Stochastic Models for Epidemics

Ziwei Wang (B00776666)

Supervisor: Professor Edward Susko

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Contents

1 Introduction

In epidemiology, Susceptible-Infective-Recovered (SIR) compartmental model is one of the famous epidemic models which is first proposed by Ross (1916). Individuals in the population are either in the class susceptible (S), infected (I) or recovered (R) and can transit between these compartments. Researches of the SIR model are conducted on either ordinary differential equations (deterministic model) or stochastic processes. This paper aims to provide a review of the deterministic SIR model and a brief introduction to methods for deriving stochastic epidemic models which are discrete time Markov chain (DTMC), continuous time Markov chain (CTMC) and stochastic differential equation, together with the discussion of their dynamics and comparisons among these models. In a discrete time Markov chain, both time and state are discrete. In a continuous time Markov chain, time becomes continuous but the state remains discrete. And when both time and state are continuous, it can be expressed as a stochastic differential equation.

	Discrete Time	Continuous Time
Discrete State	DTMC	CTMC
Continuous State		SDE (Stochastic Differential Equation)

The review of deterministic model will be discussed in Section 2 and the introduction of formulations for these stochastic epidemic models will be presented in Section 3, 4 and 5 respectively.

Comparing the stochastic models with the deterministic model, the stochastic models perform better in simulating realistic dynamics of the epidemic and can have different important characteristics. For deterministic epidemic model, it has the characteristic that it can converge to an endemic equilibrium which is derived from the ordinary differential equation, and the

long-term behavior depends on the basic reproduction number and birth rate which will be introduced in detail in Section 2. However, for any stochastic epidemic model, it will converge to disease-free state no matter what the value of the parameters are. And stochastic epidemic models have four realistic properties: probability of an outbreak, the final size distribution of an epidemic, quasi-stationary probability distribution and the expected duration of an epidemic. The first two properties will be discussed thoroughly in Section 6.

This paper is largely refer to "An Introduction to Stochastic Epidemic Models" in the book "Mathematical Epidemiology". (Allen 2008, 81-115)

2 Deterministic SIR Epidemic Model

2.1 Introduction of Basic Reproduction Number R_0

Before formulating the deterministic SIR Epidemic Model, an important factor which predominantly affects the dynamics of population called basic reproduction number R_0 is necessary to introduce first. According to Dietz (1993, 23), this concept was firstly proposed in demography as 'net production rate' by R.Böckh in 1886 aimed to estimate the average number of female babies produced by a woman throughout her entire life. Later in 1911, L-J. Dublin and A. Lotka firstly proposed the mathematical formula of R_0 as below:

$$R_0 = \int_0^\infty p(a)\beta(a)da \tag{1}$$

where $p(a)$ denotes the probability of a woman survive at age a and $\beta(a)$ represents the girl fertility rate of a female with age a. This concept was then introduced to the epidemiology area by G. McDonald in 1952 and then finally officially proposed the terminology as basic reproduction rate during the Dahlem Conference in 1982. By definition in epidemiology, R_0 represents the number of secondary infections directly produced by one infected case where all individuals in the population are susceptible. (Perasso, 2018).

It is crucial to know how to derive the mathematical formula of R_0 since it is a threshold for distinguishing different cases of dynamics in SIR Epidemic Model. Let κ be the number of people contacted by an infected individual per unit time, h be the rate of infectious among these contacts and then $\beta = \kappa h$ is defined as the contact rate with successful infections. In a

population with fixed size N, given $I_0 = i$, assume each infected individual contacts and infects susceptible individuals follows a Poisson process with rate $\beta \frac{N-i}{N} \approx \beta$ for small i. Additionally, let b be the birth rate and γ be the recovery rate. Then assume the time, T, that an infected individual remains infected is exponentially distributed with rate $b+\gamma$. Let X be the number of individuals directly infected by an infected individual.Then, R_0, the number of secondary infections directly produced by one infected case where all individuals in the population are susceptible can be calculated as:

$$R_0 = E[X] = E[E[X|T]] \tag{2}$$

Based on the assumption that infection is a Poisson process with rate t, hence

$$E[X|T = t] = \beta t \tag{3}$$

Accordingly,

$$R_0 = E[\beta T] = \beta E[T] \tag{4}$$

Since the time T during which infections individual remains infectious is exponentially distributed with rate $b+\gamma$, the mean of time T is $\frac{1}{b+\gamma}$. Mathematically, for SIR Epidemic Model, R_0 is obtained by:

$$R_0 = \frac{\beta}{b+\gamma} \tag{5}$$

where $\beta > 0$ is the contact rate, $\gamma > 0$ is the recovery rate and $b > 0$ is the birth rate. From its definition, it is reasonable to understand the value of R_0 is determined by three factors: the contact rate, the duration of the infectious period and the probability of a successful infection during one contact. Hence, the value of R_0 can be considerably different for different epidemics

and for the same epidemic, the value of R_0 also can vary among different populations.

2.2 Formulation of Deterministic SIR Epidemic Model and its Long-term Behavior

SIR, together with SIS are two well-known deterministic epidemic models. Every individuals in the population is either in the group of susceptible, infectious or immune. And the number of individuals for these three types at time t are $S(t)$, $I(t)$ and $R(t)$ respectively. In the SIR model, we have several assumptions that all individuals are born susceptible, no disease-related death and birth rate equal to death rate (the total population is fixed). After contact with an infectious individual, there is a probability for susceptible individuals to become infected and infectious and then develop immunity. The dynamic system for the SIR model is of the form:

$$\begin{aligned} \frac{dS}{dt} &= -\frac{\beta}{N}SI + b(I+R) \\ \frac{dI}{dt} &= \frac{\beta}{N}SI + (\gamma+b)I \\ \frac{dR}{dt} &= \gamma I - bR \end{aligned} \tag{6}$$

$$\text{where } S(0) \geq 0, I(0) \geq 0, R(0) \geq 0, S(0)+I(0)+R(0) = N$$

Note that $\beta > 0$ is the contact rate, $\gamma > 0$ is the recovery rate, $b > 0$ is the birth rate and $S(t)+I(t)+R(t) = N$. Basic reproduction number refers to:

$$R_0 = \frac{\beta}{b+\gamma} \tag{7}$$

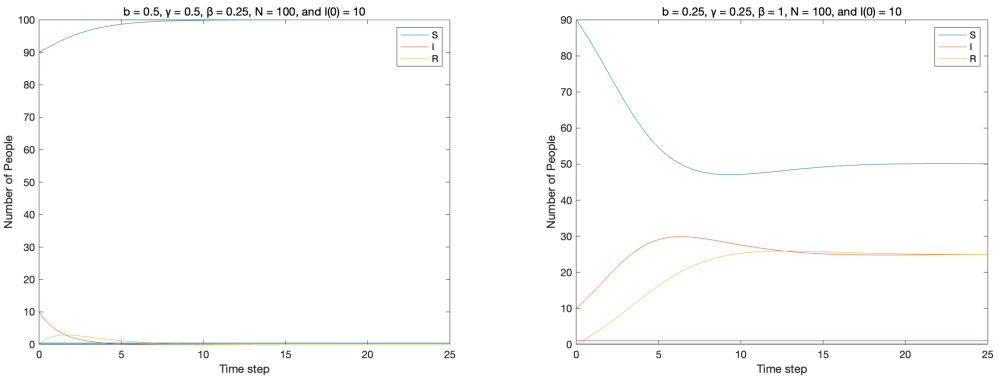
was derived in 2.1. The long-term behavior for the dynamics of the SIR model is determined by the value of R_0. If $R_0 \leq 1$, the dynamics will asymptotically converge to disease-free equilibrium, that is $\lim_{t\to\infty} I(t) = 0$. In contrast, if $R_0 > 1$, the dynamics will converge to an endemic equilibrium where $\lim_{t\to\infty}(S(t),I(t),R(t)) = (\frac{N}{R_0}, \frac{bN}{b+\gamma}(1-\frac{1}{R_0}), \frac{\gamma N}{b+\gamma}(1-\frac{1}{R_0}))$. Under the assumption of a birth rate equal to 0, the disease will finally disappear. However, the number of infected cases will initially outbreak if the initial replace number, $R_0\frac{S(0)}{N}$, which represents the expected number of infections caused by one infected case at the beginning of the infectious period, is larger than 1. Conversely, $I(t)$ will monotonically decrease to 0. The dynamics of SIR model for different cases are summarized in the following table:

Table 1: Dynamics of SIR model

$b \neq 0$	$R_0 \leq 1$	$\lim_{t\to\infty} I(t) = 0$
	$R_0 > 1$	$\lim_{t\to\infty}(S(t),I(t),R(t)) = (\frac{N}{R_0}, \frac{bN}{b+\gamma}(1-\frac{1}{R_0}), \frac{\gamma N}{b+\gamma}(1-\frac{1}{R_0}))$
$b = 0$	$R_0\frac{S(0)}{N} \leq 1$	$I(t)$ monotonically decrease to 0
	$R_0\frac{S(0)}{N} > 1$	Initially increase of $I(t)$

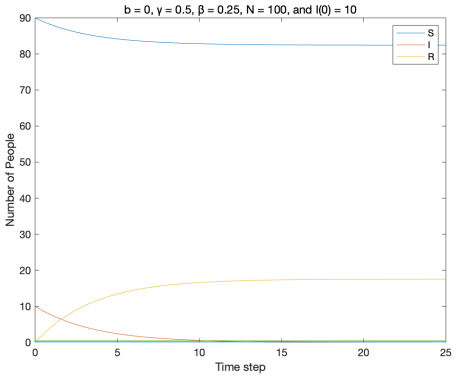
Simulating the four different cases by using MATLAB, Figure 1 shows clearly the asymptotically long term behaviors according to the different values of birth rate, basic reproduction number and initial replace number. Setting population size to be 100 and $I(0)$ to be 10 for four cases. In the case 1, taking $b = 0.5, \gamma = 0.5$ and $\beta = 0.25$ which indicates $R_0 = 0.25 \leq 1$, we can find from the Figure 1 (a) that the infected people first convert to recovered and then susceptible. By taking $b = 0.25, \gamma = 0.25$ and $\beta = 1$ instead, we got the case 2 where $R_0 = 2 > 1$. Substituting the values of variables into the corresponding case in Table 1, we know that the number of susceptible, infected and recovered will converge to 50, 25 and 25 which shows

accurately in the Figure 1 (b). In the following cases, we still fix the population size to be 100, $I(0)$ to be 10 but assuming birth rate $b = 0$. In the case 3, setting $\gamma = 0.5$ and $\beta = 0.25$ imply $R_0 \frac{S(0)}{N} = 0.45 \leq 1$. The Figure 1 (c) shows the number of infected people monotonically converge to 0 which meets the third case in Table 1. By exchanging the values of γ, β and other variables fixed, the $R_0 \frac{S(0)}{N} = 1.8 > 1$ in case 4. Figure (d) shows the number of infected people firstly experience an outbreak and then decrease which also agree with the last case shown in Table 1.

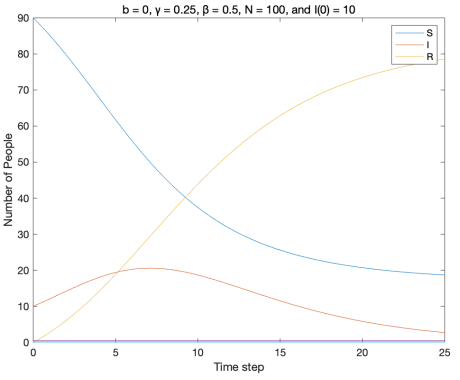


(a) Case 1: $b \neq 0, R_0 \leq 1$

(b) Case 2: $b \neq 0, R_0 > 1$



(c) Case 3: $b = 0, R_0 \frac{S(0)}{N} \leq 1$



(d) Case 4: $b = 0, R_0 \frac{S(0)}{N} > 1$

Figure 1: Simulation for Deterministic SIR Models

3 DTMC SIR Epidemic Model

3.1 Review of Markov Chain

A Russian mathematician, Andrey Markov, devoted himself to the research of stochastic process and primarily known for his work on Markov Chains and Markov Processes (Wikipedia 2021). As Ross stated (2014, 183), by definition, the Markov process is a type of stochastic process satisfying Markov property(also referred as memoryless property), which describes the distribution of the future state X_{t+1} is independent of all sequences of past states $X_0, X_1, ..., X_{t-1}$ and depends only on present sate X_t, that is,

$$P\{X_{t+1} = j | X_t = i, X_{t-1} = i_{t-1}, ..., X_1 = i_1, X_0 = i_0\} = P\{X_{t+1} = j | X_t = i\}. \tag{8}$$

Continuous time Markov process was studied as the Poisson process for a long time before the early 20th century when Markov Chain was proposed. Aiming to disprove the necessary condition, independence, for the weak law of large number declared by Pavel Nekrasov, Andrey Markov published his paper on Markov Chain in 1906 and validated his thought by proving the average outcomes of the Markov chain will finally converge to a fixed vector of values under certain conditions (Wikipedia 2021). Markov Chain, named after Andrey Markov, is defined as a sequence of discrete states satisfying Markov property (8).

There is another important principal of Markov Chain that we assume it to be time homogeneous. More specifically, a Markov Chain is said to be time homogeneous, if and only if the state transition from i to j is independent of time t. In other words, there exists a fixed value

$P_{(i,j)}$ such that

$$P_{(i,j)} = P\{X_{t+1} = j | X_t = i\} \tag{9}$$

for all times t (Wikipedia 2021).

3.2 Formulation of DTMC SIR Epidemic Model

Because of the fixed population assumption, there are two independent random variables In DTMC SIR epidemic model, $S(t)$ and $I(t)$. And $R(t)$ can be obtained by $N - S(t) - I(t)$. Since we assume birth rate equal to death rate, the total population N is fixed. The trivariate process can be regarded as bivariate process related to $S(t)$ and $I(t)$. And the joint probability for the bivariate process $\{(S(t), I(t))\}$ is

$$p_{(s,i)}(t) = Prob\{S(t) = s, I(t) = i\}. \tag{10}$$

In SIR model, susceptible people can possibly become infectious after contacting infected individuals and will then recover with immunity. Immune individual will not be infected again. Figure 2 shows the dynamic transition among population. Note that we also assume no disease

related death in SIR model, all the dotted arrows direct outside means death by nature.

