ABSTRACT

CUFFNEY, LAURIE ANN. A Comparison of Threshold Parameters in Deterministic SIS and SI_1I_2S Models and Stochastic SIS and SI_1I_2S Models. (Under the direction of John Franke.)

Epidemic models are used to predict disease spread through a population. Accurate prediction of disease spread is important in the management of outbreaks and treatment of disease. Deterministic SIS models carry with them the inherent assumption that the infection rate, α, and the recovery rate, σ, are constant throughout the population and throughout time. In reality this assumption is flawed. There are many factors which can influence the rate at which infection spreads through out a population. Over the course of time environmental changes may cause variation in the rate of infection and ability of infected individuals to recover. To account for variation in infection rate and recovery rate over time we want to add stochasticity into our epidemic model. In this paper we outline a method to introduce stochasticity into an epidemic model where each parameter is drawn from some distribution and attempt to establish a threshold parameter for this model.

A Comparison of Threshold Parameters in Deterministic SIS and SI_1I_2S Models and Stochastic SIS and SI_1I_2S Models

by
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DEDICATION

This thesis is dedicated to my parents and my close friends. Thank you for believing in me when I could not. Without you this would not exist.

BIOGRAPHY

Laurie Cuffney was born September 12th, 1988 in Cincinnati, Ohio. In 1990 Laurie and her family moved to the Raleigh area of North Carolina. After graduating from Athens Drive High School in 2006 Laurie attended Brevard College in North Carolina to purse a degree in music and mathematics. She graduated magna cum laude three years later in 2009 earning a Bachelors of Arts with a double major in music and mathematics. After graduation Laurie decided to pursue further education in mathematics. She was admitted into the Applied Mathematics graduate program at North Carolina State University in the Fall of 2009. Upon completion of her degree she plans to spend time working before returning to school to pursue a Ph.D.

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Finally, I would like to thank my peers who listened to me endlessly ramble about my project. Thank you for listening to me and allowing me to bounce ideas around out loud.

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Chapter 1

Introduction

Epidemic models are used to predict disease spread through a population. Accurate prediction of disease spread is important in the management of outbreaks and treatment of disease. Deterministic discrete and continuous time models have a rich history of study and their behavior is well known [1, 3, 10, 15]. A simple deterministic discrete time SIS model with constant population is given by

$$\begin{aligned} S(t+1) &= \left(1 - \frac{\alpha I}{N}\right) S + \sigma I \\ I(t+1) &= \frac{\alpha I}{N} S + (1-\sigma) I \end{aligned} \tag{1.1}$$

where α is the infection rate and σ is the recovery rate. The threshold parameter for this model comes from the basic reproduction number,

$$\mathcal{R}_0^d = \frac{\alpha}{\sigma}. \tag{1.2}$$

When $\mathcal{R}_0^d$ is less than one the disease is eradicated and the model goes to a disease free equilibrium. If $\mathcal{R}_0^d$ is greater than one the disease persists and spreads through the population [1, 5, 4]. The model (1.1) carries with it the inherent assumption that the infection rate, α, and the recovery rate, σ, are constant throughout the population and throughout time. In reality this assumption is flawed.

There are many factors which can influence the rate at which infection spreads throughout a population. Attributes such as age and overall health play a role in the susceptibility of individual members of the population. In the case of influenza children under 5 years old and seniors 65 years old and up are classified by the CDC as high priority during vaccination season due to their high susceptibility. If a child under 5 comes into contact with an individual infected with influenza the probability the child contracts influenza is higher than if a middle aged

individual comes into contact with the same individual. Similarly an individual who is already sick has a higher likelihood to contract influenza when in contact with someone carrying the virus.

Discrete time epidemic models measure the spread of an epidemic at distinct time intervals i.e. days, months, or years. Over the course of time environmental changes may cause variation in the rate of infection and ability of infected individuals to recover. Changes in season and weather can cause a change in the rate of infection and ability to recover from illness. Thus the rate of infection and recovery are not constant.

To account for variation in infection rate and recovery rate over time we add stochasticity into our epidemic model. There are several approaches to introduce stochasticity into epidemic models. To introduce stochasticity the SIS model can be considered a Markov chain process where S and I are random variables [2, 3, 11]. Non-Markovian models have also been used to produce a stochastic epidemic model. In non-markovian models it may be the infectious rate and the infectious duration which generate stochasticity with in the model [6].

In this paper we will review a branching process model employed by Allen and Driessche [4] in chapter 2. We then outline a different method to introduce stochasticity into an epidemic model in chapter 3. In our model the parameters governing infection rate and recovery rate vary at each time step. The parameters follow a given distribution and are assumed to be i.i.d. We consider parameters which follow a uniform or Poisson distribution for numerical examples. Through numerical simulations we observe similar behavior to other stochastic epidemic models. When the deterministic threshold $\mathcal{R}_0^d$ is greater than one, but close to one, we expect the disease to persist. However, the disease instead is effectively eradicated from the population. Through out this paper we make the consideration that if the disease is present in a very small portion of the population we will say the disease has been eradicated. If the number of infected is on the order of 10^{-5} or smaller we will consider this a disease free state.

To understand the behavior of our stochastic epidemic model we define a stochastic threshold parameter

$$\mathcal{R}_0^s = \mathrm{E}\big(\ln(\alpha + 1 - \sigma)\big)$$

for the stochastic SIS epidemic model. The form of this threshold parameter is adapted from a similar form for thresholds in populations models [7, 8, 9]. In chapter 4 we begin to expand this process into a high dimension epidemic model such as SI_1I_2S and discuss the effect of multiple stages on the threshold parameter.

Chapter 2

Literature Review

In this chapter we discuss a stochastic threshold and the threshold theorem introduced by Allen and van den Driessche [4]. We consider the discrete-time multi-stage model $SI_1 \dots I_n S$ with constant population,

$$\begin{aligned} S(t+1) &= \left(1 - \sum_{j=1}^{n} \frac{\alpha_j I_j(t)}{N}\right) S(t) + \sigma_n I_n(t) \\ I_1(t+1) &= \left(\sum_{j=1}^{n} \frac{\alpha_j I_j(t)}{N}\right) S(t) + (1-\sigma_1) I_1(t) \\ I_j(t+1) &= (1-\sigma_j) I_j(t) + \sigma_{j-1} I_{j-1}, \quad j = 2, \dots n. \end{aligned} \tag{2.1}$$

In the multi-stage epidemic model we assume that individuals transition through stages following the scheme $I_j \to I_{j+1}$ for $j = 1, ...n-1$ and $I_n \to S$. Over one time step it is also assumed that an individual transitions only one stage further i.e. an individual in I_j at time t can only stay in I_j or transition to I_{j+1}.

Multi-stage models such as this can be used to model diseases that exhibit multiple contagious stages with different infection rates. An intermediate noncontagious stage can also be modeled by allowing the corresponding α_i to be zero. We are interested in the behavior of the model near the disease free equilibrium. Linearization about the disease free equilibrium yields

$$\mathbf{I}(t+1) = \begin{pmatrix} \alpha_1 + 1 - \sigma_1 & \alpha_2 & \cdots & \cdots & \alpha_n \\ \sigma_1 & 1-\sigma_2 & 0 & \cdots & 0 \\ 0 & \sigma_2 & 1-\sigma_3 & 0 & \cdots \\ \vdots & \vdots & \ddots & \ddots & \vdots \\ 0 & 0 & \cdots & \sigma_{n-1} & 1-\sigma_n \end{pmatrix} \mathbf{I}(t), \tag{2.2}$$

where

$$\mathbf{I}(t) = \begin{pmatrix} I_1(t) \\ \vdots \\ I_n(t) \end{pmatrix}.$$

The matrix in (2.2) is a sum of two matrices F_d, the matrix of new infections, and T_d, the transition matrix [4],

$$F_d = \begin{pmatrix} \alpha_1 & \alpha_2 & \cdots & \alpha_n \\ 0 & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots \end{pmatrix} \tag{2.3}$$

$$T_d = \begin{pmatrix} 1-\sigma_1 & 0 & \cdots & 0 \\ \sigma_1 & 1-\sigma_2 & \cdots & 0 \\ 0 & \sigma_2 & 1-\sigma_3 & \vdots \\ \vdots & \vdots & \ddots & \vdots \\ 0 & \cdots & \sigma_{n-1} & 1-\sigma_n \end{pmatrix}. \tag{2.4}$$

Using these two matrices we can build the next generation matrix $K_d = F_d(\mathbb{I} - T_d)^{-1}$ [5]. The spectral radius of the next generation matrix provides the deterministic threshold $\mathcal{R}_0 = \rho(K_d)$ for the multi-stage discrete-time epidemic model (2.1). As with the single stage SIS model if the threshold parameter $\mathcal{R}_0$ is less than one the disease is eradicated. If $\mathcal{R}_0$ greater than one the disease persists within the population [4, 5]. In figure 2.1 we see two examples of an SI_1I_2S model with different parameters providing an example where $\mathcal{R}_0$ greater than one and and example where $\mathcal{R}_0$ less than one. In figure 2.1a the threshold parameter is $\mathcal{R}_0 = 3.8667$ which is greater than one and we see the disease is endemic as we would expect. For figure 2.1b the threshold parameter is $\mathcal{R}_0 = 0.9$ which is less than one and we see the population recover from the initial infection and the disease die away over time.

To add stochasticity into this model we define the probability that one individual in the I_j class infects k individuals in one time step. We notate this probability as p_{jk}. The probabilities p_{jk} follow some distribution over the interval $[0, 1]$ and $\sum_{k=0}^{\infty} p_{jk} = 1$. For the purposes of this paper we will generate p_{jk} from a Poisson distribution, with mean $\lambda_j = \alpha_j$, or a uniform distribution. In this method the transition parameters, σ_i, remain constant.

We define the offspring probability generating functions near the disease free equilibrium as

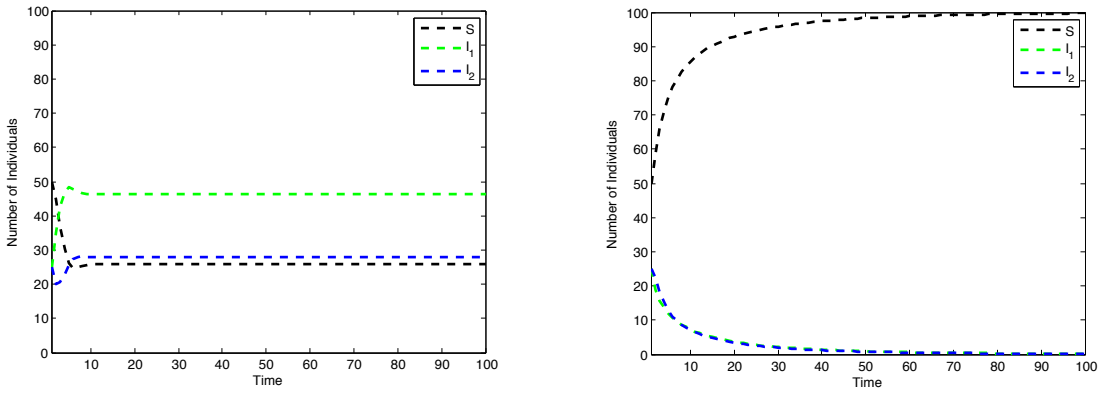
$$h_j(u) = \sum_{k_1=0}^{\infty} \cdots \sum_{k_n=0}^{\infty} P_j(k_1, \ldots, k_n) u_1^{k_1} \cdots u_n^{k_n} \tag{2.5}$$

where $P_j(k_1, \ldots, k_n)$ is the probability that in one time step one individual in the jth class

produces k_1 individuals in the I_1 class, k_2 individuals in the I_2 class etc [4]. In this model due to imposed restrictions on movement between classes $P_j(k_1, \ldots, k_n) = 0$ when $k_i \geq 2$ for any $i \geq 2$. Therefore the only nonzero probabilities we can have are $P_j(k_1, \ldots, k_n)$ where $k_i = 0, 1$ for $i \geq 2$.

