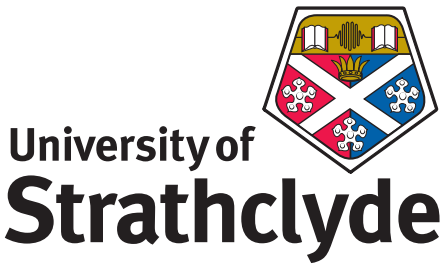

Modelling the Effect of Stochasticity in Epidemic and HIV Models

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Abstract

An epidemic of an infectious disease can be modelled by using either a deterministic model or a stochastic model. In this thesis, we consider the effect that different types of noise has on the dynamical behaviour of deterministic SIS models and SIR/SIRS models as well as an HIV model.

We start off with a literature review giving previous work and the mathematical background to the area. Next, we introduce demographic stochasticity into the well-established deterministic SIS model with births and deaths and derive a stochastic differential equation (SDE). We assume that an infected individual or a susceptible individual who dies is immediately replaced by a susceptible individual and thus the population size is kept constant. In order for our model to make sense, we then prove that the SDE has a strong unique nonnegative solution which is bounded above and establish the conditions needed for the disease to become extinct. Based on the idea of the Feller test, we also calculate the respective probabilities of the solution first hitting zero or the upper limit. Numerical simulations are then produced using the Milstein method with both theoretical and realistic parameter values to confirm our theoretical results.

Motivated by the model discussed in the first topic, we then continue our study on the effect of demographic stochasticity on the deterministic SIS model by now assuming that the births and deaths of individuals are independent of each other and thus the population size can vary with respect to time. In this case, the per capita disease contact rate may be dependent on the population size and we have shown that this model allows us to consider the cases when the population size tends to a large number and when the population size tends to a small number. First we look at the SDE model for the total population size and show that there exists a strong unique nonnegative solution. Then

we look at the two-dimensional SDE SIS model and show that there also exists a strong unique nonnegative solution which is bounded above given the total population size. We then obtain the conditions needed in order for the disease to become extinct in finite time almost surely. Numerical simulations with both theoretical and realistic parameter values are also produced to confirm our theoretical results.

Next we look at a different type of noise, namely the telegraph noise, which is an example of an environmental noise. Telegraph noise could be modelled as changing between two or more regimes of environment which differ by factors such as rainfalls or nutrition. This form of switching can be modelled using a finite-state Markov Chain. We incorporate the telegraph noise into the SIRS epidemic model. First we start with a two-state Markov Chain and show that there exists a unique nonnegative solution and establish the conditions for extinction and persistence for the stochastic SIRS model. We then explain how the results can be generalised to a finite-state Markov Chain. Furthermore we also show that the results for the SIR model with Markov switching are a special case of the SIRS model. Numerical simulations are produced using theoretical and realistic parameter values to confirm our theoretical results.

Lastly we look at the modified Kaplan HIV model amongst injecting drug users. We introduce environmental stochasticity into the deterministic HIV model by the well-known standard technique of parameter perturbation. We then prove that the resulting SDE has a unique global nonnegative solution. As well as constructing the conditions required for extinction and persistence we also show that there exists a stationary distribution for the persistence case. Simulations using the Euler-Maruyama method with realistic parameter values are then constructed to illustrate and support our theoretical results.

A brief discussion and summary section is given at the end to conclude the thesis.

Notation

a.s.	: almost surely, or $\mathbb{P}$-almost surely, or with probability 1.
$A := B$	: A is defined by B or A is denoted by B.
$A(x) \equiv B(X)$	: $A(x)$ and $B(x)$ are identically equal, i.e. $A(x) = B(x)$ for all x.
$\emptyset$	: the empty set.
$\mathbf{1}_A$	: the indicator function of a set A, i.e. $\mathbf{1}_A(x) = 1$ if $x \in A$ or otherwise 0.
A^c	: the complement of A in Ω, i.e. $A^c = \Omega - A$.
$A \subset B$	: $A \cap B^c = \emptyset$.
$a \wedge b$	: the minimum of a and b.
$a \vee b$	: the maximum of a and b.
$f : A \to B$	: the mapping f from A to B.
$\mathbb{R}_+$	: the set of all nonnegative real numbers, i.e. $\mathbb{R}_+ = [0, \infty)$.
$\mathbb{R}^d$	: the d-dimensional Euclidean space.
$\sigma(\mathcal{C})$	: the σ-algebra generated by $\mathcal{C}$.
$\mathcal{B}^d$	: the Borel σ-algebra on $\mathbb{R}^d$.
$\mathbb{R}^{d\times m}$	: the space of real $d \times m$-matrices.
$\mathcal{B}^{d\times m}$	: the Borel-σ-algebra on $\mathbb{R}^{d\times m}$.
$\lvert x \rvert$	: the Euclidean norm of a vector x.
δ_{ij}	: Dirac's delta function, that is $\delta_{ij} = 1$ if $i = j$ or otherwise 0.
V_x	: $=(V_{x_1}, \ldots, V_{x_d}) = \left(\frac{\partial V}{\partial x_1}, \ldots, \frac{\partial V}{\partial x_d}\right)$.
V_{xx}	: $=(V_{x_i x_j})_{d\times d} = \left(\frac{\partial^2 V}{\partial x_i \partial x_j}\right)_{d\times d}$.

$L^p([a,b];\mathbb{R}^d)$: the family of Borel measurable functions $h : [a,b] \to \mathbb{R}^d$ such that $\int_a^b |h(t)|^p dt < \infty$.

$\mathcal{L}^p([a,b];\mathbb{R}^d)$: the family of $\mathbb{R}^d$-valued $\mathcal{F}_t$-adapted processes $\{f(t)\}_{a\le t\le b}$ such that $\int_a^b |f(t)|^p dt < \infty$ a.s.

$\mathcal{M}^p([a,b];\mathbb{R}^d)$: the family of processes $\{f(t)\}_{a\le t\le b}$ in $\mathcal{L}^p([a,b];\mathbb{R}^d)$ such that $\mathbb{E}\int_a^b |f(t)|^p dt < \infty$.

$\mathcal{L}^p(\mathbb{R}_+;\mathbb{R}^d)$: the family of processes $\{f(t)\}_{t\ge 0}$ such that for every $T > 0$, $\{f(t)\}_{0\le t\le T} \in \mathcal{L}^p([0,T];\mathbb{R}^d)$.

$\mathcal{M}^p(\mathbb{R}_+;\mathbb{R}^d)$: the family of processes $\{f(t)\}_{t\ge 0}$ such that for every $T > 0$, $\{f(t)\}_{0\le t\le T} \in \mathcal{M}^p([0,T];\mathbb{R}^d)$.

Other notations will be explained where they first appear.

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Chapter 1

Introduction and Literature Review

1.1 Epidemic Models

Epidemics of infectious diseases have been a constant threat to our society. In the past, Europe suffered from 25 million deaths out of a population of 100 million due to the Black Death [10]; Russia suffered from about 25 million cases of typhus with a death rate of about 10 percent, whilst smallpox wiped out half of the population of the Aztecs of three and a half million in 1520 [9]. Although in the 21st century, diseases such as smallpox no longer pose a threat towards mankind, there is still a high proportion of the population that is under threat of diseases such as malaria and HIV (e.g. [10, 28]).

As a result mathematical models have been constructed in order to predict the behaviour of a disease and help to control a particular epidemic. Epidemics can be modelled by compartmental models such as SIS and SIR models where each individual has been assigned to a different subgroup representing a specific stage of disease. In 1927, Kermack and McKendrick [70] constructed the Susceptible-Infected-Removed (SIR) model to describe the behaviour of diseases such as chickenpox and measles [57]. A typical individual starts off susceptible, at some stage catches the disease and after a short infectious period becomes completely immune. Another type of epidemic model which describes a different scenario than the SIR model is the susceptible-infected-susceptible (SIS) epidemic model. This is one of the simplest possible models for how diseases spread amongst a population. 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 gonorrhea. It is sometimes used as an approximate model for tuberculosis and can also be used to model the common cold [5, 86, 93]. 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 [38].

In the next section, we would like to introduce the three different types of epidemic models that we work with in this thesis. Let $S(t)$ denote the number of susceptibles at time t, $I(t)$ denote the number of infecteds at time t and $R(t)$ denote the number of recovered individuals at time t.

1.2 The SIS Model

The spread of the disease is described by the pair of differential equations

$$\frac{dS}{dt} = \mu N - \beta S(t)I(t) + \gamma I(t) - \mu S(t), \tag{1.2.1}$$

$$\frac{dI}{dt} = \beta S(t)I(t) - (\mu + \gamma)I(t), \tag{1.2.2}$$

with appropriate starting values $S(0)$ and $I(0)$ with $S(0) + I(0) = N$. In these equations μ is the per capita 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 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 [14]. 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 [57] and Brauer et al. [14]. It is equivalent to the well-known logistic equation for population growth and has a solution given by

$$I(t) = \begin{cases} \left[\frac{\beta}{\beta N-\mu-\gamma}(1-e^{-(\beta N-\mu-\gamma)t}) + \frac{1}{I_0}e^{-(\beta N-\mu-\gamma)t}\right]^{-1}, & \text{if } R_0 \neq 1, \\ \left[\beta t + \frac{1}{I_0}\right]^{-1}, & \text{if } R_0 = 1, \end{cases} \tag{1.2.3}$$

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

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 [84] models vaccination against pneumococcus and his work is based on an SIS model. In a series of three papers Greenhalgh, Lamb and Robertson [51, 52] and Lamb, Greenhalgh and Robertson [77] 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 [76] and Weir [125] are based on SIS models for pneumococcus.

Another disease which can be modelled by using the SIS model is the common cold [5, 86, 93]. The common cold (rhinovirus) is a viral infectious disease of the upper respiratory tract which has symptoms such as sneezing and sore throat [55]. Rhinovirus is the predominant cause of common cold, it is responsible for around 30-50 percent of colds each year [55] with over 100 known serotypes, thus making it impossible to produce a unifying vaccine [55, 123]. Most importantly, exposure to one rhinovirus does not confer significant immunity against other serotypes [39]. Consequently, there have been papers that suggest that an SIS model would be suitable in analysing the behaviour of the common cold (e.g. [5, 86, 93]).

1.3 The SIR/SIRS Model

In the 1920s, Kermack and McKendrick [70] constructed the SIR and SIRS epidemic models to illustrate respectively diseases where there is a permanent acquired immunity such as measles [57] and where there is a temporary acquired immunity such as rubella. The SIR model is a special case of the SIRS model.

Let us consider the following deterministic SIRS epidemic model:

$$\begin{aligned} \frac{dS(t)}{dt} &= -\beta I(t)S(t) + \mu N - \mu S(t) + \upsilon R(t), \\ \frac{dI(t)}{dt} &= \beta I(t)S(t) - (\mu + \gamma)I(t), \\ \frac{dR(t)}{dt} &= \gamma I(t) - \mu R(t) - \upsilon R(t), \end{aligned} \tag{1.3.1}$$

where S, I and R denote respectively the number of susceptible, infected and recovered individuals in the population. N is the total size of the population, β is the disease transmission coefficient and $\beta = \lambda/N$ where λ is the disease contact rate for each individual, that is the rate at which susceptible individuals come into contact with infected individuals. μ is the per capita birth and death rate and γ is the rate at which an infected individual becomes cured and thus moves to the recovery group. υ is the rate of loss of immunity and thus making the recovered individuals susceptible to catching the virus again.

By setting the rate of loss of immunity parameter υ to zero to illustrate diseases with a permanent acquired immunity such as measles chickenpox, we have the Susceptible-Infected-Removed (SIR) model

$$\begin{aligned} \frac{dS(t)}{dt} &= -\beta I(t)S(t) + \mu N - \mu S(t), \\ \frac{dI(t)}{dt} &= \beta I(t)S(t) - (\mu + \gamma)I(t), \\ \frac{dR(t)}{dt} &= \gamma I(t) - \mu R(t). \end{aligned} \tag{1.3.2}$$

1.4 Deterministic Model and Stochastic Model

An epidemic of an infectious disease can be modelled by using either a deterministic model or a stochastic model. The deterministic model is often formulated as a system of

differential equations where its solution is uniquely dependent on the initial value. On the other hand a stochastic model is a stochastic process with a collection of random variables where its solution is a probability distribution for each of the random variables. By running a stochastic model many times, we can also build up a distribution of the possible outcomes which allows us to identify the number of infectives at a particular time t, whereas for a deterministic model we will only get a single outcome. There has been much work done on deterministic models already, however there are some limitations in using these in analysing infectious diseases. A deterministic model is more suitable than a stochastic model when we are dealing with a large population. However, if we consider an epidemic outbreak in a small community such as a school, a stochastic model would be more appropriate as the element of variability would become significant [10, 11, 15]. In addition, the real world is not deterministic, and there are many factors that can influence the behaviour of a disease and thus it is not always possible to predict with certainty what would happen. Consequently, a stochastic model is introduced to compensate for this problem. There are also many properties that are unique to the stochastic epidemic model which could enhance our understanding towards the behaviour of a particular disease, for example, the probability that an epidemic will not occur, the final size distribution of an epidemic and the expected duration of an epidemic [2]. Clearly, we can see that introducing stochasticity into an epidemic model will provide some additional information that will improve the realism of our results compared to the deterministic approach.

There are three different types of stochastic models commonly used in population biology, namely the discrete time Markov chain (DTMC), continuous time Markov chain (CTMC) and stochastic differential equations (SDEs) [2, 3]. In a DTMC model, the time and the state space variables are discrete. In a CTMC model, the time is continuous but the state variables are discrete, while the SDE is based on a diffusion process where both the time and the state variables are continuous [2]. These three stochastic models all consider the random behaviour occurring within the birth and death process of an individual [2, 3]. The SDE model is preferred over the CTMC model when it comes to computing numerical simulations to illustrate the behaviour of the model [3], which we will do later on in this thesis. This is because in order to get a good estimation of the probability distribution for the CTMC model, computational costs can be very high. The

SDE model is especially useful in situations where there are several random variables and several interacting populations as setting up the transmission matrix may be complicated when there are several random variables [3]. Allen and Allen [3] made a thorough comparison between these three epidemic models with respect to the persistence time. They found that, when consistently formulated, the three stochastic models produced similar results for the mean and variance of persistence time.

There are several ways that stochasticity can be introduced into an epidemic model. In this thesis we have introduced stochasticity into various types of epidemic model such as the SIS model, SIRS/SIR model using different approaches. In the next sections, we will discuss each stochastic model in detail.

1.5 Stochastic SIS Model with Demographic Stochasticity

Demographic stochasticity is when we introduce births and deaths into the population and derive a stochastic model. The stochastic aspects of the SIS model for infectious diseases have been studied by many authors. In [20], Cavender considered the SIS model as an example of a birth and death process, which is a stochastic population model used to model demographic stochasticity [13]. Norden [101] described the stochastic SIS model as a stochastic logistic population model and aimed to investigate the distribution of the extinction times both numerically and theoretically. Kryscio and Lefévre [73] also looked at the stochastic SIS logistic model (also known as the stochastic SIS model). They extended and combined the results mentioned by Norden and Cavender. Kryscio and Lefévre obtained the approximations of the quasi-stationary distribution by studying two approximations of the process as well as the approximation to the mean time to extinction for the stochastic SIS logistic model. Furthermore, Clancy and Pollett [23] also considered the SIS logistic model as a birth and death process with a different death/recovery rate, $\mu_i = \mu i$, than the one mentioned in [73], namely $\mu_i = \mu(i-1)$. By using Theorem 1 mentioned in Clancy and Pollett's paper, they have managed to prove one of the conjectures mentioned by Kryscio and Lefévre which Kryscio and Lefévre did not prove in their paper

[73], namely $\mathbf{q} \prec^{ST} \mathbf{m}$, where $\mathbf{q}$ and $\mathbf{m}$ represent the quasi-stationary distribution and the stationary distribution of the process respectively. The notation $\prec^{ST}$ represents the concept of stochastic ordering where it denotes the idea of one random variable being bigger than another random variable. In other words, if $A \prec^{ST} B$ where A and B are random variables then it means that $\mathbb{P}(A > x) \leq \mathbb{P}(B > x)$ for all x and $\mathbb{P}(A > x) < \mathbb{P}(B > x)$ for some x, and that A is stochastically strictly less than B (e.g. [108]). Ovaskainen [102] looked at the other aspect of the quasi-stationary distribution of the stochastic SIS model with a different infection rate of susceptible individuals, $\lambda_i = \lambda i(N - i)$, than the conventional one mentioned in most papers, namely $\lambda_i = (\lambda/N)i(N - i)$ [2, 23, 73], where N denotes the total population size. This is because by scaling λ by N, it implies that the number of contacts per person is independent of the population size while the one used by Ovaskainen [102] will take into account that there are more contacts per person in a large population than in a small population. Ovaskainen improved on previous approximation formulae and obtained a rigorous mathematical formula for the quasi-stationary distribution as $N \to \infty$. Nasell [96] showed that for the stochastic SIS model with no demography, both the quasi-stationary distribution and the expected time to extinction from quasi-stationarity have three qualitatively different behaviours as a function of N and R_0 where R_0 is the basic reproduction number which determines whether or not a disease will die out or persist. Other than the papers we have mentioned above, there are still many other papers that dealt with the stochastic SIS model [4, 97, 98, 126].

Nasell [95] mentioned that an SIS model without demography is based on the assumption that an individual will live forever and is clearly unrealistic. So adding demography makes the SIS model more realistic and stochasticity makes the SIS model more realistic in a different way by adding random fluctuation in the population size, as the birth and death of an individual is a discrete and probabilistic event [92].

Some of the literature has dealt with the stochastic SIS model with demographic stochasticity, for example Lindenstrand and Andersson [83] looked at a two dimensional Markov process and analysed the behaviour of the model close to quasi-stationarity and the time it took for the system to become extinct with the help of a diffusion approximation. On the other hand, Nasell [95] focused on finding approximations of the quasi-stationary distribution and the time to extinction for his SIS model of the form of a bivari-

ate Markov population process with appropriate transition rates. In addition, Nasell also derived an approximation for the expected time to extinction in the stochastic SIR model with demography, where he looked at two SIR models which each vary with a different demographic force.

In this thesis, we have introduced demographic stochasticity using two different ways into the deterministic SIS epidemic model given in Section 1.2 resulting in having two different types of SDE SIS model with demographic stochasticity. We will split the next section into two parts each discussing the two resulting stochastic SIS model with demographic stochasticity.

1.5.1 Stochastic SIS Model with Constant Population Size

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 [10]. 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

$$\frac{dp_0}{dt} = (\mu+\gamma)p_1(t), \tag{1.5.1}$$

$$\frac{dp_i}{dt} = \beta(i-1)(N-i+1)p_{i-1} - \beta i(N-i)p_i + (\mu+\gamma)(i+1)p_{i+1} - (\mu+\gamma)ip_i, \quad 1 \leq i \leq N-1, \tag{1.5.2}$$

$$\frac{dp_N}{dt} = \beta(N-1)p_{N-1} - (\mu+\gamma)Np_N, \tag{1.5.3}$$

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

Allen [1] and Allen [2] outline an alternative approach, namely to consider possible changes Δi in a small time interval Δt and then find the mean change $E(\Delta i)$ as well as $E((\Delta i)^2)$ for the time interval Δt and define

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

Then an SDE is inferred for this process by similarities in the forward Kolmogorov equations between the discrete and continuous stochastic processes [2]

$$dI = (\beta I(N-I) - (\mu+\gamma)I)dt + \sqrt{\beta I(N-I) + (\mu+\gamma)I}\ dW, \tag{1.5.4}$$

where W is a Brownian motion.

We have changed Allen's β to βN for consistency of notation. McCormack and Allen [91] construct an SDE approximation similar to an SIS multihost epidemic model and explore the deterministic and stochastic models numerically.

Most of the classical work on epidemiological models has assumed that the population size remains constant (e.g. [9, 10, 58]). 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 [139].

In Chapter 3, we will look at the SDE SIS model with demographic stochasticity where we have assumed that an infected individual or a susceptible individual who dies is immediately replaced by a susceptible individual or an infected individual and thus the population size is kept constant. This SDE SIS model is an approximation to the continuous time Markov Chain (CTMC) model which has been derived fully in detail in [1]. This model is discussed in detail in Chapter 3, where most of the work has been published in [47].

1.5.2 Stochastic SIS model with Varying Population Size

In the past humans have experienced many diseases that have caused a dramatic impact on the size of populations resulting in disease-related mortality. In this case, 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 [31].

As a result, in Chapter 4, 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 or a susceptible individual who dies is immediately replaced by a susceptible individual or an infected individual and thus the population size will vary with respect to time.

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 [56] 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 [74] 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, Cooke and Pozio [17] 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 [16] analysed global stability for an SIRS epidemic model with vital dynamics in a varying size population. Li et al. [81] 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, where SEIR stands for Susceptible-Exposed-Infected-Removed/Recovery.

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 to,

for example, competition for scarce resources. However in our case, the population size varies due to the effect of demographic stochasticity. This model is discussed in detail in Chapter 4 where most of the work has been published in [48].

1.6 Stochastic SIR/SIRS Model with Environmental Stochasticity

In Chapter 5, we introduce environmental stochasticity into the deterministic SIRS and the SIR models given in Section 1.3.

The dynamics of population systems are often influenced by different types of environmental noise such as the white noise, which has already been studied by various authors (e.g. [36, 40, 89, 90]). Therefore, it is important for us to consider the impact that the environmental noise has on any type of population system model. As an example, let us consider a Lotka-Volterra predator-prey model.

$$\begin{cases} \dot{x}(t) = x(t)(a - by(t)), \\ \dot{y}(t) = y(t)(-c + dx(t)), \end{cases} \tag{1.6.1}$$

where a, b, c and d are positive numbers. It is well-known that in the absence of environmental noise, the population develops periodically (e.g. [61, 114]). However, if there was environmental noise, it could have a huge impact on the behaviour of the population system. In this thesis, we will focus on another type of environmental noise, namely telegraph noise, which is an example of a simple colour noise. Telegraph noise could be demonstrated as changing between two or more regimes of environment, which differ by factors such as rainfalls or nutrition (e.g. [35, 110, 114]). The changing is memoryless and the waiting time follows an exponential distribution. As a result, the switching between two or more regimes of environment could be modelled by a finite-state Markov Chain with state space $\mathbb{S} = \{1, 2, ..., M\}$. There are already various papers which looked at the effect of telegraph noise in a population system model. For example, Takeuchi et al. [115] studied a two-species population system described by (1.6.1) perturbed by the telegraph noise. They have shown that if two equilibrium states of the subsystems differ, all positive trajectories of this system always exit from any compact set of $\mathbb{R}^2_+$ with prob-

ability one. On the other hand, if the two equilibrium states coincide, then the trajectory either leaves from any compact set of $\mathbb{R}^2_+$ or converges to the common equilibrium point. These properties imply that the population system (1.6.1) under the telegraph noise is neither permanent nor dissipative [115]. Du et al. [36] investigated the impact that telegraph noise has on the behaviour of Lotka-Volterra competition systems. The oscillatory behaviour of the solution to the systems with telegraph noise was observed.

Inspired by Takeuchi et al. [115], Gray et al. [41] introduced the effect of telegraph noise into the well-known Susceptible-Infected-Susceptible (SIS) epidemic model [57, 58] using a finite state Markov Chain. The SIS epidemic model is used to model diseases which do not develop immunity once infected individuals recover, for example gonorrhea, meningitis [57] and pneumococcus [77, 84]. Gray et al. [41] established the conditions required for almost sure (a.s.) extinction and persistence for their solution to the stochastic SIS model with finite state Markovian switching. There has been much research done on different aspects of both SIR and SIRS epidemic models already. Tornatore et al. [118] looked at the stability of the SIR model with or without delay, while Lu [87] later extended their results into a SIRS model. Yang et al. [133] looked at the stochastic SIR and SEIR epidemic models with saturated incidence while later Zhao and Jiang [138] also worked with saturated incidence but on the SIRS epidemic model instead. In this thesis, I have focused on applying Markov switching to epidemic models, but it is important to note that there are also other applications of Markov switching, for example on interest rates or on neural networks [42, 109].

Motivated by the work done in [41, 115], we will extend the results given in [41] by introducing the effect of telegraph noise into a more complicated three-dimensional SIRS epidemic model as well as the SIR epidemic model. Note that Wei et al. [124] also looked at the stochastic SIR model under regime switching but their model contains environmental noise and saturated incidence rate which is different to the classic SIRS and SIR models that we will be looking at in this thesis. This model is discussed in detail in Chapter 5 where most of the work has been published in [49].

1.7 Stochastic HIV Model

So far, we have been talking about epidemic modelling using compartmental models. In Chapter 6 we will look at a more specific type of disease namely the HIV virus and the effect of introducing environmental stochasticity on the spread of the HIV amongst a particular risk group, namely people who inject drugs (PWIDs).

HIV, Human Immunodeficiency Virus, is a deadly and infectious lentivirus which attacks and weakens the immune system by especially attacking the CD4 cells. As a result, HIV causes AIDS (Acquired Immune Deficiency Syndrome). Since the first discovery of HIV in 1981, it has already infected almost 78 million people with about 39 million lives having been taken [130]. Despite the massive improvement in technology and medical equipment, we are still unable to fully find a cure for the HIV virus. In 2014, according to the reports by the World Health Organization, there were still approximately 36.9 million people living with HIV, with around 2 million new cases globally [131]. In order to control the epidemic, it is crucial to understand the dynamical behaviour of HIV and how it spreads within our community. There are various routes by which HIV can be transmitted, for example transmission via unprotected sexual intercourse, vertically from infected mothers to their unborn children and people who inject drugs (PWIDs) sharing contaminated needles. Amongst all the possible routes of HIV transmission, PWIDs have become a significant risk group with around 3 million of them living with HIV [132]. For every 10 new cases of HIV infection, on average, one of them is caused by injecting drug use. In regions of Central Asia and Eastern Europe, injecting drug use accounts for 80 percent of HIV infections [132]. As a result, in Chapter 6, we will focus on looking at this particular risk group.

Over the past years, mathematical models have been used successfully to analyse and predict the dynamical behaviour in biological systems. The first mathematical model for the spread of HIV and AIDS amongst PWIDs in shooting galleries was created by Kaplan [66], where a shooting gallery is a place for PWIDs to purchase and inject drugs. Kaplan incorporated many factors into his model such as the injection equipment sharing rate and the effect of cleaning injection equipment in order to better understand how HIV is transmitted within this type of community. Based on the original model created in

[66], Greenhalgh and Hay [43] modified the model by changing some of the assumptions made by Kaplan to make them more realistic. These assumptions include having different visiting rates to the shooting galleries for PWIDs who have been diagnosed positive for the HIV virus and thus may have been advised to stop sharing injections and for those who either are not HIV positive or are but do not know it. The modified Kaplan model in [43] also allows for the possibility that an infected PWID may not always leave a needle infected before cleaning, as well as introducing different transmission probabilities for flushed and unflushed needles. The term "flushing" refers to the process where an infectious piece of injecting equipment is used by an uninfected PWID and thus after injecting the syringe is left uninfected. In other words, it is possible for an infectious needle to become uninfected after getting used by a susceptible PWID by getting rid of the infectious residue with the clean blood during the injecting process. The HIV model that we will be looking at in this paper is based on the modified Kaplan model given in [43]. There have been many papers that have already looked at the connection between the spread of HIV and PWIDs [12, 19, 50, 67, 44, 80]. However the models used are all deterministic models.

HIV infection is a behavioural disease and thus there are many environmental factors that can influence the spread of HIV. Rhodes et. al [106] have mentioned in detail how factors such as injecting environments, social network and neighbourhood deprivation and poverty can affect the spread of HIV amongst PWIDs. There are also other papers which emphasised how the dynamical behaviour of HIV is highly correlated with other factors [34, 54, 112]. Consequently, it is crucial for us to understand how HIV would spread under those environmental influences, especially amongst PWIDs. In this case, a stochastic model would be useful. There is also natural biological variation within people in their response to HIV. Using a stochastic model with environmental perturbation in the disease transmission parameter as we will do is one way to include this.

The stochastic aspects of the HIV model have been studied by many authors. For example, in [29], Dalal, Greenhalgh and Mao considered a stochastic model for internal HIV dynamics. They incorporated environmental stochasticity into their model by using the standard technique of parameter perturbation. They proved that the solution (representing the concentrations of uninfected cells, infected cells and virus particles) is

nonnegative and have looked at the stability aspect of their model by establishing the conditions required in order for the numbers of infected cells and virus particles to tend asymptotically to zero exponentially almost surely. Ding, Xu and Hu [34] looked at a stochastic model for AIDS transmission and control taking into consideration the treatment rate of HIV patients. They have also examined the effect that knowledge, attitude and behaviour of patients have on the spread of AIDS. Tuckwell and Le Corfec [119] used a stochastic model to analyse the behaviour of HIV-1 but focus only on the early stage after infection. Dalal, Greenhalgh and Mao [28] have also used a stochastic model to look at another aspect of HIV. Once again, by using parameter perturbation, they introduced environmental randomness into their HIV model which allows them to examine the effect that condom use has on the spread of AIDS among a homogeneous homosexual population which is split into distinct risk groups according to the tendency of individuals to use condoms. The stochastic aspects of the spread of HIV in particularly for injecting drug users have also been studied by various authors, for example, Peterson et. al [103] constructed a population-based simulation of a community of PWIDs using the Monte-Carlo technique. Similarly, Kretzchmar and Wiessing [127] also used a stochastic simulation model to describe the spread of HIV in a hypothetical population of PWIDs as well as investigating the effect of contact patterns and the frequency of needle sharing have on the spread of HIV in PWIDs. Greenhalgh and Lewis [46] modelled the spread of HIV amongst PWIDs using a set of behavioural assumptions due to Kaplan and O'Keefe [67]. They use a branching process approximation to show that if the basic reproduction number R_0 is less than or equal to unity then the disease will always go extinct. They calculate an expression for the probability of extinction. They discuss an extended model which incorporates a three-stage incubation period and again examine a branching process approximation. They then compare them to investigate whether the deterministic model provides a good approximation to the simulated stochastic model. Although there have been papers that looked at the stochastic aspect of the spread of HIV, as far as we know there are not many studies that focus on the stochastic aspect of the spread of HIV amongst PWIDs despite this particular risk group being responsible for many new HIV cases around the world. Thus it is crucial for us to examine the effect of environmental noise on this type of community.

Inspired by the model constructed in [43], in this thesis we will introduce environmental stochasticity into the model by parameter perturbation which is a standard technique in stochastic population modelling [28, 29, 40, 63]. To the best of our knowledge, this is the first time where the environmental stochasticity has been introduced into the modified Kaplan model [43]. The techniques used in this thesis are inspired by the work done in [40]. The model is discussed in detail in Chapter 6 where most of the work shown has been published in [82].

In this chapter we have introduced and discussed various types of epidemic model that we will be looking at in this thesis as well as discussing some of the work that has already been done on those models. We have discussed various ways in which stochasticity can be introduced into the epidemic models and the advantage of using a stochastic model and thus our motivation for the work carried out in this thesis. In the next chapter we will introduce some of the mathematical properties and results which will be useful throughout the thesis.

Chapter 2

Mathematical Background

This chapter gives an introduction to the properties and theorems for the SDEs as well as Markov switching which will become useful later on in the chapters. There are many books available which include the properties and the applications of SDEs, such as [64, 89, 136]. In this chapter we will talk about the basic probability theory, stochastic processes, Brownian motion, SDE, stability and convergence and stochastic integrals as well as Markov switching.

2.1 Probability Theory

There are many books that are available on probability theory, for example [53, 89, 136]. The materials given in this section is mainly from [89].

A stochastic process is a collection of random variables. In order to understand what a random variable is, we will begin this section by looking at the probability theory, which deals with mathematical models of experiments where the outcomes are random. Let us define Ω to be a set of all possible outcomes from a random experiment. In general, not all subsets of Ω are observable or interesting and thus we will group the subsets that we are interested in and are observable and form a family, $\mathcal{F}$, of subsets of Ω. A family $\mathcal{F}$ which has the following three properties is called a σ-*algebra*:

1. $\emptyset \in \mathcal{F}$,

2. $A \in \mathcal{F} \Rightarrow A^C \in \mathcal{F}$, where $A^C = \Omega - A$,

3. $\{A_i\}_{i\geq 1} \subset \mathcal{F} \Rightarrow \bigcup_{i=1}^{\infty} A_i \in \mathcal{F}$,

where $\emptyset$ denotes the empty set and A^C is the complement of A in Ω. The pair $(\Omega, \mathcal{F})$ is called a *measurable space* and the elements of $\mathcal{F}$ are now called *measurable sets*. If $\mathcal{C}$ is a family of subsets of Ω, then there exists a smallest *σ-algebra* on Ω which contains $\mathcal{C}$. This is denoted by $\sigma(\mathcal{C})$ where it is called the *σ-algebra generated by $\mathcal{C}$*. If $\Omega = \mathbb{R}^d$ and $\mathcal{C}$ is the family of all open sets in $\mathbb{R}^d$, then $\mathcal{B}^d = \sigma(\mathcal{C})$ is called the *Borel σ-algebra* and the elements of $\mathcal{B}^d$ are known as the *Borel sets*. A $\mathcal{B}^d$-measurable function is called a *Borel measurable function* if the measurable space is $(\mathbb{R}^d, \mathcal{B}^d)$.

Let us define a real-valued function X such that $X : \Omega \to \mathbb{R}$. This function is said to be *$\mathcal{F}$-measurable* if

$$\{\omega : X(\omega) \leq b\} \in \mathcal{F}, \quad \text{for all } b \in \mathbb{R}.$$

Such a function X is also called the real-valued ($\mathcal{F}$-measurable) random variable. An $\mathbb{R}^d$-valued function $\mathbf{X}(\omega) = (X_1(\omega), \ldots, X_d(\omega))^T$ is said to be $\mathcal{F}$-measurable if all the elements X_i are $\mathcal{F}$-measurable. Similarly this can be extended to a $n \times m$ matrix-valued function $\mathbf{X}(\omega) = (X_{ij}(\omega))_{n\times m}$ where it is said to be $\mathcal{F}$-measurable if all the elements X_{ij} are $\mathcal{F}$-measurable.

A *probability measure* $\mathbb{P}$ on a measurable space $(\Omega, \mathcal{F})$ is a function $\mathbb{P} : \mathcal{F} \to [0, 1]$ such that

1. $\mathbb{P}(\Omega) = 1$,

2. for any disjoint sequence $\{A_i\}_{i\geq 1} \subset \mathcal{F}$ (i.e. $A_i \cap A_j = \emptyset$ if $i \neq j$)

$$\mathbb{P}\Big(\bigcup_{i=1}^{\infty} A_i\Big) = \sum_{i=1}^{\infty} \mathbb{P}(A_i).$$

The triple $(\Omega, \mathcal{F}, \mathbb{P})$ is called a *probability space*. If $(\Omega, \mathcal{F}, \mathbb{P})$ is a *probability space*, then there exists a σ-algebra, $\bar{\mathcal{F}}$ which is called the *completion* of $\mathcal{F}$ where $\bar{\mathcal{F}}$ is set to be

$$\bar{\mathcal{F}} = \{A \subset \Omega : \exists B, C \in \mathcal{F} \quad \text{such that } B \subset A \subset C, \mathbb{P}(B) = \mathbb{P}(C)\}.$$

If $\mathcal{F} = \bar{\mathcal{F}}$, then the probability space $(\Omega, \mathcal{F}, \mathbb{P})$ is said to be *complete*. Otherwise, $\mathbb{P}$ can be extended to $\bar{\mathcal{F}}$ by defining $\mathbb{P}(A) = \mathbb{P}(B) = \mathbb{P}(C)$ for $A \in \bar{\mathcal{F}}$ where $B, C \in \mathcal{F}$ with the properties that $B \subset A \subset C$ and $\mathbb{P}(B) = \mathbb{P}(C)$. Then $(\Omega, \bar{\mathcal{F}}, \mathbb{P})$ is a complete probability space and is called the *completion* of $(\Omega, \mathcal{F}, \mathbb{P})$.

The *indicator function* $\mathbf{1}_A$ of a set $A \subset \Omega$ is defined by

$$\mathbf{1}_A(\omega) = \begin{cases} 1, & \text{for } \omega \in A, \\ 0, & \text{for } \omega \notin A. \end{cases}$$

The indicator function $\mathbf{1}_A$ is $\mathcal{F}$-measurable if and only if $A \in \mathcal{F}$, i.e. A is an $\mathcal{F}$-measurable set.

Let $(\Omega, \mathcal{F}, \mathbb{P})$ be a probability space. The number

$$\mathbb{E}X = \int_\Omega X(\omega) d\mathbb{P}(\omega)$$

is called the *expectation* of X with respect to $\mathbb{P}$ if X is a real-valued random variable and is *integrable* with respect to the probability measure $\mathbb{P}$. Furthermore, the *variance* of the random variable X is defined as

$$V(X) = \mathbb{E}(X - \mathbb{E}X)^2.$$

For $p > 0$, the term $\mathbb{E}|X|^p$ represents the pth moment of X. Let us define another real-valued random variable, Y, where the *covariance* of the random variables X and Y is given as

$$Cov(X, Y) = \mathbb{E}[(X - \mathbb{E}X)(Y - \mathbb{E}Y)].$$

If $Cov(X, Y) = 0$, then X and Y are said to be *uncorrelated*. The expectation of an $\mathbb{R}^d$-valued random variable $\mathbf{X} = (X_1, \ldots, X_d)^T$ is given as $\mathbb{E}\mathbf{X} = (\mathbb{E}X_1, \ldots, \mathbb{E}X_d)^T$. For a $n \times m$-matrix-valued random variable $\mathbf{X} = (X_{ij})_{n \times m}$, the expectation is defined as $\mathbb{E}\mathbf{X} = (\mathbb{E}X_{ij})_{n \times m}$. The *covariance matrix* for $\mathbf{X}$ and $\mathbf{Y}$ where they are both $\mathbb{R}^d$-valued random variables is given as

$$Cov(\mathbf{X}, \mathbf{Y}) = \mathbb{E}[(\mathbf{X} - \mathbb{E}\mathbf{X})(\mathbf{Y} - \mathbb{E}\mathbf{Y})^T],$$

and it is a symmetric nonnegative definite $d \times d$ matrix.

Let $A, B \in \mathcal{F}$ with $\mathbb{P}(B) > 0$. Then the *conditional probability* of A given the condition of B is

$$\mathbb{P}(A|B) = \frac{\mathbb{P}(A \cap B)}{\mathbb{P}(B)}.$$

Let us now introduce a more general concept of *conditional expectation* as very often we will have a number of conditions. Let $X \in L^1(\Omega, \mathbb{R})$ and $\mathcal{G} \subset \mathcal{F}$ where $\mathcal{G}$ is a sub-σ-algebra of $\mathcal{F}$ and thus $(\Omega, \mathcal{G})$ is a measurable space. In general, X is not $\mathcal{G}$-measurable. We now want to find an integrable $\mathcal{G}$-measurable random variable Y such that it has the same values as X on the average in the sense that

$$\mathbb{E}(\mathbf{1}_G Y) = \mathbb{E}(\mathbf{1}_G X) \quad \text{i.e.} \quad \int_G Y(\omega) d\mathbb{P}(\omega) = \int_G X(\omega) d\mathbb{P}(\omega) \quad \forall G \in \mathcal{G}.$$

By the Radon-Nikodym theorem [22], there exists one such Y, almost surely unique. It is called the *conditional expectation* of X *under the condition* $\mathcal{G}$, and we write this as

$$Y = \mathbb{E}(X|\mathcal{G}).$$

Now that we have covered the basic theorems in probability theory, we will next focus on the main results on stochastic processes.

2.2 Stochastic Processes

The materials given in this section are mainly from [136] and [89].

Let $(\Omega, \mathcal{F}, \mathbb{P})$ be a probability space. The term *filtration* is used to describe a family $\{\mathcal{F}_t\}_{t \geq 0}$ of increasing sub-σ-algebra of $\mathcal{F}$ (i.e. $\mathcal{F}_t \subset \mathcal{F}_s \subset \mathcal{F}$ for all $0 \leq t < s < \infty$). The filtration is said to be *right continuous* if $\mathcal{F}_t = \bigcap_{s>t} \mathcal{F}_s$ for all $t \geq 0$. When the probability space is complete, the filtration is said to satisfy the *usual conditions* if it is right continuous and $\mathcal{F}_0$ contains all $\mathbb{P}$-null sets.

From now on, unless stated otherwise, we shall always work on a given complete probability space $(\Omega, \mathcal{F}, \mathbb{P})$ with a filtration $\{\mathcal{F}_t\}_{t \geq 0}$ satisfying the usual conditions.

A *stochastic process* is a family of $\mathbb{R}^d$-valued random variables $\{X_t\}_{t \in I}$ with parameter set (or index set) I and *state space* $\mathbb{R}^d$, where I is usually the halfline $\mathbb{R}_+ = [0, \infty)$, but

it may also be an interval $[a, b]$, the nonnegative integers or even subsets of $\mathbb{R}^d$. For each fixed $t \in I$, we have a random variable such that

$$\Omega \ni \omega \to X_t(\omega) \in \mathbb{R}^d.$$

On the other hand, for each fixed $\omega \in \Omega$ we have a function

$$I \ni t \to X_t(\omega) \in \mathbb{R}^d,$$

which is known as a *sample path* of the process. We will denote the path by using the notation $X.(\omega)$. Note that sometimes it is easier to use the notation $X(t, \omega)$ instead of $X_t(\omega)$ and the stochastic process may be treated as a function of two variables (t, ω) from $I \times \Omega$ to $\mathbb{R}^d$. We often write a stochastic process $\{X_t\}_{t\geq 0}$ as $\{X_t\}, X_t$ or $X(t)$. Let us define an $\mathbb{R}^d$-valued stochastic process as $\{X_t\}_{t\geq 0}$. Then it is said to be continuous (resp. *right continuous, left continuous*) if for almost all $\omega \in \Omega$, the function $X_t(\omega)$ is continuous (resp. right continuous, left continuous) on $t \geq 0$. If for every $t \geq 0$, X_t is an integrable random variable then $\{X_t\}_{t\geq 0}$ is said to be *integrable*. If for every t, X_t is $\mathcal{F}_t$-measurable, then it is said to be $\{\mathcal{F}_t\}$-*adapted* (or simply, *adapted*). A real-valued stochastic process $\{A_t\}_{t\geq 0}$ is called an *increasing process* if for almost all $\omega \in \Omega$, $A_t(\omega)$ is nonnegative nondecreasing right continuous on $t \geq 0$.

Another important property that is useful when dealing with a stochastic process is *stopping time*. A random variable $\tau : \Omega \to [0, \infty]$ (it is possible to take the value ∞) is called an $\{\mathcal{F}_t\}$-*stopping time* (or simply *stopping time*) if $\{\omega : \tau(\omega) \leq t\} \in \mathcal{F}_t$ for any $t \geq 0$.

A martingale is a stochastic process which originated from betting strategies. An $\mathbb{R}^d$-valued $\{\mathcal{F}_t\}$-adapted integrable process $\{M_t\}_{t\geq 0}$ is called a *martingale with respect to* $\{\mathcal{F}_t\}$ (or simply *martingale*) if

$$\mathbb{E}(M_t|\mathcal{F}_s) = M_s \quad \text{a.s for all } 0 \leq s < t < \infty.$$

In other words, the martingale definition states that the conditional expectation of the next value, given the current and the preceding values is the current value.

Let us define a stochastic process where $X = \{X_t\}_{t\geq 0}$. If $\mathbb{E}|X_t|^2 < \infty$ for every $t \geq 0$, then the stochastic process is said to be *square-integrable*. If $M = \{M_t\}_{t\geq 0}$ is a

real-valued square-integrable continuous martingale, then there exists a unique continuous integrable adapted increasing process denoted by $\{\langle M, M\rangle_t\}$ such that $\{M_t^2 - \langle M, M\rangle_t\}$ is a continuous martingale vanishing at $t = 0$. The process $\{\langle M, M\rangle_t\}$ is known as the *quadratic variation* of M. Note that $\mathbb{E}M_\tau^2 = \mathbb{E}\langle M, M\rangle_\tau$ where τ is any finite stopping time.

Let us define a right continuous adapted process $M = \{M_t\}_{t\geq 0}$. If there exists a nondecreasing sequence $\{\tau_k\}_{k\geq 1}$ of stopping times with $\tau_k \uparrow \infty$ almost surely such that every $\{M_{\tau_k \wedge t} - M_0\}_{t\geq 0}$ is a martingale, then $M = \{M_t\}_{t\geq 0}$ is called a *local martingale*. Every martingale is a local martingale but the opposite is not true.

Theorem 2.2.1 (Strong law of large numbers) *Let $M = \{M_t\}_{t\geq 0}$ be a real-valued continuous local martingale vanishing at $t = 0$. Then*

$$\lim_{t\to\infty} \langle M, M\rangle_t = \infty \quad a.s. \quad \Rightarrow \quad \lim_{t\to\infty} \frac{M_t}{\langle M, M\rangle_t} = 0 \quad a.s.$$

and also

$$\limsup_{t\to\infty} \frac{\langle M, M\rangle_t}{t} < \infty \quad a.s. \quad \Rightarrow \quad \lim_{t\to\infty} \frac{M_t}{t} = 0 \quad a.s.$$

In general, if $A = \{A_t\}_{t\geq 0}$ is a continuous adapted increasing process such that

$$\lim_{t\to\infty} A_t = \infty \quad and \quad \int_0^\infty \frac{d\langle M, M\rangle_t}{(1 + A_t)^2} < \infty \quad a.s.$$

then

$$\lim_{t\to\infty} \frac{M_t}{A_t} = 0 \quad a.s.$$

2.3 Brownian Motion and Stochastic Integrals

The term *Brownian motion* is named after the Scottish botanist Robert Brown, who first observed the random movement of pollen grains suspended in water using a microscope in 1827. However, at that point he could not explain why this occurred. It was not until 1905, when Albert Einstein explained that the pollen grains were being moved by individual water molecules. In mathematics, Brownian motion is described by using the Wiener process which is a continuous-time stochastic process. Most of the materials given in this section can be found in [136] and [89].

2.3.1 Brownian Motion

Let $(\Omega, \mathcal{F}, \mathbb{P})$ be a probability space with a filtration $\{\mathcal{F}_t\}_{t\geq 0}$. A (standard) one-dimensional Brownian motion is a real-valued continuous $\{\mathcal{F}_t\}$-adapted process $\{B_t\}_{t\geq 0}$ satisfying the following properties:

1. $B_0 = 0$ a.s.;
2. for $0 \leq s < t < \infty$, the increment $B_t - B_s$ is normally distributed with mean zero and variance $t - s$;
3. for $0 \leq s < t < \infty$, the increment $B_t - B_s$ is independent of $\mathcal{F}_s$.

In addition, the following results hold for Brownian motion.

- $\{-B_t\}$ is a Brownian motion with respect to the same filtration $\{\mathcal{F}_t\}$.
- Let $c > 0$. For $t \geq 0$, define
$$X_t = \frac{B_{ct}}{\sqrt{c}}.$$
Then $\{X_t\}$ is a Brownian motion with respect to the filtration $\{\mathcal{F}_{ct}\}$.
- $\{B_t\}$ is a continuous square-integrable martingale and its quadratic variation $\langle B, B\rangle_t = t$ for all $t \geq 0$.
- The strong law of large numbers states that
$$\lim_{t\to\infty} \frac{B_t}{t} = 0 \quad \text{a.s.}$$
- For almost every $\omega \in \Omega$, the Brownian sample path $B.(\omega)$ is nowhere differentiable.

A d-dimensional process $\{B_t = (B_t^1, \ldots, B_t^d)\}_{t\geq 0}$ is called a d-dimensional Brownian motion if every $\{B_t^i\}$ is a one-dimensional Brownian motion, and $\{B_t^1, \}, \ldots, \{B_t^d\}$ are independent.

2.3.2 Stochastic Integrals

In this section, we will introduce the stochastic integral. Recall that the Brownian motion sample path is nowhere differentiable and thus the integral cannot be defined in the ordinary way. However we can define the integral for a large class of stochastic processes by making use of the stochastic nature of Brownian motion. As a result, the Japanese mathematician Kiyosi Itô defined the *Itô stochastic integral* to overcome this problem.

Let us define the stochastic integral

$$\int_0^t f(s)dB_s$$

with respect to an m-dimensional Brownian motion $\{B_t\}$ for a class of $n\times m$-matrix-valued stochastic processes $\{f(t)\}$.

Before we begin with the mathematical definition of Itô's integral, let us first introduce the concept of simple processes.

Definition 2.3.1 *A real-valued stochastic process $g = \{g(t)\}_{a\le t\le b}$ is called a simple (or step) process if there exists a partition $a = t_0 < t_1 < \cdots < t_k = b$ of $[a, b]$, and bounded random variable $\xi_i, 0 \le i \le k-1$ such that ξ_i is $\mathcal{F}_{t_i}$-measurable and*

$$g(t) = \xi_0 \mathbf{1}_{[t_0,t_1]}(t) + \sum_{t=1}^{k-1} \xi_i \mathbf{1}_{(t_i,t_{i+1}]}(t). \tag{2.3.1}$$

The notation $\mathcal{M}_0([a, b]; \mathbb{R})$ represents the family of all such processes.

Definition 2.3.2 *Define*

$$\int_a^b g(t)dB_t = \sum_{i=0}^{k-1} \xi_i (B_{t_{i+1}} - B_{t_i}),$$

where g is a simple process in the form of (2.3.1) in $\mathcal{M}_0([a, b]; \mathbb{R})$. This is known as the stochastic integral of g with respect to the Brownian motion $\{B_t\}$ or the Itô's integral.

If the simple process $g \in \mathcal{M}_0([a, b]; \mathbb{R})$, then the following properties hold:

- $\mathbb{E}\int_a^b g(t)dB_t = 0$,
- $\mathbb{E}|\int_a^b g(t)dB_t|^2 = \mathbb{E}\int_a^b |g(t)|^2 dt$.

Furthermore, if $g_1, g_2 \in \mathcal{M}_0([a,b];\mathbb{R})$, let c_1, c_2 be two real numbers. Then $c_1 g_1 + c_2 g_2 \in \mathcal{M}_0([a,b];\mathbb{R})$, and

$$\int_a^b [c_1 g_1(t) + c_2 g_2(t)] dB_t = c_1 \int_a^b g_1(t) dB_t + c_2 \int_a^b g_2(t) dB_t.$$

We will now extend the integral definition from simple processes to processes in $\mathcal{M}^2([a,b];\mathbb{R})$.

Definition 2.3.3 *Let $f \in \mathcal{M}^2([a,b];\mathbb{R})$. The Itô's integral of f with respect to $\{B_t\}$ is defined by*

$$\int_a^b f(t) dB_t = \lim_{n\to\infty} \int_a^b g_n(t) dB_t \quad \text{in } L^2(\Omega, \mathbb{R}),$$

where $\{g_n\}$ is a sequence of simple processes such that

$$\lim_{n\to\infty} \mathbb{E} \int_a^b |f(t) - g_n(t)|^2 dt = 0.$$

The stochastic integral has many useful properties. Let $f, g \in \mathcal{M}^2([a,b];\mathbb{R})$ and let α, β be two real numbers, then the following properties hold for the stochastic integral:

1. $\int_a^b f(t) dB_t$ is $\mathcal{F}_b$-measurable;
2. $\mathbb{E} \int_a^b f(t) dB_t = 0$;
3. $\mathbb{E}| \int_a^b f(t) dB_t|^2 = \mathbb{E}| \int_a^b f(t)|^2 dt$;
4. $\int_a^b |\alpha f(t) + \beta g(t)| dB_t = \alpha \int_a^b f(t) dB_t + \beta \int_a^b g(t) dB_t$.

2.3.3 The Itô Formula

In this section we will begin by introducing the one-dimensional Itô formula. Let $\{B_t\}_{t\geq 0}$ be a one-dimensional Brownian motion defined on the complete probability space $(\Omega, \mathcal{F}, \mathbb{P})$ adapted to the filtration $\{\mathcal{F}_t\}_{t\geq 0}$.

Definition 2.3.4 *A continuous adapted process $x(t)$ on $t \geq 0$ of the form*

$$x(t) = x(0) + \int_0^t f(s) ds + \int_0^t g(s) dB_s,$$

where $f \in \mathcal{L}^1(\mathbb{R}_+, \mathbb{R})$ *and* $g \in \mathcal{L}^2(\mathbb{R}_+, \mathbb{R})$ *is called a one-dimensional Itô process. We say that* $x(t)$ *has stochastic differential* $dx(t)$ *on* $t \geq 0$ *given by*

$$dx(t) = f(t)dt + g(t)dB_t.$$

Let $V \in C^{2,1}(\mathbb{R} \times \mathbb{R}_+, \mathbb{R})$. *Then* $V(x(t), t)$ *is again an Itô process with the stochastic differential given by*

$$dV(x(t),t) = \left[V_t(x(t),t) + V_x(x(t),t)f(t) + \frac{1}{2}V_{xx}(x(t),t)g^2(t)\right]dt + V_x(x(t),t)g(t)dB_t \quad a.s.$$

The above definition for the one-dimensional Itô formula can be generalised and extended to the multi-dimensional case. Let $\mathbf{B}(\mathbf{t}) = (B_1(t), \ldots, B_m(t))^T, t \geq 0$ be an m-dimensional Brownian motion defined on the complete probability space $(\Omega, \mathcal{F}, \mathbb{P})$ adapted to the filtration $\{\mathcal{F}_t\}_{t\geq 0}$.

Definition 2.3.5 *An* $\mathbb{R}^d$*-valued continuous adapted process* $\mathbf{x}(\mathbf{t}) = (x_1(t), \ldots, x_d(t))^T$ *on* $t \geq 0$ *of the form*

$$\mathbf{x}(t) = x(0) + \int_0^t \mathbf{f}(s)ds + \int_0^t \mathbf{g}(s)d\mathbf{B}(s),$$

where $\mathbf{f} = (f_1, \ldots, f_2)^T \in \mathcal{L}^1(\mathbb{R}_+, \mathbb{R}^d)$ *and* $\mathbf{g} = (g_{ij})_{d\times m} \in \mathcal{L}^2(\mathbb{R}_+, \mathbb{R}^{d\times m})$ *is called a* d*-dimensional Itô process. We say that* $\mathbf{x}(t)$ *has stochastic differential* $d\mathbf{x}(t)$ *on* $t \geq 0$ *given by*

$$d\mathbf{x}(t) = \mathbf{f}(t)dt + \mathbf{g}(t)d\mathbf{B}(t).$$

Let $V \in C^{2,1}(\mathbb{R}^d \times \mathbb{R}_+, \mathbb{R})$. *Then* $V(\mathbf{x}(t), t)$ *is again an Itô process with the stochastic differential given by*

$$\begin{aligned} dV(\mathbf{x}(t),t) &= \left[V_t(\mathbf{x}(t),t) + V_x(\mathbf{x}(t),t)\mathbf{f}(t) + \frac{1}{2}trace(\mathbf{g}^T(t)V_{xx}(\mathbf{x}(t),t)\mathbf{g}(t))\right]dt \\ &\quad + V_x(\mathbf{x}(t),t)\mathbf{g}(t)d\mathbf{B}(t) \quad a.s. \end{aligned}$$

2.4 Stochastic Differential Equations

In this section, we will introduce some of the main results for SDEs given in [89]. Let $(\Omega, \mathcal{F}, \mathbb{P})$ be a complete probability space with a filtration $\{\mathcal{F}_t\}_{t\geq 0}$ satisfying the usual conditions. Let $\mathbf{B}(t) = (B_1(t), \ldots, B_m(t))^T, t \geq 0$ be a m-dimensional Brownian motion

defined on the space. Let $0 \leq t_0 < T < \infty$. Let x_0 be an $\mathcal{F}_{t_0}$-measurable $\mathbb{R}^d$-valued random variable such that $\mathbb{E}|x_0|^2 < \infty$. Let $f : \mathbb{R}^d \times [t_0, T] \to \mathbb{R}^d$ and $g : \mathbb{R}^d \times [t_0, T] \to \mathbb{R}^{d\times m}$ be both Borel measurable. Consider the d-dimensional stochastic differential equation of Itô type

$$dx(t) = f(x(t), t)dt + g(x(t), t)d\mathbf{B}(t), \quad \text{on } t_0 \leq t \leq T \tag{2.4.1}$$

with initial value $x(t_0) = x_0$. By the definition of the stochastic differential, (2.4.1) is the same as the following stochastic integral equation:

$$x(t) = x_0 + \int_{t_0}^{t} f(x(s), s)ds + \int_{t_0}^{t} g(x(s), s)d\mathbf{B}(s), \quad \text{on } t_0 \leq t \leq T. \tag{2.4.2}$$

One of the most important and useful properties for SDEs is the conditions that ensure the existence and uniqueness of the solution to the SDE given by (2.4.1). Before we begin, it is important that we understand what we mean by solution.

Definition 2.4.1 *If an $\mathbb{R}^d$-valued stochastic process $\{x(t)\}_{t_0\leq t\leq T}$ has the following properties, then it is called a solution of equation (2.4.1):*

- *$\{x(t)\}$ is continuous and $\mathcal{F}_t$-adapted;*
- *$\{f(x(t), t)\} \in \mathcal{L}^1([t_0, T]; \mathbb{R}^d)$ and $\{g(x(t), t)\} \in \mathcal{L}^2([t_0, T]; \mathbb{R}^{d\times m})$;*
- *equation (2.4.2) holds for every $t \in [t_0, T]$ with probability one.*

A solution $\{x(t)\}$ is said to be unique if any other solution $\{\hat{x}(t)\}$ is indistinguishable from $\{x(t)\}$, that is

$$\mathbb{P}\{x(t) = \hat{x}(t) \quad \text{for all } t_0 \leq t \leq T\} = 1.$$

A solution is called a *strong* solution if the probability space $(\Omega, \mathcal{F}, \mathbb{P})$, the filtration $\{\mathcal{F}_t\}_{t\geq 0}$, the Brownian motion $B(t)$ and the coefficients $f(x, t), g(x, t)$ are all provided in advance and then the solution $x(t)$ is constructed. On the other hand, a solution is called a *weak* solution if only the coefficients $f(x, t)$ and $g(x, t)$ are given and we are allowed to construct a suitable probability space, a filtration, a Brownian motion and obtain a solution to the equation. If two weak solutions found under whatever probability space with a filtration and a Brownian motion are indistinguishable, then we say that *pathwise uniqueness* holds for the equation (2.4.1). The next theorem is obtained from [89].

Theorem 2.4.2 *Assume there exist two positive constants K_1 and K_2. Then there exists a unique solution $x(t)$ to the SDE (2.4.1) and the solution belongs to $\mathcal{M}^2([t_0,T],\mathbb{R}^d)$ if it satisfies the (uniform) Lipschitz condition and the linear growth condition given below respectively:*

1. *for all $x,y\in\mathbb{R}^d$ and $t\in[t_0,T]$*

$$|f(x,t)-f(y,t)|^2\vee|g(x,t)-g(y,t)|^2\leq K_1|x-y|^2, \tag{2.4.3}$$

2. *for all $(x,t)\in\mathbb{R}^d\times[t_0,T]$*

$$|f(x,t)|^2\vee|g(x,t)|^2\leq K_2(1+|x|^2). \tag{2.4.4}$$

There are some restrictions when using the (uniform) Lipschitz condition especially for functions which have discontinuities in them. As a result, we have the following theorem where the (uniform) Lipschitz condition is replaced by a less restrictive local Lipschitz condition. The next theorem is obtained from [64].

Theorem 2.4.3 *Assume that the linear growth condition (2.4.4) holds but $f(x)$ and $g(x)$ are now locally Lipschitz continuous, i.e. for every integer $n\geq 1$, there exists a positive constant K_n such that for all $t\in[t_0,T]$ and all $x,y\in\mathbb{R}^d$ with $|x|\vee|y|\leq n$,*

$$|f(x,t)-f(y,t)|^2\vee|g(x,t)-g(y,t)|^2\leq K_n|x-y|^2. \tag{2.4.5}$$

Then there exists a unique pathwise solution $x(t)$ to the SDE (2.4.1) in $\mathcal{M}^2([t_0,T],\mathbb{R}^d)$.

The localised Lipschitz condition for the pathwise uniqueness of solutions given above can be simplified in the one-dimensional case as shown below. Note that the following theorem is obtained from [64].

Theorem 2.4.4 *Suppose $f(x)$ and $g(x)$ are bounded. Assume further that the following conditions are satisfied:*

1. *there exists an increasing and concave function $\kappa(u)$ on $[0,\infty)$ such that $\kappa(0)=0$, $\int_{0^+}\kappa^{-1}(u)du=\infty$ and $|f(x)-f(y)|\leq\kappa(|x-y|)$ for all $x,y\in\mathbb{R}$ and $t\in[t_0,T]$,*

2. *there exists a strictly increasing function* $\rho(u)$ *on* $[0,\infty)$ *such that* $\rho(0)=0$, $\int_{0^+}\rho^{-2}(u)du=\infty$ *and* $|g(x)-g(y)|\le\rho(|x-y|)$ *for all* $x,y\in\mathbb{R}$ *and* $t\in[t_0,T]$.

Then the solution is pathwise unique for the SDE (2.4.1).

If $g(x)$ is Hölder continuous with exponent $1/2$ and $f(x)$ is Lipschitz continuous, then the pathwise uniqueness of solutions holds for the SDE (2.4.1) in the one-dimensional case.

We will now introduce the useful *Martingale Representation Theorem*. Let $(\Omega,\mathcal{F},\mathbb{P})$ be a complete probability space and $B(t)$ be an m-dimensional Brownian motion on it without filtration. Let $\{\mathcal{F}_t^B\}_{t\ge0}$ be the natural filtration generated by the Brownian motion, i.e. $\mathcal{F}_t^B=\sigma\{B(s):0\le s\le t\}$. Let $\{\mathcal{F}_t\}_{t\ge0}$ be the augmentation under $\mathbb{P}$ of this natural filtration. Then $\{\mathcal{F}_t\}_{t\ge0}$ is a filtration on $(\Omega,\mathcal{F},\mathbb{P})$ satisfying the usual conditions and $B(t)$ is a Brownian motion with respect to the filtration. The *martingale representation theorem* states that any continuous square-integrable martingale with respect to $\{\mathcal{F}_t\}$ can be represented as an Itô integral.

Theorem 2.4.5 *Let* $T>0$ *and* $\{\mathcal{M}_t\}_{0\le t\le T}$ *be a continuous* $\mathbb{R}^d$*-valued square-integrable martingale with respect to* $\{\mathcal{F}_t\}$*. Then there is a unique stochastic process* $f\in\mathcal{M}^2([0,T];\mathbb{R}^{d\times m})$ *such that*

$$M_t=M_0+\int_0^t f(s)dB(s)\quad \text{on } t\in[0,T].$$

By uniqueness we mean that if there is any other process $g\in\mathcal{M}^2([0,T];\mathbb{R}^{d\times m})$ *such that*

$$M_t=M_0+\int_0^t g(s)dB(s)\quad \text{on } t\in[0,T],$$

then

$$\mathbb{E}\int_0^T|f(s)-g(s)|^2ds=0.$$

2.5 Stability of the Solution

Another important property for a system to have is the stability of the solution. The term "stability" refers to the insensitivity of the system to small changes in the initial state

or the parameter of the systems. For a stable system, the trajectories which are "close" to each other at a particular point should remain close to each other at all subsequent instants. In this section, we will recall some of the important types of stability which will be useful in this thesis. Most of the materials mentioned in this section can be found in [89].

Let us consider a d-dimensional SDE given as in (2.4.1). Let us assume that the assumptions of the existence and uniqueness conditions given in Theorem 2.4.2 are satisfied. For any given initial value $x(t_0) = x_0 \in \mathbb{R}^d$, (2.4.1) has a unique global solution $x(t, t_0, x_0)$. We know that the solution has continuous sample paths and every moment is finite. Let us also assume that for all $t \geq t_0$,

$$f(0, t) = 0 \quad \text{and} \quad g(0, t) = 0.$$

Thus (2.4.1) has solution $x \equiv 0$ corresponding to the initial value $x_0 = 0$, which is the *trivial solution* or *equilibrium point*.

We will split this section into three parts, each describing a type of stability for the solution.

2.5.1 Stability in Probability

(a) If for every pair of $\varepsilon \in (0, 1)$ and $r > 0$, there exists a $\delta = \delta(\varepsilon, r, t_0) > 0$ such that

$$\mathbb{P}\{|x(t, t_0, x_0)| < r, \forall t \geq t_0\} \geq 1 - \varepsilon,$$

whenever $|x_0| < \delta$, then the trivial solution of the SDE (2.4.1) is *stochastically stable* or *stable in probability*. Otherwise, it is said to be *stochastically unstable*.

(b) If the trivial solution is stochastically stable and for every $\varepsilon \in (0, 1)$ there exists $\delta_0 = \delta_0(\varepsilon, t_0) > 0$ such that

$$\mathbb{P}\{\lim_{t \to \infty} x(t, t_0, x_0) = 0\} \geq 1 - \varepsilon,$$

whenever $|x_0| < \delta_0$, then the trivial solution is said to be *stochastically asymptotically stable*.

(c) If the trivial solution is stochastically stable and for all $x_0 \in \mathbb{R}^d$,

$$\mathbb{P}\{\lim_{t \to \infty} x(t, t_0, x_0) = 0\} = 1,$$

then it is said to be *stochastically asymptotically stable in the large*.

2.5.2 Almost Sure Exponential Stability

The trivial solution of (2.4.1) is said to be *almost surely exponentially stable* if

$$\limsup_{t\to\infty} \frac{1}{t} \log |x(t, t_0, x_0)| < 0, \quad \text{a.s.}$$

for all $x_0 \in \mathbb{R}^d$.

2.5.3 Moment Exponential Stability

In this section we will always let $p > 0$. The trivial solution of (2.4.1) is said to be *pth moment exponentially stable* if there is a pair of positive constants λ and C such that for all $x_0 \in \mathbb{R}^d$,

$$\mathbb{E}|x(t, t_0, x_0)|^p \leq C|x_0|^p e^{-\lambda(t-t_0)} \quad \text{on } t \geq t_0.$$

When $p = 2$, it is usually said to be *exponentially stable in mean square*.

The pth moment exponential stability means that the pth moment of the solution will tend to zero exponentially fast. From the above definition, we also have that

$$\limsup_{t\to\infty} \frac{1}{t} \log(\mathbb{E}|(x(t, t_0, x_0)|^p) < 0. \tag{2.5.1}$$

The left hand side of (2.5.1) is called the *pth moment Lyapunov exponent*. Therefore in this case, the pth moment Lyapunov exponent is negative.