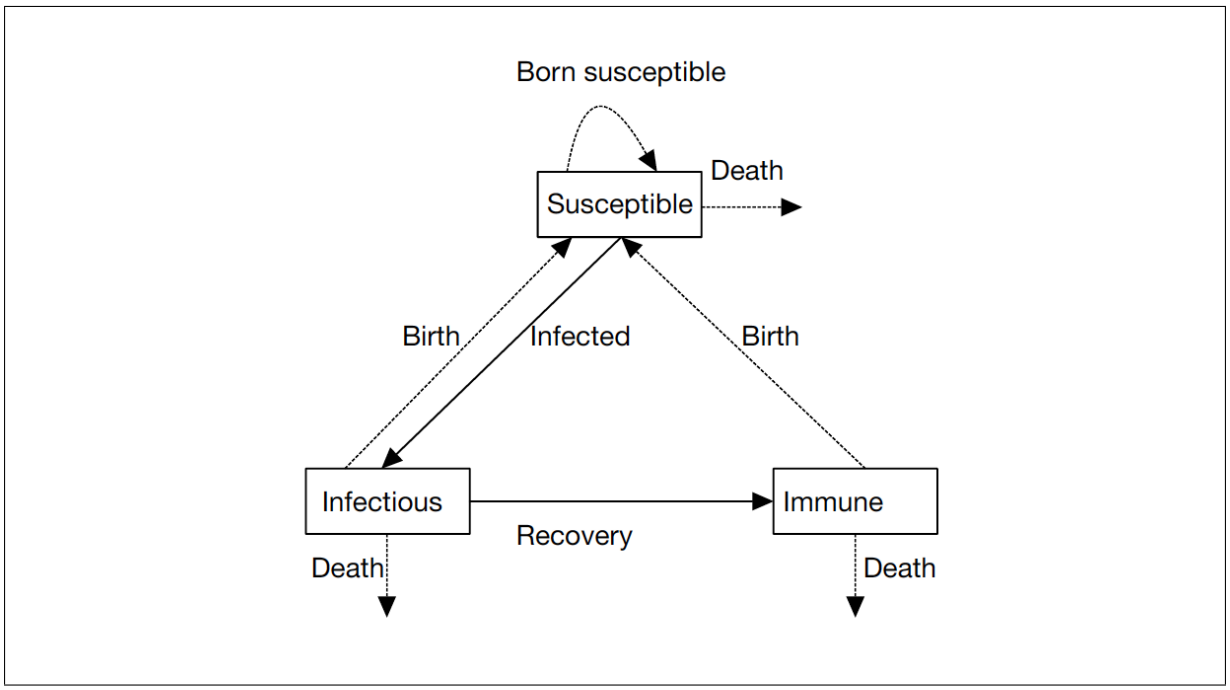


Figure 2: SIR compartmental diagram

Consider the discrete time case, we take Δt sufficiently small so that there is at most one state change, either a birth, a death, an infection or a recovery, happens during Δt. Let $N(t)$ denotes the number of events occurs during time t, then $P[N(\Delta t) \geq 2] = o(h)$. Table 2 shows the possible transition among population happens during sufficiently small Δt. Note here that $\Delta S = S(t+\Delta t) - S(t)$ and $\Delta I = I(t+\Delta t) - I(t)$.

Table 2: Possible Transition in SIR

$(\Delta S, \Delta I)$	A birth	A death	An infection	A recovery
Susceptible (S)	(1, 0)	(0, 0)	(-1, 1)	Meaningless
Infected (I)	(1, 0)	(1, -1)	Meaningless	(0, -1)
Immune (R)	(1, 0)	(1, 0)	Meaningless	Meaningless

During the sufficiently small Δt, only the above transition can happen. We also have the

probability for this bivariate process which is given by

$$p_{(s+k,i+j),(s,i)}(\Delta t) = Prob\{(\Delta S, \Delta I) = (k, j) | (S(t), I(t)) = (s, i)\}. \tag{11}$$

And the probability for each possible transition can be seen as following Table 3:

Table 3: Probability Table

$(\Delta S, \Delta I)$	Probability
(-1, 1)	$\beta is/N\Delta t$
(0, -1)	$\gamma i\Delta t$
(1, -1)	$bi\Delta t$
(1, 0)	$b(N-s-i)\Delta t$
(0, 0)	$1-\beta is/N\Delta t-[\gamma i+b(N-s)]\Delta t$

‘

Hence for the bivariate process $\{S(t), I(t)\}$, the transition matrix Q where the entry in the (r,s) row, (i,j) column represents the probability that possible transition happens during a small time interval Δt from state (i,j) to (r,s), which is denoted as $q_{(i,j),(r,s)}$. In short, $q_{(i,j),(r,s)} = Prob(S(t+\Delta t) = r, I(t+\Delta t) = s | S(t) = i, I(t) = j)$. And the values of $q_{(i,j),(r,s)}$ are defined as follows

$$q_{(i,j),(r,s)} = \begin{cases} \beta ij/N\Delta t, & (r,s) = (i-1, j+1) \\ \gamma j\Delta t, & (r,s) = (i, j-1) \\ bj\Delta t, & (r,s) = (i+1, j-1) \\ b(N-j-i)\Delta t, & (r,s) = (i+1, j) \\ 1-\beta ij/N\Delta t-[\gamma j+b(N-i)]\Delta t, & (r,s) = (0,0) \\ 0, & otherwise \end{cases} \tag{12}$$

Since this bivariate process is a discrete time Markov Chain which satisfies Markov prop-

erty and is time-homogeneous. The probability of $p_{(s,i)}(t+\Delta t)$ can be obtained by the sum of all possible previous probabilities multiply the transition probabilities

$$\begin{aligned} p_{(s,i)}(t+\Delta t) &= \sum_{all\Delta s,\Delta i} q_{(s-\Delta s,i-\Delta i)}(t) \times p_{(s-\Delta s,i-\Delta i),(s,i)}(\Delta t) \\ &= p_{(s+1,i-1)}(t)\frac{\beta}{N}(i-1)(s+1)\Delta t + p_{(s,i+1)}(t)\gamma(i+1)\Delta t \\ &+ p_{(s-1,i+1)}(t)b(i+1)\Delta t + p_{(s-1,i)}(t)b(N-s+1-i)\Delta t \\ &+ p_{(s,i)}(t)\left(1-\left[\frac{\beta}{N}is+\gamma i+b(N-s)\right]\Delta t\right). \end{aligned} \tag{13}$$

We can easily find that all states are transient except for when all individuals in population are susceptible, the state will remain unchanged forever which implies $(N,0)$ is an absorbing state namely $p_{(N,0),(N,0)}(\Delta t) = 1$.