Since we only allow an individual to either stay in the class or move to the next class, $P_j(k_1, \ldots, k_n) = 0$ if $k_i = 1$ for $i \neq j, j+1$. This leaves the only potentail nonzero probabilities $P_j(k_1, \ldots, k_n)$ when $k_i = 0$ for $i \neq 1, j, j+1$ and either $k_j = 0$ and $k_{j+1} = 1$ or $k_j = 1$ and $k_{j+1} = 0$. Multiple new infected individuals may result from one infected individual so k_1 is allowed to range from 0 to N. In practice this means $P_3(k_1, \ldots, k_n) \neq 0$ for $P_3(k_1, 0, 1, 0, \ldots, 0)$ and $P_3(k_1, 0, 0, 1, 0, \ldots, 0)$. $P_3(k_1, 0, 1, 0, \ldots, 0)$ represents the probability that one individual in I_3 stays in I_3 and infects k_1 individuals from the susceptible class successfully over one time step. Likewise the probability $P_3(k_1, 0, 0, 1, 0 \ldots, 0)$ represents the individual moving from I_3 to I_4 and infecting k_1 individuals from the susceptible class successfully over one time step.

To further simplify these probabilities we make the observation that new infections occur independently of transition between stages. Transmission of the disease from an infected individual to a susceptible individual occurs at the beginning of the time interval [4]. This means that the probabilities are independent and can be separated. Define $r_j(k)$ to be the probability that one infected individual in the jth class infects k individuals over one time step. Notice then $r_j(k) = p_{jk}$. Let $q_j(k_2, \ldots, k_n)$ be the probability that in one time step one individual in the jth class produces k_2 individuals in the I_2 class, k_3 individuals in the I_3 class etc. We can



(a) (b)

Figure 2.1: Deterministic discrete-time multi-stage SI_1I_2S models with initial conditions $N = 100$, $S(0) = 50$, and $I_1(0) = 25 = I_2(0)$ with parameters (a) $\alpha_1 = -0.2$, $\alpha_2 = 0.3$, $\sigma_1 = 0.5$, $\sigma_2 = 0.6$ and (b) $\alpha_1 = -0.8$, $\alpha_2 = 0.6$, $\sigma_1 = 0.3$, $\sigma_2 = 0.5$. The threshold parameter $\mathcal{R}_0$ for each model is; (a) $\mathcal{R}_0 = 3.8667$, (b) $\mathcal{R}_0 = 0.9$.

now rewrite $P_j(k_1, \ldots, k_n)$ as

$$P_j(k_1, \ldots, k_n) = p_{jk_1} \cdot q_j(k_2, \ldots, k_n). \tag{2.6}$$

We can define the probability q_j for all values of j as

$$q_j(k_2, \ldots, k_n) = \begin{cases} 1 - \sigma_j & \text{if } k_j = 1,\ k_i = 0 \text{ for } i \neq j \\ \sigma_j & \text{if } k_{j+1} = 1,\ k_i = 0 \text{ for } i \neq j+1 \\ 0 & \text{otherwise.} \end{cases} \tag{2.7}$$

This simplifies (2.5) with respect to our model to

$$\begin{aligned} h_j(u) &= [(1-\sigma_j)u_j + \sigma_j u_{j+1}] \sum_{k=0}^{\infty} p_{jk} u_1^k, \quad j = 1, \ldots, n-1 \\ h_n(u) &= [(1-\sigma_n)u_n + \sigma_n] \sum_{k=0}^{\infty} p_{jk} u_1^k. \end{aligned} \tag{2.8}$$

To describe this process we can calculate the expectation matrix M_d where,

$$m_{ij} = \frac{\partial h_i}{\partial u_j}\Big|_{u1=\cdots=u_n=1}[4].$$

The expectation matrix M_d satisfies the relation $M_d^T = (F_d + T_d)$. Allen and van den Driessche's [4] threshold theorem states that $\rho(M_d) < 1 (> 1)$ if and only if $\rho(K_d) < 1 (> 1)$. For this stochastic threshold when $\rho(M_d)$ less than one the process is subcritical and disease extinction occurs with probability one. When $\rho(M_d)$ greater than one the process is supercritical and the probability of disease extinction is less than one. This means that if the deterministic threshold of the deterministic model with corresponding parameters to the stochastic model is less than one we are guaranteed to see disease extinction. When the corresponding deterministic threshold is greater then one we are not guaranteed to have an endemic. It is possible to have disease extinction even with the threshold parameter greater than one.

Consider the one stage model 1.1. The offspring probability generating function for this model is

$$h(u) = [(1-\sigma)u + \sigma 1] \sum_{k=0}^{\infty} p_k u^k \tag{2.9}$$

where p_k is the probability that an infected individual produces k new infected individuals over one time step. Let p_k be poisson with mean α. Figure 2.2a shows three sample paths of this branching process. After 2,000 time steps two of the sample paths appear to be approaching a

disease free state. To determine the long term average behavior of the stochastic model we run numerical simulations for 1,000 trials at higher time steps. Figures 2.2b-d show the results of these simulations. We see through these histograms the average of the trials decreases over time and by the 100,000 time step have decreased to the point we will say the population is disease free. Here we see an instance of disease extinction where the deterministic threshold parameter is $\mathcal{R}_0 = 1.003$ which is greater than one.

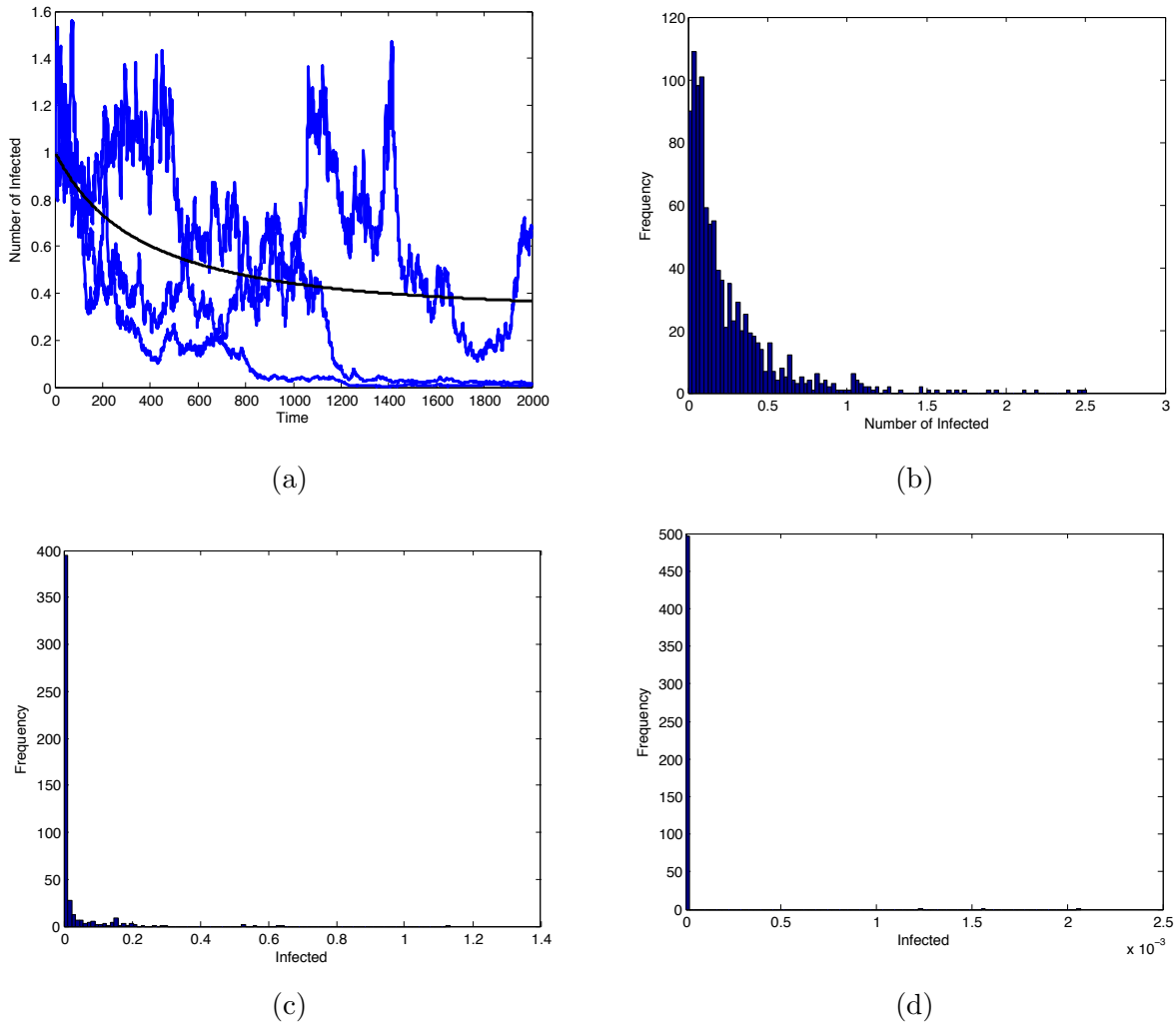


Figure 2.2: Parameter values $\alpha = .3$, $\sigma = .299$; $\mathcal{R}_0 = 1.003$. Initial conditions $I(0) = 1$, $S(0) = 99$. (a) Three sample paths of stochastic epidemic model versus deterministic model over 2000 time steps. Histograms showing frequency of infected individuals for 500 trials after (b) 1000 time steps; mean$(I(t)) = 0.2528$, (c)10000 time steps; mean$(I(t)) = 0.0253$ and (d) 100000 times steps; mean$(I(t)) = 9.7275 \cdot 10^{-6}$.

Table 2.1: Branching process SIS model where p_{jk} Poisson with $\lambda = \alpha$ infected class mean of 1000 trails after 1000, 10000 and 100000 time steps. The deterministic $\mathcal{R}_0$ and approximate deterministic endemic equilibrium or disease free state are also given.

α	σ	t=1,000	t=10,000	t=100,000	$\mathcal{R}_0$	approx. equil.
0.3	0.27	9.5599	9.7901	9.8229	$1.\bar{1}$	10
0.3	0.28	6.1755	6.4038	6.1256	1.07	$6.\bar{6}$
0.3	0.29	2.8922	3.1253	3.1229	1.03	$3.\bar{3}$
0.3	0.295	1.2102	1.2414	1.1722	1.01	$1.\bar{6}$
0.3	0.297	0.6519	0.4646	0.6226	$1.0\bar{1}0$	1
0.3	0.298	0.5439	0.2407	0.1730	1.006	$1.\bar{3}$
0.3	0.299	0.3571	0.0165	$1.5376 \cdot 10^{-9}$	1.003	$0.\bar{6}$
0.3	0.3	0.1559	$7.6995 \cdot 10^{-5}$	$1.8547 \cdot 10^{-48}$	1	0
0.3	0.35	$2.8608 \cdot 10^{-23}$	$1.6871 \cdot 10^{-235}$	$4.9407 \cdot 10^{-334}$	0.857	0

Table 2.1 shows other sample paths for the branching process. For all sample paths in table 2.1 the parameter α is the same. For each choice of the parameter σ we ran 1,000 sample paths and collected the mean of 1,000 sample paths after 1000, 10000, 100000 time steps. By running the program with different σ values we can see the change in behavior of the stochastic SIS model. For $\alpha = 0.3$ and $\sigma = 0.299$ we see the stochastic model moving to a disease free state when the deterministic model reaches an endemic equilibrium. This behavior is similar to what occurs with our model. In our stochastic epidemic model we choose to let the parameters themselves vary over time according to a chosen distribution.

Chapter 3

Stochastic one-stage SIS model

Expanding on the previous work in chapter one we allow the parameters governing infection rate and recovery rate to both follow some distribution. For simplification the model parameters are i.i.d. and we consider only the Poisson and uniform distribution. In this chapter we will focus on the one-stage model (1.1).

3.1 Uniform parameters

Assume that the parameters α and σ follow a uniform distribution over a given interval. In figure 3.1a we numerically simulate three sample paths for an SIS model with both parameters allowed to vary. At first we may assume the deterministic threshold (1.2) using the mean of α and the mean of σ to be an accurate stochastic threshold parameter. We see in figure 3.1 two examples of when this threshold fails to hold true in practice.

In figure 3.1a $\alpha \in [0, 0.3]$ and $\sigma \in [0, 0.28]$ are uniform. At time $t = 1600$ one of the sample paths goes to zero even though the deterministic threshold parameter $\mathcal{R}_0^d = 1.071428$ is greater than one suggesting an endemic disease. Figures 3.1b-d show the frequency of the number of infected individuals for 500 trials at different time steps for the stochastic SIS model with uniform parameters $\alpha \in [0, 0.8]$, $\sigma \in [0, 0.7233]$. As time increases the average over 500 trials decreases and the disease presence in the population decreases to the extent we are comfortable saying the disease has effectively been eradicated even though the deterministic threshold is greater than one. Table 3.1 shows results for the mean of the I class after time steps 1000, 10000, and 100000 and the deterministic threshold (1.2) calculated using the mean of each parameter.