2.6 Numerical Approximation

Recall in Section 2.4 we have defined the existence and uniqueness conditions required for the solution to the SDE (2.4.1), however sometimes it is not always possible to solve (2.4.1) exactly and obtain explicit solutions. As a result, we would need to approximate the solution numerically. All the simulations that are produced in this thesis are carried out using R. In this section we will give the definitions of some of the useful schemes which we could use to approximate a solution as well as their rate of convergence [60].

But first we shall remind the reader of the Euler method which is used to numerically integrate ordinary differential equations (ODEs).

Definition 2.6.1 (Euler Method) *Let us define a differential equation*

$$\frac{dx(t)}{dt} = f(x,t)$$

with initial condition $x(0) = x_0$. Sometimes it is not always possible to find the exact solution and thus numerical method would be useful to approximate the solution instead. One way to approximate the solution is by using the Euler method. Let us choose a value h for the step size and set $t_n = t_0 + nh$, then

$$x_{n+1} = x_n + hf(x_n, t_n),$$

where x_n is an approximation of the solution to the differential equation at time t_n.

Now we return to stochastic differential equations.

Definition 2.6.2 (Euler-Maruyama) *Let us divide a time interval $[0,T]$ into N subintervals by setting $\Delta t = T/N$ and $t_n = n\Delta t = n\frac{T}{N}$ where $n = 0, \ldots, N$. Let us also define $x(t_0) = x_0$, then*

$$x_{n+1} = x_n + f(x_n, t_n)\Delta t + g(x_n, t_n)\Delta W_n$$

where $\Delta W_n = W(t_{n+1}) - W(t_n)$.

Definition 2.6.3 (Milstein) *Let us divide a time interval $[0,T]$ into N subintervals by setting $\Delta t = T/N$ and $t_n = n\Delta t = n\frac{T}{N}$ where $n = 0, \ldots, N$. Let us also define $x(t_0) = x_0$, then*

$$x_{n+1} = x_n + f(x_n, t_n)\Delta t + g(x_n, t_n)\Delta W_n + \frac{1}{2}g(x_n, t_n)g'(x_n, t_n)((\Delta W_n)^2 - \Delta t)$$

where $\Delta W_n = W(t_{n+1}) - W(t_n)$ and g' denotes the first derivative of $g(x)$ with respect to x.

Note that the Euler-Maruyama method and the Milstein method mentioned above do not preserve positivity in solution. However, sometimes it might be useful to work with a numerical scheme that does preserve positivity. As a result, for the purpose of completion, we will mention one of the positive preserving numerical schemes. More details can be found in [104, 107].

Definition 2.6.4 (Balancing Implicit Method) *By using the same notations as before, the integration scheme for the Balancing Implicit Method (BIM) is given as follows:*

$$x_{n+1} = x_n + f(x_n)\Delta t + g(x_n)\Delta W + (x_n - x_{n+1})C_n(x_n),$$

$$C_n(x_n) = c_0(x_n)\Delta + c_1(x_n)|\Delta W|,$$

where c_0 and c_1 are the control functions which must be bounded and have to satisfy

$$1 + c_0(x_n)\Delta t + c_1(x_n)|\Delta W| > 0.$$

2.7 Order of Convergence

Definition 2.7.1 (Strong Convergence) *A numerical method is said to have an order of strong convergence equal to α if there exists a constant C such that*

$$\mathbb{E}|X_n - X(\tau)| \leq C\Delta t^{\alpha}, \tag{2.7.1}$$

where $\tau = n\Delta t \in [0, T]$ and Δt is sufficiently small. In other words, (2.7.1) measures the rate at which the mean of the error decays as $\Delta t \to 0$.

Definition 2.7.2 (Weak Convergence) *A numerical method is said to have an order of weak convergence equal to α if there exists a constant C such that for all functions f in some class*

$$|\mathbb{E}f(X_n) - \mathbb{E}f(X(\tau))| \leq C\Delta t^{\alpha}, \tag{2.7.2}$$

at any fixed $\tau = n\Delta t \in [0, T]$ and where Δt is sufficiently small. In other words (2.7.2) measures the rate of decay of the error of the means as $\Delta t \to 0$.

It is well known that the Euler-Maruyama method has a strong convergence rate of order 1/2 but a weak convergence rate of order 1, while the Milstein method has a strong and a weak convergence rate of order 1.

2.8 Markov Processes and Markov Chains

The results shown in this section are mainly obtained from [89] and [136].

If the following *Markov property* is satisfied then a d-dimensional $\mathcal{F}_t$-adapted process $\{X(t)\}_{t\geq 0}$ is called a *Markov process*: for all $0 \leq s \leq t < \infty$ and $A \in \mathcal{B}(\mathbb{R}^n)$,

$$\mathbb{P}(X(t) \in A|\mathcal{F}_s) = \mathbb{P}(X(t) \in A|X(s)). \tag{2.8.1}$$

The Markov property means that given a Markov process, the past and the future are independent when the present is known. One of the equivalent formulations of the Markov property is as follows: for any bounded Borel measurable function $\varphi : \mathbb{R}^n \to \mathbb{R}$ and $0 \leq s \leq t < \infty$,

$$\mathbb{E}(\varphi(X(t))|\mathcal{F}_s) = \mathbb{E}(\varphi(X(t))|X(s)). \tag{2.8.2}$$

The *transition probability or function* of the Markov process is a function $\mathbb{P}(s, x; t, A)$, defined on $0 \leq s \leq t < \infty, x \in \mathbb{R}^n$ and $A \in \mathcal{B}(\mathbb{R}^n)$, with the following properties:

1. For every $0 \leq s \leq t < \infty$ and $A \in \mathcal{B}(\mathbb{R}^n)$,

$$\mathbb{P}(s, X(s); t, A) = \mathbb{P}(X(t) \in A|X(s)).$$

2. $\mathbb{P}(s, x; t, \cdot)$ is a probability measure on $\mathcal{B}(\mathbb{R}^n)$ for every $0 \leq s \leq t < \infty$ and $x \in \mathbb{R}^n$.

3. $\mathbb{P}(s, \cdot; t, A)$ is Borel measurable for every $0 \leq s \leq t < \infty$ and $A \in \mathcal{B}(\mathbb{R}^n)$.

4. The Kolmogorov-Chapman equation

$$\mathbb{P}(s, x; t, A) = \int_{\mathbb{R}^n} \mathbb{P}(u, y; t, A)\mathbb{P}(s, x; u, dy)$$

holds for any $0 \leq s \leq u \leq t < \infty, x \in \mathbb{R}^n$ and $A \in \mathcal{B}(\mathbb{R}^n)$.

A Markov process $X = \{X(t)\}_{t\geq 0}$ is said to be *homogeneous* with respect to time if its transition probability $\mathbb{P}(s, x; t, A)$ is stationary, i.e.

$$\mathbb{P}(s + u, x; t + u, A) = \mathbb{P}(s, x; t, A)$$

for all $0 \leq s \leq t < \infty, x \in \mathbb{R}^n, u \geq 0$ and $A \in \mathcal{B}(\mathbb{R}^n)$.

A n-dimensional process $\{X_t\}_{t\geq 0}$ is called a *strong Markov process* if the following *strong Markov property* holds: for any bounded Borel measurable function $\varphi : \mathbb{R}^n \to \mathbb{R}$, any finite $\{\mathcal{F}_t\}$-stopping time τ and $t \geq 0$,

$$\mathbb{E}(\varphi(X(t + \tau))|\mathcal{F}_\tau) = \mathbb{E}(\varphi(X(t + \tau))|X(\tau)).$$

In the homogeneous case, the above expression becomes

$$\mathbb{E}(\varphi(X(t+\tau))|\mathcal{F}_\tau) = \mathbb{E}_{X(\tau)}\varphi(X(t)).$$

A stochastic process $X = \{X(t)\}_{t\geq 0}$ defined on a probability space $(\Omega, \mathcal{F}, \mathbb{P})$, with values in a countable set Ξ (to be called the *state space* of the process), is called a *continuous-time Markov chain* if for any finite set $0 < t_1 < t_2 < \cdots < t_n \leq t_{n+1}$ of "times", and corresponding set $i_1, i_2, \ldots, i_{n-1}, i, j$ of states in Ξ such that $\mathbb{P}\{X(t_n) = i, X(t_{n-1}) = i_{n-1}, \ldots, X(t_1) = i_1\} > 0$, then we have that

$$\begin{aligned}\mathbb{P}\{X(t_{n+1}) = j|X(t_n) = i, X(t_{n-1}) = i_{n-1}, \ldots, X(t_1) = i_1\} \\ = \mathbb{P}\{X(t_{n+1}) = j|X(t_n) = i\}. \qquad (2.8.3)\end{aligned}$$

The process $X = \{X(t)\}_{t\geq 0}$ is *homogeneous* if for all s, t such that $0 \leq s \leq t < \infty$ and all $i, j \in \Xi$, the conditional probability $\mathbb{P}\{X(t) = j|X(s) = i\}$ depends only on $t - s$. Then in the homogeneous case, $\mathbb{P}\{X(t) = j|X(s) = i\} = \mathbb{P}\{X(t-s) = j|X(0) = i\}$ and the *transition function* or *transition probability* of the process is given as

$$P_{ij}(t) =: \mathbb{P}\{X(t) = j|X(s) = i\}, \quad i, j \in \Xi, t \geq 0,$$

where $P_{ij}(t)$ is called *standard* if $\lim_{t\to 0} P_{ii}(t) = 1$ for all $i \in \Xi$.

Let $P_{ij}(t)$ be a standard transition function, then $\gamma_i = \lim_{t\to 0}[1 - P_{ii}(t)]/t$ exists (but may be ∞) for all $i \in \Xi$. Furthermore, if we let j be a stable state then $\gamma_{ij} = P'_{ij}(0)$ exists and is finite for all $i \in \Xi$. A state $i \in \Xi$ is *stable* if $\gamma_i < \infty$.

Let $\gamma_{ii} = -\gamma_i$ and $\Gamma = (\gamma_{ij})_{i,j\in\Xi}$ where Γ is called the *generator* of the Markov chain. Let us define a *finite* state space $\mathbb{S} = \{1, 2, \ldots, N\}$, then the process is a continuous-time *finite* Markov chain. Unless stated otherwise, from now on we assume that all Markov chains are finite and all states are stable. For this type of Markov chain, almost every sample path is a right continuous step function.

Theorem 2.8.1 *Let $P(t) = (P_{ij}(t))_{N\times N}$ be the transmission probability matrix and $\Gamma = (\gamma_{ij})_{N\times N}$ be the generator of a finite Markov chain. Then*

$$P(t) = e^{t\Gamma}.$$

Note that a continuous-time Markov chain $X(t)$ with generator $\Gamma = \{\gamma_{ij}\}_{N\times N}$ can be represented as a stochastic integral with respect to a Poisson random measure. Let Δ_{ij} be consecutive, left closed, right open intervals of the real line each having length γ_{ij} such that

$$\begin{aligned}
\Delta_{12} &= [0, \gamma_{12}), \\
\Delta_{13} &= [\gamma_{12}, \gamma_{12} + \gamma_{13}), \\
&\vdots \\
\Delta_{1N} &= \left[\sum_{j=2}^{N-1} \gamma_{1j}, \sum_{j=2}^{N} \gamma_{1j}\right), \\
\Delta_{21} &= \left[\sum_{j=2}^{N} \gamma_{1j}, \sum_{j=2}^{N} \gamma_{1j} + \gamma_{21}\right), \\
\Delta_{23} &= \left[\sum_{j=2}^{N} \gamma_{1j} + \gamma_{21}, \sum_{j=2}^{N} \gamma_{1j} + \gamma_{21} + \gamma_{23}\right), \\
&\vdots \\
\Delta_{2N} &= \left[\sum_{j=2}^{N} \gamma_{1j} + \sum_{j=1, j\neq 2}^{N-1} \gamma_{2j}, \sum_{j=2}^{N} \gamma_{1j} + \sum_{j=1, j\neq 2}^{N} \gamma_{2j}\right),
\end{aligned} \tag{2.8.4}$$

and so on. Let us define a function

$$h(i, y) = \begin{cases} j - i & \text{if } y \in \Delta_{ij}, \\ 0 & \text{otherwise,} \end{cases}$$

where $h : \mathbb{S} \times \mathbb{R} \to \mathbb{R}$. Then

$$dX(t) = \int_{\mathbb{R}} h(X(t), y)\upsilon(dt, dy),$$

with initial condition $X(0) = i_0$ where $\upsilon(dt, dy)$ is a Poisson random measure with intensity $dt \times \mu(dy)$, in which μ is the Lebesgue measure on $\mathbb{R}$.

2.8.1 The Generalised Itô's Formula

Let $(\Omega, \mathcal{F}, \{\mathcal{F}\}_{t\geq 0}, \mathbb{P})$ 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 $B(t) = (B_t^1, \ldots, B_t^m)^T$ be an m-dimensional Brownian motion defined on the probability space. Let $r(t), t \geq 0$ be a right-continuous Markov chain on the probability space taking values in a finite state space $\mathbb{S} = \{1, 2, \ldots, N\}$ with generator $\Gamma = (\gamma_{ij})_{N\times N}$ given by

$$\mathbb{P}\{r(t+\delta) = j | r(t) = i\} = \begin{cases} \gamma_{ij}\delta + o(\delta) & \text{if } i \neq j, \\ 1 + \gamma_{ii}\delta + o(\delta) & \text{if } i = j, \end{cases}$$

where $\delta > 0$. Here if $i \neq j$, then $\gamma_{ij} \geq 0$ is the transition rate from i to j, while

$$\gamma_{ii} = -\sum_{i \neq j} \gamma_{ij}.$$

We assume that the Markov chain $r(\cdot)$ is independent of the Brownian motion $B(\cdot)$.

Let $x(t)$ be a d-dimensional Itô process on $t \geq 0$ with the SDE

$$dx(t) = f(t)dt + g(t)dB(t),$$

where $f \in \mathcal{L}^1(\mathbb{R}_+; \mathbb{R}^d)$ and $g \in \mathcal{L}^2(\mathbb{R}_+; \mathbb{R}^{d\times m})$. By using the results on the Itô formula given in Section 2.3.3, we know that a $\mathcal{C}^{2,1}(\mathbb{R}^d \times \mathbb{R}_+; \mathbb{R}_+)$-function V maps the Itô process $x(t)$ into another Itô process $V(x(t), t)$. Nonetheless we will consider the paired process $(x(t), r(t))$ and we need to know how a function $V : \mathbb{R}^d \times \mathbb{R}_+ \times \mathbb{S} \to \mathbb{R}$ will map this paired process into another process $V(x(t), t, r(t))$. In this case, let us denote the family of all real-valued functions $V(x, t, i)$ on $\mathbb{R}^d \times \mathbb{R}_+ \times \mathbb{S}$ which are continuously twice differentiable in x and once in t by $\mathcal{C}^{2,1}(\mathbb{R}^d \times \mathbb{R}_+ \times \mathbb{S}; \mathbb{R})$. If $V \in \mathcal{C}^{2,1}(\mathbb{R}^d \times \mathbb{R}_+ \times \mathbb{S}; \mathbb{R})$, let us define an operator LV from $\mathbb{R}^d \times \mathbb{R}_+ \times \mathbb{S}$ to $\mathbb{R}$ such that

$$\begin{aligned} LV(x,t,i) &= V_t(x,t,i) + V_x(x,t,i)f(t) \\ &+ \frac{1}{2}trace[g^T(t)V_{xx}(x,t,i)g(t)] + \sum_{j=1}^{N} \gamma_{ij}V(x,t,j), \end{aligned} \tag{2.8.5}$$

where

$$V_t(x,t,i) = \frac{\partial V(x,t,i)}{\partial t}, \qquad V_x(x,t,i) = \left(\frac{\partial V(x,t,i)}{\partial (x_1)}, \ldots, \frac{\partial V(x,t,i)}{\partial x_d}\right),$$

and

$$V_{xx}(x,t,i) = \left(\frac{\partial^2 V(x,t,i)}{\partial x_i \partial x_j}\right)_{d\times d}.$$

Let us now introduce the useful generalised Itô formula which reveals how V maps the paired process $(x(t), r(t))$ into a new process $V(x(t), t, r(t))$.

Theorem 2.8.2 *If $V \in \mathcal{C}^{2,1}(\mathbb{R}^d \times \mathbb{R}_+ \times \mathbb{S}; \mathbb{R})$, then for any $t \geq 0$*

$$\begin{aligned} V(x(t), t, r(t)) &= V(x(0), 0, r(0)) + \int_0^t LV(x(s), s, r(s))ds \\ &+ \int_0^t V_x(x(s), s, r(s))g(x(s), s, r(s))dB(s) \\ &+ \int_0^t \int_{\mathbb{R}} (V(x(s), s, i_0 + h(r(s), l)) \\ &\quad - V(x(s), s, r(s))\mu(ds, dl), \end{aligned} \tag{2.8.6}$$

where the function h is defined as in Section 2.8 and $\mu(ds, dl) = \upsilon(ds, dl) - \mu(dl)ds$ is a martingale measure while υ and μ have been defined in the end of Section 2.8.

2.9 Other Useful Properties

In this section we will mention some of the useful properties and theorems which we use in this thesis. The materials given in this section can be found in [89].

Theorem 2.9.1 *(Gronwall inequality) Let $T > 0$ and $c \geq 0$. Let $u(\cdot)$ be a Borel measurable bounded nonnegative function on $[0, T]$, and let $v(\cdot)$ be a nonnegative integrable function on $[0, T]$. If*

$$u(t) \leq c + \int_0^t v(s)u(s)ds, \quad \textit{for all } 0 \leq t \leq T,$$

then

$$u(t) \leq c \exp \int_0^t v(s)ds, \quad \textit{for all } 0 \leq t \leq T.$$

2.9.1 Square Root Process

The purpose of this section is to give the readers the basic framework and idea for which the work in Theorem 3.3.3 in Chapter 3 is based on. The detailed workings are given in Theorem 3.3.3. Let us consider the square root process

$$dS(t) = \lambda S(t)dt + \sigma\sqrt{S(t)}dB(t). \tag{2.9.1}$$

If equation (2.9.1) becomes negative then the term $\sqrt{S(t)}$ would become a complex number and thus this would not make sense in modelling a population dynamic system.

Therefore we will show that this is not possible. This nonnegative property is clearly the equivalent to the solution of equation

$$dS(t) = \lambda S(t)dt + \sigma\sqrt{|S(t)|}dB(t) \tag{2.9.2}$$

never becoming negative as long as the initial value $S_0 \geq 0$. Let $a_0 = 1$ and $a_k = e^{-k(k+1)/2}$ for every integer $k \geq 1$. Note that

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

Let $\varphi_k(u)$ be a continuous function such that its support is contained in the interval (a_k, a_{k-1}) where $0 \leq \varphi_k(u) \leq 2/ku$ and

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

Such a function exists. Define $\varphi_k(x) = 0$ for $x \geq 0$ and for $x < 0$,

$$\varphi_k(x) = \int_0^{-x} dy \int_0^y \varphi_k(u)du.$$

It is easy to see that $\varphi_k \in \mathcal{C}^2(\mathbb{R}, \mathbb{R})$,

$$-1 \leq \varphi_k'(x) \leq 0, \quad \text{if } -\infty < x < -a_k \quad \text{or otherwise } \varphi_k'(x) = 0,$$

$$|\varphi_k''(x)| \leq \frac{2}{k|x|}, \quad \text{if } -a_{k-1} < x < -a_k \quad \text{or otherwise } \varphi_k''(x) = 0.$$

In addition, for all $x \in \mathbb{R}$,

$$x^- - a_{k-1} \leq \varphi_k(x) \leq x^-,$$

where $x^- = -x$ if $x < 0$ or otherwise $x^- = 0$. For any $t \geq 0$, by the Itô formula we have that

$$\begin{aligned}
\varphi_k(S(t)) &= \varphi_k(S_0) + \int_0^t \left[\lambda S(r)\varphi_k'(S(r)) + \frac{\sigma^2}{2}|S(r)|\varphi_k''(S(r))\right] dr \\
&+ \sigma\int_0^t \varphi_k'(S(r))\sqrt{|S(r)|}dB(r), \\
&\leq \int_0^t \lambda S^-(r)dr + \frac{\sigma^2 t}{k} + \sigma\int_0^t \varphi_k'(S(r))\sqrt{|S(r)|}dB(r),
\end{aligned} \tag{2.9.3}$$

where $S_0 = S(0)$ is the initial condition. Hence

$$\mathbb{E}S^-(t) - a_{k-1} \leq \mathbb{E}_{\varphi_k}(S(t)) \leq \lambda\int_0^t \mathbb{E}S^-(r)dr + \frac{\sigma^2 t}{k},$$

which becomes

$$\mathbb{E}S^{-}(t) \leq a_{k-1} + \frac{\sigma^2 t}{k} + \lambda \int_0^t \mathbb{E}S^{-}(r)dr.$$

By using the Gronwall inequality shown in Theorem 2.9.1, we have that

$$\mathbb{E}S^{-}(t) \leq \left(a_{k-1} + \frac{\sigma^2 t}{k}\right) e^{\lambda t}, \quad \text{for all } t \geq 0.$$

Letting $k \to \infty$, we get that $\mathbb{E}S^{-}(t) \leq 0$ and hence we must have that

$$\mathbb{E}S^{-}(t) = 0 \quad \text{for all } t \geq 0.$$

Thus

$$\mathbb{P}\{S(t) < 0\} = 0 \quad \text{for all } t \geq 0.$$

Since $S(t)$ is continuous we must have that for all $t \geq 0, S(t) \geq 0$ almost surely. This proves the nonnegative property of the solution of (2.9.2) and as a result we can write (2.9.2) as (2.9.1).

2.9.2 Feller Test for Explosions

For the purpose of completion, the purpose of this section is to introduce some useful properties in [68] that we use in Section 3.5. The materials and notations used in this section are obtained from [68].

Let us consider the one-dimensional, time-homogeneous SDE

$$dX(t) = bX(t)dt + \sigma X(t)dB(t). \tag{2.9.4}$$

Let us consider an interval $I = (l, r)$ where $-\infty \leq l < r \leq \infty$ and assume that the coefficients of the SDE $\sigma : I \to \mathbb{R}, b : I \to \mathbb{R}$ satisfy

$$\sigma^2(x) > 0, \quad \text{for all } x \in I, \tag{2.9.5}$$

$$\text{for all } x \in I, \exists \varepsilon > 0 \text{ such that } \int_{x-\varepsilon}^{x+\varepsilon} \frac{1 + |b(y)|}{\sigma^2(y)} dy < \infty. \tag{2.9.6}$$

Let us define the *scale function* $p(x)$ such that

$$p(x) = \int_c^x exp\left\{-2\int_c^\xi \frac{b(\zeta)d\zeta}{\sigma^2(\zeta)}\right\} d\xi, \tag{2.9.7}$$

where the number c in this case is in I. The function p has a continuous, strictly positive derivative and $p''(x)$ exists almost everywhere and satisfies

$$p''(x) = -\frac{2b(x)}{\sigma^2(x)}p'(x),$$

where $p'(x)$ is the first derivative of the function (2.9.7). We also introduce the *speed measure*

$$m(dx) = \frac{2dx}{p'(x)\sigma^2(x)}, \quad x \in I,$$

and the *Green's function*

$$G_{a,b}(x,y) = \frac{(p(x \wedge y) - p(a))(p(b) - p(x \wedge y))}{p(b) - p(a)}, \quad x, y \in [a,b] \subseteq I. \tag{2.9.8}$$

Let us now define $S = \inf\{t \geq 0 : X(t) \notin (l,r)\} = \lim_{n\to\infty} S_n$ and p be given by (2.9.7). Now assume that (2.9.5) and (2.9.6) hold and let X be a weak solution to the SDE (2.9.4) in I with initial condition $X_0 = x \in I$. Then the following properties hold:

1. $\mathbb{P}(l+) = -\infty, \mathbb{P}(r-) = \infty$. Then

$$\mathbb{P}[S = \infty] = \mathbb{P}\left[\sup_{0\leq t<\infty} X(t) = r\right] = \mathbb{P}\left[\inf_{0\leq t<\infty} X(t) = l\right] = 1.$$

2. $\mathbb{P}(l+) > -\infty, \mathbb{P}(r-) = \infty$. Then

$$\mathbb{P}\left[\lim_{t\uparrow S} X(t) = l\right] = \mathbb{P}\left[\sup_{0\leq t<S} X(t) < r\right] = 1.$$

3. $\mathbb{P}(l+) = -\infty, \mathbb{P}(r-) < \infty$. Then

$$\mathbb{P}\left[\lim_{t\uparrow S} X(t) = r\right] = \mathbb{P}\left[\inf_{0\leq t<S} X(t) > l\right] = 1.$$

4. $\mathbb{P}(l+) > -\infty, \mathbb{P}(r-) < \infty$. Then

$$\mathbb{P}\left[\lim_{t\uparrow S} X(t) = l\right] = 1 - \mathbb{P}\left[\lim_{t\uparrow S} X(t) = r\right] = \frac{p(r-) - p(x)}{p(r-) - p(l+)},$$

where $p(x)$ is defined as in (2.9.7), $l+$ represents tending towards l from above and $r-$ denotes reaching r from below.

Theorem 2.9.2 (Feller Test for Explosions) *Assume that (2.9.5) and (2.9.6) hold and let* $(X, W), (\Omega, \mathcal{F}, \mathbb{P}), \{\mathcal{F}_t\}$ *be a weak solution in* $I = (l, r)$ *of the SDE (2.9.4) with nonrandom initial condition* $X_0 = x \in I$*, where* W *is a standard one dimensional Brownian motion. Then the equation*

$$v(l+) = v(r-) = \infty$$

determines whether $\mathbb{P}(S = \infty) = 1$ *or* $\mathbb{P}(S = \infty) < 1$*, where*

$$v(x) = \int_c^x p'(y) \int_c^y \frac{2dz}{p'(z)\sigma^2(z)} dy = \int_c^x (p(x) - p(y)) m(dy),$$

for some fixed number c *in* I*.*

2.9.3 Mean Reverting Square Root Process

By using some of the ideas mentioned in Section 2.9.1 and Section 2.9.2, in this section we will introduce another property which will be useful in Section 3.5. The purpose of this section is to give the reader the basic framework and idea in [89] on which the proof of Theorem 3.5.1 is based. The detailed workings are shown in Section 3.5. Let us consider the following SDE

$$dS(t) = \lambda(\mu - S(t))dt + \sigma\sqrt{S(t)}dB(t). \tag{2.9.9}$$

By carrying out the same procedure as we did in Section 2.9.1, it is clear that (2.9.9) will never be negative. In fact, by using the Itô's formula given in Section 2.3.3 we have that

$$\mathbb{E}\varphi_k(S(t)) \leq \varphi_k(S_0) + \mathbb{E}\int_0^t \left[\lambda(\mu - S(t))\varphi_k'(S(r)) + \frac{\sigma^2}{2}|S(r)||\varphi_k''(S(r))|\right] dr \leq \frac{\sigma^2 t}{k}.$$

Consequently,

$$-a_{k-1} \leq \mathbb{E}S^-(t) - \alpha_{k-1} \leq \frac{\sigma^2 t}{k},$$

where $S^-(t) = -S(t)$ if $S(t) < 0$ or otherwise $S^-(t) = 0$. By letting $k \to \infty$, we have that $\mathbb{E}S^-(t) = 0$ for all $t \geq 0$. Thus we have that $S(t) \geq 0$ for all $t \geq 0$ almost surely, where a_k is defined as in Section 2.9.1. Note that if $\sigma^2 \leq 2\lambda\mu$ then $S(t) > 0$ for all $t \geq 0$ almost surely. The diffusion coefficient of (2.9.9), $g(x) := \sigma\sqrt{x}$, is continuous and obeys $g^2(x) > 0$ on $x \in (0, \infty)$ while the shift coefficient, $f(x) := \lambda(\mu - x)$, is continuous on

$x \in (0, \infty)$. By the standard result of ordinary differential equations, we know that there is a unique solution $M(x)$ to the equation

$$f(x)M'(x) + \frac{1}{2}g^2(x)M''(x) = -1, \quad a < x < b$$

for any given pair of positive constants a and b with $a < S_0 < b$, with boundary condition $M(a) = M(b) = 0$. The explicit formula for $M(x)$ is given in terms of the Green's function defined in (2.9.8), namely

$$\begin{aligned} M_{a,b} &= \int_a^b G_{a,b}(x,y)m(dy), \\ &= -\int_a^x (p(x) - p(y))m(dy) + \frac{p(x) - p(a)}{p(b) - p(a)} \int_a^b (p(b) - p(y))m(dy), \end{aligned} \tag{2.9.10}$$

where $p(x)$ is the scale function defined in (2.9.7). Let us define the stopping times

$$\tau_a = \inf\{t \geq 0 : S(t) \leq a\} \quad \text{and} \quad \tau_b = \inf\{t \geq 0 : S(t) \geq b\}.$$

By the Itô formula, it is easy to show that for any $t > 0$,

$$\mathbb{E}M(S(t \wedge \tau_a \wedge \tau_b)) = M(S_0) - \mathbb{E}(t \wedge \tau_a \wedge \tau_b), \tag{2.9.11}$$

which gives

$$\mathbb{E}(t \wedge \tau_a \wedge \tau_b) \leq M(S_0).$$

Letting $t \to \infty$ gives

$$\mathbb{E}(\tau_a \wedge \tau_b) \leq M(S_0) < \infty.$$

In other words, $S(t)$ exits from every compact subinterval of $(0, \infty)$ in finite expected time. Thus $\mathbb{P}(\tau_a \wedge \tau_b < \infty) = 1$. By returning to (2.9.11), observe from the boundary condition that $\lim_{t\to\infty} \mathbb{E}M(s(t \wedge \tau_a \wedge \tau_b)) = 0$ and thus

$$\mathbb{E}(\tau_a \wedge \tau_b) = M(S_0).$$

Let us define a function $V(x)$ such that

$$V(x) = \int_1^x \exp\left\{-\int_1^y \frac{2f(z)}{g^2(z)}dz\right\} dy, \quad x \in (0, \infty). \tag{2.9.12}$$

This function has continuous, strictly positive derivatives $V'(x)$, and $V''(x)$ which exist everywhere and obey

$$V''(x) = -\frac{2f(x)}{g^2(x)}V'(x).$$

By using the Itô formula, we have that for any $t > 0$,

$$V(S(t \wedge \tau_a \wedge \tau_b)) = V(S_0) + \int_0^{t \wedge \tau_a \wedge \tau_b} V'(S(u))g(S(u))dB(u).$$

Now taking the expectation and letting $t \to \infty$ gives that

$$V(S_0) = \mathbb{E}V(S(\tau_a \wedge \tau_b)) = V(a)\mathbb{P}(\tau_a < \tau_b) + V(b)\mathbb{P}(\tau_b < \tau_a).$$

Since two probabilities must add up to one, we have that

$$\mathbb{P}(\tau_a < \tau_b) = \frac{V(b) - V(S_0)}{V(b) - V(a)} \quad \text{and} \quad \mathbb{P}(\tau_b < \tau_a) = \frac{V(S_0) - V(a)}{V(b) - V(a)}. \tag{2.9.13}$$

By substituting $f(x)$ and $g(x)$ in (2.9.12) by the corresponding shift and drift coefficients given in (2.9.9) and computing we have that

$$\begin{aligned} V(x) &= \int_1^x \exp\left\{-\int_1^y \frac{2\lambda(\mu - z)}{\sigma^2 z} dz\right\} dy, \\ &= \int_1^x y^{-2\lambda\mu/\sigma^2} \exp\left(\frac{2\lambda\mu}{\sigma^2}(y-1)\right) dy. \end{aligned} \tag{2.9.14}$$

For the case when $2\lambda\mu \geq \sigma^2$, we have that

$$\lim_{x \downarrow 0} V(x) = -\infty \quad \text{and} \quad \lim_{x \uparrow \infty} V(x) = \infty.$$

Let us define

$$\tau_0 = \lim_{a \downarrow 0} \tau_a \quad \text{and} \quad \tau_\infty = \lim_{b \uparrow \infty} \tau_b$$

and set $\tau = \tau_0 \wedge \tau_\infty$. From (2.9.13) we have that

$$\mathbb{P}\left(\inf_{0 \leq t < \tau} S(t) \leq a\right) \geq \mathbb{P}(\tau_a < \tau_b) = \frac{1 - V(S_0)/V(b)}{1 - V(a)/V(b)}. \tag{2.9.15}$$

Letting $b \uparrow \infty$, then

$$\mathbb{P}\left(\inf_{0 \leq t < \tau} S(t) \leq a\right) = 1.$$

This holds for any $a > 0$ and thus we must have that

$$\mathbb{P}\left(\inf_{0 \leq t < \tau} S(t) = 0\right) = 1.$$

A dual argument shows that

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

Let us now suppose that $\mathbb{P}(\tau < \infty) > 0$, then

$$\mathbb{P}\left(\lim_{t\to\tau} S(t) \text{ exists and is equal to } 0 \text{ or } \infty\right) > 0.$$

Thus it is clear that $\{\inf_{0\le t<\tau} S(t) = 0\}$ and $\{\sup_{0\le t<\tau} S(t) = \infty\}$ cannot both have probability one. This is clearly a contradiction and thus

$$\mathbb{P}(\tau < \infty) = 0.$$

To sum up for the case $2\lambda\mu \ge \sigma^2$, we have

$$\mathbb{P}(\tau = \infty) = \mathbb{P}\left(\inf_{0\le t<\tau} S(t) = 0\right) = \mathbb{P}\left(\sup_{0\le t<\tau} S(t) = \infty\right) = 1.$$

For the case $2\lambda\mu < \sigma^2$, we have that

$$V(0+) := \lim_{x\downarrow 0} V(x) > -\infty \quad \text{and} \quad \lim_{x\uparrow\infty} V(x) = \infty.$$

Similarly we can show from (2.9.15) that

$$\mathbb{P}\left(\inf_{0\le t<\tau} S(t) = 0\right) = 1.$$

By letting $a \downarrow 0$ in the second equality of (2.9.13) gives

$$\mathbb{P}(\tau_b < \tau_0) = \frac{V(S_0) - V(0+)}{V(b) - V(0+)}.$$

Letting $b \to \infty$ then implies that $\mathbb{P}(\tau_\infty < \tau_0) = 0$, namely $\mathbb{P}\left(\sup_{0\le t<\tau} S(t) = \infty\right) = 0$. Hence we can conclude that if $2\lambda\mu < \sigma^2$, then

$$\mathbb{P}\left(\inf_{0\le t<\tau} S(t) = 0\right) = \mathbb{P}\left(\sup_{0\le t<\tau} S(t) < \infty\right) = 1.$$

Note that the mean reverting square root process given in equation (2.9.9) is also known as the Cox-Ingersoll-Ross model [24]. 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

$$\begin{aligned} f(r(s), s; r(t), t) &= ce^{-u-v}\Big(\frac{v}{u}\Big)^{\frac{q}{2}} I_q(2(uv)^{\frac{1}{2}}), \\ \text{where} \qquad c &= \frac{2k}{\sigma^2(1-e^{-k(s-t)})}, \\ u &= cr(t)e^{-k(s-t)}, \\ v &= cr(s), \\ q &= \frac{2k\theta}{\sigma^2} - 1, \end{aligned}$$

and $I_q(.)$ 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

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

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

In this chapter we introduced some of the mathematical properties which will be useful for us in this thesis. In the next chapter we will look at the effect of introducing demographic stochasticity on the dynamical behaviour of the SIS epidemic model given in Section 1.2.

Chapter 3

Demographic SIS Model

3.1 Introduction

In this chapter, we will look at the effect that introducing demographic stochasticity has on the dynamical behaviour of the deterministic SIS epidemic model given in Section 1.2 where we make the assumption that an infected individual or a susceptible individual who dies is immediately replaced by a susceptible individual or an infected individual, in other words, the population size is kept constant.

This chapter is organised as follows: in the next section we shall describe the basic model. In the following section we shall show the existence of a unique nonnegative solution. In Section 3.4, we shall look at conditions for extinction and in Section 3.5 we shall look at the Feller test which gives probabilities of hitting the top and bottom limits. In Section 3.6 we perform some simulations with theoretical parameter values to verify the results and simulations with realistic parameter values for gonorrhea and pneumococcus.

Most of the work mentioned in Chapter 3 has been written up as a paper and is published in [47].

3.2 Demographic Stochasticity for the SDE SIS Epidemic Model

Throughout this chapter, 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 following deterministic SIS model with two populations $S(t)$ and $I(t)$:

$$\begin{aligned} \frac{dS(t)}{dt} &= -\beta I(t)S(t) + \gamma I(t) + \mu N - \mu S(t), \\ \frac{dI(t)}{dt} &= \beta I(t)S(t) - (\mu+\gamma)I(t). \end{aligned} \tag{3.2.1}$$

Here, S and I denote two populations representing respectively the number of susceptible and infected individuals in the population. N is the total size of the population, β is the disease transmission coefficient and $\beta = \lambda/N$ where λ is the disease contact rate for each individual, that is the rate at which susceptible individuals come into contact with and are infected by infected individuals. μ is the per capita death rate and γ is the rate at which an infected individual becomes cured. By looking at the interaction occurring between the two populations, Allen [1] constructed a list of possible changes with their corresponding probabilities $p_i(t),\ i = 1, 2, 3 \ldots$ as shown in Table 3.1. Note that we have assumed that the per capita death rate is the same as the per capita birth rate, in other words the total population size remains constant.

In order to introduce demographic stochasticity into the deterministic SIS model (3.2.1), the mean change $E(\Delta\mathbf{x})$ and the covariance matrix $\mathbf{V}$ for the time interval Δt are calculated [1] where $\mathbf{V} = E(\Delta\mathbf{x}(\Delta\mathbf{x})^T)/\Delta t$. The stochastic SIS model has the form:

$$d\mathbf{x} = \boldsymbol{\mu}(t, S, I)dt + \mathbf{B}(t, S, I)d\mathbf{W}(t), \tag{3.2.2}$$

with $\mathbf{x} = (S, I)^T$, $\mathbf{x}(0) = (S(0), I(0))^T$,

$$\boldsymbol{\mu} = E(\Delta\mathbf{x})/\Delta t = \begin{bmatrix} -\beta IS + (\mu+\gamma)I \\ -(\mu+\gamma)I + \beta IS \end{bmatrix},$$

$$\mathbf{B} = \mathbf{V}^{1/2} = \begin{bmatrix} \beta IS + (\mu+\gamma)I & -\beta IS - (\mu+\gamma)I \\ -\beta IS - (\mu+\gamma)I & \beta IS + (\mu+\gamma)I \end{bmatrix} / \sqrt{2(\beta IS + (\mu+\gamma)I)}$$

Change	Probability
$\Delta \mathbf{x}_1 = [-1, 0]^T$	$p_1 = \mu S \Delta t$
$\Delta \mathbf{x}_2 = [-1, 1]^T$	$p_2 = \beta S I \Delta t$
$\Delta \mathbf{x}_3 = [0, -1]^T$	$p_3 = \mu I \Delta t$
$\Delta \mathbf{x}_4 = [0, 1]^T$	$p_4 = \mu I \Delta t$
$\Delta \mathbf{x}_5 = [1, -1]^T$	$p_5 = (\mu + \gamma) I \Delta t$
$\Delta \mathbf{x}_6 = [1, 0]^T$	$p_6 = \mu S \Delta t$
$\Delta \mathbf{x}_7 = [0, 0]^T$	$p_7 = 1 - \sum_{i=1}^{6} p_i$

Table 3.1: Possible changes between two populations with their corresponding probabilities where $\mathbf{x} = (S, I)^T$.

and $\mathbf{W}(t)$ is the two dimensional Brownian motion, namely $\mathbf{W}(t) = (W_1(t), W_2(t))^T$. In other words:

$$dS(t) = (-\beta SI + (\mu + \gamma)I)dt + \sqrt{\beta SI + (\mu + \gamma)I}\ \frac{(dW_1 - dW_2)}{\sqrt{2}}, \tag{3.2.3}$$
$$dI(t) = (\beta SI - (\mu + \gamma)I)dt - \sqrt{\beta SI + (\mu + \gamma)I}\ \frac{(dW_1 - dW_2)}{\sqrt{2}}.$$

If we write $B = (W_1 - W_2)/\sqrt{2}$ then B is a Brownian motion so the SDE SIS model with demographic stochasticity becomes:

$$dS(t) = [-\beta I(t)S(t) + \gamma I(t) + \mu N - \mu S(t)]dt - \sqrt{\beta I(t)S(t) + (\mu + \gamma)I(t)}dB, \tag{3.2.4}$$
$$dI(t) = [\beta I(t)S(t) - (\mu + \gamma)I(t)]dt + \sqrt{\beta I(t)S(t) + (\mu + \gamma)I(t)}dB.$$

In fact if in equations (5.8) and (5.9) on p.147 of [1] we replace γ by $(\mu + \gamma)$ and α by βN then equations (5.10) and (5.11) on p.148 of [1] are our equations (3.2.4). By using $S(t) + I(t) = N$, we can combine the two SDEs shown in (3.2.4) into one SDE for $I(t)$, namely:

$$dI(t) = [\beta I(t)(N - I(t)) - (\mu + \gamma)I(t)]dt + \sqrt{\beta I(t)(N - I(t)) + (\mu + \gamma)I(t)}dB. \tag{3.2.5}$$

The corresponding deterministic SIS model to the SDE SIS model (3.2.5) is given by:

$$\frac{dI(t)}{dt} = I(t)[\beta N - \beta I(t) - \mu - \gamma]. \tag{3.2.6}$$

An alternative derivation of equation (3.2.5) based on (3.2.6) is given by Allen [2] who applies the procedure outlined above to (3.2.6). Equations (3.2.4) then follow from $S+I = N$. Note that the diffusion coefficient of the SDE SIS model (3.2.5) vanishes when $I(t) = N + \frac{\mu+\gamma}{\beta}$. It is appropriate to take an initial value $I(0) = I_0 \in (0, N)$. For the rest of the chapter, we shall focus on analysing the SDE SIS model with demographic stochasticity (3.2.5). Note also that since the diffusion coefficient vanishes when $I(t) = N + \frac{\mu+\gamma}{\beta}$, this implies that it is possible for $I(t)$ to exceed N, which is slightly unusual as normally we would expect $I(t) \in (0, N)$. However it is important to note that this is caused by the way we have introduced demographic stochasticity into the model, using the techniques illustrated in [1], and this is indeed a well-established model and thus it is crucial for us to analyse the behaviour of such a model as a result of demographic stochasticity. Throughout this chapter, 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.

3.3 Existence of Unique Nonnegative Solution

In order to prove the existence and uniqueness of the solution to the SDE SIS model (3.2.5), let us denote

$$\lambda(x) = \beta x(N - x) - (\mu + \gamma)x,$$

$$\sigma(x) = \sqrt{\beta x(N - x) + (\mu + \gamma)x},$$

where $\lambda(x)$ and $\sigma(x)$ are the drift and diffusion coefficients of the SDE SIS model (3.2.5) respectively and $x \in [0, N + \frac{\mu+\gamma}{\beta}]$. We shall now extend the domain of our SDE SIS model (3.2.5) into the whole domain, i.e. $\lambda(x)$, $\sigma(x)$: $\mathbb{R} \to \mathbb{R}$, by considering the following definitions:

$$\lambda(x) = \begin{cases} 0, & \text{for } x < 0, \\ \lambda(x), & \text{for } 0 \leq x \leq N + \frac{\mu+\gamma}{\beta}, \\ \lambda(N + \frac{\mu+\gamma}{\beta}), & \text{for } x > N + \frac{\mu+\gamma}{\beta}, \end{cases} \tag{3.3.1}$$

and

$$\sigma(x) = \begin{cases} 0, & \text{for } x < 0, \\ \sigma(x), & \text{for } 0 \leq x \leq N + \frac{\mu+\gamma}{\beta}, \\ 0, & \text{for } x > N + \frac{\mu+\gamma}{\beta}. \end{cases} \tag{3.3.2}$$

As this SDE is a special case, the standard existence and uniqueness theorems on SDEs are not applicable here (e.g. [89] and Section 2.4.2) and other methods [40] do not adapt here as well. We are now ready to prove the existence and uniqueness of the solution for the SDE SIS model (3.2.5) by using the following lemma which is mentioned in [64] (Theorem 3.2 of Chapter IV) and also given as Theorem 2.4.4 in this thesis:

Lemma 3.3.1 *Suppose $\sigma(x)$ and $\lambda(x)$ are bounded. Then there exists a strong pathwise unique solution to the scalar SDE*

$$dx(t) = \lambda(x(t))dt + \sigma(x(t))dB(t) \tag{3.3.3}$$

if (i) $|\lambda(x) - \lambda(y)| \leq \kappa(|x-y|)$, where $\kappa(u)$ is a strictly increasing and concave function on $[0, \infty)$ such that $\kappa(0) = 0$ and $\int_{0+} \kappa^{-1}(u)du = \infty$ for all $x, y \in \mathbb{R}$,

(ii) $|\sigma(x) - \sigma(y)| \leq \rho(|x-y|)$, where $\rho(u)$ is a strictly increasing function on $[0, \infty)$ such that $\rho(0) = 0$ and $\int_{0+} \rho^{-2}(u)du = \infty$ for all $x, y \in \mathbb{R}$.

Theorem 3.3.2 *For any initial value $x(0) = x_0 \in [0, N + \frac{\mu+\gamma}{\beta}]$, the SDE (3.3.3) with its coefficients defined by (3.3.1) and (3.3.2) has a strong pathwise unique solution.*

Proof. We shall split the proof into two sections by showing condition (i) is satisfied first.

(i) The first derivative of equation (3.3.1) is defined as:

$$\lambda'(x) = \begin{cases} 0, & \text{for } x < 0, \\ -2\beta x + \beta N - \mu - \gamma, & \text{for } 0 < x < N + \frac{\mu+\gamma}{\beta}, \\ 0, & \text{for } x > N + \frac{\mu+\gamma}{\beta}. \end{cases} \tag{3.3.4}$$

For $x, y \in \left(0, N + \frac{\mu+\gamma}{\beta}\right)$, by the Mean Value Theorem we have that for some $\xi \in (x, y)$

$$\frac{|\lambda(x) - \lambda(y)|}{|x-y|} = |\lambda'(\xi)| \leq M = \sup_{\xi \in (0, N+\frac{\mu+\gamma}{\beta})} |\lambda'(\xi)|,$$

since $\lambda'(\xi)$ is a continuous function in $(0, N + \frac{\mu+\gamma}{\beta})$. Letting $x \to 0^+, y \to (N + \frac{\mu+\gamma}{\beta})^-$, we deduce that the same result is true if $x, y \in [0, N + \frac{\mu+\gamma}{\beta}]$. It is easy to see that the result follows for x, y in $(-\infty, \infty)$. Therefore, condition (i) is satisfied with $\kappa(u) = Mu$ for some constant M for all $x, y \in \mathbb{R}$ and $\lambda(x)$ is Lipschitz continuous. Note that a linear function can be regarded as either a concave or a convex function, and this does not contradict Lemma 3.3.1 as we do not require the function to be strictly concave.

We will now complete the proof by looking at the second condition:

(ii) From equation (3.3.2), it is clear that the Mean Value Theorem does not apply in this case. In addition, if we are able to show condition (ii) is satisfied for $x, y \in [0, N+\frac{\mu+\gamma}{\beta}]$ then the rest will follow. In other words, if we could find a constant L such that

$$\frac{|\sigma(x) - \sigma(y)|}{\sqrt{|x - y|}} \leq L, \tag{3.3.5}$$

for $x, y \in [0, N + \frac{\mu+\gamma}{\beta}]$, then condition (ii) is proved. By choosing $\varepsilon = \frac{1}{4}(N + \frac{\mu+\gamma}{\beta})$ and considering separately the regions $\varepsilon \leq x \leq N + \frac{\mu+\gamma}{\beta} - \varepsilon$, $\varepsilon \leq y \leq N + \frac{\mu+\gamma}{\beta} - \varepsilon$, $0 < x, y \leq \varepsilon$, $N + \frac{\mu+\gamma}{\beta} - \varepsilon \leq x, y \leq N + \frac{\mu+\gamma}{\beta}$, $N + \frac{\mu+\gamma}{\beta} - \varepsilon < x \leq N + \frac{\mu+\gamma}{\beta}$ and $0 < y < \varepsilon$ and $N + \frac{\mu+\gamma}{\beta} - \varepsilon < y \leq N + \frac{\mu+\gamma}{\beta}$ and $0 < x < \varepsilon$, it is straightforward to show that (3.3.5) holds. As a result, condition (ii) is satisfied with $\rho(u) = L\sqrt{u}$ for some constant L for all $x, y \in \mathbb{R}$. In other words, $\sigma(x)$ is Hölder continuous with exponent $1/2$. Moreover, by definitions (3.3.1) and (3.3.2) both $\lambda(x)$ and $\sigma(x)$ are bounded so the theorem follows from Lemma 3.3.1.

□

Note that by Theorem 2.4 of Chapter IV of [64] (given in Theorem 2.4.3), since $\sigma(I(t))$ and $\lambda(I(t))$ are bounded, the solution to the SDE SIS model (3.2.5) will not explode. Hence, we have shown that a unique strong pathwise non-explosive solution does in fact exist for our SDE SIS model (3.2.5).

All we have left to show now is the non-negativity of our solution. Note that in order for this SDE SIS model (3.2.5) to make sense, the term inside the square root has to be nonnegative. We consider the SDE (3.3.3). We show that provided that $I_0 \in (0, N)$ then $I(t) \in [0, N + \frac{\mu+\gamma}{\beta}]$.

Theorem 3.3.3 *For any given initial value $I(0) = I_0 \in (0, N)$, the probability that the SDE (3.3.3) has a unique and nonnegative solution $I(t) \in [0, N + \frac{\mu+\gamma}{\beta}]$ for all $t \geq 0$ is one, i.e.,*

$$0 \leq I(t) \leq N + \frac{\mu + \gamma}{\beta}, \tag{3.3.6}$$

almost surely for all $t \geq 0$.

Note that this result is slightly unusual as based on biological considerations we would have expected $I(t) \in (0, N)$. This is the result of introducing stochasticity into the model using the technique mentioned in [1] and this SDE SIS model (3.2.5) is a well-established model. In Section 3.6, we shall show that although it is theoretically possible for $I(t)$ to exceed N, in the numerical simulations which we performed we have not observed such a case.

Proof. The following proof for Theorem 3.3.3 is established based on the framework of the "Square Root Process" illustrated in [89] and mentioned in Section 2.9.1. We shall divide this proof into two parts. First of all, we shall prove the left hand side inequality, $I(t) \geq 0$ and by using a similar strategy we shall prove the right hand side inequality and thus complete the proof. Let $a_0 = 1$ and $a_k = e^{-k(k+1)/2}$ for every integer $k \geq 1$. Note that

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

where $a_k = e^{-k(k-1)/2}$. 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

$$\varphi_k(x) = \int_0^{-x} dy \int_0^y \Psi_k(u) du, \qquad \text{for } x < 0. \tag{3.3.7}$$

It is easy to see that $\varphi_k \in C^2(R, R)$. Furthermore, by using Leibniz integral rule we have that

$$\varphi_k'(x) = -\int_0^{-x} \Psi_k(u) du, \tag{3.3.8}$$

and $$\varphi_k''(x) = \Psi_k(-x), \tag{3.3.9}$$

respectively. As in [89]:

$$-1 \leq \varphi_k'(x) \leq 0 \text{ if } -\infty < x < -a_k \text{ or otherwise } \varphi_k'(x) = 0; \tag{3.3.10}$$

$$|\varphi_k''(x)| \leq \frac{2}{k|x|} \text{ if } -a_{k-1} < x < -a_k \text{ or otherwise } \varphi_k''(x) = 0; \tag{3.3.11}$$

and $$x^- - a_{k-1} \leq \varphi_k(x) \leq x^- \text{ for all } x \in R, \tag{3.3.12}$$

where we define $x^- = -x$ if $x < 0$ or otherwise $x^- = 0$. Now, by Itô's formula, we get that for any $t \geq 0$:

$$\begin{aligned} \varphi_k(I(t)) &= \varphi_k(I_0) + \int_0^t \left[\lambda(I(s))\varphi_k'(I(s)) + \frac{\sigma(I(s))^2}{2}\varphi_k''(I(s))\right] ds \\ &\quad + \int_0^t \sigma(I(s))\varphi_k'(I(s))dB(s), \end{aligned} \tag{3.3.13}$$

where $\lambda, \sigma : \mathbb{R} \to \mathbb{R}$ are defined as before.

As $\varphi_k'(I) = 0$ and $\varphi_k''(I) = 0$ for $I \geq 0$, from (3.3.13)

$$\varphi_k(I(t)) \leq \int_0^t \sigma(I(s))\varphi_k'(I(s))dB(s). \tag{3.3.14}$$

Taking the expectation yields:

$$\mathbb{E}\varphi_k(I(t)) \leq 0. \tag{3.3.15}$$

Hence,

$$\mathbb{E}I^-(t) - a_{k-1} \leq \mathbb{E}\varphi_k(I(t)) \leq 0. \tag{3.3.16}$$

We get that as $k \to \infty$,

$$\mathbb{E}I^-(t) \leq 0. \tag{3.3.17}$$

Now for all t, $I^-(t) \geq 0$, so $\mathbb{E}I^-(t) \geq 0$, hence from our result (3.3.17), we must have:

$$\mathbb{E}I^-(t) = 0 \quad \forall t \geq 0. \tag{3.3.18}$$

Furthermore, by using equation (3.3.18) and proof by contradiction, it is straightforward to show that for all $t > 0$,

$$\begin{aligned} &\mathbb{P}(I(t) < 0) = 0, \\ \Rightarrow &\mathbb{P}(I(t) \geq 0) = 1. \end{aligned} \tag{3.3.19}$$

Therefore, $I(t) \geq 0$ almost surely and this completes the left hand side of the proof for equation (3.3.6).

To complete the proof we shall now show that $I(t) \leq N + \frac{\mu+\gamma}{\beta}$. Let us define

$$\begin{aligned} J(I(t)) &= N + \frac{\mu+\gamma}{\beta} - I(t), \\ &= \frac{\beta N + \mu + \gamma - \beta I(t)}{\beta}. \end{aligned} \tag{3.3.20}$$

Then, we want to show that $J(I(t)) > 0$. From Itô's formula on equation (3.3.20), we get:

$$dJ(I(t)) = (-1)\lambda(J(I(t)) - \sigma(J(I(t)))dB,$$

where

$$\lambda(J(I(t)) = \begin{cases} -2(\mu+\gamma)\Big(N + \frac{\mu+\gamma}{\beta}\Big), & \text{for } J \leq 0, \\ \Big(N + \frac{\mu+\gamma}{\beta} - J(I(t))\Big)(\beta J(I(t)) - 2(\mu+\gamma)), & \text{for } 0 \leq J \leq N + \frac{\mu+\gamma}{\beta}, \\ 0, & \text{for } J \geq N + \frac{\mu+\gamma}{\beta}, \end{cases}$$

and

$$\sigma(J(I(t)) = \begin{cases} 0, & \text{for } J \leq 0, \\ \sqrt{\beta J(I(t))\Big(N + \frac{\mu+\gamma}{\beta} - J(I(t))\Big)}, & \text{for } 0 \leq J \leq N + \frac{\mu+\gamma}{\beta}, \\ 0, & \text{for } J \geq N + \frac{\mu+\gamma}{\beta}. \end{cases}$$

By Itô's formula, we derive that:

$$\varphi_k(J(t)) = \varphi_k(J_0) + \int_0^t \left[P(J(s)) + Q(J(s))\right] ds - \int_0^t \sigma(J(s))\varphi_k'(J(s))dB(s), \tag{3.3.21}$$

where $P, Q : \mathbb{R} \to \mathbb{R}$ are defined by:

$$P(x) = \begin{cases} 2(\mu+\gamma)\Big(N + \frac{\mu+\gamma}{\beta}\Big)\varphi_k'(x), & \text{for } x \leq 0, \\ \Big(N + \frac{\mu+\gamma}{\beta} - x\Big)(2(\mu+\gamma) - \beta x)\varphi_k'(x), & \text{for } 0 \leq x \leq N + \frac{\mu+\gamma}{\beta}, \\ 0, & \text{for } x \geq N + \frac{\mu+\gamma}{\beta}. \end{cases} \tag{3.3.22}$$

$$Q(x) = \begin{cases} \frac{x}{2}(\beta(N-x) + \mu + \gamma)\varphi_k''(x), & \text{for } \ 0 \leq x \leq N + \frac{\mu+\gamma}{\beta}, \\ 0, & \text{otherwise.} \end{cases} \tag{3.3.23}$$

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

Thus

$$\varphi_k(J(t)) \leq -\int_0^t \sigma(J(s))\varphi_k'(J(s))dB(s).$$

Now take the expectations to get $\mathbb{E}\varphi_k(J(t)) \leq 0$. Hence, $\mathbb{E}J^-(t) - a_{k-1} \leq \mathbb{E}\varphi_k(J(t)) \leq 0$. As $k \to \infty,\ a_{k-1} \to 0$, thus $\mathbb{E}J^-(t) \leq 0$. Similarly to the argument we used for proving the left hand side of equation (3.3.6), it is clear that for all $t > 0$,

$$\begin{aligned} &\mathbb{P}(J(t) < 0) = 0, \\ \Rightarrow\ &\mathbb{P}(J(t) \geq 0) = 1, \end{aligned} \tag{3.3.24}$$

i.e., $I(t) \leq N + \frac{\mu+\gamma}{\beta}$ almost surely $\forall t \geq 0$, which completes the entire proof. □

Hence we have proven the nonnegative property of the solution of the SDE SIS model with demographic stochasticity (3.3.3) and provided that $I(t) \in [0, N+\frac{\mu+\gamma}{\beta}]$ we can express equation (3.3.3) as equation (3.2.5). This has completed our proof on the existence of a unique nonnegative solution for the SDE SIS model (3.2.5).

3.4 Extinction of Our Solution

In this section, we shall focus on the extinction aspect of the nonnegative solution $I(t) \in [0, N + \frac{\mu+\gamma}{\beta}]$ to the SDE SIS model (3.2.5). Let us define the basic reproduction number R_0 as:

$$R_0 = \frac{\beta N}{\mu + \gamma} \tag{3.4.1}$$

where the parameters as denoted as before.

Theorem 3.4.1 *For any given initial value $I(0) = I_0 \in (0, N)$, if $R_0 \leq 1$, or if $R_0 > 1$ and $N < \frac{1}{4} + \frac{\mu+\gamma}{\beta}$, then I(t) will hit zero with probability one in finite time. In other words, the disease will certainly die out in finite time.*

Proof. Let us define the stopping time

$$\tau_n = \inf\{t : I(t) \leq n\}$$

for $0 \leq n < I_0$, where we set $\inf \emptyset = \infty$. We need to show that

$$\mathbb{P}(\tau_0 < \infty) = 1. \tag{3.4.2}$$

We will show this by using proof by contradiction. If (3.4.2) were false, then $\mathbb{P}(\tau_0 = \infty) > 0$. Noting that $\lim_{n\to 0} \tau_n = \tau_0$, we could find an n sufficiently small so that

$$\bar{\delta} := \mathbb{P}(\tau_n = \infty) > 0. \tag{3.4.3}$$

By Itô's formula, we have that

$$d(\sqrt{I(t)}) = \sqrt{I(0)} + q(I(t))dt + \frac{1}{2}\sqrt{\beta N - \beta I(t) + \mu + \gamma}dB(t) \tag{3.4.4}$$

for $0 \leq t \leq \tau_n$, where $q : \mathbb{R} \to \mathbb{R}$ is defined by:

$$q(x) = \frac{\sqrt{x}}{2}(\beta N - \mu - \gamma - \beta x) - \frac{1}{8\sqrt{x}}(\beta N - \beta x + \mu + \gamma). \tag{3.4.5}$$

In order to prove this theorem, we will now show that there exists a negative upper bound for $q(x)$ when $x \in [n, N + \frac{\mu+\gamma}{\beta}]$.

• Case 1 : $R_0 = \frac{\beta N}{\mu+\gamma} \leq 1$. By using Theorem 3.3.6, it is clear that the second term in equation (3.4.5) is negative. In addition, due to the fact that $\frac{\beta N}{\mu+\gamma} \leq 1$, then the first term for (3.4.5) is negative, which makes $q(x)$ in (3.4.5) negative. Therefore, we have that for $x \in [n, N + \frac{\mu+\gamma}{\beta}]$,

$$q(x) \leq \frac{\sqrt{x}}{2}(\beta N - \mu - \gamma) - \frac{\beta}{2}x^{3/2} \leq -\frac{\beta}{2}n^{3/2}. \tag{3.4.6}$$

As a result from (3.4.6), we could conclude that for $x \in \left[n, N + \frac{\mu+\gamma}{\beta}\right]$, $q(x)$ is negative and thus there must exist some $\varepsilon > 0$ such that $q(x) < -\varepsilon < 0$ for $t \geq 0$ for $x \in \left[n, N + \frac{\mu+\gamma}{\beta}\right]$.

Now by substituting the negative upper bound of $q(x)$ into equation (3.4.4) and integrating, we get that:

$$\sqrt{I(t \wedge \tau_n)} \leq \sqrt{I(0)} - \int_0^{t\wedge\tau_n} \varepsilon dt + \frac{1}{2}\int_0^{t\wedge\tau_n} \sqrt{\beta N - \beta I(s) + \mu + \gamma}dB(s). \tag{3.4.7}$$

By taking the expectation of equation (3.4.7) and using the result given by (3.4.3), we obtain that:

$$0 \leq \sqrt{I(0)} - \mathbb{E}\int_0^{t\wedge\tau_n} \varepsilon ds \leq \sqrt{I(0)} - \varepsilon\bar{\delta}t, \quad \forall t \geq 0. \tag{3.4.8}$$

Now letting $t \to \infty$, we have that $0 \leq -\infty$, which clearly is a contradiction. Therefore the result given by (3.4.2) must be true, in other words the disease will die out almost surely for the case where $R_0 \leq 1$. Similarly, we shall apply the same argument to the second case:

• Case 2: $R_0 = \frac{\beta N}{\mu+\gamma} > 1$ where $N < \frac{1}{4} + \frac{\mu+\gamma}{\beta}$. First of all we shall rewrite equation (3.4.5) as:

$$q(x) = \frac{1}{8\sqrt{x}} U(x), \tag{3.4.9}$$

where $U(x)$ is defined as:

$$U(x) = 4x(\beta N - (\mu+\gamma) - \beta x) - (\beta N - \beta x + \mu + \gamma), \tag{3.4.10}$$

for $x \in \left[n, N + \frac{\mu+\gamma}{\beta}\right]$. Clearly, $U(x)$ is a quadratic function so therefore it must have at most two real roots. From (3.4.10),

$$U(n) = 4n(\beta N - (\mu+\gamma) - \beta n) - (\beta N - \beta n + \mu + \gamma). \tag{3.4.11}$$

We can choose n sufficiently small, thus making $U(n)$ negative. Additionally $U\left(N + \frac{\mu+\gamma}{\beta}\right)$ is negative. So

$$-\infty < U(n) < 0, \qquad -\infty < U\left(N + \frac{\mu+\gamma}{\beta}\right) < 0. \tag{3.4.12}$$

Also, $U(x)$ has a maximum turning point at $x^* = \frac{1}{2}\left(\frac{1}{4} + N - \frac{\mu+\gamma}{\beta}\right)$. Now suppose that $x^* \in \left[n, N + \frac{\mu+\gamma}{\beta}\right]$, then by substituting x^* into (3.4.10) we could see that the second term of (3.4.10) is negative. Furthermore, the first term of (3.4.10) becomes:

$$4x^*\left(\frac{\beta N}{2} - \frac{\mu+\gamma}{2} - \frac{\beta}{8}\right), \tag{3.4.13}$$

which is negative as $N < \frac{1}{4} + \frac{\mu+\gamma}{\beta}$. So $U(x) < 0$ when $x \in \left[n, N + \frac{\mu+\gamma}{\beta}\right]$.

Now consider the case where $x^* > N + \frac{\mu+\gamma}{\beta}$. By using the fact that $U(n) < 0$ and $U(N + \frac{\mu+\gamma}{\beta}) < 0$ and that $U(x)$ has one unique turning point, at $x = x^*$, $U(x)$ is negative for $x \in \left[n, N + \frac{\mu+\gamma}{\beta}\right]$. By combining both results we could conclude from equation (3.4.10) that, for $R_0 > 1$, $\exists \varepsilon > 0$ such that $q(x) < -\varepsilon < 0$ for $x \in \left[n, N + \frac{\mu+\gamma}{\beta}\right]$.

Arguing as in case 1, we deduce that $\mathbb{P}(\tau_0 < \infty) = 1$. This completes the proof.

□

3.5 Probabilities of Hitting the Top and Bottom Limits

Now that we know under certain situations, the number of infected individuals will die out, it is also useful to know the probability of it hitting zero and the probability of it hitting $N+\frac{\mu+\gamma}{\beta}$. For the rest of this chapter, we shall work on the SDE SIS model (3.2.5), unless stated otherwise. Let $a \wedge b$ represent the minimum of $\{a, b\}$ and $a \vee b$ represent the maximum of $\{a, b\}$. For $a < I_0 < b$ define

$$\tau_a = \inf\{t \geq 0 : I(t) \leq a\},$$

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

where $\tau_0 = \lim_{a \downarrow 0} \tau_a$, $\tau_{N+\frac{\mu+\gamma}{\beta}} = \lim_{b \uparrow (N+\frac{\mu+\gamma}{\beta})} \tau_b$ and $\tau = \tau_0 \wedge \tau_{N+\frac{\mu+\gamma}{\beta}}$.

