The Stochastic Modelling of Endemic Diseases

Kurnia Susvitasari
School of Math. Science, University of Nottingham, The University Park, NG7 2RD, UK
E-mail: susvitasari@icloud.com

Titin Siswantining
Department Mathematic, University of Indonesia, Kampus UI Depok, 16424, Indonesia
E-mail: titin@sci.ui.ac.id

Abstract. A study about epidemic has been conducted since a long time ago, but genuine progress was hardly forthcoming until the end of the 19th century (Bailey, 1975). Both deterministic and stochastic models were used to describe these. Then, from 1927 to 1939 Kermack and McKendrick introduced a generality of this model, including some variables to consider such as rate of infection and recovery. The purpose of this project is to investigate the behaviour of the models when we set the basic reproduction number, $R_0$. This quantity is defined as the expected number of contacts made by a typical infective to susceptibles in the population. According to the epidemic threshold theory, when $R_0 \leq 1$, minor epidemic occurs with probability one in both approaches, but when $R_0 > 1$, the deterministic and stochastic models have different interpretation. In the deterministic approach, major epidemic occurs with probability one when $R_0 > 1$ and predicts that the disease will settle down to an endemic equilibrium. Stochastic models, on the other hand, identify that the minor epidemic can possibly occur. If it does, then the epidemic will die out quickly. Moreover, if we let the population size be large and the major epidemic occurs, then it will take off and then reach the endemic level and move randomly around the deterministic's equilibrium.

1. Introduction
Threshold theorem is the most important occurrence in the development of the mathematical theory of epidemic. It states that an epidemic can only occur if the initial number of susceptibles is larger than some critical value which depends on the parameters of the model under consideration (Ball, 1983). Nåsell (2002) also stated that the proportion of infectives in the deterministic model would converge to some equilibrium point as time approached infinity, for which we say that the epidemic enters endemic-equilibrium level or goes extinct. But the stochastic model predicted that once the epidemic is in equilibrium, it would become extinct. Both deterministic and stochastic models were important in any sense to describe this process behaviour. The deterministic model, in fact, is also an approximation of the stochastic model when the population size is sufficiently large (Nåsell, 2002). So in the other words, the stochastic model will have the same threshold value as the deterministic one, but the interpretation of this behaviour is different.

In this paper, we will investigate the behaviour of certain epidemic model, called SIS ($\text{susceptible} \rightarrow \text{infective} \rightarrow \text{susceptible}$) without demography, through its threshold. The
threshold behaviour is usually expressed in terms of epidemic basic reproduction number, $R_0$. This quantity is usually defined as the expected number of contacts made by a typical infective to susceptibles in the population. It is important to note that in general epidemic modelling, both stochastic and deterministic models have similar threshold value, which is attained at $R_0 = 1$. It then turns out that the models identify two parameter regions, $R_0 \leq 1$ and $R_0 > 1$, with qualitatively different behaviour. We will find out in later section why the threshold value is attained at $R_0 = 1$

Some simulations will be presented to understand the behaviour of the model priorly under various values of $R_0$’s and then we will provide the mathematical explanation as to why the model behaves as it is.

2. The SIS Epidemic Model without Demography

Suppose that we have a closed mixing population with initially $n$ individuals and $m$ ($m < n$) infectives. We define SIS model as follows.

At $t = 0$, there are $n - m$ susceptibles who are vulnerable to the diseases. Each infective contacts each susceptible according to independent Poisson processes with rate $\lambda n$ and if a susceptible is contacted, it immediately becomes an infective. The infectives also have an infectious period which follow iid exponential distributions with rate $\gamma$, and then removed, but once the infectives infectious period is over, the individual will immediately become vulnerable to the disease. Finally, the epidemic ends when no infective is left in the population.

Since we assume the population is closed, the SIS model without demography can be modelled using a univariate process. As we know, the SIS epidemic had two processes: infection and removal with rates $\lambda n/(n - i)$ and $\gamma i$, respectively. We can see in Figure 3 that the stochastic processes behaved similarly to deterministic ones. One could interpret the behaviour of the model by simply using deterministic approach, but some processes behave differently as shown in Figure 1, 2, and 4. It means that there is a certain random factor in the stochastic approach that can not be accounted for by deterministic approach.

Before we proceed, we will discuss the threshold behaviour of the model by deterministic approach. Suppose that we define a CTMC (continuous–time Markov chain), $\{Y_n(t) : t > 0\}$ in state space $S = \{0, 1, \ldots, n\}$ and transition rates $\Delta = \{q_{i,i+1}, q_{i,i-1}\}$, where $q_{i,i+1} = \lambda n/(n - i)$ and $q_{i,i-1} = \gamma i$. If we allow $Y_n(t)$ to be non–integer, we can interpret the transition scheme as $\frac{dY_n(t)}{dt} = \frac{\lambda}{n}Y_n(t)[n - Y_n(t)] - \gamma Y_n(t)$.

