda(N)}\right)$ a.s. Let us define

$$J(I(t \wedge \tau_n \wedge \nu_p)) = N(t \wedge \tau_n \wedge \nu_p) \left(1 + \frac{\mu + \gamma}{\lambda(N)}\right) - I(t \wedge \tau_n \wedge \nu_p). \tag{4.22}$$

Then, from Itô's formula on Eq. (4.22), we get

$$dJ(I(t \wedge \tau_n \wedge \nu_p)) = (-1)\lambda(J(I(t \wedge \tau_n \wedge \nu_p)))dt - \sigma(J(I(t \wedge \tau_n \wedge \nu_p))) dW.$$

Here

$$\lambda(J(I(t \wedge \tau_n \wedge \nu_p))) = \begin{cases} -2(\mu + \gamma) \left[N(t \wedge \tau_n \wedge \nu_p, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)} \right) \right], & \text{for } J(t \wedge \tau_n \wedge \nu_p) < 0, \\ \left[N(t \wedge \tau_n \wedge \nu_p, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)} \right) - J(I(t \wedge \tau_n \wedge \nu_p)) \right] \left(\frac{\lambda(N)J(I(t \wedge \tau_n \wedge \nu_p))}{N} - 2(\mu + \gamma) \right), \\ \quad \text{for } 0 \leq J(t \wedge \tau_n \wedge \nu_p) \leq N(t \wedge \tau_n \wedge \nu_p, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)} \right), \\ 0, & \text{for } J(t \wedge \tau_n \wedge \nu_p) > N(t \wedge \tau_n \wedge \nu_p, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)} \right), \end{cases}$$

and

$$\begin{aligned} & \sigma(J(I(t \wedge \tau_n \wedge \nu_p))) \\ &= \begin{cases} 0, & \text{for } J(t \wedge \tau_n \wedge \nu_p) < 0, \\ \sqrt{\frac{\lambda(N)J(I(t \wedge \tau_n \wedge \nu_p))}{N} \left[N(t \wedge \tau_n \wedge \nu_p, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)} \right) - J(I(t \wedge \tau_n \wedge \nu_p)) \right]}, \\ \quad \text{for } 0 \leq J(t \wedge \tau_n \wedge \nu_p) \leq N(t \wedge \tau_n \wedge \nu_p, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)} \right), \\ 0, & \text{for } J(t \wedge \tau_n \wedge \nu_p) > N(t \wedge \tau_n \wedge \nu_p, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)} \right). \end{cases} \end{aligned}$$

By Itô's formula, we derive that

$$\varphi_k(J(t \wedge \tau_n \wedge \nu_p)) = \varphi_k(J_0) + \int_0^{t \wedge \tau_n \wedge \nu_p} [P(J(s)) + Q(J(s))] ds - \int_0^{t \wedge \tau_n \wedge \nu_p} \sigma(J(s), s, \omega) \varphi'_k(J(s)) dW(s), \quad (4.23)$$

where $P, Q : \mathbb{R} \times \mathbb{R}^+ \times \Omega \rightarrow \mathbb{R}$ are defined by

$$P(x, t, \omega) = \begin{cases} 2(\mu + \gamma) N(t \wedge \tau_n \wedge \nu_p, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)} \right) \varphi'_k(x), \\ \quad \text{for } x < 0, \\ N(t \wedge \tau_n \wedge \nu_p, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)} - x \right) \left(2(\mu + \gamma) - \frac{\lambda(N)x}{N} \right) \varphi'_k(x), \\ \quad \text{for } 0 \leq x \leq N(t \wedge \tau_n \wedge \nu_p, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)} \right), \\ 0, & \text{for } x > N(t \wedge \tau_n \wedge \nu_p, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)} \right), \end{cases} \quad (4.24)$$

$$Q(x, t, \omega) = \begin{cases} \left(\frac{x}{2} \right) \left[\frac{\lambda(N)}{N} (N(t \wedge \tau_n \wedge \nu_p, \omega) - x) + (\mu + \gamma) \right] \varphi''_k(x), \\ \quad \text{for } 0 \leq x \leq N(t \wedge \tau_n \wedge \nu_p, \omega) \left(1 + \frac{\mu + \gamma}{\lambda(N)} \right), \\ 0, & \text{otherwise.} \end{cases} \quad (4.25)$$

So $P(x, t, \omega) \leq 0$ and $Q(x, t, \omega) = 0$ for all x .

Thus

$$\varphi_k(J(t \wedge \tau_n \wedge \nu_p)) \leq - \int_0^{t \wedge \tau_n \wedge \nu_p} \sigma(J(s), s, \omega) \varphi'_k(J(s)) dW(s).$$

Now take the expectations to get $\mathbb{E} \varphi_k(J(t \wedge \tau_n \wedge \nu_p)) \leq 0$. Hence, $\mathbb{E} J^-(t \wedge \tau_n \wedge \nu_p) - a_{k-1} \leq \mathbb{E} \varphi_k(J(t \wedge \tau_n \wedge \nu_p)) \leq 0$. As $k \rightarrow \infty$, $a_{k-1} \rightarrow 0$, thus $\mathbb{E} J^-(t \wedge \tau_n \wedge \nu_p) \leq 0$. Similarly to the argument we used for proving the left hand side of Eq. (4.11), it is clear that for all $t > 0$,

$$\mathbb{P}(J(t \wedge \tau_n \wedge \nu_p) < 0) = 0,$$

which implies that $\mathbb{P}(J(t \wedge \tau_n \wedge \nu_p) \geq 0) = 1$. In other words, $I(t \wedge \tau_n \wedge \nu_p) \leq N(t \wedge \tau_n \wedge \nu_p) \left(1 + \frac{\mu + \gamma}{\lambda(N)} \right)$ a.s. Once again, since $\tau_n \rightarrow \infty$ as $n \rightarrow \infty$, $I(t \wedge \nu_p) \leq N(t \wedge \nu_p) \left(1 + \frac{\mu + \gamma}{\lambda(N)} \right)$ a.s. \square

Theorem 4.4. $\lim_{p \rightarrow \infty} \nu_p = \infty$.

Proof. Clearly ν_p is increasing in p . Define $\nu_\infty = \lim_{p \rightarrow \infty} \nu_p$ (possibly infinite).