4 CTMC SIR Epidemic Model

4.1 Formulation of CTMC SIR Epidemic Model

The DTMC from the previous chapter leads to the CTMC considered in this when we let $\triangle t \to 0$ and consider rates in place of probabilities of change. Consider the case that the time $t \in [0,\infty)$ a continuous variable, and $S(t)$, $I(t)$, $R(t)$ remain discrete random variables. Similar to the DTMC SIR epidemic model, we still consider the set of ordered pairs, $\{(S(t),I(t))\}$, as a bivariate process. And the corresponding transition rate matrix for CTMC SIR epidemic model Q where the entry $q_{(i,j),(r,s)}$ in the (r,s) row, (i,j) column denotes the rate of transition from state (i,j) to (r,s). $q_{(i,j),(r,s)}$ is equal to 0 except when

$$q_{(i,j),(r,s)} = \begin{cases} \beta ij/N, & (r,s) = (i-1,j+1) \\ \gamma j, & (r,s) = (i,j-1) \\ bj, & (r,s) = (i+1,j-1) \\ b(N-i-j), & (r,s) = (i+1,j) \\ 1-\beta ij/N - [\gamma j + b(N-i)], & (r,s) = (i,j) \end{cases} \tag{14}$$

By taking $\Delta t \to 0$ of equation(13), we can also derive the system of forward Kolmogorov differential equations from the difference equation (13)

$$\begin{aligned} \frac{dp_{(s,i)}}{dt} &= p_{(s+1,i-1)}\frac{\beta}{N}(i-1)(s+1) + p_{(s,i+1)}\gamma(i+1) \\ &\quad + p_{(s-1,i+1)}b(i+1) + p_{(s-1,i)}b(N-s+1-i) \\ &\quad - p_{(s,i)}\left[\frac{\beta}{N}is + \gamma i + b(N-s)\right]. \end{aligned} \tag{15}$$

We tried to derive mean $E(I(t))$ by applying the moment generating function to the forward Kolmogorov differential equation, and ended up with finding a non-closed system which means the mean depends on the second moment and the variance depends on higher order moments. Then we need to introduce moment closure techniques to approximate the solutions. It is not our main task here.

In CTMC SIR epidemic model, we still can notice that the disease-free state is an absorbing state so that epidemic will end up with extinction.

4.2 Derivation of Deterministic SIR model from the CTMC SIR model

Similar to DTMC SIR Epidemic Model, ΔS and ΔI can take values with probabilities shown in Table 3. From Table 3, we can obtain

$$\begin{aligned} E(\Delta S|S(t)=S,I(t)=I) &= -1\cdot\frac{\beta}{N}SI\Delta t + 1\cdot(bI+b(N-S-I))\,\Delta t \\ &= -\frac{\beta}{N}SI\Delta t + b(N-S)\Delta t \\ &= -\frac{\beta}{N}SI\Delta t + b(I+R)\Delta t \end{aligned} \tag{16}$$

and

$$\begin{aligned} E(\Delta I|S(t)=S,I(t)=I) &= 1\cdot\frac{\beta}{N}SI\Delta t + (-1)\cdot(\gamma i+bi)\Delta t \\ &= \frac{\beta}{N}SI\Delta t + (\gamma+b)I\Delta t \end{aligned} \tag{17}$$

Consider the continuous time case, divide both sides by Δt and let Δt go to zero, the following ordinary differential was derived:

$$\begin{aligned} E[\frac{dS}{dt}|S(t)=S,I(t)=I] &= -\frac{\beta}{N}SI+b(I+R) \\ E[\frac{dI}{dt}|S(t)=S,I(t)=I] &= \frac{\beta}{N}SI+(\gamma+b)I \end{aligned} \tag{18}$$

Under the assumption of fixed population size, $E[\frac{dS}{dt}+\frac{dI}{dt}+\frac{dR}{dt}|S(t)=S,I(t)=I]=0$ holds, then the deterministic model can be obtained:

$$\begin{aligned} E[\frac{dS}{dt}|S(t)=S,I(t)=I] &= -\frac{\beta}{N}SI+b(I+R) \\ E[\frac{dI}{dt}|S(t)=S,I(t)=I] &= \frac{\beta}{N}SI+(\gamma+b)I \\ E[\frac{dR}{dt}|S(t)=S,I(t)=I] &= \gamma I-bR \end{aligned} \tag{19}$$

4.3 Deterministic SIR model versus CTMC SIR model

Since both deterministic SIR model and CTMC SIR model are under the assumption of continuous time, it is natural to compare these two models. Previously, we obtained the dynamic of deterministic SIR model has four possible outcomes which are determined by birth rate, basic reproduction number and initial replace number. When $b=0$ and $R_0=\frac{\beta}{b+\gamma}>1$, the final size for susceptible, infected and recovered individuals as time approaches infinity will be $\frac{N}{R_0}$, $\frac{bN}{b+\gamma}(1-\frac{1}{R_0})$ and $\frac{\gamma N}{b+\gamma}(1-\frac{1}{R_0})$ respectively. In the other three cases, the number of infected individuals will finally decrease to 0 but go through different fluctuations.

However, different from deterministic SIR model, the asymptotic dynamic of CTMC SIR epidemic model has only one outcome which is eventually converge to disease-free situation regardless of the values of parameters in the model.

5 SDE SIR Epidemic Model

5.1 Formulation of SDE SIR Epidemic Model

Previously, under the assumption of discrete states, we studied deterministic SIR epidemic model and SIR epidemic model on both discrete time and continuous time. In this section, we assume that all the random variables are continuous, that is, time $t \in [0,\infty]$ and $S(t), I(t), R(t) \in [0,N]$.

For the bivariate process $(S(t),\ I(t))$ of SIR model, It can be derived from the CTMC SIR model. Similar to CTMC model, we still have the assumptions that Δt is small enough so there at most one state change happens during the time period Δt and birth rate is equal to 0. Additionally, it is assumed that ΔS and ΔI are approximately normal distributed and independent among disjoint time periods in the SIR epidemic model.

In summary, we have the following assumptions in derivation of SDE SIR Epidemic Model:

1. Δt is sufficiently small that $E[\Delta S^k] = o(\Delta t)$ and $E[\Delta I^k] = o(\Delta t)$.

2. S and I have independent increments.

3. ΔS and ΔI have normally distribution, this assumption will be discussed in Section 5.2.