Theorem 3.5.1 *For any given initial value $I(0) = I_0 \in (0, N)$, we have that*

- *For $\frac{4(\mu+\gamma)}{\beta} \geq 1$,*

$$\mathbb{P}\left(\inf_{0 \leq t < \tau} I(t) = 0\right) = 1, \tag{3.5.1}$$

$$\mathbb{P}\left(\sup_{0 \leq t < \tau} I(t) = N + \frac{\mu+\gamma}{\beta}\right) = 0. \tag{3.5.2}$$

- *For $\frac{4(\mu+\gamma)}{\beta} < 1$ if $\mathbb{P}(\tau < \infty) = 1$,*

$$\mathbb{P}\left(\inf_{0 \leq t < \tau} I(t) = 0\right) = \frac{\int_{I_0}^{N+\frac{\mu+\gamma}{\beta}} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy}{\int_{0}^{N+\frac{\mu+\gamma}{\beta}} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy} > 0, \tag{3.5.3}$$

$$\begin{aligned} \mathbb{P}\left(\sup_{0 \leq t < \tau} I(t) = N + \frac{\mu+\gamma}{\beta}\right) &= \frac{\int_{0}^{I_0} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy}{\int_{0}^{N+\frac{\mu+\gamma}{\beta}} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy}, \\ &= 1 - \mathbb{P}\left(\inf_{0 \leq t < \tau} I(t) = 0\right) > 0. \end{aligned} \tag{3.5.4}$$

Furthermore, for the case when $\frac{4(\mu+\gamma)}{\beta} < 1$ if $\mathbb{P}(\tau = \infty) > 0$, then

$$\mathbb{P}\left(\inf_{0 \leq t < \tau} I(t) = 0\right) \geq \frac{\int_{I_0}^{N+\frac{\mu+\gamma}{\beta}} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy}{\int_{0}^{N+\frac{\mu+\gamma}{\beta}} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy} > 0, \tag{3.5.5}$$

$$\mathbb{P}\left(\sup_{0\leq t<\tau} I(t) = N + \frac{\mu+\gamma}{\beta}\right) \geq \frac{\int_0^{I_0} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy}{\int_0^{N+\frac{\mu+\gamma}{\beta}} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy}. \tag{3.5.6}$$

Proof. The proof of Theorem 3.5.1 is established based on the framework of the "Mean Reverting Square Root Process" illustrated in [89] and mentioned in Section 2.9.3. Let us define the drift and diffusion coefficients of our SDE SIS model (3.2.5) as

$$v(x) = \beta(N-x)x - (\mu+\gamma)x, \tag{3.5.7}$$

and

$$w(x) = \sqrt{x(\beta(N-x) + \mu + \gamma)}, \tag{3.5.8}$$

respectively.

As mentioned in Section 2.9.3 and [89], we know that for any given pair of nonnegative constants a and b with $a < I_0 < b$ there is a unique solution, say $M(x)$ satisfying the equation

$$v(x)M'(x) + \frac{1}{2}w^2(x)M''(s) = -1, \quad a < x < b, \tag{3.5.9}$$

with boundary conditions $M(a) = M(b) = 0$. This equation for $M(x)$ is solved in [68] and we shall outline the important aspects of the working for the purpose of completeness. Let us introduce the speed measure

$$m(dx) = \frac{2dx}{p'(x)w^2(x)}, \quad x \in [a,b], \tag{3.5.10}$$

and the Green's function

$$G_{a,b}(x,y) = \frac{(p(x \wedge y) - p(a))(p(b) - p(x \vee y))}{p(b) - p(a)}, \quad x, y \in [a,b], \tag{3.5.11}$$

where the scale function $p(x)$ is defined in [68] as

$$p(x) = \int_c^x exp\left(-2\int_c^\xi \frac{v(\zeta)d\zeta}{w^2(\zeta)}\right) d\xi, x \in \mathbb{R},$$

where $c \in \mathbb{R}$ is a fixed number. This scale function $p(x)$ is a monotonic increasing function of x. By using equations (3.5.10), (3.5.11) and applying the boundary conditions, we could

obtain the explicit solution $M(x)$ as illustrated in [68] that satisfies the equation (3.5.9), namely:

$$\begin{aligned} M_{a,b}(x) &= \int_a^b G_{a,b}(x,y)m(dy), \\ &= -\int_a^x (p(x)-p(y))m(dy) + \frac{p(x)-p(a)}{p(b)-p(a)} \times \\ &\quad \int_a^b (p(b)-p(y))m(dy), \\ &\equiv M(x). \end{aligned} \tag{3.5.12}$$

Since $G_{a,b}(x,y)$ is a nonnegative function, it is clear that $M(x) \equiv M_{a,b}(x)$ is also a nonnegative function. Now, let us define the stopping times:

$$\tau_a = \inf\{t \geq 0 : I(t) \leq a\},$$

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

where $a < I_0 < b$. By the Itô formula we get that:

$$\begin{aligned} M(I(t \wedge \tau_a \wedge \tau_b)) &= M(I_0) - \int_0^{t\wedge\tau_a\wedge\tau_b} dt + \int_0^{t\wedge\tau_a\wedge\tau_b} w(I)M'(I)dB, \\ &= M(I_0) - (t \wedge \tau_a \wedge \tau_b) + \int_0^{t\wedge\tau_a\wedge\tau_b} w(I)M'(I)dB. \end{aligned} \tag{3.5.13}$$

Taking the expectations yields the following results which are similar to the ones that have been illustrated in [89]:

$$\mathbb{E}M(I(t \wedge \tau_a \wedge \tau_b)) = M(I_0) - \mathbb{E}(t \wedge \tau_a \wedge \tau_b) \geq 0,$$

which gives

$$\mathbb{E}(t \wedge \tau_a \wedge \tau_b) \leq M(I_0) < \infty.$$

Consequently this indicates that $I(t)$ exits from every compact subinterval of $\left(0, N + \frac{\mu+\gamma}{\beta}\right)$ in finite expected time, which means that we must have $\mathbb{P}(\tau_a \wedge \tau_b < \infty) = 1$. In addition, by referring to the boundary conditions we get that

$$\lim_{t\to\infty} \mathbb{E}M(I(t \wedge \tau_a \wedge \tau_b)) = 0,$$

and so $\mathbb{E}(\tau_a \wedge \tau_b) = M(I_0)$. Let us now define

$$V(x) = \int_{x_0}^x \exp\left(-\int_{x_0}^y \frac{2v(z)}{w^2(z)}dz\right) dy, \tag{3.5.14}$$

where $x \in \left(0, N + \frac{\mu+\gamma}{\beta}\right)$ and we define $x_0 = \frac{1}{2}(N + \frac{\mu+\gamma}{\beta})$. This function has continuous first and second derivatives $V'(x)$ and $V''(x)$ in $(0, N + \frac{\mu+\gamma}{\beta})$ with strictly nonnegative $V'(x)$, and $V''(x)$ satisfies

$$V''(x) = \frac{-2v(x)}{w^2(x)}V'(x),$$

where $v(x)$ and $w(x)$ are defined as equation (3.5.7) and (3.5.8) respectively. By the Itô formula, we could derive that:

$$V(I(t \wedge \tau_a \wedge \tau_b)) = V(I_0) + \int_0^{t\wedge\tau_a\wedge\tau_b} V'(I(u))w(I(u))dB. \tag{3.5.15}$$

Taking the expectations and letting $t \to \infty$ yields that:

$$\begin{aligned} V(I_0) &= \mathbb{E}V(I(\tau_a \wedge \tau_b)), \\ &= V(a)\mathbb{P}(\tau_a < \tau_b) + V(b)\mathbb{P}(\tau_a > \tau_b). \end{aligned} \tag{3.5.16}$$

By using the fact that the two probabilities must add up to one, we obtain from equation (3.5.16) that:

$$\begin{aligned} \mathbb{P}(\tau_a < \tau_b) &= \frac{V(b) - V(I_0)}{V(b) - V(a)}, \\ &= \frac{\int_{I_0}^b \exp\left(-\int_{I_0}^y \frac{2v(z)}{w^2(z)}dz\right)dy}{\int_a^b \exp\left(-\int_{I_0}^y \frac{2v(z)}{w^2(z)}dz\right)dy}, \end{aligned} \tag{3.5.17}$$

and

$$\begin{aligned} \mathbb{P}(\tau_b < \tau_a) &= \frac{V(I_0) - V(a)}{V(b) - V(a)}, \\ &= \frac{\int_a^{I_0} \exp\left(-\int_{I_0}^y \frac{2v(z)}{w^2(z)}dz\right)dy}{\int_a^b \exp\left(-\int_{I_0}^y \frac{2v(z)}{w^2(z)}dz\right)dy}, \end{aligned} \tag{3.5.18}$$

where equation (3.5.17) represents the probability of hitting a before it reaches b and vice versa for equation (3.5.18). Now by substituting $v(z)$ and $w(z)$ into equation (3.5.14), we get that:

$$V(x) = \int_{x_0}^x \exp\left(-2\int_{x_0}^y \frac{\beta(N-z) - (\mu+\gamma)}{\beta(N-z) + (\mu+\gamma)}dz\right)dy. \tag{3.5.19}$$

In order to simplify the above expression (3.5.19), let us focus on the integral

$$\int_{x_0}^y \frac{\beta(N-z) - (\mu+\gamma)}{\beta(N-z) + (\mu+\gamma)}dz. \tag{3.5.20}$$

By making a simple substitution of the numerator by $\beta(N-z)+(\mu+\gamma)-2(\mu+\gamma)$ and integrating, (3.5.20) becomes

$$\int_{x_0}^{y} \frac{\beta(N-z)-(\mu+\gamma)}{\beta(N-z)+(\mu+\gamma)}dz = (y-x_0)+\frac{2(\mu+\gamma)}{\beta}\log\left(\frac{\beta N-\beta y+\mu+\gamma}{\beta N-\beta x_0+\mu+\gamma}\right). \quad (3.5.21)$$

Now by substituting (3.5.21) into (3.5.19) and recalling that $x_0 = \frac{1}{2}(N+\frac{\mu+\gamma}{\beta})$, we get that

$$V(x) = e^{2x_0}2^{-\frac{4(\mu+\gamma)}{\beta}}\int_{x_0}^{x}\left(\frac{\beta N-\beta y+\mu+\gamma}{\beta N+\mu+\gamma}\right)^{-\frac{4(\mu+\gamma)}{\beta}} e^{-2y}dy. \quad (3.5.22)$$

For the case where $\frac{4(\mu+\gamma)}{\beta} \geq 1$, we have that $V(x)$ tends to a finite (strictly negative) limit as $x \to 0^+$ and that $V(x)$ tends to infinity as $x \to \left[N+\frac{\mu+\gamma}{\beta}\right]^-$, namely:

$$-\infty < V(0^+) < 0 \quad \text{and} \quad V\left(\left[N+\frac{\mu+\gamma}{\beta}\right]^-\right) = \infty. \quad (3.5.23)$$

Recall that:

$$\tau_0 = \lim_{a\downarrow 0}\tau_a, \quad \tau_{N+\frac{\mu+\gamma}{\beta}} = \lim_{b\uparrow N+\frac{\mu+\gamma}{\beta}}\tau_b \quad \text{and} \quad \tau = \tau_0 \wedge \tau_{N+\frac{\mu+\gamma}{\beta}}.$$

Define $\tau_{[a,b]} = \tau_a \wedge \tau_b$. From equations (3.5.17) and (3.5.18) and the above notations, we can work out the probability of $I(t)$ hitting the bottom limit which is as follows:

For $a \in \left(0, N+\frac{\mu+\gamma}{\beta}\right)$,

$$\begin{aligned}\mathbb{P}\left(\inf_{0\leq t<\tau} I(t) \leq a\right) &\geq \mathbb{P}(\tau_a < \tau_b), \\ &= \frac{1-V(I_0)/V(b)}{1-V(a)/V(b)}. \end{aligned} \quad (3.5.24)$$

By letting $b \uparrow N+\frac{\mu+\gamma}{\beta}$, we get that

$$\mathbb{P}\left(\inf_{0\leq t<\tau} I(t) \leq a\right) = 1.$$

But since this holds for any $a > 0$ we must therefore have

$$\mathbb{P}\left(\inf_{0\leq t<\tau} I(t) = 0\right) = 1. \quad (3.5.25)$$

Similarly, the probability of $I(t)$ hitting the top limit $N+\frac{\mu+\gamma}{\beta}$ is:

$$\begin{aligned}\mathbb{P}\left(\sup_{0\leq t<\tau} I(t) \geq b\right) &\geq \mathbb{P}(\tau_b < \tau_a), \\ &= \frac{V(I_0)-V(a)}{V(b)-V(a)}. \end{aligned} \quad (3.5.26)$$

By letting $a \downarrow 0$ we get that

$$\mathbb{P}\left(\sup_{0\leq t<\tau} I(t) \geq b\right) = \frac{V(I_0) - V(0^+)}{V(b) - V(0^+)}.$$

But since this holds for any $b < N + \frac{\mu+\gamma}{\beta}$, then letting $b \uparrow N + \frac{\mu+\gamma}{\beta}$,

$$\mathbb{P}\left(\sup_{0\leq t<\tau} I(t) = N + \frac{\mu+\gamma}{\beta}\right) = 0. \tag{3.5.27}$$

As a result, for the case $\frac{4(\mu+\gamma)}{\beta} \geq 1$, $I(t)$ will reach 0 first before it reaches $N + \frac{\mu+\gamma}{\beta}$ almost surely.

By applying a similar argument for the case where $\frac{4(\mu+\gamma)}{\beta} < 1$, we get that as $x \to 0^+$, $V(x)$ tends to a finite strictly negative limit, whereas as $x \to \left[N + \frac{\mu+\gamma}{\beta}\right]^-$, $V(x)$ tends to a finite strictly nonnegative limit. In other words:

$$-\infty < V(0^+) < 0 \quad \text{and} \quad 0 < V\left[\left(N + \frac{\mu+\gamma}{\beta}\right)^-\right] < \infty. \tag{3.5.28}$$

Furthermore, the probability of $I(t)$ reaching 0 before it reaches $N + \frac{\mu+\gamma}{\beta}$ is given as follows:

$$\begin{aligned}\mathbb{P}\left(\inf_{0\leq t<\tau} I(t) \leq a\right) &\geq \mathbb{P}(\tau_a < \tau_b), \\ &= \frac{\int_{I_0}^{b} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy}{\int_{a}^{b} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy}.\end{aligned} \tag{3.5.29}$$

Letting $b \uparrow N + \frac{\mu+\gamma}{\beta}$ in equation (3.5.29), we get that:

$$\mathbb{P}\left(\inf_{0\leq t<\tau} I(t) \leq a\right) \geq \frac{\int_{I_0}^{N+\frac{\mu+\gamma}{\beta}} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy}{\int_{a}^{N+\frac{\mu+\gamma}{\beta}} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy} > 0, \tag{3.5.30}$$

and since this holds for any $a > 0$, we have that

$$\mathbb{P}\left(\inf_{0\leq t<\tau} I(t) = 0\right) \geq \frac{\int_{I_0}^{N+\frac{\mu+\gamma}{\beta}} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy}{\int_{0}^{N+\frac{\mu+\gamma}{\beta}} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy} > 0. \tag{3.5.31}$$

Similarly, the probability that $I(t)$ reaches $N + \frac{\mu+\gamma}{\beta}$ before it reaches 0 is given as:

$$\begin{aligned}\mathbb{P}\left(\sup_{0\leq t<\tau} I(t) = N + \frac{\mu+\gamma}{\beta}\right) &\geq 1 - \mathbb{P}\left(\tau_0 < \tau_{N+\frac{\mu+\gamma}{\beta}}\right), \\ &= \frac{\int_{0}^{I_0} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy}{\int_{0}^{N+\frac{\mu+\gamma}{\beta}} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy},\end{aligned} \tag{3.5.32}$$

$$> 0.$$

If $\mathbb{P}(\tau < \infty) = 1$, then

$$\mathbb{P}\left(\inf_{0\leq t<\tau} I(t) = 0\right) + \mathbb{P}\left(\sup_{0\leq t<\tau} I(t) = N + \frac{\mu+\gamma}{\beta}\right) \leq 1,$$

and thus the inequalities (3.5.31) and (3.5.32) are actually equalities. This indicates that wherever $I(t)$ starts, there is a nonnegative probability that $I(t)$ will first hit each of zero and $N + \frac{\mu+\gamma}{\beta}$. If $I(t)$ starts exactly halfway between zero and $N + \frac{\mu+\gamma}{\beta}$, then there is a higher probability that $I(t)$ will hit zero before it hits $N + \frac{\mu+\gamma}{\beta}$. However, if $\mathbb{P}(\tau = \infty) > 0$ then all that we can say is as described in inequalities (3.5.31) and (3.5.32), namely

$$\mathbb{P}\left(\inf_{0\leq t<\tau} I(t) = 0\right) \geq \frac{\int_{I_0}^{N+\frac{\mu+\gamma}{\beta}} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy}{\int_{0}^{N+\frac{\mu+\gamma}{\beta}} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy} > 0, \tag{3.5.33}$$

$$\mathbb{P}\left(\sup_{0\leq t<\tau} I(t) = N + \frac{\mu+\gamma}{\beta}\right) \geq \frac{\int_{0}^{I_0} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy}{\int_{0}^{N+\frac{\mu+\gamma}{\beta}} (\beta N - \beta y + \mu + \gamma)^{\frac{-4(\mu+\gamma)}{\beta}} e^{-2y} dy}. \tag{3.5.34}$$

□

Hence in this section we have used the Feller test to calculate the probabilities that $I(t)$ will hit zero before it hits $N + \frac{\mu+\gamma}{\beta}$ and vice versa. In the next section we shall look at some of our analytical results using computer simulations.

3.6 Simulations

In this section we shall use the Milstein numerical simulation method for SDEs (e.g. [121] and Definition 2.6.3) to numerically illustrate Theorem 3.4.1 and Theorem 3.5.1. The Milstein method is superior to the simpler Euler-Maruyama method given in Definition 2.6.2, for example used in [40], because as the integration time-step goes to zero the Milstein method is strongly convergent with order 1 as opposed to 0.5 for the Euler-Maruyama method [60]. Our numerical integration program was written in R and comprehensively verified using a large number of runs. Note that as the Milstein scheme does not preserve positivity, and since we have shown that in this particular model it is theoretically possible for $I(t) > N$, therefore it will cause the simulation to stop if the solution does in fact go below zero.

For Theorem 3.4.1, we first show that the disease will die out in finite time if $R_0 \leq 1$, or $R_0 > 1$ and $N < \frac{1}{4} + \frac{\mu+\gamma}{\beta}$, and explore numerically the situation where $R_0 > 1$ and $N \geq \frac{1}{4} + \frac{\mu+\gamma}{\beta}$.

3.6.1 Simulations on Extinction

In this section, we shall focus on highlighting the results shown in Theorem 3.4.1.

Example 3.6.1 **($R_0 \leq 1$)** *Let the following parameters be given as:*

$$N = 100, \mu = 25, \gamma = 35, \beta = 0.5, \tag{3.6.1}$$

so the SDE SIS model (3.2.5) becomes

$$dI(t) = [0.5(100 - I(t))I(t) - 60I(t)]dt + \sqrt{0.5I(t)(100 - I(t)) + 60I(t)}dB. \tag{3.6.2}$$

Clearly $R_0 = \frac{\beta N}{\mu+\gamma} = 0.833 < 1$, when we could conclude from Theorem 3.4.1 that for any initial value $I(0) = I_0 \in (0, 100)$, the disease will die out in finite time.

Moreover, by substituting the parameters (3.6.1) into the corresponding SIS deterministic model (3.2.6), we have:

$$\frac{dI(t)}{dt} = I(t)[-10 - 0.5I(t)]. \tag{3.6.3}$$

By applying the Milstein method to the SDE SIS model (3.6.2) and its corresponding SIS deterministic model (3.6.3), we have managed to construct the computer simulations illustrated in Figure 3.1 for parameters given by (3.6.1).

Figure 3.1 illustrates two different simulations constructed with different initial values. The simulation on the left hand side represents the behaviour of the model when $I(0) = 90$, while the one on the right hand side represents the behaviour of the model when $I(0) = 1$. For both cases we could see that no matter what we choose our initial value to be, I(t) will eventually die out and hit zero and thus the disease will go extinct. The simulation was repeated for about 50 times with different parameter values satisfying the condition $R_0 \leq 1$ and different initial conditions and in each case the disease died out in finite time. This supports the results of Theorem 3.4.1 on extinction. More examples of simulation where $R_0 \leq 1$ are given in Figure 3.2. Further information can also be obtained from the

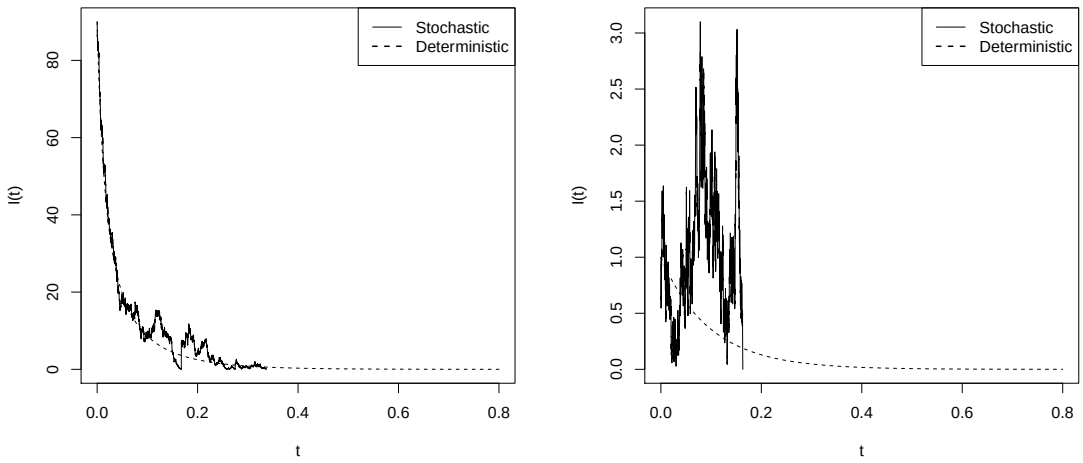

Figure 3.1: Computer simulations of the path $I(t)$ for the SDE SIS model (3.6.2) and the corresponding deterministic SIS model (3.6.3), using the Milstein method with step size $\Delta = 0.0001$ days with initial values $I(0) = 90$ (the left hand side) and $I(0) = 1$ (the right hand side).

simulations, such as the mean of the solution path, for example for Figure 3.2, the solution path on the left hand side with initial value $I(0) = 50$ *has mean value of* $I(t) = 6.295$*, a minimum value of* $I(t) = 0$ *and a maximum value* $I(t) = 55.680$*. On the right hand side of Figure 3.2, the solution path with initial value* $I(0) = 70$ *has mean value of* $I(t) = 12.2$*, a minimum value of* $I(t) = 0$ *and a maximum value of* $I(t) = 70$*. The simulations could also be repeated many times with a given initial value and fixed parameter values, to obtain similar statistics as well as the mean time to extinction and the variance of this time, for example.*

Example 3.6.2 ($R_0 > 1, N < \frac{1}{4} + \frac{\mu+\gamma}{\beta}$) *Let us use parameters*

$$N = 42, \mu = 0.9, \gamma = 20, \beta = 0.5, \tag{3.6.4}$$

so the SDE SIS model (3.2.5) becomes

$$dI(t) = [0.5(42 - I(t))I(t) - 20.9I(t)]dt + \sqrt{0.5I(t)(42 - I(t)) + 20.9I(t)}dB, \tag{3.6.5}$$

and the corresponding SIS deterministic model (3.2.6) becomes:

$$\frac{dI(t)}{dt} = I(t)[0.1 - 0.5I(t)]. \tag{3.6.6}$$

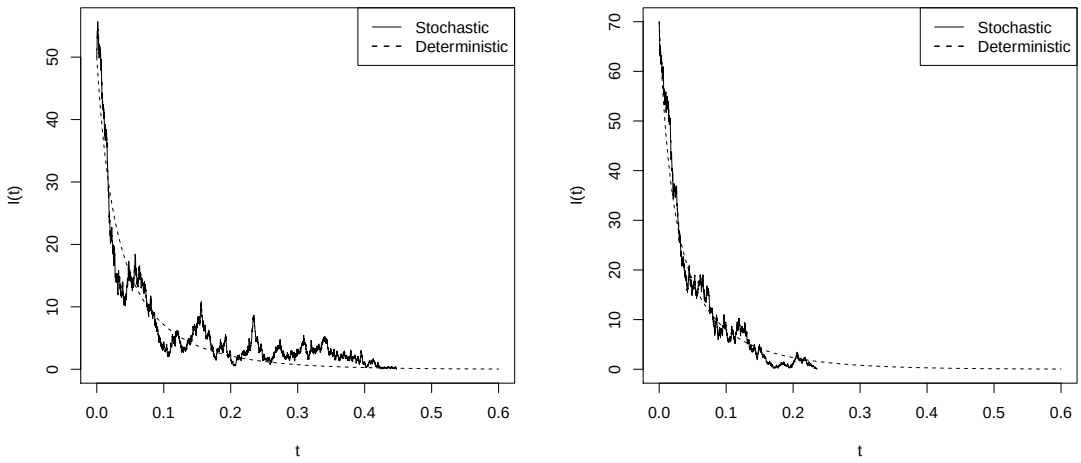

Figure 3.2: Computer simulations of the path $I(t)$ for the SDE SIS model (3.6.2) and the corresponding deterministic SIS model (3.6.3), using the Milstein method with step size $\Delta = 0.0001$ days with initial values $I(0) = 50$ (the left hand side) and $I(0) = 70$ (the right hand side).

It is easy to see that $R_0 = 1.005 > 1$, $N < \frac{1}{4} + \frac{\mu+\gamma}{\beta} = 42.05$ *and thus according to Theorem 3.4.1, for any initial value* $I(0) = I_0 \in (0, 42)$, *the disease will die out in finite time.*

The simulation was repeated with different parameter values satisfying $R_0 > 1$ *and* $N < \frac{1}{4} + \frac{\mu+\gamma}{\beta}$ *and in each case the disease died out in finite time as predicted by Theorem 3.4.1. One such simulation is shown in Figure 3.3 with parameter values as in (3.6.4). More simulations are also given in Figure 3.4 where the solution path on the left hand side has mean value of* $I(t) = 3.256$, *a minimum value of* $I(t) = 0$ *and a maximum value of* $I(t) = 9.315$. *On the right hand side of the same figure, the solution path has mean value of* $I(t) = 8.751$, *a minimum value of* $I(t) = 0$ *and a maximum value of* $I(t) = 30.570$.

Example 3.6.3 ($R_0 > 1, N \geq \frac{1}{4} + \frac{\mu+\gamma}{\beta}$) *From Theorem 3.4.1, we have obtained extinction results on the two cases where* $R_0 \leq 1$ *or where* $R_0 > 1$ *and* $N < \frac{1}{4} + \frac{\mu+\gamma}{\beta}$ *but we cannot determine any theoretical results for the case where* $R_0 > 1$ *and* $N \geq \frac{1}{4} + \frac{\mu+\gamma}{\beta}$. *However, our simulations were also inconclusive. For some parameter values the disease died out in finite time, whereas for others they did not appear to. For example for the parameter values* $N = 100, \mu = 10, \gamma = 30, \beta = 0.5$, *in this case we have that* $R_0 = 1.25 > 1$

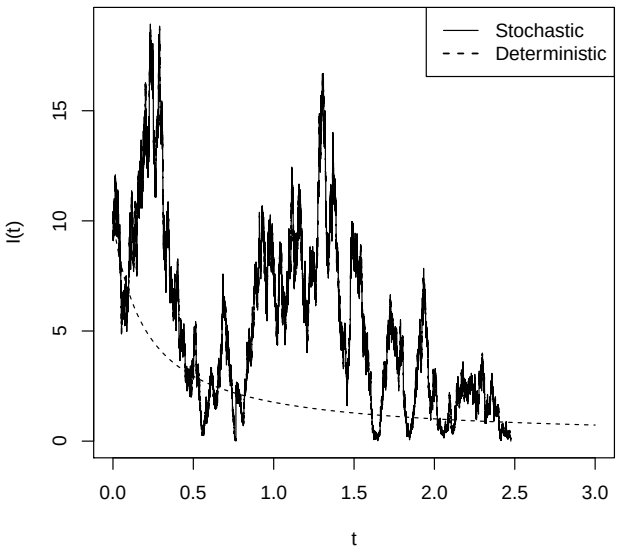

Figure 3.3: Computer simulation of the path $I(t)$ for the SDE SIS model (3.6.5) and its corresponding deterministic SIS model (3.6.6), using the Milstein method with step size $\Delta = 0.0001$ days with initial value $I(0) = 10$.

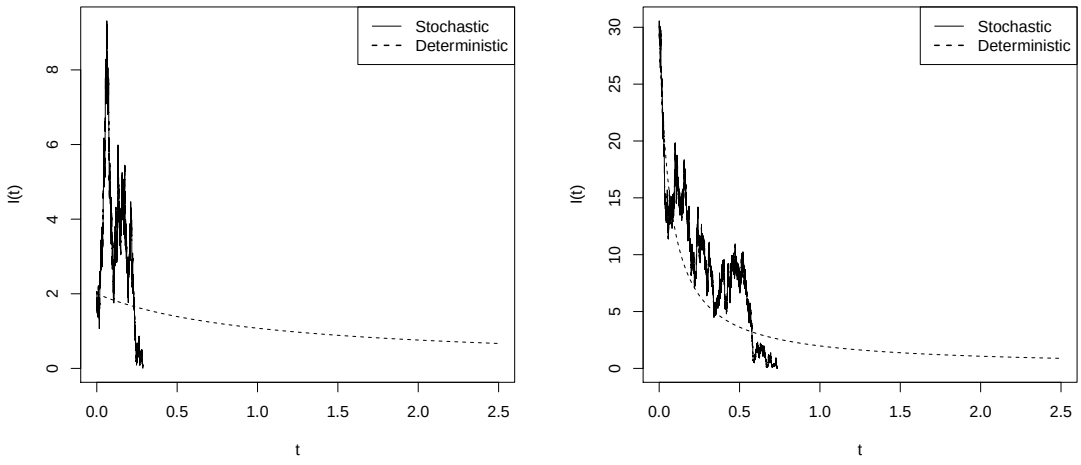

Figure 3.4: Computer simulation of the path $I(t)$ for the SDE SIS model (3.6.5) and its corresponding deterministic SIS model (3.6.6), using the Milstein method with step size $\Delta = 0.0001$ days with initial values $I(0) = 2$ (the left hand side) and $I(0) = 30$ (the right hand side).

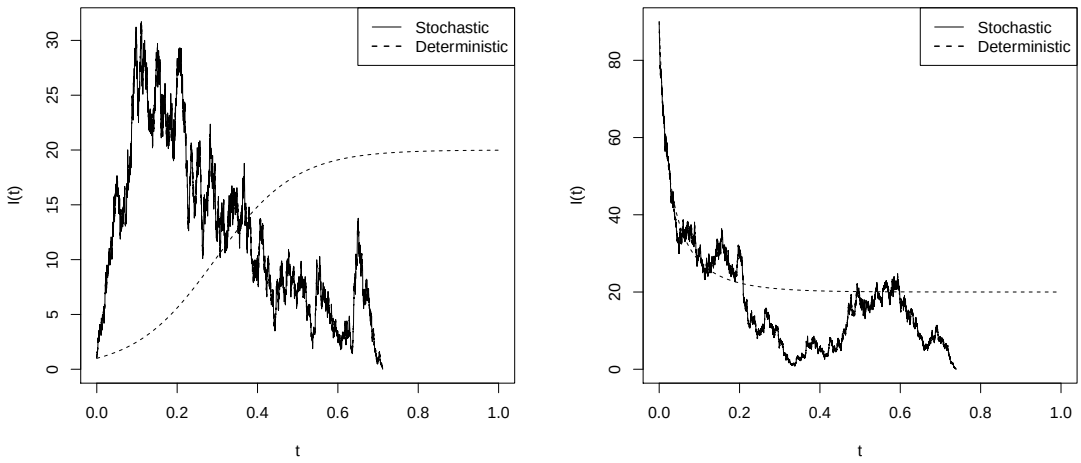

Figure 3.5: Computer simulations of the path $I(t)$ for the SDE SIS model (3.2.5) and the corresponding deterministic SIS model (3.2.6) with parameter values $N = 100, \mu = 10, \gamma = 30$ and $\beta = 0.5$, using the Milstein method with step size $\Delta = 0.0001$ days with initial values $I(0) = 1$ (the left hand side) and $I(0) = 90$ (the right hand side).

and $N > \frac{1}{4} + \frac{\mu+\gamma}{\beta} = 80.25$ *and the simulations produced by substituting these parameters into the SDE SIS model (3.2.5) died out in finite time. For the purpose of illustration, an example of the simulations is shown in Figure 3.5.*

On the other hand, for the parameter values $N = 100, \mu = 10, \gamma = 20, \beta = 0.5$*, in this case we have that* $R_0 = 1.667 > 1$ *and* $N > \frac{1}{4} + \frac{\mu+\gamma}{\beta} = 60.25$ *and here the stochastic simulations seemed to oscillate indefinitely. Here it was not clear that the disease died out in finite time. Again for the purpose of illustration, an example of the simulations is shown in Figure 3.6.*

3.6.2 Simulations on the Feller Test

Similar to Section 3.6.1, we shall apply the Milstein method to reinforce the results that we have shown in Theorem 3.5.1.

Example 3.6.4 ($\frac{4(\mu+\gamma)}{\beta} \geq 1$) *We use parameter values*

$$N = 100, \mu = 25, \gamma = 30, \beta = 0.5, \tag{3.6.7}$$

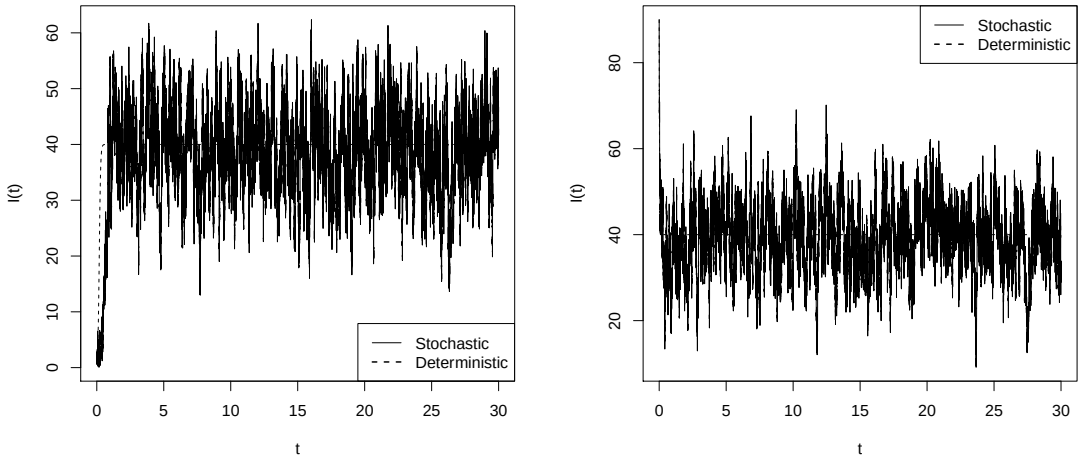

Figure 3.6: Computer simulations of the path $I(t)$ for the SDE SIS model (3.2.5) and the corresponding deterministic SIS model (3.2.6) with $N = 100, \mu = 10, \gamma = 20$ and $\beta = 0.5$, using the Milstein method with step size $\Delta = 0.0001$ days with initial values $I(0) = 1$ (the left hand side) and $I(0) = 90$ (the right hand side).

and by substituting these parameters into the SDE SIS model (3.2.5) and its corresponding SIS deterministic model (3.2.6) we get that:

$$dI(t) = [0.5(100 - I(t))I(t) - 55I(t)]dt + \sqrt{0.5I(t)(100 - I(t)) + 55I(t)}dB, \quad (3.6.8)$$

and

$$\frac{dI(t)}{dt} = I(t)[-5 - 0.5I(t)]. \quad (3.6.9)$$

It is easy to see that $\frac{4(\mu+\gamma)}{\beta} = 440 > 1$ *and thus from Theorem 3.5.1, we conclude that the disease hits zero before* $N + \frac{\mu+\gamma}{\beta}$. *The numerical simulations support these results as expected. Two typical simulations are shown in Figure 3.7. The numerical simulations were repeated with a variety of parameter values and initial conditions.*

Example 3.6.5 ($\frac{4(\mu+\gamma)}{\beta} < 1$) *Consider the parameter values*

$$N = 1, \mu = 0.025, \gamma = 0.09, \beta = 0.5, \quad (3.6.10)$$

so the SDE SIS model (3.2.5) becomes:

$$dI(t) = [0.5(1 - I(t))I(t) - 0.115I(t)]dt + \sqrt{0.5I(t)(1 - I(t)) + 0.115I(t)}dB, \quad (3.6.11)$$

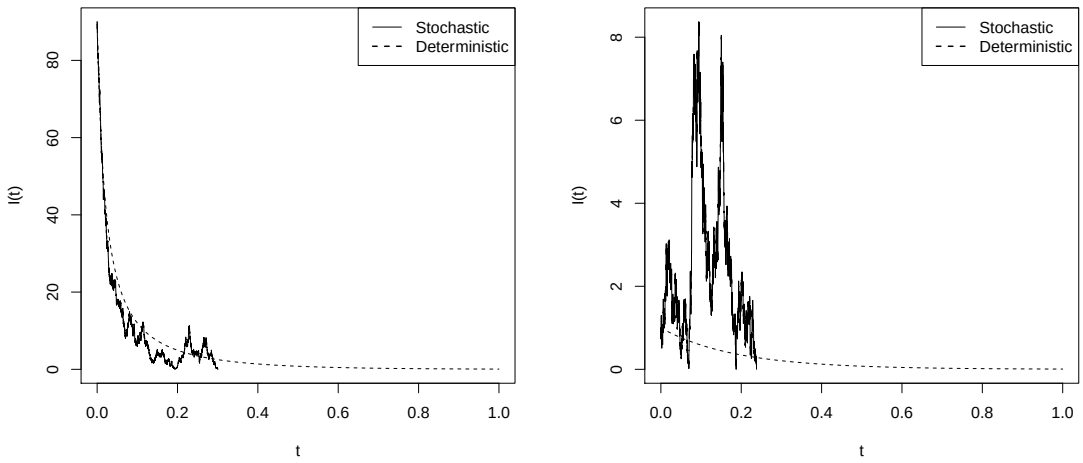

Figure 3.7: Computer simulations of the path $I(t)$ for the SDE SIS model (3.6.8) and the corresponding deterministic SIS model (3.6.9) with parameters $N = 100$, $\mu = 25$, $\gamma = 30$, $\beta = 0.5$, using the Milstein method with step size $\Delta = 0.0001$ days with initial values $I(0) = 90$ (the left hand side) and $I(0) = 1$ (the right hand side).

and its corresponding SIS deterministic model (3.2.6) becomes:

$$\frac{dI(t)}{dt} = I(t)[0.385 - 0.5I(t)]. \tag{3.6.12}$$

For this example, Theorem 3.5.1 says that it is possible for $I(t)$ to hit either zero or $N + \frac{\mu+\gamma}{\beta}$ first. Figure 3.8 illustrates simulations which clearly show that this is the case.

3.6.3 Realistic Examples Simulations

In Sections 3.6.1 and 3.6.2, we have been focusing on using arbitrary parameters to support our theories proved in Theorems 3.4.1 and 3.5.1 respectively. However, it would be better to use parameters for real-life diseases. In this section, we shall look at two different diseases for which an SIS model is suitable: gonorrhea amongst homosexuals and pneumococcus amongst very young children in Scotland. We shall first look at gonorrhea amongst homosexuals. Throughout the section the unit of time is still one day but the population sizes are not scaled as previously. Note that the step size in this section has now changed from $\Delta = 0.0001$ to $\Delta = 0.001$. This is because when running realistic example simulations, the computation time can be very long and thus by choosing a different

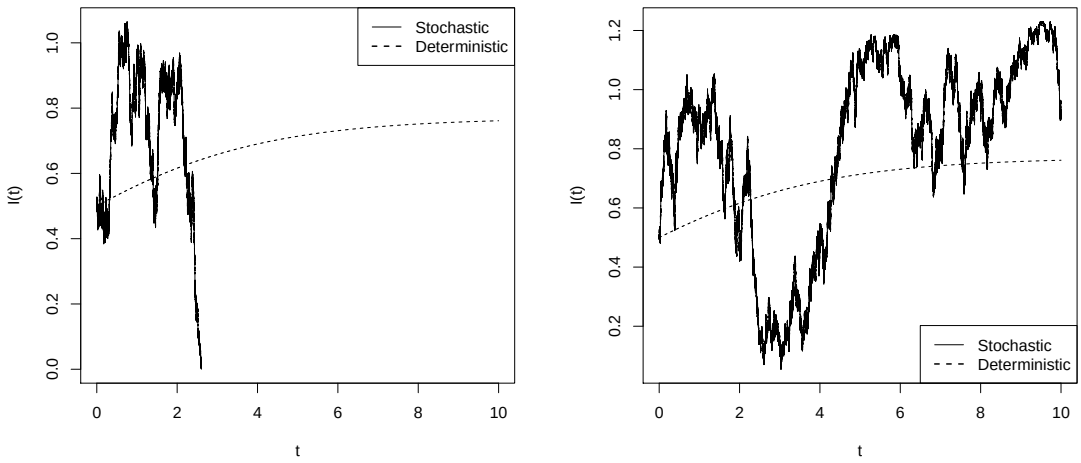

Figure 3.8: Computer simulations of the path $I(t)$ for the SDE SIS model (3.6.11) and the corresponding deterministic SIS model (3.6.12) with parameters $N = 1$, $\mu = 0.025$, $\gamma = 0.09$, $\beta = 0.5$, using the Milstein method with step size $\Delta = 0.0001$ days with initial value $I(0) = 0.5$.

step size, we hope to reduce the computation time.

Note that the demographic SDE SIS epidemic model (3.2.5) is a well established model. This model approximates the system of ordinary differential equations describing the probabilities that there are exactly I infected individuals at time t by a single stochastic differential equation. In the system of ordinary differential equations I never exceeds N but we have shown that in the stochastic differential equation approximation I may possibly exceed N. However, it is important to note that for each example in this section, we have carried out around 50 simulations with realistic parameter values and we have not experienced the case where $I(t)$ exceeds N, although the theoretical possibility remains that it could do so.

Example 3.6.6 (Gonorrhea Model) *From Hethcote and Yorke [58] and Yorke, Hethcote and Nold [135], we have the following parameters:*

$$N = 10,000, R_0 = 1.4, \mu = (1/(40 \times 365.25))/day, \gamma = (1/55)/day$$

which from the above and the equation for R_0 defined by (4.1) we can derive the value for β, namely $\beta = 2.55503 \times 10^{-6}/day$. By numerically simulating equations (3.2.5) and

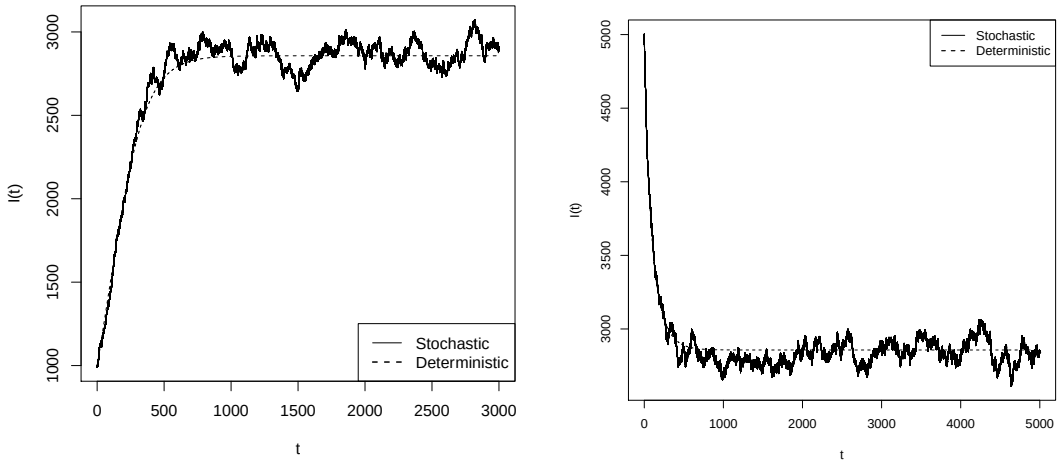

Figure 3.9: Computer simulation of the path $I(t)$ for the Gonorrhea Model with parameters $N = 10,000$, $\mu = (1/(40 \times 365.25))$/day, $\gamma = (1/55)$/day, $\beta = 2.55503 \times 10^{-6}$/day, using the Milstein method with step size $\Delta = 0.001$ days with initial values $I(0) = 1,000$ (the left hand side) and $I(0) = 5,000$ (the right hand side).

(3.2.6), Figure 3.9 is produced.

For this case, as $R_0 > 1$ *and* $N > \frac{1}{4} + \frac{\mu+\gamma}{\beta}$, *Theorem 3.4.1 is inconclusive. For this case Theorem 3.5.1 predicts that* $I(t)$ *will almost surely hit zero in finite time. However, as the time realistically looks likely to be very high it is not feasible to run the simulations for that long. For the simulations shown and the other simulations not shown with both different starting values, and different realistic parameter values with* $R_0 > 1$ *and* $N \geq \frac{1}{4} + \frac{\mu+\gamma}{\beta}$, *after an initial transient stage the stochastic simulations oscillated about the deterministic level.*

To illustrate the situation where $R_0 < 1$, *we shall change the value of* N *which realistically could change. Consider the parameter values*

$$N = 7,000, \mu = (1/(40 \times 365.25))/day, \gamma = (1/55)/day, \beta = 2.55503 \times 10^{-6}/day. \quad (3.6.13)$$

Clearly in this case, $R_0 = 0.98 < 1$ *when we could conclude from Theorem 3.4.1 that for any given initial value* $I(0) \in (0, N)$, *the solution* $I(t)$ *of the SDE SIS model (3.2.5) will die out almost surely with probability one. Furthermore* $\frac{4(\mu+\gamma)}{\beta} > 1$ *whence, from Theorem 3.5.1 we could also conclude that* $I(t)$ *will hit zero before* $N + \frac{\mu+\gamma}{\beta}$ *with probability one.*

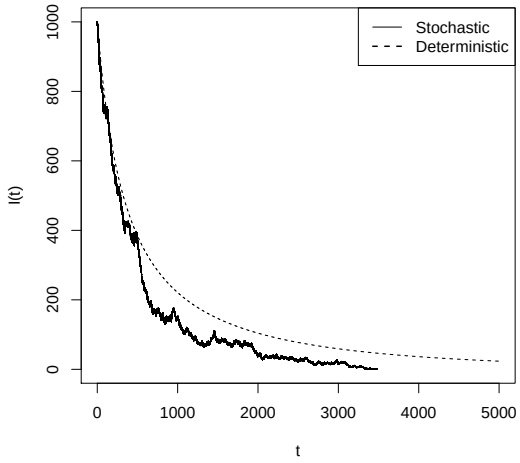

Figure 3.10: Computer simulation of the path $I(t)$ for the Gonorrhea Model with parameters $N = 7,000$, $\mu = (1/(40 \times 365.25))$/day, $\gamma = (1/55)$/day, $\beta = 2.55503 \times 10^{-6}$/day, using the Milstein method with step size $\Delta = 0.001$ days with initial value $I(0) = 1,000$.

The simulation produced by the Milstein method for SDE SIS model (3.2.5) and the corresponding SIS deterministic model (3.2.6) with parameters given by (3.6.13) supports both Theorems 3.4.1 and 3.5.1. One example of the simulations is shown in Figure 3.10. In other words the disease almost surely hits zero before the upper bound and hits zero in finite time almost surely.

The numerical simulations were repeated for around 50 times with different values of N where $R_0 < 1$, and similar results were obtained each time.

Next, we shall look at pneumococcus, especially focussing on children under two years old in Scotland mentioned in Greenhalgh, Lamb and Robertson [51].

Example 3.6.7 (Pneumococcus Model) *In Greenhalgh, Lamb and Robertson's paper [51], they have chosen $N = 150,000$, $\mu = 1/104/week = 1.37363 \times 10^{-3}/day$. In Weir's thesis [125], she chose $\gamma = 1/7.1/week = 0.02011/day$ and in Zhang et al. [137] they chose $\beta = 2 \times 10^{-6}/week = 2.857 \times 10^{-7}/day$. It is easy to see that in this case $R_0 = 2 > 1$ and $N > \frac{1}{4} + \frac{\mu+\gamma}{\beta}$ and thus from Theorem 3.4.1 we are unable to conclude anything. For these parameter values $\frac{4(\mu+\gamma)}{\beta} > 1$ and so ultimately the disease goes extinct, but the time taken for this to happen again seems very large. A numerical simulation produced by these*

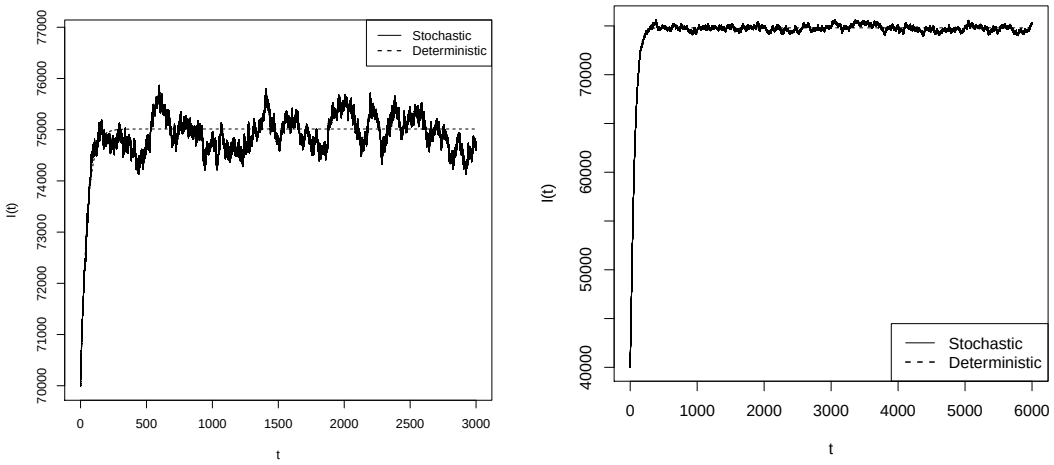

Figure 3.11: Computer simulation of the path $I(t)$ for the Pneumococcus Model with parameters $N = 150,000$, $\mu = 1.37363 \times 10^{-3}$ /day, $\gamma = 0.02011$/day and $\beta = 2.8650 \times 10^{-7}$/ day, using the Milstein method with step size $\Delta = 0.001$ days and with initial values $I(0) = 70,000$ (the left hand side) and $I(0) = 40,000$ (the right hand side).

parameters is shown in Figure 3.11. Again for other simulations not shown with different initial values and different parameter values with $R_0 > 1$ *and* $N \geq \frac{1}{4} + \frac{\mu+\gamma}{\beta}$*, after an initial transient stage the stochastic simulations oscillated about the deterministic level.*

For illustrative purposes, we change N *to* $68,000$ *so that* $R_0 = 0.904 < 1$ *and that* $\frac{4(\mu+\gamma)}{\beta} > 1$*. The numerical simulation produced for this case support both our results in Theorems 3.4.1 and 3.5.1 and thus the disease almost surely hits zero before the upper bound and hits zero in finite time almost surely. Again the numerical simulations were repeated for about 50 times with different values of* N *where* $R_0 < 1$*, and similar results were obtained each time. For the purpose of illustration, an example of the simulations is given in Figure 3.12.*

As we mentioned in Section 3.2 the theoretical results show that if we use the stochastic differential equation approximation suggested by Allen [1] to incorporate demographic stochasticity it becomes theoretically possible for the number of infected individuals to exceed the population size and the number of susceptibles to become negative. This may make us question whether the model is practically useful. However extensive simulations

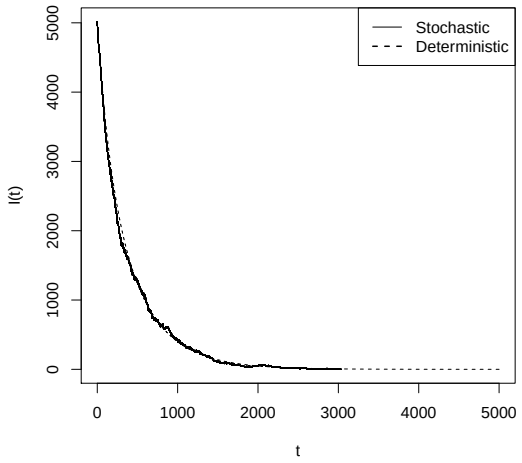

Figure 3.12: Computer simulation of the path $I(t)$ for the Pneumococcus Model with parameters $N = 68,000$, $\mu = 1.37363 \times 10^{-3}$/day, $\gamma = 0.02011$/day and $\beta = 2.8650 \times 10^{-7}$/ day, using the Milstein method with step size $\Delta = 0.001$ days and with initial value $I(0) = 5,000$.

with realistic parameter values for real diseases were performed (some examples have been illustrated above) and in these simulations we never once actually observed the number of susceptibles become negative, although it remains a theoretical possibility. Thus this approximate model may still be useful to illustrate the effect of inherent stochasticity in population dynamics.

3.7 Conclusion and Discussion

The use of epidemic models to control infectious diseases is becoming increasingly common. The SIS epidemic model is one of the simplest epidemic models possible and has been widely used practically to predict the spread of infectious diseases such as gonorrhea and pneumococcus and examine the effect of control strategies. However it ignores random variability in the population. One way to include random variation into the SIS epidemic model is to model the transitions as Markov processes with the appropriate rates and then either perform Monte-Carlo simulations, or derive the differential equations satisfied by $p_i(t)$, the probability that there are exactly i individuals infected by the

disease at time t. The latter approach is illustrated by Bailey [10]. However for realistically large population sizes these approaches rapidly become very cumbersome and use a lot of computational power. Allen [1] suggested to use a stochastic differential equation approximation to simplify the analytical stochastic model so that one had essentially a single stochastic differential equation instead of a very large set of ordinary differential equations. This model has previously been formulated but never analysed. In this chapter we have filled this gap. We showed that this SDE SIS epidemic model has a unique nonnegative bounded solution. Then we derived sufficient conditions for the disease to go extinct in a finite time. This behaviour is different than the behaviour for the SIS model with environmental stochasticity studied in [40] where environmental noise altered the threshold value R_0 from the deterministic model. If the stochastic threshold value R_0^s exceeded one then the disease would persist and oscillate about a non-zero level. In our model, the demographic noise does not alter the threshold value.

Next we used the Feller test to establish the probabilities of the number of infectious individuals hitting the lower and upper boundaries. Finally we used numerical simulations to confirm our analytical results and examine the behaviour of the model for realistic parameter values for gonorrhea and pneumococcus.

The analytical results show that it is theoretically possible for the number of susceptibles to become negative in the solution to the stochastic differential equation model. However in many simulation runs with realistic parameter values this was never actually observed so the stochastic differential equation model remains a useful approximation to illustrate the possible effects of demographic stochasticity on population dynamics.

Motivated by the work done in this chapter, in Chapter 4 we also introduce demographic stochasticity into the deterministic SIS model but now in a different way by modelling births and deaths of individuals independently. Consequently this removes the assumption that an infected individual or a susceptible individual who dies is immediately replaced by a susceptible individual or an infected individual and instead we have a more realistic (and complicated) assumption where the total population size will vary with respect to time.

Chapter 4

Demographic SIS Model with Varying Population Size

4.1 Introduction

In this chapter we will look 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 or a susceptible individual who dies is immediately replaced by a susceptible individual or an infected individual and thus the population size will vary with respect to time. However the reader might argue that the SIS epidemic model given by (1.2.1)-(1.2.2) 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 a school or a large city where doubling the population size could arguably double the number of contacts [30, 139]. However, there are many diseases such as gonorrhea 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. [58]). As a result, it is reasonable to assume that the per capita

disease contact rate λ depends on the population size N [30, 117, 139]. Inspired by this, we obtain the following alternative SIS epidemic model with transmission term $\frac{\lambda(N)}{N}S(t)I(t)$:

$$\frac{dS}{dt} = \mu N - \frac{\lambda(N)}{N}S(t)I(t) + \gamma I(t) - \mu S(t), \tag{4.1.1}$$

$$\frac{dI}{dt} = \frac{\lambda(N)}{N}S(t)I(t) - (\mu + \gamma)I(t). \tag{4.1.2}$$

There are various choices for $\lambda(N)$, for example Anderson and May [6] assume that $\lambda(N)$ is linearly proportional to N for small population size while Busenberg and van den Driessche [16] assume that $\lambda(N)$ does not depend on N. One important conclusion that Anderson [7] obtained is that as N becomes sufficiently large, the function $\lambda(N)$ becomes less dependent on N. In other words, the correlation between N and $\lambda(N)$ becomes weaker for sufficiently large N. This 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 chapter aims to take into consideration cases when the population size tends to a large number and when the population size tends to a small number. We will show that the SIS epidemic model (1.2.1)-(1.2.2) could be derived from (4.1.1)-(4.1.2) 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, we hope this work would fill the gap by providing a thorough analysis of the behaviour of this model.

The chapter is organised as follows: In Section 4.2 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 4.3, 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 nonnegative non-explosive solution is also shown. In Section 4.4 we shall look at the existence of a unique nonnegative solution $(S(t), I(t))$ to the two dimensional SDE SIS epidemic model. In Section 4.5 we examine the conditions for our disease in 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 4.6 and 4.7 respectively.

Most of the work in this chapter has been written up as a paper and is published in [48].

4.2 Demographic Stochasticity for the Two-Dimensional SDE SIS Epidemic Model

Throughout this chapter, 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 (4.1.1)-(4.1.2) 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 $\lambda(0) = \lim_{N\to 0} \lambda(N)$, where it is biologically reasonable to assume that it represents a small population.

We follow the model of Allen [1] outlined above. Unlike the model discussed in Chapter 3, in this case the births and deaths are introduced independently where we are now assuming all individuals (susceptible and infected) are born susceptible which then later may become infected. Furthermore, we have removed the assumption in Chapter 3 that a susceptible or an infected individual who dies is immediately replaced by another susceptible individual. As a result, we have five possible interactions that could occur in the overall population.

These changes and their probabilities to the first order in Δt are shown in Table 4.1 with $\mathbf{x} = (S, I)^T$ and $\mathbf{x}(0) = (S(0), I(0))^T$.

Change	Probability
$\Delta\mathbf{x}_1 = [-1, 0]^T$	$p_1 = \mu S \Delta t$
$\Delta\mathbf{x}_2 = [0, -1]^T$	$p_2 = \mu I \Delta t$
$\Delta\mathbf{x}_3 = [1, 0]^T$	$p_3 = \mu(S + I)\Delta t$
$\Delta\mathbf{x}_4 = [1, -1]^T$	$p_4 = \gamma I \Delta t$
$\Delta\mathbf{x}_5 = [-1, 1]^T$	$p_5 = (\frac{\lambda(N)SI}{N})\Delta t$

Table 4.1: Possible changes between two populations with their corresponding probabilities with births and deaths introduced independently of each other where $\mathbf{x} = (S, I)^T$.

Similar to Chapter 3, the mean change $E(\Delta\mathbf{x})$ and the covariance matrix $\mathbf{V}$ for the time interval Δt are calculated. We use the notation

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

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

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

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 [1] and Allen [2], the SDE SIS model with demographic stochasticity for the dynamics of two interacting populations takes the form:

$$dS(t) = \left[-\frac{\lambda(N)SI}{N} + (\mu+\gamma)I\right]dt + \frac{a+w}{d}\,dW_1 + \frac{b}{d}\,dW_2, \tag{4.2.1}$$

$$dI(t) = \left[\frac{\lambda(N)SI}{N} - (\mu+\gamma)I\right]dt + \frac{b}{d}\,dW_1 + \frac{c+w}{d}\,dW_2, \tag{4.2.2}$$

where $W(t) = (W_1, W_2)^T$ is a two-dimensional Brownian motion. Let us integrate (4.2.1) to get

$$S(t) = S(0) + \int_0^t \left[-\frac{\lambda(N)S(s)I(s)}{N(s)} + (\mu+\gamma)I(s) \right] ds + \int_0^t \frac{a(s)+w(s)}{d(s)}\, dW_1(s) + \int_0^t \frac{b(s)}{d(s)}\, dW_2(s). \tag{4.2.3}$$

Now we define

$$M(t) = \int_0^t \frac{a(s)+w(s)}{d(s)}\, dW_1(s) + \int_0^t \frac{b(s)}{d(s)}\, dW_2(s). \tag{4.2.4}$$

This is a martingale with respect to the filtration [89]. Hence its quadratic variation is given by:

$$\begin{aligned} < M(t) > &= \int_0^t \frac{(a(s)+w(s))^2}{d(s)^2}\, ds + \int_0^t \frac{b(s)^2}{d(s)^2}\, ds, \\ &= \int_0^t \left(\frac{\lambda(N)S(s)I(s)}{N(s)} + (\mu+\gamma)I(s) + 2\mu S(s) \right) ds. \end{aligned} \tag{4.2.5}$$

By the Martingale Representation Theorem in terms of Brownian motion [89], equation (4.2.5) could be written as an Itô integral (e.g. [89]). Hence there exists a Brownian motion W_3 such that

$$M(t) = \int_0^t \sqrt{\frac{\lambda(N)S(s)I(s)}{N(s)} + (\mu+\gamma)I(s) + 2\mu S(s)}\, dW_3(s). \tag{4.2.6}$$

As a result, equation (4.2.3) becomes

$$S(t) = S(0) + \int_0^t \left[-\frac{\lambda(N)S(s)I(s)}{N(s)} + (\mu+\gamma)I(s) \right] ds + \int_0^t \sqrt{\frac{\lambda(N)S(s)I(s)}{N(s)} + (\mu+\gamma)I(s) + 2\mu S(s)}\, dW_3(s), \tag{4.2.7}$$

and thus, equation (4.2.1) could be written as

$$dS(t) = \left[-\frac{\lambda(N)SI}{N} + (\mu+\gamma)I \right] dt + \sqrt{\frac{\lambda(N)SI}{N} + (\mu+\gamma)I + 2\mu S}\, dW_3. \tag{4.2.8}$$

Similarly, the same procedure could be applied to equation (4.2.2) to get

$$dI(t) = \left[\frac{\lambda(N)SI}{N} - (\mu+\gamma)I \right] dt + \sqrt{\frac{\lambda(N)SI}{N} + (\mu+\gamma)I}\, dW_4, \tag{4.2.9}$$

where W_4 is also a Brownian motion.

By using (4.2.1)-(4.2.2) and the fact that $S+I=N$, we have constructed the following SDE model illustrating the behaviour for N:

$$dN(t) = \frac{a+b+w}{d}\, dW_1 + \frac{b+c+w}{d}\, dW_2. \tag{4.2.10}$$

Again, by using the same technique as we have done to obtain equations (4.2.8)-(4.2.9), equation (4.2.10) could be simplified to get

$$dN(t) = \sqrt{2\mu N(t)}\, dW_5 \tag{4.2.11}$$

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 (4.2.11) we get that $N(t)$ satisfies the implicit equation

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

Note that equation (4.2.11) is a very specialised case (with $k=0$) of the mean-reverting square root process or Cox-Ingersoll-Ross model [24, 89] which is given in Section 2.9.3.

The system of SDEs

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

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

$$dI(t) = \left[\frac{\lambda(N)}{N} I(N-I) - (\mu+\gamma)I\right] dt + \sqrt{\frac{\lambda(N)}{N} I(N-I) + (\mu+\gamma)I}\, dW_4, \tag{4.2.12}$$

$$\text{and} \quad dN(t) = \sqrt{2\mu N(t)}\, dW_5, \tag{4.2.13}$$

where $N(t) = S(t) + I(t) > 0$. In the remainder of the chapter we shall focus on showing existence, uniqueness, boundedness, extinction and persistence of the system of equations

(4.2.12)-(4.2.13). In the next section we focus solely on the second of these equations (4.2.13). Throughout this chapter, 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.

4.3 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 $N(t)$ (4.2.13). 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

$$\tau_a = \inf\{t \geq 0 : N(t) \leq a\},$$

$$\tau_n = \inf\{t \geq 0 : N(t) \geq n\},$$

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 4.3.1 *For any given initial value $N(0) = N_0 > 0$, the probability that the SDE (4.2.13) has a unique and nonnegative solution $N(t)$ for all $t \geq 0$ is one, i.e., $N(t) > 0$ almost surely for all $t \geq 0$ and that the solution is non explosive.*

Proof. It is easy to see that our SDE (4.2.13) is a special case of the SDE considered in the "Mean reverting square root process" mentioned by Mao [89] and illustrated in Section 2.9.3 with parameters $\bar{\lambda} = \bar{\mu} = 0$ and $\bar{\sigma} = \sqrt{2\mu}$. Thus, it is easy to see that $N(t) > 0$ for all $t \geq 0$ almost surely. Furthermore, since $\bar{\sigma}^2 > 2\bar{\lambda}\bar{\mu}$, we could conclude from [89] that $\sup_{0 \leq t < \tau} N(t) < \infty$ almost surely where τ is defined as above. Our SDE (4.2.13) also satisifies the localised version of Theorem 3.2 and condition (2.18) mentioned in Chapter IV of [64] which represent the uniqueness theorem and the sufficient condition for non-explosion of solutions respectively. These two requirements are given in Theorem 2.4.3 and Theorem 2.4.4 respectively in this thesis. As a result, we have reached our desired result that there exists a unique, nonnegative and non-explosive solution to the SDE (4.2.13).

□

As a result, this completes our proof on the properties for the SDE (4.2.13), and that we have shown there exists a unique and nonnegative solution $N(t)$ for the SDE (4.2.13).