If $\mathbb{P}(v_\infty < \infty) > 0$ then as $(v_\infty < \infty) = \cup_{T \geq 0} (v_\infty \leq T) \exists T < \infty$ with $\mathbb{P}(v_\infty < T) = \delta > 0$. Hence \exists an integer p_0 such that for $p \geq p_0, \mathbb{P}(v_p < T) \geq \delta/2 > 0$. So

$$\mathbb{E}(I(T \wedge v_p)^2) \geq \frac{\delta p^2}{2} \rightarrow \infty \text{ as } p \rightarrow \infty.$$

However now consider the one dimensional SDE (2.13) for $N(t)$. By the proof of Theorem 2.4 in Chapter IV of [51],

$$M_T = \sup_{t \in [0, T]} \mathbb{E}(N(t)^2) < \infty.$$

Hence for $t \in [0, T]$

$$\mathbb{E}|N(t)| \leq \left[\mathbb{E}|N(t)|^2 \right]^{\frac{1}{2}} \leq \left[\sup_{t \in [0, T]} \mathbb{E}(N(t)^2) \right]^{\frac{1}{2}} = M_{1T} < \infty.$$

For any nonnegative integer $p \geq |I(0)|$ and $t \in [0, T]$, we have that

(i) In Case A

$$\mathbb{E}[I(t \wedge v_p)^2] \leq \mathbb{E}[N(t \wedge v_p)^2] \left(1 + \frac{\mu + \gamma}{\lambda(0)} \right)^2 \leq M_T \left(1 + \frac{\mu + \gamma}{\lambda(0)} \right)^2 = M_{2T} < \infty, \tag{4.26}$$

or

(ii) In Case B by considering the regions $N \in [0, 1]$ and $N \in [1, \infty)$ separately it is straightforward to show that there is a constant K such that $I \leq K(1 + N)$. Hence

$$\mathbb{E}(I(t \wedge v_p)^2) \leq K^2(1 + 2\mathbb{E}|N(t \wedge v_p)| + \mathbb{E}N(t \wedge v_p)^2) < K^2(1 + 2M_{1T} + M_T) = M_{3T} < \infty. \tag{4.27}$$

In both cases, this is a contradiction hence $\mathbb{P}(v_\infty < \infty) = 0$, i.e. $v_\infty = \infty$ a.s. This completes the proof of Theorem 4.4. \square

Corollary 4.5. The solution $(I(t), N(t))$ to the SDE system (2.12) and (2.13) is non-explosive.

Proof. This is straightforward. Given $T > 0$ we already know that

$$M_T = \sup_{t \in [0, T]} \mathbb{E}(N(t)^2) < \infty.$$

Letting $p \rightarrow \infty$ in (4.26) and (4.27) we deduce that

$$\sup_{t \in [0, T]} \mathbb{E}(I(t)^2) \leq \max(M_{2T}, M_{3T}) < \infty.$$

Hence if $\mathbf{x}(t) = (I(t), N(t))$,

$$\sup_{t \in [0, T]} \mathbb{E}[\mathbf{x}(t)\mathbf{x}(t)^T] < \infty$$

as required. \square

Corollary 4.6. $0 \leq I(t) \leq N(t)(1 + \frac{\mu + \gamma}{\lambda(N)})$ a.s.

Proof. This is straightforward letting $p \rightarrow \infty$ in Theorem 4.3. \square

Corollary 4.7. There exists a unique strong pathwise solution to the SDEs (2.12) and (2.13) for all t .

Proof. Suppose that there are two distinct solutions $\mathbf{x}_1(t, \omega) = (N_1(t, \omega), I_1(t, \omega))$, $\mathbf{x}_2(t, \omega) = (N_2(t, \omega), I_2(t, \omega))$ to (2.12) and (2.13) with the same initial conditions, then they must differ on a set Ω_1 where $\mathbb{P}(\Omega_1) > 0$. Hence they must differ for $t \in [0, T]$, where $T < \infty$, on a set Ω_2 where $\mathbb{P}(\Omega_2) > 0$. However $\tau_n \rightarrow \infty$ as $n \rightarrow \infty$ and $v_p \rightarrow \infty$ as $p \rightarrow \infty$ so for some strictly nonnegative integers n and p the solutions $\mathbf{x}_1(t \wedge \tau_n \wedge v_p, \omega)$ and $\mathbf{x}_2(t \wedge \tau_n \wedge v_p, \omega)$ must differ on a set Ω_3 with $\mathbb{P}(\Omega_3) > 0$. This contradicts Theorem 4.1. Hence the solution is unique. \square

So we have shown that there is a unique pathwise strong non-explosive solution to the SDEs (2.12) and (2.13). The same result is true for the system (S, I, N) given by $S = N - I$, (2.12) and (2.13). In the next section we shall look at extinction of our SDE system.

5. Extinction of the number of infecteds and the total number of individuals

For the rest of this paper we shall focus on analysing the behaviour for the two dimensional SDE SIS model (2.12) and (2.13). When looking at an epidemic model, one of the key aspects that we would like to look at is the extinction condition on our SDE SIS model. Therefore, throughout this section we shall investigate this key aspect and show that the solution for $N(t)$ to our SDE model (2.13) does become extinct a.s. and then deduce that $I(t)$ becomes extinct a.s.

Corollary 5.1. For any given initial value of $N_0 = N(0)$, there exists some $t > 0$ such that $N(t)$ will reach 0 with probability one in finite time. In other words, $\mathbb{P}(\tau_0 < \infty) = 1$.

Proof. Recall that the SDE model (2.13) is a special case of the mean-reverting square root process with zero drift coefficient and thus from [49]

$$\mathbb{P}\left(\sup_{0 \leq s < \tau} N(s) < \infty\right) = 1.$$

We shall show that $\mathbb{P}(\tau_0 < \infty) = 1$ by contradiction. Let us assume that the opposite is true i.e. $\mathbb{P}(\tau_0 = \infty) = \delta > 0$. For given t , $\lim_{a \downarrow 0} \mathbb{P}(\tau_a \geq t) = \mathbb{P}(\tau_0 \geq t) \geq \delta$. So by choosing a , with $0 < a < N(0)$, small enough $\mathbb{P}(\Omega_1) \geq \frac{2\delta}{3} > 0$ where $\Omega_1 = \{\omega : \tau_a \geq t\}$. Now $\exists M$ such that $\mathbb{P}(\Omega_2) \geq 1 - \frac{\delta}{3}$ where

$$\Omega_2 = \left\{ \omega : \sup_{0 \leq s \leq \tau} N(s) \leq M \right\}$$

so $\mathbb{P}(\Omega_1 \cap \Omega_2) \geq \frac{\delta}{3} > 0$.