4. For simplicity we assume the birth rate $b = 0$.

Let $\Delta \boldsymbol{X}(t) = (\Delta S, \Delta I)^T$. From Table 3, we have

$$p_{(s+k,i+j),(s,i)}(\Delta t) = \begin{cases} \beta is/N\Delta t, & (k,j) = (-1,1) \\ \gamma i \Delta t, & (k,j) = (0,-1) \\ bi\Delta t, & (k,j) = (1,-1) \\ b(N-s-i)\Delta t, & (k,j) = (1,0) \\ 1-\beta is/N\Delta t - [\gamma i + b(N-s)]\delta t, & (k,j) = (0,0) \\ 0, & otherwise \end{cases} \tag{20}$$

The expectations of ΔS and ΔI can be computed:

$$\begin{aligned} E(\Delta S) &\approx -1 \cdot \frac{\beta}{N} SI\Delta t + 1 \cdot (bI + b(N-S-I))\,\Delta t \\ &= -\frac{\beta}{N} SI\Delta t \qquad Since\ b = 0 \end{aligned} \tag{21}$$

and

$$\begin{aligned} E(\Delta I) &\approx 1 \cdot \frac{\beta}{N} SI\Delta t + (-1) \cdot (\gamma I + bI)\Delta t \\ &= \left(\frac{\beta}{N} SI - \gamma I\right)\Delta t \qquad Since\ b = 0 \end{aligned} \tag{22}$$

We assume $\Delta \boldsymbol{X}(t)$ is approximately multivariate normal in what follows. When this is a good approximation will be discussed later. In terms of $\Delta \boldsymbol{X}(t)$, the expectation is

$$E(\Delta \boldsymbol{X}(t)) \approx \begin{pmatrix} -\frac{\beta}{N} SI \\ \frac{\beta}{N} SI - \gamma I \end{pmatrix} \Delta t = \boldsymbol{\mu}(t)\Delta t \tag{23}$$

According to the definition, we know that the covariance matrix of $\Delta \boldsymbol{X}(t)$ can be obtained by $E(\Delta \boldsymbol{X}(t)[\Delta \boldsymbol{X}(t)]^T) - E(\Delta \boldsymbol{X}(t))E(\Delta \boldsymbol{X}(t))^T$. Since all the elements of $E(\Delta \boldsymbol{X}(t))E(\Delta \boldsymbol{X}(t))^T$

are $o([\Delta t]^2)$, we can approximate the covariance matrix by $E(\Delta \boldsymbol{X}(t)[\Delta \boldsymbol{X}(t)]^T)$:

$$\begin{aligned} E(\Delta \boldsymbol{X}(t)[\Delta \boldsymbol{X}(t)]^T) &= E([\Delta S, \Delta I][\Delta S, \Delta I]^T) \\ &= E(\begin{pmatrix} \Delta S^2 & \Delta S \Delta I \\ \Delta S \Delta I & \Delta I^2 \end{pmatrix}) \end{aligned} \tag{24}$$

From Table 3,

$$\begin{aligned} E(\Delta S^2) &\approx (-1)^2 \cdot \frac{\beta}{N} SI\Delta t = \frac{\beta}{N} SI\Delta t \\ E(\Delta I^2) &\approx (-1)^2 \cdot (\gamma I + bI)\Delta t + 1^2 \cdot \frac{\beta}{N} SI\Delta t \approx \left(\frac{\beta}{N} SI + \gamma I\right)\Delta t \\ E(\Delta S \Delta I) &= (-1 \cdot 1)\left(\frac{\beta}{N} SI + bI\right)\Delta t = -\frac{\beta}{N} SI\Delta t \end{aligned}$$

We have

$$V(\Delta \boldsymbol{X}(t)) = E\begin{pmatrix} \Delta S^2 & \Delta S \Delta I \\ \Delta S \Delta I & \Delta I^2 \end{pmatrix} \approx \begin{pmatrix} \frac{\beta}{N} SI & -\frac{\beta}{N} SI \\ -\frac{\beta}{N} SI & \frac{\beta}{N} SI + \gamma I \end{pmatrix} \Delta t = V\Delta t \tag{25}$$

with $t \to 0$. So we got $\Delta \boldsymbol{X}(t) \sim N(\boldsymbol{\mu}(t)dt, Vdt)$. Then we can approximate $\boldsymbol{X}(t+\Delta t)$ by

$$\boldsymbol{X}(t+\Delta t) = \boldsymbol{X}(t) + \Delta \boldsymbol{X}(t) \approx \boldsymbol{X}(t) + \boldsymbol{\mu}(t)\Delta t + \sqrt{V\Delta t} \tag{26}$$

Since V is symmetric and positive definite, there exists a unique matrix B such that $\Delta t V = \Delta t B^2$. Let $\boldsymbol{U}(t) = \begin{pmatrix} U_1 \\ U_2 \end{pmatrix}$ be a two-dimension vector consists of two standard normal distributions normalized from $\Delta \boldsymbol{X}(t)$:

$$\boldsymbol{U}(t) = B^{-1} \frac{\Delta \boldsymbol{X}(t) - \boldsymbol{\mu}(t)\Delta t}{\sqrt{\Delta t}} \sim N(0, I) \tag{27}$$

Then we have

$$\begin{aligned}\Delta \boldsymbol{X}(t) &= \boldsymbol{X}(t+\Delta t) - \boldsymbol{X}(t) \\ &= B\sqrt{\Delta t}\cdot \boldsymbol{U}(t) + \boldsymbol{\mu}(t)\Delta t\end{aligned} \tag{28}$$

Dividing both sides by dt gives:

$$\frac{\boldsymbol{X}(t+\Delta t) - \boldsymbol{X}(t)}{\Delta t} = \boldsymbol{\mu}(t) + \frac{B\sqrt{\Delta t}\cdot \boldsymbol{U}(t)}{\Delta t} \tag{29}$$

Note that $\sqrt{\Delta t}\boldsymbol{U}(t) \sim N(0, \Delta \boldsymbol{t})$ has the same distribution with a two-dimension vector consists of two standard Brownian Motions $\{\boldsymbol{W}(t) = \begin{pmatrix} W_1 \\ W_2 \end{pmatrix}\}$ where $\boldsymbol{W}(t+\Delta t) - \boldsymbol{W}(t) \sim N(0, \Delta \boldsymbol{t})$ and W_1, W_2 are two independent Weiner Processes. Hence

$$\frac{\boldsymbol{X}(t+\Delta t) - \boldsymbol{X}(t)}{\Delta t} = \boldsymbol{\mu}(t) + \frac{B\{\boldsymbol{W}(t+\Delta t) - \boldsymbol{W}(t)\}}{\Delta t}. \tag{30}$$

By taking $\Delta t \to 0$, we have the differential equation

$$\begin{aligned}\frac{d\boldsymbol{X}(t)}{dt} &= \boldsymbol{\mu}(t) + B\frac{d\boldsymbol{W}(t)}{dt} \\ &= \begin{pmatrix} \mu_1 \\ \mu_2 \end{pmatrix} + \begin{pmatrix} B_{11} & B_{12} \\ B_{21} & B_{22} \end{pmatrix} \begin{pmatrix} \frac{dW_1}{dt} \\ \frac{dW_2}{dt} \end{pmatrix}.\end{aligned} \tag{31}$$

Substitute the values into equation (31), we get the solution $\boldsymbol{X}(t)$ of equation(26) converges to the solution of the following system of Itô SDEs:

$$\begin{aligned}\frac{dS}{dt} &= -\frac{\beta}{N}SI + B_{11}\frac{dW_1}{dt} + B_{12}\frac{dW_2}{dt} \\ \frac{dI}{dt} &= \frac{\beta}{N}SI - \gamma I + B_{21}\frac{dW_1}{dt} + B_{22}\frac{dW_2}{dt}\end{aligned} \tag{32}$$