Let $y(t) = \frac{Y_n(t)}{n}$ represent the proportion of infective in the population at time $t$, then

$$\frac{dy(t)}{dt} = \lambda y(t) \cdot (1 - y(t)) - \gamma y(t).$$

Obviously, according to (1), the major epidemic occurs if and only if $\frac{dy}{dt} > 0$ and otherwise. At some time $t$, the increment of $y(t)$ will reach stationary and the process will hit the equilibrium point, as shown in Figure 1, 2, 3, and 4. So, it is possible to determine the equilibrium of $y(t)$ by letting $\frac{dy}{dt} = 0$, which are attained when $y(t) = 0$ or $y(t) = 1 - \frac{\gamma}{\lambda}$.

Now, if $R_0 = \frac{\lambda}{\gamma} \leq 1$, the only possible equilibrium point is at $y(t) = 0$, otherwise, if $R_0 > 1$, the equilibrium is reached at $y(t) = 1 - \frac{\gamma}{\lambda} = 1 - R_0^{-1}$. This is not surprising at all because if the infection rate is negative, the equilibrium is attained when the epidemic dies out. Similar explanation is applied if the infection rate is positive. The point $y(t) = 1 - R_0^{-1}$ is then called the endemic–equilibrium level.
In the later section, we will show that the SIS model approached by stochastic process can be approximated by deterministic process if we let \( n \to \infty \) in special case.

3. Branching Process

Suppose that in a closed population, just by the end of its lifetime, each individual has independently produced \( j \geq 0 \) offsprings with probability \( P_j \). Let \( X_n \) denote the size of \( n \)-th generation, then the process \( \{X_n : n = 0, 1, 2, \cdots \} \) is a Markov chain having non-negative integer state space, where state 0 is a recurrent state and others are transient. Since any finite transient state will be visited finitely often, this leads to the conclusion that if \( P_j > 0 \), then the population will either die out or take off.

Let \( \mu \) be the mean number of offspring from a single individual, then

\[
E(X_n) = E \left( E \left( \sum_{j=1}^{X_{n-1}} \zeta_j \mid X_{n-1} \right) \right), \quad \zeta_j \text{ is number of } j\text{th individual’s offspring}
\]

\[
= \mu^2 E(X_{n-2}) = \cdots = \mu^n E(X_0) = \mu^n, \quad \text{given } X_0 = 1.
\]

Suppose that \( \pi_0 = \lim P(X_n = 0 \mid X_0 = 1) \) denotes the probability that the population dies out. Note that if \( \mu < 1 \), then \( P(X_n \geq 1) \to 0 \) almost surely as \( n \to \infty \). This concept is very useful in epidemic modelling because when the expected number of infection is less than 1, then the epidemic will obviously die out. But, if \( \mu > 1 \), by conditioning on the \( X_1 \),

\[
\pi_0 = \sum_{j=0}^{\infty} P(\text{population dies out} \mid X_1 = j)P_j.
\]
Note that given $X_1 = j$, the population will eventually die out if and only if each of the $j$ families started by the members of the first generation die out. This statement is supported by the fact that the probability of extinction occurring in the early stage is non-zero. Moreover, the probability that the members of a typical family to die out is $\pi_0$. Thus, assuming that each individual acts independently, $P(\text{population dies out}|X_1 = j) = \pi_0$.

Hence, $\pi_0$ must satisfy

$$\pi_0 = \sum_{j=0}^{\infty} \pi_0^j P_j = E\left(\frac{X_i}{\pi_0}\right) = f(\pi_0)$$

where $f(\pi_0)$ is the pgf (probability generating function) of $X_1$, in such a way that $\pi_0$ is the smallest root in $[0, 1]$ satisfying equation (2).