4.4 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 (4.2.12)-(4.2.13). The existence, uniqueness and non-explosivity of a solution to the SDE (4.2.13) was discussed above. We refer to Ikeda and Watanabe [64] as it is a classic work on this topic. The existence theorem mentioned in [64] (Theorem 2.2 in Chapter IV) holds for a d-dimensional stochastic process, so as a result the existence of a (possibly explosive) solution for our two-dimensional SDE SIS model (4.2.12) -(4.2.13) (or (4.2.8)-(4.2.9)) follows directly. However, the uniqueness theorem mentioned in [64] (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 $b(x) : \mathbb{R} \to \mathbb{R}$ and $\sigma(x) : \mathbb{R} \to \mathbb{R}$ 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 [64] and show that it can be extended to a one-dimensional SDE where the coefficients $b(x, t, \omega) : \mathbb{R} \times \mathbb{R}^+ \times \Omega \to \mathbb{R}$ and $\sigma(x, t, \omega) : \mathbb{R} \times \mathbb{R}^+ \times \Omega \to \mathbb{R}$ are time-dependent stochastic functions where $\omega \in \Omega$. For the purposes of the uniqueness theorem proof we will consider the one-dimensional SDE SIS model (4.2.12) with $N(t, \omega)$ as a given stochastic function $\mathbb{R} \times \Omega \to \mathbb{R}$ (which is the unique nonnegative non-explosive solution to (4.2.13)). We will then prove that the solution to the SDE SIS model (4.2.12) 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 (4.2.12)-(4.2.13) is valid only for $I(t, \omega) \in \left[0, N(t, \omega)\left(1 + \frac{\mu+\gamma}{\lambda(N)}\right)\right]$, as otherwise the term under the square root is negative. Furthermore, as $N \to 0$, $\lambda(N) \to \lambda(0)$. 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. [6, 7]). In Section 4.2, 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 $N \to 0$, or

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

Suppose that n is a given nonnegative integer with $n > |N(0)|$. We now extend the domain of (4.2.12)-(4.2.13) into the whole domain by defining $\lambda_n(x,t,\omega),\ \sigma_n(x,t,\omega) : \mathbb{R} \times \mathbb{R}^+ \times \Omega \to \mathbb{R}$ by

$$\lambda_n(x,t,\omega) = \begin{cases} 0, & \text{for } x < 0, \\ \frac{\lambda(N)x}{N}(N(t\wedge\tau_n,\omega) - x) - (\mu+\gamma)x, & \text{for } 0 \le x \le N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right), \\ \lambda_n\left(N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right), t, \omega\right), & \text{for } x > N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right), \end{cases} \tag{4.4.1}$$

and

$$\sigma_n(x,t,\omega) = \begin{cases} 0, & \text{for } x < 0, \\ \sqrt{\frac{\lambda(N)x}{N}(N(t\wedge\tau_n,\omega) - x) + (\mu+\gamma)x}, & \text{for } 0 \le x \le N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right), \\ 0, & \text{for } x > N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right), \end{cases} \tag{4.4.2}$$

in Case A, or in Case B if $N(t) > 0$. In Case A, if $N(t) \to 0$ and $x \ge 0$ we interpret $\lambda_n(x,t,\omega)$ as zero, and if $N(t) \to 0$ and $x = 0$ we interpret $\sigma_n(x,t,\omega)$ as zero. It is easy to see from (4.4.1)-(4.4.2) that in Case A then as $N(t) \to 0$, then $\lambda_n(x,t,\omega) \to 0$ and $\sigma_n(x,t,\omega) \to 0, \forall x,t,\omega$. In Case B then in the limit as $N(t) \to 0$, (4.4.1)-(4.4.2) become

$$\lambda_n(x,t,\omega) = \begin{cases} 0, & \text{for } x < 0, \\ -\lambda'(0)x^2 - (\mu+\gamma)x, & \text{for } 0 \le x \le \frac{\mu+\gamma}{\lambda'(0)}, \\ \frac{-2(\mu+\gamma)^2}{\lambda'(0)}, & \text{for } x > \frac{\mu+\gamma}{\lambda'(0)}, \end{cases} \tag{4.4.3}$$

and

$$\sigma_n(x,t,\omega) = \begin{cases} 0, & \text{for } x < 0, \\ \sqrt{x\{(\mu+\gamma) - \lambda'(0)x\}}, & \text{for } 0 \le x \le \frac{\mu+\gamma}{\lambda'(0)}, \\ 0, & \text{for } x > \frac{\mu+\gamma}{\lambda'(0)}. \end{cases} \tag{4.4.4}$$

Hence here we take (4.4.3)-(4.4.4) as the definitions of $\lambda_n(x,t,\omega)$ and $\sigma_n(x,t,\omega)$ at $N(t) \to 0$. Note that equations (4.4.3)-(4.4.4) also represent the case with disease transmission term βSI as $N(t) \to 0$. Throughout the rest of the chapter in Case B for $N(t) \to 0$ we interpret $N\left(1 + \frac{\mu+\gamma}{\lambda(N)}\right)$ as $\frac{\mu+\gamma}{\lambda'(0)}$.

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

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

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

$$\lambda(x,t,\omega) = \begin{cases} 0, & \text{for } x < 0, \\ \frac{\lambda(N)x}{N}(N(t,\omega) - x) - (\mu+\gamma)x, & \text{for } 0 \le x \le N(t,\omega)\left(1 + \frac{\mu+\gamma}{\lambda(N)}\right), \\ \lambda\left(N(t,\omega)\left(1 + \frac{\mu+\gamma}{\lambda(N)}\right), t, \omega\right), & \text{for } x > N(t,\omega)\left(1 + \frac{\mu+\gamma}{\lambda(N)}\right), \end{cases} \tag{4.4.5}$$

and

$$\sigma(x,t,\omega) = \begin{cases} 0, & \text{for } x < 0, \\ \sqrt{\frac{\lambda(N)x}{N}(N(t,\omega) - x) + (\mu+\gamma)x}, & \text{for } 0 \le x \le N(t,\omega)\left(1 + \frac{\mu+\gamma}{\lambda(N)}\right), \\ 0, & \text{for } x > N(t,\omega)\left(1 + \frac{\mu+\gamma}{\lambda(N)}\right), \end{cases} \tag{4.4.6}$$

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

The following is the localised version of the uniqueness theorem mentioned in [64]:

Theorem 4.4.1 (Localised version of Uniqueness Theorem) *Suppose that* $x : \mathbb{R}^+ \times \Omega \to \mathbb{R}$. *Consider the SDE*

$$dx(t) = \lambda_n(x,t,\omega)dt + \sigma_n(x,t,\omega)\ dW(t), \tag{4.4.7}$$

with given initial condition $x_n(0)$, *for* $t \le \tau_n$, *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 (4.4.7) for* $t \le \tau_n$ *if for each nonnegative integer* $M \ge 1$*:*

(i) $|\lambda_n(x,t,\omega)-\lambda_n(y,t,\omega)| \leq \kappa_{n,M}(|x-y|)$*, where* $\kappa_{n,M} : [0,M] \to \mathbb{R}$ *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* $\rho_{n,M} : [0,M] \to \mathbb{R}$ *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 [64].

The next stage is to show that our SDE SIS model (4.2.12) satisfies the conditions mentioned in Theorem 4.4.1, in other words the functions $\kappa_{n,M}$ and $\rho_{n,M}$ exist for each n, M.

Lemma 4.4.2 *$\lambda_n(x,t,\omega)$ and $\sigma_n(x,t,\omega)$ defined by (4.4.1) and (4.4.2) satisfy conditions (i) and (ii) of Theorem 4.4.1.*

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

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

for $\mid x \mid \vee \mid y \mid \leq M$, where K_n is independent of ω, x, y and M. Note that the first partial derivative of (4.4.1) is given as

$$\lambda_{n,x}(x,t,\omega) = \begin{cases} 0, & \text{for } x < 0, \\ \lambda(N) - \frac{2\lambda(N)x}{N(t\wedge\tau_n,\omega)} - \mu - \gamma, & \text{for } 0 \leq x \leq N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right), \\ 0, & \text{for } x > N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right), \end{cases} \tag{4.4.8}$$

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 $\xi(t,\omega) \in (x,y) \subset \left[0, N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right)\right]$

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

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

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

Letting $x \to 0^+, y \to \left(N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right)\right)^-$, we deduce that the same result is true if $x, y \in \left[0, N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right)\right]$. It is easy to see that the result follows for $(x,y) \in \mathbb{R}^2$ in Case A.

We will now show that the condition (i) is also satisfied for Case B. Before we begin, it is important for us to show that the term $\frac{N(t\wedge\tau_n,\omega)}{\lambda(N)}$ is bounded away from zero. Let us recall $\lambda(N) = \lambda'(0)N + o(N)$ for $N(t) > 0, N(t) \to 0$ and $\lambda(0) = 0$ where $\lambda'(0) > 0$. Let us consider the following expression

$$\lim_{N\to 0^+} \frac{N(t\wedge\tau_n,\omega)}{\lambda(N)} = \lim_{N\to 0^+} \frac{N(t\wedge\tau_n,\omega)}{\lambda'(0)N(t\wedge\tau_n,\omega) + o(N)} = \frac{1}{\lambda'(0)}, \tag{4.4.9}$$

then $\exists \bar{\varepsilon} > 0$ such that for $N(t\wedge\tau_n,\omega) \leq \bar{\varepsilon}$,

$$0 < \frac{1}{2\lambda'(0)} < \frac{N(t\wedge\tau_n,\omega)}{\lambda(N)} < \frac{2}{\lambda'(0)} < \infty. \tag{4.4.10}$$

In other words, for $N(t\wedge\tau_n,\omega) \in [0,\bar{\varepsilon}]$, the term $\frac{N(t\wedge\tau_m,\omega)}{\lambda(N)}$ is bounded above and below away from zero, while if $N(t\wedge\tau_n,\omega) \in [\bar{\varepsilon}, n]$, then

$$0 < \frac{\bar{\varepsilon}}{\lambda(n)} < \frac{N(t\wedge\tau_n,\omega)}{\lambda(N)} < \frac{n}{\lambda(\bar{\varepsilon})}. \tag{4.4.11}$$

It is easy to see that for $N(t\wedge\tau_n,\omega) \in [0,n]$,

$$0 < \min\left\{\frac{1}{2\lambda'(0)}, \frac{\bar{\varepsilon}}{\lambda(n)}\right\} = k_{1,n} \leq \frac{N(t\wedge\tau_n,\omega)}{\lambda(n)} < \max\left\{\frac{2}{\lambda'(0)}, \frac{n}{\lambda(\bar{\varepsilon})}\right\} = k_{2,n}. \tag{4.4.12}$$

Now by applying a similar method as in Case A, 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 $x, y \in \left[0, N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right)\right]$, as the rest will follow. Therefore, if there exists a constant L_n independent of ω, x, y and M such that

$$\frac{|\sigma_n(x,t,\omega) - \sigma_n(y,t,\omega)|}{\sqrt{|x(t,\omega) - y(t,\omega)|}} \leq L_n, \tag{4.4.13}$$

for $x(t,\omega), y(t,\omega) \in \left[0, N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right)\right]$, then the proof is complete. By choosing $\varepsilon = \frac{1}{4}N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right)$ we then consider separately the regions:

(a) $\varepsilon \le x, y \le N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right) - \varepsilon$,

(b) $0 < x, y \le \varepsilon$,

(c) $N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right) - \varepsilon \le x, y \le N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right)$,

(d) $N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right) - \varepsilon < x \le N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right), 0 < y < \varepsilon$,

and

(e) $0 < x < \varepsilon,\ N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right) - \varepsilon < y \le N(t\wedge\tau_n,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right)$,

it is straightforward to show that (4.4.13) holds $\forall N \ge 0$ in both cases. For (a) similarly to above we find an upper bound for the derivative of $\sigma_n(t,x,\omega)$ in $\left[\varepsilon, N(t\wedge\tau_n)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right)-\varepsilon\right]$. Case B where $N=0$ needs a separate argument but follows the same basic idea. For (b) we multiply the top and bottom of (4.4.13) 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 $|x| \vee |y| \le M$, $\forall t \in \mathbb{R}^+, \omega \in \Omega$. This completes the proof of Lemma 4.4.2.

□

We wish to extend the localised uniqueness Theorem 4.4.1 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 (4.2.12). We cannot use Theorem 2.4 in Chapter IV of [64] 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 $p >\mid I(0) \mid$ define the stopping time for $I(t)$

$$\upsilon_p = \inf\{t \geq 0 :\mid I(t) \mid \geq p\}. \tag{4.4.14}$$

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 equation (4.2.12) is nonnegative and bounded. We can then deduce non-explosivity of the SDEs (4.2.12)-(4.2.13) as a corollary.

Theorem 4.4.3 *For any given initial value $I(0) = I_0 \in (0, N(0))$ and any nonnegative integer $p >\mid I(0) \mid$,*

$$0 \leq I(t \wedge \upsilon_p) \leq N(t \wedge \upsilon_p)\left(1 + \frac{\mu+\gamma}{\lambda(N)}\right), \qquad \text{a.s.} \tag{4.4.15}$$

for all $t \geq 0$.

Note that the result (4.4.15) differs from what one might expect on biological considerations, namely $I(t \wedge \upsilon_p) \in (0, N(t \wedge \upsilon_p))$. However, this is caused by the method we adopted using the idea illustrated in [1] to introduce stochasticity into our two-dimensional process (I, N) given by (4.2.12) - (4.2.13). 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 around 50 simulations with realistic parameter values with some illustrated and discussed later in the chapter and although it is theoretically possible for $I(t)$ to exceed $N(t)$, in practice this was not observed for the simulations with realistic parameter values that we performed. Furthermore, the result (4.4.15) 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 4.4.1 the equation (4.2.12) has a unique non-explosive solution in $[0, T \wedge \tau_n \wedge \upsilon_p]$. The proof for Theorem 4.4.3 is established based on a similar mechanism as the "Square root process" mentioned in [89]. 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 $\Psi_k(a_{k-1}) = \Psi_k(a_k) = 0$

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

We have shown that such a function exists however since the proof is very long and we do not use the workings in the rest of the chapter, the proof is omitted. Define $\varphi_k(x) = 0$ for $x \geq 0$ and

$$\varphi_k(x) = \int_0^{-x} dy \int_0^y \Psi_k(u)du, \qquad \text{for } x < 0. \tag{4.4.16}$$

It is easy to see that $\varphi_k \in C^2(\mathbb{R}, \mathbb{R})$. As in [89]:

$$-1 \leq \varphi_k'(x) \leq 0 \text{ if } -\infty < x < -a_k \text{ or otherwise } \varphi_k'(x) = 0; \tag{4.4.17}$$

$$|\varphi_k''(x)| \leq \frac{2}{k|x|} \text{ if } -a_{k-1} < x < -a_k \text{ or otherwise } \varphi_k''(x) = 0; \tag{4.4.18}$$

and
$$x^- - a_{k-1} \leq \varphi_k(x) \leq x^- \text{ for all } x \in \mathbb{R}, \tag{4.4.19}$$

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 $I(t \wedge \upsilon_p)$ given by (4.4.15). We shall first show that the left hand side of expression (4.4.15) in Theorem 4.4.3 holds. By using Itô's formula, we obtain that for any $t > 0$:

$$\begin{aligned}
&\varphi_k(I(t \wedge \tau_n \wedge \upsilon_p)) \\
&\quad = \quad \varphi_k(I_0) + \int_0^{t\wedge\tau_n\wedge\upsilon_p} \left[\lambda_n(I(s), s, \omega)\varphi_k'(I(s,\omega)) + \frac{\sigma_n(I(s), s, \omega)^2}{2}\varphi_k''(I(s,\omega))\right] ds \\
&\qquad + \int_0^{t\wedge\tau_n\wedge\upsilon_p} \sigma_n(I(s), s, \omega)\varphi_k'(I(s,\omega))\ dW(s),
\end{aligned} \tag{4.4.20}$$

Now from results (4.4.17) and (4.4.18), we know that for $I(t \wedge \tau_n \wedge \upsilon_p) \geq 0$, $\varphi_k'(I(t \wedge \tau_n \wedge \upsilon_p)) = 0$ and $\varphi_k''(I(t \wedge \tau_n \wedge \upsilon_p)) = 0$, thus for all $N \geq 0$ in both cases, (4.4.20) yields:

$$\varphi_k(I(t \wedge \tau_n \wedge \upsilon_p)) \leq \int_0^{t\wedge\tau_n\wedge\upsilon_p} \sigma_n(I(s), s, \omega)\varphi_k'(I(s,\omega))\ dW(s). \tag{4.4.21}$$

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

$$\mathbb{E}\varphi_k(I(t \wedge \tau_n \wedge \upsilon_p)) \leq 0. \tag{4.4.22}$$

Thus,

$$\mathbb{E}I^{-}(t \wedge \tau_n \wedge \upsilon_p) - a_{k-1} \leq \mathbb{E}\varphi_k(I(t \wedge \tau_n \wedge \upsilon_p)) \leq 0. \tag{4.4.23}$$

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

$$\mathbb{E}I^{-}(t \wedge \tau_n \wedge \upsilon_p) \leq 0. \tag{4.4.24}$$

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

$$\mathbb{E}I^{-}(t \wedge \tau_n \wedge \upsilon_p) = 0. \tag{4.4.25}$$

By using proof by contradiction and equation (4.4.25), it is easy to see that for all $t \geq 0$

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

which implies that $\mathbb{P}(I(t \wedge \tau_n \wedge \upsilon_p) \geq 0) = 1$. As a result, $I(t \wedge \tau_n \wedge \upsilon_p) \geq 0$ almost surely. But we have shown in Theorem 4.3.1 that $\tau_n \to \infty$ as $n \to \infty$ almost surely. Hence the left hand side of (4.4.15) holds for all t where $N(t \wedge \upsilon_p) \geq 0$.

By using the same framework and a similar technique as we did previously to prove $I(t \wedge \tau_n \wedge \upsilon_p) \geq 0$, we will now complete the boundedness proof by proving that $I(t \wedge \tau_n \wedge \upsilon_p) \leq N(t \wedge \tau_n \wedge \upsilon_p)\left(1 + \frac{\mu+\gamma}{\lambda(N)}\right)$ a.s. Let us define

$$J(I(t \wedge \tau_n \wedge \upsilon_p)) = N(t \wedge \tau_n \wedge \upsilon_p)\left(1 + \frac{\mu+\gamma}{\lambda(N)}\right) - I(t \wedge \tau_n \wedge \upsilon_p), \tag{4.4.26}$$

if $\lambda(0) > 0, N(t \wedge \tau_n \wedge \upsilon_p) \geq 0$ and

$$J(I(t \wedge \tau_n \wedge \upsilon_p)) = \frac{\mu+\gamma}{\lambda'(0)} - I(t \wedge \tau_n \wedge \upsilon_p), \tag{4.4.27}$$

if $\lambda(0) = 0, N(t \wedge \tau_n \wedge \upsilon_p) \geq 0$ and $\lambda'(0) > 0$. Note that (4.4.27) is similar to the case with transmission rate βSI with $N(t \wedge \tau_n \wedge \upsilon_p, \omega) \to 0$. Let us now focus on Case A where $\lambda(0) > 0$ for $N(t \wedge \tau_n, \wedge \upsilon_p) \geq 0$, as we will show later that the results for the case $\lambda(0) = 0$ will follow. Then, from Itô's formula on equation (4.4.26), we get:

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

Here

$$\lambda(J(I(t\wedge\tau_n\wedge\upsilon_p)) \;=\; \begin{cases} -2(\mu+\gamma)\left[N(t\wedge\tau_n\wedge\upsilon_p,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right)\right], \\ \qquad \text{for } J(t\wedge\tau_n\wedge\upsilon_p)<0, \\ \left[N(t\wedge\tau_n\wedge\upsilon_p,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right)-J(I(t\wedge\tau_n\wedge\upsilon_p))\right]\times \\ \qquad\qquad \left(\frac{\lambda(N)J(I(t\wedge\tau_n\wedge\upsilon_p))}{N}-2(\mu+\gamma)\right), \\ \qquad \text{for } 0\le J(t\wedge\tau_n\wedge\upsilon_p)\le N(t\wedge\tau_n\wedge\upsilon_p,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right), \\ 0, \qquad \text{for } J(t\wedge\tau_n\wedge\upsilon_p)>N(t\wedge\tau_n\wedge\upsilon_p,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right), \end{cases}$$

and

$$\sigma(J(I(t\wedge\tau_n\wedge\upsilon_p))$$

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

Note that for the case where $\lambda(0)=0$, we can obtain the corresponding $\lambda(J(I(t\wedge\tau_n\wedge\upsilon_p))$ and $\sigma(J(I(t\wedge\tau_n\wedge\upsilon_p))$ by simply setting $\lambda(N)=\lambda'(0)N(t\wedge\tau_n\wedge\upsilon_p,\omega)+o(N)$ in the above expressions. Again the result in this case is similar to the model with transmission term βSI with $N(t\wedge\tau_n\wedge\upsilon_p,\omega)\to 0$.

By Itô's formula, we derive that:

$$\begin{aligned}\varphi_k(J(t\wedge\tau_n\wedge\upsilon_p)) &= \varphi_k(J_0)+\int_0^{t\wedge\tau_n\wedge\upsilon_p}\left[P(J(s))+Q(J(s))\right]ds \\ &\quad -\int_0^{t\wedge\tau_n\wedge\upsilon_p}\sigma(J(s),s,\omega)\varphi_k'(J(s))\;dW(s), \qquad (4.4.28)\end{aligned}$$

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

$$P(x,t,\omega) = \begin{cases} 2(\mu+\gamma)N(t\wedge\tau_n\wedge\upsilon_p,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right)\varphi_k'(x), \\ \qquad\qquad \text{for } x<0, \\ N(t\wedge\tau_n\wedge\upsilon_p,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}-x\right)\left(2(\mu+\gamma)-\frac{\lambda(N)x}{N}\right)\varphi_k'(x), \\ \qquad\qquad \text{for } 0\le x\le N(t\wedge\tau_n\wedge\upsilon_p,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right), \\ 0, \qquad\qquad \text{for } x> N(t\wedge\tau_n\wedge\upsilon_p,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right), \end{cases} \tag{4.4.29}$$

$$Q(x,t,\omega) = \begin{cases} \left(\frac{x}{2}\right)\left[\frac{\lambda(N)}{N}(N(t\wedge\tau_n\wedge\upsilon_p,\omega)-x)+(\mu+\gamma)\right]\varphi_k''(x), \\ \qquad\qquad \text{for } \ 0\le x\le N(t\wedge\tau_n\wedge\upsilon_p,\omega)\left(1+\frac{\mu+\gamma}{\lambda(N)}\right), \\ 0, \qquad\qquad \text{otherwise.} \end{cases} \tag{4.4.30}$$

Again, we can obtain the expressions for $P(x,t,\omega)$ and $Q(x,t,\omega)$ for the case $\lambda(0)=0$ by simply setting $\lambda(N)=\lambda'(0)N(t\wedge\tau_n\wedge\upsilon_p,\omega)+o(N)$ in the above expressions. So $P(x,t,\omega)\le 0$ and $Q(x,t,\omega)=0$ for all x.

Thus

$$\varphi_k(J(t\wedge\tau_n\wedge\upsilon_p)) \le -\int_0^{t\wedge\tau_n\wedge\upsilon_p} \sigma(J(s),s,\omega)\varphi_k'(J(s))\,dW(s).$$

Now take the expectations to get $\mathbb{E}\varphi_k(J(t\wedge\tau_n\wedge\upsilon_p))\le 0$. Hence, $\mathbb{E}J^-(t\wedge\tau_n\wedge\upsilon_p)-a_{k-1}\le \mathbb{E}\varphi_k(J(t\wedge\tau_n\wedge\upsilon_p))\le 0$. As $k\to\infty,\ a_{k-1}\to 0$, thus $\mathbb{E}J^-(t\wedge\tau_n\wedge\upsilon_p)\le 0$. Similarly to the argument we used for proving the left hand side of equation (4.4.15), it is clear that for all $t>0$,

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

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

Theorem 4.4.4 $\lim_{p\to\infty}\upsilon_p=\infty$.

Proof. Clearly υ_p is increasing in p. Define $\upsilon_\infty=\lim_{p\to\infty}\upsilon_p$ (possibly infinite). We will prove this theorem by proof by contradiction. Let us assume that the opposite is true.

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

$$\mathbb{E}(I(T \wedge \upsilon_p)^2) \geq \tfrac{\delta p^2}{2} \to \infty \text{ as } p \to \infty.$$

However now consider the one dimensional SDE (4.2.13) for $N(t)$. By the proof of Theorem 2.4 in Chapter IV of [64],

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

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

$$\mathbb{E}[I(t \wedge \upsilon_p)^2] \leq \mathbb{E}[N(t \wedge \upsilon_p)^2] \left(1 + \frac{\mu + \gamma}{\lambda(0)}\right)^2 \leq M_T \left(1 + \frac{\mu + \gamma}{\lambda(0)}\right)^2 = M_{2T} < \infty, \quad (4.4.31)$$

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

$$\mathbb{E}(I(t \wedge \upsilon_p)^2) \leq K^2(1 + 2\mathbb{E}|N(t \wedge \upsilon_p)| + \mathbb{E}N(t \wedge \upsilon_p)^2) < K^2(1 + 2M_{1T} + M_T) = M_{3T} < \infty. \quad (4.4.32)$$

In both cases, this is a contradiction, hence $\mathbb{P}(\upsilon_\infty < \infty) = 0$, i.e. $\upsilon_\infty = \infty$ almost surely. This completes the proof of Theorem 4.4.4. □

Corollary 4.4.5 *The solution $(I(t), N(t))$ to the SDE system (4.2.12)-(4.2.13) 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 $p \to \infty$ in (4.4.31) and (4.4.32) 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.

Corollary 4.4.6 $0 \leq I(t) \leq N(t)\left(1 + \frac{\mu+\gamma}{\lambda(N)}\right)$ *a.s.*

Proof. This is straightforward letting $p \to \infty$ in Theorem 4.4.3.

Corollary 4.4.7 *There exists a unique strong pathwise solution to the SDEs (4.2.12)-(4.2.13) 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 (4.2.12)-(4.2.13) 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 $\tau_n \to \infty$ as $n \to \infty$ and $\upsilon_p \to \infty$ as $p \to \infty$ so for some strictly nonnegative integers n and p the solutions $\mathbf{x}_1(t \wedge \tau_n \wedge \upsilon_p, \omega)$ and $\mathbf{x}_2(t \wedge \tau_n \wedge \upsilon_p, \omega)$ must differ on a set Ω_3 with $\mathbb{P}(\Omega_3) > 0$. This contradicts Theorem 4.4.1. Hence the solution is unique.

So we have shown that there is a unique pathwise strong non-explosive solution to the SDEs (4.2.12) and (4.2.13). The same result is true for the system (S, I, N) given by $S = N - I$, (4.2.12) and (4.2.13). In the next section we shall look at extinction of our SDE system.

4.5 Extinction of the Number of Infecteds and the Total Number of Individuals

For the rest of this chapter we shall focus on analysing the behaviour for the two dimensional SDE SIS model (4.2.12)-(4.2.13). 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 (4.2.13) does become extinct almost surely and then deduce that $I(t)$ becomes extinct almost surely.

Corollary 4.5.1 *For any given initial value of $N_0 = N(0) > 0$, 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 (4.2.13) is a special case of the mean-reverting square root process with zero drift coefficient and thus from [89]

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

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

$$\sqrt{N(t\wedge\tau_a,\omega)} = \sqrt{N(0)} + \int_0^{t\wedge\tau_a} q(N(s,\omega))ds + \int_0^{t\wedge\tau_a} \frac{\sqrt{2\mu}}{2} dW(s), \tag{4.5.1}$$

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

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

Letting $t \to \infty$ 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.

Theorem 4.5.2 *For any given initial value $I(0) = I_0 \in (0, N)$, the solution to our two-dimensional SDE SIS model (4.2.12)-(4.2.13), $I(t)$, will reach zero with probability one in finite time and thus the disease will die out almost surely.*

Proof. From Corollary 4.5.1, we have shown that $\exists t_0 < \infty$ such that $N(t_0) = 0$ almost surely. From Corollary 4.4.6, 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 as $N(t) \to 0$, $N(t)\left(1 + \frac{\mu+\gamma}{\lambda(N)}\right) \to 0$, so there exists t_0 such that $N(t_0) = 0$ almost surely. By letting $t \to t_0$, $I(t_0) = 0$ almost surely.

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

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

where we set $\inf \emptyset = \infty$. The aim of our proof is to show that $\mathbb{P}(\upsilon_0 < \infty) = 1$, where $\upsilon_0 = \lim_{b \downarrow 0} \upsilon_b$ and this can be shown by proof by contradiction. Let us assume the opposite is true, i.e. $\mathbb{P}(\upsilon_0 = \infty) = \bar{\delta} > 0$. As $\tau_0 < \infty$ almost surely, we can choose T such that $\mathbb{P}(\tau_0 \leq T) \geq 1 - \frac{\bar{\delta}}{3}$. For $t \geq T$, $\lim_{b \downarrow 0} \mathbb{P}(\upsilon_b \geq t) = \mathbb{P}(\upsilon_0 \geq t) \geq \bar{\delta}$. So by choosing $b > 0$ small enough $\mathbb{P}(\upsilon_b \geq t) \geq \frac{2\bar{\delta}}{3} > 0$. Hence

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

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

$$\sqrt{I(t \wedge \upsilon_b)} = \sqrt{I(t \wedge \tau_0)} + \int_{t\wedge\tau_0}^{t\wedge\upsilon_b} U(I(s), s, \omega)ds + \frac{1}{2}\int_{t\wedge\tau_0}^{t\wedge\upsilon_b} \sqrt{\frac{\lambda(N)}{N}(N - I) + \mu + \gamma}\, dW(s), \tag{4.5.2}$$

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

$$U(x, t, \omega) = \frac{\sqrt{x}}{2}\left(\frac{\lambda(N)}{N}(N - x) - \mu - \gamma\right) - \frac{1}{8\sqrt{x}}\left(\frac{\lambda(N)}{N}(N - x) + \mu + \gamma\right). \tag{4.5.3}$$

Here $\frac{\lambda(N)}{N}$ is interpreted as $\lambda'(0)$ as $N = 0$. Taking expectations of (4.5.2) we deduce that

$$0 \leq \mathbb{E}\Big(\sqrt{I(t \wedge \upsilon_b)}\Big) \leq \mathbb{E}\Big(\sqrt{I(t \wedge \tau_0)}\Big) + \mathbb{E}\int_{t\wedge\tau_0}^{t\wedge\upsilon_b} U(I, s, \omega)ds. \tag{4.5.4}$$

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

$$\begin{aligned} U(x,s,\omega) &= \frac{\sqrt{x}}{2}(-\lambda'(0)x - \mu - \gamma) - \frac{1}{8\sqrt{x}}(-\lambda'(0)x + \mu + \gamma), \\ &\leq -\frac{\lambda'(0)}{2}x^{\frac{3}{2}} - (\mu+\gamma)\frac{\sqrt{x}}{2}, \text{ by letting } p \to \infty \text{ in (4.4.15) with } N = 0. \\ &\leq -\frac{\lambda'(0)}{2}b^{\frac{3}{2}}, \qquad \text{if } x \geq b. \end{aligned}$$

Hence there exists an $\varepsilon_1 > 0$ such that $U(x,s,\omega) \leq -\varepsilon_1$ when $x \geq b$. From (4.5.4) we deduce that for $t \geq T$,

$$0 \leq \mathbb{E}\Big(\sqrt{I(t \wedge \tau_0)}\Big) - \bar{\delta}_1\varepsilon_1(t-T),$$

so
$$\bar{\delta}_1\varepsilon_1(t-T) \leq \mathbb{E}\Big(\sqrt{I(t \wedge \tau_0)}\Big). \tag{4.5.5}$$

But by the Fatou-Lebesgue Theorem

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

This contradicts (4.5.5) hence we have $\mathbb{P}(\upsilon_0 = \infty) = 0$ and this completes the proof of Theorem 4.5.2. □

So in the two dimensional SIS model both $N(t)$ and $I(t)$ (hence also $S(t)$) die out almost surely in finite time. Note that the extinction results given in Corollary 4.5.1 and Theorem 4.5.2 are caused by the assumptions that we made at the beginning of this chapter where individuals are all introduced as susceptibles and we have introduced deomographic stochasticity into the model by assuming the births and deaths are independent of each other.

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 4.5.

4.6 Simulations to Illustrate the Analytical Results

In the previous sections, we managed to prove several theorems for our two-dimensional SDE SIS model (4.2.12)-(4.2.13). In this section, we will focus on applying the Milstein

method (e.g. [121]) to produce simulations using R to support the results that we have shown. In this chapter, we have decided to use the Milstein method instead of the simpler Euler-Maruyama method which is commonly used in many papers, for example [40]. 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 [60]. Note that since we are using the Milstein method which does not preserve positivity, therefore the simulations will stop if the solution path goes below zero.

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

$$dI(t) = [\beta I(t)(N(t) - I(t)) - (\mu + \gamma)I]dt + \sqrt{\beta I(N - I) + (\mu + \gamma)I}\, dW_6, \quad (4.6.1)$$

$$\text{and } dN(t) = \sqrt{2\mu N(t)}\, dW_7, \quad (4.6.2)$$

where again W_6 and W_7 are Brownian motions and illustrate the result given by Corollary 4.5.1, namely there exists some $t > 0$ such that $N(t) = 0$ almost surely. Then we will integrate the two-dimensional system for $(I(t), N(t))$ given by (4.6.1)-(4.6.2). Simulations are produced to support the results shown in Theorem 4.5.2 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 (with around 50 simulations being carried out for each example) and also in both cases the simulations were repeated using different parameter values and in each case the analytical results were verified. Note that in some examples we have chosen a different step size Δt in order to improve on the computation time.

4.6.1 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 4.5.1.

Example 4.6.1 *Suppose that the population size is measured in units of one million. By*

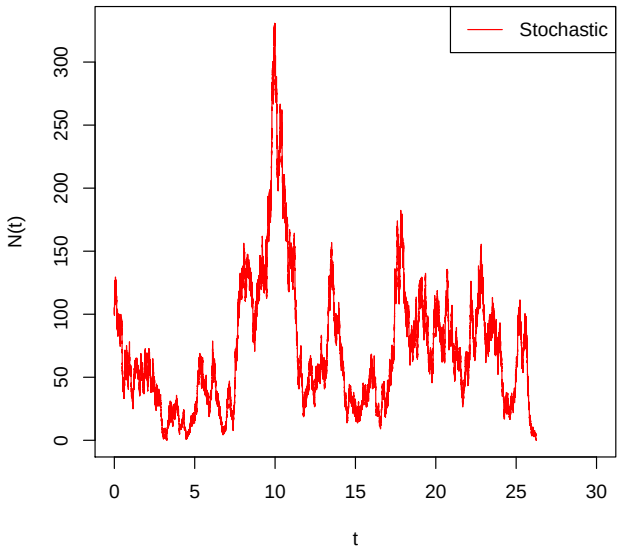

Figure 4.1: Computer simulation of the path $N(t)$ for the SDE model (4.6.3) using the Milstein method with step size $\Delta = 0.001$ days with initial value $N(0) = 100$.

choosing $\mu = 25$*, the SDE model for* $N(t)$ *(4.6.2) becomes*

$$dN(t) = \sqrt{50N(t)}\, dW(t). \tag{4.6.3}$$

By Corollary 4.5.1, we could conclude that there exists $t > 0$ *such that* $N(t) = 0$ *almost surely.*

Clearly, Figure 4.1 supports the result illustrated in Corollary 4.5.1 and that the solution $N(t)$ *to the SDE model for N (4.2.13) does in fact die out in finite time. In addition, Figure 4.1 also supports the results shown in Theorem 4.3.1 by showing that the solution* $N(t)$ *will not explode in finite time. The simulation was repeated around 50 times with different values of* μ *and similar results were obtained each time to support the results shown in Corollary 4.5.1 and Theorem 4.3.1.*

4.6.2 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 equations (4.6.1)-(4.6.2) to support the results given in Theorem 4.5.2.

Example 4.6.2 *($R_0 < 1$) Again suppose that the population size is measured in units of one million. Let us choose the following parameter values*

$$N_1 = 80, \mu = 15, \gamma = 35, \beta = 0.5, \tag{4.6.4}$$

where N_1 is the N value we choose for our deterministic SIS model given by (1.2.1)-(1.2.2) with $R_0 = 0.8$. By substituting the parameter values (4.6.4) into the SDE SIS model (4.6.1) - (4.6.2) we have that

$$dI(t) = [0.5I(t)(N(t) - I(t)) - 50I(t)]dt + \sqrt{0.5I(t)(N(t) - I(t)) + 50I(t)}\, dW_6(t),$$

and

$$dN(t) = \sqrt{30}\, dW_7(t), \tag{4.6.5}$$

with the corresponding SIS deterministic model as:

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

and

$$\frac{dI(t)}{dt} = [-50 + 0.5S(t)]I(t). \tag{4.6.6}$$

Based on the result shown in Theorem 4.5.2, we would expect to see the solution $I(t)$ to the SDE SIS model (4.6.1)-(4.6.2) die out in finite time almost surely. From both figures illustrated in Figure 4.2, we can see that the numerical simulations support the result given in Theorem 4.5.2 by illustrating that the solution $I(t)$ dies out in finite time. Similarly, the numerical simulations were repeated around 50 times with different parameter values where $R_0 \leq 1$ and the same conclusion is obtained verifying the results obtained in Corollary 4.5.1 and Theorem 4.5.2 for our two-dimensional SDE SIS model (4.6.1)-(4.6.2).

Next we would like to verify that the result illustrated in Theorem 4.5.2 also holds for the case where $R_0 > 1$.

Example 4.6.3 *($R_0 > 1$) Suppose that the population size is measured in units of one million. Let us now choose the following parameter values*

$$N_1 = 100, \mu = 10, \gamma = 25, \beta = 0.5, \tag{4.6.7}$$

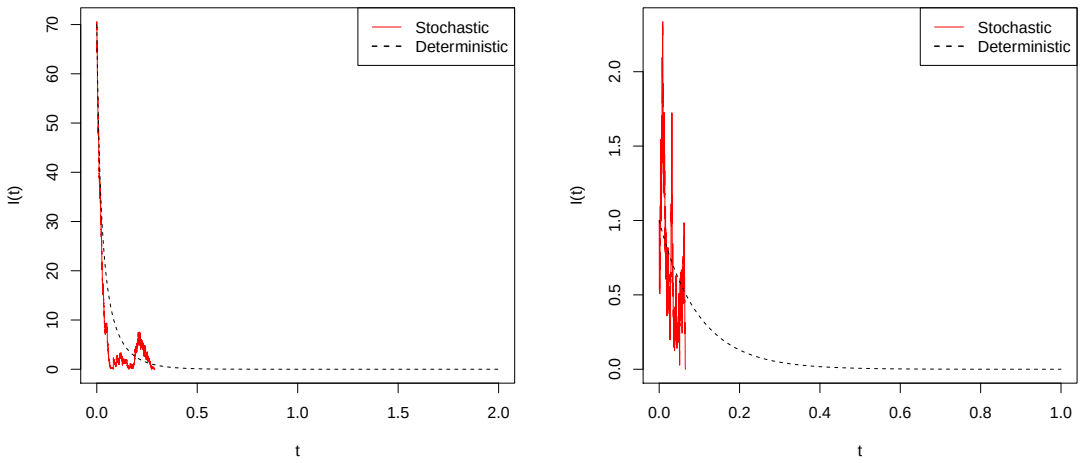

Figure 4.2: Computer simulations of the path $I(t)$ for the SDE SIS model (4.6.5) and the solution $I(t)$ for the corresponding deterministic SIS model (4.6.6), using the Milstein method with step size $\Delta = 0.0001$ days with initial values $I(0) = 70$ (the left hand side) and $I(0) = 1$ (the right hand side) both with $N(0) = 80$.

where N_1 is the N value we choose for our deterministic SIS model given by (1.2.1)-(1.2.2) where now $R_0 = 1.43$. Similar to Example 4.6.2, by substituting the parameter values (4.6.7) into the SDE SIS model (4.6.1) - (4.6.2) we have that

$$dI(t) = [0.5I(t)(N(t) - I(t)) - 35I(t)]dt + \sqrt{0.5I(t)(N(t) - I(t)) + 35I(t)}\, dW_6(t),$$

and

$$dN(t) = \sqrt{20}\, dW_7(t), \tag{4.6.8}$$

with the corresponding SIS deterministic model as:

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

and

$$\frac{dI(t)}{dt} = [-35 + 0.5S(t)]I(t). \tag{4.6.9}$$

For the case where $R_0 > 1$, we could see from Figure 4.3 that the simulations produced once again support our results mentioned in Theorem 4.5.2, namely the solution $I(t)$ to (4.6.1)-(4.6.2) dies out in finite time. Similar to Example 4.6.2, the numerical simulations were carried out about 50 times with different parameter values where $R_0 > 1$, and the

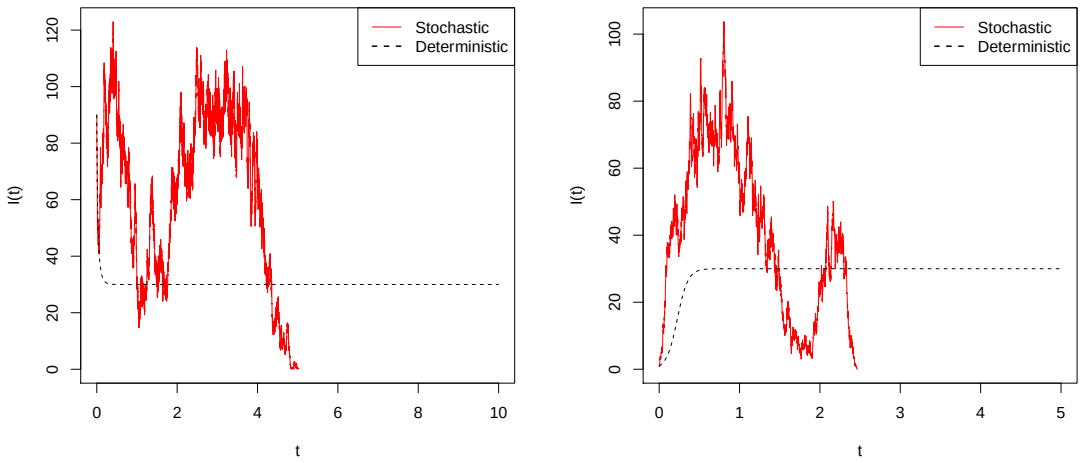

Figure 4.3: Computer simulations of the path $I(t)$ for the SDE SIS model (4.6.8) and the solution $I(t)$ for the corresponding deterministic SIS model (4.6.9), using the Milstein method with step size $\Delta = 0.001$ days with initial values $I(0) = 90$ (the left hand side) and $I(0) = 1$ (the right hand side) both with $N(0) = 100$.

same conclusion is drawn to support the results obtained in Corollary 4.5.1 and Theorem 4.5.2 for (4.6.1)-(4.6.2).

4.7 Realistic Simulations

In Section 4.6 we have been focusing on using theoretical parameter values to show that the solution (I, N) to (4.6.1)-(4.6.2) shown in Corollary 4.5.1 and Theorem 4.5.2 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 in Greenhalgh, Lamb and Robertson [51] 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

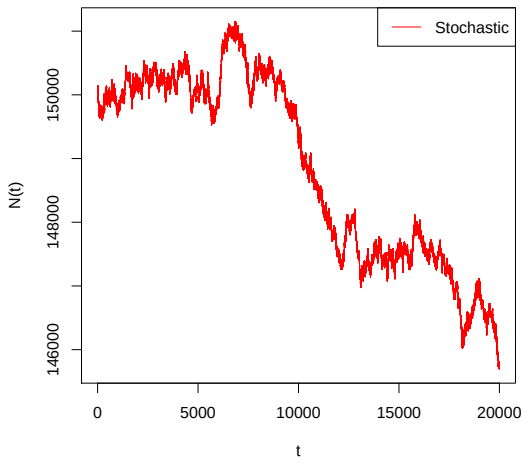

Figure 4.4: Computer simulation of the path $N(t)$ for the SDE model (4.6.2) for pneumococcus, using the Milstein method with parameter value $\mu = 1.37363 \times 10^{-3}$/day with step size $\Delta = 0.05$ days with initial value $N(0) = 150,000$.

but the population sizes are not scaled as previously.

Example 4.7.1 (Pneumococcus Model) *The population of Scottish children under two years old is of approximate size* $150,000$. *The per capita death rate is* $\mu = \frac{1}{104}$*/week*$=9.615\times 10^{-3}$*/week*$=1.37363 \times 10^{-3}$*/day [51]. For the per capita rate* γ *at which infected individuals become immune we note that in her Ph.D. thesis Weir [125] deduces from a systematic review that* $\gamma = 0.02011$*/day,* $(1/\gamma) = 49.7$ *days. The basic reproduction number for pneumococcus is estimated to be 1.49 [37], 1.4 [62] and 1.8-2.2 [137] so we take* $\beta = 2.857 \times 10^{-7}$*/day corresponding to a basic reproduction number of 2.0.*

Based on the result shown in Corollary 4.5.1, 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 and thus we suspect the solution* $N(t)$ *might not die out in a realistic time period with these parameter values.*

The numerical simulation produced for the solution of $N(t)$ *is illustrated in Figure 4.4.*

From Theorem 4.5.2, we would also expect the solution $I(t)$ *to equations (4.6.1)-(4.6.2) to die out in finite time almost surely. The simulations for* $I(t)$ *are shown in*

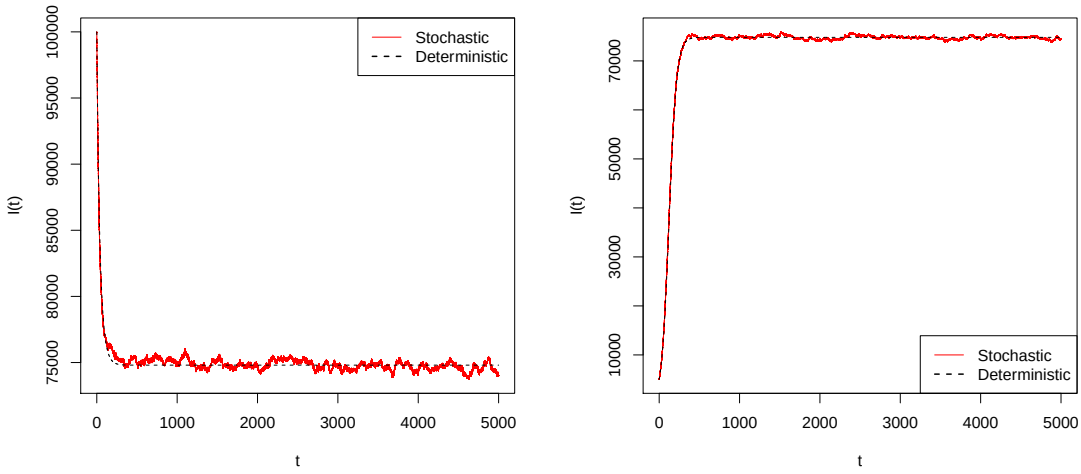

Figure 4.5: Computer simulations of the path $I(t)$ for the SDE SIS model with $N(t)$ as a random variable for pneumococcus, using the Milstein method with parameter values $\beta = 2.857 \times 10^{-7}$/day, $\gamma = 0.02011$/day and $\mu = 1.37363 \times 10^{-3}$/day with step size $\Delta = 0.01$ days 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.

Figure 4.5. 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 [105], This does not contradict our theoretical result, we expect that the disease dies out eventually after a long but finite time [105]. Note that on the timescale shown, the total population size is still large, therefore it seems the disease might not die out in a more realistic time frame. 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 4.7.2 (Common Cold Model) *Heikkinen and Järvinen [55], 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* $\gamma = 0.125/day$. *Sun et al. [113], 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 [113] and (ii) where* $R_0 > 1$, *so we choose* $R_0 = 1.6$ *which corresponds to 6 people per dormitory [113]. According to statistics of WHO [128] the crude death rate per year per 1,000 population in the UK was 8.9 in 2012, hence* $\mu = 0.000024384/day$. *By using the above parameter values and the definition for* R_0, *we derived* β *for both cases: (i)* $\beta = 0.02917/day$ *where* $N = 3$ *to correspond to* $R_0 = 0.7$ *and (ii)* $\beta = 0.03334/day$ *where* $N = 6$ *to correspond to* $R_0 = 1.6$.

The numerical simulation on the solution $N(t)$ *to the SDE model (4.6.2) with the realistic parameter values for the common cold is shown in Figure 4.6. Based on the results in Corollary 4.5.1 we would expect the solution* $N(t)$ *to die out in finite time. However, from Figure 4.6, it appears that the computation time required in order for it to happen might be too large. The simulations were repeated around 50 times with different initial values and the same conclusion is drawn.*

We will now show the simulations for the solution $I(t)$ *to the SDE SIS model (4.6.1) for the two cases where* $R_0 = 0.7$ *and* $R_0 = 1.6$ *corresponding to* $N = 3$ *and* $N = 6$ *respectively as mentioned in [113].*

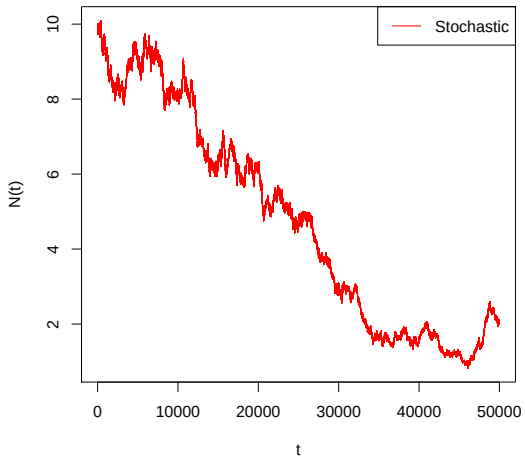

Figure 4.6: Computer simulation of the path $N(t)$ for the SDE model (4.6.2) for the common cold, using the Milstein method with parameter value
$\mu = 0.000024384$/day with step size $\Delta = 0.1$ days with initial value $N(0) = 10$.

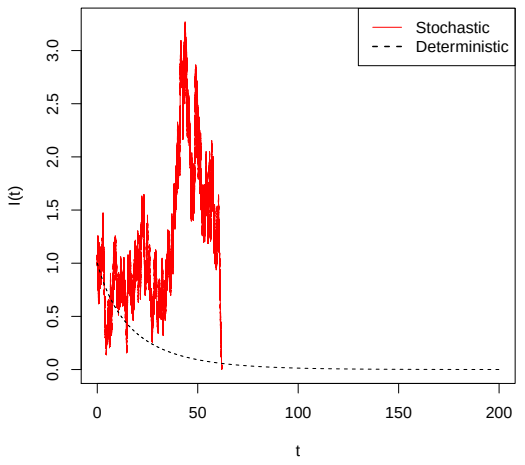

Figure 4.7: Computer simulation of the path $I(t)$ for the SDE SIS model with $N(t)$ as a random variable for the common cold, using the Milstein method where $R_0 < 1$ with parameter values $\beta = 0.02917$/day, $\gamma = 0.125$/day and $\mu = 0.000024384$/day with step size $\Delta = 0.001$ days with initial values $I(0) = 1, N(0) = 3$, $N_1 = 3$, where N_1 is the N value for the deterministic model.

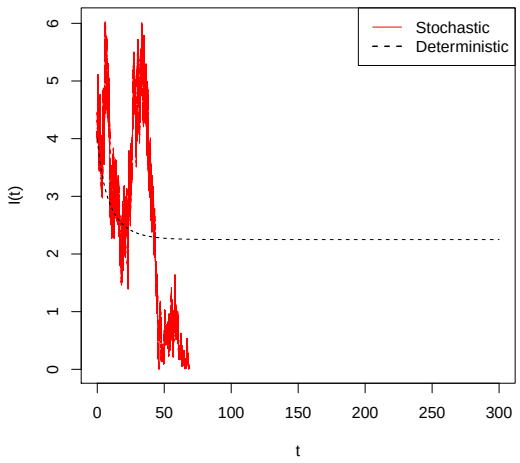

Figure 4.8: Computer simulation of the path $I(t)$ for the SDE SIS model with $N(t)$ as a random variable for the common cold, using the Milstein method where $R_0 > 1$ with parameter values $\beta = 0.03334$/day, $\gamma = 0.125$/day and $\mu = 0.000024384$/day with step size $\Delta = 0.001$ days with initial values $I(0) = 4, N(0) = 6$, $N_1 = 6$, where N_1 is the N value for the deterministic model.

From Theorem 4.5.2 we would expect the solution to the SDE SIS model (4.6.1), $I(t)$ with $N(t)$ as a random variable to become extinct in finite time almost surely. This is clearly the case illustrated in Figure 4.7 and Figure 4.8 for the case where $R_0 < 1$ and $R_0 > 1$ respectively. The solution path illustrated in Figure 4.7 has mean value of $I(t) = 1.22$, a minimum value of $I(t) = 0$ and a maximum value of $I(t) = 3.27$. The solution path illustrated in Figure 4.8 has mean value of $I(t) = 2.54$, a minimum value of $I(t) = 0$ and a maximum value of $I(t) = 6.03$. Our simulations for the common cold have verified our results shown in Theorem 4.5.2. 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 simulations with larger population size such as $N(0) = 100$ 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 4.4.3, although theoretically, $I(t)$ might exceed $N(t)$, as far as we could see from our realistic simulations produced based on realistic parameter values 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 (4.2.12)-(4.2.13) do indeed apply to the SDE SIS model (4.6.1)-(4.6.2) with transmission term $\beta S(t)I(t)$.

4.8 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 gonorrhea, pneumococcus, tuberculosis or the common cold.

In this chapter 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 [1] and Allen [2] 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 chapter 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 nonnegative, 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. This is a surprising result as we have shown theoretically that the total population size will become extinct and as a result of that the disease will die out in finite time. We believe this is caused by the assumptions

which we made on the formulation of this stochastic SIS model, where we have introduced births and deaths independently of each other. 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. [33], [40], [87] and [118]). 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 chapter 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 ([1], [2], [10]). Although similar models have been formulated, but not analysed, previously ([1], [2]) our work is one of the first to analyse such models.

In the next chapter we move onto looking at the effect of environmental stochasticity on the deterministic SIRS/SIR epidemic model introduced in Section 1.3.

Chapter 5

Modelling the Effect of Telegraph Noise in the SIRS Epidemic Model Using Markovian Switching

5.1 Introduction

Motivated by the work done in [41, 115], in this chapter we will introduce the effect of telegraph noise into a more complicated three-dimensional SIRS epidemic model as well as the SIR epidemic model introduced in Section 1.3.

The chapter is organised as follows. In Section 5.2, we will introduce the SIRS epidemic model with Markovian switching. A recap of some of the fundamental concepts of finite state Markov Chains will also be given. In Section 5.3, the existence of a unique nonnegative solution will be proven. In Section 5.4, we will look at the conditions needed for extinction for the SIRS model with Markovian switching. In Section 5.5, we will obtain the conditions needed for persistence. In Section 5.6, by using the Lyapunov Theorem, we continue to get a better understanding of the persistence conditions on the stochastic SIRS model. In Section 5.7 we explain how the results for the SIR model are a special case of our results and in Section 5.8 we explain how the results can be extended from a two-state Markov Chain to an M-state Markov Chain. Throughout this chapter, numerical simulations with theoretical parameter values and realistic parameter values for measles

are produced in R to support our theoretical results.

Most of the work mentioned in Chapter 5 has been written up as a paper and is published in [49].

5.2 SIRS Epidemic Model with Markovian Switching

Throughout this chapter, unless stated otherwise, 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 following deterministic SIRS epidemic model:

$$\begin{aligned} \frac{dS(t)}{dt} &= -\beta I(t)S(t) + \mu N - \mu S(t) + \upsilon R(t), \\ \frac{dI(t)}{dt} &= \beta I(t)S(t) - (\mu + \gamma)I(t), \\ \frac{dR(t)}{dt} &= \gamma I(t) - \mu R(t) - \upsilon R(t), \end{aligned} \tag{5.2.1}$$

where S, I and R denote respectively the number of susceptible, infected and recovered individuals in the population. N is the total size of the population, β is the disease transmission coefficient and $\beta = \lambda/N$ where λ is the disease contact rate for each individual, that is the rate at which susceptible individuals come into contact with infected individuals. μ is the per capita birth and death rate and γ is the rate at which an infected individual becomes cured and thus moves to the recovery group. υ is the rate of loss of immunity and thus making the recovered individuals susceptible to catching the virus again.

Throughout this chapter, 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. Before we begin analysing the SIRS model with Markovian switching, it is important to recall some of the fundamental theories of Markov Chains with a finite state space. Some other useful properties can be found in Section 2.8.

5.2.1 M-State Markov Chain

Let $r(t)$, $t \geq 0$, be a right-continuous Markov Chain on the probability space taking values in finite state space $\mathbb{S} = \{1, 2, ..., M\}$ with the generator $\Gamma = (\nu_{ij})_{M \times M}$ defined as

$$\mathbb{P}\{r(t+\delta) = j | r(t) = i\} = \begin{cases} \nu_{ij}\delta + o(\delta), & \text{if } i \neq j, \\ 1 + \nu_{ii}\delta + o(\delta), & \text{if } i = j, \end{cases} \tag{5.2.2}$$

where $\delta > 0$, $\nu_{ij} \geq 0$ is the transition rate from state i to j for $i \neq j$ and $\nu_{ii} = -\sum_{1 \leq j \leq M, j \neq i} \nu_{ij}$. It is well known that almost every sample path of $r(\cdot)$ is a right-continuous step function with a finite number of sample jumps in any finite subinterval of $\mathbb{R}_+ = [0, \infty)$ [9]. There is a sequence $\{\tau_k\}_{k \geq 0}$ of finite-valued $\mathcal{F}_t$-stopping times such that $0 = \tau_0 < \tau_1 < ... < \tau_k \to \infty$ almost surely and

$$r(t) = \sum_{k=0}^{\infty} r(\tau_k) \mathbf{1}_{[\tau_k, \tau_{k+1})}(t), \tag{5.2.3}$$

where $\mathbf{1}_A$ denotes the indicator function of set A. The switching is memoryless and the waiting time for the next switch has an exponential distribution. Therefore if $r(\tau_k) = i$, the random variable $\tau_{k+1} - \tau_k$ will follow the exponential distribution with parameter $-\nu_{ii}$, namely

$$\mathbb{P}(\tau_{k+1} = j | \tau_k = i) = \frac{\nu_{ij}}{\sum_{j \neq i} \nu_{ij}} = \frac{\nu_{ij}}{-\nu_{ii}}, \quad i \neq j, \tag{5.2.4}$$

$$\mathbb{P}(\tau_{k+1} - \tau_k \geq T | r(\tau_k) = i) = e^{\nu_{ii} T}, \qquad \forall T \geq 0. \tag{5.2.5}$$

In addition, let us define $\mathbf{\Pi} = (\pi_1, \pi_2, ..., \pi_M)$ to be the unique stationary distribution of this Markov Chain where

$$\mathbf{\Pi\Gamma} = \mathbf{0} \qquad \text{and} \qquad \sum_{i=1}^{M} \pi_i = 1. \tag{5.2.6}$$

In order to make the theories easier to understand and follow, we will begin by only looking at a two-state Markov Chain, namely $\mathbb{S} = \{1, 2\}$. In the next section we will give the fundamental concepts for a two-state Markov Chain.

5.2.2 Two-State Markov Chain

Similarly, let $r(t)$, $t \geq 0$, be a right-continuous Markov Chain on the probability space taking values in finite state space $\mathbb{S} = \{1, 2\}$ with the generator

$$\mathbf{\Gamma} = \begin{bmatrix} -\nu_{12} & \nu_{12} \\ \nu_{21} & -\nu_{21} \end{bmatrix}$$

where $\nu_{12} > 0$ is the transition rate from state 1 to state 2 and $\nu_{21} > 0$ is the transition rate from state 2 to state 1, in other words for $\delta > 0$,

$$\mathbb{P}\{r(t+\delta) = 2 | r(t) = 1\} = \nu_{12}\delta + o(\delta) \quad \text{and} \quad \mathbb{P}\{r(t+\delta) = 1 | r(t) = 2\} = \nu_{21}\delta + o(\delta).$$

If $r(\tau_k) = 1$, the random variable $\tau_{k+1} - \tau_k$ will follow the exponential distribution with parameter $-\nu_{12}$, namely

$$\mathbb{P}(\tau_{k+1} - \tau_k \geq T | r(\tau_k) = 1) = e^{-\nu_{12}T}, \qquad \forall T \geq 0, \tag{5.2.7}$$

and similarly if $r(\tau_k) = 2$.

This Markov Chain has a unique stationary distribution $\mathbf{\Pi} = (\pi_1, \pi_2)$ given by

$$\pi_1 = \frac{\nu_{21}}{\nu_{12} + \nu_{21}} \qquad \text{and} \qquad \pi_2 = \frac{\nu_{12}}{\nu_{12} + \nu_{21}}. \tag{5.2.8}$$

Note that $\sum_{i=1}^{2} \pi_i = 1$.

Now that we have finished recalling the important concepts for M-state and two-state Markov Chains we will introduce the two-state Markov switching into the SIRS epidemic model (5.2.1). Consequently, (5.2.1) will evolve into the SIRS epidemic model with two-state Markovian switching, namely

$$\begin{aligned} \frac{dS(t)}{dt} &= -\beta_{r(t)} I(t) S(t) + \mu_{r(t)} N - \mu_{r(t)} S(t) + \upsilon_{r(t)} R(t), \\ \frac{dI(t)}{dt} &= \beta_{r(t)} I(t) S(t) - (\mu_{r(t)} + \gamma_{r(t)}) I(t), \\ \frac{dR(t)}{dt} &= \gamma_{r(t)} I(t) - \mu_{r(t)} R(t) - \upsilon_{r(t)} R(t), \end{aligned} \tag{5.2.9}$$

where $r(t)$ is a Markov Chain with a finite state space $\mathbb{S} = \{1, 2\}$. For the rest of this chapter, unless stated otherwise, we will focus on analysing this SIRS model with

Markovian switching (5.2.9). We will later describe an extension of the results to a more generalised case and an SIR epidemic model with Markovian switching.

5.3 Existence of Unique Nonnegative Solution

Theorem 5.3.1 *For any given initial value $S(0) = S_0 \in (0, N), I(0) = I_0 \in (0, N)$ and $R(0) = R_0 \in (0, N)$, there exists a unique and nonnegative solution for the SIRS model with Markovian switching (5.2.9) for all t.*

Proof. Fix any sample path of the Markov Chain. Without loss of generality, we may assume $r(t) = 1$ in $[0, \tau_1)$ where $\tau_1 < \infty$ is the first switching time. Let us rewrite (5.2.9) as

$$\frac{d\,\boldsymbol{U}(t)}{dt} = \boldsymbol{f}(\,\boldsymbol{U}(t)) \tag{5.3.1}$$

where $\boldsymbol{U}(t) = (S(t), I(t), R(t))$. Let us define $(x_1, x_2, x_3) = (S, I, R)$, then $\boldsymbol{f} : \mathbb{R}^3 \to \mathbb{R}^3$ such that

$$\begin{aligned} f_1(x_1, x_2, x_3) &= -\beta_{r(t)} x_1 x_2 + \mu_{r(t)} N - \mu_{r(t)} x_1 + \upsilon_{r(t)} x_3, \\ f_2(x_1, x_2) &= \beta_{r(t)} x_1 x_2 - (\mu_{r(t)} + \gamma_{r(t)}) x_2, \\ f_3(x_2, x_3) &= \gamma_{r(t)} x_2 - \mu_{r(t)} x_3 - \upsilon_{r(t)} x_3. \end{aligned} \tag{5.3.2}$$

It is easy to show that f_1, f_2 and f_3 are Lipschitz continuous functions and thus $\boldsymbol{f}(\,\boldsymbol{U}(t))$ is also a Lipschitz continuous function where

$$|\boldsymbol{f}(\,\boldsymbol{U}_1(t)) - \boldsymbol{f}(\,\boldsymbol{U}_2(t))| \leq \rho_{r(t)}(|x_1 - y_1| + |x_2 - y_2| + |x_3 - y_3|),$$

for some constant $\rho_{r(t)}$, where $\boldsymbol{U}_1 = (x_1, x_2, x_3)$ and $\boldsymbol{U}_2 = (y_1, y_2, y_3)$. By the Picard-Lindelöf Theorem, there exists a unique local solution for $r(t) = 1$ for all t or $r(t) = 2$ for all t. Let us now define $[0, \tau_e)$ to be the maximum interval where a solution exists and $S(t), I(t)$ and $R(t)$ remain in $(0, N)$ for each time ξ in $[0, \tau_e)$. We will now show by using the Picard-Lindelöf Theorem that $\tau_e > 0$ and $S(t), I(t), R(t) \in (0, N)$ on $[0, \tau_e]$ and then using continuity we will extend this to the whole region $[0, \infty)$. We will split the proof into three different cases. Let us assume that $\tau_e < \tau_1$.

Case (i): Let us assume $I(0) > 0$. By the Picard-Lindelöf Theorem, $\exists \Delta t > 0$ such that a solution exists in $[0, \Delta t]$. For $S(0) > 0, I(0) > 0$ and $R(0) > 0$, it is easy to see that

$S(t) > 0, I(t) > 0$ and $R(t) > 0$ in $[0, \Delta t]$ if Δt is small enough. If $R(0) = 0$ then from (5.2.9) we have that

$$R(\Delta t) = \gamma_1 I(0)\Delta t + o(\Delta t) > 0. \tag{5.3.3}$$

Thus it is clear that $R(t) > 0$ in $[0, \Delta t]$ for Δt small enough. Similarly, if $S(0) = 0, S(t) = 0$ then we have that

$$S(\Delta t) = \mu_1 N\Delta t + \upsilon_1 R(0)\Delta t + o(\Delta t) > 0, \tag{5.3.4}$$

where we have that $S(t) > 0$ in $[0, \Delta t]$ for Δt small enough. Hence we have shown that $\tau_e > 0$.

Now by integrating the expression of $dI(t)/dt$ given in (5.2.9), we have that for $t \in [0, \tau_e)$, where $\tau_e < \infty$,

$$I(t) = I(0) \exp\left[\int_0^t \beta_1 S - (\mu_1 + \gamma_1)ds\right] > 0. \tag{5.3.5}$$

Let us define $I(\tau_e) = \lim_{t\to\tau_e} I(t)$, then it is obvious from above that $I(t) > 0$ in $[0, \tau_e]$. Similarly by integrating the expression of $dS(t)/dt$ given in (5.2.9), we deduce the following

$$S(t) \geq \frac{1}{\exp(\beta_1 N + \mu_1)t}\left[S(0) + \int_0^t \mu_1 N \exp((\beta_1 N + \mu_1)\xi)d\xi\right] > 0. \tag{5.3.6}$$

By defining $S(\tau_e) = \lim_{t\to\tau_e} S(t)$, we have that $S(t) > 0$ in $[0, \tau_e]$. Similarly we can show the same for $R(t)$. Thus we have shown that $S(t), I(t), R(t) \in (0, N)$ on $[0, \tau_e]$. If $\tau_e < \tau_1$ then by continuity, we could extend the interval of existence to $[0, \tau_e + \Delta t]$ for some $\Delta t > 0$. This is clearly a contradiction, thus $\tau_e \geq \tau_1$. The same procedure follows for $r(t) = 2$, and allows us to extend the region of existence to $[0, \tau_2]$. Continuing in this manner we extend the existence region to $[0, \infty)$.

The other two cases where we look at the situation where $I(0) = 0, R(0) > 0$ and $I(0) = R(0) = 0$ can be carried out in a similar manner as above and we obtain the same result.