Then we apply Itô's formula choosing $V = \sqrt{N}$ for $N > 0$. We have that

$$\sqrt{N(t \wedge \tau_a, \omega)} = \sqrt{N(0)} + \int_0^{t \wedge \tau_a} q(N(s, \omega)) ds + \int_0^{t \wedge \tau_a} \frac{\sqrt{2\mu}}{2} dW(s), \tag{5.1}$$

where $q(x, \omega) = -\frac{\mu}{4\sqrt{x}} \leq -\frac{\mu}{4\sqrt{M}} = -\varepsilon$ for $M \geq x$. Here $\varepsilon = \frac{\mu}{4\sqrt{M}} > 0$. Hence

$$\mathbb{E}(\sqrt{N(t \wedge \tau_a, \omega)}) \leq \sqrt{N(0)} + \int_0^{t \wedge \tau_a} \mathbb{E}(q(N(s, \omega))) ds, \leq \sqrt{N(0)} + \int_0^{t \wedge \tau_a} \mathbb{E}(I_{\Omega_1 \cap \Omega_2} q(N(s, \omega))) ds, \leq \sqrt{N(0)} - \frac{\varepsilon \delta t}{3}.$$

Letting $t \rightarrow \infty$ we deduce a contradiction. Thus we must have $\mathbb{P}(\tau_0 < \infty) = 1$, so $\exists t_0 < \infty$ such that $N(t_0) = 0$ a.s. \square

Theorem 5.2. For any given initial value $I(0) = I_0 \in (0, N)$, the solution to our two-dimensional SDE SIS model (2.12) and (2.13), $I(t)$, will reach zero with probability one in finite time and thus the disease will die out a.s.

Proof. $\exists t_0 < \infty$ such that $N(t_0) = 0$ a.s. From Corollary 4.6, we have that in Case A, and in Case B if $N > 0$

$$0 \leq I(t) \leq N(t) \left(1 + \frac{\mu + \gamma}{\lambda(N)}\right).$$

In Case A at $t = t_0$, $I(t_0) = 0$ a.s.

In order to complete the proof, let us now consider Case B. Let us define the stopping time

$$\nu_b = \inf\{t \geq \tau_0 : I(t) \leq b\},$$

where we set $\inf \emptyset = \infty$. The aim of our proof is to show that $\mathbb{P}(\nu_0 < \infty) = 1$, where $\nu_0 = \lim_{b \downarrow 0} \nu_b$ and this can be shown by proof by contradiction. Let us assume the opposite is true, i.e. $\mathbb{P}(\nu_0 = \infty) = \bar{\delta} > 0$. As $\tau_0 < \infty$ a.s. we can choose T such that $\mathbb{P}(\tau_0 \leq T) \geq 1 - \frac{\bar{\delta}}{3}$. For $t \geq T$, $\lim_{b \downarrow 0} \mathbb{P}(\nu_b \geq t) = \mathbb{P}(\nu_0 \geq t) \geq \bar{\delta}$. So by choosing $b > 0$ small enough $\mathbb{P}(\nu_b \geq t) \geq \frac{2\bar{\delta}}{3} > 0$. Hence

$$\bar{\delta}_1 = \mathbb{P}(\nu_b \geq t \text{ and } \tau_0 \leq T) > \frac{\bar{\delta}}{3}.$$

By using Itô's formula and choosing $V(I) = \sqrt{I}$, we have that for $N(t) \geq 0$,

$$\sqrt{I(t \wedge \nu_b)} = \sqrt{I(t \wedge \tau_0)} + \int_{t \wedge \tau_0}^{t \wedge \nu_b} U(I(s), s, \omega) ds + \frac{1}{2} \int_{t \wedge \tau_0}^{t \wedge \nu_b} \sqrt{\frac{\lambda(N)}{N} (N - I) + \mu + \gamma} dW(s), \tag{5.2}$$

where $U : \mathbb{R} \times \mathbb{R}^+ \times \Omega \rightarrow \mathbb{R}$ is defined by

$$U(x, t, \omega) = \frac{\sqrt{x}}{2} \left(\frac{\lambda(N)}{N} (N - x) - \mu - \gamma \right) - \frac{1}{8\sqrt{x}} \left(\frac{\lambda(N)}{N} (N - x) + \mu + \gamma \right). \tag{5.3}$$

Here $\frac{\lambda(N)}{N}$ is interpreted as $\lambda'(0)$ as $N = 0$. Taking expectations of (5.2) we deduce that

$$0 \leq \mathbb{E}(\sqrt{I(t \wedge \nu_b)}) \leq \mathbb{E}(\sqrt{I(t \wedge \tau_0)}) + \mathbb{E} \int_{t \wedge \tau_0}^{t \wedge \nu_b} U(I, s, \omega) ds. \tag{5.4}$$

For $s \in [t \wedge \tau_0, t \wedge \nu_b]$,

$$\begin{aligned}
 U(x, s, \omega) &= \frac{\sqrt{x}}{2} (-\lambda'(0)x - \mu - \gamma) - \frac{1}{8\sqrt{x}} (-\lambda'(0)x + \mu + \gamma), \\
 &\leq -\frac{\lambda'(0)}{2} x^{\frac{3}{2}} - (\mu + \gamma) \frac{\sqrt{x}}{2}, \text{ by letting } p \rightarrow \infty \text{ in (4.11) with } N = 0. \\
 &\leq -\frac{\lambda'(0)}{2} b^{\frac{3}{2}}, \quad \text{if } x \geq b.
 \end{aligned}$$

