COMPARISON OF CONTINUOUS TIME MARKOV CHAIN (CTMC) SIRS AND SIQRS EPIDEMIC MODEL SIMULATION RESULTS ON THE SPREAD OF MONKEYPOX DISEASE

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ABSTRACT

The uncontrolled spread of infectious diseases over a long period of time can cause epidemic. The pattern of spread of an infectious disease can be described through a mathematical model called an epidemic model. The development of the SIR epidemic model which assumes that recovered individuals have temporary immunity so that they can be re-infected is called the SIRS epidemic model. Quarantine is an effort to restrict movement to prevent the transmission of disease among individuals in a society. The SIQRS epidemic model is a modification of the SIRS model which assumes a quarantine phase for infected individuals. The SIQRS epidemic model that follows the Markov process and changes in the number of individuals are viewed in continuous time is the SIQRS continuous time Markov chain (CTMC) epidemic model. Monkeypox or monkeypox is an infectious disease that has hit several countries in Central and West Africa. The aims of this research are to explain the CTMC SIQRS epidemic model and compare the simulation results between the CTMC SIQRS and CTMC SIRS epidemic models on the spread of monkeypox. The research's method is literature study by discussing relevant theories and previous research. The results of this research are the CTMC SIQRS model in the form of transition probabilities. The simulation of CTMC SIRS epidemic model on the spread of monkeypox shows that the end of epidemic occur at $t = 8768.42$ *days* $= 24$ *years, whereas in the CTMC SIQRS model, the end of epidemic occur at* $t = 1046.98$ *days* $= 2.8$ *years. Therefore, it was concluded that the quarantine phase can speed up the end of the epidemic.*

Keywords: *Epidemic Model, CTMC, SIQRS, SIRS, Monkeypox*

1. INTRODUCTION

Infectious diseases are diseases that can be transmitted from infected individuals to healthy individuals through direct or indirect contact (Notoatmodjo, 2003). The uncontrolled spread of infectious diseases for a long period of time can cause epidemic. An epidemic is the emergence of an infectious disease in a certain population, within a certain time period, with a high rate of spread and causing many losses (Kemenkes RI, 2022). The pattern of spread of an infectious disease can be described through a mathematical model called an epidemic model (Kasbawati, 2011).

The SIR epidemic model was initially introduced in 1927 by Kermack and Mckendrick. The population in this epidemic model is divided into three groups including susceptible (S), infected (I), and recovered (R). The disease transmission in the SIR epidemic model occurs when individuals in the susceptible group come into contact with infected individuals. Once individuals become infected, they remain in the infectious group for a period of time before recovering. After recovering, they will have a permanent level of immunity. The development of the SIR epidemic model which assumes that recovered individuals have temporary immunity so that they can be re-infected is called the SIRS epidemic model (Ma & Li, 2009).

A quarantine is an effort to restrict the movement of exposed and infected individuals to prevent disease transmission in society (Hossain et al., 2020). The purposes of quarantine are to restrict the movement of people who have been exposed to an infectious disease and periodically monitor whether they are likely to become infected. According to The Law of the Republic of Indonesia Number (No). 11 of 2018 concerning health quarantine, a quarantine process for individuals who have been infected and need health services is called isolation. The SIQRS epidemic model is a modification of the SIRS model which assumes a quarantine phase for infected individuals (Fatimatuzzahroh et al., 2021).

Epidemic models can be viewed deterministically or stochastically. The stochastic epidemic model is formulated as a stochastic process from a collection of random variables and the result is a probability distribution (Allen, 2008). In the stochastic epidemic model, the spread of disease is seen as a random process. Epidemic models that are reviewed stochastically and follow the Markov process are continuous-time Markov chain (CTMC) and discrete-time Markov chain (DTMC). The CTMC epidemic model reviews changes in the number of individuals in each group over continuous time.

The research conducted by Fatimatuzzahroh et al. (2021) discusses the CTMC SIQRS epidemic model and its application in understanding the spread of tuberculosis disease. In this research, the quarantine phase for infected individuals is symbolized by Q. The results of this research are transition probabilities for the CTMC SIQRS epidemic model and numerical simulations. Based on numerical simulations, it is known that increasing the quarantine rate will reduce the estimated time of disease extinction, R_0 and m (the expected value of the number of infected individuals).