□

5.4 Extinction

Extinction is one of the most important aspects when studying the behaviour of a particular disease. It is important for us to find out the conditions that are needed in order for a disease to die out. Therefore, in this section we will focus on discussing the conditions for extinction for our SIRS model with Markovian switching (5.2.9). For the deterministic SIRS model, the criterion used to determine whether a disease will go extinct or persist is based on the basic reproduction number $R_0^D = \frac{\beta N}{\mu+\gamma}$. This represents the expected number of secondary infections caused by an infected individual entering the disease free equilibrium (DFE) which consists of susceptible and removed individuals only (e.g. [9, 32, 57, 59]). If $R_0^D > 1$ then we expect that the disease will persist, while $R_0^D \leq 1$ indicates that the disease will die out. Note that the basic reproduction number for the stochastic SIRS model with Markovian switching (5.2.9), R_0^S, could be derived exactly the same way as in [41] for their stochastic SIS model with Markovian switching. Detailed calculations can be found in [41]. In this chapter we will be using another type of threshold to determine whether the disease will die out or persist almost surely, namely

$$T_0^S = \frac{\pi_1\beta_1 N + \pi_2\beta_2 N}{\pi_1(\mu_1+\gamma_1) + \pi_2(\mu_2+\gamma_2)}. \tag{5.4.1}$$

This threshold T_0^S is used by Gray et al. in their paper [41] to analyse the extinction and persistence issue for their SIS model with Markovian switching. By working with the same threshold we will extend the results Gray et al. have already obtained to a more complex three-dimensional stochastic SIRS model (5.2.9).

Proposition 5.4.1 *Let us define $\alpha_{r(t)} = \beta_{r(t)}N - \mu_{r(t)} - \gamma_{r(t)}$, then we have the following alternative ways of interpreting T_0^S :*

- $T_0^S < 1 \Leftrightarrow \pi_1\alpha_1 + \pi_2\alpha_2 < 0$,
- $T_0^S = 1 \Leftrightarrow \pi_1\alpha_1 + \pi_2\alpha_2 = 0$,
- $T_0^S > 1 \Leftrightarrow \pi_1\alpha_1 + \pi_2\alpha_2 > 0$.

Proof. The proof is straightforward.

Theorem 5.4.2 *If $T_0^S < 1$, then for any given initial value $(S_0, I_0, R_0) \in (0, N)^3$, the solution of the stochastic SIRS epidemic model (5.2.9) obeys*

(i) $\limsup_{t\to\infty} \frac{1}{t} log(I(t)) \leq \alpha_1\pi_1 + \alpha_2\pi_2 < 0$ *a.s.,*

(ii) $\lim_{t\to\infty} R(t) = 0$ *a.s.,*

(iii) $\lim_{t\to\infty} S(t) = N$ *a.s.*

By Proposition 5.4.1, we hence conclude that $I(t)$ tends to zero exponentially and $R(t)$ tends to zero as $t \to \infty$, thus making $S(t)$ tend to N as $t \to \infty$ almost surely. In other words, the disease will die out with probability one and the solution will tend to its DFE $(N, 0, 0)$.

Proof. We will prove the three results separately.

(i) Recall from (5.2.9) that

$$\frac{dI(t)}{dt} = \beta_{r(t)}S(t)I(t) - (\mu_{r(t)} + \gamma_{r(t)})I(t),$$

then by making the substitution that $S(t) = N - I(t) - R(t)$, it is easy to see that

$$\begin{aligned} \frac{d\log(I(t))}{dt} &= \alpha_{r(t)} - \beta_{r(t)}(I(t) + R(t)), \\ &\leq \alpha_{r(t)}, \end{aligned} \tag{5.4.2}$$

where $\alpha_r(t)$ is defined as in Proposition 5.4.1. This implies that for any $t > 0$

$$\frac{\log I(t)}{t} \leq \frac{\log I(0)}{t} + \frac{1}{t}\int_0^t \alpha_{r(s)}ds, \tag{5.4.3}$$

since $\beta_{r(t)} > 0$ and $I(t), R(t) \in (0, N)$. By letting $t \to \infty$, we hence obtain

$$\limsup_{t\to\infty} \frac{1}{t}\log I(t) \leq \limsup_{t\to\infty} \frac{1}{t}\int_0^t \alpha_{r(s)}ds. \tag{5.4.4}$$

Hence by using the ergodic theory of the Markov Chain (e.g. [9]), we have that

$$\lim_{t\to\infty} \frac{1}{t}\int_0^t \alpha_{r(s)}ds = \alpha_1\pi_1 + \alpha_2\pi_2, \quad \text{a.s.} \tag{5.4.5}$$

Therefore equation (5.4.4) becomes

$$\limsup_{t\to\infty} \frac{1}{t}\log I(t) \leq \alpha_1\pi_1 + \alpha_2\pi_2, \quad \text{a.s.} \tag{5.4.6}$$

As a result we have shown that $I(t)$ tends to zero exponentially almost surely. Note that this proof is similar to the proof for Theorem 4.2 in [41].

We will now prove Theorem 5.4.2(ii). Suppose that $\limsup_{t\to\infty} R(t) > 0$ on a set Ω_1 where $\mathbb{P}(\Omega_1) = \delta$ for some $\delta > 0$. Then $I(t) \to 0$ as $t \to \infty$ on a set Ω_2 where $\mathbb{P}(\Omega_2) \geq 1 - \frac{\delta}{2}$. For $\omega \in \Omega_2$ then given $\epsilon > 0$ let us choose ϵ_1 small enough so that

$$\frac{\varepsilon_1 \max(\gamma_1, \gamma_2)}{\min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2)} < \frac{\varepsilon}{2}. \tag{5.4.7}$$

$\exists t_0$ such that for $t \geq t_0,\ 0 \leq I(t) \leq \epsilon_1$. Let us now recall the $R(t)$ equation in (5.2.9), namely

$$\frac{dR(t)}{dt} = \gamma_{r(t)} I(t) - (\mu_{r(t)} + \upsilon_{r(t)}) R(t). \tag{5.4.8}$$

By integrating the above $R(t)$ equation, we have that for $t \geq t_0$,

$$\begin{aligned} R(t) &= R(t_0)e^{-Q(t)} + e^{-Q(t)} \int_{t_0}^{t} \gamma_r(s) I(s) e^{Q(s)} ds, \\ &\leq Ne^{-Q(t)} + \int_{t_0}^{t} \gamma_{r(s)} \varepsilon_1 e^{-\int_s^t (\mu_{r(u)} + \upsilon_{r(u)}) du} ds, \end{aligned} \tag{5.4.9}$$

where $Q(t) = \int_{t_0}^{t} (\mu_r(s) + \upsilon_r(s)) ds \geq \min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2)(t - t_0)$. By carrying out the integrations, (5.4.9) becomes

$$\begin{aligned} R(t) &\leq Ne^{-Q(t)} + \varepsilon_1 \max(\gamma_1, \gamma_2) \int_{t_0}^{t} e^{-\min(\mu_1+\upsilon_1, \mu_2+\upsilon_2)(t-s)} ds, \\ &= Ne^{-Q(t)} + \frac{\varepsilon_1 \max(\gamma_1, \gamma_2)}{\min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2)} \left[e^{-\min(\mu_1+\upsilon_1, \mu_2+\upsilon_2)(t-s)} \right]_{t_0}^{t}, \\ &\leq Ne^{-Q(t)} + \frac{\varepsilon_1 \max(\gamma_1, \gamma_2)}{\min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2)}. \end{aligned} \tag{5.4.10}$$

By choosing $t_1 \geq t_0$ such that for $t \geq t_1,\ Ne^{-Q(t)} \leq \frac{1}{2}\varepsilon$ and using (5.4.7) we have that for $t \geq t_1,\ R(t) \leq \varepsilon$. Hence for $\omega \in \Omega_2, \limsup_{t\to\infty} R(t) = 0$. This is a contradiction. Hence we have obtained our desired result that as $t \to \infty, R(t) \to 0$ almost surely.

Theorem 5.4.2(iii) is obvious by using the fact that $S + I + R = N$. Thus we have completed the entire proof by showing that for $T_0^S < 1$, the disease will die out almost surely and that the solution to the SIRS model with Markovian switching will tend to its DFE $(N, 0, 0)$. $\square$

Note that if both $\alpha_1 < 0$ and $\alpha_2 < 0$, then clearly the corresponding $R_{0,i}^D$ values for both subsystems (state 1 and state 2) are less than one, thus both subsystems will die out. However, the readers may wonder what would happen if one subsystem, say state 1, has $\alpha_1 < 0$ while in state 2 $\alpha_2 > 0$? In other words, one subsystem will go extinct whilst the other subsystem will persist, what would happen to the overall model? This interesting idea highlights the significance of the Markov Chain in dealing with extinction, as in real life it is possible for a particular disease to switch between two or more regimes of environment. It turns out that if the time it takes for the Markov Chain to switch from state 2 to state 1 is relatively faster than from state 1 to 2, so that $\pi_1\alpha_1 + \pi_2\alpha_2 < 0$, then the effect from state 1 will predominate, thus making the overall system die out.

Example 5.4.3 *Let us define the system parameters to be*

$$\mu_1 = 0.65, \quad \mu_2 = 0.10, \quad \gamma_1 = 0.45, \quad \gamma_2 = 0.25, \quad \upsilon_1 = 0.15, \quad \upsilon_2 = 0.75$$

$$\beta_1 = 0.01, \quad \beta_2 = 0.002, \quad \nu_{12} = 0.5, \quad \nu_{21} = 0.8 \quad \textit{and} \quad N = 100.$$

Thus by using the definition of $\alpha_{r(t)}$ defined in Proposition 5.4.1 and (5.2.8), we deduce that $\alpha_1 = -0.10, \alpha_2 = -0.15, \pi_1 = 8/13$ and $\pi_2 = 5/13$, where clearly $\pi_1\alpha_1 + \pi_2\alpha_2 = -0.1192 < 0$ to four d.p. As a result, from Theorem 5.4.2, we expect that for any initial value $(S(0), I(0), R(0)) \in (0, N)^3$, the solution to (5.2.9) satisfies:

1. $\limsup_{t\to\infty} \frac{1}{t} log(I(t)) \leq -0.1192 < 0$ *a.s.,*
2. $\lim_{t\to\infty} R(t) = 0$ *a.s.,*
3. $\lim_{t\to\infty} S(t) = N$ *a.s.*

So the disease will die out almost surely.

The numerical simulations generated by using the Euler method given in Definition 2.6.1 as shown in Figure 5.1 clearly support our theoretical results given in Theorem 5.4.1 by illustrating that the solution path for $S(t)$ tends towards N while $I(t)$ and $R(t)$ tend to zero as $t \to \infty$, in other words, the disease will die out almost surely. Furthermore, in this example, both $\alpha_1 < 0$ and $\alpha_2 < 0$. This implies that both the subsystems will die out.

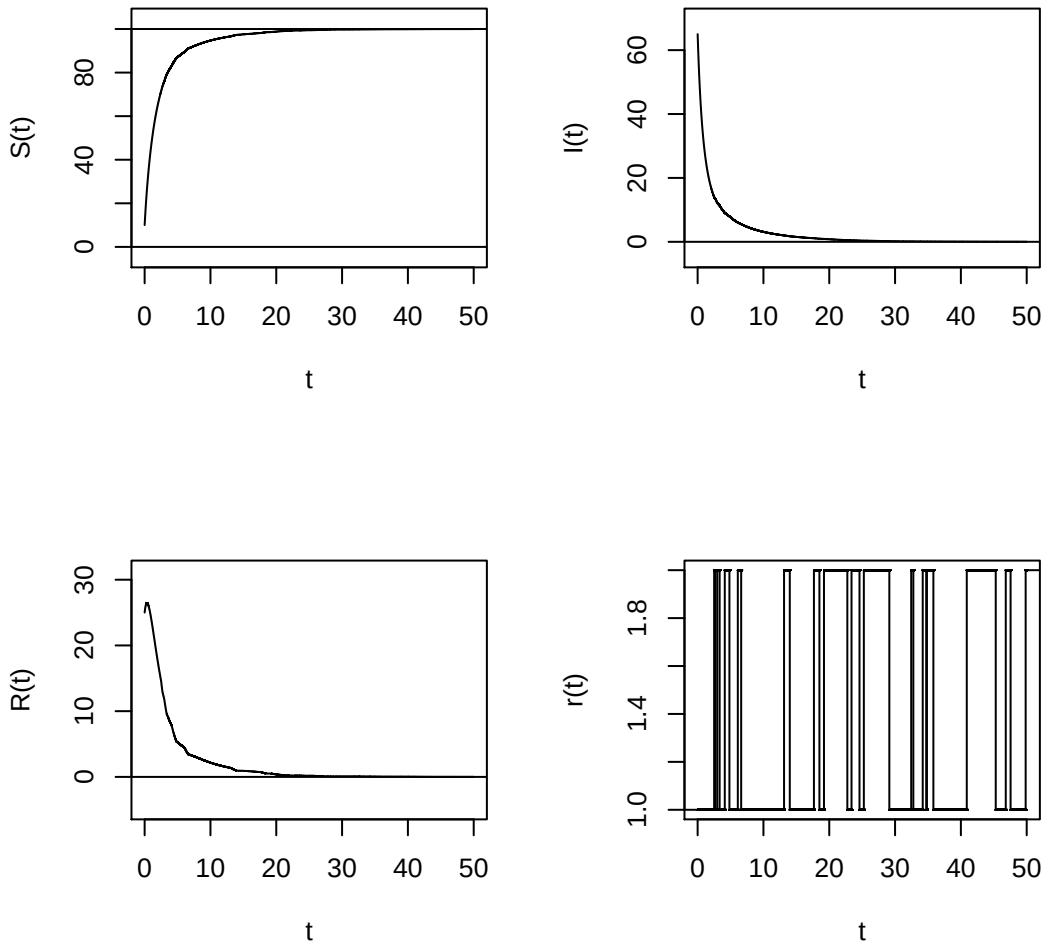

Figure 5.1: Numerical simulations for our solution to (5.2.9) with $T_0^S < 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.4.3 with $\Delta = 0.001$ days and initial values $S(0) = 10, I(0) = 65, R(0) = 25$ and $r(0) = 1$.

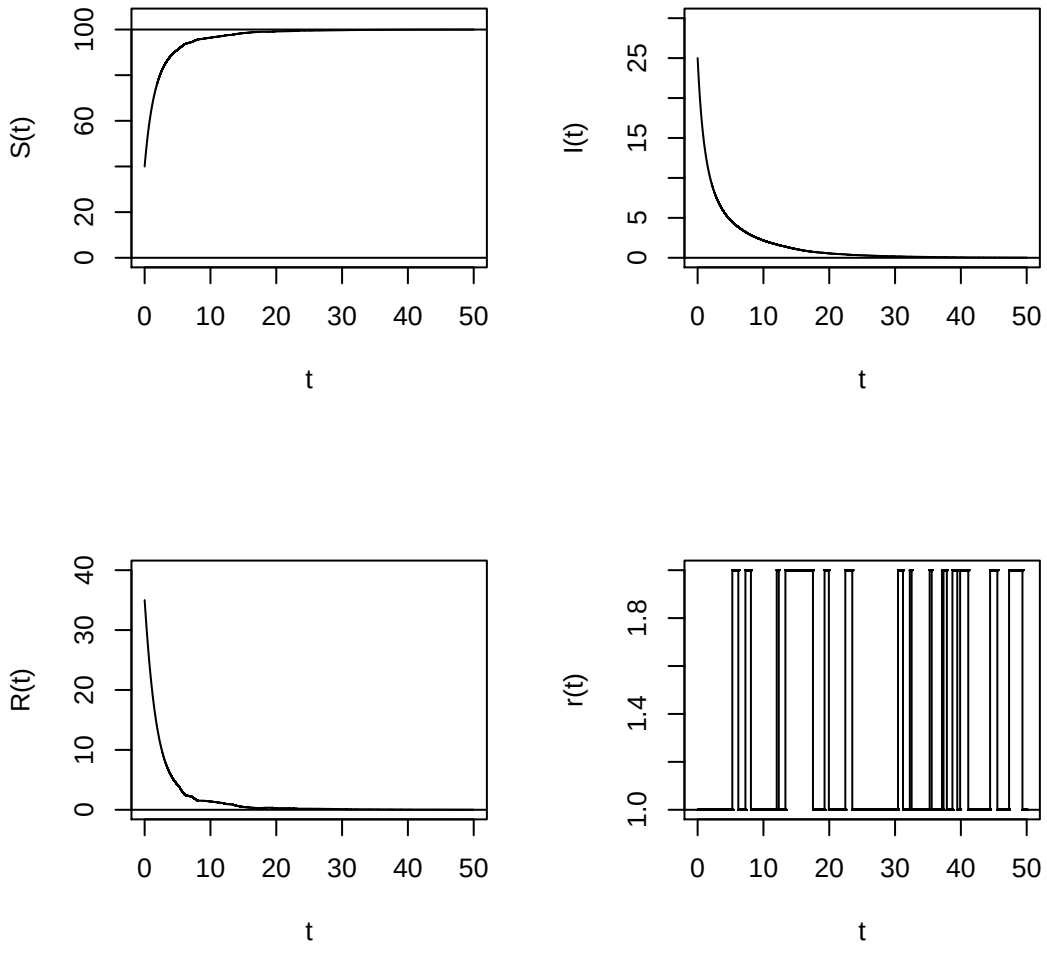

Figure 5.2: Numerical simulations for our solution to (5.2.9) with $T_0^S < 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.4.3 with $\Delta = 0.001$ days and initial values $S(0) = 40, I(0) = 25, R(0) = 25$ and $r(0) = 1$.

In order to reinforce our theoretical results given in Theorem 5.4.1, we have produced two more simulations with different initial values than the ones used in Figure 5.1.

Figure 5.2 shows another simulation with the same system parameter values given in Example 5.4.3 but with a different initial values. In order to understand the simulation better, we have obtained some useful information such as the mean and the variance of the solution path illustrated in Figure 5.2. The solution path for $S(t), I(t)$ *and* $R(t)$ *has mean values of* $96.6, 1.659, 1.737$ *and variance values (to four d.p.) of* $65.8613, 11.4337, 22.7255$ *respectively.*

Another simulation with the system parameter values given in Example 5.4.3 with initial values $S(0) = 70, I(0) = 20, R(0) = 10$ *is shown in Figure 5.3. The solution path for* $S(t), I(t)$ *and* $R(t)$ *has mean values of* $97.16, 1.74, 1.098$ *and variance values (to four d.p.) of* $29.2736, 10.5544, 4.7510$ *respectively.*

The numerical simulations were repeated around 50 times with different parameter values and initial values and all supported our results.

Example 5.4.4 *Let us now define the system parameters to be*

$$\mu_1 = 0.65, \quad \mu_2 = 0.10, \quad \gamma_1 = 0.45, \quad \gamma_2 = 0.25, \quad \upsilon_1 = 0.15, \quad \upsilon_2 = 0.75$$

$$\beta_1 = 0.002, \quad \beta_2 = 0.005, \quad \nu_{12} = 0.5, \quad \nu_{21} = 0.8 \quad \textit{and} \quad N = 100.$$

Again, by using the definition of $\alpha_{r(t)}$ *defined in Proposition 5.4.1 and (5.2.8), we deduce that* $\alpha_1 = -0.90, \alpha_2 = 0.15, \pi_1 = 8/13$ *and* $\pi_2 = 5/13$*, where clearly* $\pi_1\alpha_1 + \pi_2\alpha_2 = -0.4962 < 0$ *to four d.p. Similarly, by using Theorem 5.4.2, we expect that for any initial value* $(S(0), I(0), R(0)) \in (0, N)^3$*, the solution to our stochastic SIRS model (5.2.9) satisfies*

1. $\limsup_{t\to\infty} \frac{1}{t} log(I(t)) \leq -0.4962 < 0$ *a.s.,*
2. $\lim_{t\to\infty} R(t) = 0$ *a.s.,*
3. $\lim_{t\to\infty} S(t) = N$ *a.s.*

In other words, the disease will die out almost surely.

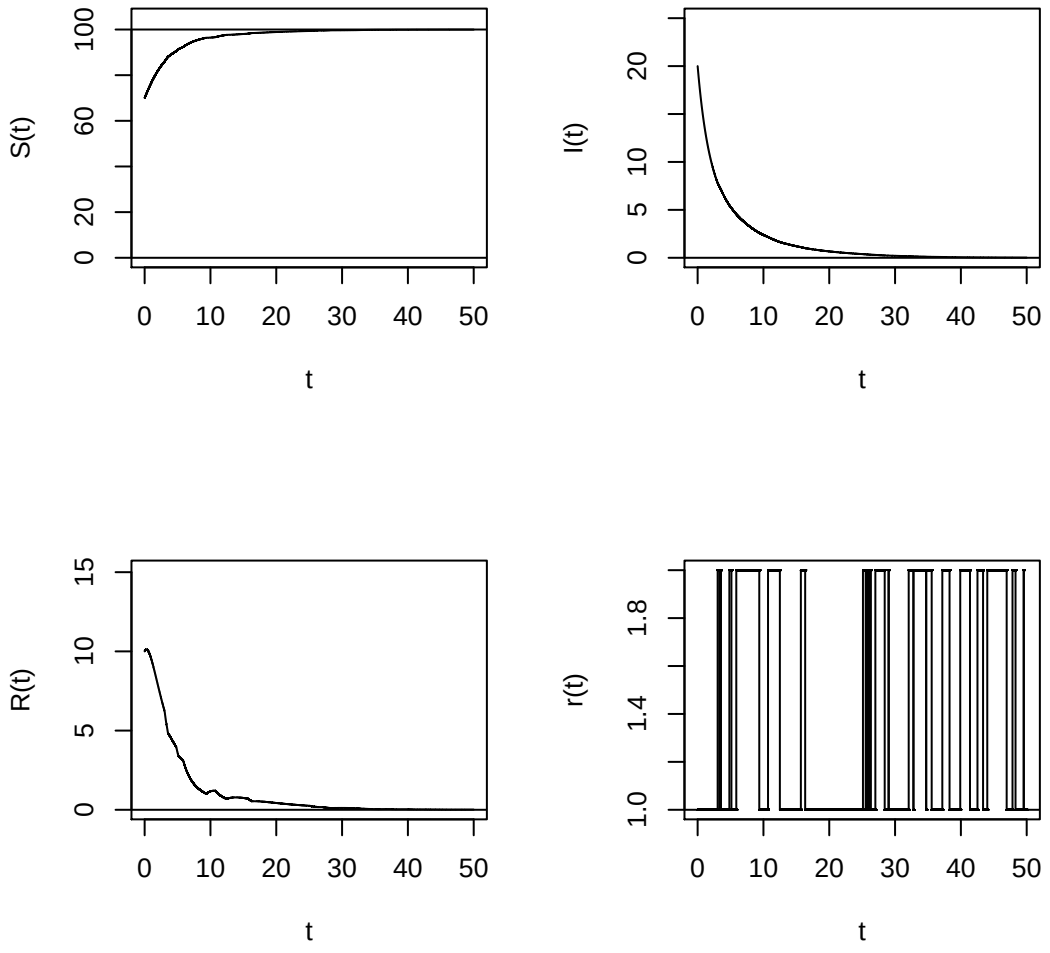

Figure 5.3: Numerical simulations for our solution to (5.2.9) with $T_0^S < 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.4.3 with $\Delta = 0.001$ days and initial values $S(0) = 70, I(0) = 20, R(0) = 10$ and $r(0) = 1$.

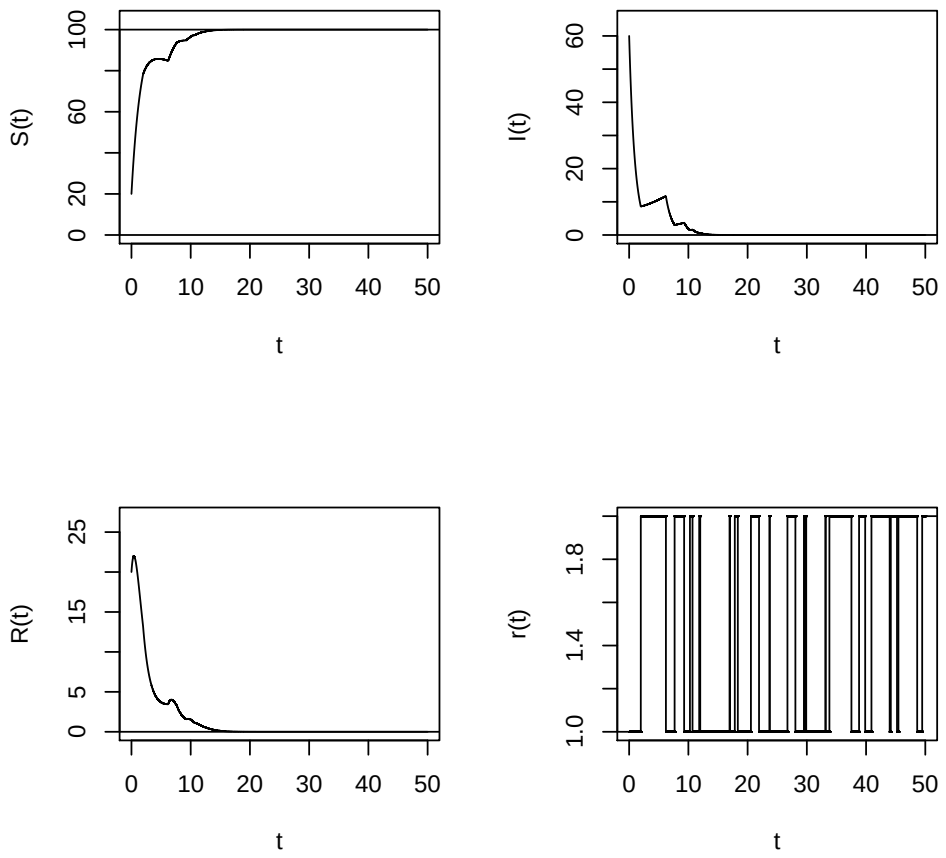

Figure 5.4: Numerical simulations for our solution to (5.2.9) with $T_0^S < 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.4.4 with $\Delta = 0.001$ days with initial values $S(0) = 20, I(0) = 60, R(0) = 20$ and $r(0) = 1$.

Again, the numerical simulations produced by using the Euler method support our results in Theorem 5.4.2, namely the disease dies out almost surely. Note that in this case, $\alpha_1 < 0$ *while* $\alpha_2 > 0$*. This represents that one subsystem will die out while the other subsystem will persist. This scenario is clearly illustrated in Figure 5.4, where we see clearly that there are points where the solution path of* $I(t)$ *increases then decreases, but the overall number of cases of the disease tends to zero as time becomes large.*

In order to illustrate the results given in Theorem 5.4.2 better, we will now produce more simulations with the same system parameter values given in Example 5.4.4 but increasing the population size from $N = 100$ *to* $N = 200$ *and changing the initial values for* S_0, I_0 *and* R_0*. As a result, we now have* $\alpha_1 = -0.7, \alpha_2 = 0.65$ *while* π_1 *and* π_2 *and other parameter values stay the same as before and thus we have* $\pi_1\alpha_1 + \pi_2\alpha_2 = -0.1808 < 0$ *to four d.p. By using Theorem 5.4.2, we expect that for any initial value* $(S(0), I(0), R(0)) \in (0, N)^3$*, the solution to our stochastic SIRS model (5.2.9) satisfies*

1. $\limsup_{t\to\infty} \frac{1}{t} log(I(t)) \leq -0.1808 < 0$ *a.s.,*
2. $\lim_{t\to\infty} R(t) = 0$ *a.s.,*
3. $\lim_{t\to\infty} S(t) = N$ *a.s.*

In other words, the disease will die out almost surely.

The simulation produced is illustrated in Figure 5.5 and clearly we can see that the simulation supports our theoretical results. Again since we have $\alpha_1 < 0$ *but* $\alpha_2 > 0$*, we have the situation again where one subsystem dies out while the other subsystem persists. Similarly to Figure 5.4, we can see the solution path of* $I(t)$ *in Figure 5.5 increases then decreases, but the overall number of cases of the disease tends to zero as time becomes large. This is again expected. The solution path* $S(t), I(t)$ *and* $R(t)$ *has mean values* $196.9, 1.733, 1.384$ *and variance values (to four d.p.)* $56.3394, 15.1458, 14.2500$ *respectively.*

In order to illustrate that the results given in Theorem 5.4.2 also apply to large population size, we will now increase the total population size again from $N = 200$ *to* $N = 300$*. Let us now choose* $\nu_{12} = 0.3$ *and* $\nu_{21} = 0.8$*. As a result, we have* $\pi_1 = 8/11$ *and* $\pi_2 = 3/11$*, and keeping other parameter values the same as before we have that* $\alpha_1 = -0.5, \alpha_2 = 1.15$

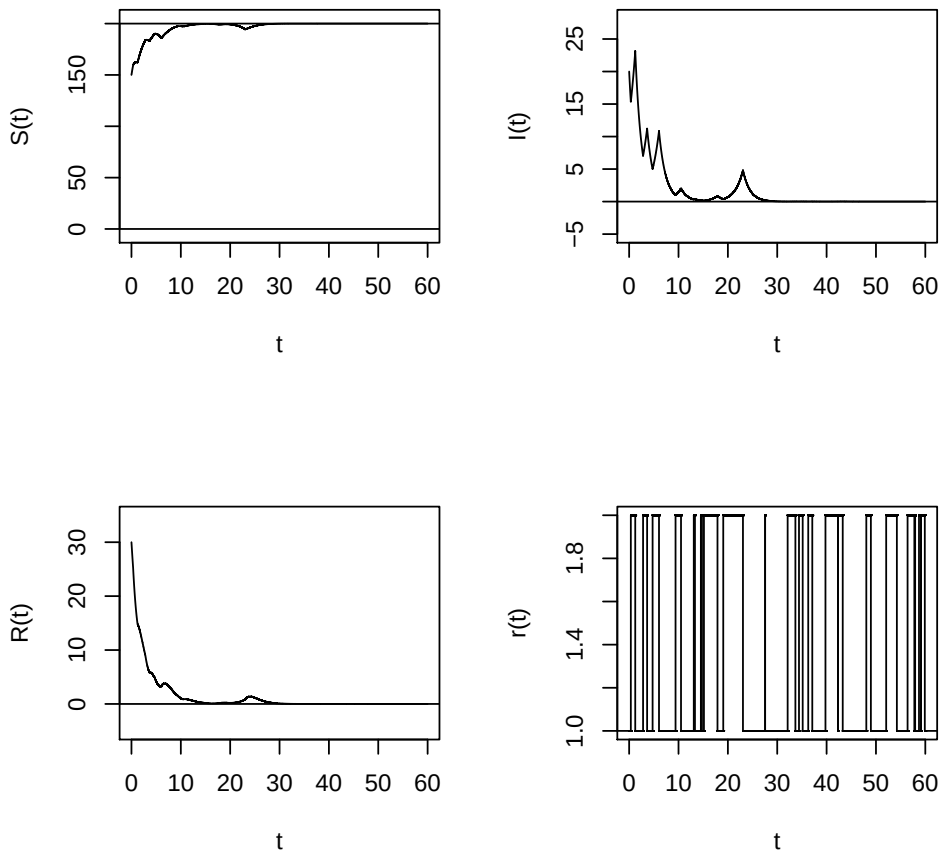

Figure 5.5: Numerical simulations for our solution to (5.2.9) with $T_0^S < 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.4.4 with $\Delta = 0.001$ days, $N = 200$ with initial values $S(0) = 150, I(0) = 20, R(0) = 30$ and $r(0) = 1$.

and hence $\pi_1\alpha_1+\pi_2\alpha_2 = -0.05 < 0$. *Similarly, by using Theorem 5.4.2, we expect that for any initial value* $(S(0), I(0), R(0)) \in (0, N)^3$, *the solution to our stochastic SIRS model (5.2.9) satisfies*

1. $\limsup_{t\to\infty} \frac{1}{t} log(I(t)) \leq -0.05 < 0 \quad a.s.,$
2. $\lim_{t\to\infty} R(t) = 0 \quad a.s.,$
3. $\lim_{t\to\infty} S(t) = N \quad a.s.$

In other words, the disease will die out almost surely.

The simulation produced is illustrated in Figure 5.6 and clearly we can see that the simulation supports our theoretical results. Similarly since we have $\alpha_1 < 0$ *but* $\alpha_2 > 0$, *we have the situation again where one subsystem dies out while the other subsystem persists. Similarly to Figures 5.4 and 5.5, we can see the solution path of* $I(t)$ *in Figure 5.6 increases then decreases, but the overall number of cases of the disease tends to zero as time becomes large. This is again expected. The solution path* $S(t), I(t)$ *and* $R(t)$ *has mean values* $280.9, 12.41, 6.659$ *and variance values* $1553.49, 771.3875, 157.9767$ *respectively.*

Similarly, the numerical simulations were repeated around 50 times with different parameter values and initial values and all support our results.

5.5 Persistence

Apart from extinction, the aspect of persistence of a disease is very important when analysing an epidemic model for a particular disease. As a result, in this section we will be looking at different types of conditions on persistence for the SIRS model with Markovian switching (5.2.9) when $T_0^S > 1$. Note that there are two possible cases that could arise from the condition $T_0^S > 1$, i.e. $\pi_1\alpha_1 + \pi_2\alpha_2 > 0$, namely:

(a) Both α_1 and α_2 are positive. Without loss of generality, we will assume that $0 < \frac{\alpha_1}{\beta_1} \leq \frac{\alpha_2}{\beta_2}$.

(b) One of α_1 and α_2 is positive. Without loss of generality, we will assume that $\frac{\alpha_1}{\beta_1} \leq 0 < \frac{\alpha_2}{\beta_2}$.

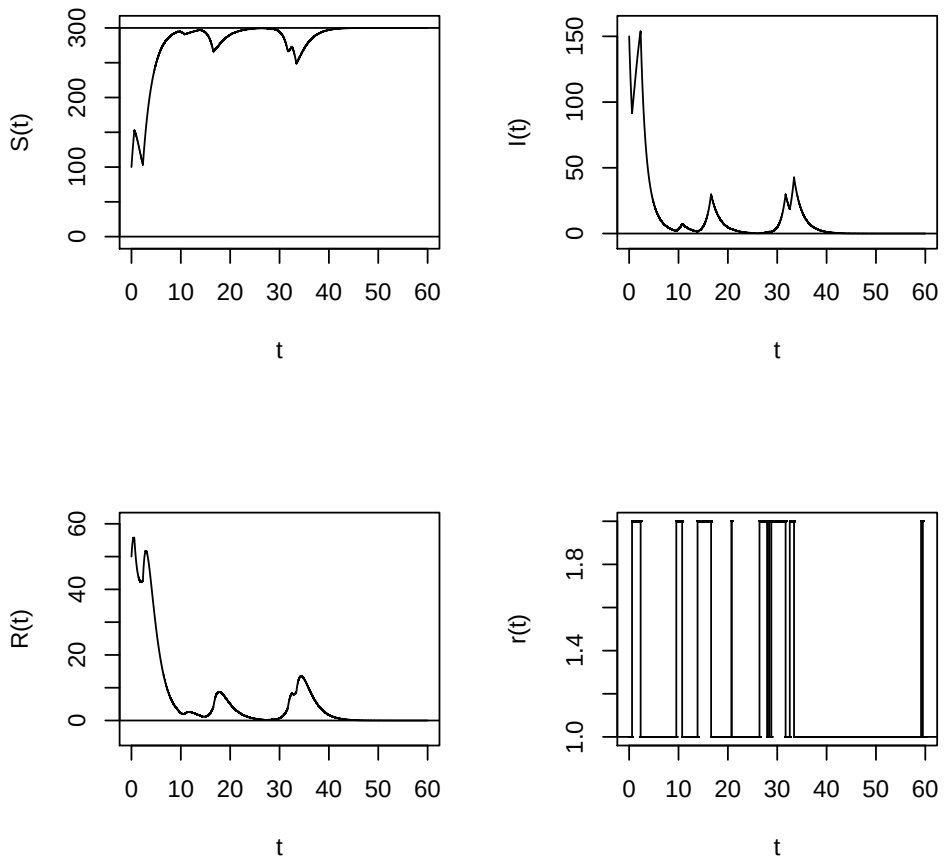

Figure 5.6: Numerical simulations for our solution to (5.2.9) with $T_0^S < 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.4.4 with $\Delta = 0.001$ days, $N = 300$, $\nu_{12} = 0.3$ and $\nu_{21} = 0.8$ with initial values $S(0) = 100, I(0) = 150, R(0) = 50$ and $r(0) = 1$.

First, we will examine in detail the persistence condition $T_0^S > 1$ by looking at the above two cases separately in order to give us a better understanding of the persistence results for the SIRS model with Markovian switching (5.2.9). Before we begin with the main theorems in this section, we will look at another aspect of persistence which is given by using the uniform persistence theorem (e.g [18, 122]). We will prove that our solution $I(t)$ for our stochastic SIRS model (5.2.9) under both cases for $T_0^S > 1$ is uniformly strong persistent.

Theorem 5.5.1 (Uniform strong persistence) *Suppose that $I(0) > 0$.*

Case (a): If $0 < \frac{\alpha_1}{\beta_1} \leq \frac{\alpha_2}{\beta_2}$, $\exists \varepsilon^{'} > 0$ independent of the initial conditions such that

$$\liminf_{t\to\infty} I(t) \geq \varepsilon^{'} > 0 \ a.s. \tag{5.5.1}$$

In other words the SIRS model with Markov switching is almost surely uniformly persistent.

Case (b): If $\frac{\alpha_1}{\beta_1} \leq 0 < \frac{\alpha_2}{\beta_2}$, given $\delta_1 > 0, \exists \varepsilon' > 0$ such that $\forall t_1 > 0,\ I(t) \geq \varepsilon'$ for some $t \geq t_1$ on a set Ω_1 where $\mathbb{P}(\Omega_1) \geq 1 - \delta_1$. To put this another way,

$$\liminf_{t\to\infty} I(t) > 0 \ a.s.$$

Proof. Case (a): Let us choose $\varepsilon > 0$ small enough such that

$$\varepsilon < \frac{\alpha_1}{\beta_1} \frac{\min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2)}{\min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2) + 2\max(\gamma_1, \gamma_2)}.$$

Suppose that $I(t) < \varepsilon$ for all $t \geq t_0$ and $I(0) > 0$. Then from the third equation in (5.2.9) for $t \geq t_0$

$$\frac{dR(t)}{dt} \leq \max(\gamma_1, \gamma_2)\varepsilon - \min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2)R(t). \tag{5.5.2}$$

By integrating (5.5.2), it is easy to obtain the following expression:

$$\begin{aligned} R(t) &\leq R(t_0)e^{-\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)(t-t_0)} \\ &\quad + \frac{\max(\gamma_1, \gamma_2)\varepsilon}{\min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2)}\left(1 - e^{-\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)(t-t_0)}\right), \\ &\leq R(t_0)e^{-\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)(t-t_0)} + \frac{\max(\gamma_1, \gamma_2)\varepsilon}{\min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2)}, \\ &\leq Ne^{-\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)(t-t_0)} + \frac{\max(\gamma_1, \gamma_2)\varepsilon}{\min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2)}. \end{aligned} \tag{5.5.3}$$

Let us choose $t_1 > t_0$ such that for $t \geq t_1$, we have

$$Ne^{-\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)(t-t_0)} \leq \frac{\max(\gamma_1,\gamma_2)\varepsilon}{\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)}. \tag{5.5.4}$$

By using (5.5.4), (5.5.3) becomes

$$R(t) \leq \frac{2\max(\gamma_1,\gamma_2)\varepsilon}{\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)}, \tag{5.5.5}$$

for $t \geq t_1$.

Recall from (5.4.2), we have that

$$\frac{1}{I(t)}\frac{dI(t)}{dt} = \alpha_{r(t)} - \beta_{r(t)}(I(t)+R(t)) \geq \alpha_{r(t)} - \beta_{r(t)}(\varepsilon + R(t)). \tag{5.5.6}$$

By substituting (5.5.5) into the above equation, we have that

$$\frac{1}{I(t)}\frac{dI(t)}{dt} \geq \min_{r=\{1,2\}}\left[\alpha_r - \beta_r\varepsilon\left(1+\frac{2\max(\gamma_1,\gamma_2)}{\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)}\right)\right] = K_1 > 0. \tag{5.5.7}$$

This implies that $I(t)$ is an increasing function and it must eventually increase above ε. Moreover, from our argument we know that by time t_1, $R(t)$ must drop to a level at most $\frac{2\max(\gamma_1,\gamma_2)\varepsilon}{\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)}$, where from (5.5.4) we have that

$$t_1 - t_0 = \begin{cases} \frac{-1}{\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)}\log\left(\frac{\max(\gamma_1,\gamma_2)\varepsilon}{N\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)}\right), & \text{if } \frac{\max(\gamma_1,\gamma_2)\varepsilon}{\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)} < N, \\ 0, & \text{if } \frac{\max(\gamma_1,\gamma_2)\varepsilon}{\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)} \geq N. \end{cases} \tag{5.5.8}$$

Furthermore, from the second equation of (5.2.9) $I(t_1) \geq I(0)e^{-\max(\mu_1+\gamma_1,\mu_2+\gamma_2)t_1} > 0$. For $t \geq t_1, I(t) \geq I(t_1)e^{K_1(t-t_1)} \geq I(0)e^{-\max(\mu_1+\gamma_1,\mu_2+\gamma_2)t_1}e^{K_1(t-t_1)}$, hence $I(t)$ must reach level ε by a time at most t_2 where $\varepsilon = I(0)e^{-\max(\mu_1+\gamma_1,\mu_2+\gamma_2)t_1}e^{K_1(t_2-t_1)}$ and thus by rearranging we have that

$$t_2 = t_1 + \frac{1}{K_1}\left[\log\left(\frac{\varepsilon}{I(0)}\right) + \max(\mu_1+\gamma_1,\mu_2+\gamma_2)t_1\right]. \tag{5.5.9}$$

As a result, we have shown that if $I(0) < \varepsilon$, then $I(t)$ will reach the level ε by at most time t_2. In other words, $I(t)$ will always at some time be greater than ε provided we start below it. However the proof is not finished as it is possible for $I(t)$ to go below ε again later. Consequently, we will now assume that $I(0) = \varepsilon$ and from the above if $I(t)$ does go below ε, it will eventually rise back up again by time at most

$$t_2' = t_1'\left[1 + \frac{1}{K_1}\max(\mu_1+\gamma_1,\mu_2+\gamma_2)\right], \tag{5.5.10}$$

where t_1' is defined by (5.5.8) with $t_0 = 0$.

In general, let us define t^* with $I(t^*) = \varepsilon$ to be the first time that $I(t)$ drops beneath ϵ. Recall again that

$$\begin{aligned} \frac{dI(t)}{dt} &= \beta_{r(t)} S(t) I(t) - \max(\mu_{r(t)} + \mu_{r(t)}) I(t), \\ &\geq -\max(\mu_1 + \gamma_1, \mu_2 + \gamma_2) I(t). \end{aligned} \tag{5.5.11}$$

Then a similar argument as before and by integrating will show that for $t \geq t^*$,

$$\begin{aligned} I(t) &\geq \varepsilon e^{-\max(\mu_1+\gamma_1, \mu_2+\gamma_2)(t-t^*)}, \\ &\geq \varepsilon e^{-\max(\mu_1+\gamma_1, \mu_2+\gamma_2)t_2'} = \varepsilon' > 0, \end{aligned} \tag{5.5.12}$$

where $t^* \leq t \leq t^* + t_2'$. So we have shown that our solution $I(t)$ to the stochastic SIRS model (5.2.9) is uniformly strong persistent in case (a).

Case (b): In this case, we have that $\alpha_1 < 0$, which indicates that $R_{0,1}^D < 1$ in state 1 while in state 2 we have $R_{0,2}^D > 1$. In other words, if we stay in state 1 long enough, $I(t)$ will tend to 0 thus making our solution $(S(t), I(t), R(t))$ for (5.2.9) tend towards the DFE $(N, 0, 0)$. As a result, unlike in case (a), the uniform strong persistence result will not hold for all the domain as there will be a region where it is possible for $I(t)$ to approach 0 arbitrarily closely with a small but non-zero probability. However, we can make the probability of that happening as small as we want it to be.

Choose ε small enough so that

$$\begin{aligned} \pi_1 \left[\alpha_1 - \beta_1 \varepsilon \left(1 + \frac{2\max(\gamma_1, \gamma_2)}{\min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2)} \right) \right] \\ + \pi_2 \left[\alpha_2 - \beta_2 \varepsilon \left(1 + \frac{2\max(\gamma_1, \gamma_2)}{\min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2)} \right) \right] > K_2 > 0. \end{aligned} \tag{5.5.13}$$

Now suppose that $\liminf_{t\to\infty} I(t) = 0$ on a set Ω_1 where $\mathbb{P}(\Omega_1) = \delta_1 > 0$. By the ergodic theory of the Markov Chain, $\exists\ T$ independent of the initial state such that on a set Ω_2 where $\mathbb{P}(\Omega_2) \geq\ 1 - \frac{\delta}{2}$ for $t \geq T$,

$$\begin{aligned} &\lim_{t\to\infty} \frac{1}{t} \int_0^t \left\{ \alpha_{r(s)} - \beta_{r(s)} \varepsilon \left(1 + \frac{2\max(\gamma_1, \gamma_2)}{\min(\mu_1 + \nu_1, \mu_2 + \nu_2)} \right) \right\} ds \\ &= \pi_1 \left[\alpha_1 - \beta_1 \varepsilon \left(1 + \frac{2\max(\gamma_1, \gamma_2)}{\min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2)} \right) \right] \\ &\quad + \pi_2 \left[\alpha_2 - \beta_2 \varepsilon \left(1 + \frac{2\max(\gamma_1, \gamma_2)}{\min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2)} \right) \right] > K_2. \end{aligned} \tag{5.5.14}$$

Consider any $\omega \in \Omega_1 \cap \Omega_2$. Suppose that $\exists\, t_0(\omega)$ such that $I(t) \leq \varepsilon$ for all $t \geq t_0(\omega)$. Similarly to case (a) we have that $R(t)$ falls beneath a level at most $\frac{2\max(\gamma_1,\gamma_2)\varepsilon}{\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)}$ from time $t_1(\omega) = t_0(\omega) + t_1'$ onwards. Again similarly to case (a), $I(t_1) \geq I(0)e^{-\max(\mu_1+\gamma_1,\mu_2+\gamma_2)t_1} > 0$. By integrating (5.4.2) and substituting $R(t)$ by its upper bound given by (5.5.5) and substituting $I(t)$ by its upper bound, namely ε, we have that for $t \geq t_1(\omega)$,

$$\log\left(\frac{I(t)}{I(t_1)}\right) \geq \int_{t_1}^{t} \left[\alpha_{r(s)} - \beta_{r(s)}\varepsilon\left(1 + \frac{2\max(\gamma_1,\gamma_2)}{\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)}\right)\right] ds. \tag{5.5.15}$$

$$\begin{aligned}\Rightarrow \frac{1}{t-t_1}\frac{\log I(t)}{\log I(t_1)} \;\geq\; & \int_{t_1}^{t} \frac{\mathbf{1}(r(s)=1)}{t-t_1}\left[\alpha_1 - \beta_1\varepsilon\left(1 + \frac{2\max(\gamma_1,\gamma_2)}{\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)}\right)\right] ds \\ & + \int_{t_1}^{t} \frac{\mathbf{1}(r(s)=2)}{t-t_1}\left[\alpha_2 - \beta_2\varepsilon\left(1 + \frac{2\max(\gamma_1,\gamma_2)}{\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)}\right)\right] ds,\end{aligned}$$

where $\mathbf{1}$ is the indicator function. Hence using (5.5.14) for $t \geq t_1(\omega) + T$,

$$\lim_{t\to\infty} \frac{1}{t - t_1(\omega)} \log\left(\frac{I(t)}{I(t_1(\omega))}\right) \geq K_2 > 0, \tag{5.5.16}$$

so for $t \geq t_1(\omega) + T,\ I(t) \geq I(t_1)e^{K_2(t-t_1)}$. In other words, from time $t_1 + T$ onwards, $I(t)$ is bounded below by an increasing unbounded function and thus we have a contradiction and $I(t)$ must rise above the level ε by a time at most $\max(t_2(\omega), t_1(\omega) + T)$ where $\varepsilon = I(t_1(\omega))e^{K_2(t_2(\omega)-t_1(\omega))}$.

Starting at $\max(t_2(\omega), t_1(\omega)+T),\ \exists\, t_3(\omega) > \max(t_2(\omega), t_1(\omega)+T)$ with $I(t_3(\omega)) = \epsilon$. Moreover arguing as previously every time that $I(t)$ drops beneath ε it must rise up again to this level by time at most t_4' where

$$t_4' = (t_1' + T)\left(1 + \frac{1}{K_2}\max(\mu_1+\gamma_1, \mu_2+\gamma_2)\right) > t_1'.$$

Then similarly to (a) we have that $\liminf_{t\to\infty} I(t) \geq \varepsilon'$ for some $\varepsilon' > 0$, contradicting $\omega \in \Omega_1$. This completes the proof of Theorem 5.5.1. □

Let us now look at more conditions on persistence for our SIRS model with Markovian switching (5.2.9).

Theorem 5.5.2 *If $T_0^S > 1$, then for any given initial value $(S(0), I(0), R(0)) \in (0, N)^3$, then the solution $S(t)$ of the stochastic SIRS model has the properties that:*

(a) $\liminf_{t\to\infty} S(t) \leq N - \frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2}$ *a.s.,*

(b) $\limsup_{t\to\infty} S(t) \geq N - \frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2}$ *a.s.*

In other words, the number of susceptibles will reach the neighbourhood of the level $N - \frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2}$ *infinitely many times almost surely.*

Proof.

Case (a): Assume the statement given in Theorem 5.5.2(a) is not true, then $\exists\varepsilon > 0$ sufficiently small such that $\mathbb{P}(\Omega_1) > 0$ where

$$\Omega_1 = \left\{\omega \in \Omega : \liminf_{t\to\infty} S(t) > N - \frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2} + 2\varepsilon\right\}.$$

In addition, by the ergodic theory of the Markov Chain, we have that $\mathbb{P}(\Omega_2) = 1$ where for any $\omega \in \Omega_2$,

$$\begin{aligned}\lim_{t\to\infty}\frac{1}{t}\int_0^t &\left\{\alpha_{r(s)} - \beta_{r(s)}\left(\frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2} - \varepsilon\right)\right\} ds \\ &= \pi_1\left\{\alpha_1 - \beta_1\left(\frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2} - \varepsilon\right)\right\} + \pi_2\left\{\alpha_2 - \beta_2\left(\frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2} - \varepsilon\right)\right\}, \\ &= (\pi_1\beta_1 + \pi_2\beta_2)\varepsilon. \end{aligned} \tag{5.5.17}$$

Now consider any $\omega \in \Omega_1 \cap \Omega_2$. Then there is a positive number $T = T(\omega)$ such that

$$S(t) \geq N - \frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2} + \varepsilon, \quad \forall t \geq T(\omega), \tag{5.5.18}$$

which we can easily rearrange by setting $N = S(t) + I(t) + R(t)$ to get

$$I(t) + R(t) \leq \frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2} - \varepsilon, \quad \forall t \geq T(\omega). \tag{5.5.19}$$

By integrating (5.4.2) and using (5.5.19), we have that for all $t \geq T(\omega)$,

$$\begin{aligned}&log(I(t)) \geq \\ &log(I(0)) + \int_0^T [\alpha_{r(s)} - \beta_{r(s)}(I(s) + R(s))]ds + \int_T^t \left[\alpha_{r(s)} - \beta_{r(s)}\left(\frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2} - \varepsilon\right)\right] ds.\end{aligned}$$

Dividing both sides by t and letting $t \to \infty$, we could simplify the above expression to

$$\liminf_{t\to\infty}\frac{1}{t}\log(I(t)) \geq (\pi_1\beta_1 + \pi_2\beta_2)\varepsilon > 0 \tag{5.5.20}$$

by using (5.5.17). So $I(t) \to \infty$ as $t \to \infty$, which clearly contradicts our statement (5.5.19). As a result, it is obvious that our assumption at the beginning is false and thus we must have

$$\liminf_{t\to\infty} S(t) \leq N - \frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2}, \quad a.s.$$

as required.

Case (b): This can be proven in a similar way as in (a). By following the same technique as in (a), we will assume that there exists $\varepsilon > 0$ sufficiently small such that $\mathbb{P}(\Omega_3) > 0$ where

$$\Omega_3 = \left\{\omega \in \Omega : \limsup_{t\to\infty} S(t) < N - \frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2} - 2\varepsilon\right\}.$$

Consider any $\omega \in \Omega_2 \cap \Omega_3$. Then there is a positive number $T = T(\omega)$ such that

$$S(t) \leq N - \frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2} - \varepsilon, \quad \forall t \geq T(\omega), \tag{5.5.21}$$

which can be easily rearranged to get

$$I(t) + R(t) \geq \frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2} + \varepsilon, \quad \forall t \geq T(\omega). \tag{5.5.22}$$

By integrating (5.4.2) and using (5.5.22) , we have that for all $t \geq T(\omega)$,

$$log(I(t)) \leq$$
$$log(I(0)) + \int_0^T [\alpha_{r(s)} - \beta_{r(s)}(I(s) + R(s))]ds + \int_T^t \left[\alpha_{r(s)} - \beta_{r(s)}\left(\frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2} + \varepsilon\right)\right] ds. \tag{5.5.23}$$

Dividing both sides by t and letting $t \to \infty$, we deduce that,

$$\limsup_{t\to\infty} \frac{1}{t} \log(I(t)) \leq -(\pi_1\beta_1 + \pi_2\beta_2)\varepsilon < 0. \tag{5.5.24}$$

Hence, $I(t) \to 0$ as $t \to \infty$. Thus by using this result and integrating the equation for $R(t)$ given in (5.2.9), namely $\frac{dR(t)}{dt} = \gamma_{r(t)}I(t) - (\mu_{r(t)} + \upsilon_{r(t)})R(t)$, then it is easy to see also that $R(t) \to 0$ as $t \to \infty$. This again contradicts (5.5.22). We have arrived at our desired result,

$$\limsup_{t\to\infty} S(t) \geq N - \frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2} \quad a.s.$$

As a result we have proved that the number of susceptibles will persist and it will reach the neighbourhood of the level $N - \frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2}$ infinitely many times almost surely. $\square$

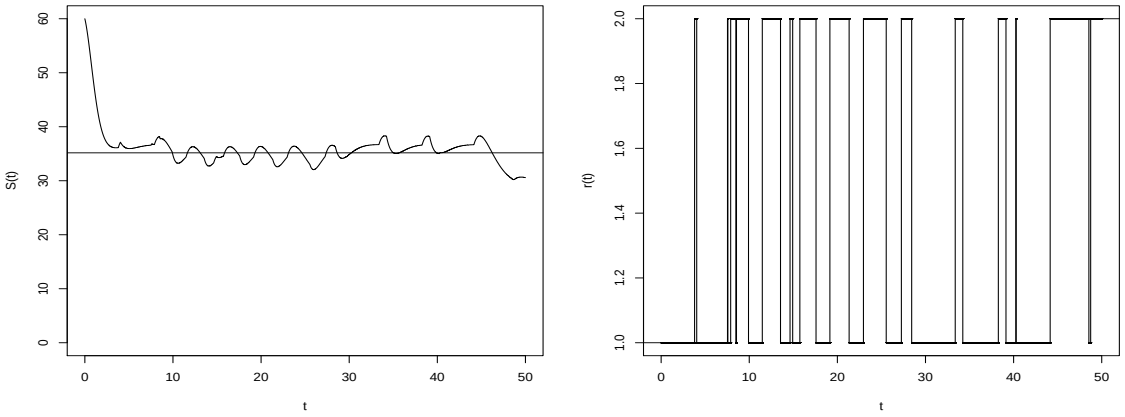

Figure 5.7: Numerical simulation for our solution $S(t)$ to (5.2.9) with $T_0^S > 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.5.3 with initial values $S(0) = 60, I(0) = 20, R(0) = 20$ and $r(0) = 1$.

Example 5.5.3 *Let us now define the system parameters to be*

$$\mu_1 = 0.65, \quad \mu_2 = 0.10, \quad \gamma_1 = 0.45, \quad \gamma_2 = 0.25, \quad \upsilon_1 = 0.15, \quad \upsilon_2 = 0.75$$

$$\beta_1 = 0.03, \quad \beta_2 = 0.012, \quad \nu_{12} = 0.5, \quad \nu_{21} = 0.8 \quad \textit{and} \quad N = 100.$$

By using the definition of $\alpha_{r(t)}$ *defined in Proposition 5.4.1 and (5.2.8), we deduce that* $\alpha_1 = 1.90, \alpha_2 = 0.85, \pi_1 = 8/13$ *and* $\pi_2 = 5/13$*, where clearly* $\pi_1\alpha_1 + \pi_2\alpha_2 = 1.4962 > 0$ *to four d.p. Similarly, by using Theorem 5.5.2, we expect that for any initial value* $(S(0), I(0), R(0)) \in (0, N)^3$*, the solution to (5.2.9) satisfies the following:*

(a) $\liminf_{t\to\infty} S(t) \leq N - \frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2} = 35.1667$ *a.s.,*

(b) $\limsup_{t\to\infty} S(t) \geq N - \frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2} = 35.1667$ *a.s.*

In other words, the number of susceptibles will oscillate around the level 35.1667 *(to four d.p.) almost surely.*

The numerical simulation shown in Figure 5.7 clearly supports our results in Theorem 5.5.2.

In order to prove our results in Theorem 5.5.2 further, we will show another example where we have increased the total population size N *from* 100 *to* 200 *but keeping all the*

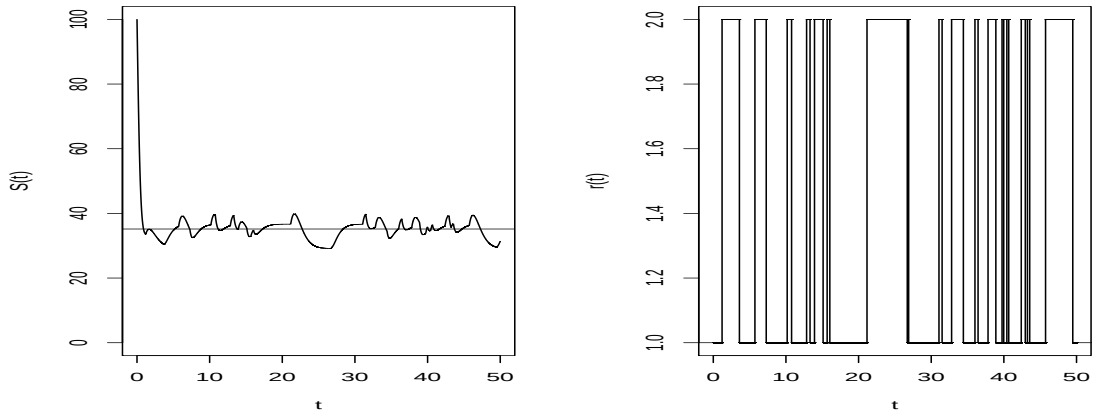

Figure 5.8: Numerical simulation for our solution $S(t)$ to (5.2.9) with $T_0^S > 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.5.3 with $\Delta = 0.001$ days, $N = 200$ and initial values $S(0) = 100, I(0) = 70, R(0) = 30$ and $r(0) = 1$.

other parameter values the same as in Example 5.5.3. As a result we have that $\alpha_1 = 4.90, \alpha_2 = 2.05$ *and* $\pi_1\alpha_1 + \pi_2\alpha_2 = 3.8038 > 0$ *to four d.p. Therefore by using Theorem 5.5.2, we expect that for any initial value* $(S(0), I(0), R(0)) \in (0, N)^3$*, the solution to (5.2.9) satisfies the following:*

(a) $\liminf_{t\to\infty} S(t) \leq N - \frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2} = 35.1667$ *a.s.,*

(b) $\limsup_{t\to\infty} S(t) \geq N - \frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2} = 35.1667$ *a.s.*

In other words, the number of susceptibles will oscillate around the level 35.1667 *(to four d.p.) almost surely.*

The numerical simulation shown in Figure 5.8 clearly supports our results in Theorem 5.5.2. In addition, the solution path shown in Figure 5.8 has mean and variance values of 35.36 *and* 21.0859 *to four d.p. respectively.*

The numerical simulations were repeated around 50 times with different initial values and the same result was observed.

Before we look at the persistence theorem for $I(t)$ we need the following lemma:

Lemma 5.5.4 *Given $\varepsilon_1 > 0$,*

(i) If $I(t) \geq \xi$ for $t \geq t_0, \exists t_1 \geq t_0$ such that for $t \geq t_1$,

$$R(t) \geq \xi \min\left(\frac{\gamma_1}{\mu_1 + \upsilon_1}, \frac{\gamma_2}{\mu_2 + \upsilon_2}\right)(1 - \varepsilon_1).$$

(ii) If $I(t) \leq \xi$ for $t \geq t_0, \exists t_1 \geq t_0$ such that for $t \geq t_1$,

$$R(t) \leq \xi \max\left(\frac{\gamma_1}{\mu_1 + \upsilon_1}, \frac{\gamma_2}{\mu_2 + \upsilon_2}\right)(1 + \varepsilon_1).$$

Proof. Case (i): Let us define a sequence of stopping times $t_0 = \tau_0 < \tau_1 < ... < \tau_m < t$ where τ_{m+1} is interpreted as t. Then for the case $I(t) \geq \xi$, the equation $\frac{dR(t)}{dt}$ for our stochastic SIRS model defined in (5.2.9) gives:

$$\frac{d}{dt}\left(R(t)e^{F(t)}\right) \geq \gamma_{r(t)}\xi e^{F(t)}, \tag{5.5.25}$$

where
$$\begin{aligned} F(t) &= \int_{t_0}^{t} \mu_{r(t)} + \upsilon_{r(t)} ds, \\ &= \sum_{k=0}^{m} \int_{\tau_k}^{\tau_{k+1}} (\mu_{r(\tau_k)} + \upsilon_{r(\tau_k)}) \mathbf{1}_{[\tau_k, \tau_{k+1})} ds, \\ &= \sum_{k=0}^{m} (\mu_{r(\tau_k)} + \upsilon_{r(\tau_k)})(\tau_{k+1} - \tau_k), \end{aligned} \tag{5.5.26}$$

and $\mathbf{1}$ represents the indicator function. By integrating equation (5.5.25), replacing the term $F(t)$ with (5.5.26) and some rearranging, we deduce that:

$$\begin{aligned} &R(t)e^{F(t)} - R(t_0) \\ &\geq \int_{t_0}^{t} \gamma_{r(s)}\xi \exp\left[(\mu_{r(\tau_0)} + \upsilon_{r(\tau_0)})(\tau_1 - \tau_0) + ... + (\mu_{r(\tau'_m)} + \upsilon_{r(\tau'_m)})(s - \tau'_m)\right] ds, \\ &\qquad\qquad \text{where } t_0 = \tau_0 < \tau_1 < ... < \tau'_m \leq s \ ... \leq \tau_m \leq t, \\ &= \sum_{k=0}^{m} \int_{\tau_k}^{\tau_{k+1}} \gamma_{r(s)}\xi \exp\left[(\mu_{r(\tau_0)} + \upsilon_{r(\tau_0)})(\tau_1 - \tau_0) + ... + (\mu_{r(\tau_k)} + \upsilon_{r(\tau_k)})(s - \tau_k)\right] ds, \\ &= \sum_{k=0}^{m} \frac{\gamma_{r(\tau_k)}}{\mu_{r(\tau_k)} + \upsilon_{r(\tau_k)}} \xi \exp\left[(\mu_{r(\tau_0)} + \upsilon_{r(\tau_0)})(\tau_1 - \tau_0) + ... + (\mu_{r(\tau_k)} + \upsilon_{r(\tau_k)})(s - \tau_k)\right]_{\tau_k}^{\tau_{k+1}} \\ &= \frac{\gamma_{r(\tau_0)}}{\mu_{r(\tau_0)} + \upsilon_{r(\tau_0)}} \xi \left(e^{F(\tau_1)} - e^{F(\tau_0)}\right) + ... + \frac{\gamma_{r(\tau_m)}}{\mu_{r(\tau_m)} + \upsilon_{r(\tau_m)}} \xi \left(e^{F(t)} - e^{F(\tau_m)}\right), \\ &\qquad\qquad \text{where } e^{F(\tau_0)} = 1, \\ &\geq \xi \min\left(\frac{\gamma_1}{\mu_1 + \upsilon_1}, \frac{\gamma_2}{\mu_2 + \upsilon_2}\right)(e^{F(t)} - 1). \end{aligned} \tag{5.5.27}$$

As a result,

$$R(t) \geq R(t_0)e^{-F(t)} + \xi \min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)(1-e^{-F(t)}). \tag{5.5.28}$$

Given $\varepsilon_1 > 0$ by choosing t large enough, we have that for $t \geq t_1$,

$$R(t) \geq \xi \min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)(1-\varepsilon_1). \tag{5.5.29}$$

We have thus completed the proof for Lemma 5.5.4(i). The proof for case (ii) follows similarly. In this case we have that $I(t) \leq \xi$, and thus the expression (5.5.25) becomes

$$\frac{d}{dt}\left(R(t)e^{F(t)}\right) \leq \gamma_{r(t)}\xi e^{F(t)}, \tag{5.5.30}$$

where $F(t)$ is defined as in (5.5.26). Now by carrying out a similar procedure as in case (i), it is easy to obtain our desired result. □

Theorem 5.5.5 *If $T_0^S > 1$, then for any given initial value $(S(0), I(0), R(0)) \in (0, N)^3$, the solution $I(t)$ of the stochastic SIRS model has the properties that:*

(a) $\liminf_{t\to\infty} I(t) \leq \left(\frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2}\right)\frac{1}{1+\min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)}$ *a.s.,*

(b) $\limsup_{t\to\infty} I(t) \geq \left(\frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2}\right)\frac{1}{1+\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)}$ *a.s.*

So given $\epsilon > 0$ the number of infectives will enter between the levels

$$\left\{\frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2} - \epsilon\right\}\frac{1}{1+\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)} \text{ and } \left\{\frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2} + \epsilon\right\}\frac{1}{1+\min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)}$$

infinitely often almost surely.

Proof.

