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# A Novel Technology-Based Stochastic Epidemic Model

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**Abstract** In this article, we propose a new discrete-time stochastic epidemic compartment model to study and analyze the spread of disease. The SUQIHR model consists of six compartments; Susceptible ($S$), Unsafe ($U$), Quarantined ($Q$), Infected ($I$), Hospitalized ($H$) and Recovered ($R$). The Unsafe class ($U$) comprises individuals who are at higher risk of infection compared to the general susceptible population, such as those with close contact to infected individuals. Transitions between compartments are assumed to follow certain probability distributions that capture the movement of individuals. The advancement of tracking technologies enables the differentiation of unsafe individuals from susceptible ones through the use of tracking equipment or mobile applications. Therefore, this model finds relevance in technology-ready societies. In this study, we utilize the SUQIHR model to forecast the future spread of diseases. The model incorporates both the transmission dynamics of epidemics and measures to control their spread. We examine the mathematical analysis of the model such as long-term behavior, the basic reproduction number and sensitivity analysis. Moreover, the Monte Carlo simulation can be employed to study the survival distribution of the outbreak, the final size of infected individuals, and the expected duration of the epidemic. By this comprehensive approach, our model provides valuable insights for understanding and managing disease outbreaks in various scenarios.

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**Keywords:** discrete stochastic model; epidemic model; mathematical biology; public health; basic reproduction number

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## 1. Introduction

The Centers for Disease Control and Prevention (CDC) describes an epidemic as an increase, often sudden, in the number of cases of a disease above what is normally expected in a given population [1]. The examples of human-related epidemics include Ebola, Yellow fever, MERS, SARS, Influenza and, recently, COVID-19. An epidemic can cause

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enormous damage through social, financial and economic losses in addition to impaired health and loss of life.

Mathematical models can project how infectious diseases progress to show the likely outcome of an epidemic. The modelling is a tool that has been used to study the dynamics of disease transmission, analyze the causes and risk factors for the outbreaks, predict the spread of disease, and evaluate strategies to control an epidemic. The classic epidemic models include SI, SIS, SIR, and SEIR models, where S, E, I, and R denote susceptible, exposed, infected, and recovered populations, respectively. The models can also be classified in two different types; deterministic and stochastic. Both can be used to describe the dynamics of epidemics, but there is a significant difference. In deterministic models, the variables are not random and are functions of time only. For a given set of parameters and initial conditions, the solution is unique. But stochastic models are formulated in terms of random variables which depend on time and probability. The same set of parameter values and initial conditions will lead to many different outcomes.

Several mathematical modeling studies have been conducted to describe the epidemic in the past. The list of deterministic models are as follows: Giraldo and Palacio [2] propose SIR models for varicella outbreaks in children. Kibona et al. [3] propose SIPA model for HIV/AIDS. Aldila and Asrianti [4] propose SVIQR model for measles infection. Okyere et al. [5] propose SIR and SEIR models for Ebola. Demongeot et al. [6] propose SI model for COVID-19. Ndamuzi and Gahungu [7] propose SLIR model for malaria parasite in mosquito and human populations. Some examples of stochastic models are: Lekone and Finkenstdt [8] propose SEIR model for Ebola. Maki and Hirose [9] propose SIR model for SARS outbreak in Hong Kong. Greenhalgh et al. [10] propose SIS model for gonorrhea and pneumococcus. Ming et al. [11] propose SIR model for 2009 H1N1 pandemic. Chanu and Singh [12] propose SEQIR model for COVID-19. He et al. [13] propose a discrete-time stochastic epidemic model with binomial distributions for COVID-19. Allen [14] proposes deterministic and stochastic SIR model for malaria. Getz and Dougherty [15] propose deterministic and stochastic SEIR model for Ebola. Rihan et al. [16] propose deterministic and stochastic SIRC model for COVID-19. Fortunately, due to the current technology of tracking and recording devices, it is possible to keep track of people in technology-ready communities who had direct contact with the patients or/and may have been to place where there is an outbreak or superspreading. This class of people can be defined as the unsafe class ($U$). To be precise, people who have close contact with infected individuals but have not been confirmed as patients are in the unsafe class. The example of this technology includes NOVID which is a contact tracing app that uses ultrasound technology and Bluetooth to follow people's exposure to COVID-19 [17]. These sorts of technology will help us classified the number of people in unsafe class.

In this research, we introduce a novel discrete-time stochastic epidemic model where the unsafe compartment, justified by tracking technology, is included. We propose a susceptible-unsafe-quarantine-infected-hospitalized-recovered (SUQIHR) compartment model. Since quarantine is one of a commonly used way to control the spread of epidemic, the quarantine and hospitalized classes are included to the model. Both classes are related to the unsafe individuals as follows. The quarantined class ($Q$) is the class of unsafe individuals which are not confirmed to be safe of infected that are quarantined and isolated from people. The hospitalized class ($H$) is the unsafe individuals who are confirmed patients that are admitted to hospital and isolated to prevent spread of the virus to others. The dynamics of the model are assumed based on certain probability distributions. The

models are studied based on various levels of the quarantine rates and the probability of isolation of the patients to other people. We mainly focus on three quantities; the survival function of the outbreak, the final size of total infected population, and the expected duration of the epidemic. These quantities are investigated via Monte Carlo simulation. Moreover, we also analyze the epidemic as a Markov chain perspective and outline some interesting quantities such as the long-term behavior, the basic reproduction number and the sensitivity analysis.