Through numerical simulations we can make several preliminary observations. When the α and σ intervals are non-overlapping deterministic threshold is an accurate representation of the behavior of the stochastic epidemic model. Since the intervals do not overlap the probability

that the ratio $\frac{\alpha}{\sigma}$ is greater than one at one time step and less than one at another time step is zero. The ratio $\frac{\alpha}{\sigma}$ is either always greater than one or always less than one. When the two intervals overlap it is possible for the ratio $\frac{\alpha}{\sigma}$ to be greater than one at one time step and less than one at another time step. The question then is at what point does the overlap cause the stochastic model to become disease free when we would expect based on the means to have an endemic disease.

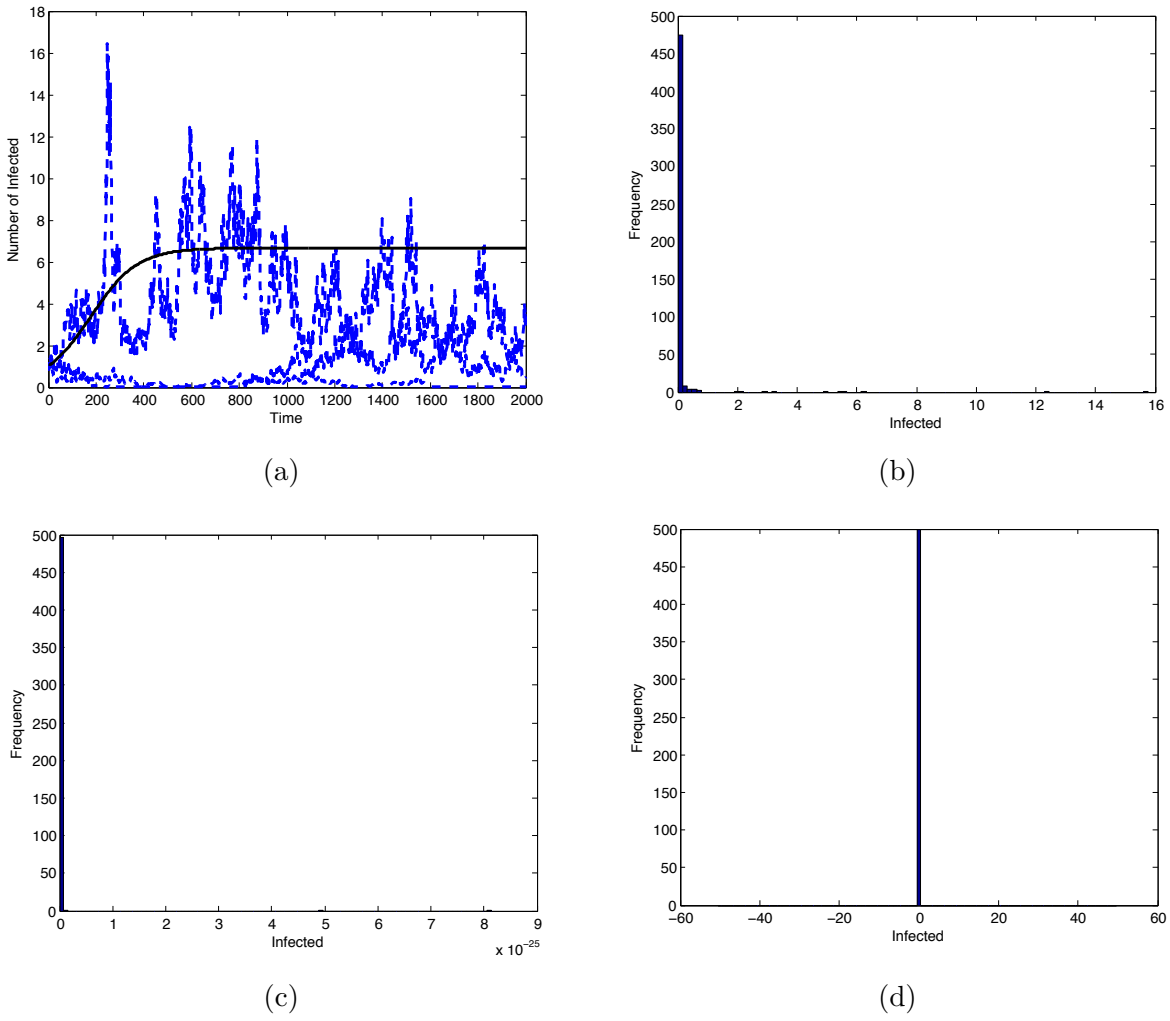


Figure 3.1: Initial conditions $I(0) = 1$, $S(0) = 99$. (a) Three sample paths of stochastic epidemic model versus deterministic model over 2000 time steps with uniform parameters $\alpha \in [0, 0.3]$, $\sigma \in [0, 0.28]$; $\mathcal{R}_0 = 1.071428$. (b)-(d) Uniform parameters $\alpha \in [0, 0.8]$, $\sigma \in [0, 0.7233]$; $\mathcal{R}_0 = 1.1058$. Histograms showing frequency of infected individuals for 500 trials after (b) 1000 time steps; mean$(I(t)) = 0.1365$, (c)10000 time steps; mean$(I(t)) = 2.6410 \cdot 10^{-27}$ and (d) 100000 time steps; mean$(I(t))) = 0$.

To answer this question we run simulations with the α interval fixed and vary the σ interval. For all simulations the intervals are of the form $[0, \alpha_{\max}]$ and $[0, \sigma_{\max}]$. To find the smallest $\mathcal{R}_0$ that shows a disease epidemic we compare the mean values for 1,000 trials at the time steps 100,000 and 300,000. If the mean at 300,000 differs from the mean at 100,000 by a factor of 30 and neither mean is on the order of 1×10^{-5} we say there is an epidemic. If either of the means is less than or equal to 1×10^{-5} or the means differ by more than a factor of 30 we say that the model is approaching a disease free equilibrium. Refer to Appendix A.2 for a detailed view of the program. This is repeated for the α endpoints $0.2, 0.3, \ldots, 1$. The results of this experiment

Table 3.1: Multiple trial run results for our stochastic SIS model with uniform parameters. Infected class mean of 1000 trails after 1000, 10000 and 100000 time steps and deterministic $\mathcal{R}_0^d$.

α	σ	$\mathcal{R}_0^d$	t=1,000	t=10,000	t=100,000
$[0, .4]$	$[.5, .7]$	$0.\bar{3}$	$1.1506 \cdot 10^{-227}$	0	0
$[.3, .4]$	$[.1, .2]$	$2.\bar{3}$	34.1231	34.3557	34.0874
$[.4, .6]$	$[.35, .55]$	$1.\bar{1}$	5.5527	5.6389	5.5010
$[.3, .7]$	$[.25, .65]$	$1.\bar{1}$	6.5698	6.9806	7.4433
$[.2, .8]$	$[.25, .75]$	$1.\bar{1}$	2.6205	3.1808	3.9760
$[.4, .6]$	$[.3, .5]$	1.25	19.1799	19.3276	19.8807
$[.3, .7]$	$[.3, .5]$	1.25	18.1380	18.3112	18.1623
$[0, .5]$	$[0, .4]$	1.25	13.6954	14.3214	14.3711
$[0, .5]$	$[0, .47]$	1.0638	0.3614	$1.4550 \cdot 10^{-5}$	$7.1654 \cdot 10^{-169}$

Table 3.2: Approximation of the smallest value of $\sigma_{\max}$ for the interval $[0, \sigma_{\max}]$ which results in an endemic disease. The parameters α and σ follow a uniform distribution and $\alpha \in [0, \alpha_{\max}]$.

$\alpha_{\max}$	$\sigma_{\max}$
0.2	0.1906
0.3	0.2717
0.4	0.3751
0.5	0.4608
0.6	0.5411
0.7	0.6140
0.8	0.7017
0.9	0.7763
1.0	0.8452

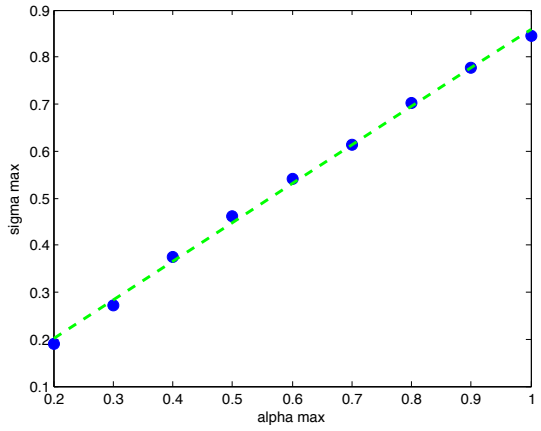


Figure 3.2: Linear regression describing an approximate relationship between $\alpha_{\max}$ and $\sigma_{\max}$ when α and σ follow a uniform distribution. This line represents the dividing line between epidemic and disease free parameter sets. The regression is $\sigma = 0.8235\alpha + 0.0365$ with $r^2 = 0.9979$.

are show in table 3.2.

From this data we find the linear regression shown in figure 3.2 given by $\sigma = 0.8235\alpha + 0.0365$. In the deterministic case the slope of this line would be one. We see here that by adding stochasticity into our model the behavior of the threshold parameter changes. If the α interval and the σ interval both begin at zero and the choice for $\alpha_{\max}$ and $\sigma_{\max}$ give a point above the line in figure 3.2 we should expect the disease be eradicated over time. If the choice of $\alpha_{\max}$ and $\sigma_{\max}$ is below the line we expect the disease to persist.

3.2 Poisson parameters

Using the same approach as the uniform distribution we examine similar experiments for the model (1.1) with parameters that follow a Poisson distribution. Figure 3.3 shows three sample paths for the stochastic model with Poisson parameters α and σ. The parameter ranges are the same as those in figure 3.1. Comparing these two images we can see that a shift has occurred when we change from uniform to Poisson. Intervals which produced a disease free result with uniform parameters may produce an endemic result when the parameters follow Poisson distribution. Based on the difference between figure 3.1 and figure 3.3 we predict an increase in the $\sigma_{\max}$ endpoint of the interval $[0, \sigma_{\max}]$ when we run simulations to generate a table for poisson parameters similar to table 3.2.

We run the same simulations as before when considering uniform parameters but now with

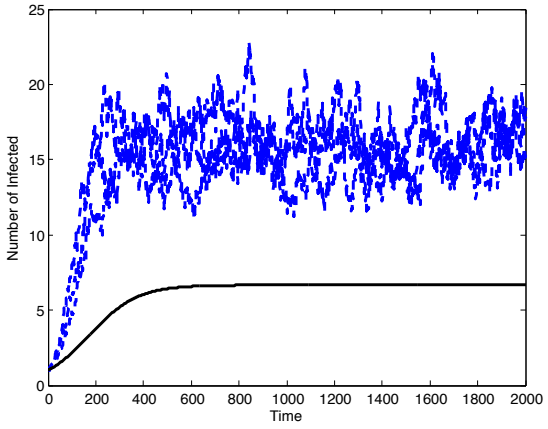


Figure 3.3: Three sample paths of stochastic epidemic model versus deterministic model over 2000 time steps. Parameters are Poisson with $\lambda = .15$ for $\alpha \in [0, 0.3]$ and $\lambda = .14$ for $\sigma \in [0, 0.28]$; $\mathcal{R}_0 = 1.071428$.

poisson parameters. For all simulations the intervals are of the form $[0, \alpha_{\max}]$ and $[0, \sigma_{\max}]$.The approximated values for the smallest $\sigma_{\max}$ in the σ interval $[0, \sigma_{\max}]$ are show in table 3.3. Looking at the values in table 3.3 and comparing them to the values found for uniform distributions in table 3.2 we can see that value for $\sigma_{\max}$ has increased for all $\alpha_{\max}$ as we predicted.