Hence there exists an $\varepsilon_1 > 0$ such that $U(x, s, \omega) \leq -\varepsilon_1$ when $x \geq b$. From (5.4) we deduce that for $t \geq T$,

$$\begin{aligned}
 0 &\leq \mathbb{E}\left(\sqrt{I(t \wedge \tau_0)}\right) - \bar{\delta}_1 \varepsilon_1 (t - T), \\
 \text{so} \quad \bar{\delta}_1 \varepsilon_1 (t - T) &\leq \mathbb{E}\left(\sqrt{I(t \wedge \tau_0)}\right). \tag{5.5}
 \end{aligned}$$

But by the Fatou–Lebesgue Theorem

$$\begin{aligned}
 \limsup_{t \rightarrow \infty} \mathbb{E}\left(\sqrt{I(t \wedge \tau_0)}\right) &\leq \mathbb{E}\left(\limsup_{t \rightarrow \infty} \sqrt{I(t \wedge \tau_0)}\right), \\
 &= \sqrt{\frac{\mu + \gamma}{\lambda'(0)}} < \infty.
 \end{aligned}$$

This contradicts (5.5) hence we have $\mathbb{P}(v_0 = \infty) = 0$ and this completes the proof of Theorem 5.2. \square

So in the two dimensional SIS model both $N(t)$ and $I(t)$ (hence also $S(t)$) die out a.s. in finite time.

In the next section we will be using the Milstein numerical simulation method to produce analytical results to reinforce the results we have shown in Section 5.

6. Simulations to illustrate the analytical results

In the previous sections, we managed to prove several theorems for our two-dimensional SDE SIS model (2.12) and (2.13). In this section, we will focus on applying the Milstein method (e.g. [52]) to produce simulations using R to support the results that we have shown. In our paper, we have decided to use the Milstein method instead of the simpler Euler–Maruyama method which is commonly used in many papers, for example [7]. The reason is that the Milstein method is strongly convergent with order 1 as the integration time-step goes to zero, which is better than the Euler–Maruyama method which only has a convergence order of 0.5 [53].

We shall apply our results to the case where $\lambda(N) = \beta N$ corresponding to Case B and disease transmission term βSI as in the classical epidemic model. We simulate this model

$$dI(t) = [\beta I(t)(N(t) - I(t)) - (\mu + \gamma)I]dt + \sqrt{\beta I(N - I) + (\mu + \gamma)I} dW_6, \tag{6.1}$$

$$\text{and } dN(t) = \sqrt{2\mu N(t)} dW_7, \tag{6.2}$$

where again W_6 and W_7 are Brownian motions and illustrate the result given by Corollary 5.1, namely there exists some $t > 0$ such that $N(t) = 0$ a.s. Then we will integrate the two-dimensional system for $(I(t), N(t))$ given by (6.1) and (6.2). Simulations are produced to support the results shown in Theorem 5.2 that the disease will die out in finite time. Our numerical simulation program was comprehensively verified using detailed output from a large number of runs and also in both cases the simulations were repeated using different parameter values and in each case the analytical results were verified.

6.1. Simulations on the total number of individuals

In this section, we will use simulation produced by the Milstein method to show the results given in Corollary 5.1.

Example 6.1. Suppose that the population size is measured in units of one million. By choosing $\mu = 25$, the SDE model for $N(t)$ (6.2) becomes

$$dN(t) = \sqrt{50N(t)} dW(t). \tag{6.3}$$

By Corollary 5.1, we could conclude that there exists $t > 0$ such that $N(t) = 0$ a.s.

Clearly, Fig. 1 supports the result illustrated in Corollary 5.1 and that the solution $N(t)$ to the SDE model for N (2.13) does in fact die out in finite time. In addition, Fig. 1 also supports the results shown in Theorem 3.1 by showing that the solution $N(t)$ will not explode in finite time. The simulation was repeated many times with different values of μ and similar results were obtained each time to support the results shown in Corollary 5.1 and Theorem 3.1.

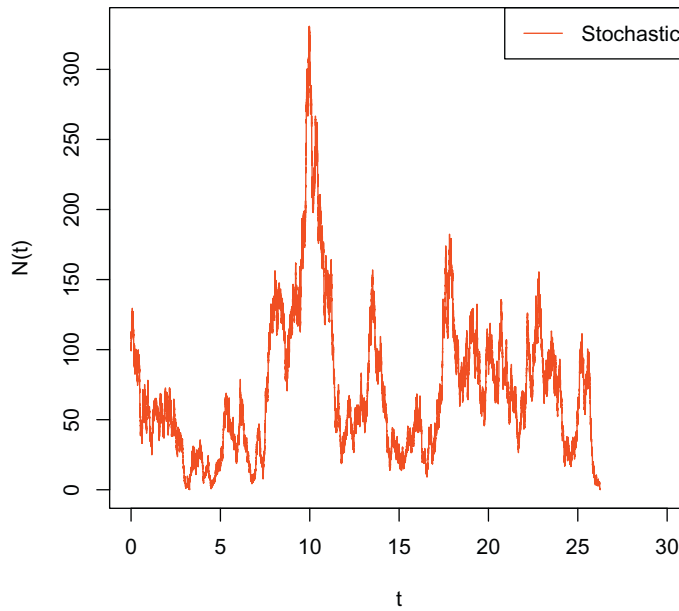


Fig. 1. Computer simulation of the path $N(t)$ for the SDE model (6.3) using the Milstein method with step size $\Delta = 0.001$ with initial value $N(0) = 100$.

6.2. Simulations on the total number of infecteds

In this section we will use the combined integration program for the system $(I(t), N(t))$ given by the system of differential Eqs. (6.1) and (6.2) to support the results given in Theorem 5.2.

Example 6.2 ($R_0 < 1$). Again suppose that the population size is measured in units of one million. Let us choose the following parameter values:

$$N_1 = 80, \mu = 15, \gamma = 35, \beta = 0.5, \tag{6.4}$$

where N_1 is the N value we choose for our deterministic SIS model given by (1.1) and (1.2) with $R_0 = 0.8$. By substituting the parameter values (6.4) into the SDE SIS model (6.1) and (6.2) we have that

$$dI(t) = [0.5I(t)(N(t) - I(t)) - 50I(t)]dt + \sqrt{0.5I(t)(N(t) - I(t)) + 50I(t)} dW_4(t),$$

and

$$dN(t) = \sqrt{30} dW_5(t), \tag{6.5}$$

with the corresponding SIS deterministic model as

$$\frac{dS(t)}{dt} = 1200 - 0.5S(t)I(t) + 35I(t) - 15S(t),$$

and

$$\frac{dI(t)}{dt} = [-50 + 0.5S(t)]I(t). \tag{6.6}$$

Based on the result shown in Theorem 5.2, we would expect to see the solution $I(t)$ to the SDE SIS model (6.1) and (6.2) die out in finite time a.s. From both figures illustrated in Fig. 2, we can see that the numerical simulations support the result given in Theorem 5.2 by illustrating that the solution $I(t)$ dies out in finite time. Similarly, the numerical simulations were repeated many times with different parameter values where $R_0 \leq 1$ and the same conclusion is obtained verifying the results obtained in Corollary 5.1 and Theorem 5.2 for our two-dimensional SDE SIS model (6.1) and (6.2).

