

## A QUASI-BIRTH-DEATH PERSPECTIVE OF SUSCEPTIBLE-INFECTIOUS-RECOVERED TYPE MODEL

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**ABSTRACT.** This research focuses on the development of a Susceptible-Infectious-Recovered (SIR) model to study the spread of the disease using stochastic approaches. Specifically, the emphasis is on the stochastic perspective, employing a Discrete Markov Chain as the stochastic model for the SIR model. Furthermore, the quasi-birth-death (QBD) process is used to formulate the stochastic model for the SIR model. The SIR model consists of three compartments representing susceptible (S), infected (I), and recovered (R) individuals. Initially formulated as a set of differential equations, the SIR model is then transformed into a probabilistic model. To proceed with the QBD process, the transition matrix and state space are constructed, forming the P matrix. Within the QBD process, a P matrix is prepared containing submatrices derived from the transition matrix. Furthermore, steady-state analysis is performed on the P matrix using the QBD process. This approach enables a probabilistic perspective for studying disease spread through the SIR model, allowing for a deeper understanding of the dynamics and potential outcomes.

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Key words and phrases. SIR model; stochastic approaches; discrete Markov chain; quasi-birth-death process; disease spread.

### 1. INTRODUCTION

In recent years, there has been a growing diversity in mathematical research, especially in modeling a problem in real life. An example of modeling using a mathematical model is the disease case model. In recent years, infectious diseases caused by viruses and bacteria have infected and plagued human life. Many diseases last a long time, and there are also diseases that spread only temporarily, such as dengue fever (DHF), influenza, to the disease that has become a recent pandemic, namely COVID-19. In various studies, epidemic diseases have been discussed to have a negative impact on society in

various sectors, including education, tourism, and especially socioeconomic aspects in areas where disease outbreaks spread throughout the world [1].

The spread of disease occurs due to viruses and bacteria that infect human pathogenic cells. The spread of epidemic diseases can occur through physical contact with infected people, the environment, bites, and attacks from animals contaminated with viruses and bacteria that can cause the spread of disease, as well as the consumption of food and drink containing viruses or bacteria. There are many cases of epidemic diseases that occur in densely populated cities, and the spread occurs very quickly, so epidemic diseases often cause many cases of death [2].

The spread of infected diseases according to their proportions can be divided into three options, namely endemic, epidemic, and pandemic diseases, depending on the extent of the area contaminated with viruses or bacteria [3]. Many impacts resulted from the three types of disease spread. Starting from the economic aspect, education, and even social life for developed and developing countries. Therefore, a mathematical model was formed that served to interpret how the effects of disease spread in a population [4]. Incidence, prevention, infection rates, and deaths can be predicted and interpreted by mathematical models.

Predictions in the case of mathematical modeling are helpful in understanding the extent of disease infecting a population, the effects of widespread disease, and how long the disease will last [4]. By analyzing the effect and extent of disease spread using a mathematical model, accurate predictions can be made regarding how the infection will spread, so that preventive and treatment measures can be taken against the spread of the disease in a population [5].

The mathematical model that will be studied in this paper is an SIR model (Susceptible-Infected-Recovery). The SIR model can be solved using deterministic and stochastic models. Numerous studies have been conducted to develop deterministic models for the SIR model. Research related to the mathematical model of SIR began with research conducted by Daniel Bernoulli, who examined the effect of cowpox inoculation on the spread of smallpox in 1760 [6], then research carried out by Meghan related to a simple mathematical model that was implemented for the number of people infected with infectious diseases such as chickenpox in a closed population [7]. Some of the following studies are studies conducted with a deterministic model. However, there have been limited studies in exploring stochastic modeling for the SIR model.

The deterministic model assumes that the parameters of susceptible individuals who come into contact with infected individuals and the parameters of individuals who have recovered are fixed and do not change periodically. However, in reality, the numbers on these parameters differ from one individual to another. Thus, it is necessary to identify the randomness of the parameter numbers obtained from one individual and another. The stochastic model is used to overcome the randomness of the model parameters.

The disease model that will be studied in this study is the SIR model with an addition of the birth-and-death rate with reference to the SIR model with a constant population [8]. The model to be studied in this study is a discrete Markov chain SIR model in which the stability of the system will be sought using the Quasi-Birth-Death (QBD) process. The QBD process on non-negative integers is a Markov process in which transitions in the system are only allowed from state  $n$  to the next higher state  $n + 1$  for every  $n \geq 0$  and from  $n$  to  $n - 1$  for every  $n \geq 1$  [9].