This occurs because the Poisson distribution is concentrated near the mean and the probability of hitting a value far from the mean is small. In the uniform distribution the probability is equal for all values in the interval. This means that the overlap for the two intervals describing α and σ may be larger for Poisson parameters then uniform parameters before we encounter a deterministic threshold $\mathcal{R}_0^d$ greater than one but see disease eradication in practice. The linear regression, figure 3.4, $\sigma = 0.9874\alpha + 0.0022$ with $r^2 = 0.9999$ shows a visible increase in the α coefficient of the regression from uniform to poisson. As before if the α interval and the σ interval both begin at zero and the choice for $\alpha_{\max}$ and $\sigma_{\max}$ give a point above the line in figure 3.4 we should expect the disease be eradicated over time. If the choice of $\alpha_{\max}$ and $\sigma_{\max}$ is below the line we expect the disease to persist.

In table 3.4 we see the effect of the σ interval on the stochastic model behavior. The α interval is fixed for each set of trial runs. We illustrate the behavior of the infected class mean for 1,000 trials for different choices of the σ interval. The table shows us that when $\sigma_{\max} = 0.695$ the disease persists in a very small portion of the population and when $\sigma_{\max}$ is increased to 0.699 the disease is eradicated. This indicates at some point between 0.695 and 0.699 the model changes behavior. If we look at table 3.3 we approximated $\sigma_{\max} = 0.6958$ when $\alpha \in [0, 0.7]$ which is between 0.695 and 0.699 as we expected.

Table 3.3: Approximation of the smallest value of $\sigma_{\max}$ for the interval $[0, \sigma_{\max}$ which results in an endemic disease. The parameter $\alpha \in [0, \alpha_{\max}$ and α and σ follow a Poisson distribution.

$\alpha_{\max}$	$\sigma_{\max}$
0.2	0.1986
0.3	0.2988
0.4	0.3977
0.5	0.4966
0.6	0.5943
0.7	0.6958
0.8	0.7876
0.9	0.8923
1.0	0.9899

Table 3.4: Multiple trial run results for our stochastic SIS model with poisson parameters. Infected class mean of 1000 trails after 1000, 10000 and 100000 time steps and deterministic $\mathcal{R}_0^d$ are shown.

α	λ_α	σ	λ_σ	mean $\mathcal{R}_0$	t=1,000	t=10,000	t=100,000
$[0, .7]$	.35	$[0, .6]$	.3	$1.\bar{6}$	13.8054	13.6855	13.6347
$[0, .7]$	.35	$[0, .675]$	.3375	1.037	2.9662	2.9247	2.9111
$[0, .7]$	.35	$[0, .695]$	.3475	1.0072	0.0879	0.0434	0.0248
$[0, .7]$	.35	$[0, .699]$	.3495	1.00143	$0.417 \cdot 10^{-4}$	$40.1212 \cdot 10^{-28}$	$0.75 \cdot 10^{-62}$

3.3 Stochastic threshold parameter

It is apparent that the deterministic threshold does not accurately predict the behavior of our stochastic model . To descibe the long term behavior of our stochastic model we must establish a new stochastic threshold. We adapt the ideas of Lewontin and Cohen[12] from population models to epidemic models to build our stochastic threshold. The linearization of (1.1) is

$$I(t+1) = (\alpha + 1 - \sigma)I(t). \tag{3.1}$$

In the deterministic model we can rewrite this linearization as

$$I(n) = (\alpha + 1 - \sigma)^n I(0). \tag{3.2}$$

In our stochastic model the parameters α and σ vary over time and the coefficient $(\alpha + 1 - \sigma)$ is different at each time step. Thus the linearization for the stochastic model is

$$I(n) = \big(\alpha(n) + 1 - \sigma(n)\big) \cdots \big(\alpha(1) + 1 - \sigma(1)\big) I(0) \tag{3.3}$$

where $\alpha(i)$ and $\sigma(i)$ are the values of the parameters α and σ at time i. The parameters α and σ are assumed to be i.i.d. and have finite mean since $0 \leq \alpha, \sigma \leq 1$. This means that if we consider a new parameter $l_i = \alpha(i) + 1 - \sigma(i)$, the l_i are i.i.d. and also have finite mean. To show there is disease persistence in the model we need to know the probability that $\lim_{t\to\infty} I(t)$ greater

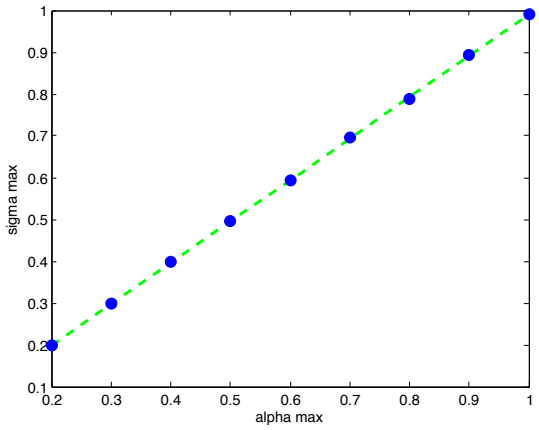


Figure 3.4: Linear regression of approximation relationship between the α max and σ max. This line represents the dividing line between epidemic and disease free parameter sets with Poisson parameters. The regression is $\sigma = 0.9874\alpha + 0.0022$ with $r^2 = 0.9999$.

than zero. In our model since the population is constant we first consider the probability

$$Pr\{A \leq I(n) \leq B\} \tag{3.4}$$

where $0 < A, B < N$ and N is the total population. Since the natural logarithm is a monotone function we can say

$$Pr\{A \leq I(n) \leq B\} = Pr\{\ln(A) \leq \ln(I(n)) \leq \ln(B)\} \text{ [12].} \tag{3.5}$$

For our model

$$\ln(I(n)) = \ln\Big[\Big(\big(\alpha(n) + 1 - \sigma(n)\big) \cdots \big(\alpha(1) + 1 - \sigma(1)\big)\Big) I(0)\Big] \tag{3.6}$$

which can be simplified to

$$\ln(I(n)) = \sum_{i=1}^{n} \ln\Big(\big(\alpha(i) + 1 - \sigma(i)\big)\Big) + \ln\big(I(0)\big) = \sum_{i=1}^{n} \ln(l_i) + \ln\big(I(0)\big). \tag{3.7}$$

We substitute this into (3.5) and simplify to get

$$Pr\{A \leq I(n) \leq B\} = Pr\left\{\ln\left(\frac{A}{I(0)}\right) \leq \sum_{i=1}^{n} \ln(l_i) \leq \ln\left(\frac{B}{I(0)}\right)\right\} \text{ [12].} \tag{3.8}$$

We can take the time average of the right hand side of (3.8) to get

$$Pr\{A \leq I(n) \leq B\} = Pr\left\{\frac{1}{n}\ln\left(\frac{A}{I(0)}\right) \leq \hat{\ln}(l_i) \leq \frac{1}{n}\ln\left(\frac{B}{I(0)}\right)\right\} \tag{3.9}$$

where $\hat{\ln}(l_i)$ is the arithmetic mean of $\ln(l_i)$ over n time steps[12]. Since we have already established the l_i are i.i.d. and have finite mean then $\ln(l_i)$ has mean $\mu_{\ln(l_i)}$ and variance $\rho_{\ln(l_i)}$ the Central Limit Theorem tells us that $\hat{\ln}(l_i)$ over large samples is normally distributed with mean $\mu_{\ln(l_i)}$ and variance $\rho_{\ln(l_i)}$[12]. Lewontin and Cohen[12] define the values

$$\tau_1 = \frac{\frac{1}{n}\ln\left(\frac{A}{I(0)}\right) - \mu_{\ln(l_i)}}{\rho_{\ln(l_i)}/\sqrt{n}}, \quad \tau_2 = \frac{\frac{1}{n}\ln\left(\frac{B}{I(0)}\right) - \mu_{\ln(l_i)}}{\rho_{\ln(l_i)}/\sqrt{n}}, \tag{3.10}$$

so that

$$Pr\{A \leq I(t) \leq B\} \approx Pr\{\tau_1 \leq \tau \leq \tau_2\}. \tag{3.11}$$

The way τ_1 and τ_2 are defined $Pr\{\tau_1 \leq \tau \leq \tau_2\}$ is the standardized normal integral between τ_1 and τ_2 [12]. When $\mu_{\ln(l_i)}$ is less than zero the value τ_1 is positive and grows towards infinity.

As τ_1 grows the normal integral between τ_1 and τ_2 shrinks and approaches zero. This means if $\mu_{\ln(l_i)}$ is less than zero the model approaches a disease free equilibrium. If $\mu_{\ln(l_i)}$ is greater than zero the disease persists over time with in the population[12]. We use these results by Lewontin and Cohen[12] to build a stochastic threshold parameter for our model.

We define this new threshold as

$$\mathcal{R}_0^s = \mathrm{E}(ln(\alpha + 1 - \sigma)). \tag{3.12}$$

If $\mathcal{R}_0^s$ is less than zero we expect our stochastic SIS model to approach a disease free equilibrium If $\mathcal{R}_0^s$ is greater than zero we expect the disease to persist over time. This type of threshold parameter has been employed previously in work on populations models but has yet to find prominence in the application to disease models [9, 7, 12, 13]. This new threshold parameter allows us see a clearer picture of the behavior of the stochastic model over time.

Table 3.5 demonstrates the improvement over the deterministic threshold $\mathcal{R}_0^d$ by using the new stochastic threshold parameter $\mathcal{R}_0^s$. One important example given in table 3.5 is when $\alpha \in [0, .8]$ and $\sigma \in [0, .71224]$. In this example $\mathcal{R}_0^d$ is greater than one which tells us that the disease may remain in the population. The numerical simulation in table 3.5 show the model goes to what we consider a disease free state. In table 3.5 we see that $\mathcal{R}_0^s$ is less than zero which agrees with what we see numerically. Using this new threshold parameter we can more accurately predict the behavior of our stochastic model.

Table 3.5: Stochastic epidemic model infected class mean of 1000 trails after 1000, 10000 and 100000 time steps with uniform parameters from various intervals. The deterministic $\mathcal{R}_0^d$ and stochastic threshold $\mathcal{R}_0^s$ are given.

α	σ	t=1,000	t=10,000	t=100,000	$\mathcal{R}_0^d$	$\mathcal{R}_0^s$
$[0, .5]$	$[0, .5]$	$2.3919 \cdot 10^{-4}$	$1.6118 \cdot 10^{-71}$	$4.9407 \cdot 10^{-324}$	1	-0.00549
$[0, .2]$	$[0, .213]$	0.0051	$4.3004 \cdot 10^{-34}$	$5.6389 \cdot 10^{-83}$	0.9389	-0.01016
$[0, .2]$	$[0, .1813]$	6.4936	6.4995	6.5383	1.1031	0.00635
$[0, .3]$	$[0, .2717]$	5.1390	5.0421	5.3456	1.6547	0.00731
$[0, .4]$	$[0, .3739]$	1.3223	0.4341	0.2723	1.0698	0.00042
$[0, .8]$	$[0, .71224]$	0.4525	0.0059	$9.2660 \cdot 10^{-54}$	1.1232	-0.01338
$[0, .2]$	$[0, .199]$	0.4147	$3.2471 \cdot 10^{-5}$	$1.9081 \cdot 10^{-35}$	1.00502	-0.00284

Chapter 4

Multi-Stage stochastic epidemic model

4.1 Overview

To further expand this model we now incorporate our stochastic parameters into the multi-stage model (2.1). In this model each parameter α_i and σ_i for, $i = 1, \ldots, n$, is i.i.d. and follow a uniform distribution. If we wish to apply our threshold parameter from chapter 3 we consider the linearization (2.2). In the one stage model the form of the $\mathbf{I}(t)$ coefficient allowed us to simplify (3.1) to (3.2). In the multistage $SI_1 \cdots I_n S$ model linearization (2.2) the $\mathbf{I}(t)$ coefficient is

$$L = \begin{pmatrix} \alpha_1 + 1 - \sigma_1 & \alpha_2 & \cdots & \cdots & \alpha_n \\ \sigma_1 & 1 - \sigma_2 & 0 & \cdots & 0 \\ 0 & \sigma_2 & 1 - \sigma_3 & 0 & \cdots \\ \vdots & \vdots & \ddots & \ddots & \vdots \\ 0 & 0 & \cdots & \sigma_{n-1} & 1 - \sigma_n \end{pmatrix}. \tag{4.1}$$

This raises several questions. If we approach building a new threshold parameter in the same way we have

$$\mathcal{R}_0^s = \mathrm{E}(\ln(L_n \cdots L_1)). \tag{4.2}$$

This would result in a matrix valued threshold parameter. This does not provide us the information we desire so we have to adapt the threshold parameter to the multi-stage model. We would like to adapt the threshold parameter in a way that preserves the integrity of the our threshold parameter for the single stage model (3.12).