## 2. Background

**Definition 2.1.** [18] A discrete-time stochastic process $\{X_n\}_{n=0}^{\infty}$ is said to have the Markov property if

$$\mathbb{P}(X_n = i_n | X_0 = i_0, \ldots, X_{n-1} = i_{n-1}) = \mathbb{P}(X_n = i_n | X_{n-1} = i_{n-1}),$$

where the values of $i_k \in \{1, 2, ...\}$ for $k = 1, 2, \ldots, n$. The stochastic process is then called a Markov chain or, more specifically, a discrete-time Markov chain (DTMC).

**Definition 2.2.** [18] The one-step transition probability, denoted as $p_{ij}(n)$, is defined as the following conditional probability

$$p_{ij}(n) = \mathbb{P}(X_{n+1} = j \mid X_n = i),$$

the probability that the process is in state $j$ at time $n + 1$ given that the process was in state $i$ at the previous time $n$, for $i,\ j = 1,\ 2, \ldots$.

**Definition 2.3.** [18] If the transition probabilities $p_{ij}(n)$ in a Markov chain do not depend on time $n$, they are said to be time-homogeneous. In this case, the notation $p_{ij}$ is used. If the transition probabilities are time dependent, $p_{ij}(n)$, then they are said to be time-nonhomogeneous.

**Definition 2.4.** [19] A state $s_i$ of a Markov chain is called absorbing if it is impossible to leave it (i.e., $p_{ii} = 1$). A Markov chain is absorbing if it has at least one absorbing state, and if from every state it is possible to go to an absorbing state.

**Definition 2.5.** [19] For a finite absorbing Markov chain, the probability that the Markov chain is being absorbed is 1 and not depends on the initial distribution.

**Definition 2.6.** [20] The normalized forward sensitivity index of the basic reproduction number $R_0$, that depends differentiably on a parameter $p$, is defined by

$$\Upsilon_p^{R_0} = \frac{\partial R_0}{\partial p} \times \frac{p}{R_0}.$$

## 3. Model Setup

We construct a discrete-time stochastic epidemic model, namely the SUQIHR model, to describe the transmission of epidemics, to understand the dynamics of disease transmission and to predict the spread of disease in technology-ready communities. This model is invented based on the development of modern world technology. Compare to the past, it is much easier and cheaper to have tracking devices for population. The devices can be appeared as items in various form such as microchips, mobile phones or animal collars. The aim of tracking is to keep track of people in who may have had direct contact with the population from the infected class. Therefore, the devices could further help us to classify

the unsafe individuals from the susceptible individuals. The model can be used not only for humans but also for farm animals. In SUQIHR model, the population is partitioned into six compartments as susceptible ($S$), unsafe ($U$), quarantined ($Q$), infected ($I$), hospitalized ($H$), and recovered ($R$) individuals. Let $N = S(t)+U(t)+Q(t)+I(t)+H(t)+R(t)$ denote the total population size. The flow diagram is shown in Figure 1.

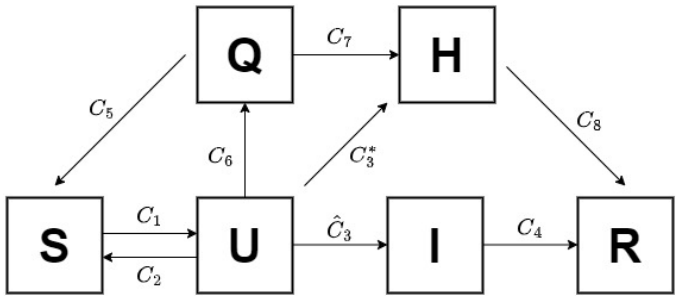


FIGURE 1. Diagram of the SUQIHR model.

The susceptible class ($S$) is the individuals who are not infected but could become infected.

The unsafe class ($U$) is the susceptible individuals who have close contact with infected individuals.

The quarantined class ($Q$) is the unsafe individuals who are quarantined and isolated from people.

The infected class ($I$) is the individuals who have already been infected and can spread the virus to the susceptible individuals.

The hospitalized class ($H$) is the confirmed patients who are admitted to hospital and isolated to prevent spread of the virus to others.

The recovered class ($R$) is the infected individuals who have recovered and are assumed to be immune and have died from disease.

As indicated in Figure 1, the susceptible individuals move to the unsafe class ($U$) if they contact the infected individuals. Note that the number of people in unsafe class is classified by tracking technology. The unsafe individuals may move to the quarantined class ($Q$) when they are quarantined and isolated from people, either by themselves or by the societys order. After a period of time, the unsafe and quarantined individuals who are not infected return to the susceptible class ($S$). On the other hand, a group of unsafe individuals who get infected may move to the infected class ($I$), or the hospitalized class ($H$) depends on their decisions. Additionally, the quarantined individuals who get infected are assumed to move to the hospitalized class ($H$). After recovery or death, the infected and hospitalized individuals move to the recovered class ($R$).

We consider discrete-time point series $t = 1, 2, \ldots$ as the time progression of the disease. At this timescale, the number of each compartment is dependent on the number in the previous period and the inflows and removals from other compartments during the time. Let $C_i(t)$ be the number of individual transportations between compartments. The transition from each state is listed as follows:

$C_1(t)$ is the number of susceptible individuals who have contact with infected individuals at time $t$.

$C_2(t)$ is the number of unsafe individuals who are not infected and go back to the susceptible class at time $t$.

$C_3(t)$ is the number of unsafe individuals who become infected at time t.