Next we would like to verify that the result illustrated in Theorem 5.2 also holds for the case where $R_0 > 1$.

Example 6.3 ($R_0 > 1$). Suppose that the population size is measured in units of one million. Let us now choose the following parameter values:

$$N_1 = 100, \mu = 10, \gamma = 25, \beta = 0.5, \tag{6.7}$$

where N_1 is the N value we choose for our deterministic SIS model given by (1.1) and (1.2) where now $R_0 = 1.43$. Similar to Example 6.2, by substituting the parameter values (6.7) into the SDE SIS model (6.1) and (6.2) we have that

$$dI(t) = [0.5I(t)(N(t) - I(t)) - 35I(t)]dt + \sqrt{0.5I(t)(N(t) - I(t)) + 35I(t)} dW_4(t),$$

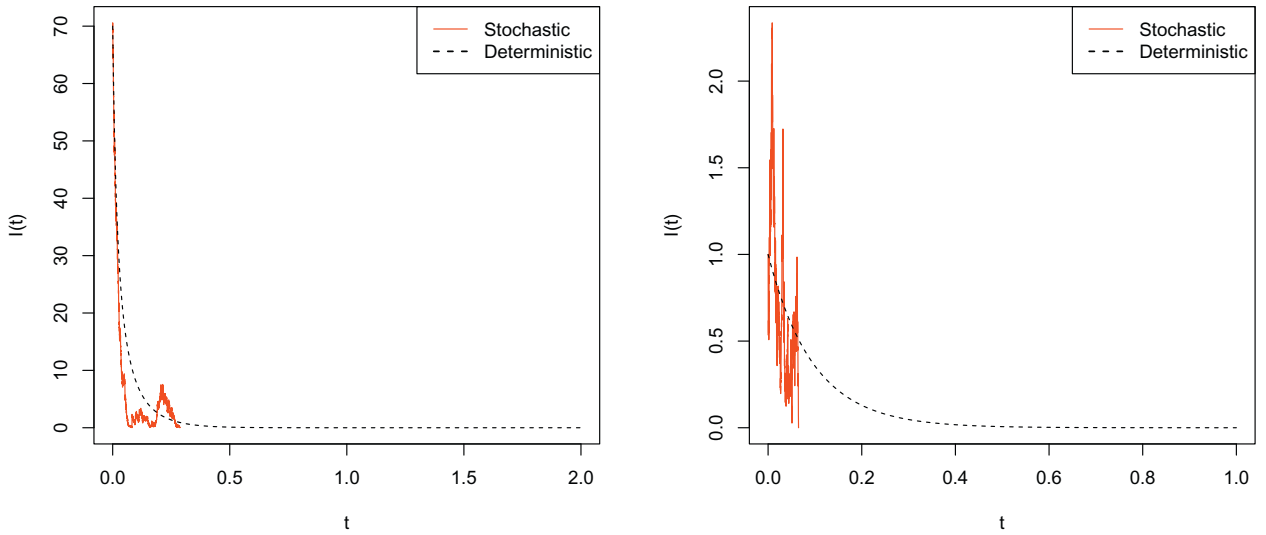


Fig. 2. Computer simulation of the path $I(t)$ for the SDE SIS model (6.5) and the solution $I(t)$ for the corresponding deterministic SIS model (6.6), using the Milstein method with step size $\Delta = 0.0001$ with initial values $I(0) = 70$ (the left hand side) and $I(0) = 1$ (the right hand side) both with $N(0) = 80$.

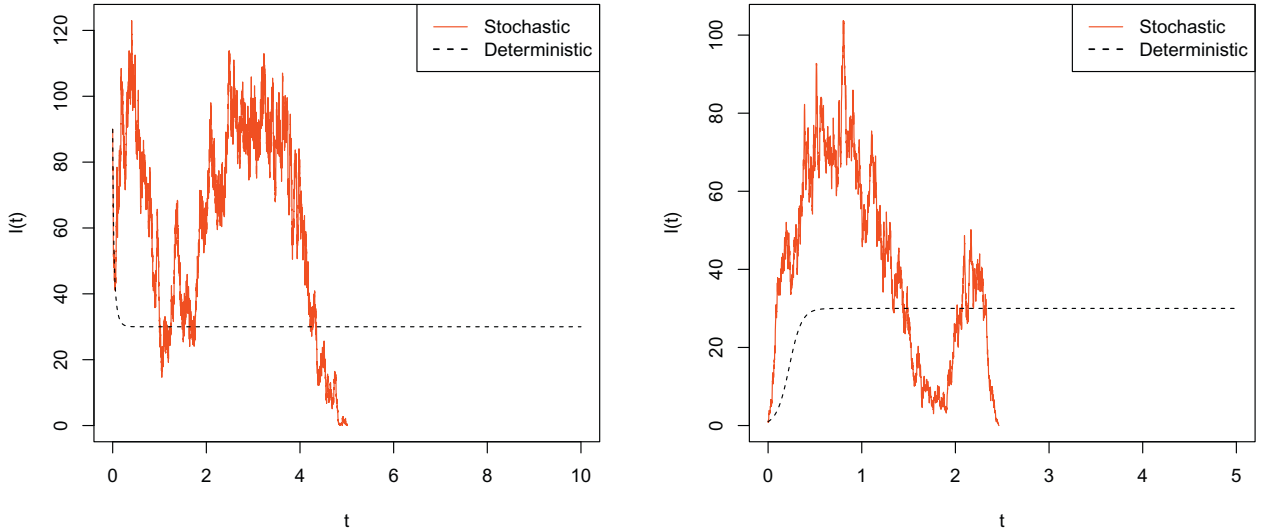


Fig. 3. Computer simulation of the path $I(t)$ for the SDE SIS model (6.8) and the solution $I(t)$ for the corresponding deterministic SIS model (6.9), using the Milstein method with step size $\Delta = 0.001$ with initial values $I(0) = 90$ (the left hand side) and $I(0) = 1$ (the right hand side) both with $N(0) = 100$.