Based on the description that has been explained, a model of epidemic SIR will be formed as a Discrete Time Markov Chain (DTMC). The transition probabilities and transition matrix of the DTMC SIR model will be sought, and the stability of the system will be sought using numerical simulations generated from the QBD process using the rate matrix. In the end, from the QBD process that has been made, further studies can be made on the steady-state analysis of the DTMC SIR model.

## 2. MODELLING FORMULATION

The next section will discuss the form of the Susceptible-Infected-Recovered (SIR) model in the form of a Markov chain and will look for the stability of the discrete Markov chain SIR model system. The simple epidemiological model was first proposed by Kermack and McKendrick [10]. The method used to find stability from the Discrete Markov Chain SIR model is to form a rate matrix which will be used to analyze steady state using the QBD process in order to obtain stability from the system.

**2.1. The Stochastic SIR Model.** In this section, the formation of an SIR model will be discussed. First, a SIR model will be formed with three compartments, namely susceptible individuals (Susceptible), infected individuals (Infected), and recovered individuals (Recovered). Then, from the three compartments formed, the deterministic SIR model compartment is described, which consists of the variables  $S$ ,  $I$ , and  $R$  as described in Figure 1.

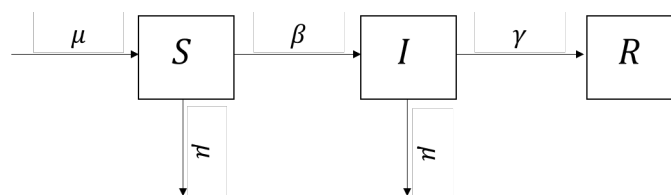


FIGURE 1. SIR Mathematical Model

The SIR model described has parameters  $\mu$ ,  $\beta$ , and  $\gamma$  each of which shows the birth or death rate with the assumption that the birth and death rates are equal, the contact rate of disease spread, and disease cure rate, respectively.

**2.2. Discrete Time Markov Chain (DTMC) SIR Model.** Furthermore, from the SIR epidemic model, a discrete Markov model will be formulated with the population in the system denoted by the variables

$S(t)$ ,  $I(t)$ , and  $R(t)$  with  $t \in T = \{0, \Delta t, 2\Delta t, \dots\}$  and  $S(t), I(t), R(t) \in \{0, 1, 2, \dots, N\}$ . The recovered individual is no longer susceptible and immune to the infection that spreads the disease. The assumptions made for a constant population produce a value of  $N$  at time  $t$  as follows,

$$N = S(t) + I(t) + R(t) \quad (1)$$

so that

$$\frac{dN}{dt} = \frac{dS(t)}{dt} + \frac{dI(t)}{dt} + \frac{dR(t)}{dt} = 0. \quad (2)$$

Two *states*, i.e.,  $S$  and  $I$ , are used to construct probabilities in the Markov process, with the number of recovered individuals depending on the susceptible and infected individuals, so that it applies

$$R(t) = N - S(t) - I(t). \quad (3)$$

It is assumed that every time there is a transition, there will be a movement for each individual, both susceptible, infected, and cured. For each  $\Delta t$ , the possible transitions that occur between individuals are:

- (1)  $(s, i) \xrightarrow{\Delta t} (s - 1, i + 1)$  for each susceptible individual that switches to an infected individual.
- (2)  $(s, i) \xrightarrow{\Delta t} (s + 1, i)$  for each individual born, the birth rate is assumed to be constant.
- (3)  $(s, i) \xrightarrow{\Delta t} (s - 1, i)$  for each susceptible individual who dies, it is assumed that the death rate is constant and equal to the birth rate.
- (4)  $(s, i) \xrightarrow{\Delta t} (s, i - 1)$  for each infected individual who has recovered or dies, the death rate is assumed to be constant and equal to the birth rate.
- (5)  $(s, i) \xrightarrow{\Delta t} (s, i)$  if there are no individual transition changes.

For each change in time, there are six transitions in the system, namely infected individuals increase by one from the infected susceptible population, susceptible individuals increase by one with births, susceptible individuals also decrease by one due to natural death, infected individuals recover and cannot return to susceptible individuals, so that one less infected individual, and no change in the number of infected cases in the population. In the case of the SIR model, *trajectory* is defined as the set of  $U$  from *state*  $s$  and  $i$  formed on the Markov system

$$U = ((s_0, i_0), \Delta t, (s_{\Delta t}, i_{\Delta t}), \Delta t, \dots, (s, i), \Delta t, (k, j)). \quad (4)$$

Equation (4) represents the system starts at  $(s_0, i_0)$ . After a unit time period  $\Delta t$ , the system switches to *state*  $(s_{\Delta t}, i_{\Delta t})$ . The system remains in *state*  $(s_{\Delta t}, i_{\Delta t})$  until the next unit time period  $\Delta t$  the system switches back and forth until *state*  $(k, j)$ . Figure 2 shows the *trajectory* of the Discrete Time Markov Chain SIR model.