$C_3^*(t)$ is the number of new patients from the unsafe class who are admitted to hospital at time $t$.

$\hat{C}_3(t)$ is the number of newly infected individuals from unsafe class at time $t$.

$C_4(t)$ is the number of newly recovered or death individuals from infected class at time $t$.

$C_5(t)$ is the number of quarantined individuals who are not infected and go back to the susceptible class at time $t$.

$C_6(t)$ is the number of unsafe individuals who are quarantined at time $t$.

$C_7(t)$ is the number of new patients from quarantined class who are admitted to hospital at time $t$.

$C_8(t)$ is the number of newly recovered and death individuals from hospitalized class at time $t$.

The dynamic of the SUQIHR model can be written in the system of equations as follows:

$$\begin{aligned}
S(t+1) &= S(t) - C_1(t) + C_2(t) + C_5(t),\\
U(t+1) &= U(t) + C_1(t) - C_2(t) - C_3(t) - C_6(t),\\
Q(t+1) &= Q(t) - C_5(t) + C_6(t) - C_7(t),\\
I(t+1) &= I(t) + \hat{C}_3(t) - C_4(t),\\
H(t+1) &= H(t) + C_3^*(t) + C_7(t) - C_8(t),\\
R(t+1) &= R(t) + C_4(t) + C_8(t),
\end{aligned} \tag{3.1}$$

where the random variables can be assumed with binomial distributions Bin($n$,$p$), trinomial distribution Trin($n, p, q$) and multinomial distribution Mult($n$,$\vec{p}$)as follows:

$$\begin{aligned}
&C_1(t) \sim Bin(S(t), q_1(t)),\\
&C_2(t), C_3(t), C_6(t) \sim Mult(U(t), q_2, q_3, q_6) \quad \text{where } C_3(t) = \hat{C}_3(t) + C_3^*(t),\\
&C_3^*(t) \sim Bin(C_3(t), \theta),\\
&C_4(t) \sim Bin(I(t), q_4),\\
&C_5(t), C_7(t) \sim Trin(Q(t), q_5, q_7),\\
&C_8(t) \sim Bin(H(t), q_8),
\end{aligned}$$

with probabilities:

$$\begin{aligned}
q_1(t) &= 1 - exp\left(\frac{-\beta I(t)}{N}\right),\\
q_2 &= q_5 = 1 - exp(-\alpha),\\
q_3 &= q_7 = 1 - exp(-\sigma),\\
q_4 &= q_8 = 1 - exp(-\gamma),\\
q_6 &= 1 - exp(-\delta).
\end{aligned}$$

The parameter $\beta$ is the contact rate, $\alpha$ is the transition rate from unsafe and quarantined class to susceptible class, $\sigma$ is the infection rate, $\delta$ is the quarantine rate, $\theta$ is the

probability that the unsafe individuals are admitted to hospital, and $\gamma$ is the recovery rate. Additionally, the assumption of SUQIHR model includes

1. The transition of an individual from one state to the next state is considered as a stochastic process.
2. The time length that an individual has been in a certain compartment obeys exponential distribution. Note that, the exponential distribution has a memoryless property. This implies that for the exponential distribution with parameter $\lambda(t)$, the probability that individuals leave the current state at the next time is $1 - e^{-\lambda(t)}$ uniformly at all time $t$. By the memoryless property, this implies that the transition probabilities remain constant throughout the time.
3. The numbers of inflows and removals from other compartments during the time step can be generated by a binomial distribution, trinomial distribution, or a multinomial distribution. This assumption is valid since the transition events are independent and that the probabilities of individuals leaving from one to another state are constants. For example, people in the unsafe class, one may move to the susceptible class, the quarantined class, the hospitalized class, infected class, or otherwise stay in the unsafe class. Therefore, the random variables $C_2(t)$, $C_3(t)$, and $C_6(t)$ are assumed to follow multinomial distribution. The number of experiments in these distributions is the number of individuals in the current compartment. The successful probabilities in the random variables of transitions are $\theta$ and $q_i$, $i = 1, \ldots, 8$ where $\theta, q_i \in [0, 1]$. Note that the probability $q_1$ is the only parameter that depends on the number of infected individuals $I$ at time $t$, while the other transition probabilities are constants.
4. The transmission of the disease is presumed to occur in the context of close contact between susceptible and infected individuals.
5. Population size $N$ is constant. There are no births or deaths.
6. The parameters $\beta, \alpha, \sigma, \delta, \theta$, and $\gamma$ are constants.

## 4. Model Analysis

By the assumption of the SUQIHR model, it can be concluded that the model is a time-homogeneous Markov chain where the set of states is $\{(S, U, Q, I, H, R)$ where $S + U + Q + I + H + R = N\}$. The transition probabilities, denoted by,

$$p_{(s,u,q,i,h,r),(s+j,u+k,q+l,i+m,h+n,r+o)}$$

which is equivalent to

$$\mathbb{P}\left((\Delta S, \Delta U, \Delta Q, \Delta I, \Delta H, \Delta R) = (j, k, l, m, n, o) | (S, U, Q, I, H, R)(t) = (s, u, q, i, h, r)\right)$$

where $\Delta S = S(t+1) - S(t)$. The transition probabilities are complicated since the states are 6-tuple and the transition probabilities depend on the possibility of transportation between compartments from previous unit time. The set of states $\{(S, 0, 0, 0, 0, N - S)\}_{S=0}^{N}$ are absorbing states while the remaining states are transient states. Since the SUQIHR model is a finite Markov chain, the probability that the chain will be absorbed to absorbing states is 1. This implies that, in the long run, the disease would extinct from the community with probability 1.