and

$$dN(t) = \sqrt{20} dW_5(t), \tag{6.8}$$

with the corresponding SIS deterministic model as

$$\frac{dS(t)}{dt} = 1000 - 0.5S(t)I(t) + 25I(t) - 10S(t),$$

and

$$\frac{dI(t)}{dt} = [-35 + 0.5S(t)]I(t). \tag{6.9}$$

For the case where $R_0 > 1$, we could see from Fig. 3 that the simulations produced once again support our results mentioned in Theorem 5.2, namely the solution $I(t)$ to (6.1) and (6.2) dies out in finite time. Similar to Example 6.2, the numerical simulations were carried out numerous times with different parameter values where $R_0 > 1$, and the same conclusion is drawn to support the results obtained in Corollary 5.1 and Theorem 5.2 for (6.1) and (6.2).

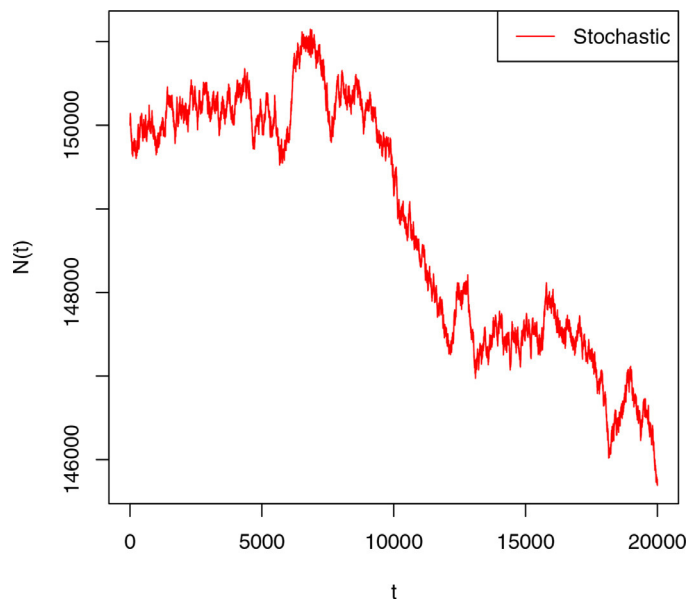


Fig. 4. Computer simulation of the path $N(t)$ for the SDE model (6.2) for pneumococcus, using the Milstein method with parameter value $\mu = 1.37363 \times 10^{-3}/\text{day}$ with step size $\Delta = 0.05$ with initial values $N(0) = 150,000$.

7. Realistic simulations

In Section 6 we have been focusing on using theoretical parameter values to show that the solution (I, N) to (6.1) and (6.2) shown in Corollary 5.1 and Theorem 5.2 are supported by our numerical simulation produced using the Milstein method. As mentioned before the SIS model is suitable for modelling diseases such as the common cold, and pneumococcus where infected individuals, once recovered, will not obtain immunity to the disease. In this section we will focus on producing numerical simulations using realistic parameter values for the common cold, and pneumococcus amongst children aged two years and under in Scotland. A similar situation but examining the spread of *Streptococcus pneumoniae* with transmission due to genetic sequence type (part of the genetic material) is discussed by Greenhalgh et al. [12] and we have taken some of their parameter values to use in our simulations. Throughout this section, the unit of time is still one day but the population sizes are not scaled as previously.

Example 7.1 (Pneumococcus model). The population of Scottish children under two years old is of approximate size 150,000. The per capita death rate is therefore $\mu = \frac{1}{104}/\text{wk} = 9.615 \times 10^{-3}/\text{wk} = 1.37363 \times 10^{-3}/\text{day}$ [12]. For the per capita rate γ at which infected individuals become immune we note that in her Ph.D. thesis Weir [16] deduces from a systematic review that $\gamma = 0.02011/\text{day}$, $(1/\gamma) = 49.7$ days. The basic reproduction number for pneumococcus is estimated to be 1.49 [54], 1.4 [55] and 1.8–2.2 [56] so we take $\beta = 2.857 \times 10^{-7}/\text{day}$ corresponding to a basic reproduction number of 2.0.

Based on the result shown in Corollary 5.1, we would expect the solution $N(t)$ to die out in finite time. Our simulations do not contradict this but it appears that the time taken to die out with realistic parameter values is very large. The numerical simulation produced for the solution of $N(t)$ is illustrated in Fig. 4.

From Theorem 5.2, we would also expect the solution $I(t)$ to Eqs. (6.1) and (6.2) to die out in finite time a.s. The simulations for $I(t)$ are shown in Fig. 5. We observe that after an initial transient stage, the stochastic simulations appear to oscillate about the deterministic endemic equilibrium level which acts as a quasi-equilibrium [57]. This does not contradict our theoretical result, we expect that the disease dies out eventually after a long but finite time [57]. Note that on the timescale shown, the total population size is still large. The numerical simulations were repeated with different starting values and similar results were obtained each time.

Next we shall look at the simulations for the common cold.

Example 7.2 (Common cold model). Heikkinen and Järvinen [17], mentioned that the mean duration of the common cold is around 7–10 days. For our simulation, we choose the mean duration of the common cold to be 8 days and thus $\gamma = 0.125/\text{day}$. Sun et al. [58], calculated the estimated basic reproduction number of the common cold, R_0 , in a dormitory to be between 0.7–1.6 depending on the number of people in each dormitory. For our simulations, we shall demonstrate two cases: (i) where $R_0 < 1$, so we choose R_0 to be 0.7 which corresponds to 3 people per dormitory and (ii) where $R_0 > 1$, so we choose $R_0 = 1.6$ which corresponds to 6 people per dormitory. According to statistics of WHO [59] the crude death rate per year per 1000 population in the UK was 8.9 in 2012, hence $\mu = 0.000024384/\text{day}$. By using the above parameter values and the definition for R_0 , we derived β for both cases: (i) $\beta = 0.02917/\text{day}$ where $N = 3$ to correspond to $R_0 = 0.7$ and (ii) $\beta = 0.03334/\text{day}$ where $N = 6$ to correspond to $R_0 = 1.6$.