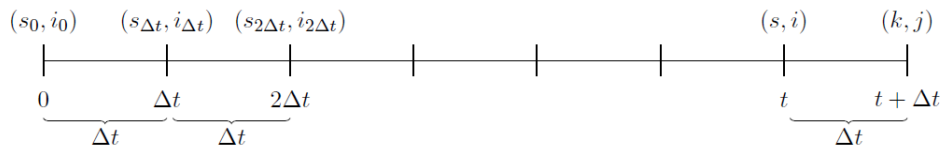


FIGURE 2. DTMC SIR Model Trajectory

**2.3. Transition Probability.** Next, the transition probabilities of the DTMC SIR model will be formulated from the transitions that have been obtained. The transitional change in a susceptible individual at time  $t$  is given as follows

$$\frac{dS(t)}{dt} = \mu - \frac{\beta S(t)I(t)}{N} - \mu S(t). \tag{5}$$

In susceptible individuals, the population will increase from the birth of individuals and decrease from natural death and disease infection. Based on Equation (5), the number of susceptible individuals will increase or decrease over time. This means that when susceptible individuals decrease due to infection, then infected individuals increase. Three transitions are obtained in vulnerable populations, namely,  $(s, i)$  to  $(s - 1, i + 1)$ ,  $(s, i)$  to  $(s + 1, i)$ , or  $(s, i)$  to  $(s - 1, i)$ . The probability of each vulnerable population transition is

$$p_{(s,i) \rightarrow (s-1,i+1)}(\Delta t) = \frac{\beta si}{N} \Delta t \tag{6}$$

$$p_{(s,i) \rightarrow (s+1,i)}(\Delta t) = \mu N \Delta t \tag{7}$$

$$p_{(s,i) \rightarrow (s-1,i)}(\Delta t) = \mu s \Delta t. \tag{8}$$

Next, individuals in the infected compartment experience a transition, namely when infected individuals recover or die naturally. Changes that occur in infected individuals at time  $t$  are

$$\frac{dI(t)}{dt} = \beta S(t)I(t) - (\gamma + \mu)I(t) + \omega R(t). \tag{9}$$

The transition that occurs in infected individuals who recover or die is  $(s, i)$  to  $(s, i - 1)$ . The probability of an infected individual recovering or an infected individual experiencing a natural death is

$$p_{(s,i) \rightarrow (s,i-1)}(\Delta t) = (\gamma + \mu)i \Delta t. \tag{10}$$

Further, because it is assumed that the population is constant, a transition is obtained that the susceptible and infected populations do not experience compartmentalization so that the probability of the population remains constant as given below.

$$p_{(s,i) \rightarrow (s,i)}(\Delta t) = 1 - [\beta si + \mu N + \mu s + (\gamma + \mu)i] \Delta t. \tag{11}$$

From Equation (6)-(8), (10), and (11), the transition probability of the DTMC SIR model is obtained as follows

$$P_{(s,i) \rightarrow (s+k,i+j)}(\Delta t) = \begin{cases} \frac{\beta si}{N} \Delta t, & (k, j) = (s-1, i+1) \\ \mu \Delta t, & (k, j) = (s+1, i) \\ \mu s \Delta t, & (k, j) = (s-1, i) \\ (\gamma + \mu) i \Delta t, & (k, j) = (s, i-1) \\ 1 - \left[ \frac{\beta si}{N} + \mu + \mu s + (\gamma + \mu) i \right] \Delta t, & (k, j) = (s, i) \\ 0, & (k, j) \text{ otherwise.} \end{cases} \quad (12)$$

From the transition probability and state used, it is obtained that set of  $\{(S(t), I(t)) | t \geq 0\}$  is a two-dimensional discrete Markov process with state space  $\{(s, i) | 0 \leq s, i \leq N, s + i \leq N\}$ . Next, we will discuss the state space transition matrix of the DTMC SIR model.

**2.4. Transition Matrix and Diagram.** The  $P(\Delta t)$  matrix is defined as the transition matrix and the transition diagram used to describe the transitions that occur in the DTMC SIR model is given below.