Case (a): Suppose that the assertion is false. Then there exists $\varepsilon > 0$ such that $\mathbb{P}(\Omega_5) > 0$ where

$$\Omega_5 = \left\{\omega \in \Omega : \liminf_{t\to\infty} I(t) > \left(\frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2}\right)\frac{1}{1+\min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)} + 2\varepsilon\right\}.$$

Now by considering any $\omega \in \Omega_5$, there is a positive number $T = T(\omega)$ such that

$$I(t) \geq \left(\frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2}\right)\frac{1}{1+\min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)} + \varepsilon, \tag{5.5.31}$$

for all $t \geq T(\omega)$. From Lemma 5.5.4(i), given $\varepsilon_1 > 0$ and $I(t) \geq \xi + \varepsilon$, $\exists T_1(\omega) \geq T(\omega)$ such that for $t \geq T_1(\omega) \geq T(\omega)$,

$$R(t) \geq (\xi + \varepsilon) \min\left(\frac{\gamma_1}{\mu_1 + \upsilon_1}, \frac{\gamma_2}{\mu_2 + \upsilon_2}\right)(1 - \varepsilon_1), \tag{5.5.32}$$

where $\xi = \left(\frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2}\right) \frac{1}{1 + \min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)}$. By using the fact $S(t) + I(t) + R(t) = N$, (5.5.32) becomes

$$S(t) \leq N - (\xi + \varepsilon)\left[1 + \min\left(\frac{\gamma_1}{\mu_1 + \upsilon_1}, \frac{\gamma_2}{\mu_2 + \upsilon_2}\right)(1 - \varepsilon_1)\right], \tag{5.5.33}$$

whence

$$\limsup_{t\to\infty} S(t) \leq N - (\xi + \varepsilon)\left[1 + \min\left(\frac{\gamma_1}{\mu_1 + \upsilon_1}, \frac{\gamma_2}{\mu_2 + \upsilon_2}\right)(1 - \varepsilon_1)\right]. \tag{5.5.34}$$

Now let $\varepsilon_1 \to 0$ as it is arbitrary. By making a substitution using the result shown in Theorem 5.5.2, we have that

$$N - \frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2} \leq N - (\xi + \varepsilon)\left[1 + \min\left(\frac{\gamma_1}{\mu_1 + \upsilon_1}, \frac{\gamma_2}{\mu_2 + \upsilon_2}\right)\right]. \tag{5.5.35}$$

Then by rearranging and replacing ξ by its definition defined above, we arrive at the following contradiction

$$0 \leq -\varepsilon\left[1 + \min\left(\frac{\gamma_1}{\mu_1 + \upsilon_1}, \frac{\gamma_2}{\mu_2 + \upsilon_2}\right)\right], \tag{5.5.36}$$

and we must therefore have

$$\liminf_{t\to\infty} I(t) \leq \left(\frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2}\right) \frac{1}{1 + \min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)} \ a.s. \tag{5.5.37}$$

Case (b): Similarly by using a similar method as in Case (a), we will now assume that there exists $\varepsilon > 0$ sufficiently small such that $\mathbb{P}(\Omega_6) > 0$ where

$$\Omega_6 = \left\{\omega \in \Omega : \limsup_{t\to\infty} I(t) < \left(\frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2}\right) \frac{1}{1 + \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)} - 2\varepsilon\right\}.$$

Now by considering any $\omega \in \Omega_6$, there is a positive number $T = T(\omega)$ such that

$$I(t) \leq \left(\frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2}\right) \frac{1}{1 + \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)} - \varepsilon, \tag{5.5.38}$$

Now by using Lemma 5.5.4(ii), it is easy to see that given $\varepsilon_1 > 0$ and $I(t) \leq \xi_1 + \varepsilon$, $\exists T_2(\omega) \geq T(\omega)$ such that for $t \geq T_2(\omega) \geq T(\omega)$,

$$R(t) \leq (\xi_1 - \varepsilon) \max\left(\frac{\gamma_1}{\mu_1 + \upsilon_1}, \frac{\gamma_2}{\mu_2 + \upsilon_2}\right)(1 + \varepsilon_1), \tag{5.5.39}$$

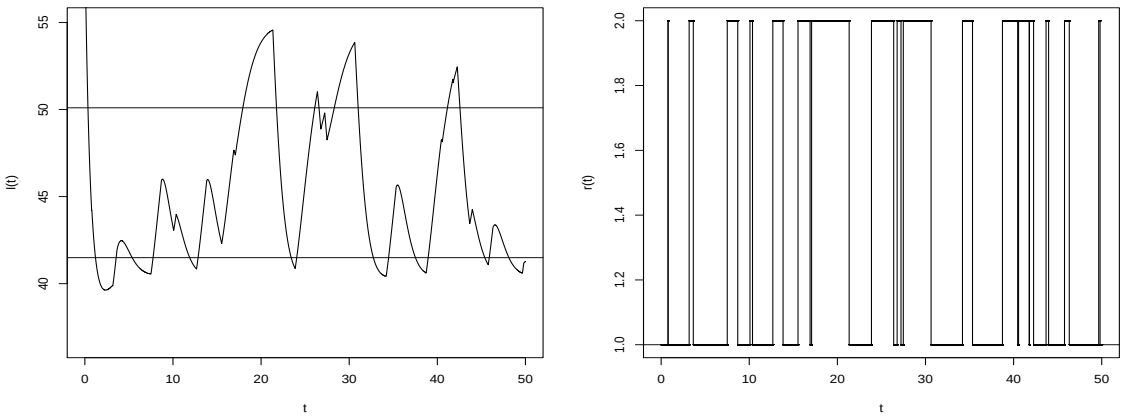

Figure 5.9: Numerical simulation for our solution $I(t)$ to (5.2.9) $T_0^S > 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.5.3 with $\Delta = 0.001$ days, initial values $S(0) = 15, I(0) = 60, R(0) = 25$ and $r(0) = 1$.

where $\xi_2 = \left(\frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2}\right)\frac{1}{1+\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1},\frac{\gamma_2}{\mu_2+\upsilon_2}\right)}$. Now by carrying out the same procedure as we did in Case (a), it is straightforward to see that the result follows.

□

Example 5.5.6 *By using the same parameter values we used in Example 5.5.3, we would expect the solution $I(t)$ to our Markov switching SIRS (5.2.9) to obey*

(a) $\liminf_{t\to\infty} I(t) \leq \left(\frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2}\right)\frac{1}{1+\min\left(\frac{\gamma_1}{\mu_1+\upsilon_1},\frac{\gamma_2}{\mu_2+\upsilon_2}\right)} = 50.0985 \quad a.s.,$

(b) $\limsup_{t\to\infty} I(t) \geq \left(\frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2}\right)\frac{1}{1+\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1},\frac{\gamma_2}{\mu_2+\upsilon_2}\right)} = 41.4933 \quad a.s.,$

to four d.p.

The numerical simulation produced using the Euler method shown in Figure 5.9 clearly supports our results in Theorem 5.5.5 by showing that the solution path for $I(t)$ does in fact enter into the region between the lower and upper levels, namely 41.4933 and 50.0985 (to four d.p.) respectively, almost surely.

Let us now change the total population size from $N = 100$ to $N = 200$ but keeping all the other parameter values the same. Again, in this case we would have $\alpha_1 = 4.90, \alpha_2 =$

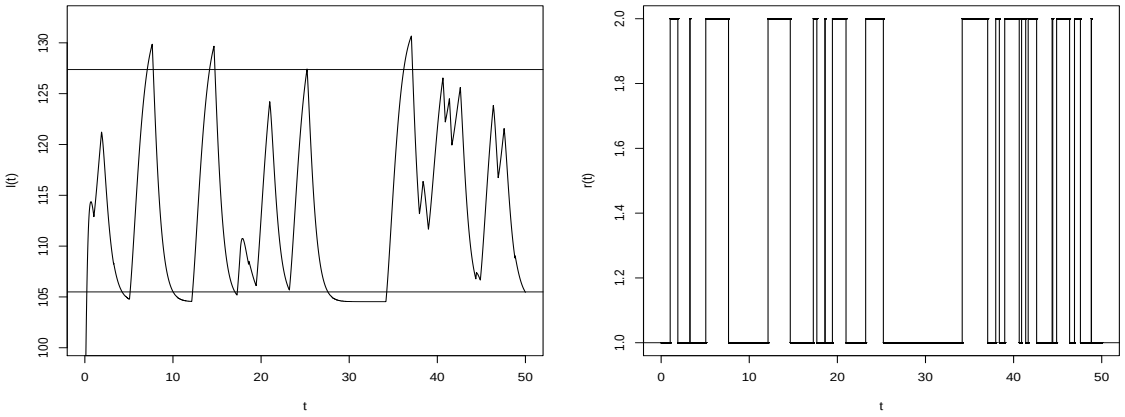

Figure 5.10: Numerical simulation for our solution $I(t)$ to (5.2.9) $T_0^S > 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.5.3 with $\Delta = 0.001$ days, $N = 200$ and initial values $S(0) = 70, I(0) = 90, R(0) = 40$ and $r(0) = 1$.

2.05 *and thus* $\pi_1\alpha_1 + \pi_2\alpha_2 = 3.8038 > 0$ *to four d.p. By Theorem 5.5.5, we would expect our solution* $I(t)$ *to obey*

(a) $\liminf_{t\to\infty} I(t) \leq \left(\frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2}\right) \frac{1}{1+\min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)} = 127.3712$ *a.s.,*

(b) $\limsup_{t\to\infty} I(t) \geq \left(\frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2}\right) \frac{1}{1+\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)} = 105.4933$ *a.s.*

In other words, the solution path for $I(t)$ *would enter the region bounded above and below by 127.3712 and 105.4933 respectively almost surely.*

This is clearly confirmed by the results shown in Figure 5.10. In addition, the solution path in Figure 5.10 has mean and variance values of 113.30 *and* 59.6727 *to four d.p. respectively.*

The numerical simulations were repeated about 50 times with different initial values and the same conclusion was drawn.

Theorem 5.5.7 *If* $T_0^S > 1$*, then for any given initial value* $(S(0), I(0), R(0)) \in (0, N)^3$*, then the solution* $R(t)$ *of the stochastic SIRS model (5.2.9) has the properties that:*

(a) $\liminf_{t\to\infty} R(t) > 0$ *a.s.,*

(b) $\limsup_{t\to\infty} R(t) < \frac{N\max(\gamma_1,\gamma_2)}{\max(\gamma_1,\gamma_2)+\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)} < N \quad a.s.$

In other words, the limiting value of the number of recovered individuals will be strictly positive and will not ultimately exceed $\frac{N\max(\gamma_1,\gamma_2)}{\max(\gamma_1,\gamma_2)+\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)}$ *almost surely.*

Proof.

Case (a): We will prove this case using proof by contradiction. Let us assume that $\liminf_{t\to\infty} R(t) = 0$ on a set Ω_1 where $\mathbb{P}(\Omega_1) \geq \delta > 0$, then by the uniform strong persistence results shown in Theorem 5.5.1, $\exists\varepsilon > 0$ and t_0 such that $I(t) \geq \varepsilon > 0$ for $t \geq t_0$ on a set Ω_2 where $\mathbb{P}(\Omega_2) \geq 1 - \frac{\delta}{2} > 0$. By Lemma 5.5.4 $\exists\varepsilon' > 0$ and $t_1 > t_0$ such that for $t \geq t_1$,

$$R(t) \geq \varepsilon \min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)(1-\varepsilon_1) = \varepsilon' > 0$$

on Ω_2. In other words, $\liminf_{t\to\infty} R(t) > 0$ which clearly is a contradiction and thus proves the result.

Case (b): Let us choose

$$\xi = \frac{N\max(\gamma_1,\gamma_2)}{\max(\gamma_1,\gamma_2)+\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)} < N.$$

From (5.2.9),

$$\begin{aligned}\frac{dR(t)}{dt} &\leq \max(\gamma_1,\gamma_2)(N-R) - \min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)R(t), &(5.5.40)\\ &= N\max(\gamma_1,\gamma_2) - [\max(\gamma_1,\gamma_2)+\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)]R(t). &(5.5.41)\end{aligned}$$

By integrating the above equation for $R(t)$ and rearranging, we have that

$$R(t) \leq R(t_0)e^{-(\max(\gamma_1,\gamma_2)+\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2))(t-t_0)} + \xi, \tag{5.5.42}$$

where ξ is defined above. Then by letting $t \to \infty$, the result of Theorem 5.5.7(b) follows. □

Example 5.5.8 *Again, by using the same parameter values given in Example 5.5.3, the following conclusion can be concluded from the results in Theorem 5.5.7:*

(a) $\liminf_{t\to\infty} R(t) > 0 \quad a.s.,$

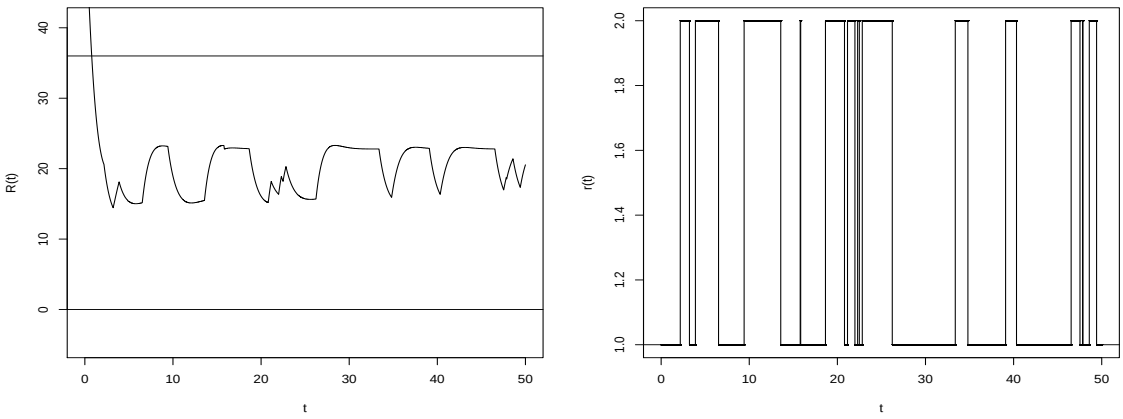

Figure 5.11: Numerical simulation for our solution to (5.2.9) $T_0^S > 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.5.3 where $\Delta = 0.001$ days with initial values $S(0) = 25, I(0) = 15, R(0) = 60$ and $r(0) = 1$.

(b) $\limsup_{t\to\infty} R(t) < \frac{N\max(\gamma_1,\gamma_2)}{\max(\gamma_1,\gamma_2)+\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)} = 36 < N \quad a.s.$

In other words, whatever the starting values, the value of $R(t)$ *asymptotically approaches the region* $(0, 36)$.

The numerical simulation given in Figure 5.11 clearly supports the results given in Theorem 5.5.7 as expected.

Let us now change the $N = 100$ *to* $N = 300$ *to show that the results shown in Theorem 5.5.7 also applies for large population size but keeping all the other parameter values the same. As a result of increasing the population size, we have* $\alpha_1 = 7.90$ *and* $\alpha_2 = 3.25$. *Thus* $\pi_1\alpha_1 + \pi_2\alpha_2 = 6.1115$ *to four d.p. By using Theorem 5.5.7 we would expect the solution* $R(t)$ *to obey*

(a) $\liminf_{t\to\infty} R(t) > 0 \quad a.s.,$

(b) $\limsup_{t\to\infty} R(t) < \frac{N\max(\gamma_1,\gamma_2)}{\max(\gamma_1,\gamma_2)+\min(\mu_1+\upsilon_1,\mu_2+\upsilon_2)} = 108 < N \quad a.s.$

In other words, whatever the starting values, the value of $R(t)$ *asymptotically approaches the region* $(0, 108)$.

Again the simulation shown in Figure 5.12 confirmed the result. In addition the solution path $R(t)$ *shown in Figure 5.12 has mean and variance values of* 86.18 *and* 128.3396

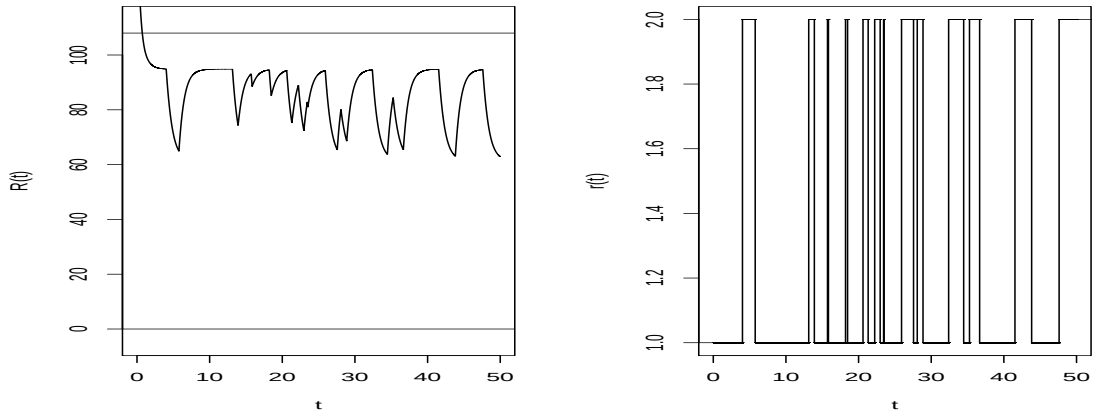

Figure 5.12: Numerical simulation for our solution to (5.2.9) $T_0^S > 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.5.3 where $\Delta = 0.001$ days and $N = 300$ with initial values $S(0) = 100, I(0) = 50, R(0) = 150$ and $r(0) = 1$.

respectively.

The numerical simulations were repeated around 50 times with different initial values and the same conclusion was drawn. Note that for the simulations that we have done and the ones that are shown in Figures 5.11 and 5.12, we suspect that maybe it is possible to improve on the lower and upper bounds for $R(t)$ given in Theorem 5.5.7 to reduce the region that $R(t)$ will enter. We are unable to prove this analytically though the simulations seem to suggest this could be the case.

We will continue to investigate the persistence aspect of the model by looking at the two cases that could possibly arise from $T_0^S > 1$.

Theorem 5.5.9 *Assume that $T_0^S > 1$ and let $I(0) \in (0, N)$ be arbitrary. If $\frac{\alpha_1}{\beta_1} \leq 0 < \frac{\alpha_2}{\beta_2}$, then the following statements hold almost surely:*

(i) $\liminf_{t\to\infty} S(t) \geq N - \frac{\alpha_2}{\beta_2}\left(1 + \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)\right)$.

(ii) $\limsup_{t\to\infty} I(t) \leq \frac{\alpha_2}{\beta_2}$.

(iii) $\limsup_{t\to\infty} R(t) \leq \frac{\alpha_2}{\beta_2} \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)$.

Proof. We will prove this using proof by contradiction. Note that $I(t) > 0$ for all t. Let us assume that $\limsup_{t\to\infty} I(t) > \frac{\alpha_2}{\beta_2}$. Then using Theorem 5.5.5(b), $\exists t_1$ and t_2 with $t_1 < t_2$, such that $\frac{\alpha_2}{\beta_2} < I(t_1) < I(t_2)$ and $I(t)$ is strictly monotonic increasing in $[t_1, t_2]$. Let us now choose $t_3 \in (t_1, t_2)$, not a jump point of the Markov Chain such that $\frac{dI(t)}{dt} > 0$. For $r(t) = 1$ and $r(t) = 2$, from (5.2.9):

$$\frac{1}{I(t_3)}\frac{dI(t)}{dt}\bigg|_{t_3} = \alpha_i - \beta_i(I(t_3) + R(t_3)) < 0, \quad \text{for} \quad i = 1, 2. \tag{5.5.43}$$

For $r(t) = 1$, equation (5.5.43) becomes

$$\frac{1}{I(t_3)}\frac{dI(t)}{dt}\bigg|_{t_3} = \frac{\alpha_1}{\beta_1}\beta_1 - \beta_1(I(t_3) + R(t_3)) < 0, \quad \text{since} \quad \frac{\alpha_1}{\beta_1} \leq 0. \tag{5.5.44}$$

Similarly for $r(t) = 2$, equation (5.5.43) becomes

$$\begin{aligned} \frac{1}{I(t_3)}\frac{dI(t)}{dt}\bigg|_{t_3} &= \frac{\alpha_2}{\beta_2}\beta_2 - \beta_2(I(t_3) + R(t_3)), \\ &\leq \beta_2\left(\frac{\alpha_2}{\beta_2} - \rho\right) < 0 \quad \text{for} \quad \frac{\alpha_2}{\beta_2} < \rho < I(t_3). \end{aligned} \tag{5.5.45}$$

Thus clearly, for both states we have that $\frac{dI(t)}{dt} < 0$ which is a contradiction. Theorem 5.5.9(ii) follows. Subsequently, by using Lemma 5.5.4(ii), we have that

$$\limsup_{t\to\infty} R(t) \leq \frac{\alpha_2}{\beta_2}\max\left(\frac{\gamma_1}{\mu_1 + \upsilon_1}, \frac{\gamma_2}{\mu_2 + \upsilon_2}\right), \tag{5.5.46}$$

whence by using the fact that $S(t) + I(t) + R(t) = N$, we obtain the desired result that

$$\liminf_{t\to\infty} S(t) \geq N - \frac{\alpha_2}{\beta_2}\left(1 + \max\left(\frac{\gamma_1}{\mu_1 + \upsilon_1}, \frac{\gamma_2}{\mu_2 + \upsilon_2}\right)\right). \qquad \square$$

Example 5.5.10 *Let us now define the system parameters to be*

$$\mu_1 = 0.65, \quad \mu_2 = 0.40, \quad \gamma_1 = 0.45, \quad \gamma_2 = 0.20, \quad \upsilon_1 = 0.15, \quad \upsilon_2 = 0.75$$

$$\beta_1 = 0.009, \quad \beta_2 = 0.012, \quad \nu_{12} = 0.5, \quad \nu_{21} = 0.8 \quad \textit{and} \quad N = 100.$$

We see that $\alpha_1 = -0.2, \alpha_2 = 0.60, \pi_1 = 8/13$ *and* $\pi_2 = 5/13$*, where clearly* $\pi_1\alpha_1 + \pi_2\alpha_2 = 0.1077 > 0$ *to four d.p. From Theorem 5.5.9, we expect that for any initial value* $(S(0), I(0), R(0)) \in (0, N)^3$*, the solution to our stochastic SIRS model (5.2.9) satisfies the following:*

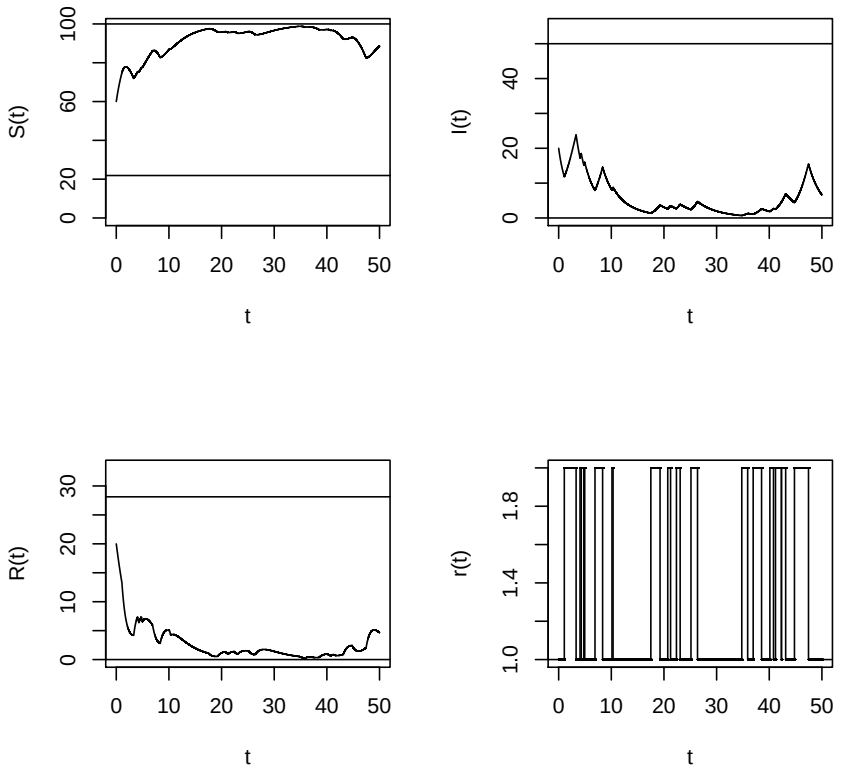

Figure 5.13: Numerical simulations for our solution to (5.2.9) $T_0^S > 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.5.10 where $\Delta = 0.001$ days with initial values $S(0) = 60, I(0) = 20, R(0) = 20$ and $r(0) = 1$.

(i) $\liminf_{t\to\infty} S(t) \geq N - \frac{\alpha_2}{\beta_2}\left(1 + \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)\right) = 21.875,$

(ii) $\limsup_{t\to\infty} I(t) \leq \frac{\alpha_2}{\beta_2} = 50,$

(iii) $\limsup_{t\to\infty} R(t) \leq \frac{\alpha_2}{\beta_2} \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right) = 28.125,$

to three d.p.

Again, the numerical simulations generated by the Euler method illustrated in Figure 5.13 support our results in Theorem 5.5.9.

We will continue to look at the case where $T_0^S > 1$ and $\frac{a_1}{\beta_1} \leq 0 < \frac{a_2}{\beta_2}$ but with a different set of parameter values than the ones mentioned in Example 5.5.10.

Example 5.5.11 *Let us now define the system parameters to be*

$$\mu_1 = 0.95, \quad \mu_2 = 0.80, \quad \gamma_1 = 0.90, \quad \gamma_2 = 0.20, \quad \upsilon_1 = 0.85, \quad \upsilon_2 = 0.65$$

$$\beta_1 = 0.009, \quad \beta_2 = 0.012, \quad \nu_{12} = 0.5, \quad \nu_{21} = 0.8 \quad \textit{and} \quad N = 200.$$

We see that $\alpha_1 = -0.05, \alpha_2 = 1.40, \pi_1 = 8/13$ *and* $\pi_2 = 5/13$*, where clearly* $\pi_1\alpha_1 + \pi_2\alpha_2 = 0.5077 > 0$ *to four d.p. From Theorem 5.5.9, we expect that for any initial value* $(S(0), I(0), R(0)) \in (0, N)^3$*, the solution to our stochastic SIRS model (5.2.9) satisfies the following:*

(i) $\liminf_{t\to\infty} S(t) \geq N - \frac{\alpha_2}{\beta_2}\left(1 + \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)\right) = 25,$

(ii) $\limsup_{t\to\infty} I(t) \leq \frac{\alpha_2}{\beta_2} = 116.6667,$

(iii) $\limsup_{t\to\infty} R(t) \leq \frac{\alpha_2}{\beta_2} \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right) = 58.3333,$

to four d.p.

The results shown in Figure 5.14 clearly confirm the results given in Theorem 5.5.9. In addition, the solution path for $S(t), I(t)$ *and* $R(t)$ *illustrated in Figure 5.14 has mean values of* $132.70, 53.40, 13.920$ *and variance values of* $1226.131, 1022.368, 66.8854$ *(to four d.p.) respectively.*

The results shown in Example 5.5.10 and Example 5.5.11 indicate that regardless of where we choose our starting values, whether they begin above or below the required bound, the results given in Theorem 5.5.9 are still satisfied.

Theorem 5.5.12 *(a) Assume that* $T_0^S > 1$ *and let* $I(0) \in (0, N)$ *be arbitrary. If* $0 < \frac{\alpha_1}{\beta_1} \leq \frac{\alpha_2}{\beta_2}$*, then the following statements hold a.s.:*

(i) $\liminf_{t\to\infty} S(t) \geq N - \frac{\alpha_2}{\beta_2}\left(1 + \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)\right).$

(ii) $\limsup_{t\to\infty} I(t) \leq \frac{\alpha_2}{\beta_2}.$

(iii) $\limsup_{t\to\infty} R(t) \leq \frac{\alpha_2}{\beta_2} \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right).$

(b) If $I(0) > 0$ *under the same conditions the following statements hold almost surely:*

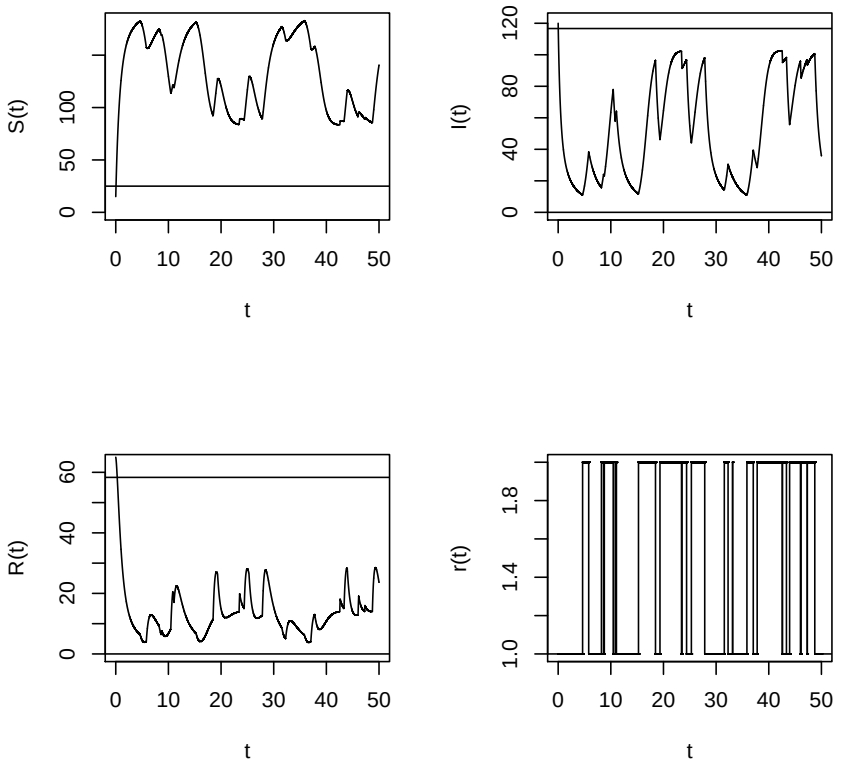

Figure 5.14: Numerical simulations for our solution to (5.2.9) $T_0^S > 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.5.10 where $\Delta = 0.001$ days with initial values $S(0) = 15, I(0) = 120, R(0) = 65$ and $r(0) = 1$.

(i) $\limsup_{t\to\infty} S(t) \leq N - \left(\frac{\alpha_1}{\beta_1} - \frac{\alpha_2}{\beta_2}\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)\right) \times \left(1 + \min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)\right).$

(ii) $\liminf_{t\to\infty} I(t) \geq \frac{\alpha_1}{\beta_1} - \frac{\alpha_2}{\beta_2}\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right).$

(iii) $\liminf_{t\to\infty} R(t) \geq \left(\frac{\alpha_1}{\beta_1} - \frac{\alpha_2}{\beta_2}\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)\right) \times \min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right).$

Proof. The proof for case (a) follows as in Theorem 5.5.9. In order to prove Theorem 5.5.12(b), without loss of generality we may assume that

$$\frac{\alpha_1}{\beta_1} > \frac{\alpha_2}{\beta_2}\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right).$$

Suppose that Theorem 5.5.12(bii) is false and choose $\varepsilon > 0$ such that

$$\liminf_{t\to\infty} I(t) < \frac{\alpha_1}{\beta_1} - \frac{\alpha_2}{\beta_2}\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right) - \varepsilon \tag{5.5.47}$$

on a set Ω_1 where $\mathbb{P}(\Omega_1) = \delta_1 > 0$. Moreover by the results of Theorem 5.5.5(b) and Theorem 5.5.12$(aiii)$

$$\begin{aligned} \limsup_{t\to\infty} I(t) &\geq \left(\frac{\pi_1\alpha_1 + \pi_2\alpha_2}{\pi_1\beta_1 + \pi_2\beta_2}\right)\frac{1}{1+\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)} \\ \text{and} \qquad \limsup_{t\to\infty} R(t) &\leq \frac{\alpha_2}{\beta_2}\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right), \end{aligned}$$

on a set Ω_2 where $\mathbb{P}(\Omega_2) = 1$.

For $\omega \in \Omega_1 \cap \Omega_2, \exists t_4(\omega)$ such that for $t \geq t_4$,

$$R(t) < \frac{\alpha_2}{\beta_2}\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right) + \varepsilon. \tag{5.5.48}$$

Also by using $\frac{a_1}{\beta_1} \leq \frac{\alpha_2}{\beta_2}$, (5.5.47) becomes

$$\begin{aligned} \liminf_{t\to\infty} I(t) &< \frac{\alpha_1}{\beta_1} - \frac{\alpha_2}{\beta_2}\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right), \\ &< \frac{\alpha_1}{\beta_1}\left(1 - \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)\right), \\ &< \limsup_{t\to\infty} I(t). \end{aligned} \tag{5.5.49}$$

Hence from (5.5.47) there must exist some t_5 and t_6 where $t_4 < t_5 < t_6$ such that

$$\begin{aligned} I(t_6) < I(t_5) &< \frac{\alpha_1}{\beta_1} - \frac{\alpha_2}{\beta_2}\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right) - \varepsilon, \\ &\leq \frac{\alpha_2}{\beta_2}\left(1 - \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right)\right) - \varepsilon, \end{aligned} \tag{5.5.50}$$

and $I(t)$ is strictly monotonic decreasing in $[t_5, t_6]$.

Let us now choose $t_7 \in (t_5, t_6)$, not a jump point of the Markov Chain, such that $\frac{dI(t)}{dt}\big|_{t_7} < 0$. Similar to the proof for Theorem 5.5.9, for $r(t) = 1$ we have that

$$\begin{aligned}
\frac{1}{I(t_7)}\frac{dI(t)}{dt}\bigg|_{t_7} &= \alpha_1 - \beta_1(I(t_7) + R(t_7)), \\
&\geq \alpha_1 - \beta_1 I(t_7) - \beta_1\left(\frac{\alpha_2}{\beta_2}\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right) + \varepsilon\right), \\
&\geq \alpha_1 + \beta_1\left(I(t_5) - \frac{\alpha_1}{\beta_1} - I(t_7)\right) > 0, \text{ from (5.5.50).} \qquad (5.5.51)
\end{aligned}$$

Similarly for $r(t) = 2$, by using $\frac{\alpha_1}{\beta_1} \leq \frac{\alpha_2}{\beta_2}$, we have that

$$\begin{aligned}
\frac{1}{I(t_7)}\frac{dI(t)}{dt}\bigg|_{t_7} &\geq \alpha_2 - \beta_2 I(t_7) - \beta_2\left(\frac{\alpha_2}{\beta_2}\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right) + \varepsilon\right), \\
&= \beta_2\left(\frac{\alpha_2}{\beta_2} - I(t_7) - \frac{\alpha_2}{\beta_2}\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right) - \varepsilon\right), \\
&\geq \beta_2\left(\frac{\alpha_1}{\beta_1} - I(t_7) - \frac{\alpha_2}{\beta_2}\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right) - \varepsilon\right), \\
&\geq \frac{\beta_2}{\beta_1}\left[\alpha_1 - \beta_1 I(t_7) - \beta_1\left(\frac{\alpha_2}{\beta_2}\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}\right) + \varepsilon\right)\right], \\
&> 0 \text{ from (5.5.50).}
\end{aligned}$$

As a result we have $\frac{dI(t)}{dt}\big|_{t_7} > 0$ which again is a contradiction proving Theorem 5.5.12(*bii*).

Again, by using Lemma 5.5.4 and that $S(t) + I(t) + R(t) = N$, we obtain the required results $(bi) - (biii)$. □

Therefore for the case $0 < \frac{\alpha_1}{\beta_2} \leq \frac{\alpha_2}{\beta_2}$, we have obtained both an upper and lower bound for our solution (S, I, R) for our stochastic SIRS model (5.2.9), which is a better result than in the case $\frac{\alpha_1}{\beta_1} \leq 0 < \frac{\alpha_2}{\beta_2}$.

Example 5.5.13 *Let us define the system parameter values to be*

$$\mu_1 = 0.85, \quad \mu_2 = 0.50, \quad \gamma_1 = 0.55, \quad \gamma_2 = 0.20, \quad \upsilon_1 = 0.15, \quad \upsilon_2 = 0.75$$

$$\beta_1 = 0.02, \quad \beta_2 = 0.012, \quad \nu_{12} = 0.5, \quad \nu_{21} = 0.8 \quad \textit{and} \quad N = 100.$$

By using the definition of $\alpha_{r(t)}$ defined in Proposition 5.4.1 and (5.2.8), we deduce that $\alpha_1 = 0.6, \alpha_2 = 0.5, \pi_1 = 8/13$ and $\pi_2 = 5/13$, where clearly $\pi_1\alpha_1 + \pi_2\alpha_2 = 0.5615 > 0$ to four d.p. By substituting the appropriate parameter values into Theorem 5.5.12, we would expect that for any initial value $(S(0), I(0), R(0)) \in (0, N)^3$,

(a) $35.4167 \leq \liminf_{t\to\infty} S(t) \leq \limsup_{t\to\infty} S(t) \leq 91.7833$,

(b) $7.0833 \leq \liminf_{t\to\infty} I(t) \leq \limsup_{t\to\infty} I(t) \leq 41.6667$,

(c) $1.1333 \leq \liminf_{t\to\infty} R(t) \leq \limsup_{t\to\infty} I(t) \leq 22.9167$,

to four d.p. almost surely. This implies that regardless of whatever the initial values, the solution $(S(t), I(t), R(t))$ asymptotically approaches the appropriate region above.

Once again, we could conclude from Figures 5.15 - 5.16 that the numerical simulations support our results proved in Theorem 5.5.12. The numerical simulations were repeated many times with various initial values and the same conclusion was obtained.

We will continue to look at the case where $T_0^S > 1$ with $0 < \frac{\alpha_1}{\beta_2} \leq \frac{\alpha_2}{\beta_2}$, but in the next example we will show that the results given in Theorem 5.5.12 also hold for a larger population size.

Example 5.5.14 *Let us define the system parameter values to be*

$$\mu_1 = 0.85, \quad \mu_2 = 0.70, \quad \gamma_1 = 0.75, \quad \gamma_2 = 0.50, \quad \upsilon_1 = 0.15, \quad \upsilon_2 = 0.75$$

$$\beta_1 = 0.02, \quad \beta_2 = 0.009, \quad \nu_{12} = 0.5, \quad \nu_{21} = 0.8 \quad \text{and} \quad N = 300.$$

By using the definition of $\alpha_{r(t)}$ defined in Proposition 5.4.1 and (5.2.8), we deduce that $\alpha_1 = 4.4, \alpha_2 = 1.5, \pi_1 = 8/13$ and $\pi_2 = 5/13$, where clearly $\pi_1\alpha_1 + \pi_2\alpha_2 = 3.2846 > 0$ to four d.p. By substituting the appropriate parameter values into Theorem 5.5.12, we would expect that for any initial value $(S(0), I(0), R(0)) \in (0, N)^3$,

(a) $8.3333 \leq \liminf_{t\to\infty} S(t) \leq \limsup_{t\to\infty} S(t) \leq 172.2414$,

(b) $96 \leq \liminf_{t\to\infty} I(t) \leq \limsup_{t\to\infty} I(t) \leq 166.6667$,

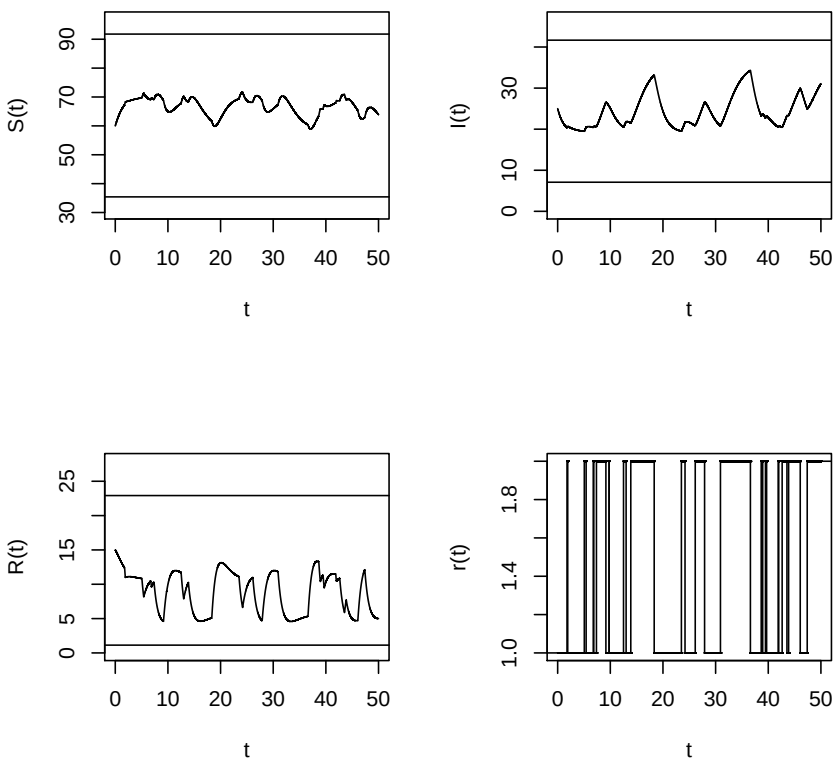

Figure 5.15: Numerical simulations for our solution $(S(t), I(t), R(t))$ to (5.2.9) $T_0^S > 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.5.13 where $\Delta = 0.001$ days with initial values $S(0) = 60, I(0) = 25, R(0) = 15$ and $r(0) = 1$.

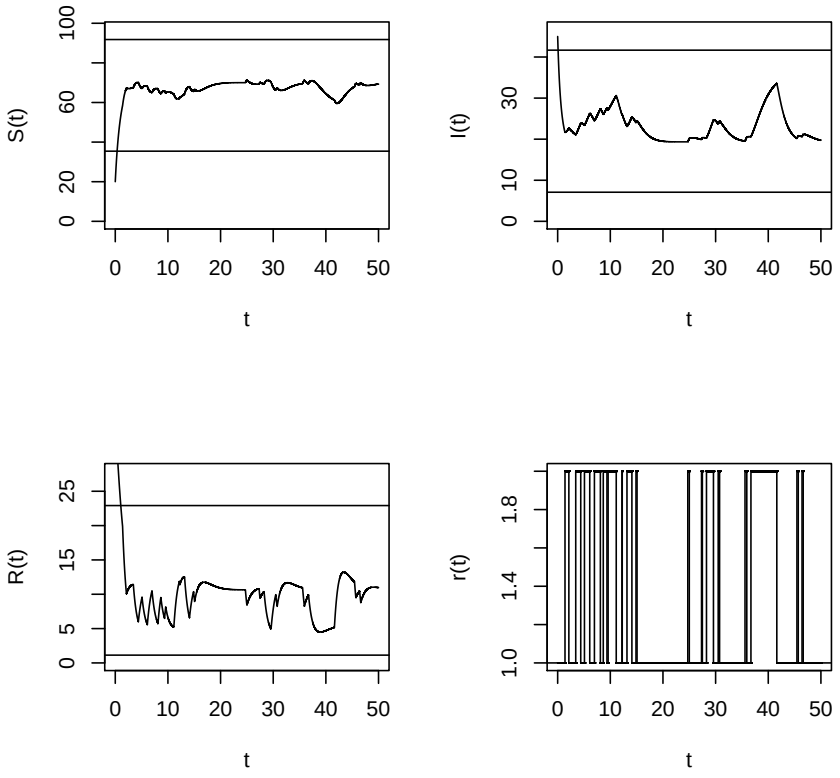

Figure 5.16: Numerical simulations for our solution $(S(t), I(t), R(t))$ to (5.2.9) $T_0^S > 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.5.13 where $\Delta = 0.001$ days with initial values $S(0) = 20, I(0) = 45, R(0) = 35$ and $r(0) = 1$.

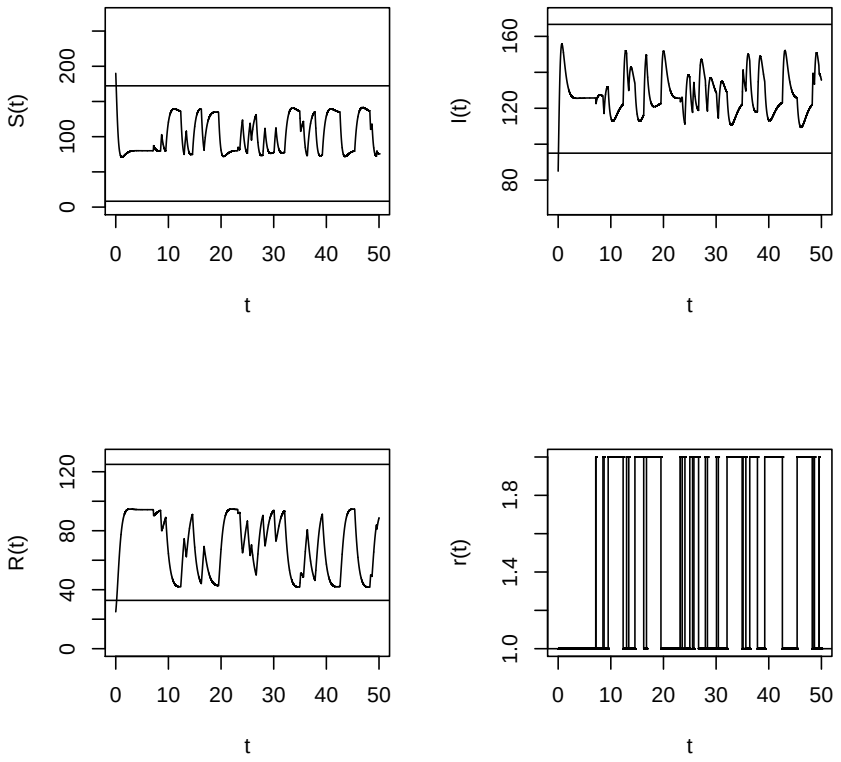

Figure 5.17: Numerical simulations for our solution $(S(t), I(t), R(t))$ to (5.2.9) $T_0^S > 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.5.14 where $\Delta = 0.001$ days with initial values $S(0) = 190, I(0) = 85, R(0) = 25$ and $r(0) = 1$.

(c) $32.7586 \leq \liminf_{t\to\infty} R(t) \leq \limsup_{t\to\infty} I(t) \leq 125$,

to four d.p. almost surely. This implies that regardless of whatever the initial values, the solution $(S(t), I(t), R(t))$ *asymptotically approaches the appropriate region above.*

The results are again confirmed by Figure 5.17 showing clearly that even if we choose some initial values that are outside the regions, the solution path for $S(t), I(t)$ *and* $R(t)$ *will eventually enter the appropriate required region. Moreover, the solution path* $S(t), I(t)$ *and* $R(t)$ *shown in Figure 5.17 has mean values* $101.70, 128, 70.34$ *and variance values* $646.6665, 119.3072, 381.0576$ *respectively.*

5.5.1 $T_0^S = 1$ case

So far, we have looked into great detail on the dynamic behaviour of (5.2.9) under the thresholds $T_0^S < 1$ and $T_0^S > 1$. The reader may ask what about the case when $T_0^S = 1$? Unfortunately, we are unable to prove the behaviour of our solution $(S(t), I(t), R(t))$ in this situation. We have however carried out some numerical simulations using the Euler method to hopefully illustrate the possible behaviour and thus attempt to fill the gap.

Example 5.5.15 *Let us define the system parameter values to be*

$$\mu_1 = 0.60, \quad \mu_2 = 0.25, \quad \gamma_1 = 0.30, \quad \gamma_2 = 0.15, \quad \upsilon_1 = 0.15, \quad \upsilon_2 = 0.75,$$

$$\beta_1 = 0.005, \quad \beta_2 = 0.01, \quad \nu_{12} = 0.6, \quad \nu_{21} = 0.9 \quad \textit{and} \quad N = 100.$$

Consequently we deduce that $\alpha_1 = -0.40, \alpha_2 = 0.60, \pi_1 = 0.60$ *and* $\pi_2 = 0.40$*, where clearly* $\pi_1\alpha_1 + \pi_2\alpha_2 = 0$.

From the numerical simulations shown in Figure 5.18, it appears that the disease will die out in the case for $T_0^S = 1$*. Note that in this case, we have* $\alpha_1 < 0$ *and* $\alpha_2 > 0$*, thus we can see that there are some increasing and decreasing patterns to the solution path for* $I(t)$ *given in Figure 5.18 which exactly demonstrates the situation where one subsystem dies out while the other persists. The numerical simulations were repeated around 50 times with different initial values and the same result was concluded for each simulation.*

In order to help us understand the situation where $T_0^S = 1$ better, in the next example we will increase the total population size from $N = 100$ to $N = 200$ and analyse the behaviour of our system with a different set of parameter values.

Example 5.5.16 *Let us define the system parameter values to be*

$$\mu_1 = 0.80, \quad \mu_2 = 0.25, \quad \gamma_1 = 0.30, \quad \gamma_2 = 0.15, \quad \upsilon_1 = 0.15, \quad \upsilon_2 = 0.75,$$

$$\beta_1 = 0.005, \quad \beta_2 = 0.00275, \quad \nu_{12} = 0.40, \quad \nu_{21} = 0.60 \quad \textit{and} \quad N = 200.$$

Consequently we deduce that $\alpha_1 = -0.10, \alpha_2 = 0.15, \pi_1 = 0.60$ *and* $\pi_2 = 0.40$*, where clearly* $\pi_1\alpha_1 + \pi_2\alpha_2 = 0$.

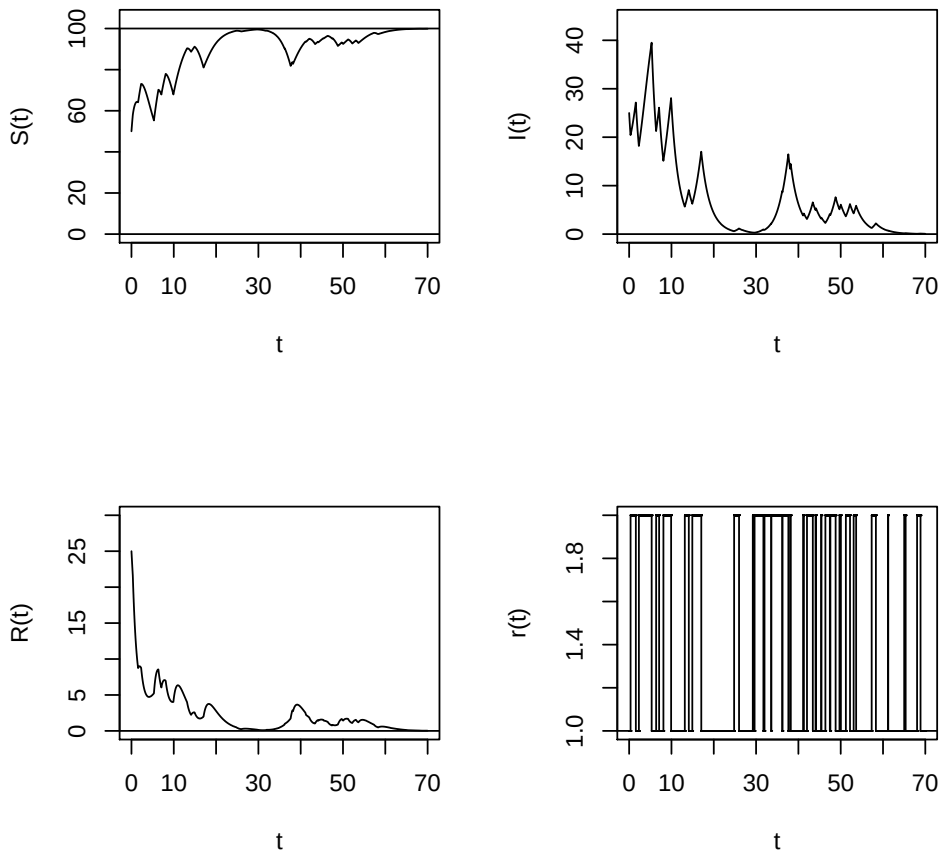

Figure 5.18: Numerical simulations for our solution to (5.2.9) with $T_0^S = 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.5.15 where $\Delta = 0.001$ days with initial values $S(0) = 50, I(0) = 25, R(0) = 25$ and $r(0) = 1$.

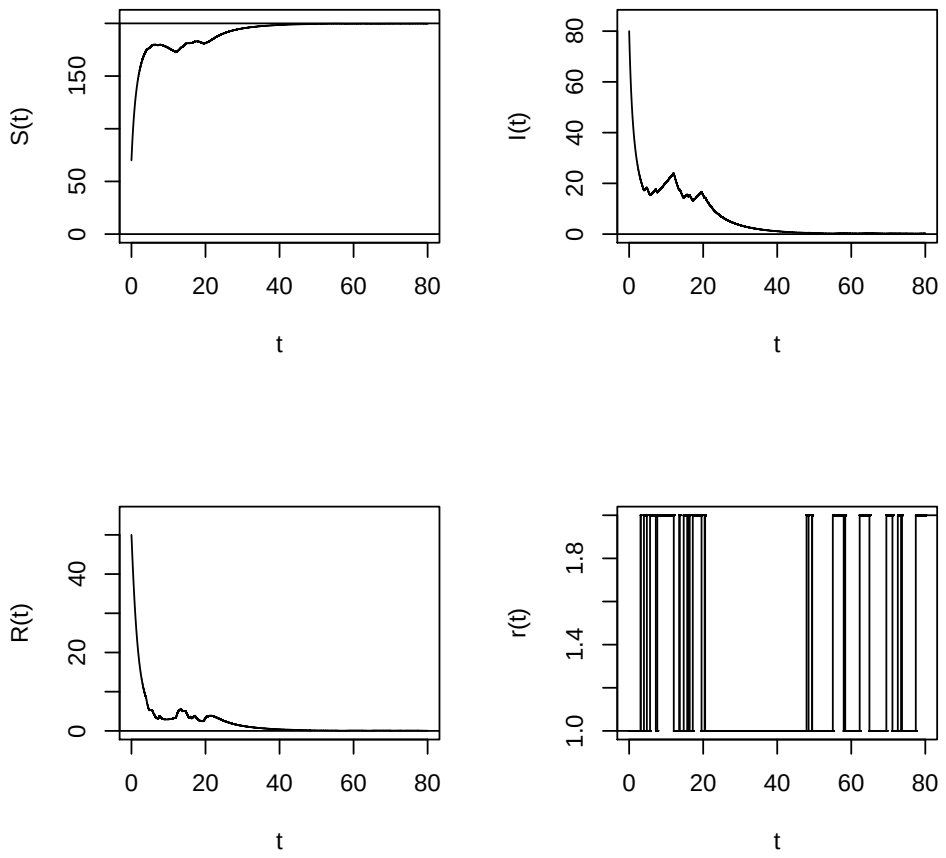

Figure 5.19: Numerical simulations for our solution to (5.2.9) with $T_0^S = 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.5.16 where $\Delta = 0.001$ days with initial values $S(0) = 70, I(0) = 80, R(0) = 50$ and $r(0) = 1$.

From Figure 5.19, it appears that the disease will also die out in this case for $T_0^S = 1$. *Similarly since we have* $\alpha_1 < 0$ *and* $\alpha_2 > 0$ *we have the case where one subsystem will die out while the other will persist. This is again shown clearly by the increasing and decreasing pattern in the solution path* $I(t)$ *illustrated in Figure 5.19. In addition the solution path* $S(t), I(t)$ *and* $R(t)$ *has mean values* $191, 6.6650, 2.353$ *and variance values of* $228.6190, 101.3616, 29.8320$ *to four d.p. respectively.*

In the next section, we will continue to investigate the persistence aspect of our SIRS model with Markovian switching (5.2.9), but we will be using the theory of Lyapunov stability (e.g. [69, 72, 120]) as well as the uniform strong persistence theorem, Theorem 5.5.1, to obtain results on the convergence of the solution (S, I, R) to its corresponding endemic and disease-free equilibria in both state 1 and state 2 under the persistence conditions $0 < \frac{\alpha_1}{\beta_1} \leq \frac{\alpha_2}{\beta_2}$ and $\frac{\alpha_1}{\beta_1} \leq 0 < \frac{\alpha_2}{\beta_2}$.

5.6 Lyapunov Stability

When analysing the behaviour of a dynamical system, one of the significant aspects would be the stability of the solution. There are various types of stability, but the most important one is the stability of a solution near its equilibrium point, in other words will the solution converge to its equilibrium point or will it diverge? This aspect of stability could be discussed by using a Lyapunov Theorem, which is what we shall look at in this section. By combining the results from the uniform strong persistence theorem, Theorem 5.5.1, we have obtained some very useful results which further enhance our understanding about the SIRS model with Markovian switching. Before we begin, it is important to find out what are our endemic and disease-free equilibria for both states 1 and state 2. By setting $\frac{dS(t)}{dt} = \frac{dI(t)}{dt} = \frac{dR(t)}{dt} = 0$, it is easy to see that the DFE is $(N, 0, 0)$ while the endemic equilibria for state 1 and 2 are:

$$S_i^* = \frac{N}{R_{0,i}}, \tag{5.6.1}$$

$$I_i^* = \frac{\mu_i + \upsilon_i}{\mu_i + \upsilon_i + \gamma_i}\left(1 - \frac{1}{R_{0,i}}\right)N = \frac{\mu_i + \upsilon_i}{\mu_i + \upsilon_i + \gamma_i}\left(\frac{\alpha_i}{\beta_i}\right), \tag{5.6.2}$$

$$R_i^* = \frac{\gamma_i}{\mu_i + \upsilon_i + \gamma_i}\left(1 - \frac{1}{R_{0,i}}\right)N = \frac{\gamma_i}{\mu_i + \upsilon_i + \gamma_i}\left(\frac{\alpha_i}{\beta_i}\right), \tag{5.6.3}$$

where $R_{0,i}^D = \frac{\beta_i N}{\mu_i + \gamma_i}$ is the basic reproduction number when the Markov Chain is in state i for $i = 1, 2$.

Theorem 5.6.1 *Assume that $T_0^S > 1$ and $0 < \frac{\alpha_1}{\beta_1} \leq \frac{\alpha_2}{\beta_2}$ and let $(S(0), I(0), R(0)) \in (0, N)^3$ be arbitrary and let the switching times of the Markov Chain be $0 = \tau_0 < \tau_1 < ... < \tau_k$ where $\tau_k \to \infty$ as $k \to \infty$. Define the Lyapunov function to be:*

$$V_i(\boldsymbol{x}) = I - I_i^* - I_i^* \log\left(\frac{I}{I_i^*}\right) + \frac{\beta_i}{2\gamma_i}(R - R_i^*)^2, \tag{5.6.4}$$

where $\boldsymbol{x} = (S(t), I(t), R(t))$, for $i = 1, 2$. Let us define

$$\begin{aligned} f_1(I) &= \frac{(I - I_i^*)^2}{4I_i^*}, \\ f_2(I) &= I - I_i^* - I_i^* \log\left(\frac{I}{I_i^*}\right), \\ f_3(I) &= \frac{(I - I_i^*)^2}{I_i^*}. \end{aligned}$$

Then it is easy to see that $f_1(I_i^*) = f_2(I_i^*) = f_3(I_i^*) = f_1'(I_i^*) = f_2'(I_i^*) = f_3'(I_i^*) = 0$ and

$$f_1''(I_i^*) = \frac{1}{2I_i^*}, \quad f_2''(I_i^*) = \frac{1}{I_i^*}, \quad f_3(I_i^*) = \frac{2}{I_i^*}.$$

Note that by considering the Taylor series expansion about $I = I_i^*$ for ϵ small enough, say $\varepsilon \leq \varepsilon_1$ then

$$\frac{1}{4I_i^*}(I - I_i^*)^2 \leq I - I_i^* - I_i^* \log\left(\frac{I}{I_i^*}\right) \leq \frac{(I - I_i^*)^2}{I_i^*}, \tag{5.6.5}$$

in $(I_i^* - \varepsilon, I_i^* + \varepsilon)$, for $i = 1, 2$.

For any $\varepsilon \leq \varepsilon_1$ sufficiently small, the Lyapunov function (5.6.4) for our SIRS model with Markovian switching has the properties that:

$$\mathbb{P}\left\{\liminf_{t\to\infty} V_1(t) < \frac{\varepsilon^2\beta_1}{2(\mu_1 + \upsilon_1)}\left(1 + \frac{2(\mu_1 + \upsilon_1 + \gamma_1)}{\alpha_1}\right)\right\} \geq e^{-\nu_{12}T_1(\varepsilon)}, \tag{5.6.6}$$

and

$$\mathbb{P}\left\{\liminf_{t\to\infty} V_2(t) < \frac{\varepsilon^2\beta_2}{2(\mu_2 + \upsilon_2)}\left(1 + \frac{2(\mu_2 + \upsilon_2 + \gamma_2)}{\alpha_2}\right)\right\} \geq e^{-\nu_{21}T_2(\varepsilon)}, \tag{5.6.7}$$

where $T_1(\varepsilon) = \frac{W}{\varepsilon^2\beta_1} > 0$ and $T_2(\varepsilon) = \frac{W}{\varepsilon^2\beta_2} > 0$ for some constant W.

Proof. By differentiating the Lyapunov function (5.6.4) and using that $R_i^* = \frac{\gamma_i I_i^*}{\mu_i+\upsilon_i}$, thus $-\gamma_i I_i^* + (\mu_i + \upsilon_i)R_i^* = 0$ we have that

$$\begin{aligned}
\frac{dV_i}{dt} &= \frac{\partial V_i}{\partial I}\frac{dI}{dt} + \frac{\partial V_i}{\partial R}\frac{dR}{dt}, \\
&= (\beta_i SI - (\mu_i + \gamma_i)I)\left(1 - \frac{I_i^*}{I}\right) + \left(\frac{\beta_i}{\gamma_i}\right)(R - R_i^*)(\gamma_i I - (\mu_i + \upsilon_i)R), \\
&= (\beta_i S - \mu_i - \gamma_i)(I - I_i^*), \\
&\quad + \left(\frac{\beta_i}{\gamma_i}\right)(R - R_i^*)(\gamma_i(I - I_i^*) - (\mu_i + \upsilon_i)(R - R_i^*)). \qquad (5.6.8)
\end{aligned}$$

After some simple algebraic manipulations, consequently, (5.6.8) becomes

$$\frac{dV_i}{dt} = -\beta_i(I - I_i^*)^2 - \frac{(\mu_i + \upsilon_i)\beta_i}{\gamma_i}(R - R_i^*)^2 < 0. \qquad (5.6.9)$$

Thus, $V_i(\mathbf{x}) \geq 0$ and $\dot{V}_i(\mathbf{x}) \leq 0$ with equality if and only if $I = I_i^*$ and $R = R_i^*$. If there is no switching then $V_i(\mathbf{x})$ is a Lyapunov function and the endemic equilibria (S_i^*, I_i^*, R_i^*) given by (5.6.1)-(5.6.3) are globally asymptotically stable, i.e. $S \to S_i^*, I \to I_i^*$ and $R \to R_i^*$ as $t \to \infty$, whatever the initial condition.

We shall now prove the results with switching time involved. The proof will split into two parts, corresponding to the Lyapunov functions for state 1 and state 2. First of all, we will show that the result holds in state 1.

(i) By the uniform strong persistence result shown in Theorem 5.5.1, $\exists t_1, W < \infty$ such that for $t \geq t_1$,

$$V_i(\mathbf{x}) = I - I_i^* - I_i^* \log\left(\frac{I}{I_i^*}\right) + \frac{\beta_i}{2\gamma_i}(R - R_i^*)^2 \leq W < \infty, \qquad (5.6.10)$$

and $\max(V_1(t), V_2(t)) \leq W$.

Define a stopping time

$$\sigma_1 = \inf\{t \geq t_1 : r(t) = 1\}.$$

Clearly, $\mathbb{P}(\sigma_1 < \infty) = 1$, and by the right-continuity of the Markov Chain, $r(\sigma_1) = 1$. Define

$$T_1'(\varepsilon) = \frac{V_1(\sigma_1)}{\varepsilon^2\beta_1} < \infty, \qquad (5.6.11)$$

and note that

$$T_1'(\varepsilon) = \frac{V_1(\sigma_1)}{\varepsilon^2\beta_1} \leq T_1(\varepsilon) = \frac{W}{\varepsilon^2\beta_1} \text{ a.s.} \qquad (5.6.12)$$

By the memoryless property of an exponential distribution, the probability that the Markov Chain will not jump to state 2 before $\sigma_1 + T_1'(\varepsilon)$ is

$$\mathbb{P}(\Omega_1) = e^{-\nu_{12} T_1'(\varepsilon)},$$

where $\Omega_1 = \{\omega : r(\sigma_1 + t) = 1, \text{for all } t \in [0, T_1'(\varepsilon)]\}$. Consider any $\omega \in \Omega_1$ on $[\sigma_1, \sigma_1 + T_1'(\varepsilon)]$ and suppose that

$$-\beta_1 (I - I_1^*)^2 - \frac{(\mu_1 + \upsilon_1)\beta_1}{\gamma_1}(R - R_1^*)^2 \leq -\varepsilon^2 \beta_1, \tag{5.6.13}$$

in this region, which by rearranging implies that

$$(I - I_1^*)^2 + \frac{(\mu_1 + \upsilon_1)}{\gamma_1}(R - R_1^*)^2 \geq \varepsilon^2 > 0, \tag{5.6.14}$$

for $t \in [\sigma_1, \sigma_1 + T_1'(\varepsilon)]$. As a result, for $t \in [\sigma_1, \sigma_1 + T_1'(\varepsilon)]$, (5.6.9) becomes

$$\frac{dV_i}{dt} \leq -\varepsilon^2 \beta_1. \tag{5.6.15}$$

Thus, after integrating we deduce the following:

$$0 \leq V_1(\sigma_1 + T_1'(\varepsilon)) \leq V_1(\sigma_1) - \varepsilon^2 \beta_1 (T_1'(\varepsilon)), \tag{5.6.16}$$

from which by substituting $T_1'(\varepsilon)$ by its definition in (5.6.11), we could conclude that

$$V_1(\sigma_1 + T_1'(\varepsilon)) = 0. \tag{5.6.17}$$

However, if we recall the Lyapunov function given by (5.6.4), it is only equal to zero if and only if $I(\sigma_1 + T_1'(\varepsilon)) = I_1^*$ and $R(\sigma_1 + T_1'(\varepsilon)) = R_1^*$. This clearly contradicts our assumption given by (5.6.14) for $t \in [\sigma_1, \sigma_1 + T_1'(\varepsilon)]$. Thus, we must have instead

$$\beta_1 (I - I_1^*)^2 + \frac{(\mu_1 + \upsilon_1)\beta_1}{\gamma_1}(R - R_1^*)^2 < \varepsilon^2 \beta_1, \tag{5.6.18}$$

for some $s \in [\sigma_1, \sigma_1 + T_1'(\varepsilon)]$. Note that at time s, from (5.6.18) we have that

$$\frac{(I - I_1^*)^2}{I_1^*} < \frac{\varepsilon^2}{I_1^*} \quad \text{and} \quad (R - R_1^*)^2 < \frac{\varepsilon^2 \gamma_1}{\mu_1 + \upsilon_1}. \tag{5.6.19}$$

Therefore, if $\varepsilon \leq \varepsilon_1$, then by using (5.6.5)

$$0 \leq I - I_1^* - I_1^* \log\left(\frac{I}{I_1^*}\right) \leq \frac{(I - I_1^*)^2}{I^*} \leq \frac{\varepsilon^2}{I_1^*}. \tag{5.6.20}$$

By using (5.6.19) and (5.6.20), the Lyapunov function (5.6.4) at time s is bounded above by

$$\begin{aligned} V_1(s) &< \frac{\varepsilon^2}{I_1^*} + \frac{\beta_1}{2\gamma_1}\left(\frac{\varepsilon^2\gamma_1}{\mu_1+\upsilon_1}\right), \\ &= \varepsilon^2\left(\frac{1}{I_1^*} + \frac{\beta_1}{2(\mu_1+\upsilon_1)}\right). \end{aligned} \tag{5.6.21}$$

Recall from (5.6.2) that $I_1^* = \frac{\mu_1+\upsilon_1}{\mu_1+\upsilon_1+\gamma_1}\left(\frac{\alpha_1}{\beta_1}\right)$ hence (5.6.21) becomes

$$V_1(s) < \varepsilon^2\left[\frac{(\mu_1+\upsilon_1+\gamma_1)\beta_1}{(\mu_1+\upsilon_1)\alpha_1} + \frac{\beta_1}{2(\mu_1+\upsilon_1)}\right]. \tag{5.6.22}$$

Consequently, if $T \geq 0$,

$$\begin{aligned} \mathbb{P}\left\{\inf_{T\leq t<\infty} V_1(t) < \frac{\varepsilon^2\beta_1}{2(\mu_1+\upsilon_1)}\left(\frac{2(\mu_1+\upsilon_1+\gamma_1)}{\alpha_1}+1\right)\right\} \geq \mathbb{P}(\Omega_1) &= e^{-\nu_{12}T_1'(\varepsilon)}, \\ &\geq e^{-\nu_{12}T_1(\varepsilon)}, \end{aligned} \tag{5.6.23}$$

where $T_1(\varepsilon) = \frac{W}{\varepsilon^2\beta_1}$ defined as before.