4. Density Dependent Population Process

Suppose that $\{X_n(t) : t \geq 0\}$ is the CTMC process defined on $d$-dimensional integer lattice $\mathbb{Z}^d$ with finite number of possible transitions, given by $q_{i,i+t} = n \beta_i \left(\frac{k}{n}\right)$ where we define $\beta_i : \mathbb{Z}^d \to [0, \infty)$, $l \in \Delta \subseteq \mathbb{Z}^d$, $\beta_i(x) < \infty$ for all $x \in \mathbb{Z}^d$. In this context, we interpret $n$ as the area of region occupied by a certain population. According to Ethier and Kurtz (1986), if the the size of a certain population was $k$, then the density of that population was $k/n$ with intensities approximated proportionally to its size. For example, in the epidemic case, suppose that there are $i$-susceptible individuals who are vulnerable to the disease and $j$-infectious individuals. We assume that the disease transmission has constant rate $\lambda/n$ and the diseased-individual recovers with rate $\gamma$. An infection occurs when an infective makes contact to a susceptible. Therefore, the contact intensity and recovery intensity are $q_{j,j+1} = \frac{\lambda}{n} ij = n \lambda \left(\frac{i}{n}\right) \left(\frac{j}{n}\right)$ and $q_{j,j-1} = \gamma j = n \gamma \left(\frac{j}{n}\right)$, respectively. Both intensities are density-dependent functions.

Now, suppose that $Y_l$ is a independent standard Poisson process, defined for each of possible transition $l \in \Delta$. Therefore, by letting $X_n(0)$ be non-random,

$$X_n(t) = X_n(0) + \sum_{l \in \Delta} l Y_l \left(n \int_0^t \beta_l \left(\frac{X_n(s)}{n}\right) \, ds\right).$$

(3)

Note that the process $Y_l$ is a function of density-dependent. Therefore, the process $\{X_n(t) : t \geq 0\}$ equals to the summation of its initial value and the total increment given by the standard Poisson process during time interval $[0, t]$.

Now let $\tilde{Y}_l(u) = Y_l(u) - u$ be a centered Poisson process at its expectation and $\tilde{X}_n(t) = \frac{X_n(t)}{n}$. Following equation (3) and letting $F(x) = \sum_{l \in \Delta} l \beta_l(x)$, we can write equation (3) into

$$\tilde{X}_n(t) = \tilde{X}_n(0) + \frac{1}{n} \sum_{l \in \Delta} l \tilde{Y}_l \left(n \int_0^t \beta_l (\tilde{X}_n(s)) \, ds\right) + \int_0^t F(\tilde{X}_n(s)) \, ds.$$

(4)

We will show in a later section that the stochastic process in equation (4) can be approximated by non-random quantity when we let the population size become sufficiently large.

5. The Fundamental Result of Poisson Processes

To start this section, the readers are expected to have prior knowledge of martingale and stopping theorem.
The theorem introduced in this section is called fundamental result of Poisson process. But before that, consider the followings

**Theorem 5.1.** Let \(\{X_n; n \geq 0\}\) be a submartingale with respect to itself for which \(X_n \geq 0\) for all \(n \geq 0\). Then, for any \(\lambda > 0\),

\[
\lambda P\left(\max_{0 \leq k \leq n} X_k > \lambda\right) \leq E(X_n).
\]

(Ball, 2016)

**Lemma 5.2.** (Borel-Cantelli). Suppose that \(\{E_n: n \geq 1\}\) denotes a sequence of events in probability space \(\Omega\). If

\[
\sum_{n=1}^{\infty} P(E_n) < \infty,
\]

then \(P\{E_n \text{ occurs infinitely often for some } n\} = 0\).

Finally, the fundamental result of the Poisson process will be stated formally in the following theorem.

**Theorem 5.3.** If \(\{Y(t), t \geq 0\}\) is a standard Poisson process, then for all \(s \leq t\),

\[
\lim_{n \to \infty} \sup_{s \leq t} |n^{-1}Y(ns) - s| = 0
\]

almost surely.

**Proof.** Note that \(Y(ns) \sim \text{Poisson}(ns)\), for \(s \geq 0\) since it is a Poisson process. We can show easily that \((Y(ns) - ns)\) is a martingale. Further, \((Y(ns) - ns)^4\) is a submartingale. Therefore, by applying Theorem 5.1, for any \(\varepsilon > 0\)

\[
P\left(\sup_{0 \leq s \leq t} |Y(ns) - ns| \geq \varepsilon\right) = P\left(\sup_{0 \leq s \leq t} (Y(ns) - ns)^4 \geq \varepsilon^4 n^4\right)
\]

\[
\leq \frac{E(Y(nt) - nt)^4}{\varepsilon^4 n^4} \leq \frac{C(\varepsilon, t)}{n}.
\]

Consider equation (5). If we let \(n \to \infty\), then \(P\left(\sup_{0 \leq s \leq t} |Y(ns) - ns| \geq \varepsilon n\right) \to 0\). It implies that \(\lim_{n \to \infty} \sum_{n=1}^{\infty} P(|Y(ns) - ns|) < \infty\) since the probability of its supremum tends to zero as \(n\) goes to infinity. Therefore, according to Lemma 5.2, \(P\left(\sup_{0 \leq s \leq t} |n^{-1}Y(s) - s| \to 0 \text{ as } n \to \infty\right) = 1\). Hence, \(\lim_{n \to \infty} \sup_{s \leq t} |n^{-1}Y(ns) - s| = 0\) almost surely.