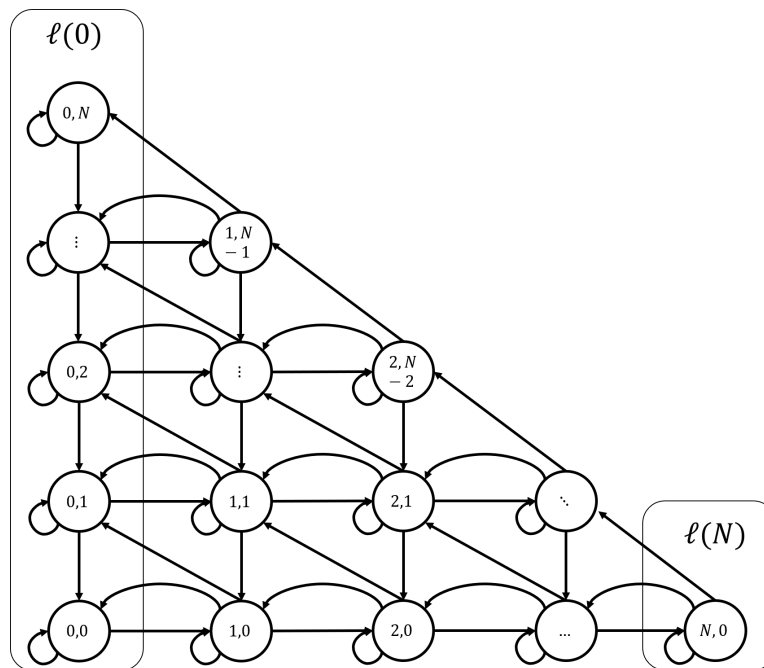


FIGURE 3. DTMC SIR Model Transition Diagram

Based on the state space diagram shown in Figure 3 the transition in the model shown vertically starts from level zero, denoted by  $\ell(0)$  to  $\ell(N)$ . The arrows on state starting from state  $(s, i) = (0, 0)$  indicate the transitions that occur in that state.

Next, the transition matrix  $\mathbf{P}$  where the transition matrix with size  $\frac{(N+1)(N+2)}{2}$  describe the transition probability that happen from the susceptible and infected population  $(s, i)$  to  $(k, j)$  will be formulated

in which the elements of the matrix are tridiagonal block matrix with submatrices, namely  $A_{00}$ ,  $A_{01}$ ,  $A_{10}$ ,  $\dots$ , on the level  $\ell(0)$ ,  $\ell(1)$ ,  $\dots$ ,  $\ell(N)$ . The transition matrix  $\mathbf{P}$  is given as follow.

$$\mathbf{P} = \begin{bmatrix} A_{00} & A_{01} & 0 & 0 & \dots & 0 & 0 & 0 \\ A_{10} & A_{11} & A_{12} & 0 & \dots & 0 & 0 & 0 \\ 0 & A_{20} & A_{21} & A_{22} & \dots & 0 & 0 & 0 \\ \vdots & \vdots & \vdots & \vdots & \ddots & \vdots & \vdots & \vdots \\ 0 & 0 & 0 & 0 & \dots & A_{N-1,N-2} & A_{N-1,N-1} & A_{N-1,N} \\ 0 & 0 & 0 & 0 & \dots & 0 & A_{N,N-1} & A_{N,N} \end{bmatrix}, \quad (13)$$

where

$$A_{00} = \begin{bmatrix} 1 - b(0,0)\Delta t & 0 & 0 & \dots & 0 \\ d(0,1)\Delta t & 1 - [b(0,1) + d(0,1)] & 0 & \dots & 0 \\ 0 & d(0,2)\Delta t & 1 - [b(0,2) + d(0,2)]\Delta t & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \dots & 1 - [b(0,N) + d(0,N)]\Delta t \end{bmatrix},$$

$$A_{01} = \begin{bmatrix} b(0,0)\Delta t & 0 & 0 & \dots & 0 \\ 0 & b(0,1)\Delta t & 0 & \dots & 0 \\ 0 & 0 & b(0,2)\Delta t & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \dots & b(0,N-1)\Delta t \\ 0 & 0 & 0 & \dots & 0 \end{bmatrix},$$

$$A_{10} = \begin{bmatrix} c(1,0)\Delta t & a(1,0)\Delta t & 0 & \dots & 0 \\ 0 & c(1,1)\Delta t & a(1,1)\Delta t & \dots & 0 \\ 0 & 0 & c(1,2)\Delta t & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \dots & a(1,N-1)\Delta t \end{bmatrix},$$