5.2 Normal Approximation for SDE

To discuss why we can approximate ΔS and ΔI to be normal distributions, detailed explanation for ΔI as follows will be an example and the derivation procedure for ΔS will be similar. Let

$$\Delta I(t) = \sum_{j=0}^{I(t)} \delta_j(\Delta t) - \sum_{k=0}^{I(t)} r_j(\Delta t) \tag{33}$$

where δ_j and r_j are indicator random variables:

$$\delta_j(\Delta t) = \begin{cases} 1, & \text{if individual j infects someone} \\ 0, & otherwise \end{cases} \tag{34}$$

and

$$r_j(\Delta t) = \begin{cases} 1, & \text{if individual j recovers} \\ 0, & otherwise \end{cases} \tag{35}$$

Since infections and recoveries are independent,

$$\Delta I(t) = \sum_{j=0}^{I(t)} \{\delta_j(\Delta t) - r_j(\Delta t)\} = \sum_{j=0}^{I(t)} dI_j(\Delta t) \tag{36}$$

When I(t) is large enough, the Central Limit Theorem can be applied to approximate $\Delta I(t)$ as normal distributed random variable. Similar approaches applied to ΔS have the same result as well.

6 Important Properties of the SIR Epidemic Model

For stochastic SIR epidemic models, it has four crucial properties that distinguish them from deterministic epidemic models and depend on the stochastic nature which are:

1. Probability of an outbreak.

2. Final size distribution.

3. Quasi-stationary probability distribution.

4. Expected duration of an epidemic.

The first two properties will be discussed in details in the following two subsections.

6.1 Probability of an Outbreak

Formally, an outbreak is the situation where a larger number of people, N_0 say, in the population gets infected. For the SIR model, when a disease go through an outbreak, it is called epidemic. It is important to know the probability of an outbreak during an epidemic. I will argue that $I(t) \in \{0,1,2,...\}$ which represents the number of infected individuals at time t is a random walk. Note here that 0 and $N_0 << N$ are two absorbing states, $p_{00} = p_{N_0N_0} = 1$. Thus this process can be regarded as a Gambler's Ruin Problem where the probability of win \$1 is p, lose \$1 is q and $p+q=1$. In the Gambler's Ruin Problem, $X(t)$ start with \$k and stop if broke or money reached a predetermined value N. Then the probability that begin with \$k and end with N will be

$$a_k = \frac{1-(\frac{q}{p})^k}{1-(\frac{q}{p})^N} \tag{37}$$

Note that equation(37) is meaningful if and only if $q < p$, or this will always ends with break and the probability becomes negative.

In the SIR epidemic model, $I(t)$ represents the number of infected individuals at time t and $\{I(t)\}$ is a Markov Chain with rates q_{ij}. Let y_n be the number of infected individuals at the nth change. Then $\{y_n\}$ is an embedded discrete time Markov Chain corresponding to $\{I(t)\}$ with the property (Ross 2014, 446):

$$Prob(y_n = j | y_{n-1} = i) = \frac{q_{ij}}{\sum_{i \neq j} q_{ij}} \tag{38}$$

Under the assumption of birth rate equal to 0, the equation (14) is simplified as:

$$q_{(i,j),(r,s)} = \begin{cases} \beta ij/N, & (r,s) = (i-1, j+1) \\ \gamma j, & (r,s) = (i, j-1) \\ 1 - \beta ij/N - \gamma j, & (r,s) = (i,j) \end{cases} \tag{39}$$

We only consider the changes of $I(t)$, then we have the probabilities of transition corresponding to $I(t)$ are as follow:

$$\begin{aligned} q_{ii+1} &= \beta is/N \\ q_{ii-1} &= \gamma i \end{aligned} \tag{40}$$

where s is the number of susceptible individuals. Since $N_0 << N$ and $i \leq N_0$, the number of infected people also much smaller than N. Then the number of susceptible, s, is relatively large

enough to approximate $\frac{s}{N}$ by 1. Hence the equation (40) can be simplified:

$$\begin{aligned} q_{ii+1} &= \beta i \\ q_{ii-1} &= \gamma i \end{aligned} \tag{41}$$

Applying the equation (38), we have

$$\begin{aligned} Prob(y_n = i+1 | y_{n-1} = i) &= \frac{\beta i}{\beta i + \gamma i} = \frac{\beta}{\beta + \gamma} \\ Prob(y_n = i-1 | y_{n-1} = i) &= \frac{\gamma i}{\beta i + \gamma i} = \frac{\gamma}{\beta + \gamma} \end{aligned} \tag{42}$$

Hence y_n can be regarded as a random walk model start with i_0 infected individuals, and considered as a Gambler's Ruin Problem where $p = \frac{\beta}{\beta+\gamma}$ and $q = \frac{\gamma}{\beta+\gamma}$. Substitute the value of p and q into equation (37), we have $\frac{q}{p} = \frac{\gamma}{\beta}$ and assume $q < p$, he probability of the pandemic end with all individuals are infected can be computed by the equation(37):

$$a_{i_0} = \frac{1 - \left(\frac{\gamma}{\beta}\right)^{i_0}}{1 - \left(\frac{\gamma}{\beta}\right)^{N}} \tag{43}$$

Let N goes to infinity, then

$$a_{i_0} = 1 - \left(\frac{\gamma}{\beta}\right)^{i_0} \tag{44}$$

Since the epidemic will absorb into either 0 or N, then

$$\lim_{t \to \infty} Prob\{I(t) = 0\} = 1 - \left(1 - \left(\frac{\gamma}{\beta}\right)^{i_0}\right) = \left(\frac{\gamma}{\beta}\right)^{i_0} \tag{45}$$

In this case, the probability of absorption to 0 state is $\left(\frac{\gamma}{\beta}\right)^{i_0}$. In contrast, the probability of pop-

ulation persistence which also can be approximate as outbreak is $1-\left(\frac{\gamma}{\beta}\right)^{i_0}$. This approximation will be more accurate when the population size N is large and initial number of infections i_0 os small. In summary,

$$\lim_{t\to\infty} Prob\{I(t)=0\} = \begin{cases} 1, & \text{if } \beta \le \gamma \\ \left(\frac{\gamma}{\beta}\right)^{i_0}, & \text{if } \beta < \gamma \end{cases} \tag{46}$$

Review that when $b=0$, $R_0=\frac{\beta}{\gamma}$, therefore the probability that the epidemic ends with 0 infection is:

$$\lim_{t\to\infty} Prob\{I(t)=0\} \approx \begin{cases} 1, & \text{if } \beta \le \gamma \\ \left(\frac{1}{R_0}\right)^{i_0}, & \text{if } \beta > \gamma \end{cases} \tag{47}$$

And the probability of an outbreak is

$$Prob[\text{An outbreak happens}] \approx \begin{cases} 0, & \text{if } \beta \le \gamma \\ 1-\left(\frac{1}{R_0}\right)^{i_0}, & \text{if } \beta \le \gamma \end{cases} \tag{48}$$

6.2 *Final Size of an Epidemic*

In the deterministic model, the final size of an epidemic, which is defined as the number of individuals who ever got infected, depends on the different values of basic reproduction number R_0. However, in the stochastic model, the epidemic will finally end, $I(t)$ will converge to 0 eventually. It is interested to know the oscillations during the epidemic. In this section, the final size of the deterministic model will be discussed first. Then an R code in Appendix A is provided to get the final size distribution for the stochastic SIR model.