## Basic Reproduction Number

A quantity of major importance within mathematical epidemic theory is the basic reproduction number $R_0$. The basic reproduction number $R_0$ is defined as the expected number of secondary cases produced by a single (typical) infection in a completely susceptible population. Many researchers obtained the basic reproduction number in stochastic epidemic model, see [13, 21–23]. We calculate the basic reproduction number for SUQIHR model using the next generation matrix method [13, 24] as follows. Firstly, we consider the infection subsystem from Equation (3.1) as

$$\begin{aligned} U(t+1) &= U(t) + C_1(t) - C_2(t) - C_3(t) - C_6(t), \\ I(t+1) &= I(t) + \hat{C}_3(t) - C_4(t). \end{aligned} \tag{4.1}$$

Next, we take the expectations to both sides of Equation (4.1). Hence, the equation is transformed to

$$\begin{aligned} U'(t) &= \frac{\beta}{N} I(t)S(t) - \alpha U(t) - \sigma U(t) - \delta U(t), \\ I'(t) &= \sigma(1-\theta)U(t) - \gamma I(t). \end{aligned} \tag{4.2}$$

Next, by the next generation matrix method, the vectors $\mathcal{F}$ and $\mathcal{V}$ are given as follows:

$$\mathcal{F} = \begin{bmatrix} \frac{\beta S}{N} \\ 0 \end{bmatrix}, \qquad \mathcal{V} = \begin{bmatrix} (\alpha+\sigma+\delta)U \\ \sigma(\theta-1)U - \gamma I \end{bmatrix}.$$

The Jacobian matrices of $\mathcal{F}$ and $\mathcal{V}$ evaluated at the disease-free equilibrium are given by

$$F = \begin{bmatrix} 0 & \beta \\ 0 & 0 \end{bmatrix}, \qquad V = \begin{bmatrix} \alpha+\sigma+\delta & 0 \\ \sigma(\theta-1) & \gamma \end{bmatrix},$$

and

$$FV^{-1} = \begin{bmatrix} \frac{(1-\theta)\sigma\beta}{\gamma(\alpha+\sigma+\delta)} & \frac{\beta}{\gamma} \\ 0 & 0 \end{bmatrix}.$$

The eigenvalues of $FV^{-1}$ are

$$\lambda_1 = \frac{(1-\theta)\sigma\beta}{\gamma\,(\alpha+\sigma+\delta)} \quad \text{and} \quad \lambda_2 = 0.$$

Therefore, the basic reproduction number of the SUQIHR model is

$$R_0 = \frac{(1-\theta)\sigma\beta}{\gamma\,(\alpha+\sigma+\delta)}. \tag{4.3}$$

Note that, $R_0$ varies depending on a variety of parameters. The parameters $\beta, \alpha, \sigma, \delta, \theta$ and $\gamma$ are dependent of the epidemic.

If $R_0 > 1$ or, equivalently, $(1-\theta)\sigma\beta > \gamma\,(\alpha+\sigma+\delta)$, then the disease will spread faster and the epidemic occurs. It will result in an increase in the number of infected individuals because each existing infection causes more than one new infection.

If $R_0 \leq 1$ or, equivalently, $(1-\theta)\sigma\beta \leq \gamma\,(\alpha+\sigma+\delta)$, then the number of infected individuals will decrease because each existing infection causes less than one new infection. The disease eventually disappears from the population.

## Sensitivity Analysis

Sensitivity analysis shows how each parameter affects the basic reproduction number to control the spread of disease. When the values of parameters change, we can use the sensitivity index to measure the relative change in a variable. The sensitivity index of each parameter is derived from the basic reproduction number $R_0$ and by Definition 2.6. All sensitivity indices can be calculated as follows:

$$\Upsilon_{\beta}^{R_0} = \frac{\partial R_0}{\partial \beta} \times \frac{\beta}{R_0} = 1, \tag{4.4}$$

$$\Upsilon_{\alpha}^{R_0} = \frac{\partial R_0}{\partial \alpha} \times \frac{\alpha}{R_0} = \frac{-\alpha}{\alpha+\sigma+\delta}, \tag{4.5}$$

$$\Upsilon_{\sigma}^{R_0} = \frac{\partial R_0}{\partial \sigma} \times \frac{\sigma}{R_0} = \frac{\alpha+\delta}{\alpha+\sigma+\delta}, \tag{4.6}$$

$$\Upsilon_{\delta}^{R_0} = \frac{\partial R_0}{\partial \delta} \times \frac{\delta}{R_0} = \frac{-\delta}{\alpha+\sigma+\delta}, \tag{4.7}$$

$$\Upsilon_{\theta}^{R_0} = \frac{\partial R_0}{\partial \theta} \times \frac{\theta}{R_0} = \frac{-\theta}{1-\theta}, \tag{4.8}$$

$$\Upsilon_{\gamma}^{R_0} = \frac{\partial R_0}{\partial \gamma} \times \frac{\gamma}{R_0} = -1. \tag{4.9}$$

For example, in the case that $\beta = 31$, $\alpha = 0.7$, $\sigma = 0.095, \delta = 0.3$, $\theta = 0.6$ and $\gamma = 1/14$, all sensitivity indices are calculated by Equations (4.4)-(4.9), as shown in Table 1.

| Parameter | Sensitivity Index |
|---|---|
| $\beta$ | 1 |
| $\alpha$ | -0.639 |
| $\sigma$ | 0.913 |
| $\delta$ | -0.274 |
| $\theta$ | -1.5 |
| $\gamma$ | -1 |

Table 1. The sensitivity index of each parameter given that $\beta = 31$, $\alpha = 0.7$, $\sigma = 0.095$, $\delta = 0.3$, $\theta = 0.6$ and $\gamma = 1/14$.