$$\begin{aligned}
A_{11} &= \begin{bmatrix} 1 - [a(1,0) & 0 & 0 & \dots & 0 \\ +b(1,0) \\ +c(1,0)]\Delta t & & & & \\ d(1,1)\Delta t & 1 - [a(1,1) & 0 & \dots & 0 \\ +b(1,1) \\ +c(1,1) \\ +d(1,1)]\Delta t & & & & \\ 0 & d(1,2)\Delta t & 1 - [a(1,2) + b(1,2) & \dots & 0 \\ +c(1,2) + d(1,2)]\Delta t & & & & \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \dots & 1 - [a(1, N-1) \\ +c(1, N-1) \\ +d(1, N-1)]\Delta t \end{bmatrix}, \\
A_{12} &= \begin{bmatrix} b(1,0)\Delta t & 0 & 0 & \dots & 0 \\ 0 & b(1,1)\Delta t & 0 & \dots & 0 \\ 0 & 0 & b(1,2)\Delta t & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \dots & b(1, N-1)\Delta t \\ 0 & 0 & 0 & \dots & 0 \end{bmatrix}, \\
&\vdots \\
A_{N-1, N-2} &= \begin{bmatrix} a(N-1, N-2)\Delta t & c(N-1, N-2)\Delta t & 0 \\ 0 & a(N-1, N-1)\Delta t & c(N-1, N-1)\Delta t \end{bmatrix}, \\
A_{N-1, N-1} &= \begin{bmatrix} 1 - [a(N-1, N-2) + b(N-1, N-2) & 0 \\ +c(N-1, N-2) + d(N-1, N-2)]\Delta t & \\ 0 & 1 - [a(N-1, N-1) \\ +c(N-1, N-1)]\Delta t \end{bmatrix}, \\
A_{N-1, N} &= \begin{bmatrix} b(N-1, 0)\Delta t \\ 0 \end{bmatrix}, \\
A_{N, N-1} &= \begin{bmatrix} c(N, 0)\Delta t & a(N, 0)\Delta t \end{bmatrix}, \\
A_{N, N} &= \begin{bmatrix} 1 - [a(N, 0) + c(N, 0)]\Delta t \end{bmatrix}.
\end{aligned}$$



It is clear that  $\{X(t), t \geq 0\} = \{(S(t), I(t)) | t \geq 0\}$  is a non-homogeneous QBD process. The following section will focus on examining the steady-state distribution of the process.

### 3. STEADY-STATE ANALYSIS

Assume that the matrix  $\mathbf{P}$  in Equation (13) is irreducible and  $\{X(t), t \geq 0\}$  is ergodic, so that the non-homogeneous QBD processes of the DTMC SIR model have a stationary distribution. The stationary probability vector is denoted by  $\pi$ , where  $\pi$  is a unique solution to the balance equation  $\pi = \pi P$  and  $\sum \pi e = 1$ , where  $\pi_{si}$  is given as follow.

$$\pi_{si} = (\pi_{00}, \pi_{01}, \dots) \quad (14)$$

**3.1. Steady-State Analysis.** The stationary probability vector  $\pi$  of the Markov chain  $\{(S(t), I(t)), t \geq 0\}$  satisfies the following equations

$$\pi_{si} \mathbf{P} = \pi_{si}, \quad (15)$$

$$\sum \pi_{si} e = 1, \quad (16)$$

where  $s, i = 0, \dots, N$  and  $e$  is a  $\frac{(N+1)(N+2)}{2}$  column vector of 1.

The vector  $\pi_{si}$  represents the stationary probability of the DTMC SIR model of susceptible and infected individuals at level  $s$  and phase  $i$ , where  $0 \leq s, i \leq N$  and  $s + i \leq N$ . Based on the form of transition matrix  $P$  as given in Equation (13), then for every  $0 \leq s, i, k \leq N$  and  $0 \leq s + i \leq N$ , the vector  $\pi$  can be expressed as

$$\pi = (\pi^{(0)}, \pi^{(1)}, \dots, \pi^{(N)}), \quad \text{where } \pi^{(k)} = (\pi_{si}^{(k)}). \quad (17)$$

For  $k = 1, 2, \dots, N - 1$ , the stationary probability  $\pi^{(k)}$  can be expressed as follow.

$$\begin{aligned} \pi^{(0)} &= (\pi_{00}^{(0)}, \pi_{01}^{(0)}, \dots, \pi_{0,N-1}^{(0)}, \pi_{0N}^{(0)}) \\ \pi^{(1)} &= (\pi_{10}^{(1)}, \pi_{11}^{(1)}, \dots, \pi_{1,N-1}^{(1)}) \\ &\vdots \\ \pi^{(N)} &= (\pi_{N0}^{(N)}). \end{aligned}$$