Note that

$$\begin{aligned} &\left(\liminf_{t\to\infty} V_1(t) < \frac{\varepsilon^2\beta_1}{2(\mu_1+\upsilon_1)}\left(\frac{2(\mu_1+\upsilon_1+\gamma_1)}{\alpha_1}+1\right)\right) \\ &\qquad = \bigcap_{0<T<\infty}\left(\inf_{T\leq t<\infty} V_1(t) < \frac{\varepsilon^2\beta_1}{2(\mu_1+\upsilon_1)}\left(\frac{2(\mu_1+\upsilon_1+\gamma_1)}{\alpha_1}+1\right)\right). \end{aligned} \tag{5.6.24}$$

By letting $T \to \infty$ in (5.6.23), we have obtained our desired result (5.6.6).

(ii) The proof for state 2 follows similarly and thus we have the desired result (5.6.7).

□

Theorem 5.6.1 shows that our solution $(S(t), I(t), R(t))$ can approach either endemic equilibrium $(S_i^*, I_i^*, R_i^*), i = 1, 2$ arbitrarily closely with strictly positive probability.

From Theorem 5.6.1, we could derive another way of analysing the rate of convergence.

Corollary 5.6.2 *If $\varepsilon \leq \varepsilon_1$, then*

$$\mathbb{P}\left\{ \liminf_{t\to\infty} \max\{|S-S_1^*|, |I-I_1^*|, |R-R_1^*|\} \right.$$
$$\left. < \varepsilon \left(\sqrt{4 + \frac{2\alpha_1}{\mu_1+\upsilon_1+\gamma_1}} + \sqrt{\frac{\gamma_1}{\mu_1+\upsilon_1}\left(\frac{2(\mu_1+\upsilon_1+\gamma_1)}{\alpha_1}+1\right)}\right) \right\}$$
$$\geq e^{-\nu_{12}T_1(\varepsilon)}, \tag{5.6.25}$$

and

$$\mathbb{P}\left\{ \liminf_{t\to\infty} \max\{|S-S_2^*|, |I-I_2^*|, |R-R_2^*|\} \right.$$
$$\left. < \varepsilon \left(\sqrt{4 + \frac{2\alpha_2}{\mu_2+\upsilon_2+\gamma_2}} + \sqrt{\frac{\gamma_2}{\mu_2+\upsilon_2}\left(\frac{2(\mu_2+\upsilon_2+\gamma_2)}{\alpha_2}+1\right)}\right) \right\}$$
$$\geq e^{-\nu_{21}T_2(\varepsilon)}, \tag{5.6.26}$$

where $T_1(\varepsilon) = \frac{W}{\varepsilon^2\beta_1}, T_2(\varepsilon) = \frac{W}{\varepsilon^2\beta_2}$, and ε_1 is defined as in Theorem 5.6.1. Recall that $\alpha_i = \beta_i N - \mu_i - \gamma_i$.

Proof. Similar to the proof for Theorem 5.6.1, we shall split this proof into two parts, each dealing with the results for state 1 and state 2. We shall begin by looking at state 1 and the result will follow similarly for state 2.

(*i*) Recall from (5.6.5) that for $I \in (I_i^* - \varepsilon, I_i^* + \varepsilon)$ and $\varepsilon < \varepsilon_1$

$$\frac{1}{4I_1^*}(I-I_1^*)^2 \leq I_i - I_i^* - I_i^* \log\left(\frac{I}{I_i^*}\right) \leq \frac{(I-I_i^*)^2}{I_i^*}, \tag{5.6.27}$$

which implies that if (5.6.18) holds for $t \in [\sigma_1, \sigma_1 + T_1'(\varepsilon)]$ then for some $s \in [\sigma_1, \sigma_1 + T_1'(\varepsilon)]$,

$$\frac{1}{4I_i^*}(I-I_i^*)^2 \leq V_1(s) \leq \frac{\varepsilon^2\beta_1}{2(\mu_1+\upsilon_1)}\left(\frac{2(\mu_1+\upsilon_1+\gamma_1)}{\alpha_1}+1\right). \tag{5.6.28}$$

By rearranging the above expression, and taking the square root we deduce that

$$|I-I_1^*| \leq \varepsilon\sqrt{4 + \frac{2\alpha_1}{\mu_1+\upsilon_1+\gamma_1}}. \tag{5.6.29}$$

Recall again from (5.6.4) that

$$V_1(s) = I - I_1^* - I_1^* \log\left(\frac{I}{I_1^*}\right) + \frac{\beta_1}{2\gamma_1}(R - R_1^*)^2, \tag{5.6.30}$$

which by using (5.6.28) and some simple rearrangement gives that

$$|R(s) - R_1^*| \leq \varepsilon \sqrt{\frac{\gamma_1}{\mu_1 + \upsilon_1}\left(\frac{2(\mu_1 + \upsilon_1 + \gamma_1)}{\alpha_1} + 1\right)}. \tag{5.6.31}$$

By using $S(s) = N - I(s) - R(s)$ and $S_1^* = N - I_1^* - R_1^*$, then

$$\begin{aligned} |S(s) - S_1^*| &= |N - I(s) - R(s) - (N - I_1^* - R_1^*)|, \\ &\leq |I(s) - I_1^*| + |R(s) - R_1^*|, \\ &\leq \varepsilon\left(\sqrt{4 + \frac{2\alpha_1}{\mu_1 + \upsilon_1 + \gamma_1}} + \sqrt{\frac{\gamma_1}{\mu_1 + \upsilon_1}\left(\frac{2(\mu_1 + \upsilon_1 + \gamma_1)}{\alpha_1} + 1\right)}\right). \end{aligned} \tag{5.6.32}$$

So $\max\{|S(s) - S_1^*|, |I(s) - I_1^*|, |R(s) - R_1^*|\}$

$$< \varepsilon\left(\sqrt{4 + \frac{2\alpha_1}{\mu_1 + \upsilon_1 + \gamma_1}} + \sqrt{\frac{\gamma_1}{\mu_1 + \upsilon_1}\left(\frac{2(\mu_1 + \upsilon_1 + \gamma_1)}{\alpha_1} + 1\right)}\right).$$

Arguing as in the proof of Theorem 5.6.1 it is easy to see that (5.6.25) holds.

(*ii*) The proof for state 2 follows similarly. □

Corollary 5.6.2 shows similarly to Theorem 5.6.1, but using the Euclidean metric instead of the metric induced by the Lyapunov function, that the solution $(S(t), I(t), R(t))$ can approach either endemic equilibrium (S_i^*, I_i^*, R_i^*) arbitrarily closely with strictly positive probability.

In Theorem 5.6.1 and Corollary 5.6.2 we have been focusing on analysing the persistence condition where $0 < \frac{\alpha_1}{\beta_1} \leq \frac{\alpha_2}{\beta_2}$ by using Lyapunov stability. We will now complete the results on persistence by obtaining results on the convergence of the solution (S, I, R) to its corresponding disease-free and endemic equilibria under the condition $\frac{\alpha_1}{\beta_1} \leq 0 < \frac{\alpha_2}{\beta_2}$.

Theorem 5.6.3 *Assume that $T_0^S > 1$ (namely $\pi_1\alpha_1 + \pi_2\alpha_2 > 0$) and $\frac{\alpha_1}{\beta_1} \leq 0 < \frac{\alpha_2}{\beta_2}$. Let $(S_0, I_0, R_0) \in (0, N)$ be arbitrary. Then the solution to (5.2.9) has the properties that*

(i) If $\varepsilon > 0$, then

$$\mathbb{P}\left(\lim_{t\to\infty} \inf \max(|N - S|, |I|, |R|) \leq \varepsilon\left(1 + \frac{2\gamma_1}{\mu_1 + \upsilon_1}\right)\right) \geq e^{-\nu_{12}T_1(\varepsilon)}, \tag{5.6.33}$$

where $T_1(\varepsilon) = \bar{t}_1(\varepsilon) + \bar{t}_2(\varepsilon)$ *and* $\bar{t}_1(\varepsilon)$ *and* $\bar{t}_2(\varepsilon)$ *are defined as:*

$$\bar{t}_1(\varepsilon) = \begin{cases} \frac{1}{\beta_1 \varepsilon} \log\left(\frac{N}{\varepsilon}\right), & \text{if } N \geq \varepsilon, \\ 0, & \text{if } N < \varepsilon. \end{cases} \text{ and } \bar{t}_2(\varepsilon) = \begin{cases} \frac{-1}{\mu_1 + \upsilon_1} \log\left(\frac{\gamma_1 \varepsilon}{(\mu_1+\upsilon_1)N}\right), & \text{if } \frac{(\mu_1+\upsilon_1)N}{\gamma_1} \geq \varepsilon, \\ 0, & \text{if } \frac{(\mu_1+\upsilon_1)N}{\gamma_1} < \varepsilon, \end{cases} \tag{5.6.34}$$

respectively.

(ii) If $\varepsilon > 0$ *is small enough such that*

$$\pi_1 \left[\alpha_1 - \beta_1 2\varepsilon \left(1 + \frac{2\max(\gamma_1, \gamma_2)}{\min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2)}\right)\right] + \pi_2 \left[\alpha_2 - \beta_2 2\varepsilon \left(1 + \frac{2\max(\gamma_1, \gamma_2)}{\min(\mu_1 + \upsilon_1, \mu_2 + \upsilon_2)}\right)\right] > 0, \tag{5.6.35}$$

$$\textit{then} \qquad \mathbb{P}\left\{\lim_{t\to\infty} \inf V_2(t) \leq \frac{\varepsilon^2 \beta_2}{2(\mu_2 + \upsilon_2)} \left(1 + \frac{2(\mu_2 + \upsilon_2 + \gamma_2)}{\alpha_2}\right)\right\} \geq e^{-\nu_{21} T_2(\varepsilon)}, \tag{5.6.36}$$

where $T_2(\varepsilon) = \frac{W(\varepsilon)}{\beta_2 \varepsilon^2}$ *and* $W(\varepsilon) = \max\left\{N - I_2^* - I_2^* \log\left(\frac{N}{I_2^*}\right), \left|\varepsilon - I_2^* - I_2^* \log\left(\frac{\varepsilon}{I_2^*}\right)\right|\right\} + \frac{\beta_2}{2\gamma_2} N^2 < \infty$. *Note that* $V_i(\boldsymbol{x})$ *denotes the Lyapunov function which is defined as in (5.6.4) in Theorem 5.6.1, for* $i = 1, 2$.

Proof. As mentioned previously, due to the condition $\frac{\alpha_1}{\beta_1} \leq 0 < \frac{\alpha_2}{\beta_2}$, we have $R_{0,1}^D \leq 1$ in state 1 and thus if we stay in state 1 long enough, the system will tend towards its DFE which is illustrated by (5.6.33) in case (i). If, however, the system stays in state 2 long enough, then the solution will tend to its endemic equilibrium and thus the disease will persist, which is given by (5.6.36) in case (ii). First we will prove the result in case (i).

(i): Suppose that $\varepsilon > 0$. Define a stopping time such that

$$\sigma_1 = \inf\{t \geq 0 : r(t) = 1\}.$$

Clearly, $\mathbb{P}(\sigma_1 < \infty) = 1$ and by the right-continuity of the Markov Chain, $r(\sigma_1) = 1$. By the memoryless property of an exponential distribution, the probability that the Markov Chain will not jump to state 2 before $\sigma_1 + T_1(\varepsilon)$ is

$$\mathbb{P}(\Omega_1) = e^{-\nu_{12} T_1(\varepsilon)},$$

where $\Omega_1 = \{\omega : r(\sigma_1 + t) = 1, \text{for all } t \in [0, T_1(\varepsilon)]\}$. Consider any $\omega \in \Omega_1$ on $[0, T_1(\varepsilon)]$, then by using $S(t) = N - I(t) - R(t)$, it is easy to see that

$$\begin{aligned}
\frac{dI(t)}{dt} &= \beta_1 S(t) I(t) - (\mu_1 + \gamma_1) I(t), \\
&\leq \alpha_1 I(t) - \beta_1 I(t)^2, \\
&\leq -\beta_1 I(t)^2, \\
&\leq -\beta_1 \varepsilon I(t). \qquad (5.6.37)
\end{aligned}$$

provided $I \geq \varepsilon > 0$, which after integration becomes

$$I(\sigma_1 + t) \leq I(\sigma_1) e^{-\beta_1 \varepsilon t} \leq N e^{-\beta_1 \varepsilon t}. \qquad (5.6.38)$$

If $N \geq \varepsilon$ then (5.6.38) shows that by time $\bar{t}_1(\varepsilon)$, $I(t)$ must drop to a level at most ε where

$$\bar{t}_1(\varepsilon) = \frac{1}{\beta_1 \varepsilon} \log\left(\frac{N}{\varepsilon}\right). \qquad (5.6.39)$$

On the other hand if $N < \varepsilon$ then $I(0) < N < \varepsilon$ and thus $\bar{t}_1(\varepsilon) = 0$. Arguing as in the uniform strong persistence theorem, Theorem 5.5.1, and using (5.5.8) we know that for $t \geq \bar{t}_1(\varepsilon) + \bar{t}_2(\varepsilon)$,

$$R(\sigma_1 + t) \leq \frac{2\gamma_1 \varepsilon}{\mu_1 + \upsilon_1}, \qquad (5.6.40)$$

$$\text{where} \qquad \bar{t}_2(\varepsilon) = \begin{cases} \frac{-1}{\mu_1 + \upsilon_1} \log\left(\frac{\gamma_1 \varepsilon}{N(\mu_1 + \upsilon_1)}\right), & \text{if } \varepsilon \leq \frac{(\mu_1 + \upsilon_1)N}{\gamma_1}, \\ 0, & \text{if } \varepsilon > \frac{(\mu_1 + \upsilon_1)N}{\gamma_1}. \end{cases} \qquad (5.6.41)$$

Hence for $t \geq \bar{t}_1(\varepsilon) + \bar{t}_2(\varepsilon)$, we have that

$$|N - S(\sigma_1 + t)| = I(\sigma_1 + t) + R(\sigma_1 + t) \leq \varepsilon \left(1 + \frac{2\gamma_1}{\mu_1 + \upsilon_1}\right). \qquad (5.6.42)$$

Thus we could see from (5.6.42) that

$$\begin{aligned}
&\max\left[N - S(\sigma_1 + \bar{t}_1(\varepsilon) + \bar{t}_2(\varepsilon)), I(\sigma_1 + \bar{t}_1(\varepsilon) + \bar{t}_2(\varepsilon)), R(\sigma_1 + \bar{t}_1(\varepsilon) + \bar{t}_2(\varepsilon))\right] \\
&\qquad \leq \varepsilon \left(1 + \frac{2\gamma_1}{\mu_1 + \upsilon_1}\right). \qquad (5.6.43)
\end{aligned}$$

As this result is true for each $\omega \in \Omega_1$, we have that

$$\begin{aligned}
\mathbb{P}\Bigg\{ &\max\left[|N - S(\sigma_1 + \bar{t}_1(\varepsilon) + \bar{t}_2(\varepsilon))|, I(\sigma_1 + \bar{t}_1(\varepsilon) + \bar{t}_2(\varepsilon)), R(\sigma_1 + \bar{t}_1(\varepsilon) + \bar{t}_2(\varepsilon))\right] \\
&\qquad \leq \varepsilon \left(1 + \frac{2\gamma_1}{\mu_1 + \upsilon_1}\right) \Bigg\} \geq e^{-\nu_{12} T_1(\varepsilon)}, \qquad (5.6.44)
\end{aligned}$$

where $T_1(\varepsilon) = \bar{t}_1(\varepsilon) + \bar{t}_2(\varepsilon)$. Consequently, if $T \geq 0$, then

$$\mathbb{P}\left\{\inf_{T\leq t<\infty} \max\left(|N - S(t)|, I(t), R(t)\right) \leq \varepsilon\left(1 + \frac{2\gamma_1}{\mu_1 + \upsilon_1}\right)\right\} \geq e^{-\nu_{12}T_1(\varepsilon)}. \tag{5.6.45}$$

Note that

$$\begin{aligned}\Bigg(\liminf_{t\to\infty} \max\left(|N - S(t)|, I(t), R(t)\right) \leq \varepsilon\left(1 + \frac{2\gamma_1}{\mu_1 + \upsilon_1}\right)\Bigg) \\ = \bigcap_{0<T<\infty}\left(\inf_{T\leq t<\infty} \max\left(|N - S(t)|, I(t), R(t)\right) \leq \varepsilon\left(1 + \frac{2\gamma_1}{\mu_1 + \upsilon_1}\right)\right).\end{aligned} \tag{5.6.46}$$

By letting $T \to \infty$ in (5.6.45), we have obtained our desired result (5.6.33).

(ii) Recall that (5.6.35) holds which is inequality (5.5.13) with ε replaced by 2ε since ε is small and thus we can extend the result to 2ε. Note also that when $r(t) = 1, R_{0,1}^D \leq 1$ and also $\frac{dI}{dt} < (\alpha_1 - \beta_1 I(t))I(t) < 0$. Hence, if Ω denotes the whole sample space, given $\omega \in \Omega$ and $t_3(\omega) > 0$, for $t \geq t_3(\omega), I(t)$ must rise up and over the level ε at some time $t_4(\omega) > t_3(\omega)$. So $\exists t_5(\omega) > t_3(\omega)$ with $I(t_5(\omega)) = \varepsilon$ and $r(t_5(\omega)) = 2$. Also note that $V_2(t_5(\omega)) \leq W(\varepsilon)$ where $V_2(t)$ denotes the Lyapunov function in state 2 given by (5.6.4) in Theorem 5.6.1 and $W(\varepsilon)$ is a constant.

Now arguing as in the proof of Theorem 5.6.1 but now starting at $t_5(\omega)$ not σ_1, i.e. define a new stopping time

$$t_5(\omega) = \inf\{t \geq 0 : r(t_5(\omega)) = 2,\ I(t_5(\omega)) = \varepsilon\},$$

we will have the required result namely,

$$\mathbb{P}\left\{\liminf_{t\to\infty} V_2(t) < \frac{\varepsilon^2\beta_2}{2(\mu_2 + \upsilon_2)}\left(\frac{2(\mu_2 + \upsilon_2 + \gamma_2)}{\alpha_2} + 1\right)\right\} \geq e^{-\nu_{21}T_2(\varepsilon)}, \tag{5.6.47}$$

where $T_2(\varepsilon) = \frac{W(\varepsilon)}{\varepsilon^2\beta_2}$ and $W(\varepsilon) = \max\big\{N - I_2^* - I_2^*\log\big(\frac{N}{I_2^*}\big), \big|\varepsilon - I_2^* - I_2^*\log\big(\frac{\varepsilon}{I_2^*}\big)\big|\big\} + \frac{\beta_2}{2\gamma_2}N^2 < \infty$, which could be easily derived from (5.6.10). □

In this theorem, we have obtained interesting probabilistic results on the convergence of the solution $(S(t), I(t), R(t))$ to the stochastic SIRS model (5.2.9) to its corresponding disease-free and endemic equilibria.

The following corollary follows from Theorem 5.6.3.

Corollary 5.6.4 *If $\varepsilon < \varepsilon_1$, then:*

$$\mathbb{P}\left\{ \liminf_{t\to\infty} \max\{|S - S_2^*|, |I - I_2^*|, |R - R_2^*|\} \right.$$
$$\left. < \varepsilon \left(\sqrt{4 + \frac{2\alpha_2}{\mu_2 + \upsilon_2 + \gamma_2}} + \sqrt{\frac{\gamma_2}{\mu_2 + \upsilon_2} \left(\frac{2(\mu_2 + \upsilon_2 + \gamma_2)}{\alpha_2} + 1 \right)} \right) \right\}$$
$$\geq e^{-\nu_{21} T_2(\varepsilon)}, \tag{5.6.48}$$

where $T_2(\varepsilon) = \frac{W(\varepsilon)}{\varepsilon^2 \beta_2}$ and ε_1 is defined as in Theorem 5.6.1.

Proof. The proof is similar to the proof for Corollary 5.6.2.

5.7 SIR Model with Markovian Switching and Measles

The Susceptible-Infected-Removed (SIR) model with two-state Markovian switching

$$\begin{aligned} \frac{dS(t)}{dt} &= -\beta_{r(t)} I(t) S(t) + \mu_{r(t)} N - \mu_{r(t)} S(t), \\ \frac{dI(t)}{dt} &= \beta_{r(t)} I(t) S(t) - (\mu_{r(t)} + \gamma_{r(t)}) I(t), \\ \frac{dR(t)}{dt} &= \gamma_{r(t)} I(t) - \mu_{r(t)} R(t), \end{aligned} \tag{5.7.1}$$

is a special case of the SIRS model (5.2.9) which we have been looking at throughout the chapter. In fact, we could easily derive the corresponding extinction and persistence results for the SIR model with Markovian switching by simplying setting one of the parameters, namely $\upsilon_{r(t)}$, in (5.2.9) to zero. In order to illustrate the results for the SIR model with two-state Markovian switching (5.7.1), we have constructed realistic numerical simulations using realistic parameter values based on the real life disease measles.

5.7.1 Measles

The measles virus is a single stranded RNA paramyxovirus, genus *Morbillivirus* where its nucleocapsid is surrounded by two types of envelopes, the lipid- and glycoprotein-containing envelope (e.g. [94, 111]). As mentioned before, there are many environmental factors that could affect the behaviour of a virus, for example temperature, humidity,

pollution and sunlight [116]. It turns out that airborne viruses with lipid envelopes such as measles virus are more likely to survive better and longer at a lower relative humidity $(20-30\%)$ condition as opposed to a higher relative humidity $(70-90\%)$ condition [65, 116]. As a result switching between two seasons where the relative humidity differs greatly could have an impact on the measles virus survival rate in the air and thus possibly affect the disease transmission rate to switch. Although in real life, things are more complex, we hope that by choosing the appropriate parameter values for measles in the UK, we could construct numerical simulations to illustrate such a situation. Note that in this section, the unit of time is still one day but the population sizes are now unscaled.

Example 5.7.1 *According to the Global Health Observatory Data Repository of the World Health Organisation [129], the total UK population size in 2012 was* $62,783,000$ *while the UK crude death rate per* $1,000$ *population in the same year was* 8.9*, hence making* $\mu = 2.43836 \times 10^{-5}/day$*. The average infection period for measles in the UK is* 7 *days, thus making* $\gamma_1 = \gamma_2 = 1/7/day$ *[9]. Furthermore, let us now define* $\beta_1 = 3.072 \times 10^{-8}/day$ *(to four significant figures) corresponding to* $R_{01}^D = 13.5$ *and* $\beta_2 = 3.641 \times 10^{-8}/day$ *(to four significant figures) corresponding to* $R_{02}^D = 16$*. Note that both* β_1 *and* β_2 *are chosen so that* R_{01}^D *and* R_{02}^D *lie in the range* $11-18$*, which is the* R_0 *range for measles [9].*

As a result, we have that $\alpha_1 = 1.785812/day$ *and* $\alpha_2 = 2.143048/day$*. Moreover, let us set* $\nu_{12} = 0.0005/day$ *and* $\nu_{21} = 0.0008/day$*, then* $\pi_1 = 8/13$ *and* $\pi_2 = 5/13$*. As a result, we deduce that* $\alpha_1\pi_1 + \alpha_2\pi_2 = 1.92321 > 0$*. In other words, we have that* $T_0^S > 1$*. Note that for this case we have* $\frac{\gamma_1}{\mu_1} = \frac{\gamma_2}{\mu_2}$*. By setting* $\upsilon_{r(t)} = 0$*, we could conclude from Theorems 5.5.2-5.5.7 that, for any given initial value* $(S(0), I(0), R(0)) \in (0, N)^3$*, the solution to the stochastic SIR model (5.7.1) satisfies*

(a) $\liminf_{t\to\infty} S(t) \leq N - \frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2} = 4,341,787 \quad a.s.,$

(b) $\limsup_{t\to\infty} S(t) \geq N - \frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2} = 4,341,787 \quad a.s.,$

(c) $\liminf_{t\to\infty} I(t) \leq \left(\frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2}\right) \frac{1}{1+\min\left(\frac{\gamma_1}{\mu_1}, \frac{\gamma_2}{\mu_2}\right)} = 9,973 \quad a.s.,$

(d) $\limsup_{t\to\infty} I(t) \geq \left(\frac{\pi_1\alpha_1+\pi_2\alpha_2}{\pi_1\beta_1+\pi_2\beta_2}\right) \frac{1}{1+\max\left(\frac{\gamma_1}{\mu_1}, \frac{\gamma_2}{\mu_2}\right)} = 9,973 \quad a.s.,$

(e) $R_\infty = \liminf_{t\to\infty} R(t) > 0 \quad a.s.,$

(f) $R^\infty = \limsup_{t\to\infty} R(t) < \frac{N\max(\gamma_1,\gamma_2)}{\max(\gamma_1,\gamma_2)+\min(\mu_1,\mu_2)} = 62,772,286 < N \quad a.s.$

In other words, the number of susceptible and infected individuals will always return to the vicinity of the level $4,341,787$ *and* $9,973$ *respectively almost surely, while the limiting number of recovered individuals has almost surely a strictly positive limiting lower limit whilst its limiting upper limit is at most* $62,772,286$ *almost surely.*

From Figure 5.20, we could see clearly that the numerical simulations support our theoretical results by showing our solution to the SIR model with Markov switching (5.7.1) oscillating about the levels we expected. Again the numerical simulations were repeated for around 50 times with different initial values and the same conclusion was achieved.

5.8 Generalisation

As mentioned at the beginning, in order to allow us to understand the results better, we have been focusing on analysing the behaviour of our SIRS model with two-state Markovian switching (5.2.9). However, all the results we have obtained in this chapter could be easily extended to a finite state space Markov Chain $\mathbb{S} = \{1, 2, ..., M\}$ by using the fundamental concepts for finite state Markov Chains mentioned in Section 5.2.1. Note that by following a similar procedure as for the two-state Markov switching, we can show that for any given initial values $(S_0, I_0, R_0) \in (0, N)$, there exists a unique solution such that $(S(t), I(t), R(t)) \in (0, N)$ with probability 1 for all $t \geq 0$. In the general finite state space Markov Chain, it is possible to derive an explicit expression for the basic reproduction number R_0^S in the stochastic Markov switching model analogues to the corresponding R_0^S for the two-state Markov switching case [41], namely

$$R_0^S = \frac{a_1 + a_2 + \sqrt{(a_1 + a_2)^2 - 4a_1a_2(1 - p)}}{2(1 - p)}, \tag{5.8.1}$$

expressed as the largest eigenvalue of a positive matrix.

Let us first generalise the expression T_0^S given in (5.4.1) as

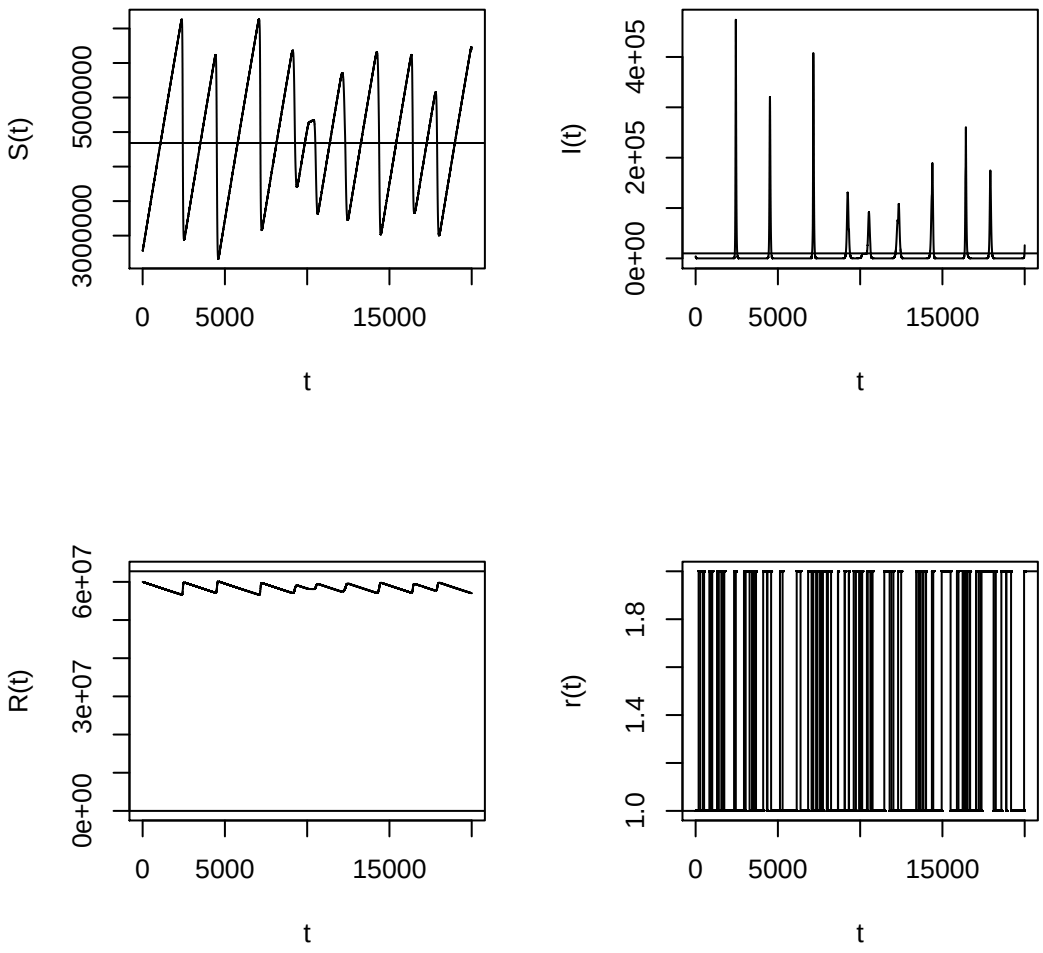

Figure 5.20: Numerical simulations for our solution to (5.7.1) $T_0^S > 1$ and the corresponding Markov Chain $r(t)$ using the system parameter values given in Example 5.7.1 with $\Delta = 0.001$ days with initial values $S(0) = 2,779,000$, $I(0) = 4,000$, $R(0) = 60,000,0000$ and $r(0) = 1$.

$$T_0^S = \frac{\sum_{k=1}^{M} \pi_k \beta_k N}{\sum_{k=1}^{M} \pi_k (\mu_k + \gamma_k)}. \tag{5.8.2}$$

Similar to Proposition 5.4.1, we have the following alternative conditions on the value T_0^S for a finite state space Markov switching.

Proposition 5.8.1 *Let us define $\alpha_{r(t)}$ as before, then we have the following alternative ways of interpreting T_0^S*

- $T_0^S < 1 \Leftrightarrow \sum_{k=1}^{M} \pi_k \alpha_k < 0$,
- $T_0^S = 1 \Leftrightarrow \sum_{k=1}^{M} \pi_k \alpha_k = 0$,
- $T_0^S > 1 \Leftrightarrow \sum_{k=1}^{M} \pi_k \alpha_k > 0$.

For $T_0^S < 1$, Theorem 5.4.2 can be generalised as follows:

Theorem 5.8.2 *If $T_0^S < 1$, then for any given initial value $(S_0, I_0, R_0) \in (0, N)^3$, the solution of the stochastic SIRS epidemic model obeys*

(i) $\limsup_{t\to\infty} \frac{1}{t} log(I(t)) \leq \sum_{k=1}^{M} \pi_k \alpha_k < 0$ *a.s.,*

(ii) $\lim_{t\to\infty} R(t) = 0$ *a.s.,*

(iii) $\lim_{t\to\infty} S(t) = N$ *a.s.*

By the above result, we hence conclude that $I(t)$ tends to zero exponentially and $R(t)$ tends to zero as $t \to \infty$, thus making $S(t)$ tend to N as $t \to \infty$ almost surely. In other words, the disease will die out with probability one and the solution will tend to its DFE $(N, 0, 0)$.

For the case of $T_0^S > 1$, the uniform strong persistence result given in Theorem 5.5.1 can be generalised as follows:

Theorem 5.8.3 (Generalised uniform strong persistence) *Suppose that* $I(0) > 0$

Case (a): If $0 < \frac{\alpha_1}{\beta_1} \leq \frac{\alpha_2}{\beta_2} \leq \cdots \leq \frac{\alpha_M}{\beta_M}$, $\exists \varepsilon^{'} > 0$ *independent of the initial conditions such that*

$$\liminf_{t\to\infty} I(t) \geq \varepsilon^{'} > 0 \ a.s. \tag{5.8.3}$$

In other words the SIRS model with Markov switching is almost surely uniformly persistent.

Case (b): If $T_0^S > 1$, *that is* $\sum_{k=1}^{M} \pi_k \alpha_k > 0$ *and* $\frac{\alpha_j}{\beta_j} \leq 0$ *for some* $j \in (1, M-1)$, *then given* $\delta_1 > 0, \exists \varepsilon' > 0$ *such that* $\forall t_1 > 0,\ I(t) \geq \varepsilon'$ *for some* $t \geq t_1$ *on a set* Ω_1 *where* $\mathbb{P}(\Omega_1) \geq 1 - \delta_1$. *To put this another way,*

$$\liminf_{t\to\infty} I(t) > 0 \ a.s.$$

The results shown in Theorem 5.5.2 for the two-state Markov switching can be extended to a more generalised case.

Theorem 5.8.4 *If* $T_0^S > 1$, *then for any given initial value* $(S(0), I(0), R(0)) \in (0, N)^3$, *then the solution* $S(t)$ *of the stochastic SIRS model has the properties that:*

(a) $\liminf_{t\to\infty} S(t) \leq N - \frac{\sum_{k=1}^{M} \pi_k \alpha_k}{\sum_{k=1}^{M} \pi_k \beta_k} \quad a.s.,$

(b) $\limsup_{t\to\infty} S(t) \geq N - \frac{\sum_{k=1}^{M} \pi_k \alpha_k}{\sum_{k=1}^{M} \pi_k \beta_k} \quad a.s.$

In other words, the number of susceptibles will reach the neighbourhood of the level $N - \frac{\sum_{k=1}^{M} \pi_k \alpha_k}{\sum_{k=1}^{M} \pi_k \beta_k}$ *infinitely many times almost surely.*

Lemma 5.5.4 can be generalised as follows:

Lemma 5.8.5 *Given* $\varepsilon_1 > 0$,

(i) If $I(t) \geq \xi$ *for* $t \geq t_0, \exists t_1 \geq t_0$ *such that for* $t \geq t_1$,

$$R(t) \geq \xi \min\left(\frac{\gamma_1}{\mu_1 + \upsilon_1}, \frac{\gamma_2}{\mu_2 + \upsilon_2}, \ldots, \frac{\gamma_M}{\mu_M + \upsilon_M}\right)(1 - \varepsilon_1).$$

(ii) If $I(t) \leq \xi$ *for* $t \geq t_0, \exists t_1 \geq t_0$ *such that for* $t \geq t_1$,

$$R(t) \leq \xi \max\left(\frac{\gamma_1}{\mu_1 + \upsilon_1}, \frac{\gamma_2}{\mu_2 + \upsilon_2}, \ldots, \frac{\gamma_M}{\mu_M + \upsilon_M}\right)(1 + \varepsilon_1).$$

Theorem 5.5.5 and Theorem 5.5.7 respectively can be generalised as follows:

Theorem 5.8.6 *If $T_0^S > 1$, then for any given initial value $(S(0), I(0), R(0)) \in (0, N)^3$, the solution $I(t)$ of the stochastic SIRS model has the properties that:*

(a) $\liminf_{t\to\infty} I(t) \leq \left(\frac{\sum_{k=1}^{M} \pi_k \alpha_k}{\sum_{k=1}^{M} \pi_k \beta_k}\right) \frac{1}{1+\min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}, ..., \frac{\gamma_M}{\mu_M+\upsilon_M}\right)}$ *a.s.,*

(b) $\limsup_{t\to\infty} I(t) \geq \left(\frac{\sum_{k=1}^{M} \pi_k \alpha_k}{\sum_{k=1}^{M} \pi_k \beta_k}\right) \frac{1}{1+\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}, ..., \frac{\gamma_M}{\mu_M+\upsilon_M}\right)}$ *a.s.*

So given $\epsilon > 0$ the number of infectives will enter between the levels

$$\left\{\frac{\sum_{k=1}^{M} \pi_k \alpha_k}{\sum_{k=1}^{M} \pi_k \beta_k} - \epsilon\right\} \frac{1}{1+\max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}, ..., \frac{\gamma_M}{\mu_M+\upsilon_M}\right)} \text{ and } \left\{\frac{\sum_{k=1}^{M} \pi_k \alpha_k}{\sum_{k=1}^{M} \pi_k \beta_k} + \epsilon\right\} \frac{1}{1+\min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \frac{\gamma_2}{\mu_2+\upsilon_2}, ..., \frac{\gamma_M}{\mu_M+\upsilon_M}\right)}$$

infinitely often almost surely.

Theorem 5.8.7 *If $T_0^S > 1$, then for any given initial value $(S(0), I(0), R(0)) \in (0, N)^3$, then the solution $R(t)$ of the stochastic SIRS model has the properties that:*

(a) $\liminf_{t\to\infty} R(t) > 0$ *a.s.,*

(b) $\limsup_{t\to\infty} R(t) < \frac{N \max(\gamma_1, \gamma_2, ..., \gamma_M)}{\max(\gamma_1, \gamma_2, ..., \gamma_M) + \min(\mu_1+\upsilon_1, \mu_2+\upsilon_2, ..., \mu_M+\upsilon_M)} < N$ *a.s.*

In other words, the limiting value of the number of recovered individuals will be strictly positive and will not ultimately exceed $\frac{N \max(\gamma_1, \gamma_2, ..., \gamma_M)}{\max(\gamma_1, \gamma_2, ..., \gamma_M) + \min(\mu_1+\upsilon_1, \mu_2+\upsilon_2, ..., \mu_M+\upsilon_M)}$ almost surely.

Theorem 5.5.9 can be generalised as follows:

Theorem 5.8.8 *Assume that $T_0^S > 1$ and let $I(0) \in (0, N)$ be arbitrary. If $\frac{\alpha_j}{\beta_j} \leq 0$ for some $j \in (1, M-1)$ and $\frac{\alpha_1}{\beta_1} \leq \frac{\alpha_2}{\beta_2} \leq \cdots \leq \frac{\alpha_M}{\beta_M}$, then the following statements hold almost surely:*

(i) $\liminf_{t\to\infty} S(t) \geq N - \frac{\alpha_M}{\beta_M}\left(1 + \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \ldots, \frac{\gamma_M}{\mu_M+\upsilon_M}\right)\right).$

(ii) $\limsup_{t\to\infty} I(t) \leq \frac{\alpha_M}{\beta_M}.$

(iii) $\limsup_{t\to\infty} R(t) \leq \frac{\alpha_M}{\beta_M} \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \ldots, \frac{\gamma_M}{\mu_M+\upsilon_M}\right).$

Theorem 5.5.12 can be generalised as follows:

Theorem 5.8.9 *(a) Assume that $T_0^S > 1$ and let $I(0) \in (0, N)$ be arbitrary. If $0 < \frac{\alpha_1}{\beta_1} \leq \frac{\alpha_2}{\beta_2} \leq \ldots \frac{\alpha_M}{\beta_M}$, then the following statements hold almost surely:*

(i) $\liminf_{t\to\infty} S(t) \geq N - \frac{\alpha_M}{\beta_M}\left(1 + \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \ldots, \frac{\gamma_M}{\mu_M+\upsilon_M}\right)\right)$.

(ii) $\limsup_{t\to\infty} I(t) \leq \frac{\alpha_M}{\beta_M}$.

(iii) $\limsup_{t\to\infty} R(t) \leq \frac{\alpha_M}{\beta_M} \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \ldots, \frac{\gamma_M}{\mu_M+\upsilon_M}\right)$.

(b) If $I(0) > 0$ under the same conditions the following statements hold almost surely:

(i) $\limsup_{t\to\infty} S(t) \leq N - \left(\frac{\alpha_1}{\beta_1} - \frac{\alpha_M}{\beta_M} \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \ldots, \frac{\gamma_M}{\mu_M+\upsilon_M}\right)\right) \times \left(1 + \min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \ldots, \frac{\gamma_M}{\mu_M+\upsilon_M}\right)\right)$.

(ii) $\liminf_{t\to\infty} I(t) \geq \frac{\alpha_1}{\beta_1} - \frac{\alpha_M}{\beta_M} \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \ldots, \frac{\gamma_M}{\mu_M+\upsilon_M}\right)$.

(iii) $\liminf_{t\to\infty} R(t) \geq \left(\frac{\alpha_1}{\beta_1} - \frac{\alpha_M}{\beta_M} \max\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \ldots, \frac{\gamma_M}{\mu_M+\upsilon_M}\right)\right) \times \min\left(\frac{\gamma_1}{\mu_1+\upsilon_1}, \ldots, \frac{\gamma_M}{\mu_M+\upsilon_M}\right)$.

The results on Lyapunov stability shown in Section 5.6 can also be extended to the finite state Markov chain. Theorem 5.6.1 can be generalised as follows:

Theorem 5.8.10 *Assume that $T_0^S > 1$ and $0 < \frac{\alpha_1}{\beta_1} \leq \frac{\alpha_2}{\beta_2} \leq \cdots \leq \frac{\alpha_M}{\beta_M}$ and let $(S(0), I(0), R(0)) \in (0, N)^3$ be arbitrary and let the switching times of the Markov Chain be $0 = \tau_0 < \tau_1 < ... < \tau_k$ where $\tau_k \to \infty$ as $k \to \infty$. Define the Lyapunov function to be:*

$$V_i(\boldsymbol{x}) = I - I_i^* - I_i^* \log\left(\frac{I}{I_i^*}\right) + \frac{\beta_i}{2\gamma_i}(R - R_i^*)^2, \tag{5.8.4}$$

where $\boldsymbol{x} = (S(t), I(t), R(t))$, for $i = 1, 2, \ldots, M$. Let us define

$$\begin{aligned} f_1(I) &= \frac{(I - I_i^*)^2}{4I_i^*}, \\ f_2(I) &= I - I_i^* - I_i^* \log\left(\frac{I}{I_i^*}\right), \\ f_3(I) &= \frac{(I - I_i^*)^2}{I_i^*}. \end{aligned} \tag{5.8.5}$$

Then it is easy to see that $f_1(I_i^*) = f_2(I_i^*) = f_3(I_i^*) = f_1'(I_i^*) = f_2'(I_i^*) = f_3'(I_i^*) = 0$ *and*

$$f_1''(I_i^*) = \frac{1}{2I_i^*}, \quad f_2''(I_i^*) = \frac{1}{I_i^*}, \quad f_3(I_i^*) = \frac{2}{I_i^*}.$$

Note that by considering the Taylor series expansion about $I = I_i^*$ *for* ϵ *small enough, say* $\varepsilon \leq \varepsilon_1$ *then*

$$\frac{1}{4I_i^*}(I - I_i^*)^2 \leq I - I_i^* - I_i^* \log\left(\frac{I}{I_i^*}\right) \leq \frac{(I - I_i^*)^2}{I_i^*}, \tag{5.8.6}$$

in $(I_i^* - \varepsilon, I_i^* + \varepsilon)$, *for* $i = 1, 2, \ldots, M$.

For any $\varepsilon \leq \varepsilon_1$ *sufficiently small, the Lyapunov function (5.8.4) for our SIRS model with Markovian switching has the properties that:*

$$\mathbb{P}\left\{\liminf_{t\to\infty} V_i(t) < \frac{\varepsilon^2\beta_i}{2(\mu_i + \upsilon_i)}\left(1 + \frac{2(\mu_i + \upsilon_i + \gamma_i)}{\alpha_i}\right)\right\} \geq e^{\Phi_{ii}T_i(\varepsilon)}, \tag{5.8.7}$$

where $T_i(\varepsilon) = \frac{W}{\varepsilon^2\beta_i} > 0$ *for* $i = 1, 2, \ldots, M$ *and for some constant* W. *Note that* $\Phi_{ii} = \nu_{ii}$ *where* ν_{ii} *is defined as in Section 5.2.1.*

Corollary 5.6.2 can be generalised as follows:

Corollary 5.8.11 *If* $\varepsilon \leq \varepsilon_1$, *then*

$$\mathbb{P}\left\{\liminf_{t\to\infty} \max\{|S - S_i^*|, |I - I_i^*|, |R - R_i^*|\}\right.$$
$$\left. < \varepsilon\left(\sqrt{4 + \frac{2\alpha_i}{\mu_i + \upsilon_i + \gamma_i}} + \sqrt{\frac{\gamma_i}{\mu_i + \upsilon_i}\left(\frac{2(\mu_i + \upsilon_i + \gamma_i)}{\alpha_i} + 1\right)}\right)\right\}$$

$$\geq e^{\Phi_{ii}T_i(\varepsilon)}, \tag{5.8.8}$$

where $T_i(\varepsilon) = \frac{W}{\varepsilon^2\beta_1}$, *for* $i = 1, 2, \ldots, M$ *and for some constant* W. *Note that* ε_1 *is defined as in Theorem 5.8.10. Recall that* $\alpha_i = \beta_i N - \mu_i - \gamma_i$.

Theorem 5.6.3 can be generalised as follows:

Theorem 5.8.12 *Assume that* $T_0^S > 1$ *(namely* $\sum_{k=1}^{M} \pi_k\alpha_k > 0$*) and* $\frac{\alpha_j}{\beta_j} \leq 0$ *for some* $j \in (1, M-1)$. *Let* $(S_0, I_0, R_0) \in (0, N)$ *be arbitrary. Then the solution of the stochastic SIRS model has the properties that*

(i) If $\varepsilon > 0$, then

$$\mathbb{P}\left(\liminf_{t\to\infty} \max(|N-S|,|I|,|R|) \leq \varepsilon\left(1+\frac{2\gamma_j}{\mu_j+\upsilon_j}\right)\right) \geq e^{\Phi_{jj}T_1(\varepsilon)}, \tag{5.8.9}$$

where $T_1(\varepsilon) = \bar{t}_1(\varepsilon) + \bar{t}_2(\varepsilon)$ and $\bar{t}_1(\varepsilon)$ and $\bar{t}_2(\varepsilon)$ are defined as:

$$\bar{t}_1(\varepsilon) = \begin{cases} \frac{1}{\beta_j\varepsilon}\log\left(\frac{N}{\varepsilon}\right), & \text{if } N \geq \varepsilon, \\ 0, & \text{if } N < \varepsilon, \end{cases} \text{ and } \bar{t}_2(\varepsilon) = \begin{cases} \frac{-1}{\mu_j+\upsilon_j}\log\left(\frac{\gamma_j\varepsilon}{(\mu_j+\upsilon_j)N}\right), & \text{if } \frac{(\mu_j+\upsilon_j)N}{\gamma_j} \geq \varepsilon, \\ 0, & \text{if } \frac{(\mu_j+\upsilon_j)N}{\gamma_j} < \varepsilon, \end{cases} \tag{5.8.10}$$

respectively.

(ii) If $\varepsilon > 0$ is small enough such that

$$\pi_1\left[\alpha_1 - \beta_1 2\varepsilon\left(1+\frac{2\max(\gamma_1,\ldots,\gamma_M)}{\min(\mu_1+\upsilon_1,\ldots,\mu_M+\upsilon_M)}\right)\right] + \cdots + \pi_M\left[\alpha_M - \beta_M 2\varepsilon\left(1+\frac{2\max(\gamma_1,\ldots,\gamma_M)}{\min(\mu_1+\upsilon_1,\ldots,\mu_M+\upsilon_M)}\right)\right] > 0, \tag{5.8.11}$$

then
$$\mathbb{P}\left\{\liminf_{t\to\infty} V_i(t) \leq \frac{\varepsilon^2\beta_i}{2(\mu_i+\upsilon_i)}\left(1+\frac{2(\mu_i+\upsilon_i+\gamma_i)}{\alpha_i}\right)\right\} \geq e^{\Phi_{ii}T_2(\varepsilon)}, \tag{5.8.12}$$

where $T_2(\varepsilon) = \frac{W(\varepsilon)}{\beta_i\varepsilon^2}$ and $W(\varepsilon) = \max\{N - I_i^* - I_i^*\log(\frac{N}{I_i^*}), |\varepsilon - I_i^* - I_i^*\log(\frac{\varepsilon}{I_i^*})|\} + \frac{\beta_i}{2\gamma_i}N^2 < \infty$. Note that $V_i(\boldsymbol{x})$ denotes the Lyapunov function which is defined as in (5.8.4) in Theorem 5.8.10, for $i = 1, 2, \ldots, M$.

Corollary 5.6.4 can be generalised as follows:

Corollary 5.8.13 *If $\varepsilon < \varepsilon_1$, then:*

$$\mathbb{P}\left\{\liminf_{t\to\infty} \max\{|S-S_i^*|, |I-I_i^*|, |R-R_i^*|\} < \varepsilon\left(\sqrt{4+\frac{2\alpha_i}{\mu_i+\upsilon_i+\gamma_i}} + \sqrt{\frac{\gamma_i}{\mu_i+\upsilon_i}\left(\frac{2(\mu_i+\upsilon_i+\gamma_i)}{\alpha_i}+1\right)}\right)\right\}$$

$$\geq e^{\Phi_{ii}T_2(\varepsilon)}, \tag{5.8.13}$$

where $T_2(\varepsilon) = \frac{W(\varepsilon)}{\varepsilon^2\beta_i}$ and ε_1 is defined as in Theorem 5.8.10, for $i = 1, 2, \ldots, M$.

5.9 Summary

There are many environmental factors that could affect the behaviour of a population system such as the availability of food and temperature [116]. Motivated by Gray et al. [41] we have examined the effect of environmental noise on a more complicated model, the SIRS model, by using the concept of Markovian switching to include telegraph noise into the SIRS model with two-state Markov switching (5.2.9). We have obtained the conditions needed for almost surely extinction and persistence using the threshold T_0^S which was also used in [41]. In Theorem 5.4.2, we showed that if $T_0^S < 1$ then the disease will go extinct almost surely. On the other hand if $T_0^S > 1$, then the disease will persist almost surely (Theorems 5.5.2, 5.5.5 and 5.5.7). In Theorems 5.5.9 and 5.5.12 we obtained two sets of persistence conditions for the two possible cases in which $T_0^S > 1$, namely $\frac{\alpha_1}{\beta_1} \leq 0 < \frac{\alpha_2}{\beta_2}$ and $0 < \frac{\alpha_1}{\beta_1} \leq \frac{\alpha_2}{\beta_2}$. Furthermore by using the uniform strong persistence result for $I(t)$, (Theorem 5.5.1) and the Lyapunov stability theorem, we managed to obtain probabilistic results on convergence of our solution to the disease-free and endemic equilibria in Section 5.6.

Throughout the chapter, numerical simulations were produced to support and illustrate our theoretical results. The results obtained for the two-state Markov Chain $\mathbb{S} = \{1, 2\}$ could be easily extended into a more general Markov Chain $\mathbb{S} = \{1, 2, ..., M\}$. Furthermore the SIR model with Markov switching is a special case of the SIRS model and more importantly the extinction and persistence results for the SIR model could be obtained simply by setting $\upsilon_1 = \upsilon_2 = 0$. As a practical example, we constructed a numerical simulation using realistic parameter values for measles to support the theoretical results for the SIR model with Markov switching after setting $\upsilon_1 = \upsilon_2 = 0$.

Most of the work mentioned in this chapter has been written up as a paper and has been submitted to a journal and is currently under review.

In the next chapter we will look at a more specific model with environmental stochasticity introduced using a different method than we have done in Chapter 5.

Chapter 6

A Stochastic Differential Equation Model for the Spread of HIV Amongst People Who Inject Drugs

6.1 Introduction

Inspired by the model constructed in [43], in this chapter we will introduce environmental stochasticity into the model by parameter perturbation which is a standard technique in stochastic population modelling [28, 29, 40, 63]. To the best of our knowledge, we are the first to examine the effect that environmental stochasticity has on the dynamical behaviour of the modified Kaplan model [43]. The techniques used in this chapter are inspired by the work done in [40]. The chapter is organised as follows. In the next section, we will describe the formulation of the stochastic HIV model amongst PWIDs. In Section 6.3, we shall prove the existence of a unique nonnegative solution. In Sections 6.4 and 6.5, we will investigate two of the main important properties of any biological system, namely the conditions required for extinction and persistence respectively. Then in Section 6.6, we shall show that there exists a stationary distribution for our system. Finally, we will perform some numerical simulations with realistic parameter values to verify the result.

Most of the work in this chapter has been written up as a paper and has been published in [82].

6.2 The Stochastic HIV Model

Throughout this chapter, 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 following deterministic HIV model, which has been constructed by Greenhalgh and Hay [43] based on the model of Kaplan [66]. Define the following parameters:

λ_1 : shooting gallery visiting rate for susceptible PWIDs and the PWIDs who are infected but do not know they are infected;

λ_2 : shooting gallery visiting rate for infected PWIDs who know that they are infected;

P_1 : probability that the needle is flushed and the PWID is infected;

P_2 : probability that the needle is flushed and the PWID remains uninfected;

P_3 : probability that the PWID becomes infected without the needle being flushed;

P_4 : probability that the PWID remains uninfected and the needle is not flushed;

ϕ_1 : probability that an infected PWID leaves uninfected a syringe that was initially uninfected;

θ_1 : probability that an infected PWID leaves uninfected a syringe that was initially infected;

ξ : fraction of all PWIDs (susceptible or not) who bleach their injection equipment after use;

γ : gallery ratio, where $\gamma = \frac{n}{m}$ and n represents the PWID population and m represents the number of shooting galleries or syringes that each PWID visits at random;

p : probability that infected PWIDs know that they are infected;

μ: per capita rate at which infected PWIDs cease to share injection equipment (including those who cease sharing because of developing AIDS).

Note that $P_1 + P_2 + P_3 + P_4 = 1$. In real life situation, whether or not a needle is left infectious after being used by an infected addict may depend on various factors, for example the volume of blood left in the needle and the average viral load of that blood. As a result, it is possible for $\phi_1 > 0$ though the probability might be small.

Define the following new composite parameters:

$$\begin{aligned}
\sigma &= [\lambda_1(1-p) + \lambda_2 p]\,\gamma(1-\xi)(1-\phi_1), \\
\eta &= [\lambda_1(1-p) + \lambda_2 p]\,\gamma\,[\xi + \theta_1(1-\xi)]\,, \\
\rho &= \lambda_1\gamma\,[1-(1-\xi)(1-P_1-P_2)]\,, \\
\upsilon &= \lambda_1(P_1+P_3).
\end{aligned} \tag{6.2.1}$$

In the expression for σ the factor $(1-\xi)(1-\phi_1)$ represents the probability that an initially uninfected syringe is left infected and not cleaned by an infected PWID. The term $\lambda_1(1-p)+\lambda_2 p$ represents the average rate at which an infected PWID visits syringes. Hence $\sigma = \gamma\bar{\sigma}$ where $\gamma = \frac{n}{m}$ is the gallery ratio and $\bar{\sigma}$ is the rate at which an infected PWID visits syringes multiplied by the probability that he or she leaves an uninfected syringe infected after use. Similarly $\eta = \gamma\bar{\eta}$ where $\bar{\eta}$ is the rate at which an infected PWID visits syringes multiplied by the probability that he or she leaves an infected syringe uninfected after use.

λ_1 represents the rate at which a susceptible PWID visits syringes and $1-(1-\xi)(1-P_1-P_2)$ represents the probability that an initially infected syringe is left uninfected after use by that PWID. Hence $\rho = \gamma\bar{\rho}$ where $\bar{\rho}$ is the rate at which a susceptible PWID visits syringes multiplied by the probability that he or she leaves an infected syringe uninfected after use. υ represents the rate at which a susceptible PWID visits syringes multiplied by the probability that he or she becomes infected given that the syringe which they visit is infected. Thus $\upsilon\beta$ represents the rate at which a susceptible PWID visits syringes and becomes infected. υ can thus be regarded as the "potential" infection rate of a susceptible PWID.

Let $\pi(t)$ and $\beta(t)$ denote the proportion of infected PWIDs and proportion of infected needles respectively. Thus the absolute numbers of infected PWIDs and infected needles are $n\pi(t)$ and $m\beta(t)$. The spread of the disease amongst syringes can be described by the following differential equation:

$$\frac{d(m\beta(t))}{dt} = n\pi(t)\bar{\sigma}(1-\beta(t)) - n\pi(t)\bar{\eta}\beta(t) - n(1-\pi(t))\bar{\rho}\beta(t).$$

Dividing by m,

$$\begin{aligned}\frac{d\beta(t)}{dt} &= \pi(t)\sigma(1-\beta(t)) - \pi(t)\eta\beta(t) - (1-\pi(t))\rho\beta(t), \\ &= \pi(t)(\sigma - \tau\beta(t)) - (1-\pi(t))\rho\beta(t),\end{aligned} \tag{6.2.2}$$

where

$$\tau = \sigma + \eta = \gamma(\bar{\sigma} + \bar{\eta}), \tag{6.2.3}$$

is the gallery ratio multiplied by the rate at which an infected PWID visits syringes multiplied by the sum of the probability that he or she leaves an uninfected syringe infected after use plus the probability that he or she leaves an infected syringe uninfected after use.

The spread of the disease amongst PWIDs can be described by the differential equation:

$$\frac{d(n\pi(t))}{dt} = n(1-\pi(t))\upsilon\beta(t) - \mu(n\pi(t)).$$

Dividing by n,

$$\frac{d\pi(t)}{dt} = (1-\pi(t))\upsilon\beta(t) - \mu\pi(t). \tag{6.2.4}$$

So in summary the equations describing the deterministic HIV model are:

$$\begin{aligned}\frac{d\beta(t)}{dt} &= \pi(t)(\sigma - \tau\beta(t)) - (1-\pi(t))\rho\beta(t), \\ \frac{d\pi(t)}{dt} &= (1-\pi(t))\upsilon\beta(t) - \mu\pi(t).\end{aligned} \tag{6.2.5}$$

Greenhalgh and Hay define the basic reproduction number for the modified Kaplan model to be

$$R_0^D = \frac{\upsilon\sigma}{\rho\mu}, \tag{6.2.6}$$

where in Section 4.5 they have shown in detail that it corresponds to the usual biological definition, that is the expected number of secondary infected PWIDs (infected PWIDs who became infected from sharing a syringe with the original infected PWID) caused during his or her entire infectious period by a single newly infected PWID entering a disease free population at equilibrium. They also point out that it is also the expected number of secondary infected needles caused by a single newly infected needle entering the disease free population at equilibrium.

Greenhalgh and Hay then show that the disease dies out if $R_0^D < 1$ or $R_0^D = 1$ and $\tau > \rho$. If $R_0^D > 1$ there are two possible equilibria, one with no disease present and the other with disease present. Thus this value of R_0^D clearly satisfies the usual properties of the deterministic threshold value in epidemic models. There is a unique endemic equilibrium

$$\beta^* = \frac{\sigma}{\tau}\left(1 - \frac{\rho\mu}{\sigma\upsilon}\right), \ \pi^* = \frac{\sigma\upsilon - \rho\mu}{\mu\tau + \sigma\upsilon - \rho\mu}.$$

If $R_0^D > 1$ then the unique endemic equilibrium is locally stable. If $\tau > \rho$ and $R_0^D > 1$ then $\beta(t) \to \beta^*$ and $\pi(t) \to \pi^*$ as $t \to \infty$ provided that $\pi(0) > 0$ or $\beta(0) > 0$.

Note that the average rate at which PWIDs leave the sharing, injecting population is around 0.25/year [43] so they each share for on average four years. $P_1 + P_3$, the probability of HIV transmission to a susceptible PWID on making a single injection with an infected syringe is quite small (for example one estimate is 0.01 [43]). On the other hand PWIDs inject on a timescale of every few days. Hence changes in the fraction of syringes infected will typically happen a lot faster than changes in the fraction of PWIDs infected. In other words, $\pi(t)$ is more likely to remain constant over an intermediate timescale, whereas the rate of change for $\beta(t)$ will happen much faster and thus it is more likely for $\beta(t)$ to approach its equilibrium value from equation (6.2.5)

$$\frac{\pi(t)\sigma}{\pi(t) + \rho - \rho\pi(t)}. \tag{6.2.7}$$

By substituting (6.2.7) into the second equation in (6.2.5) we deduce that

$$\frac{d\pi(t)}{dt} = \frac{(1 - \pi(t))\pi(t)\upsilon\sigma}{\pi(t)\tau + \rho - \pi(t)\rho} - \mu\pi(t). \tag{6.2.8}$$

A similar technique of reducing the dimensions of the model by assuming that the needle equations are at equilibrium is used in models of variable infectivity of spread of HIV amongst PWIDs discussed by Greenhalgh and Lewis [44, 80] and Corson, Greenhalgh and Hutchinson [26, 27].

In this section, we introduce environmental stochasticity into the system (6.2.8) by replacing the parameter υ by $\upsilon + \bar{\upsilon}\frac{dB(t)}{dt}$ where $B(t)$ is a Brownian motion and $\bar{\upsilon} > 0$ is the intensity of the noise which is associated with the potential rate of infection υ. It is therefore clear that the total number of new PWIDs infected during the small time

interval $[t, t+dt)$ is normally distributed with mean

$$\frac{n(1-\pi(t))\pi(t)\upsilon\sigma}{\pi(t)\tau+\rho-\pi(t)\rho}dt$$

and variance

$$\frac{n^2(1-\pi(t))^2\pi(t)^2\bar{\upsilon}^2\sigma^2}{(\pi(t)\tau+\rho-\pi(t)\rho)^2}dt.$$

Notice that both this mean and variance tend to zero as dt goes to zero which is a biologically desirable property. This is a standard technique of introducing random noise in stochastic modelling [28, 29, 87, 88, 134, 133] and corresponds to some stochastic environmental factor acting on each individual in the population.

To justify why simple white noise is appropriate for our model suppose that we consider a timescale on which $\beta(t)$ and $\pi(t)$ are approximately constant. We consider the changes in a small time interval $[t, t+T_0)$ and divide it into a series of n_0 equal width subintervals $[t, t+T), [t+T, t+2T),$ ... $[t+(n_0-1)T, t+n_0T)$ where $n_0T = T_0$ and n_0 is very large. Then the number of new infections caused by a single susceptible PWID visiting one infected syringe during each of the subintervals $[t, t+T), [t+T, t+2T)$, ... $[t+(n_0-1)T, t+n_0T)$ are identically distributed random variables say with common mean μ_0 and common variance σ_0^2. We assume that $\sigma_0^2 < \infty$. So by the Central Limit Theorem the total number of PWIDs who visit infected syringes and become infected in $[t, t+n_0T) = [t, t+T_0)$ is approximately normally distributed with mean $n_0\mu_0$ and variance $n_0\sigma_0^2$. Moreover keeping T fixed and doubling T_0 doubles n_0, thus the mean and variance of the number of susceptible PWIDs who become infected from visiting an infected syringe in $[t, t+T_0)$ are both proportional to T_0. Hence it is appropriate to consider simple white noise where the mean number of infections in $[t, t+dt)$ caused by a given susceptible PWID visiting a given infected syringe is υdt (hence proportional to dt), the same as in the deterministic model, and the variance of this number is also proportional to dt.

As a result, we obtain the following SDE HIV model:

$$d\pi(t) = \left[\frac{(1-\pi(t))\pi(t)\upsilon\sigma}{\pi(t)\tau+\rho-\pi(t)\rho} - \mu\pi(t)\right]dt + \left[\frac{(1-\pi(t))\pi(t)\bar{\upsilon}\sigma}{\pi(t)\tau+\rho-\pi(t)\rho}\right]dB(t). \tag{6.2.9}$$

The reason why we chose to peturb the parameter υ, corresponding to the total rate at which PWIDs visit syringes and potentially become infected is because as it multiplies

the term $\pi(1-\pi)$ in (6.2.8) it is a key parameter in the transmission of HIV amongst PWIDs and we thought that this would be the most interesting and important parameter when analysing the effect that environmental noise would have on the spread of HIV.

There are some environmental factors which can cause a perturbation in υ, for example natural biological variation between people and between HIV viruses. These factors affect the probability $P_1 + P_3$ of HIV transmission to a susceptible PWID. It is possible that environmental noise causes variation in other parameters too, but it would be quite complicated to include these as well. Analysis of the model with environmental stochasticity in υ provides theoretical insight into the behaviour of the model. A similar approach of introducing environmental stochasticity into only the disease transmission prameter was discussed in stochastic studies of epidemic models by Ding, Xu and Hu [34], Gray et al. [40], Lu [87], Tornatore, Buccellato and Vetro [118] and others.