The parameters $\beta$ and $\sigma$ have a positive sensitivity index which means that the parameters $\beta$ and $\sigma$ have a positive effect on the basic reproduction number. In other words, the basic reproduction number shall increase (decrease) when the parameter value increases (decreases). Generally, if $\beta$ (respectively, $\sigma$) increases by 10%, the basic reproduction number should increase 10% (9.13%). On the contrary, the parameters $\alpha, \delta, \theta$ and $\gamma$ have a negative sensitivity index. It means that the parameters $\alpha, \delta, \theta$ and $\gamma$ have a negative effect on the basic reproduction number, that is, the basic reproduction number should decrease (increase) when the parameter value increases (decreases). If $\alpha, \delta, \theta$ or $\gamma$ is increased by 10%, then the basic reproduction number should decrease by 6.39%, 2.74%, 15%, and 10%, respectively. In order to prevent the spread of infection, we aim to reduce the number of patients by reducing the basic reproduction number $R_0$ to less than 1. One of things we can do to reduce the basic reproduction number. Decreasing the value of the contact rate ($\beta$) and increasing the value of the quarantine rate ($\delta$) and the probability

that the unsafe individuals are admitted to hospital ($\theta$) will lead to decreases in the basic reproduction number.

## 5. Monte Carlo Simulations

Due to the stochastic dynamic of the model, it is very challenging to obtain the behaviors of the model since it depends on many factors such as parameter values, initial population, probability distributions and randomness. Since we focus on the survival function of the outbreak, the final size of total infected population and the expected duration of the epidemic, it is possible to analyses these empirical results via Monte Carlo simulations.

### 5.1. A Monte Carlo Simulation Example of SUQIHR Model

**Example 5.1.** We give a simulation of SUQIHR model under COVID-19 situation with the total population size $N = 10,000$. In addition, at the beginning of the epidemic, we assume the initial number of infected individuals $I(0) = 5$. We provide Monte Carlo simulations for SUQIHR model with the parameter values are given in Table 2 and initial values: $S(0) = 9,995$, $I(0) = 5$, and $U(0) = Q(0) = H(0) = R(0) = 0$.

| Parameters | Value | Source |
|---|---|---|
| $\beta$ | 31 | [13] |
| $\alpha$ | 0.7 | assumed |
| $\sigma$ | 0.095 | [13] |
| $\delta$ | 0.3 | assumed |
| $\theta$ | 0.6 | assumed |
| $\gamma$ | 1/14 | [25] |

Table 2. Parameter values used in Example 5.1.

The simulation is done for 1,000 times. The dynamic of population in each class according to time is plotted. Moreover, we obtain the survival function, the final size of total infected population and the expected duration of the epidemic from the simulation empirically. The survival function of the outbreak is calculated from the ratio of the simulations that disease still occur compare with the total samples. The expected final size of total infected population and the expected duration of the epidemic are obtained from the average of total infected population and the average of the duration of epidemic from the simulations respectively. For the last two quantities, the 95% confidence intervals are also calculated. The simulation results are displayed on Figure 2, Table 3 and Figure 3.

| **Duration of Epidemic** | | | **Final size of infected population** | | |
|---|---|---|---|---|---|
| Lower 95% C.I. | Expected | Upper 95% C.I. | Lower 95% C.I. | Expected | Upper 95% C.I. |
| 140 | 174.619 | 225 | 9,859.975 | 9,892.397 | 9,922 |

Table 3. The final size of total infected population and the expected duration of the epidemic with 95% confidence intervals of Example 5.1.

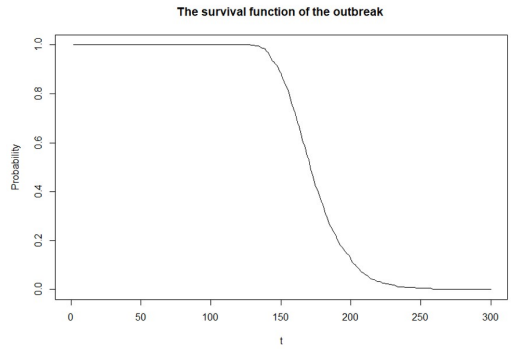


FIGURE 2. The survival distribution of the outbreak from Example 5.1.