Refer to Ramaswami [9], the stationary distribution of a non-homogeneous discrete time Markov chain can be expressed as

$$\pi^{(k)} = \pi^{(k+1)} R^{(k)}, \quad k = 1, 2, \dots, N - 1, \quad (18)$$

where the rate matrix  $R^{(k)} = \{R_{si}^{(k)}\}$  is the expected value of the number of visits to  $(k, j)$  before returning to level  $\ell(k + 1) \cup \dots \cup \ell(N)$  and the process starts from  $(k + 1, i)$ . On one hand, by applying

the balance equation which are  $\pi \mathbf{P} = \pi$  and  $\sum \pi e = 1$  it yields

$$\pi^{(0)} A_{00} + \pi^{(1)} A_{10} = \pi^{(0)} \quad (19)$$

$$\pi^{(0)} A_{01} + \pi^{(1)} A_{11} + \pi^{(2)} A_{21} = \pi^{(1)} \quad (20)$$

$$\pi^{(1)} A_{12} + \pi^{(2)} A_{22} + \pi^{(3)} A_{32} = \pi^{(2)}$$

$$\vdots$$

$$\pi^{(N-1)} A_{N-1,N} + \pi^{(N)} A_{NN} = \pi^{(N)}$$

and

$$\sum_{i=0}^{\infty} \pi^{(i)} e = 1. \quad (21)$$

From Equation (19) we have

$$\begin{aligned} \pi^{(0)} &= \pi^{(1)} A_{10} (I - A_{00})^{-1} \\ \pi^{(0)} &= \pi^{(1)} R^{(0)}, \end{aligned} \quad (22)$$

where  $R^{(0)} = A_{10} (I - A_{00})^{-1}$ . By substituting Equation (18) into the Equation (20), it yields

$$\begin{aligned} \pi^{(0)} A_{01} + \pi^{(1)} A_{11} + \pi^{(2)} A_{21} &= \pi^{(1)} \\ \pi^{(2)} R^{(1)} R^{(0)} A_{01} + \pi^{(2)} R^{(1)} A_{11} + \pi^{(2)} A_{21} &= \pi^{(2)} R^{(1)} \\ \pi^{(2)} (R^{(1)} R^{(0)} A_{01} + R^{(1)} A_{11} + A_{21}) &= \pi^{(2)} (R^{(1)}) \\ R^{(1)} R^{(0)} A_{01} + R^{(1)} A_{11} + A_{21} &= R^{(1)}. \end{aligned} \quad (23)$$

From Equation (18) vector  $\pi^{(0)}$  can be formed recursively as

$$\pi^{(0)} = \pi_N R^{(N-1)} \dots R^{(0)}, \quad (24)$$

then Equation (19) can be written as

$$\begin{aligned} \pi^{(0)} A_{00} + \pi^{(1)} A_{10} &= \pi^{(0)} \\ \pi^{(N)} (R^{(N-1)} \dots R^{(0)} A_{00} + R^{(N-2)} \dots R^{(1)} A_{10} - R^{(N-1)} \dots R^{(0)}) &= 0. \end{aligned} \quad (25)$$

Next, based on Equation (18) and (21) we obtain

$$\begin{aligned} \sum_{i=0}^{\infty} \pi^{(i)} e &= 1 \\ (\pi^{(0)} + \pi^{(1)} + \dots + \pi^{(N)}) e &= 1 \\ \pi^{(N)} (R^{(N-1)} \dots R^{(0)} + R^{(N-2)} \dots R^{(1)} + \dots + I) e &= 1. \end{aligned} \quad (26)$$

WLOG, based on Ramaswami [9] and Equations (23)-(26), the matrix  $\mathbf{P}$  is positive recurrent if and only if rate matrix  $R$  is a minimal and non-negative solution of the equation

$$R^{(k)} R^{(k-1)} A_{k-1,k} + R^{(k)} A_{k,k} + A_{k+1,k} = R^{(k)}, \quad \text{for } k = 1, 2, \dots, N-1, \quad (27)$$

and  $\pi^{(k)}$  is the unique solution that satisfies

$$\pi^{(k)} (R^{(k-1)} \dots R^{(0)} A_{00} + R^{(k-2)} \dots R^{(1)} A_{10} - R^{(k-1)} \dots R^{(0)}) = 0, \quad (28)$$

$$\pi^{(N)} (R^{(N-1)} \dots R^{(0)} + R^{(N-2)} \dots R^{(1)} + \dots + R^{(N-1)} + I)e = 1. \quad (29)$$

**3.2. Performance Analysis.** Having acquired the steady-state distribution  $\pi$ , we now analyze the performance of the DTMC SIR model. Here, we adapt a two-dimensional queueing system to assess the model's performance. The probability that there are  $s$  susceptible individuals in the system is

$$P\{L_s = s\} = \sum_{i=0}^N \pi_{si}, \quad (30)$$

where  $0 \leq s \leq N$ .

On other hand, denote  $P\{L_i = i\}$  is the probability that an infected individual is in *phase*  $i$ ,  $0 \leq i \leq N$ .