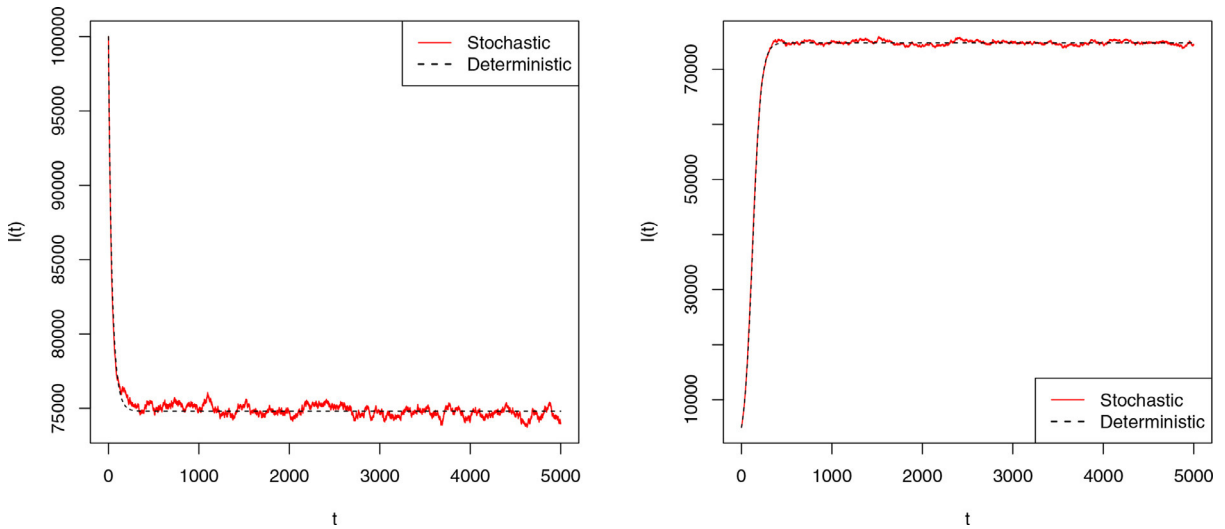


Fig. 5. Computer simulation of the path $I(t, \omega)$ for the SDE SIS model with $N(t)$ as a random variable for pneumococcus, using the Milstein method with parameter values $\beta = 2.857 \times 10^{-7}/\text{day}$, $\gamma = 0.02011/\text{day}$ and $\mu = 1.37363 \times 10^{-3}/\text{day}$ with step size $\Delta = 0.01$ with initial values $I(0) = 100,000$ (the left hand side) and $I(0) = 5,000$ (the right hand side) both with $N(0) = 150,000$ and $N_1 = 150,000$, where N_1 is the N value for the deterministic model.

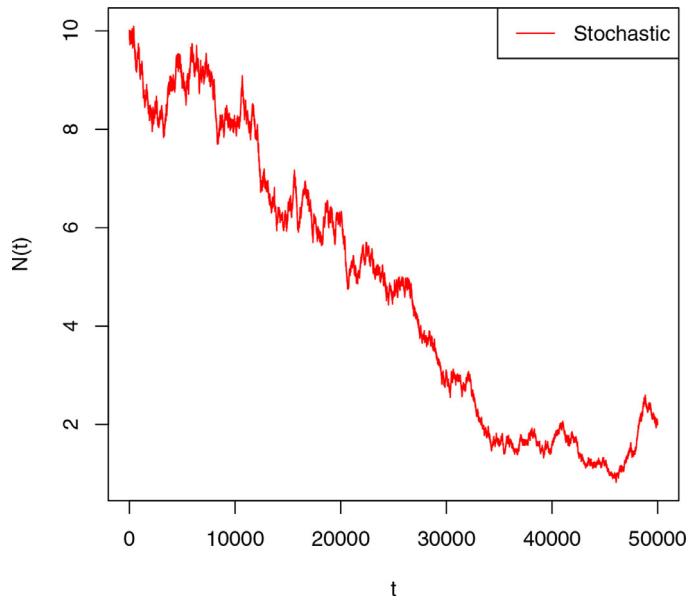


Fig. 6. Computer simulation of the path $N(t)$ for the SDE model (6.2) for the common cold, using the Milstein method with parameter value $\mu = 0.000024384/\text{day}$ with step size $\Delta = 0.1$ with initial value $N(0) = 10$.

The numerical simulation on the solution $N(t)$ to the SDE model (6.2) with the realistic parameter values for the common cold is shown in Fig. 6. Based on the results in Corollary 5.1 we would expect the solution $N(t)$ to die out in finite time. However, from Fig. 6, it appears that the computational time required in order for it to happen might be too large, but we could see that the simulation is approaching zero as time increases. The simulations were repeated various times with different initial values and the same conclusion is drawn.

We will now show the simulations for the solution $I(t, \omega)$ to the SDE SIS model (6.1) for the two cases where $R_0 = 0.7$ and $R_0 = 1.6$.