For the rest of the chapter, we shall focus on analysing the SDE HIV model (6.2.9). Throughout this chapter, unless stated otherwise, we shall assume that the unit of time is one day.

6.3 Existence of Unique Nonnegative Solution

Before we begin to investigate the dynamical behaviour of the SDE HIV model (6.2.9), it is important for us to show whether this SDE has a unique global nonnegative solution. It is well known that in order for an SDE to have a unique global solution for any given initial value, the coefficients of the equation are generally required to satisfy the linear growth condition and the local Lipschitz conditions [89]. It is clear that our coefficients in (6.2.9) satisfy the linear growth condition and they are locally Lipschitz continuous. As a result there is a unique, non-explosive solution to (6.2.9). The following theorem shows that the solution remains in (0,1) if it starts there.

Theorem 6.3.1 *For any given initial value $\pi(0) = \pi_0 \in (0,1)$, the SDE HIV model (6.2.9) has a unique global nonnegative solution $\pi(t) \in (0,1)$ for all $t \geq 0$ with probability one, namely*

$$\mathbb{P}\big\{\pi(t) \in (0,1), \forall t \geq 0\big\} = 1. \tag{6.3.1}$$

Proof. For any given initial value $\pi_0 \in (0,1)$, there is a unique global solution $\pi(t)$ for $t \geq 0$. Let $k_0 \geq 0$ be sufficiently large so that π_0 lies within the interval $(1/k_0, 1-(1/k_0))$. Then for each integer $k \geq k_0$, define the stopping time

$$\tau_k = \inf\big\{t \geq 0 : \pi(t) \notin (1/k, 1-(1/k))\big\},$$

where $\inf \emptyset = \infty$. It is easy to see that τ_k is increasing as $k \to \infty$. Let us also define $\tau_\infty = \lim_{k\to\infty} \tau_k$. To complete the proof, we need to show that $\tau_\infty = \infty$ almost surely. We will carry this proof out by contradiction. Let us therefore assume that the statement is false and thus there exists a pair of constants $T > 0$ and $\varepsilon \in (0,1)$ such that

$$\mathbb{P}\big\{\tau_\infty \leq T\big\} > \varepsilon. \tag{6.3.2}$$

Hence, there is an integer $k_1 \geq k_0$ such that

$$\mathbb{P}\big\{\tau_k \leq T\big\} > \varepsilon \quad \text{for all } k \geq k_1. \tag{6.3.3}$$

Let us define a function $V : (0,1) \to \mathbb{R}$,

$$V(x) = \frac{1}{x} + \frac{1}{1-x}. \tag{6.3.4}$$

Now by Itô's formula, we have that for any $t \in [0,T]$ and $k \geq k_1$,

$$\mathbb{E}V(\pi(t \wedge \tau_k)) = V(\pi_0) + \mathbb{E}\int_0^{t\wedge\tau_k} LV(\pi(s))ds, \tag{6.3.5}$$

where $LV : (0,1) \to \mathbb{R}$ is defined by

$$\begin{aligned} LV(x) &= \frac{-(1-x)\upsilon\sigma}{x(x\tau+\rho-x\rho)} + \frac{x\upsilon\sigma}{(x\tau+\rho-x\rho)(1-x)} + \frac{\mu}{x} - \frac{\mu x}{(1-x)^2} \\ &\quad + \frac{(1-x)^2\bar{\upsilon}^2\sigma^2}{(x\tau+\rho-x\rho)^2 x} + \frac{x^2\bar{\upsilon}^2\sigma^2}{(1-x)(x\tau+\rho-x\rho)^2}. \end{aligned} \tag{6.3.6}$$

Furthermore, since $x\tau + \rho(1-x) \geq \min(\tau,\rho)$, then it is easy to see that

$$\begin{aligned} LV(x) &\leq \frac{x\upsilon\sigma}{\min(\tau,\rho)(1-x)} + \frac{\mu}{x} + \frac{\bar{\upsilon}^2\sigma^2}{\min(\tau,\rho)^2}\left[\frac{(1-x)^2}{x} + \frac{x^2}{1-x}\right], \\ &\leq \frac{\upsilon\sigma}{\min(\tau,\rho)(1-x)} + \frac{\mu}{x} + \frac{\bar{\upsilon}^2\sigma^2}{\min(\tau,\rho)^2}\left[\frac{1}{x} + \frac{1}{1-x}\right] \leq CV(x), \end{aligned} \tag{6.3.7}$$

where

$$C = \left\{\left[\frac{\upsilon\sigma}{\min(\tau,\rho)}\right] \vee \mu\right\} + \frac{\bar{\upsilon}^2\sigma^2}{\min(\tau,\rho)^2}.$$

Here $a \vee b$ denotes the maximum of a and b. By substituting this into (6.3.5), we have that for any $t \in [0, T]$

$$\mathbb{E}V(\pi(t \wedge \tau_k)) \leq V(\pi_0) + C \int_0^t \mathbb{E}V(\pi(s \wedge \tau_k))ds. \tag{6.3.8}$$

Then by using the Gronwall inequality we have that

$$\mathbb{E}V(\pi(t \wedge \tau_k)) \leq V(\pi_0)e^{Ct} \leq V(\pi_0)e^{CT}.$$

Let us set $\Omega_k = \{\tau_k \leq T\}$ for $k \geq k_1$, and so by (6.3.3), we have that $\mathbb{P}(\Omega_k) \geq \varepsilon$. For every $\omega \in \Omega_k, \pi(\tau_k, \omega)$ equals either $1/k$ or $1 - (1/k)$ and thus $V(\pi(\tau_k, \omega)) \geq k$. Consequently we have that

$$\begin{aligned} V(\pi_0)\varepsilon^{CT} &\geq \mathbb{E}\big[\mathbf{1}_{\Omega_k}(\omega)V(\pi(\tau_k, \omega))\big], \\ &\geq k\mathbb{P}(\Omega_k), \\ &\geq \varepsilon k. \end{aligned} \tag{6.3.9}$$

Letting $k \to \infty$, we have a contradiction where $\infty > V(\pi_0)e^{CT} = \infty$. Therefore, our assumption at the beginning must be false and thus we obtained our desired result that $\tau_\infty = \infty$ almost surely. □

In this section we have managed to show that there exists a unique nonnegative global solution for the SDE HIV model (6.2.9) which remains in (0,1).

6.4 Extinction

When studying the dynamical behaviour of a population system, it is important for us to consider the conditions required in order for the HIV amongst PWIDs to die out, in other words when the disease will become extinct. We will split this proof into two parts, each considering two different scenarios of the noise intensity, namely $\bar{v}$. Before we begin the proof, let us recall the basic reproduction number for the deterministic model of Greenhalgh and Hay [43]:

$$R_0^D = \frac{\upsilon\sigma}{\rho\mu}, \tag{6.4.1}$$

where all the parameters are defined as before.

For the stochastic model we define the stochastic basic reproduction number

$$R_0^S = R_0^D - \frac{\bar{\upsilon}^2\sigma^2}{2\rho^2\mu}.$$

This is the deterministic basic reproduction number R_0^D corrected for the effect of stochastic noise and plays a role in the stochastic model with many similarities to R_0^D in the deterministic one.

Theorem 6.4.1 *If the stochastic reproduction number*

$$R_0^S = R_0^D - \frac{\bar{\upsilon}^2\sigma^2}{2\rho^2\mu} < 1, \quad \textit{and} \quad \bar{\upsilon}^2 \leq \frac{\upsilon\rho}{\sigma}, \tag{6.4.2}$$

then for any given initial value $\pi(0) = \pi_0 \in (0,1)$, the solution of (6.2.9) obeys

$$\limsup_{t\to\infty} \frac{1}{t}\log\pi(t) \leq \frac{\upsilon\sigma}{\rho} - \frac{\bar{\upsilon}^2\sigma^2}{2\rho^2} - \mu = \mu(R_0^S - 1) < 0 \quad a.s. \tag{6.4.3}$$

In other words, $\pi(t)$ will tend to zero exponentially almost surely. Thus the fraction of the population that is infected with HIV at time t will approach zero.

Proof. Let us define a function $V(x) = \log(x)$, where by Itô's formula we have that

$$\log(\pi(t)) = \log(\pi_0) + \int_0^t f(\pi(s))ds + \int_0^t \frac{(1-\pi(s))\bar{\upsilon}\sigma}{\pi(s)\tau + \rho - \pi(s)\rho} dB(s). \tag{6.4.4}$$

Here $f : (0,1) \to \mathbb{R}$ is defined as

$$\begin{aligned} f(x) &= \frac{(1-x)\upsilon\sigma}{x\tau + \rho - x\rho} - \mu - \frac{(1-x)^2\bar{\upsilon}^2\sigma^2}{2(x\tau+\rho-x\rho)^2}, &(6.4.5)\\ &= \frac{\upsilon\sigma}{\varphi+\rho} - \mu - \frac{\bar{\upsilon}^2\sigma^2}{2(\varphi+\rho)^2}, &(6.4.6)\end{aligned}$$

where $\varphi = x\tau/(1-x)$. Moreover

$$\begin{aligned} f'(\varphi) &= -\frac{\upsilon\sigma}{(\varphi+\rho)^2} + \frac{\bar{\upsilon}^2\sigma^2}{(\varphi+\rho)^3},\\ &\leq -\frac{\upsilon\sigma}{(\varphi+\rho)^2} + \frac{\upsilon\rho\sigma}{(\varphi+\rho)^3}, \quad \text{as } \bar{\upsilon}^2 \leq \frac{\upsilon\rho}{\sigma},\\ &= \frac{\upsilon\sigma}{(\varphi+\rho)^2}\left[-1 + \frac{\rho}{\varphi+\rho}\right],\\ &= -\frac{\upsilon\sigma\varphi}{(\varphi+\rho)^2},\\ &< 0. \end{aligned}$$

Hence $f(\varphi)$ is a monotone decreasing function of φ for $\varphi > 0$, and thus we must have that

$$f(x) \leq f(x)|_{\varphi=0} = \mu(R_0^S - 1) < 0, \tag{6.4.7}$$

where R_0^S is the stochastic reproduction number defined in Theorem 6.4.1. As a result, equation (6.4.4) becomes

$$\log(\pi(t)) \leq \log(\pi_0) + t\mu(R_0^S - 1) + \int_0^t \frac{(1-\pi(s))\bar{\upsilon}\sigma}{\pi(s)\tau + \rho - \pi(s)\rho} dB(s). \tag{6.4.8}$$

This implies that

$$\limsup_{t\to\infty} \frac{1}{t}\log(\pi(t)) \leq \mu(R_0^S - 1) + \limsup_{t\to\infty} \frac{1}{t}\int_0^t \frac{(1-\pi(s))\bar{\upsilon}\sigma}{\pi(s)\tau + \rho - \pi(s)\rho} dB(s). \tag{6.4.9}$$

However, since

$$0 \leq \frac{(1-\pi(s))}{\pi(s)\tau + \rho - \pi(s)\rho} \leq \frac{1}{\min(\tau, \rho)},$$

then by the large number theorem of martingales (e.g. [134]), we have that

$$\limsup_{t\to\infty} \frac{1}{t}\int_0^t \frac{(1-\pi(s))\bar{\upsilon}\sigma}{\pi(s)\tau + \rho - \pi(s)\rho} dB(s) = 0 \quad \text{a.s.} \tag{6.4.10}$$

Hence, we have arrived at our desired result where

$$\limsup_{t\to\infty} \frac{1}{t}\log(\pi(t)) \leq \mu(R_0^S - 1) < 0 \quad \text{a.s.} \tag{6.4.11}$$

In other words, $\pi(t)$ tends to zero exponentially almost surely. □

In Theorem 6.4.1, we have focused on discussing the extinction conditions for our SDE HIV model (6.2.9) and we have considered a partial case where the noise intensity satisfies the condition $\bar{\upsilon}^2 \leq \frac{\upsilon\rho}{\sigma}$. In order to get a better picture of the dynamical behaviour of our SDE HIV model (6.2.9), it is important for us to investigate what happens to the population system when $\bar{\upsilon}^2 > \frac{\upsilon\rho}{\sigma}$.

Theorem 6.4.2 *If*

$$R_0^S = R_0^D - \frac{\bar{\upsilon}^2\sigma^2}{2\rho^2\mu} \leq 1, \quad \textit{and} \quad \bar{\upsilon}^2 > \frac{\upsilon\rho}{\sigma} \vee \frac{\upsilon^2}{2\mu}, \tag{6.4.12}$$

then for any given initial value $\pi(0) = \pi_0 \in (0,1)$, the solution of (6.2.9) obeys

$$\limsup_{t\to\infty} \frac{1}{t}\log\pi(t) \leq \frac{\upsilon^2}{2\bar{\upsilon}^2} - \mu < 0 \quad \textit{a.s.} \tag{6.4.13}$$

In other words, $\pi(t)$ will tend to zero exponentially almost surely. Thus the fraction of the population that are infected with HIV at time t will become zero.

Proof. In order to simplify the computation, throughout this proof, we will be working with equation (6.4.6). It is easy to see that this function has a maximum turning point at

$$\varphi = \hat{\varphi} = \frac{\bar{\upsilon}^2\sigma}{\upsilon} - \rho. \tag{6.4.14}$$

Note that, by substituting (6.4.14) back into the expression $\varphi = x\tau/(1-x)$, we could easily obtain the same result as we would if we decided to work with the alternative function

$$x = \hat{x} = \frac{\bar{\upsilon}^2\sigma - \rho\upsilon}{\upsilon(\tau - \rho + \bar{\upsilon}^2\sigma)}, \tag{6.4.15}$$

where $\hat{x} \in (0,1)$. Note also that $\hat{\varphi} > 0$ by (6.4.12). Furthermore, by substituting the maximum turning point $\hat{\varphi}$ given in (6.4.14) into (6.4.6), we have that $f(x)|_{\varphi=\hat{\varphi}} = \frac{\upsilon^2}{2\bar{\upsilon}^2} - \mu$ which is negative by condition (6.4.12). Therefore, arguing as before in Theorem 6.4.1, we have that

$$\log(\pi(t)) \leq \log(\pi_0) + t\left(\frac{\upsilon^2}{2\bar{\upsilon}^2} - \mu\right) + \int_0^t \frac{(1-\pi(s))\bar{\upsilon}\sigma}{\pi(s)\tau + \rho - \pi(s)\rho} dB(s), \tag{6.4.16}$$

which similarly implies that

$$\limsup_{t\to\infty} \frac{1}{t}\log(\pi(t)) \leq \frac{\upsilon^2}{2\bar{\upsilon}^2} - \mu < 0 \quad \text{a.s.} \tag{6.4.17}$$

In other words, $\pi(t)$ will also tend to zero exponentially almost surely for $\bar{\upsilon}^2 > \frac{\upsilon\rho}{\sigma} \vee \frac{\upsilon^2}{2\mu}$ and thus we have completed the proof. □

Note that $R_0^S < R_0^D$, which implies that the condition for extinction is weaker in the stochastic case compared to the deterministic case. In addition, as $\bar{\upsilon}$ increases, the stochastic reproduction number R_0^S will become smaller and thus it will be more likely for the HIV virus to die out for large noise intensity. As a result, this highlights the fact that environmental factors play an important role in the dynamical behaviour of HIV amongst PWIDs.

Note also that there is a gap in our results. We have not shown what will happen if $R_0^S \leq 1$ and $\frac{\upsilon\rho}{\sigma} < \bar{\upsilon}^2 < \frac{\upsilon^2}{2\mu}$ or if $R_0^S = 1$ and $\bar{\upsilon}^2 \leq \frac{\upsilon\rho}{\sigma}$, but we conjecture that in both cases the disease will die out almost surely. This is confirmed by the simulations shown in Section 6.7.

6.5 Persistence

Another very important aspect of the behaviour of a dynamical system is the conditions for persistence. In this section we will discuss the persistence conditions required for our SDE HIV model (6.2.9).

Theorem 6.5.1 *If*

$$R_0^S = R_0^D - \frac{\bar{\upsilon}^2\sigma^2}{2\rho^2\mu} > 1, \tag{6.5.1}$$

then for any given initial value $\pi(0) = \pi_0 \in (0,1)$*, the solution of (6.2.9) satisfies*

$$\lim_{t\to\infty} \sup \pi(t) \geq \eta \quad a.s. \tag{6.5.2}$$

and

$$\lim_{t\to\infty} \inf \pi(t) \leq \eta \quad a.s. \tag{6.5.3}$$

where

$$\eta = \frac{\upsilon\sigma - 2\mu\rho + \sqrt{\upsilon^2\sigma^2 - 2\mu\bar{\upsilon}^2\sigma^2}}{2\mu\tau + \upsilon\sigma - 2\mu\rho + \sqrt{\upsilon^2\sigma^2 - 2\mu\bar{\upsilon}^2\sigma^2}} > 0, \tag{6.5.4}$$

which is the unique root in $(0,1)$ *of the function*

$$f(x) = \frac{(1-x)\upsilon\sigma}{x\tau + \rho - x\rho} - \mu - \frac{(1-x)^2\bar{\upsilon}^2\sigma^2}{2(x\tau + \rho - x\rho)^2} = 0, \tag{6.5.5}$$

defined in (6.4.5). In other words, the solution $\pi(t)$ *will persist and oscillate around the level* η *infinitely often with probability one.*

Proof. Let us recall the function $f : (0,1) \to \mathbb{R}$ defined in (6.4.6). Throughout this proof, we will be working with this function in order to simplify the computation.

By setting $f(x) = 0$ and rearranging, we have the following quadratic function of φ, namely

$$\mu\varphi^2 + \varphi(2\mu\rho - \upsilon\sigma) + \mu\rho^2 - \upsilon\sigma\rho + 0.5\bar{\upsilon}^2\sigma^2 = 0.$$

By solving for φ using the quadratic formula, we obtain one positive and one negative root where the positive root is

$$\varphi^* = \frac{1}{2\mu}\left[\sqrt{(\upsilon\sigma - 2\mu\rho)^2 + 4\mu(\upsilon\sigma\rho - \mu\rho^2 - 0.5\bar{\upsilon}^2\sigma^2)} + (\upsilon\sigma - 2\mu\rho)\right] > \hat{\varphi}, \tag{6.5.6}$$

where $\hat{\varphi}$ is the maximum turning point of (6.4.6) defined in (6.4.14). Note that $(\upsilon\sigma\rho - \mu\rho^2 - 0.5\bar{\upsilon}^2\sigma^2) > 0$ by (6.5.1). For the purpose of consistency, we will now substitute (6.5.6) into the expression $\varphi^* = x^*\tau/(1-x^*)$ to get that

$$x^* = \eta = \frac{\upsilon\sigma - 2\mu\rho + \sqrt{\upsilon^2\sigma^2 - 2\mu\bar{\upsilon}^2\sigma^2}}{2\mu\tau + \upsilon\sigma - 2\mu\rho + \sqrt{\upsilon^2\sigma^2 - 2\mu\bar{\upsilon}^2\sigma^2}} > \hat{x}, \tag{6.5.7}$$

where $x^* \in (0,1)$ and that $\hat{x}$ is the equivalent maximum turning point of (6.4.5) defined in (6.4.15). Moreover, it is easy to see that

$$f(0) = \frac{\upsilon\sigma}{\rho} - \mu - \frac{\bar{\upsilon}^2\sigma^2}{2\rho^2} > 0 \quad \text{and} \quad f(1) = -\mu < 0.$$

As a result we have that

$$f(x) > 0 \quad \text{is strictly increasing on} \quad x \in (0, 0 \vee \hat{x}), \tag{6.5.8}$$

$$f(x) > 0 \quad \text{is strictly decreasing on} \quad x \in (0 \vee \hat{x}, x^*), \tag{6.5.9}$$

$$f(x) < 0 \quad \text{is strictly decreasing on} \quad x \in (x^*, 1), \tag{6.5.10}$$

where again $\hat{x}$ and x^* are the maximum turning point and the positive root of (6.4.5) respectively as defined as before. Let us now prove that result (6.5.2) is true by contradiction. Assume that (6.5.2) is false and thus there must exist an $\varepsilon \in (0,1)$ small enough such that

$$\mathbb{P}(\Omega_1) > \varepsilon$$

where $\Omega_1 = \{\omega \in \Omega : \lim_{t\to\infty} \sup \pi(t) \leq \eta - 2\varepsilon\}$. Hence for every $\omega \in \Omega_1$, there is a $T = T(\omega) > 0$ such that

$$\pi(t,\omega) \leq \eta - \varepsilon \quad \text{for} \quad t \geq T(\omega). \tag{6.5.11}$$

Clearly we can choose an ε so small such that $f(0) > f(\eta - \varepsilon)$. Therefore, from (6.5.8), (6.5.9) and (6.5.11), we have that $f(\pi(t,\omega)) > f(\eta - \varepsilon)$ for $t \geq T(\omega)$. Let us now recall that for $t \geq 0$,

$$\log(\pi(t)) = \log(\pi_0) + \int_0^t f(\pi(s))ds + \int_0^t \frac{(1-\pi(s))\bar{\upsilon}\sigma}{\pi(s)\tau + \rho - \pi(s)\rho} dB(s),$$

then arguing as before, by the large number theorem of martingales, there is an $\Omega_2 \subset \Omega$ with $\mathbb{P}(\Omega_2) = 1$, such that for every $\omega \in \Omega_2$,

$$\lim_{t\to\infty} \frac{1}{t} \int_0^t \frac{(1-\pi(s))\bar{\upsilon}\sigma}{\pi(s)\tau + \rho - \pi(s)\rho} dB(s) = 0. \tag{6.5.12}$$

Therefore by fixing any $\omega \in \Omega_1 \cap \Omega_2$, then for $t \geq T(\omega)$,

$$\begin{aligned} \log(\pi(t,\omega)) &\geq \log(\pi_0) + \int_0^{T(\omega)} f(\pi(s,\omega))ds + f(\eta-\varepsilon)(t-T(\omega)) \\ &\quad + \int_0^t \frac{(1-\pi(s))\bar{v}\sigma}{\pi(s)\tau + \rho - \pi(s)\rho} dB(s,\omega), \end{aligned} \tag{6.5.13}$$

which implies that

$$\liminf_{t\to\infty} \frac{1}{t} \log(\pi(t,\omega)) \geq f(\eta-\varepsilon) > 0, \tag{6.5.14}$$

and thus we have that $\lim_{t\to\infty} \pi(t,\omega) = \infty$. This is clearly a contradiction to (6.5.11). Thus, our assumption at the beginning must be wrong and therefore we obtained our desired result that

$$\limsup_{t\to\infty} \pi(t) \geq \eta \quad \text{a.s.}$$

Similarly, we will prove (6.5.3) by assuming again that it is false and thus there must exist a $\delta \in (0,1)$ such that

$$\mathbb{P}(\Omega_3) > \delta,$$

where $\Omega_3 = \{\omega \in \Omega : \lim_{t\to\infty} \inf \pi(t) \geq \eta + 2\delta\}$. Hence for every $\omega \in \Omega_3$, there is a $\tau = \tau(\omega) > 0$ such that

$$\pi(t,\omega) \geq \eta + \delta \quad \text{for} \quad t \geq \tau(\omega). \tag{6.5.15}$$

Thus, we have from (6.5.10) that $f(\pi(t,\omega)) \leq f(\eta+\delta)$ for $t \geq \tau(\omega)$. Let us now fix any $\omega \in \Omega_2 \cap \Omega_3$, then similarly to before, we would get that for $t \geq \tau(\omega)$,

$$\begin{aligned} \log(\pi(t,\omega)) &\leq \log(\pi_0) + \int_0^{\tau(\omega)} f(\pi(s,\omega))ds + f(\eta+\delta)(t-\tau(\omega)) \\ &\quad + \int_0^t \frac{(1-\pi(s))\bar{v}\sigma}{\pi(s)\tau + \rho - \pi(s)\rho} dB(s,\omega), \end{aligned} \tag{6.5.16}$$

$$\Rightarrow \limsup_{t\to\infty} \frac{1}{t} \log(\pi(t,\omega)) \leq f(\eta+\delta) < 0, \tag{6.5.17}$$

and thus

$$\Rightarrow \lim_{t\to\infty} \pi(t,\omega) = 0.$$

This is clearly a contradiction to (6.5.15) and thus we have completed our proof. $\square$

In order to allow us to better understand the effect of the noise intensity $\bar{\upsilon}$ on the dynamical behaviour of our SDE HIV model (6.2.9) and its connection to the corresponding deterministic model (6.2.8), we have the following proposition.

Proposition 6.5.2 *Suppose that $R_0^S > 1$. Consider η as defined by (6.5.4) as a function of $\bar{\upsilon}$ for*

$$0 < \bar{\upsilon} < \frac{\sqrt{2\rho(\upsilon\sigma - \mu\rho)}}{\sigma} = \hat{\upsilon}, \tag{6.5.18}$$

then η is strictly decreasing and

$$\lim_{\bar{\upsilon}\to 0} \eta = \frac{\upsilon\sigma - \mu\rho}{\upsilon\sigma - \mu\rho + \mu\tau}, \tag{6.5.19}$$

which is the equilibrium state of the deterministic HIV model (6.2.8) and

$$\lim_{\bar{\upsilon}\to \hat{\upsilon}} \eta = \begin{cases} 0 & \text{if } 1 \leq R_0^D \leq 2, \\ \frac{\upsilon\sigma - 2\mu\rho}{\upsilon\sigma - 2\mu\rho + \mu\tau} & \text{if } R_0^D > 2. \end{cases} \tag{6.5.20}$$

In other words, η lies between the deterministic equilibrium value for $\pi(t)$, namely $\frac{\upsilon\sigma - \mu\rho}{\upsilon\sigma - \mu\rho + \mu\tau}$, and $\max\left(0, \frac{\upsilon\sigma - 2\mu\rho}{\upsilon\sigma - 2\mu\rho + \mu\tau}\right)$. Furthermore, if the noise intensity decreases to zero, then η will increase to the deterministic equilibrium value, namely $\frac{\upsilon\sigma - \mu\rho}{\upsilon\sigma - \mu\rho + \mu\tau}$. If R_0^D is large then η will be close to but beneath the deterministic equilibrium value for $\pi(t)$.

Proof. Let us recall that

$$\eta = \frac{\upsilon\sigma - 2\mu\rho + \sqrt{\upsilon^2\sigma^2 - 2\mu\bar{\upsilon}^2\sigma^2}}{2\mu\tau + \upsilon\sigma - 2\mu\rho + \sqrt{\upsilon^2\sigma^2 - 2\mu\bar{\upsilon}^2\sigma^2}}. \tag{6.5.21}$$

Then,

$$\frac{d\eta}{d\bar{\upsilon}} = \frac{-4\mu^2\bar{\upsilon}\sigma^2\tau}{(\upsilon^2\sigma^2 - 2\mu\bar{\upsilon}^2\sigma^2)^{1/2}(2\mu\tau + \upsilon\sigma - 2\mu\rho + (\upsilon^2\sigma^2 - 2\mu\bar{\upsilon}^2\sigma^2)^{1/2})^2}. \tag{6.5.22}$$

Clearly, $\frac{d\eta}{d\bar{\upsilon}} < 0$ since $\sigma > 0$ and thus η is strictly decreasing as $\bar{\upsilon}$ increases. By letting $\bar{\upsilon}$ tend to zero in the function for η defined above, we have the desired result given in (6.5.19). Moreover, as $\bar{\upsilon} \to \hat{\upsilon}$, we have that

$$\lim_{\bar{\upsilon}\to \hat{\upsilon}} \eta = \frac{\upsilon\sigma - 2\mu\rho + \sqrt{\upsilon^2\sigma^2 - 2\mu\hat{\upsilon}^2\sigma^2}}{2\mu\tau + \upsilon\sigma - 2\mu\rho + \sqrt{\upsilon^2\sigma^2 - 2\mu\hat{\upsilon}^2\sigma^2}}. \tag{6.5.23}$$

By substituting $\hat{v}$ by its definition given in (6.5.18) and rearranging, the numerator of the above expression is equal to

$$|\upsilon\sigma - 2\mu\rho| + \upsilon\sigma - 2\mu\rho. \tag{6.5.24}$$

As a result, if $1 \leq R_0^D \leq 2$, in other words, $1 \leq \frac{\upsilon\sigma}{\mu\rho} \leq 2$, then it is obvious that $\lim_{\bar{v}\to\hat{v}} \eta = 0$. On the other hand, if $R_0^D > 2$, then $\lim_{\bar{v}\to\hat{v}} \eta = \frac{\upsilon\sigma - 2\mu\rho}{\upsilon\sigma - 2\mu\rho + \mu\tau}$. We have completed the proof. □

6.6 Stationary Distribution

In this section, we will use the well known Khasminskii theorem [71] to prove that there exists a stationary distribution for our stochastic HIV model (6.2.9). Before we begin, let us recall the conditions for the existence of a stationary distribution mentioned in [71].

Lemma 6.6.1 *The SDE HIV model (6.2.9) has a unique stationary distribution if there is a strictly proper subinterval (a, b) of $(0, 1)$ such that $\mathbb{E}(\tau) < \infty$ for all $\pi_0 \in (0, a) \cup (b, 1)$, where*

$$\tau = \inf\{t \geq 0 : \pi(t) \in (a, b)\}, \tag{6.6.1}$$

and

$$\sup_{\pi_0 \in [\bar{a}, \bar{b}]} \mathbb{E}(\tau) < \infty \quad \textit{for every interval} \quad [\bar{a}, \bar{b}] \subset (0, 1). \tag{6.6.2}$$

Note that in the original Khasminskii theorem, there is an additional condition which states that the square of the diffusion coefficient of the SDE HIV model (6.2.9), namely

$$\left(\frac{(1 - \pi(t))\pi(t)\bar{\upsilon}\sigma}{\pi(t)\tau + \rho - \pi(t)\rho}\right)^2,$$

is bounded away from zero for $\pi(t) \in (a, b)$. However, recall from the proof of Theorem 6.3.1, we have already shown that the denominator, $(\pi(t)\tau + \rho - \pi(t)\rho)$, is bounded away from zero (it is at least $\min(\tau, \rho)$). Thus it is therefore clear that this condition holds for our model.

Theorem 6.6.2 *If $R_0^S > 1$, then the SDE HIV model (6.2.9) has a unique stationary distribution.*

Proof. Let us fix any $0 < a < \pi(t) < b < 1$. From conditions (6.5.8)-(6.5.10) in the proof for Theorem 6.5.1 we can see that

$$f(x) \geq f(0) \wedge f(a) > 0 \quad \text{if} \quad 0 < x \leq a, \qquad f(x) \leq f(b) < 0 \quad \text{if} \quad b \leq x < 1. \tag{6.6.3}$$

Let us now define the stopping time τ as we did in Lemma 6.6.1. Recall that

$$\log(\pi(t)) = \log(\pi_0) + \int_0^t f(\pi(s))ds + \int_0^t \frac{(1-\pi(s))\bar{\upsilon}\sigma}{\pi(s)\tau + \rho - \pi(s)\rho} dB(s),$$

then by using (6.6.3), we have that for all $t \geq 0$ and for any $\pi_0 \in (0, a)$,

$$\log(a) \geq \mathbb{E}\log(\pi(t \wedge \tau)) \geq \log(\pi_0) + (f(0) \wedge f(a))\mathbb{E}(t \wedge \tau), \tag{6.6.4}$$

then

$$\log\left(\frac{a}{\pi_0}\right) \geq (f(0) \wedge f(a))\mathbb{E}(t \wedge \tau). \tag{6.6.5}$$

By letting $t \to \infty$, we have that for all $\pi_0 \in (0, a)$

$$\mathbb{E}(\tau) \leq \frac{\log(a/\pi_0)}{f(0) \wedge f(a)}. \tag{6.6.6}$$

Similarly, for any $\pi_0 \in (b, 1)$, we have that

$$\log(b) \leq \mathbb{E}\log(\pi(t \wedge \tau)) \leq \log(\pi_0) - |f(b)|\mathbb{E}(t \wedge \tau), \quad \forall t \geq 0 \tag{6.6.7}$$

then

$$\log\left(\frac{b}{\pi_0}\right) \leq -|f(b)|\mathbb{E}(t \wedge \tau). \tag{6.6.8}$$

By letting $t \to \infty$, we have that

$$\mathbb{E}(\tau) \leq \frac{\log(\pi_0/b)}{|f(b)|} \leq \frac{\log(1/b)}{|f(b)|} \quad \forall \pi_0 \in (b, 1). \tag{6.6.9}$$

Clearly, the conditions required for existence of a unique stationary distribution mentioned in Lemma 6.6.1 are satisfied by (6.6.6) and (6.6.9) and thus we have completed our proof and our SDE HIV model (6.2.9) has a unique stationary distribution. □

6.7 Simulations

In this section we will support our analytical results using numerical simulations produced in R. Throughout this section, various simulations are produced using realistic parameter values but our main objective is to verify the analytic results. Before we begin, let us make the same assumptions as in [43]. Without loss of generality, let us take $p = 0$ and assume that all PWIDs visit shooting galleries at the same rate whether or not they are infected and thus $\lambda_1 = \lambda_2$. In addition, we take $\phi_1 = \theta_1 = 0$ as these probabilities are very small. Note that it is also possible for us to carry out simulations by choosing alternative values for p, ϕ_1 and θ_1, however since the simulations are produced for illustrative purpose we have decided to make the same assumptions as in [43] and setting them to be zero.

Note that the numerical simulations produced in this section are carried out using the Euler-Maruyama method which is different to the Milstein method that we used in Chapter 3 and Chapter 4. This is because the diffusion term in the stochastic HIV model given in (6.2.9), namely $\frac{(1-\pi(t))\pi(t)\bar{\upsilon}\sigma}{\pi(t)\tau+\rho-\pi(t)\rho}$, is slightly complicated and thus we might end up with a complicated first derivative of the diffusion term which is needed as part of the computations in the Milstein method. Furthermore, the computational time for the simulations are relatively fast and thus we feel the Euler-Maruyama method is sufficient in this case especially when the simulations are only for illustrative purposes.

6.7.1 Simulations on Extinction

In this section, we will focus on looking at the numerical simulations produced which support the analytical results given in Theorems 6.4.1 and 6.4.2.

Example 6.7.1 *($R_0^S < 1$, $\bar{\upsilon}^2 \leq \frac{\upsilon\rho}{\sigma}$.) Let us choose realistic parameter values $\mu = 0.258/year = 7.06849\times10^{-4}/day$ [19], $\lambda_1 = \lambda_2 = 0.143, \alpha = (P_1 + P_3) = 0.01, \theta = (P_1+P_2) = 0.25, \gamma = 1$ (based on [43]) and $\xi = 0.6$ [67], then from (6.2.1) and (6.2.3), we have that $\sigma = 0.0572/day$, $\tau = 0.143/day$, $\rho = 0.1001/day$ and $\upsilon = 0.00143/day$. Then by choosing $\bar{\upsilon} = 0.046/day^{-1/2}$ we have that*

$$\bar{\upsilon}^2 = 0.002116 < \frac{\upsilon\rho}{\sigma} = 0.0025025,$$

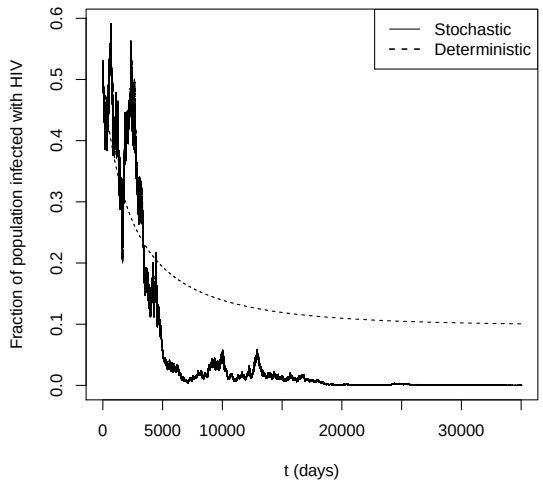

Figure 6.1: Computer simulation of the path $\pi(t)$ for the SDE HIV model (6.2.9) and its corresponding deterministic HIV model (6.2.8) with step size $\Delta = 0.01$ days with parameter values given in Example 6.7.1 with initial value $\pi(0) = 0.5$.

where $R_0^S = 0.66729 < 1$ *while* $R_0^D = 1.156$. *Note that in this case we have* $R_0^S < 1$ *while* $R_0^D > 1$, *in other words in the deterministic case the disease will persist, however due to the effect of environmental stochasticity the disease will actually die out in the stochastic case. This once again highlights the importance and the effect of environmental stochasticity on the spread of HIV amongst PWIDs. Recall that we have introduced environmental stochasticity by replacing* υ *by* $\upsilon + \bar{\upsilon}\frac{dB(t)}{dt}$ *where* $\upsilon + \bar{\upsilon}\frac{dB(t)}{dt}$ *is per unit time. Here,* $dB(t)$ *is* $\sqrt{unit\ time}$, υ *is per unit time and thus* $\bar{\upsilon}$ *is* $(unit\ time)^{-1/2}$ *which in this case is per day.*

By Theorem 6.4.1, we would expect the solution $\pi(t)$ *to reach zero with probability one.*

The computer simulation produced in R using the Euler-Maruyama method ([40, 89]) with the above parameter values is given in Figure 6.1, which clearly illustrates that $\pi(t)$ *hits zero in finite time almost surely. The numerical simulations were repeated around 50 times with different initial value of* $\pi_0 \in (0, 1)$ *and similar results were obtained each time.*

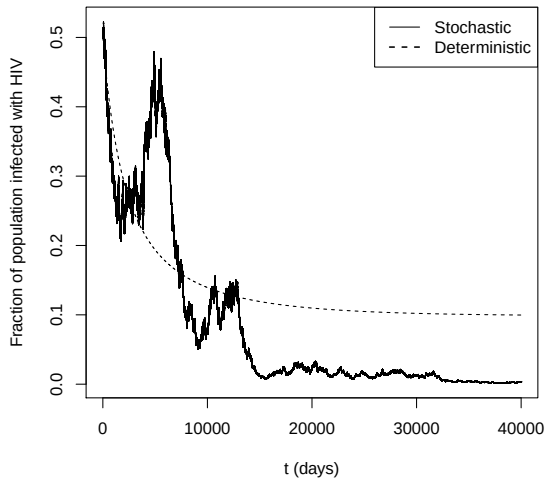

Figure 6.2: Computer simulation of the path $\pi(t)$ for the SDE HIV model (6.2.9) and its corresponding deterministic HIV model (6.2.8) with step size $\Delta = 0.01$ days with parameter values given in Example 6.7.2 with initial value $\pi(0) = 0.5$.

In the next example we will now confirm one of the two conjectures that we made, namely the case where $R_0^S = 1$ and $\bar{\upsilon}^2 \leq \frac{\upsilon\rho}{\sigma}$.

Example 6.7.2 *($R_0^S = 1,\ \bar{\upsilon}^2 \leq \frac{\upsilon\rho}{\sigma}$.) Let us use the same parameter values as in Example 6.7.1 but now choosing $\upsilon = 0.02599131/day^{-1/2}$ such that*

$$\bar{\upsilon}^2 = 0.0006755479 < \frac{\upsilon\rho}{\sigma} = 0.0025025,$$

where $R_0^S = 1$ while $R_0^D = 1.156035 > 1$.

Figure 6.2 clearly supports our conjecture by showing that the disease dies out in finite time. The solution path shown in Figure 6.2 has mean 0.08256 *and variance* 0.01460998.

The numerical simulations were again repeated around 50 times with different values and similar results were obtained each time.

Example 6.7.3 *($R_0^S \leq 1,\ \bar{\upsilon}^2 > \frac{\upsilon\rho}{\sigma} \vee \frac{\upsilon^2}{2\mu}$.) By using the same parameter values as in Example 6.7.1 but choosing $\bar{\upsilon}$ to be $0.07/day^{-1/2}$ and thus $\bar{\upsilon}^2 = 0.0049/day$, we have that*

$$\bar{\upsilon}^2 > \frac{\upsilon\rho}{\sigma} \vee \frac{\upsilon^2}{2\mu}$$

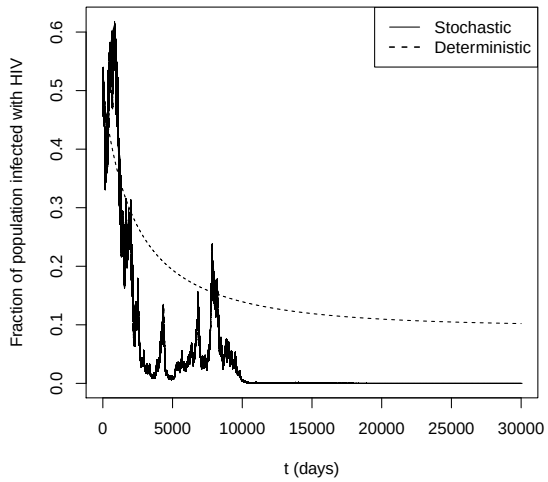

Figure 6.3: Computer simulation of the path $\pi(t)$ for the SDE HIV model (6.2.9) and its corresponding deterministic HIV model (6.2.8) with step size $\Delta = 0.01$ days using parameter values given in Example 6.7.3 with initial value $\pi(0) = 0.5$.

where $R_0^S = 0.02425249 < 1$ *while* $R_0^D = 1.156035$. *As a result, by Theorem 6.4.2, we could conclude that for any initial value* $\pi(0) = \pi_0 \in (0, 1)$, *the solution* $\pi(t)$ *obeys*

$$\limsup_{t\to\infty} \frac{1}{t} \log(\pi(t)) \leq -0.000498186 < 0 \quad a.s.$$

Clearly Figure 6.3 supports this result by showing that the solution $\pi(t)$ *reaches zero at finite time. Again, the numerical simulations were repeated around 50 times with different initial values and the same results were concluded.*

We will now confirm the other conjecture which we made, namely for $R_0^S \leq 1, \frac{\upsilon\rho}{\sigma} < \bar{\upsilon}^2 < \frac{\upsilon^2}{2\mu}$ using the following example.

Example 6.7.4 ($R_0^S \leq 1, \frac{\upsilon\rho}{\sigma} < \bar{\upsilon}^2 < \frac{\upsilon^2}{2\mu}$) *Let us use the same parameter values as in Example 6.7.1 but again changing* μ *to* $0.125/year$ *and thus* $3.42466 \times 10^{-4}/day$ *[66]. Let us now define* $\bar{\upsilon} = 0.054/day^{-1/2}$ *such that*

$$\frac{\upsilon\rho}{\sigma} = 0.002502 < \bar{\upsilon}^2 = 0.002916 < \frac{\upsilon^2}{2\mu} = 0.002985554.$$

In this case, we have that $R_0^D = 2.386057$ *and* $R_0^S = 0.9958988 < 1$.

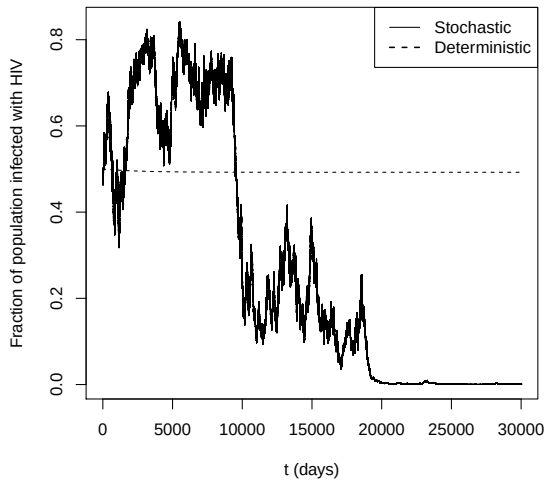

Figure 6.4: Computer simulation of the path $\pi(t)$ for the SDE HIV model (6.2.9) and its corresponding deterministic HIV model (6.2.8) with step size $\Delta = 0.01$ days using parameter values given in Example 6.7.4 with initial value $\pi(0) = 0.5$.

Figure 6.4 clearly supports our conjecture by showing that the fraction of population that is infected with HIV at time t approaches zero almost surely. Again the numerical simulations were repeated and the same conclusion could be drawn each time.

6.7.2 Simulations on Persistence

We will now move on to the numerical simulations for results given in Theorem 6.5.1 and Proposition 6.5.2.

Example 6.7.5 *($R_0^S > 1$) Let us use the same parameter values as in Example 6.7.1 but changing μ to $0.125/year$ and thus $3.42466\times10^{-4}/day$ [66]. Let us define $\bar{v} = 0.05/day^{-1/2}$ and thus $R_0^D = 2.386057$ and $R_0^S = 1.1942 > 1$. Therefore by Theorem 6.5.1, for any given initial value $\pi_0 = \pi(0) \in (0,1)$, the solution $\pi(t)$ for the SDE HIV model (6.2.9) should obey*

$$\liminf_{t\to\infty} \pi(t) \leq \eta = 0.3206092 \leq \limsup_{t\to\infty} \pi(t) \quad a.s.$$

Figure 6.5 clearly supports our analytical results given in Theorem 6.5.1 by showing the solution path of $\pi(t)$ oscillates around the level η in finite time. Again the numerical

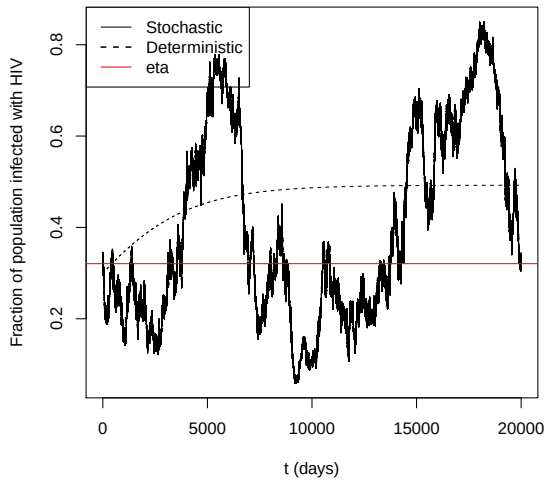

Figure 6.5: Computer simulation of the path $\pi(t)$ for the SDE HIV model (6.2.9) and its corresponding deterministic HIV model (6.2.8) with step size $\Delta = 0.01$ days using parameter values given in Example 6.7.5 with initial value $\pi(0) = 0.3$ and $\eta = 0.3206092$.

simulations were repeated and the same conclusion could be drawn each time.

In order to further illustrate the effect of the noise intensity $\bar{\upsilon}$ has on the solution, in the next example we will keep all the parameter values the same as in Example 6.7.5 but reducing the noise intensity.

Example 6.7.6 *By keeping the parameter values the same as in Example 6.7.5 and reducing* $\bar{\upsilon}$ *to* $0.02/day^{-1/2}$*, we have that* $R_0^D = 2.38605, R_0^S = 2.195363 > 1$ *and* $\eta = 0.4770654$*. By Theorem 6.5.1 and Proposition 6.5.2, we would expect the solution* $\pi(t)$ *to persist and oscillate around the level* η*. Furthermore by Proposition 6.5.2, as* $\bar{\upsilon} \to 0/day^{-1/2}$*, we would expect* η *to tend towards the deterministic equilibrium value for the corresponding deterministic model given by (6.2.8), namely* $\frac{\upsilon\sigma - \mu\rho}{\upsilon\sigma - \mu\rho + \mu\tau} = 0.4924476$*.*

From Figure 6.6, we can clearly see that the solution path $\pi(t)$ *does indeed oscillate about the level* η*. Moreover, by comparing Figure 6.5 and Figure 6.6, we can also see that as we reduce the noise intensity from* $0.05/day^{-1/2}$ *to* $0.02/day^{-1/2}$*, the level* η *does indeed tend towards the deterministic equilibrium value as expected.*

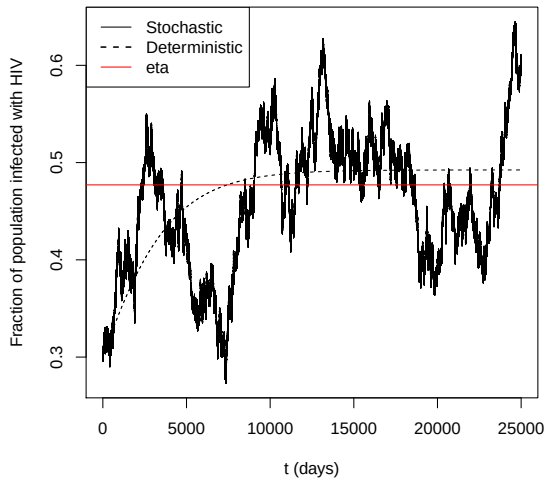

Figure 6.6: Computer simulation of the path $\pi(t)$ for the SDE HIV model (6.2.9) and its corresponding deterministic HIV model (6.2.8) with step size $\Delta = 0.01$ days using parameter values given in Example 6.7.6 with initial value $\pi(0) = 0.3$ and $\eta = 0.4770654$.

In the next example we will use histograms to see how the solution of the SDE HIV model oscillates around the level η as we vary the noise intensity $\bar{v}$.

Example 6.7.7 *Let us use the same parameter values as in Example 6.7.5 and choose* $\bar{v}$ *to be* $0.05, 0.04, 0.03, 0.005$ *and* $0.001/day^{-1/2}$. *We then let the simulations run for 1 million iterations but disregard the first 800,000 iterations in order to allow* $\pi(t)$ *to reach its recurrent level.*

From Figure 6.7, we can see from the histograms that for larger $\bar{v}$, *the distribution of the solution is more skewed, while for smaller* $\bar{v}$, *the distribution is more normally distributed about the level* η. *This is further confirmed by the sample skewness coefficients, namely* $0.8380437, 0.7711584, 0.299269, 0.2371403$ *and* -0.1524738 *corresponding to* $\bar{v} = 0.05, 0.04, 0.03, 0.005$ *and* $0.001/day^{-1/2}$ *respectively.*

Figure 6.8 shows the corresponding normal QQ plot for the histograms shown in Figure 6.7 for $\bar{v} = 0.03, 0.005$ *and* $0.001/day^{-1/2}$. *There is clearly curvature in those plots, indicating some departure from normality.*

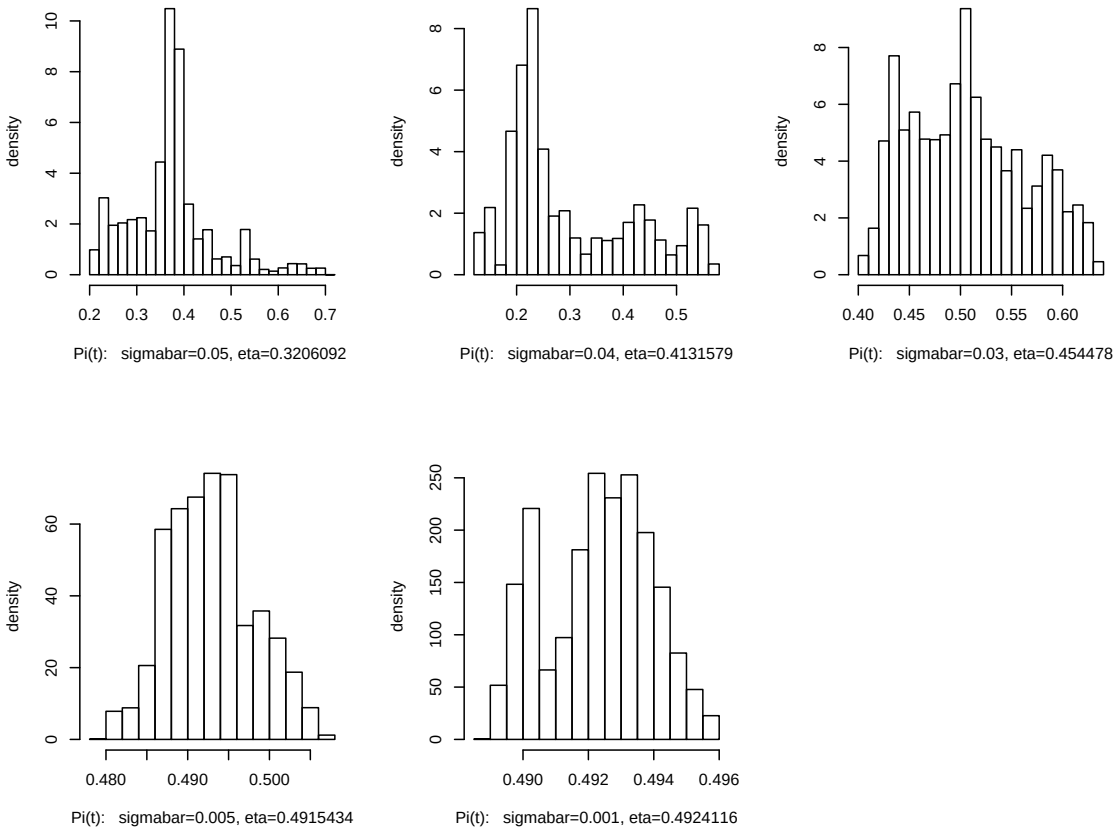

Figure 6.7: Histograms for the solution path $\pi(t)$ for the SDE HIV model (6.2.9) with step size $\Delta = 0.01$ days using parameter values given in Example 6.7.7 with initial value $\pi(0) = 0.5$ and $\bar{v} = 0.05, 0.04, 0.03, 0.005$ and $0.001/\text{day}^{-1/2}$.

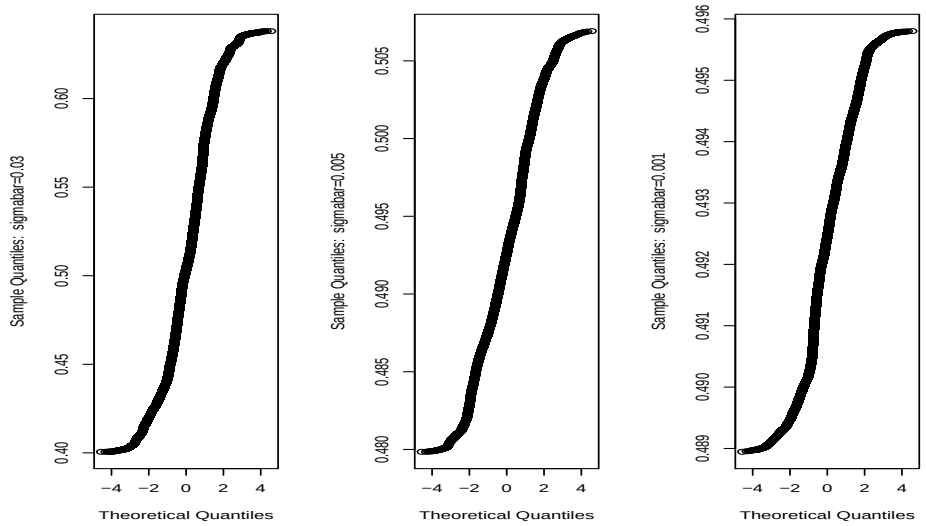

Figure 6.8: QQ plot for the solution path $\pi(t)$ for the SDE HIV model (6.2.9) corresponding to the histograms shown in Figure 6.7 for $\bar{\upsilon} = 0.03, 0.005$ and $0.001/\text{day}^{-1/2}$.

6.8 Conclusion and Discussion

In this chapter we have introduced environmental stochasticity into the extended Kaplan model for the spread of HIV amongst PWIDs constructed by Greenhalgh and Hay [43]. Inspired by the work done on introducing stochasticity by parameter perturbation into the SIS epidemic model in [40], we explored the properties for the resulting stochastic HIV model by first proving that there exists a unique nonnegative solution $\pi(t)$ for any given initial value $\pi_0 \in (0, 1)$. Furthermore, we have constructed the basic reproduction number for the stochastic model, namely R_0^S, and the conditions required for extinction and persistence for our solution $\pi(t)$. In general, if $R_0^S < 1$, the solution will almost surely go extinct as shown in Theorems 6.4.1 and Theorem 6.4.2. There is a gap in our results if $R_0^S \leq 1$ and $\frac{\upsilon\rho}{\sigma} < \bar{\upsilon}^2 < \frac{\upsilon^2}{2\mu}$ or if $R_0^S = 1$ and $\bar{\upsilon}^2 \leq \frac{\upsilon\rho}{\sigma}$, but here we conjecture that disease will always die out. Both conjectures were supported by simulations. On the other hand, the solution will almost surely persist and oscillate around the level η if $R_0^S > 1$ as shown in Theorem 6.5.1. Most importantly, we have shown that by altering the noise intensity $\bar{\upsilon}$, it will affect the dynamical behaviour of our system.

By using the well-known Khasminskii theorem [71], we have shown that the SDE HIV model has a unique stationary distribution. Lastly, numerical simulations using realistic

parameter values are constructed to support our analytical results.

Note that R_0^S has a natural interpretation as follows: If we consider introducing a single newly infected individual into the disease-free equilibrium (DFE) and consider the number of secondary cases that he or she produces then near the DFE equation (6.2.9) becomes

$$d\pi(t) = \pi\left(\frac{\upsilon\sigma}{\rho} - \mu\right)dt + \frac{\bar{\upsilon}\sigma}{\rho}\pi dB.$$

By using the Itô's formula and choosing a function $V(x) = \log(x)$, we have the solution

$$\pi(t) = \pi_0 \exp\left[\left\{\left(\frac{\upsilon\sigma}{\rho} - \mu\right) - \frac{1}{2}\frac{\bar{\upsilon}^2\sigma^2}{\rho^2}\right\}t + \frac{\bar{\upsilon}\sigma}{\rho}B(t)\right].$$

Also $\lim_{t\to\infty} |B(t)|/t = 0$ almost surely. Hence we expect that if

$$R_0^S = \left(\frac{\upsilon\sigma}{\mu\rho}\right) - \frac{\bar{\upsilon}^2\sigma^2}{2\rho^2\mu} < 1$$

then the disease dies out whereas if $R_0^S > 1$ the disease takes off. Thus this is a natural biological interpretation of the stochastic basic reproduction number R_0^S. Note that R_0^S is negative if $\bar{\upsilon}^2 > \frac{2\rho\upsilon}{\sigma}$.

Deterministic models have in the past proved very useful in describing the spread of HIV amongst PWIDs but they have their faults. The real world is stochastic and in general stochastic models are more realistic than deterministic ones. Recall that

$$R_0^S = R_0^D - \frac{\bar{\upsilon}^2\sigma^2}{2\rho^2\mu} \tag{6.8.1}$$

where R_0^D represents the basic reproduction number in the deterministic model. So in the deterministic model R_0^D is the expected number of secondary cases caused by a single newly infected PWID entering a population consisting entirely of susceptible PWIDs and uninfected needles. The second term in (6.8.1) is an adjustment factor for the stochastic model.

In the deterministic model we have a straightforward scenario where if the basic reproduction number $R_0^D \leq 1$ then it is known that the disease will die out, whereas if $R_0^D > 1$ then the disease will persist. The results in this section show that in the stochastic model, if $R_0^S < 1$ then the disease dies out (almost surely), whereas if $R_0^S > 1$ then the disease ultimately persists and oscillates about a non-zero level. These theoretical results

are confirmed by numerical simulations. Moreover the argument above shows that if a single newly infected PWID enters the DFE then we expect the disease to die out if $R_0^S < 1$ and take off if $R_0^S > 1$.

These findings provide new insights into the spread of HIV amongst PWIDs. This is because as the stochastic basic reproduction number R_0^S is less than the deterministic one it is possible for the noise to drive the disease to extinction, that is if $R_0^D > 1$ so that in the deterministic model the disease will persist, then if the stochastic noise is large enough, in the stochastic model the disease will die out. This has important implications for control strategies. Deterministic models have often been used to predict control strategies, for example the fraction of PWIDs who must clean their needles after use, the effects of HIV testing, or the amount that PWIDs need to decrease their syringe sharing rates in order to reduce R_0^D beneath one and eliminate disease. Examples of this applied to HIV amongst PWIDs include Greenhalgh and Lewis [45], Lewis [79] and Lewis and Greenhalgh [78]. Examples applied to hepatitis C virus (HCV) control include Corson [25] and Corson, Greenhalgh and Hutchinson [26].

The analytical and numerical results of this chapter provide new insight into this. If there is significant stochastic noise in the system then these estimates will be overestimated, that is a smaller fraction of PWIDs cleaning their needles, or a smaller reduction in PWID syringe sharing rates will still be sufficient for elimination of disease transmission.

In the next chapter we would like to conclude the thesis by summarising the work we have done.

Chapter 7

Conclusion and Summary

In this thesis we have explored the effect that demographic stochasticity and environmental stochasticity has on the dynamical behaviour of four different types of stochastic models. The real world is stochastic, with many factors that can influence the behaviour of an infectious diease. Very often we cannot predict with certainity what would happen to an epidemic. Therefore in order to fully understand and thus control a particular epidemic, stochasticity plays an important role.

In Chapter 3 we discuss the stochastic differential equation (SDE) susceptible-infected-susceptible (SIS) epidemic model with demographic stochasticity. First we prove that the SDE has a unique nonnegative solution which is bounded above. Then we give conditions needed for the solution to become extinct. Next we use the Feller test to calculate the respective probabilities of the solution first hitting zero or the upper limit. We confirm our theoretical results with numerical simulations and then give simulations with realistic parameter values for two example diseases: gonorrhea and pneumococcus. This SDE SIS model is a well established model constructed in [1]. As far as we know, this is the first piece of work that gives a detailed analysis on this model and therefore we hope to have filled this gap.

Motivated by the work done in Chapter 3, we continue to look at the effect that demographic stochasticity has on the deterministic SIS model but introducing stochasticity in a different way and thus causing the population size to vary with respect to time. In this chapter we work with a more challenging and complicated two dimensional stochas-

tic 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 nonnegative solution. Then we look at the two dimensional SDE SIS model and show that there exists a unique nonnegative 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. Due to the fact that the population size can vary, then the transmission term $\beta S(t)I(t)$ that we used in Chapter 3 corresponding to per capita disease contact rate $\lambda = \beta N$ might not be realistic and suitable when analysing models where population size is allowed to change as the transmission rate β may not remain constant when N is large. Consequently, in this chapter we decide to work with an alternative transmission term, namely $\frac{\lambda(N)}{N}S(t)I(t)$, where we have made some assumptions on the parameter $\lambda(N)$ to take into consideration both of the extreme population sizes and it is reasonable to assume that the per capita disease contact rate λ depends on the population size. Later on we have shown that provided that the population size is small, the results we obtained with the transmission term $\frac{\lambda(N)}{N}S(t)I(t)$ can be applied to the SIS epidemic model with transmission term $\beta S(t)I(t)$, as expected.

In Chapter 5 we discuss the effect of introducing the telegraph noise, which is an example of an environmental noise, into the susceptible-infected-recovered-susceptible (SIRS) model by examining the model using a finite-state Markov Chain. First we start with a two-state Markov Chain and show that there exists a unique nonnegative solution and establish the conditions for extinction and persistence for the stochastic SIRS epidemic model. We then explain how the results can be generalised from a two-state Markov Chain to a finite-state Markov Chain. The results for the SIR (susceptible-infected-removed) model with Markovian switching are a special case of the SIRS model. Numerical simulations are produced to confirm our theoretical results on the SIRS epidemic model. Realistic simulation on a real-life disease, measles, is also given as an example for the SIR epidemic model. In this chapter we constructed a new threshold value T_0^S which deter-

mines whether a particular disease would die out or persist in the stochastic environment. In general, if $T_0^S < 1$ then the disease would die out, otherwise it would persist. For the persistence case we have obtained two further sets of persistence conditions for the two possible cases in which $T_0^S > 1$. One important thing we have discovered is that although in a deterministic environment, if $R_0^D \leq 1$ then the disease would always die out, this is not always the case when we incorporated telegraph noise into the SIRS/SIR epidemic model. If one subsystem has $R_0^D < 1$ while the other has $R_0^D > 1$, in other words one subsystem will go extinct while the other subsystem will persist, then the behaviour of the overall system is not so straightforward in the stochastic environment. The behaviour of the disease will then depend on the average time it takes for the disease to switch from one environment to the other. If for example, the average time it takes for the Markov Chain to switch from state 2 to state 1 is relatively faster than from state 2 to state 1, then the effect from state 1 will predominate. This interesting scenario highlights the important effect that environmental stochasticity has on the dynamical behaviour of an infectious disease as there are various types of factor such as rainfall or nutrition that could cause a particular disease to switch between two or more regimes of environment.

From Chapter 3 to Chapter 5 we have looked at three different types of epidemic models. Another epidemic model which will be interesting to look at is the Susceptible-Exposed-Infectious-Susceptible (SEIS) model. In this case the term "Exposed" referred to exposed individuals in the latent period. In other words, the individual is infected but not yet infective. This model would be suitable for infectious diseases which have a significantly long incubation period such as AIDS and schistosomiasis. It would be interesting to find out how stochasticity will affect the behaviour of such disease. We believe that the techniques we developed in this thesis can be applied to the SEIS model and other more complicated epidemic models with more compartments.

In Chapter 6, we introduced environmental stochasticity using the well-known standard technique of parameter perturbation into the modified Kaplan model given in [43], which describes the spread of HIV amongst PWIDs. We derive a stochastic differential equation (SDE) for the fraction of PWIDs who are infected with HIV at time t. We first prove that the resulting SDE for the fraction of infected PWIDs has a unique solution in (0,1) provided that some infected PWIDs are initially present, and next construct the

conditions required for extinction and persistence. We have obtained a new basic reproduction number in the stochastic case, namely $R_0^S = R_0^D - \frac{\bar{v}^2\sigma^2}{2\rho^2\mu}$ where R_0^D is the basic reproduction number in the deterministic model. If $R_0^S < 1$, then we have shown that the disease will die out and if $R_0^S > 1$ then the disease will persist. Note that in this case $R_0^S < R_0^D$, which means if the environmental noise is large enough then it is possible for the disease to persist in the deterministic case ($R_0^D > 1$) but it will die out in the stochastic case ($R_0^S < 1$). This has once again highlighted the importance of taking into consideration the effect of environmental factors.

Furthermore, we also show that there exists a stationary distribution for the persistence case. Simulations using realistic parameter values are then constructed to illustrate and support our theoretical results.

Our results provide new insight into the spread of HIV amongst PWIDs. The results show that the introduction of stochastic noise into a model for the spread of HIV amongst PWIDs can cause the disease to die out in scenarios where deterministic models predict disease persistence. Hence in situations where stochastic noise is important predictions of control measures such as needle cleaning or reduction of needle sharing rates needed to eliminate disease may be overly conservative. As far as we know this is the first literature which looks at the effect of environmental stochasticity on the extended Kaplan model and we hope this would fill the gap.

We believe that the technique used in this chapter can be applied to other types of HIV models which deal with different risk groups to examine the effect that environmental stochasticity has on the dynamical behaviour of the disease.

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