Then, the probability that the environment is in the  $i$  phase is obtained

$$P\{L_i = i\} = \sum_{s=0}^N \pi_{si}. \quad (31)$$

Suppose  $E(L_s)$  and  $W(L_s)$  represent the average number of susceptible individuals at the system and the average waiting time for susceptible individuals before entering infected compartment in the system, respectively, then we have

$$\begin{aligned} E(L_s) &= \sum_{s=0}^{\infty} s P\{L_s = s\} \\ &= \sum_{s=0}^{\infty} s \sum_{i=0}^N \pi_{si}^{(k)}, \end{aligned} \quad (32)$$

and

$$\begin{aligned} W(L_s) &= \frac{E(L_s)}{\sum_{i=0}^N P\{L_i = i\} \lambda_i} \\ &= \frac{\sum_{s=0}^{\infty} s \sum_{i=0}^N \pi_{si}^{(k)}}{\sum_{i=0}^N \lambda_i \sum_{i=0}^N \pi_{si}^{(k)}}. \end{aligned} \quad (33)$$

**3.3. Numerical Example.** In this numerical simulation, we assume that the number of population is 100. The parameter values of the DTMC SIR model are given in Table 1 based on research conducted by [11], [12], [13], and [14].

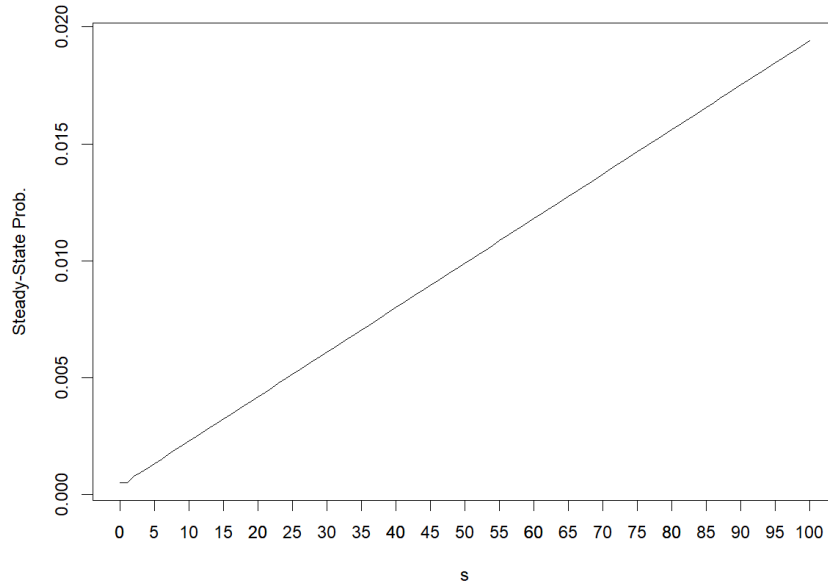
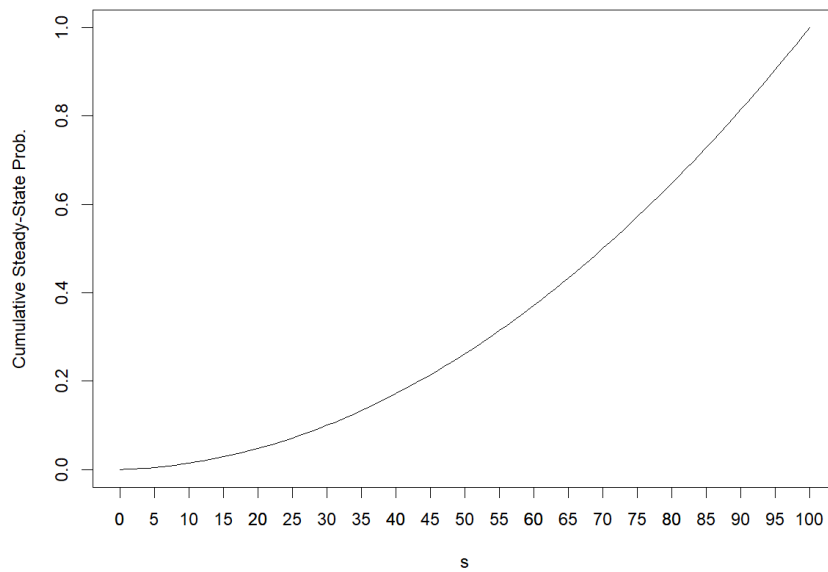
Parameter	Value
$\beta$	0.02
$\gamma$	0.08
$\mu$	0.01

TABLE 1. Parameter values

Further, the steady-state probabilities  $\pi^{(k)}$  presented in Table 2 were computed using R software. Figure 4 and 5 represent the steady-state probability  $\pi^{(k)}$  and cumulative steady-state probability  $\sum_{s=0}^k \pi^{(s)}$  over  $s$  individuals, respectively.