We begin by considering a simplified example to demonstrate the same behavior from one

stage models carries over into multi-stage models. Here we consider the two stage SI_1I_2S model

$$\begin{aligned} S(t+1) &= \left(1 - \frac{\alpha_1 I_1(t)}{N} - \frac{\alpha_2 I_2(t)}{N}\right) S(t) + \sigma_2 I_2(t) \\ I_1(t+1) &= \left(\frac{\alpha_1 I_1(t)}{N} + \frac{\alpha_2 I_2(t)}{N}\right) S(t) + (1-\sigma_1) I_1(t) \\ I_2(t+1) &= \sigma_1 I_1(t) + (1-\sigma_2) I_2(t). \end{aligned} \tag{4.3}$$

The linearization of the two stage SI_1I_2S model is

$$\mathbf{I}(t+1) = \begin{pmatrix} \alpha_1 + 1 - \sigma_1 & \alpha_2 \\ \sigma_1 & 1 - \sigma_2 \end{pmatrix} \mathbf{I}(t). \tag{4.4}$$

The deterministic threshold parameter $\mathcal{R}_0 = \rho(K_d)$ for (4.3) is

$$\mathcal{R}_0^d = \frac{\alpha_1}{\sigma_1} + \frac{\alpha_2}{\sigma_2}. \tag{4.5}$$

For the two stage model the matrix L is

$$L = \begin{pmatrix} \alpha_1 + 1 - \sigma_1 & \alpha_2 \\ \sigma_1 & 1 - \sigma_2 \end{pmatrix}. \tag{4.6}$$

Unlike before the linearization does not simplify nicely. Because we are now dealing with matrices it is important to realize that at each time step the entries within matrix L change and as a result L_i may not commute with L_{i+1} for any i. We can write our model as

$$\mathbf{I}(n) = L_n L_{n-1} \cdots L_1 \mathbf{I}(0) \tag{4.7}$$

where L_i is the matrix (4.6) at time i. Where we were previously able to simplify the natural logarithm we can not because the matrices do not commute and $\ln(AB) = \ln(A) + \ln(B)$ only if the matrices A and B commute.

4.2 Numerical simulations

To begin our analysis of muti-stage models we look at numerical simulations of the SI_1I_2S model (4.3). In the two stage model we have four parameters α_1, α_2, σ_1 and σ_2 which vary over time. The four parameters each follow a uniform distribution over some interval. Let α_1 and α_2 be chosen from the same interval and σ_1 and σ_2 from the same interval. We create a program in MATLAB to run 1,000 trials of our SI_1I_2S model and calculate the mean for the I_1 and I_2 class at certain time steps. Refer to appendix A.3. Table 4.1 shows the results for different

interval choices and also provides the deterministic threshold calculated using the parameter means.

As we would expect the our stochastic model may go to a disease free equilibrium when the deterministic threshold based on parameter means is greater than one. An interesting observation we can make from these numerical examples is that when $\sigma_{\max}$ approaches twice $\alpha_{\max}$ we have a deterministic threshold greater one but in practice the model goes to a disease free equilibrium. The deterministic threshold (4.5) simplifies to

$$\mathcal{R}_0^d = 2\frac{\mu(\alpha_1)}{\mu(\sigma_1)} \tag{4.8}$$

Table 4.1: Numerical examples of a stochastic SI_1I_2S model where α_1 is uniform over the same interval as α_2. Similarly the parameter σ_1 is uniform over the same interval as σ_2. The table contains the two infected class means of 1000 trails after 1000, 10000 and 100000 time steps with initial conditions $S(0) = 99$, $I_1(0) = 1$, and $I_2(0) = 1$. The deterministic $\mathcal{R}_0^d$ is calculated using the means value of each parameter.

α_1, α_2	σ_1,σ_2	t=1,000	t=10,000	t=100,000	$\mathcal{R}_0^d$
$[0, 0.2]$	$[0, 0.35]$	5.2626	5.2272	5.3399	1.14286
$[0, 0.2]$	$[0, 0.39]$	0.1602	$0.4413 \cdot 10^{-5}$	$0.5925 \cdot 10^{-92}$	1.02564
$[0, 0.3]$	$[0, 0.5]$	6.9422	6.9458	7.0635	1.2
$[0, 0.3]$	$[0, 0.59]$	0.1362	$1.0224 \cdot 10^{-4}$	$8.0984 \cdot 10^{-119}$	1.01695
$[0, 0.3]$	$[0, 0.6]$	0.0280	$1.2046 \cdot 10^{-12}$	$6.1544 \cdot 10^{-270}$	0.9836
$[0, 0.4]$	$[0, 0.75]$	0.9871	0.8282	0.9618	$1.0\bar{6}$
$[0, 0.4]$	$[0, 0.78]$	0.0719	$5.9337 \cdot 10^{-13}$	$1.5511 \cdot 10^{-215}$	1.0256
$[0, 0.4]$	$[0, 0.8]$	0.0015	$0.2566 \cdot 10^{-42}$	0	1

(a) I1

α_1, α_2	σ_1,σ_2	t=1,000	t=10,000	t=100,000	$\mathcal{R}_0^d$
$[0, 0.2]$	$[0, 0.35]$	5.3874	5.2678	5.2922	1.14286
$[0, 0.2]$	$[0, 0.39]$	0.1616	$0.3554 \cdot 10^{-5}$	$0.5125 \cdot 10^{-92}$	1.02564
$[0, 0.3]$	$[0, 0.5]$	6.9852	6.9737	6.9994	1.2
$[0, 0.3]$	$[0, 0.59]$	0.1386	$9.8186 \cdot 10^{-5}$	$5.8915 \cdot 10^{-119}$	1.01695
$[0, 0.3]$	$[0, 0.6]$	0.0250	$1.7066 \cdot 10^{-12}$	$2.6788 \cdot 10^{-270}$	0.9836
$[0, 0.4]$	$[0, 0.75]$	0.9576	0.7957	0.8449	$1.0\bar{6}$
$[0, 0.4]$	$[0, 0.78]$	0.0777	$1.2560 \cdot 10^{-12}$	$9.3813 \cdot 10^{-216}$	1.0256
$[0, 0.4]$	$[0, 0.8]$	0.0013	$0.2468 \cdot 10^{-42}$	0	1

(b) I2

since α_1 and α_2 are over the same interval they have the same mean, $\mu(\alpha_1)$. The same can be said of the parameters σ_1 and σ_2. Thus for the deterministic threshold $\mathcal{R}_0^d$ to equal one $\mu(\sigma_1)$ must be greater than or equal to twice $\mu(\alpha_1)$. Since we expect to see disease extinction when the deterministic threshold is greater one is is not surprising to see the shift happen when $\sigma_{\max}$ close to twice $\alpha_{\max}$.

For our next set of numerical simulations we assign an interval to each parameter and observe the behavior of each infected class over time. These simulations are shown in table 4.2. We see that more most of our simulations the deterministic threshold $\mathcal{R}_0^d$ is a good indicator of the model behavior. The simulations of interest in table 4.2 are the last three simulations. In these simulations the parameters α_1, σ_1 and σ_2 are uniform over the same interval for all three trials. The σ_1 interval is the only change between simulations. Looking at these three simulations we see the deterministic threshold $\mathcal{R}_0^d$ decrease and the behavior of the model switch from disease persistence to disease extinction. When $\sigma_1 \in [0, 0.55]$ the deterministic threshold is greater than one but the model goes to a disease free state.

4.3 Commuting matrices

To simplify our analysis we now consider the rare case where the matrices L_i do commute. Commuting matrices provide a simple example since (4.2) can now be simplified to,

$$\mathcal{R}_0^s = \mathrm{E}\left(\sum_{i=1}^{n} \ln(L_i)\right). \tag{4.9}$$

If we follow the same basic argument and take the time average we can express the threshold parameter more simply as

$$\mathcal{R}_0^s = \mathrm{E}\big(\ln(L)\big). \tag{4.10}$$

This $\mathcal{R}_0^s$ is matrix valued and does not provide the information we want for the model. To cope with this issue we observe the eigenvalues for the matrices.

First we must find commuting matrices that satisfy the conditions on the parameters α_i and σ_i, $0 \leq \alpha_1, \alpha_2, \sigma_1, \sigma_2 \leq 1$. Choose a matrix B,

$$B = \begin{pmatrix} 0.7 & 0.2 \\ 0.8 & 0.5 \end{pmatrix} \tag{4.11}$$

where $\alpha_1 = 0.5$, $\alpha_2 = 0.2$, $\sigma_1 = 0.8$ and $\sigma_2 = 0.5$. If we consider this matrix in the deterministic model $\mathcal{R}_0^d = 1.025$ which means the disease is endemic. Fixing this matrix we find matrices with valid entries which commute with B.

The first commuting matrix we chose is

$$A_1 = \begin{pmatrix} 0.3 & 0.2 \\ 0.8 & 0.1 \end{pmatrix} \tag{4.12}$$

where $\alpha_1 = 0.1$, $\alpha_2 = 0.2$, $\sigma_1 = 0.8$ and $\sigma_2 = 0.9$. If we consider this matrix in the deterministic model $\mathcal{R}_0^d = 0.34722$ and the disease is eradicated. We now have two commuting matrices with different deterministic $\mathcal{R}_0^d$ values. The product of these two matrices

$$BA_1 = \begin{pmatrix} 0.37 & 0.16 \\ 0.64 & 0.21 \end{pmatrix} \tag{4.13}$$

has a deterministic $\mathcal{R}_0^d = 0.2181566$.

We use these two matrices to generate a simple stochastic SI_2I_2S model by randomly

Table 4.2: Numerical examples of a stochastic SI_1I_2S model. Parameters α_1, α_2, σ_1 and σ_2 are uniform over the interval given. The table contains the two infected class means of 1000 trails after 1000, 10000 and 100000 time steps with initial conditions $S(0) = 99$, $I_1(0) = 1$, and $I_2(0) = 1$. The deterministic $\mathcal{R}_0^d$ is calculated using the means value of each parameter.

α_1	α_2	σ_1	σ_2	t=1,000	t=10,000	t=100,000	$\mathcal{R}_0^d$
$[0.2, 0.3]$	$[0.3, 0.4]$	$[0, 0.2]$	$[0, 0.2]$	41.6579	41.5514	41.5605	6
$[0, 0.2]$	$[0, 0.2]$	$[0.6, 0.8]$	$[0, 0.5]$	$0.1150 \cdot 10^{-49}$	0	0	0.54285
$[0, 0.1]$	$[0, 0.5]$	$[0, 1]$	$[0, 1]$	$5.3272 \cdot 10^{-61}$	0	0	0.6
$[0, 0.2]$	$[0.4, 0.6]$	$[0, 0.25]$	$[0, 0.8]$	38.0228	38.3215	38.1930	2.05
$[0, 0.2]$	$[0.4, 0.6]$	$[0, 0.6]$	$[0, 0.8]$	19.8131	19.8854	19.7090	$1.58\bar{3}$
$[0, 0.2]$	$[0, 0.6]$	$[0, 0.6]$	$[0, 0.8]$	1.9263	1.9943	2.0670	$1.08\bar{3}$
$[0, 0.2]$	$[0, 0.55]$	$[0, 0.6]$	$[0, 0.8]$	0.1454	$2.4367 \cdot 10^{-5}$	$2.7525 \cdot 10^{-151}$	1.02083
$[0, 0.2]$	$[0, 0.4]$	$[0, 0.6]$	$[0, 0.8]$	$8.5438 \cdot 10^{-16}$	$2.0028 \cdot 10^{-176}$	0	$0.8\bar{3}$

(a) I1

α_1	α_2	σ_1	σ_2	t=1,000	t=10,000	t=100,000	$\mathcal{R}_0^d$
$[0.2, 0.3]$	$[0.3, 0.4]$	$[0, 0.2]$	$[0, 0.2]$	41.4177	41.4582	41.4795	6
$[0, 0.2]$	$[0, 0.2]$	$[0.6, 0.8]$	$[0, 0.5]$	$0.6163 \cdot 10^{-49}$	0	0	0.54285
$[0, 0.1]$	$[0, 0.5]$	$[0, 1]$	$[0, 1]$	$6.4059 \cdot 10^{-61}$	0	0	0.6
$[0, 0.2]$	$[0.4, 0.6]$	$[0, 0.25]$	$[0, 0.8]$	12.1596	11.6508	11.8227	2.05
$[0, 0.2]$	$[0.4, 0.6]$	$[0, 0.6]$	$[0, 0.8]$	14.7394	14.8360	15.1986	$1.58\bar{3}$
$[0, 0.2]$	$[0, 0.6]$	$[0, 0.6]$	$[0, 0.8]$	1.4257	1.5367	1.5173	$1.08\bar{3}$
$[0, 0.2]$	$[0, 0.55]$	$[0, 0.6]$	$[0, 0.8]$	0.1028	$4.7676 \cdot 10^{-5}$	$2.8302 \cdot 10^{-151}$	1.02083
$[0, 0.2]$	$[0, 0.4]$	$[0, 0.6]$	$[0, 0.8]$	$8.9781 \cdot 10^{-16}$	$2.4334 \cdot 10^{-176}$	0	$0.8\bar{3}$

(b) I2

choosing which of the two matrices to apply at each time step. Each of the two matrices has equal probability, $\frac{1}{2}$, of being applying at any time step. Figure 4.1a shows two sample runs of the model (4.3) with the commuting matrices A_1 and B. In the case of these choices for commuting matrices the model goes disease free.