From Theorem 5.2 we would expect the solution to the SDE SIS model (6.1), $I(t, \omega)$ with $N(t)$ as a random variable to become extinct in finite time a.s. This is clearly the case illustrated in Fig. 7 and Fig. 8 for the case where $R_0 < 1$ and $R_0 > 1$ respectively. Hence our simulations for the common cold have verified our results shown in Theorem 5.2. Again, numerical simulations were repeated with different initial values and the same conclusion is obtained for both cases. Note that we have also carried out

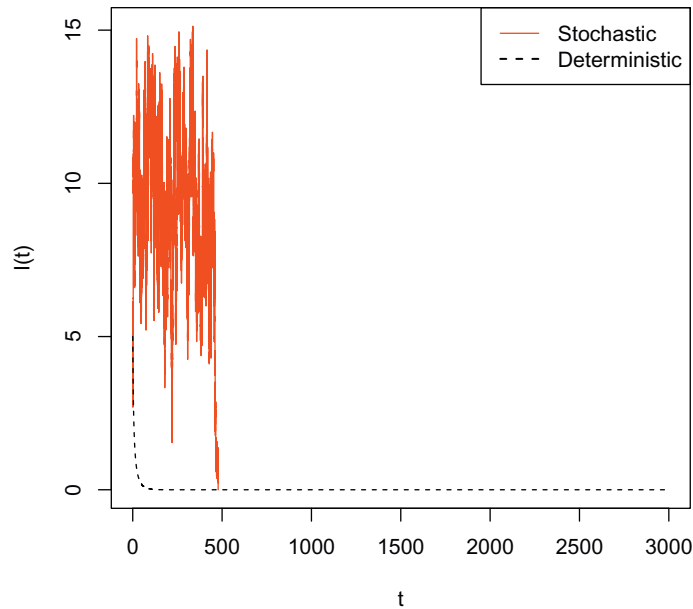


Fig. 7. Computer simulation of the path $I(t, \omega)$ for the SDE SIS model with $N(t)$ as a random variable for the common cold, using the Milstein method where $R_0 < 1$ with parameter values $\beta = 0.02917/\text{day}$, $\gamma = 0.125/\text{day}$ and $\mu = 0.000024384/\text{day}$ with step size $\Delta = 0.05$ with initial values $I(0) = 5$, $N(0) = 15$, $N_1 = 3$, where N_1 is the N value for the deterministic model.

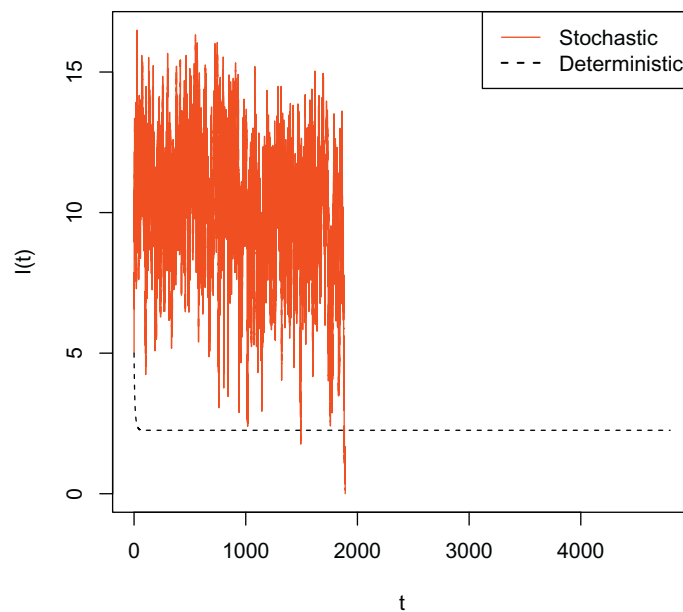


Fig. 8. Computer simulation of the path $I(t, \omega)$ for the SDE SIS model with $N(t)$ as a random variable for the common cold, using the Milstein method where $R_0 > 1$ with parameter values $\beta = 0.03334/\text{day}$, $\gamma = 0.125/\text{day}$ and $\mu = 0.000024384/\text{day}$ with step size $\Delta = 0.08$ with initial values $I(0) = 5$, $N(0) = 15$, $N_1 = 6$, where N_1 is the N value for the deterministic model.

simulations with larger population size such as $N(t) = 100$ and the simulations obtained do not contradict with our theorems but again the time taken to die out with realistic parameter values is very large.

Recall from [Theorem 4.3](#), although theoretically, $I(t)$ might exceed $N(t)$, we could see from our realistic simulations produced based on realistic parameter values that we never practically encounter the situation where $I(t)$ does exceed $N(t)$, even though it is theoretically possible.

From the simulations created using theoretical and realistic parameter values, we could see that the results obtained for the SDE SIS model [\(2.12\)](#) and [\(2.13\)](#) do indeed apply to the SDE SIS model [\(6.1\)](#) and [\(6.2\)](#) with transmission term $\beta S(t)I(t)$.

8. Conclusion and discussion

Epidemiological models have become increasingly important in predicting and controlling the spread of infectious diseases. The SIS epidemic model is one of the simplest models which is suitable in analysing diseases where individuals do not gain immunity after recovery, for example gonorrhoea, pneumococcus, tuberculosis or the common cold.

In this paper we have constructed the SDE SIS model with full demographic stochasticity with transmission term $\frac{\lambda(N)S(t)I(t)}{N(t)}$. The deterministic SDE SIS model assumes that the total population size is constant thus susceptible or infected individuals who die are immediately replaced by new susceptible individuals. Allen [21] and Allen [22] discuss an SDE model which retains this assumption and this is a direct analogue of the deterministic SIS epidemic model. However this assumption was made in the deterministic model to maintain a tractable model structure. In the stochastic model it is not really necessary to retain this assumption so in this paper we have assumed that births and deaths of infected individuals were completely independent, so that the total number of individuals formed a stochastic birth and death process. We derived a pair of coupled SDEs which describe how the number of susceptible and infected individuals vary with time. However it was more convenient to work with the SDEs in terms of the total number of individuals and the total number of infected individuals. We showed that there was a unique non-negative, non-explosive solution and obtained an upper bound for the number of infected individuals at time t in terms of the total number of individuals. We then showed that both the total number of individuals and the number of infected individuals will become extinct in finite time almost surely. We next demonstrated that that SDE SIS model with transmission term $\beta S(t)I(t)$ is a special case of our SDE SIS model. The analytical results were confirmed with numerical simulations. Finally examples of pneumococcus and the common cold with real-life parameters were discussed, providing further numerical verification of our analytical results.

SDEs are increasingly being used in a wide range of areas, for example finance and biology. There has recently been a large explosion in the number of papers using SDEs to model how diseases spread (e.g. [7,60–62]). However these papers introduce stochasticity in a different way by parameter perturbation which is appropriate if one of the parameters is a random variable. In this paper the SDEs look similar but have a different explanation as they are an SDE approximation to the continuous time Markov Chain models that have traditionally been used to introduce stochasticity into epidemic models ([20–22]). Although similar models have been formulated, but not analysed, previously ([21,22]) our paper is one of the first to analyse such models.

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