Another example of an infectious disease is monkeypox. Monkeypox is an infectious disease that has hit several countries in Central Africa (Democratic Republic of Congo, Cameroon, and Gabon) and West Africa (Nigeria, Liberia, and Benin). This disease is caused by a virus from the *Poxviridae* family called *monkeypox* virus (MPXV). This virus was first discovered in 1958 in captive monkeys in Copenhagen (Husna & Wicaksono, 2020). In 1970, the first case of this disease was reported in the Democratic Republic of Congo affecting a nine-month-old toddler with a history of never having received the smallpox vaccine (Budiyarto et al., 2023). Since 2003, several cases of monkeypox have been reported outside Africa, such as America, England, Israel, and Singapore. Transmitted by citizens of endemic countries who traveled abroad or through the import of wild animals. Many cases of monkeypox reemerged in early May 2022 across several countries in North America and Europe. The number of cases of monkeypox increased every week until June 23, 2022, when this disease was declared a global health emergency by the World Health Organization (Amato et al., 2022). As of September 10, 2023, there were 90,302 cases of monkeypox with 157 deaths reported (Mathieu et al., 2022).

The transmission from human to human can occur through direct or indirect contact (World Health Organization, 2023). Direct transmission occurs through physical contact with an infected individual. The virus can spread through lesions on the skin or body fluids (droplets). In general, symptoms that appear in exposed individuals include skin rashes, fever, muscle aches, sore throat, headache, and backache. These symptoms usually appear 1 to 21 days following exposure and may persist for 2 to 4 weeks.

The spread of monkeypox can be controlled by tracing contact between infected individuals and the people around them (Budiyarto et al., 2023). Restricting movement for individuals who have contact with infected individuals and implementing isolation for infected individuals will reduce the rate of transmission. A specific vaccine to prevent monkeypox infection has not yet been found. However, the smallpox vaccine is believed to have a cross-protective effect against the monkeypox virus so it can be used in monkeypox. Smallpox vaccination was The vaccination of smallpox officially stopped in 1979 by WHO after global success in eradicating the disease. However, in 2007, a new smallpox vaccine called ACAM2000 was produced (Britannica, 2024). Stopping smallpox vaccination for a long period is thought to result in decreased immunity against the smallpox virus and other viruses in the same genus such as monkeypox virus.

Similar to smallpox, monkeypox infection stimulates the human immune system to generate antibodies that can offer long-term protection against possible reinfection (Musumeci et al., 2023). In addition, the cross-immunity reaction in the smallpox vaccine has an 85% success rate in preventing monkeypox infection and can last for years. However, based on research conducted by Musumeci et al. (2023), several cases of monkeypox reinfection were found to be reported in 2022 with varying time periods after the first infection. Two cases occurred in Milan, one case in Geneva, Paris, and London. The five cases occurred in men in their 30s who had a history of having gay-sex after recovering from the first infection. Musumeci et al. (2023) stated that these cases reveal that long-term natural immunity does not appear to guarantee avoidance of reinfection. However, research on reinfection with monkeypox is still being carried out due to the small number of reinfection cases (Carstens, 2023).

The research conducted by Peter et al. (2022) discusses the SEICR-SEI deterministic epidemic model on the spread of monkeypox in Nigeria. In this research, there is a quarantine phase denoted by "C" for individuals who are infected and require medical care. The numerical simulation results indicate that high contact rates potentially result in a higher number of individuals becoming infected. Therefore, contact between susceptible individuals and infected individuals must be controlled by considering quarantine factors.

This research discusses the CTMC SIQRS stochastic epidemic model and compares the simulation results of CTMC SIQRS and CTMC SIRS epidemic models on the spread of monkeypox.