We can calculate the expected value for the matrix L at each time step. In this case there are only two possibilities each of equal probability, $\frac{1}{2}$, i.e. at each time step $L = B$ or $L = A_1$.

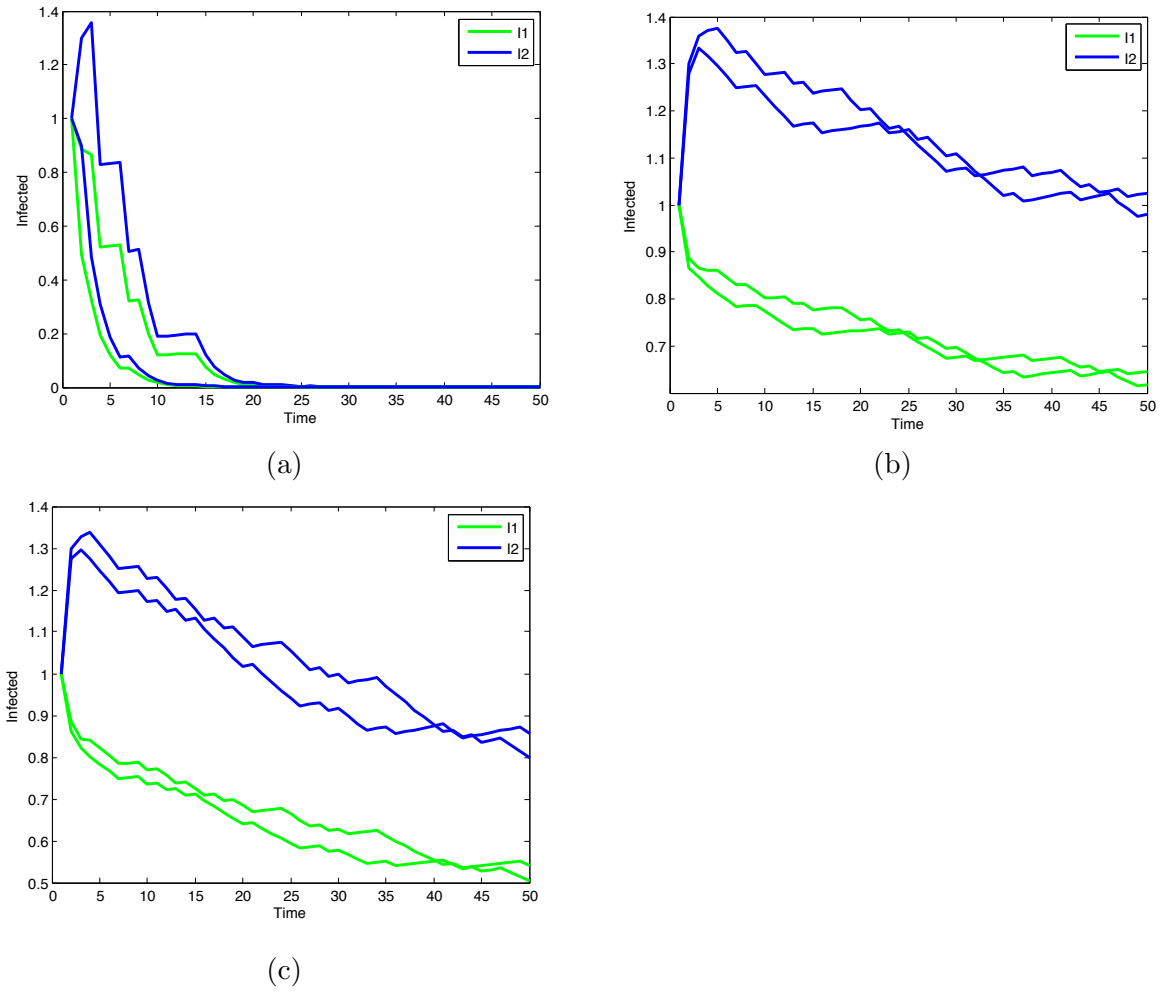


Figure 4.1: Initial conditions $S(0) = 99$, $I_1(0) = 1$, $I_2(0) = 1$. Two sample paths of a stochastic SI_1I_2S epidemic model 50 time steps. With commuting matrices B and (a)A_1, (b) A_2, and (c) A_3.

Table 4.3: Comparison of the deterministic threshold $\mathcal{R}_0^d$ and eigenvalues for matrix B and our choices for a commuting matrix; A_1, A_2, A_3.

Matrix	ρ	$\mathcal{R}_0^d$
B	1.01231	1.025
A_1	0.612311	0.34722
BA_1	0.619848	0.2181566
$\frac{1}{2}(B+A_1)$	0.812311	0.66071
A_2	0.992311	0.98461
BA_2	1.00453	1.0077
$\frac{1}{2}(B+A_2)$	1.00231	1.0046
A_3	0.987811	0.97569
BA_3	0.999971	0.99995
$\frac{1}{2}(B+A_3)$	1.00006	1.001219

The expectation matrix is $\mathrm{E}(L) = \frac{1}{2}(A_1 + B)$,

$$\mathrm{E}(L) = \begin{pmatrix} 0.5 & 0.2 \\ 0.8 & 0.3 \end{pmatrix}. \tag{4.14}$$

If we consider this matrix for a deterministic model the parameters are $\alpha_1 = 0.3$, $\alpha_2 = 0.2$, $\sigma_1 = 0.8$ and $\sigma_2 = 0.7$ with $\mathcal{R}_0 = 0.6671$.

To investigate the threshold parameter we calculate the eigenvalues for the matrices B, A_1, BA_1, and $\mathrm{E}(L)$. We see in table 4.3 for B the deterministic threshold $\mathcal{R}_0^d$ is greater than one and the spectral radius $\rho(B) = 1.01231$ is greater than one. Similarly we see for matrices A_1 and BA_1, $\mathcal{R}_0^d$ is less than one and the spectral radius for these matrices is also less than one. For this example the behavior of the stochastic model aligns with the deterministic threshold for the product matrix BA_1 and the deterministic threshold for the expectation matrix.

Consider a different commuting matrix

$$A_2 = \begin{pmatrix} 0.68 & 0.2 \\ 0.8 & 0.48 \end{pmatrix} \tag{4.15}$$

where $\alpha_1 = 0.48$, $\alpha_2 = 0.2$, $\sigma_1 = 0.8$ and $\sigma_2 = 0.52$. The deterministic model for A_2 is disease free with $\mathcal{R}_0^d = 0.9846$ less than one. Again the commuting matrices B and A_2 have different

deterministic behavior. Their product

$$BA_2 = \begin{pmatrix} 0.636 & 0.236 \\ 0.944 & 0.4 \end{pmatrix} \tag{4.16}$$

$\mathcal{R}_0^d = 1.0077$ so the disease is endemic. With this choice of commuting matrices we have two matrices with different deterministic behavior whose product results in a model with endemic behavior. The previous choice for a commuting matrix also had different deterministic behavior than B but the product resulted in a disease free model. This shows that it is possible to mix matrices with different deterministic behavior and get either a disease free or epidemic result.

We can calculate the expected value for the matrix L at each time step. In this case there are only two possibilities each of equal probability, $\frac{1}{2}$, i.e. at each time step $L = B$ or $L = A_2$. The expectation matrix is $\mathrm{E}(L) = \frac{1}{2}(A_2 + B)$,

$$\mathrm{E}(L) = \begin{pmatrix} 0.69 & 0.2 \\ 0.8 & 0.49 \end{pmatrix}. \tag{4.17}$$

If we consider this matrix for a deterministic model the parameters are $\alpha_1 = 0.49$, $\alpha_2 = 0.2$, $\sigma_1 = 0.8$ and $\sigma_2 = 0.51$ with $\mathcal{R}_0 = 1.00231$.

Figure 4.1b shows two trial runs of (4.3) with commuting matrices A_2 and B. In this case it is harder to see the behavior of the stochastic model. To investigate the long term behavior of the model we run a larger number trials over large time steps to determine the expected behavior. In figure 4.2 the mean value of I_1 over 1,000 trials is 0.1763 at 100,000 time steps. After $300,000$ times steps the mean value of I_1 is 0.1752. The difference between the mean at 100,000 times steps and 300,000 times steps is small enough that we say there is an epidemic. We observe a similar variation in the I_2 mean at 100,000 and 300,000. The spectral radius for A_2, $\rho(A_2) = 0.98461$ is less than one and for the product matrix BA_2, $\rho(BA_2) = 1.00453$ is greater than one and agrees with the deterministic threshold for A_2 and BA_2 as we see in table 4.3. The deterministic threshold for the expectation matrix is also greater than one.

The previous two examples give the false impression that the stochastic threshold parameter is equivalent to the deterministic threshold parameter of the expectation matrix or the deterministic threshold of the product matrix. To show this does not hold for all commuting matrices consider the matrix

$$A_3 = \begin{pmatrix} 0.6755 & 0.2 \\ 0.8 & 0.4755 \end{pmatrix} \tag{4.18}$$

where $\alpha_1 = 0.4755$, $\alpha_2 = 0.2$, $\sigma_1 = 0.8$ and $\sigma_2 = 0.5245$. The deterministic model for A_3 goes to a disease free equilibrium with $\mathcal{R}_0 = 0.97569$. As with the previous examples the two commuting matrices B and A_3 have different deterministic behavior. Figure 4.1c shows two

trial runs of (4.3) with commuting matrices B and A_3. After 50 time steps the behavior of the stochastic model is unclear. In figure 4.3 we observe I_1 and I_2 after 100,000 and 300,000 time steps and 1,000 trials. After 100,000 and 300,000 time steps there is a noticeable shift in the I_2 mean from 0.0016 to $4.8823 \cdot 10^{-4}$. After 300,000 times steps the infected class means are small enough we say the disease has been effectively eradicated and the model goes to a disease free state.

The product matrix for B and A_3

$$BA_3 = \begin{pmatrix} 0.63285 & 0.2351 \\ 0.9404 & 0.39775 \end{pmatrix} \tag{4.19}$$

where $\alpha_1 = 0.57325$, $\alpha_2 = 0.2351$, $\sigma_1 = 0.9404$ and $\sigma_2 = 0.60225$ with deterministic $\mathcal{R}_0 = 0.99995$.

We can calculate the expected value for the matrix L at each time step. In this case there are only two possibilities each of equal probability, $\frac{1}{2}$, i.e. at each time step $L = B$ or $L = A_3$. The expectation matrix is $\mathrm{E}(L) = \frac{1}{2}(A_3 + B)$,

$$\mathrm{E}(L) = \begin{pmatrix} 0.68775 & 0.2 \\ 0.8 & 0.48775 \end{pmatrix}. \tag{4.20}$$

If we consider this matrix for a deterministic model the parameters are $\alpha_1 = 0.48775$, $\alpha_2 = 0.2$, $\sigma_1 = 0.8$ and $\sigma_2 = 0.51225$ with $\mathcal{R}_0 = 1.001219$.