$k$	$\pi^{(k)}$	$\sum_{s=0}^k \pi^{(s)}$
0	0.0005177895	0.0005177895
1	0.0005177895	0.001035579
2	0.0007766842	0.001812263
3	0.0009492807	0.002761544
4	0.001143452	0.003904996
5	0.001333308	0.005238304
10	0.002285809	0.01476252
20	0.004190650	0.04809724
30	0.006095492	0.1004804
40	0.008000333	0.1719119
50	0.009905174	0.2623919
60	0.01181001	0.3719202
70	0.01371486	0.500497
80	0.01561970	0.6481222
90	0.01752454	0.8147958
100	0.01942938	1

TABLE 2. Some steady-state probabilities  $\pi^{(k)}$

FIGURE 4. Steady-state probability over  $s$  individualsFIGURE 5. Cumulative steady-state probability over  $s$  individuals

Moreover, by applying Equation (32) and (33), the average number of susceptible individuals in the system and the average number of susceptible individuals entering the infectious compartment are 1 and 100, respectively. It means that every susceptible individuals will enter  $i$  phase to infectious compartment.

#### 4. CONCLUSIONS

The DTMC SIR model provides valuable insights into the dynamics of disease spread in populations. It effectively captures the transitions among susceptible, infected, and recovered individuals, accounting for the stochastic nature of disease transmission. Utilizing state transitions and transition probabilities, this model aids in comprehending the progression of epidemics, including the initial exponential growth, saturation of infections, and eventual decline as individuals recover and gain immunity. For the DTMC SIR model featuring the compartments S, I, and R, non-homogeneous QBD processes offer a suitable analytical tool. The stationary vector and rate matrix enable performance analysis based on susceptible and infected individuals.

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#### CONFLICTS OF INTEREST

The authors declare that there are no conflicts of interest regarding the publication of this paper.

#### REFERENCES

- [1] K.M. Smith, C.C. Machalaba, R. Seifman, Y. Feferholtz, W.B. Karesh, Infectious disease and economics: The case for considering multi-sectoral impacts, *One Health*. 7 (2019), 100080. <https://doi.org/10.1016/j.onehlt.2018.100080>.
- [2] P. Armitage, T. Colton, *Encyclopedia of biostatistics*, 2nd ed, J. Wiley, Chichester, 2005.
- [3] R. Chakraborty, *Epidemics*, Springer, Dordrecht, (2015).
- [4] O. Ige, *Markov chain epidemic models and parameter estimation*, Theses, Dissertations and Capstones, 1307, (2020). <https://mds.marshall.edu/etd/1307>.
- [5] S. Banerjee, *Mathematical modeling: models, analysis and applications*, CRC Press, Hoboken, 2014.
- [6] M. Keeling, *The mathematics of diseases*, Millennium Mathematics Project, University of Cambridge, Cambridge, 2001.
- [7] M. Burke, *Epidemiology Model (Differential Equations) Part I*, College of Science & Mathematics, Kennesaw University, 2011.
- [8] M.G.M. Gomes, L.J. White, G.F. Medley, Infection, reinfection, and vaccination under suboptimal immune protection: epidemiological perspectives, *J. Theor. Biol.* 228 (2004), 539–549. <https://doi.org/10.1016/j.jtbi.2004.02.015>.
- [9] G. Latouche, V. Ramaswami, *Introduction to matrix analytic methods in stochastic modeling*, SIAM, Philadelphia, 1999.
- [10] E.W. Weisstein, *Kermack-McKendrick model*, MathWorld—A Wolfram Web Resource, <https://mathworld.wolfram.com/Kermack-McKendrickModel.html>.
- [11] A. Bernoussi, A. Kaddar, S. Asserda, Global stability of a delayed SIRI epidemic model with nonlinear incidence, *Int. J. Eng. Math.* 2014 (2014), 487589. <https://doi.org/10.1155/2014/487589>.
- [12] T. Caraballo, M. El Fatini, R. Pettersson, et al. A stochastic SIRI epidemic model with relapse and media coverage, *Discr. Contin. Dyn. Syst. - B*. 23 (2018), 3483–3501. <https://doi.org/10.3934/dcdsb.2018250>.

- 
- [13] S. Side, A. Zaki, S. Sartika, Pemodelan matematika SIRI pada penyebaran penyakit tifus di Sulawesi Selatan, *J. Math. Comput. Stat.* 4 (2021), 55–65. <https://doi.org/10.35580/jmathcos.v4i2.24439>.
- [14] N. Stollenwerk, M. Aguiar, The SIRI stochastic model with creation and annihilation operators, arXiv:0806.4565, (2008). <http://arxiv.org/abs/0806.4565>.