Since the epidemic always happens rapidly, we assume no birth and death in SIR Epidemic

Model. And review that the SIR epidemic model with $b = 0$:

$$\begin{aligned}
\frac{dS}{dt} &= -\frac{\beta}{N}SI \\
\frac{dI}{dt} &= \frac{\beta}{N}SI - \gamma I \\
\frac{dR}{dt} &= \gamma I
\end{aligned} \tag{49}$$

with initial condition $S(0) = s_0$, $I(0) = i_0$, $R(0) = r_0$ and $S+I+R = N$ always holds. The equilibrium points for this model are every point on the S axis where $I = 0$. The equilibrium points where on the left of the threshold $S = \frac{1}{R_0}$ are neutrally stable and the equilibrium points on the other side are neutrally unstable. Since $S(t)$ is non-increasing and $S(t) \geq 0$, there must exist a unique limit $S(\infty)$. Moreover, $R(t)$ is increasing and bound above by N, $R(\infty)$ exists. It follows that $I(\infty)$ also exists because of $I(t) = N - S(t) - R(t)$. In addition, proof by contradiction, if $I(\infty) > 0$, $R(\infty) = \infty$ for sufficiently large t. However, $R(\infty) \leq \infty$ which contradicts. Hence $I(\infty) = 0$ is proved. Divide $\frac{dS}{dt}$ by $\frac{dI}{dt}$, a differential equation of $\frac{dI}{dS}$ can be obtained:

$$\begin{aligned}
\frac{dI}{dS} &= \frac{\beta SI - \gamma IN}{-\beta SI} \\
&= -1 + \frac{N}{R_0 S}
\end{aligned} \tag{50}$$

and the function of I can be solved from equation (50):

$$I = N - r_0 - S + \frac{N}{R_0} ln\left(\frac{S}{s_0}\right) \tag{51}$$

In conclusion, when $\frac{R_0 s_0}{N} \leq 1$, then $\frac{dI}{dS} > 0$ which means I and S will increase or decrease at the same time. With $t \to \infty$, $S(t)$ will decrease and converge to a finite limit $S(\infty)$ since $\frac{dS}{dt} < 0$. Correspondingly, $I(t)$ will also decrease and converge to $I(\infty) = 0$. On the other side, if $\frac{R_0 s_0}{N} > 1$, then $\frac{dI}{dS} < 0$ at first. With $S(t)$ decrease along t, $\frac{N}{R_0 S(t)}$ will reach 1 and $\frac{dI}{dS} > 0$

afterwards. So $I(t)$ will achieve its maximum when $\frac{N}{R_0 S} = 1$, which is $S = \frac{N}{R_0}$. Hence, $I(t)$ will first increase to its maximum

$$N - r_0 - \frac{N}{R_0} + \frac{N}{R_0} ln\left(\frac{N}{R_0 s_0}\right) \tag{52}$$

and then decrease to 0. For the limit of number of susceptible people $S(\infty)$ is when $I(t) = 0$, the unique root in the range $\left(0, \frac{1}{R_0}\right)$ of the equation

$$N - r_0 - S(\infty) + \frac{N}{R_0} ln\left(\frac{S(\infty)}{s_0}\right) = 0 \tag{53}$$

And the final size, $R(\infty)$ of the epidemic can be obtained by

$$R(\infty) = N - S(\infty) \tag{54}$$

Note that in most case, we assume there is no recovered case at first, $r_0 = 0$. Review the case 4 in Section 2.2 where $R_0 = 2$, $i_0 = 10$, $s_0 = 90$ and $N = 100$. Applying the equation (52), the $I(t)$ will reach its maximum equal to 20.61 which is consistent with Figure 1(d). Refer to the data in the book "Mathematical Epidemiology" (Allen 2008, 112), the final size of the deterministic model is summarized in the following table where $\gamma = 1$ and $I(0) = 1$.

Table 4: Expectation of the Final Size when $\gamma = 1, I(0) = 1$

R_0	$N = 20$	$N = 100$
0.5	1.87	1.97
1	5.74	13.52
2	16.26	80.02
5	19.87	99.31
10	20.00	100.00

For stochastic SIR model, the methods to compute final size distribution is more complex.

A simpler method introduced by Foster is discussed here. The stochastic SIR model is regarded as a bivariate process where the ordered pair (s,i) ,which consists of the number of susceptible and infected people, is a random variable.

For a simple case where $N=3$, (s,i) can take values from the ordered set $A=\{(3,0),(2,0),$ (1,0), $(0,0),(2,1),(1,1),(0,1),(1,2),(0,2),(0,3)\}$. Since we assume no birth and death here, only two kinds of transitions, recovery and infection, can happen, the probability for recovery, $(s,i)\to(s,i-1)$ can be calculated by divide the recovery rate over the rate of transition happens:

$$p_s=\frac{\gamma i}{\gamma i+(\beta/N)is}=\frac{\gamma}{\gamma+(\beta/N)s},s=0,1,2 \tag{55}$$

and infection,$(s,i)\to(s-1,i+1)$ with probability $1-p_s$. Under these rules, the transition matrix for $N=3$ is obtained in the form:

$$T=\begin{pmatrix}
1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0\\
0 & 1 & 0 & 0 & p_2 & 0 & 0 & 0 & 0 & 0\\
0 & 0 & 1 & 0 & 0 & p_1 & 0 & 0 & 0 & 0\\
0 & 0 & 0 & 1 & 0 & 0 & p_0 & 0 & 0 & 0\\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0\\
0 & 0 & 0 & 0 & 0 & 0 & 0 & p_1 & 0 & 0\\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & p_0 & 0\\
0 & 0 & 0 & 0 & 1-p_2 & 0 & 0 & 0 & 0 & 0\\
0 & 0 & 0 & 0 & 0 & 1-p_1 & 0 & 0 & 0 & p_0\\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 1-p_1 & 0 & 0
\end{pmatrix}$$

The entry in the ith row and the jth column of the matrix T represents the transition from the

jth state in A to the ith state in A. It is easily to find that the upper left 4 x 4 matrix is a closed cycle consist of four absorbing states. Since the epidemic is always begin with one infected and the left are susceptible, the initial condition $p(0)$ for $N = 3$ is $(0,0,0,0,1,0,0,0,0,0)^T$. Each entry in $p(0)$ corresponds to the distribution probability of the ordered set A. Therefore in this case, the process starts with the state $(2,1)$. Then the final size distribution can be obtained from the first four rows of $\lim_{t\to\infty} T^t p(0)$ where T is the transition matrix and $p(0)$ is the initial condition of the distribution of the population. The limit can be obtained when we take t relatively large to N. By computing $T^5 p(0)$, we get the final distribution size will be 1, 2 or 3 with probabilities of p_2, $p_1^2(1-p_2)$ and $(1-p_1^2)(1-p_2)$ respectively. However, when N is large, it is impossible to calculate manually. The code in Appendix A provides a function in R to calculate the final size distribution for different N (population size) and R_0 (basic reproduction number). By employing R, set $N = 20$, $\gamma = 1$ and $I(0) = 1$, the final size distributions for different R_0 show in the following Figure:

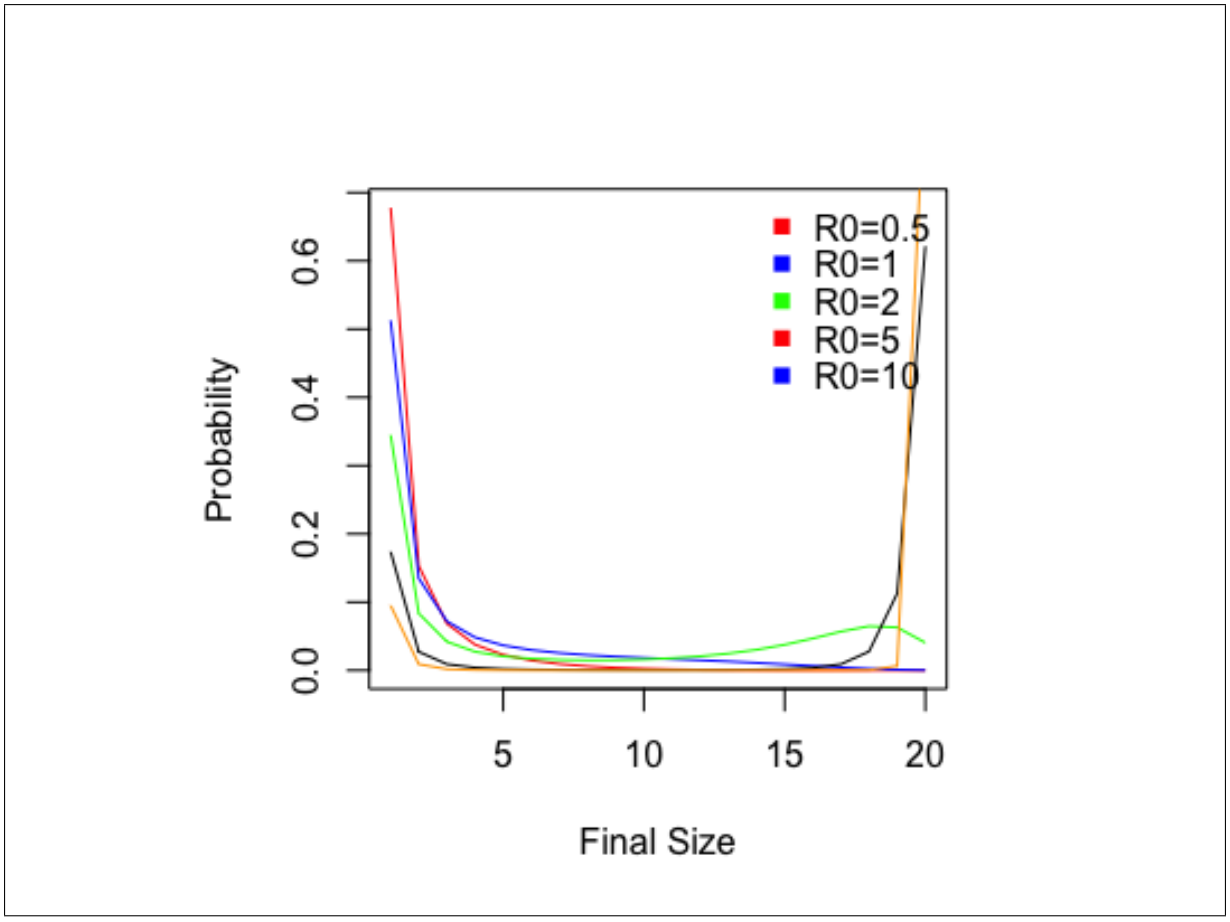


Figure 3: Final Size Distribution for different R_0 with N = 20, $\gamma = 1$ and I(0) = 1

The Figure inferred that when $R_0 < 1$ or around 1, then the final size distribution is right skewed. Otherwise, it is left skewed. By employing R, the expectations of the final size for different values of R_0 can be calculated and summarized in the following table:

Table 5: Expectation of the Final Size when $\gamma = 1, I(0) = 1$

R_0	$N = 20$	$N = 100$
0.5	1.757177	1.931314
1	3.341303	6.099598
2	8.117944	38.34319
5	15.66162	79.27778
10	17.97618	89.98004

Comparing the values in Table 4 and Table 5, we can conclude that when R_0 less than 1 or much larger than 1, the expectations of the final size for the deterministic model and stochastic model are closer.

7 Conclusion

This paper provides a detailed introduction to the SIR epidemic model conducted on ordinary differential equation, discrete time Markov Chain, continuous time Markov Chain and stochastic differential equation. Section 2 gives a derivation of the basic reproduction number, R_0 and an introduction of dynamics of the deterministic SIR epidemic model in terms of various R_0. Comparing to the deterministic model, run SIR epidemic model with stochastic framework is more realistic. In section 3, the SIR epidemic model under the assumption of discrete time, discrete state, which is known as DTMC SIR epidemic model, is discussed. Then assume time is continuous, the derivation of CTMC SIR epidemic model is presented in section 4, along with the connection and comparison between deterministic SIR model and CTMC SIR model. Section 5 studies the formulation of SDE SIR epidemic model. In section 6, two of four important properties is thoroughly discussed which are probability of an outbreak and the final size distribution.

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1 Appendix A

```r
#Define a function to obtain the final size distribution with its probability
finaldist <- function(N, R0){
  #Matrix size
  n <- (N+1)*(N+2)/2
  #Function to calculate p_s
  ps <- function(s){
    return(1/(1+R0*s/N))
  }
  #Create a matrix of the possible distribution of population
  #x - the number of susceptible
  x<-c()
  for(i in N:0){
    for(j in i:0){
      x<-append(x,j)
    }
  }
  #x - the number of infected
  y<-c()
  for(i in 0:N){
    y<-append(y,rep(i, N+1-i))
  }
  A <- cbind(x,y)
  #Create the transition matrix
  transMat <- matrix(data = rep(0, n^2), nrow = n)
  for(i in 1:n){
    for(j in 1:n){
      a <- A[j,1]
      b <- A[j,2]
      c <- A[i,1]
      d <- A[i,2]
      if((b == 0) & (d == 0) & (a == c)){
        transMat[i,j] = 1
      }
      else if((a == c) & (d == (b-1))){
        transMat[i,j] = ps(a)
      }
      else if((b != 0) & (c == (a-1)) & (d == (b+1))){
        transMat[i,j] = 1 - ps(a)
      }
    }
  }
  #Obtain the limit of transition matrix
  B <- transMat %^% (2*N-1)
  finalsize <- B[1:N+1, N+2]
  return(finalsize)
}
```

1

Figure 4: Code for Obtaining Final Size Distribution