In this example we encounter the first disagreement between the deterministic threshold for the product matrix and the deterministic threshold for the expectation matrix. The deterministic threshold for the product matrix points to the stochastic model approaching a disease free state. The expectation matrix threshold predicts an endemic disease state for the model. In our numerical examples we observe that the model with commuting matrices A_3 and B goes to a disease free state. This tells us that the expectation matrix is not a good indicator of the behavior of the stochastic model.

In this overly simplified model it appears as though an appropriate threshold would be

$$\mathcal{R}_0^s = \mathrm{E}(\rho(AB)). \tag{4.21}$$

There are several problems with this threshold. The first issues is that when we apply this to our one stage model we would have a threshold parameter $\mathcal{R}_0 = \mathrm{E}(\alpha + 1 - \sigma)$. We know this type of parameter does not give an accurate representation of the behavior of the model based on our findings in chapter 2. This means we should not use (4.21) as our threshold parameter.

Consider the application of the method in one stage models to multi-stage that gave (4.10).

Table 4.4: Eigenvalues of natural logarithms of commuting matrix products.

Matrices	λ_1	λ_2
$\ln(BA_1)$	$-0.4782 + 7.6478 \cdot 10^{-10}i$	$-3.2267 + 3.14159i$
$\ln(BA_2)$	0.0045	-3.458608
$\ln(BA_3)$	-0.0000029	-3.4858101

In the deterministic model we utilize the spectral radius to describe the overall behavior of the model. In a similar fashion we look at the eigenvalues of the product matrix BA_i and look at the maximum eigenvalue instead of the maximum absolute value. Let λ_1 and λ_2 be the eigenvalues of the matrix L. We can rewrite (4.10) as

$$\mathcal{R}_0^s = \mathrm{E}\left(\max\{\mathrm{Real}(\lambda_1), \mathrm{Real}(\lambda_2)\}\right). \tag{4.22}$$

where $\mathrm{Real}(\lambda_i)$ is the real part of λ_i. Table 4.4 shows the results for this threshold parameter with our three choices of commuting matrices. We see based on the table that when the real part of the largest eigenvalue is less than zero the model goes to a disease free state and when it is greater than zero the disease persists within the population. Now that we have an idea for the two-stage model in a simplified case we investigate the reliability of the threshold in a more complex setting.

4.4 Non-commuting matrices

Consider now the case where we are not guaranteed that any of the matrices L_i commute. Our argument for the threshold parameter (4.22) now breaks down since we can no longer simplify the natural logarithm of the product $L_n \cdots L_1$. Through numerical simulations we can see that the inability to simplify the natural logarithm nullifies the usability of the threshold parameter (4.22). In the SI_1I_2S model we now choose each parameter randomly at time t based on a distribution. This changes the way we calculate the expected value. First we calculate the eigenvalues of $\ln(L)$ in the two-stage model,

$$\lambda_{1,2} = \ln\left(\frac{1}{2}\left(r + 1 - \sigma_2 \pm \sqrt{(\sigma_2 - 1 - r)^2 - 4(r - r\sigma_2 - \alpha_2\sigma_1)}\right)\right). \tag{4.23}$$

Calculating the expected value for the eigenvalues can become difficult very quickly. Here in the two-stage model we already see a large increase in computational difficultly from the one-stage model.

To simplify our calculations we consider the case where the parameters α_1, σ_1, and σ_2 are fixed and we allow only α_2 to vary over time. In table 4.5 we see the mean of the I_1 and I_2 classes as time progress in comparison to both the deterministic threshold, calculated using the parameter means, and our theoretical stochastic threshold (4.22). In this table we see that (4.22) correctly predicts the model behavior for most cases including several which have deterministic threshold greater than one but go to a disease free equilibrium. The case of interest is when $\alpha_2 \in [0, 0.85]$ where the numerical simulation shows the disease persisting in the population but $\mathcal{R}_0^s$ is less than zero. This occurs because our choice of $\mathcal{R}_0^s$ require that the matrices commute which is not true.

We see that when the deterministic threshold is close to one $\mathcal{R}_0^s$ is not reliable. The threshold $\mathcal{R}_0^s$ passes zero and changes sign earlier then it should. Since $\mathcal{R}_0^s$ is an increasing function we can conclude that it accurately predicts behavior when the deterministic threshold is less than 1. Once the deterministic threshold is greater than 1 $\mathcal{R}_0^s$ may become inaccurate. However as the deterministic threshold increases from 1 there is a higher likely hood that $\mathcal{R}_0^s$ describes the model.

While this is an interesting observation we would like to determine a stochastic threshold parameter that does not rely on the deterministic threshold and is accurate for all parameter choices. This requires more research. In special case where the determinate of the matrix is one matrix norms have been used to establish a threshold parameter Watkins[14]. The determinate for the matrix L is not one and the matrix norm approach raises more questions and requires the calculations of random Liapounov characteristics which are known to be computationally complex. More analysis is required to further understand the stochastic model and determine an accurate stochastic threshold to predict disease epidemics and eradication.

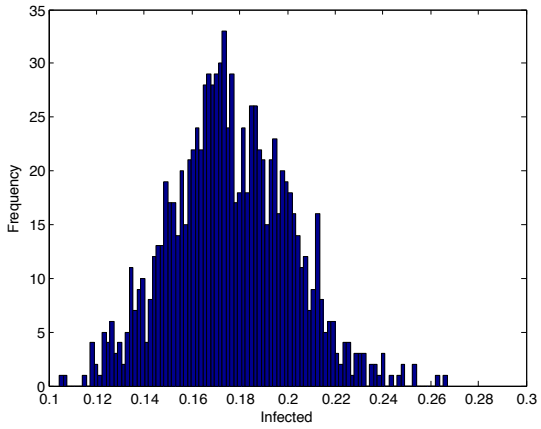
Table 4.5: Numerical examples of a stochastic SI_1I_2S model. The parameters α_1, σ_1 and σ_2 are fixed and parameter α_2 is uniform over the given interval. The table contains the two infected class means of 1000 trails after 1000, 10000 and 100000 time steps with initial conditions $S(0) = 99$, $I_1(0) = 1$, and $I_2(0) = 1$. The deterministic $\mathcal{R}_0^d$ is calculated using the means value of each parameter. $\mathcal{R}_0^s$ is the expectation of the maximum of the real part of the eigenvalues of L.

α_1	α_2	σ_1, σ_2	t=1,000	t=10,000	t=100,000	$\mathcal{R}_0^d$	$\mathcal{R}_0^s$
0 .4	$[0, 0.2]$	$\sigma_1 = .4$, $\sigma_2 = .5$	9.2080	9.1498	9.1775	1.2	0.010518
0 .4	$[0, 0.3]$	$\sigma_1 = .4$, $\sigma_2 = .5$	12.7051	12.6299	12.6808	1.3	0.02727
0 .4	$[0, 0.5]$	$\sigma_1 = .4$, $\sigma_2 = .5$	18.2603	18.2938	18.3252	1.5	0.671718
0 .4	$[0, 1]$	0.8	4.0182	4.1669	4.3129	1.125	0.01537
0 .4	$[0, 0.85]$	0.8	0.3812	0.3066	0.2653	1.03125	-0.02198
0 .4	$[0, 0.81]$	0.8	0.0062	$0.1062 \cdot 10^{-22}$	0	1.00625	-0.03056
0 .4	$[0, 0.8]$	0.8	0.0020	$0.1523 \cdot 10^{-39}$	0	1	-0.03260
0 .4	$[0, 0.6]$	0.8	$0.5248 \cdot 10^{-32}$	0	0	0.875	-0.06462
0 .4	$[0, 0.4]$	0.8	$0.2801 \cdot 10^{-71}$	0	0	0.75	-0.07662

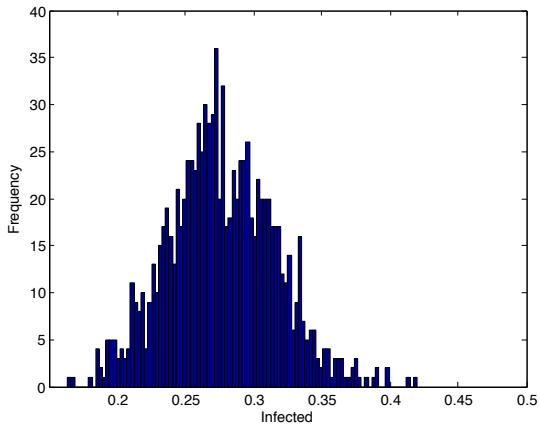
(a) I1

α_1	α_2	σ_1, σ_2	t=1,000	t=10,000	t=100,000	$\mathcal{R}_0^d$	$\mathcal{R}_0^s$
0 .4	$[0, 0.2]$	$\sigma_1 = .4$, $\sigma_2 = .5$	7.3653	7.3293	7.3444	1.2	0.010518
0 .4	$[0, 0.3]$	$\sigma_1 = .4$, $\sigma_2 = .5$	10.1958	10.1139	10.1380	1.3	0.02727
0 .4	$[0, 0.5]$	$\sigma_1 = .4$, $\sigma_2 = .5$	14.6418	14.6588	14.6361	1.5	0.671718
0 .4	$[0, 1]$	0.8	3.9519	4.1401	4.3308	1.125	0.01537
0 .4	$[0, 0.85]$	0.8	0.3922	0.3078	0.2648	1.03125	-0.02198
0 .4	$[0, 0.81]$	0.8	0.0060	$0.0851 \cdot 10^{-22}$	0	1.00625	-0.03056
0 .4	$[0, 0.8]$	0.8	0.0020	$0.1339 \cdot 10^{-39}$	0	1	-0.03260
0 .4	$[0, 0.6]$	0.8	$0.6083 \cdot 10^{-32}$	0	0	0.875	-0.06462
0 .4	$[0, 0.4]$	0.8	$0.3726 \cdot 10^{-71}$	0	0	0.75	-0.07662