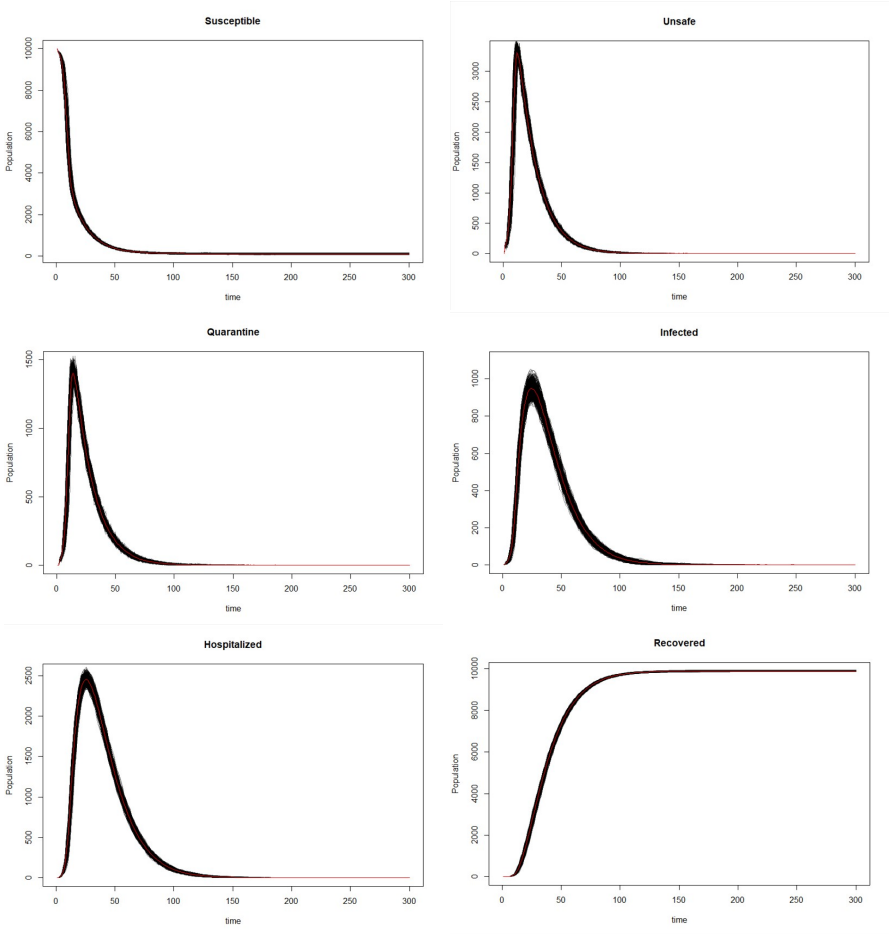


FIGURE 3. The Monte Carlo simulation result of Example 5.1. The red lines represent the average values of each compartment.

For this example, note that $R_0 = \frac{0.7\times0.095\times31}{\frac{1}{14}(0.7+0.095+0.3)} = 27.18$. Therefore, the outbreak is expected to occur. From Figure 3, it can be seen that the outbreak reaches the peak around $t = 30$ to 40. The number of infected individuals peak at around 1,000 patients, while the unsafe individuals can be as high as 3,300. The number of quarantine individuals can be as much as 1,500 while the number of hospitalized individuals, which may come either from quarantine class or unsafe class, may go up to around 2,500. At the end, almost everyone would have had the disease. From Figure 2 and Table 3, it can be seen that the duration of the outbreak is around 174, with a 95% confidence interval from 140 to 225. The expected final size is 9,892.397 with a 95% confidence interval from 9,859.975 to 9,922.

### 5.2. Effects of Quarantine and Isolation to the Epidemic

The aim of this section is to study the effects of quarantine and isolation to the epidemic. Clearly, by introducing the quarantine measure, it is expected to reduce the final size of infected individuals. However, it is not straightforward to justify the effect on the duration of the epidemic. Since the basic reproduction number, the parameter values and the initial distribution all play role in these two quantities, we shall fix the parameter values and the initial condition as

- $S(0) = 9,995,\ I(0) = 5$, and $U(0) = Q(0) = H(0) = R(0) = 0$.
- $\beta = 5,\ \alpha = 0.1,\ \sigma = 0.095$ and $\gamma = 1/14$.

The simulation is done for 1,000 times. The values $\delta$ and $\theta$, which reflects on the isolation rate and hospitalized rate (if infected), are varied to make various reproduction number. Note that the number of unsafe individuals who decide (or force) to quarantine themselves in each day is $q_6 = 1-e^{-\delta}$. It is more sensible to choose $\delta$ based on quarantine rate. Hence, if we believe, for example, that 30% of unsafe individuals will be quarantined on the next day, then the value of $\delta$ should be

$$\delta = -\ln(1-q_6) = -\ln(0.7) = 0.35667.$$

The value $\theta$ can assumed to be independent with quarantine rate, $q_6$. However, we would expect the value of $\theta$ to be greater than $q_6$. The unsafe individuals who are confirmed patients should have more probability to get isolate from the community compare to the unconfirmed ones.

The simulation results for various values of $\delta$ and $\theta$ are displayed on Table 4. Clearly, by setting $\theta = q_6 = 100\%$ this is the best-case scenario and it will give the minimum values for both expected duration of the epidemic and the final size of total infected population. For $q_6 = 0\%,\ 25\%,\ 50\%,\ 75\%$ the best case is, obviously, still with $\theta = 100\%$. When $\theta$ increase, the expected final size of total infected population decreases. However, when $\theta$ increase, the expected duration of outbreak seems to increase until it reaches a certain turning point and starts decreasing again. This implies that when the quarantine measure is applied, the final size of total infected population will decrease, but the duration of epidemic will increase. To confirm this conclusion, we provide another result when the quarantine rate is set to be 10% and $\theta = 10\%,\ 20\%,\ \ldots,\ 100\%$, as displayed in Table 5.