Note that the second term of (4) will converge to 0 if we let \(n\) be large according to Theorem 5.3. This suggests that \(\bar{X}_n(t)\) will be non-random as \(n \to \infty\). So, the process \(\bar{X}_n(t)\), given \(\bar{X}_n(0)\) is non-random, can be approximated by quantity \(\bar{X}_n(0) + \int_0^t F(\bar{X}_n(s))ds\) as \(n \to \infty\).

Before proving this statement, consider the following lemma.

**Lemma 5.4.** (Gronwall’s inequality). Suppose that \(f: \mathbb{R} \to \mathbb{R}\) satisfying \(0 < f(t) \leq a + b \int_0^t f(u)du\) for some \(a, b > 0\) and \(\forall t \geq 0\). Then \(\forall t \geq 0\), \(f(t) \leq ae^{bt}\.\)
Now, we will prove the previous statement by proving the below theorem.

Theorem 5.5. Let \( \lim_{n \to \infty} \bar{X}_n(0) = x_0 \) and \( x(t) = x_0 + \int_0^t F(x(u))du \) be the deterministic version of equation (4). Suppose that for each compact \( K \subset \mathbb{R}^d, \exists M_K > 0 \) such that \( \forall x, y \in K, |F(x) - F(y)| \leq M_K |x - y| \). Then, for \( 0 \leq s \leq t \),

\[
\lim_{n \to \infty} \sup_{s \leq t} |\bar{X}_n(s) - x(s)| = 0
\]

almost surely.

Proof. Given \( x(t) = x_0 + \int_0^t F(x(u))du \), thus

\[
|\bar{X}_n(t) - x(t)| \leq |\bar{X}_n(0) - x(0)| + \frac{1}{n} \sum_{l \in \Delta} |l| \sup_{s \leq t} |\bar{Y}_1(n \beta_l (\bar{X}_n(s)))| + \int_0^t M_k |\bar{X}_n(s) - x(s)| \, ds.
\]

Now consider the second term of the right hand side of equation (6).

\[
\frac{1}{n} \sum_{l \in \Delta} |l| \sup_{s \leq t} |\bar{Y}_1(n \beta_l (\bar{X}_n(s)))| = \sum_{l \in \Delta} |l| \sup_{s \leq t} n^{-1} \beta_l (\bar{X}_n(t)) - \beta_l (\bar{X}_n(t)) \leq 0.
\]

But, according to Theorem 5.3, if we let \( n \to \infty \), then \( n^{-1} \beta_l (\bar{X}_n(t)) \to 0 \) almost surely. Therefore, equation (6) now becomes

\[
|\bar{X}_n(t) - x(t)| = |\bar{X}_n(0) - x(0)| + \int_0^t M_k |\bar{X}_n(s) - x(s)| \, ds.
\]

as \( n \to \infty \). By applying Lemma 5.4, \( \lim_{n \to \infty} |\bar{X}_n(t) - x(t)| \leq |\bar{X}_n(0) - x(0)| \cdot e^{M_K t} = 0 \) since \( \lim_{n \to \infty} \bar{X}_n(0) = x(0) \). Therefore, \( 0 \leq \lim_{n \to \infty} \sup_{s \leq t} |\bar{X}_n(s) - x(s)| \leq \lim_{n \to \infty} |\bar{X}_n(t) - x(t)| = 0 \).

Hence, by sanwich property, \( \lim_{n \to \infty} \sup_{s \leq t} |\bar{X}_n(s) - x(s)| = 0 \).

Theorem 5.5 suggests that as \( n \to \infty \), the process \( \{\bar{X}_n(t), t \geq 0\} \) will resemble the deterministic version \( x(t) \). It means that for large \( n \), the process will settle down and randomly move around its mean. We can use this analogy to approximate the stochastic epidemic model when it reaches endemic-equilibrium.