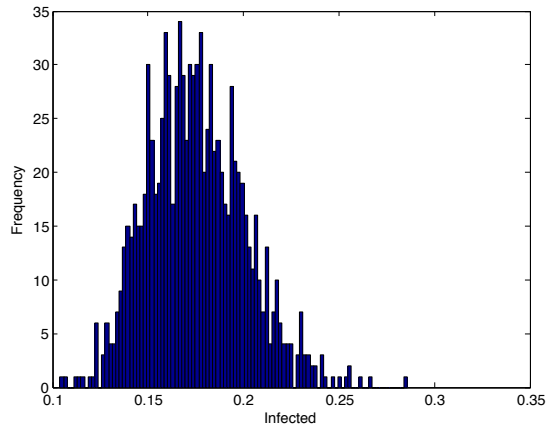
(b) I2



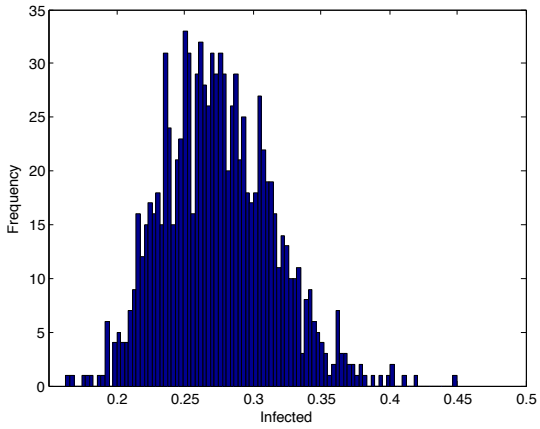
(a) I1



(b) I2

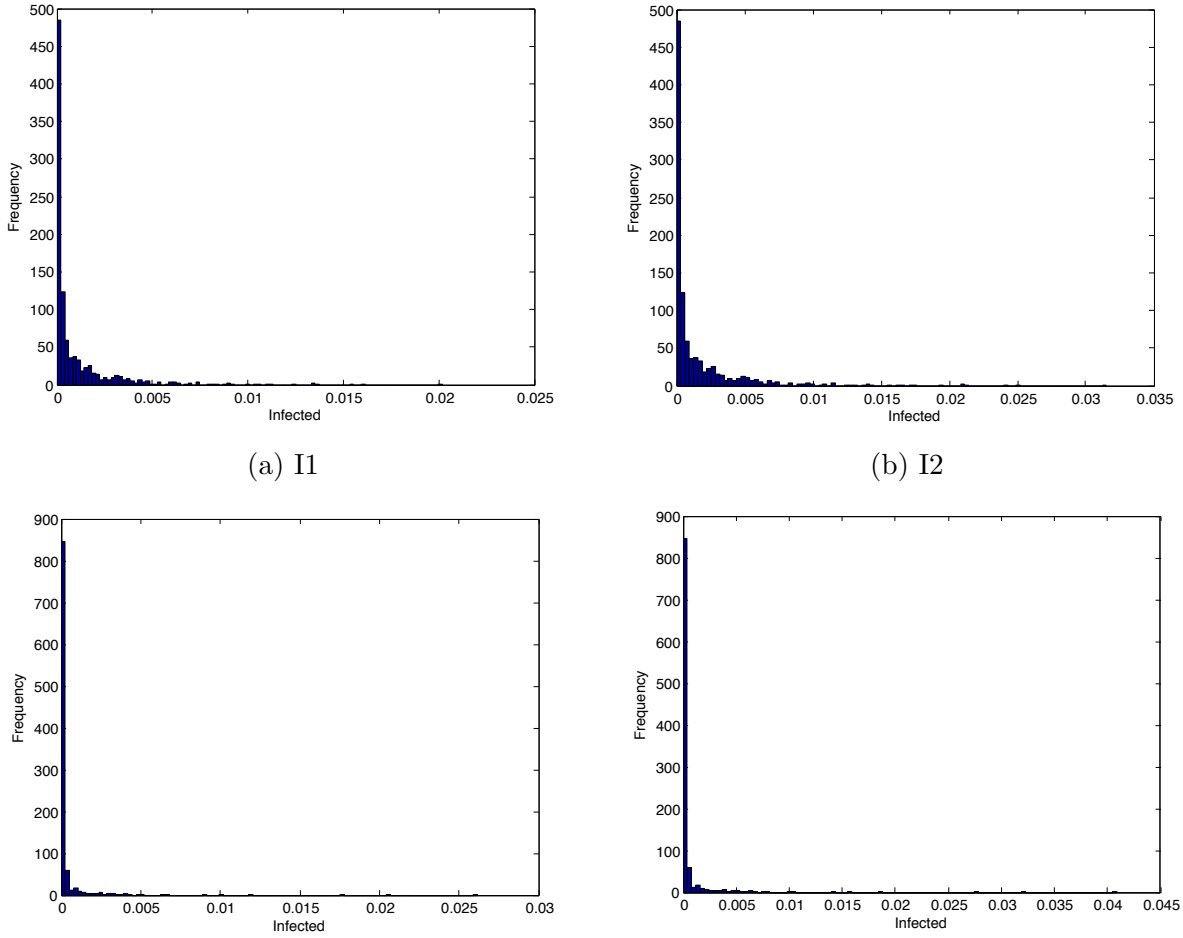


(c) I1



(d) I2

Figure 4.2: Histogram of infected class means of 1,000 trial runs after 100,000 (a) and (b) and 300,000 (c) and (d) of the SI_1I_2S model with commuting matrices B and A_2. After 100,000 times steps and 1,000 trials the mean $\mu(I1) = 0.1763$ and $\mu(I2) = 0.2766$. At 300,000 times steps the means are $\mu(I1) = 0.1752$ and $\mu(I2) = 0.2748$. Initial conditions $S(0) = 99$, $I_1(0) = 1$, $I_2(0) = 1$.



(a) I1

(b) I2

(c) I1

(d) I2

Figure 4.3: Histogram of infected class means of 1,000 trial runs after 100,000 (a) and (b) and 300,000 (c) and (d) of the SI_1I_2S model with commuting matrices B and A_3. After 100,000 times steps and 1,000 trials the mean $\mu(I1) = 9.9738 \cdot 10^{-4}$ and $\mu(I2) = 0.0016$. At 300,000 times steps the means are $\mu(I1) = 3.1260 \cdot 10^{-4}$ and $\mu(I2) = 4.8823 \cdot 10^{-4}$. Initial conditions $S(0) = 99$, $I_1(0) = 1$, $I_2(0) = 1$.

Chapter 5

Conclusion

Stochastic epidemic models are important in providing a more realistic model of disease spread in populations. The infection rate and recovery rate in practice are not constant and change over time as a result of many factors. The environment is in a constant state of change and effects a population's ability to fight an infectious disease. To account for variation in infection rate and recovery rate over time we add stochasticity into our epidemic model. There are several approaches to introduce stochasticity into epidemic models. We have chosen to introduce stochasticity by allowing the individual parameters which govern infection rate and recovery rate to vary over time according to a distribution. We can limit the interval over which the parameter varies. This means given data we can determine an approximate range and distribution for each parameter and build a model.

We aimed to determine a threshold parameter for this stochastic model. In the one-stage SIS model we were successful. The stochastic threshold $\mathcal{R}_0^s = \mathrm{E}\big(\ln(\alpha + 1 - \sigma)\big)$ determines the expected behavior of the stochastic model. If $\mathcal{R}_0^s$ is less than zero the disease is eradicated and the population reaches a disease free equilibrium. If $\mathcal{R}_0^s$ greater than zero then the disease persists in the population. The parameter was derived from a similar threshold for populations models.

When we try to expand this stochastic threshold parameter into multi-stage models we encounter issues with random matrices. The random matrices for our model do not commute and the stochastic threshold expanded into multi-stage models breaks down. It is possible that the expansion of our one-stage threshold parameter breaks down at the start and we have approach the multi-stage model in a entirely different way. More research into a stochastic threshold for these models is required.

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APPENDIX

Appendix A

Programs

A.1 SIS Uniform

```
t =  50;
trials = 2;

alpha = [0 0.4];
sigma = [0 0.9];

for n = 1:trials
    W = RandStream('mt19937ar','Seed','shuffle');
    RandStream.setGlobalStream(W);

    alpha = alpha(1)+(alpha(2)-alpha(1)).*rand(W,t,1);
    sigma = sigma(1)+(sigma(2)-sigma(1)).*rand(t,1);

    N= 100;
    I = 1;
    S = N-I;
    PredI(1) = I;

    for i =2:t
        Snew = (1-Ich(i)*I/N)*S  + sigma*I;
        Inew = (Ich(i)*I/N)*S + (1-sigma)*I;
        S = Snew;
        I = Inew;
```

```
        PredI(i) = I;
    end

    figure(1)
    plot(1:1:t, PredI,'r--','LineWidth',2)
    hold on
    xlabel('Time')
    ylabel('Infected')

end

%Deterministic Model
I = 1;
S = N-I;
DetI(1)=I;

alpha = (alpha(2)-alpha(1))/2;
sigma = (sigma(2)-sigma(1))/2;

for i =2:t
    Snew = (1-alpha*I/N)*S  + sigma*I;
    Inew = (alpha*I/N)*S + (1-sigma)*I;
    S = Snew;
    I = Inew;
DetI(i) = I;
end

plot(1:1:t,DetI,'LineWidth',2)
hold off
```

A.2 Regression

A.2.1 Endpoint search

```
%seed [S0 I0]
s = [50 50];
```

```
%time
N1 = 100000;
N2 = 300000;
%trials
R = 1000;

%alpha
a = 0.5;
b= 0.2;
%sigma
c = 0.5;
cprime =0.5;

for b=0.5:0.1:1
    b
    d=1;
    i = 1;
    clearvars endpoints
while 3<4
    SIS = histmean(s,N1,N2,R,a,b,c,d);
    endpoints(i,:) = [d, SIS(1), SIS(2)];
    i = i+1;
    if min(SIS)<= 0.00001
        dnew = (cprime+d)/2;
        dfe = 0;
        if abs(dnew - d) <= 0.001
           break
        end
        d = dnew;
    else
        cprime=d;
        dnew = (d+b)/2;
        endemic = 1;
        if abs(d-dnew) <= 0.001
            break
        end
        d = dnew;
```

```
    end
end
endpoints
end
```

A.2.2 histmean function

```
function[Means] = histmean(s,N1,N2,R,a,b,c,d)
close all;

matlabpool 2
%s is the seed (input an ordered pair [S(0) I(0)])
%N = number of iterations
%R = number of trials, or realizations
B=zeros(1,R);
C=zeros(1,R);
A=zeros(N2,R);


parfor r=1:R
    W = RandStream('mt19937ar','Seed','shuffle');
    RandStream.setGlobalStream(W);

    S0=s(1);
    I0=s(2);
    alpha=a+(b-a).*rand(W,N2,1);
    A(:,r)=alpha;
    sigma=c+(d-c).*rand(N2,1);
    for ic=1:N2
    S1=(1-alpha(ic).*I0./sum(s)).*S0+sigma(ic).*I0; %loop function, generates orbits
    I1=alpha(ic).*I0./sum(s).*S0+(1-sigma(ic)).*I0;
    S0=S1;
    I0=I1;
    if ic == N1
        B(r) = I1;
    end
    end
```

```
    C(r)=I1;
    if mod(r,50)==0
        r
    end
end

M1 = mean(B);
M2 = mean(C);
Means = [M1 M2];

matlabpool close
end
```

A.3 SI_1I_2S Uniform

```
t =  70
trails = 2;

%alpha intervals
a1 = 0;
b1 = .2;
a2 =0;
b2= .4;
% sigma intervals
c1 = 0;
d1 = 0.8;
c2 =0;
d2 =0.85;

for j = 1:n
    W = RandStream('mt19937ar','Seed','shuffle');
    RandStream.setGlobalStream(W);

    N= 100;
    I1 = 1;
    I2 =1;
```

```
    S = N-I1-I2;
    yInit = [N-I1 I1 I2]; %initial size of each group [S I1 I2]
    PredY(:,1)=yInit;

    alpha1 = a1+(b1-a1)*rand(W,t,1);
    alpha2 = a2+(b2-a2)*rand(W,t,1);
    sigma1 = c1+(d1-c1)*rand(t,1);
    sigma2 = c2+(d2-c2)*rand(t,1);

    for i =2:t
        Snew = (1-(alpha1(i)*I1/N+alpha2(i)*I2/N))*S + sigma2(i)*I2;
        I1new = (alpha1(i)*I1/N+alpha2(i)*I2/N)*S + (1-sigma1(i))*I1;
        I2new = sigma1(i)*I1 + (1-sigma2(i))*I2;
        S = Snew;
        I1 = I1new;
        I2 = I2new;
        PredY(:,i) =[S I1 I2];
    end

    PredS = PredY(1,:);
    PredI1 = PredY(2,:);
    PredI2 = PredY(3,:);

    figure(k)
         plot(1:t, PredI1, 'g--','LineWidth',2)
         hold on
         plot(1:t, PredI2, 'b--','LineWidth',2)
         hold on
         xlim([1 t])
         xlabel('Time')
         ylabel('Number of Infected')
         legend('I1','I2')

end

%Deterministic Model
N= 100;
```

```
I1 = 1;
I2 = 1;
S = N-I1-I2;
Det(:,1) = [N-I1 I1 I2];

for i =2:t
    Snew = (1-((b1+a1)/2*I1/N+(b2+a2)/2*I2/N))*S +(d2+c2)/2*I2;
    I1new = ((b1+a1)/2*I1/N+(b2+a2)/2*I2/N)*S + (1-(d1+c1)/2)*I1;
    I2new = (d1+c1)/2*I1 + (1-(d2+c2)/2)*I2;
    S = Snew;
    I1 = I1new;
    I2 = I2new;
    Det(:,i) =[S I1 I2];
 end

DetS = Det(1,:);
DetI1 = Det(2,:);
DetI2 = Det(3,:);

plot(1:t, DetI1, 'g','LineWidth',2)
hold on
plot(1:t, DetI2, 'b','LineWidth',2)
hold off
```

A.4 Commuting Matrices

```
t =  300000;
trials = 1000;

alpha1 = [.5 .48];
alpha2 = [.2 .2];
sigma1 = [.8 .8];
sigma2 = [.5 .52];

for n= 1:trials
N= 100;
I1 = 50;
```

```
I2 = 0;
S = N-I1-I2;
for i =1:t
        k = randi([1,2]);
        Snew = (1-(alpha1(k)*I1/N+alpha2(k)*I2/N))*S + sigma2(k)*I2;
        I1new = (alpha1(k)*I1/N+alpha2(k)*I2/N)*S + (1-sigma1(k))*I1;
        I2new = sigma1(k)*I1 + (1-sigma2(k))*I2;
        S = Snew;
        I1 = I1new;
        I2 = I2new;
end
I1trial(n) = I1;
I2trial(n) = I2;
end

I1mean = mean(I1trial)
I2mean = mean(I2trial)
```