| $q_6$ | $\theta$ | $R_0$ | Duration of Epidemic | | | Final size of total infected population | | |
|---|---|---|---|---|---|---|---|---|
| | | | Lower 95% C.I. | Expected | Upper 95% C.I. | Lower 95% C.I. | Expected | Upper 95% C.I. |
| 0% | 0% | 34.10 | 153 | 180.909 | 231.025 | 9,975 | 9,984.430 | 9,992 |
| | 25% | 25.57 | 154 | 182.455 | 232.025 | 9,966 | 9,976.410 | 9,986 |
| | 50% | 17.05 | 160 | 189.107 | 241 | 9,943.975 | 9,957.441 | 9,970.025 |
| | 75% | 8.52 | 173 | 204.981 | 260.025 | 9,839.975 | 9,873.246 | 9,903 |
| | 100% | 0 | 65 | 102.333 | 153.025 | 67.975 | 179.073 | 354.05 |
| 25% | 25% | 11.80 | 159 | 189.425 | 242.025 | 9,985 | 9,908.936 | 9,932 |
| | 50% | 7.89 | 167 | 198.140 | 251 | 9,790 | 9,831.607 | 9,868.025 |
| | 75% | 3.93 | 189 | 225.441 | 284.05 | 9,331 | 9,441.753 | 9,568 |
| | 100% | 0 | 64 | 103.853 | 164 | 67.95 | 181.407 | 368 |
| 50% | 50% | 4.63 | 174.975 | 211.487 | 273 | 9,573 | 9,469.464 | 9,719 |
| | 75% | 2.32 | 208.925 | 253.273 | 321.3 | 8,392.925 | 8,700.815 | 9,001 |
| | 100% | 0 | 62 | 103.217 | 157.05 | 61.975 | 181.77 | 360.225 |
| 75% | 75% | 1.46 | 127.3 | 279.42 | 369 | 225.5 | 7,478.620 | 8,234.9 |
| | 100% | 0 | 61.975 | 102.42 | 156 | 65 | 178.005 | 349.025 |
| 100% | 100% | 0 | 66 | 103.245 | 156 | 65.95 | 180.875 | 342.15 |

TABLE 4. The final size of total infected population and the expected duration of the epidemic with 95% confidence intervals for SUQIHR model for the different values of $\delta$, $\theta$ and $N = 10,000$, $S(0) = 9,995$, $I(0) = 5$, $\beta = 5$, $\alpha = 0.1$, $\sigma = 0.095$ and $\gamma = 1/14$.

| $q_6$ | $\theta$ | $R_0$ | Duration of Epidemic | | | Final size of total infected population | | |
|---|---|---|---|---|---|---|---|---|
| | | | Lower 95% C.I. | Expected | Upper 95% C.I. | Lower 95% C.I. | Expected | Upper 95% C.I. |
| 10% | 10% | 21.381 | 153.975 | 184.19 | 231.025 | 9,950 | 9,963.892 | 9,976.025 |
| | 20% | 19.005 | 156 | 184.105 | 234.025 | 9,942 | 9,957.341 | 9,972 |
| | 30% | 16.629 | 158.975 | 187.593 | 237.025 | 9,929 | 9,947.717 | 9,963 |
| | 40% | 14.254 | 159 | 189.098 | 241.025 | 9,915.975 | 9,935.005 | 9,952.025 |
| | 50% | 11.878 | 162 | 191.84 | 243 | 9,890 | 9,914.418 | 9,936 |
| | 60% | 9.503 | 166 | 197.276 | 249.025 | 9,850 | 9,879.46 | 9,910 |
| | 70% | 7.167 | 174 | 205.289 | 255 | 9,765 | 9,807.627 | 9,851 |
| | 80% | 4.751 | 187 | 223.945 | 290 | 9,524 | 9,610.902 | 9,688.025 |
| | 90% | 2.376 | 228 | 282.104 | 358 | 7,962 | 8,416.176 | 8,803.3 |
| | 100% | 0 | 65 | 102.488 | 156 | 61 | 175.698 | 351.125 |

TABLE 5. The final size of total infected population and the expected duration of the epidemic with 95% confidence intervals for SUQIHR model for $q_6 = 10\%$, $\theta = 10\%,\ 20\%, \ldots, 100\%$, and $N = 10,000$, $S(0) = 9,995$, $I(0) = 5$, $\beta = 5$, $\alpha = 0.1$, $\sigma = 0.095$ and $\gamma = 1/14$.

### 5.3. Effects of the Basic Reproduction Number to the Epidemic

From Section 5.2, it can be noticed that the final size of total infected individuals and the duration of the outbreak may depend on the basic reproduction number of the model. In this section, we shall verify the dependence between them. We fix the parameter values and the initial condition as

- $S(0) = 9,995,\ I(0) = 5$, and $U(0) = Q(0) = H(0) = R(0) = 0$
- $\beta = 10,\ \alpha = 0.1,\ \sigma = 0.095$ and $\gamma = 1/14$.

The simulation is done for 1,000 times. To quarantine rate is set to be 10% and various values of $\theta$ are chosen to make different values $R_0$ from 0 to 20. Figure 4 provides the plot between the expected final size of total infected individuals against the basic reproduction number. Figure 5 provides the plot between the expected duration of the epidemic against the basic reproduction number. From these figures and subject to the quarantine rate of 10%, it can be concluded that

1. The case $R_0 = 0$, equivalent to $\theta = 1$, is the best-case scenario which minimise both the expected final size and the expected duration of the outbreak.
2. The expected final size of total infected individuals depends on $R_0$. Higher basic reproduction number implies higher expected final size.
3. The expected duration of epidemic is maximized when the basic reproduction number is close to 1. For $0 < R_0 < 1$, smaller $R_0$ implies smaller expected duration, while for $R_0 > 1$, higher $R_0$ implies smaller expected duration. Also, $R_0 \to \infty$ provide larger expected duration than the case $R_0 \to 0$, but smaller expected duration than $R_0 = 1$.