Now, see Figure 1, 2, and 4. In stochastic approximation, even though \( R_0 > 1 \), there is a non-zero probability that the epidemic will die out. This fact violates our deterministic approximation. Therefore, we will investigate why such scenario occurred. Note that in the stochastic version of the SIS model, if the number of susceptibles \( n \) is large, the process of infectives can be approximated by a branching process. Following the definition of the SIS model with each shape of an epidemic with few initial infectives, we know that contacts made by a typical infective to susceptibles follow a Poisson process of rate \( \beta = \lambda/n \). Suppose that \( T_i \) is infection period of \( i \)-th typical infective, which is assumed to follow independent exponential distributions with intensity \( \gamma \) and let \( R \) be the total number of contacts made by a typical infective in the epidemic model. Then,

\[
R \mid T = t \sim \text{Poisson}(\beta t), \quad (7a)
\]

\[
T \sim \text{exponential}(\gamma). \quad (7b)
\]
Table 1: Comparison table of probability the epidemics to die out approximated by branching process and empirical with $m = 1$

| $R_0$ | Population Size | Branching Process | Empirical (10000 runs) |
|-------|-----------------|-------------------|------------------------|
| ≤ 1   | $N = 100$       | 1                 | 1                      |
|       | $N = 1000$      | 1                 | 1                      |
| 3.0   | $N = 100$       | 0.3333            | 0.3420                 |
|       | $N = 1000$      | 0.3333            | 0.3331                 |
| 5.0   | $N = 100$       | 0.2               | 0.1997                 |
|       | $N = 1000$      | 0.2               | 0.1996                 |
| 8.0   | $N = 100$       | 0.125             | 0.1273                 |
|       | $N = 1000$      | 0.125             | 0.1282                 |

Now, suppose that $f(s), s \in [0, 1]$ is the pgf of $R$ and $g(t) (t \geq 0)$ is the pdf of $T$. Then,

$$f(s) = \sum_{k=0}^{\infty} s^k \int_0^\infty P(R = k \mid T = t)g(t)dt = \frac{\gamma}{\beta + \gamma} \sum_{k=0}^{\infty} \left( \frac{s\beta}{\beta + \gamma} \right)^k.$$

Note that according to Section 3, we find $s$, such that $f(s) = s$. Therefore, $s = 1$ or $s = \frac{\gamma}{\beta}$.

If $\gamma \geq \beta$, then the smallest root is 1, but if $\gamma < \beta$, then the smallest root is $\frac{\gamma}{\beta}$. Hence, suppose there are $m$ initial infectives in the population and assuming that the contacts made are mutually independent, then

$$P\text{(epidemic dies out)} \approx \begin{cases} 1 & \text{if } \gamma \geq \beta \\ \left(\frac{\gamma}{\beta}\right)^m & \text{if } \gamma < \beta. \end{cases}$$

Once again, the above result explains threshold behaviour of the process. All figures confirm the interpretation of threshold behaviour of the SIS deterministic model, that if $R_0 > 1$, major epidemic will occur despite of its initial values and population size. But in the stochastic model (which are displayed in jagged plots), some plots do not mimic the deterministic paths. For example, in Figure 1, the epidemic with $R_0 = 1.5$ and $R_0 = 1.25$ quickly die in a very short time. If we apply branching process approximation, the probability that an epidemic dies out in Figure 1 are 0.11, 0.25, 0.44, and 0.64, respectively. It seems that as $R_0$ approaches 1 from the right ($R_0 \downarrow 1$), the greater the probability of an epidemic to die out. But look at Figure 3. Despite similar population size and $R_0$’s, the last two epidemic models (indicated by green and orange colours) do not die out. It turns out that by using the branching process, the probability that the last two epidemics in Figure 3 to die out decreases to 0.017 and 0.107, respectively. So, we could safely claim that when $R_0 > 1$, the stochastic model of the SIS epidemic to die out quickly depends upon the proportion of its initial infectives since intuitively, if there are few initial infectives present in the population, according to the branching process theory, there is non-zero probability that their infectious periods will be over before they make contact with any susceptibles. Another simulation is provided in Table 1, where we compare the probability of the epidemics to die out approximated by branching process and empirical.

6. Conclusion
We have successfully showed that both deterministic and stochastic models performed similar results when $R_0 \leq 1$. That is, the disease-free stage in the epidemic. But when $R_0 > 1$, the deterministic and stochastic approaches had different interpretations. In the deterministic
models, both the SIS and SIR models showed an outbreak of the disease and after some time \( t \), the disease persisted and reached endemic-equilibrium stage. The stochastic models, on the other hands, had different interpretations. If we let the population size be sufficiently large, the epidemic might die out or survive. There were essentially two stages to this model. First, the infection might die out in the first cycle. If it did, then it would happen very quickly, just like the branching process theory described. Second, if it survived the first cycle, the outbreak was likely to occur, but after some time \( t \), it would reach equilibrium just like the deterministic version. In fact, the stochastic models would mimic the deterministic’s paths and be scattered randomly around their equilibrium point.