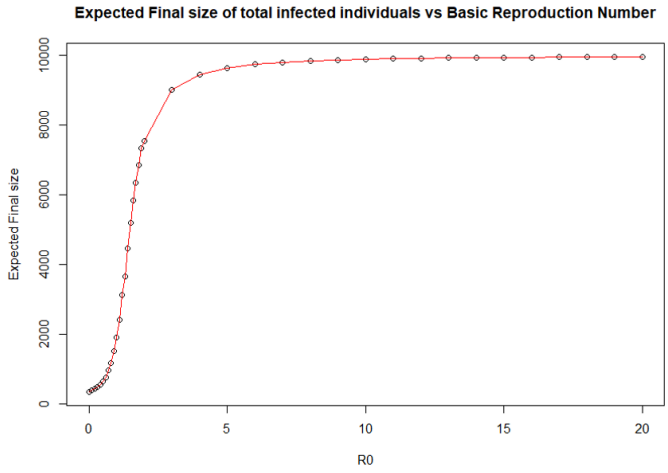


Figure 4. The plot between the expected final size of total infected individuals against the basic reproduction number for SUQIHR model for the quarantine rate 10% and $N = 10000$, $S(0) = 9995$, $I(0) = 5$, $\beta = 5$, $\alpha = 0.1$, $\sigma = 0.095$ and $\gamma = 1/14$.

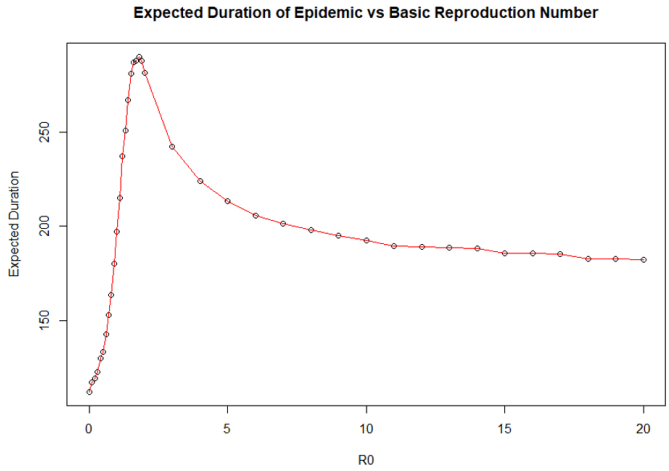


FIGURE 5. The plot between the expected duration of epidemic against the basic reproduction number for SUQIHR model for the quarantine rate 10% and $N = 10000,\ S(0) = 9995,\ I(0) = 5,\ \beta = 5,\ \alpha = 0.1,\ \sigma = 0.095$ and $\gamma = 1/14$.

## 6. Conclusion

In this article, we propose a new discrete-time stochastic epidemic compartment model to study and analyze the spread of disease for the modern world. The proposed SUQIHR model consists of six compartments; Susceptible ($S$), Unsafe ($U$), Quarantined ($Q$), Infected ($I$), Hospitalized ($H$) and Recovered ($R$). The numbers of individual transportations between compartments are assumed to follow certain probability distributions. The model is introduced due to the development of modern worlds technology of tracking, which help us to classify the unsafe individuals from the susceptible ones. This model can be applied in technology-ready societies such as in the big cities or in animal farms.

The findings of this work are as follows. First, we examine the mathematical analysis of the model such as long-term behavior, the basic reproduction number and sensitivity analysis. The analysis show that the disease would extinct from the community with probability 1, but may take a long time in some cases. The basic reproduction number ($R_0$) can be computed via the next generation matrix method displayed on Equation (4.3). The sensitivity analysis of the parameters in the model provides that decreasing the value of the contact rate ($\beta$), increasing the value of the quarantine rate ($\delta$) and increasing the probability that the unsafe individuals are admitted to hospital ($\theta$) are the best ways to control the transmission of the disease since these controls lead to the reduction of the basic reproduction number.

Second, since the dynamic of the stochastic model is sophisticated, the analysis of the model can be discussed via Monte Carlo simulation. The simulation can be used to obtain the survival function of the outbreak, the final size of the total infected population, and the expected duration of the epidemic for SUQIHR model.

Third, we study the effects of the basic reproduction number to the epidemic for SUQIHR model. As a result, it can be seen that the final size of total infected individuals

and the duration of the outbreak depends on the basic reproduction number. The large $R_0$ implies big spread of the disease, but the epidemic duration may be short. The small $R_0$ implies small spread of the disease, but the epidemic duration may take a long time if $R_0$ is close to 1. The model can be applied to forecast epidemics and help in making decisions about the quarantine measure to mimimise the damage caused by in terms of social, financial, economic and life losses.

Since the model is developed based on the assumptions that all the population in the communities can be tracked, it is currently impossible to find the real data to fit the model. Hence, the model analysis can only be done via mathematical modelling. For further study, a real experiment that mimic the model situation can be conducted. The experiment can be done, for example, in a small population community or in an animal farm. The experimental data will enable us to make informed comparisons between the results obtained in the experiment and the theoretical predictions, ultimately aiding us in making more informed decisions regarding public health policy.

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