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2. METHODS

The research's method is a literature study by discussing epidemic models, monkeypox disease, and theories relevant to the problems in this research through various references such as journals, articles, books, and other sources. This research aims to explain the continuous-time Markov chain susceptible-infected-quarantined-recovered-susceptible (CTMC SIQRS) epidemic model and to compare the simulation results of CTMC SIRS and CTMC SIQRS epidemic models on the spread of monkeypox. The following are several steps implemented in this research.

1. Explaining the CTMC SIRS and CTMC SIQRS epidemic model.
    a. Explaining the phenomenon of disease spread on the CTMC SIRS and CTMC SIQRS epidemic model.
    b. Determining the assumptions of the CTMC SIRS and CTMC SIQRS epidemic model.
    c. Determining the parameters and random variables of the CTMC SIRS and CTMC SIQRS epidemic model.
    d. Determining the transition probability of the CTMC SIRS and CTMC SIQRS epidemic model.
2. Simulating and interpreting CTMC SIRS and CTMC SIQRS epidemic models on the spread of monkeypox.
    a. Determining the parameter values of transmission rate (β), recovery rate without quarantine (ε), quarantine rate (δ), recovery rate with quarantine (α)and rate of return to susceptibility (γ).
    b. Determining the population size N and the initial values of each group $S(0), I(0), Q(0)$, $R(0)$.
    c. Determining the number of individuals in each group at each time t by generating random numbers with uniform distribution.
    d. Interpreting and comparing simulation results of the CTMC SIRS and CTMC SIQRS epidemic models on the spread of monkeypox.

3. RESULTS & DISCUSSION

a. Continuous Time Markov Chain (CTMC)

A stochastic process $\{X(t) : t \in T\}$ is a collection of random variables X indexed by t, which represents time or another index parameter (Taylor & Karlin, 1998). The collection of possible values of the random variable X in a stochastic process is called the state space, usually denoted by S. The time index and the state space in a stochastic process can be a continuous or discrete.

A stochastic process is called a Markov process when given the value $X(t)$, the value $X(s)$ is not influenced by $X(u)$ for $u < t < s$. In other words, the probaility of states in the future depends only on the current state and is not influenced by states in the past. A Markov process $\{X(t)\}$ with a discrete state space $S = \{0,1,2,\dots\}$ and continuous time index $T = [0,\infty)$ is called continuous time Markov chain (CTMC). Let n is integer in the time index set $T = \{t_0, t_1, t_2, t_3, \dots, t_{n-1}, t_n, t_{n+1}\}$ and the state space $S = \{i_0, i_1, i_2, \dots, i_{n-1}, i, j\}$, therefore :

$$P\{X(t_0) = i_0, X(t_1) = i_1, \dots, X(t_{n-1}) = i_{n-1}, X(t_n) = i\} = P\{X(t_n) = i\} \tag{1}$$

b. CTMC SIRS epidemic model

The spread of disease can occur when susceptible individuals come into contact with infected individuals, causing the individual to become infected with the disease. After a certain period of time, infected individuals will recover and have immunity to the disease. Immunity to a disease can be temporary or permanent. Permanent immunity is long-term, so there is little chance of re-infection. Meanwhile, temporary immunity is short-term. The body's defense ability against disease only lasts in a short time and will decrease over time, so that the body will become susceptible to disease again. Epidemic models that consider the existence of temporary immunity are called SIRS epidemic models (Ma & Li, 2009). The following are the assumptions used in the SIRS epidemic model.

1. The population size is constant, meaning that no individuals enter or leave the population.
2. Populations are homogeneous, meaning that each individual in the population has the same probability of being infected.
3. Death rates and birth rates are ignored.
4. There is only one type of disease that spreads in the population.
5. Recovered individuals have temporary immunity so they can become susceptible individuals again and have the potential to be infected again.

The population in the SIRS epidemic model is categorized into three groups including susceptible group (S), infected group (I), and recovered group (R). The spread of disease in the SIRS epidemic model occurs if there is a transmission of individuals from the susceptible to the infected group with a contact rate of β, from the infected to the recovered group with a natural recovery rate of ε, and from the recovered to the susceptible group with a contact rate of γ. The pattern diagram of the SIQRS epidemic model is shown in Figure 1.

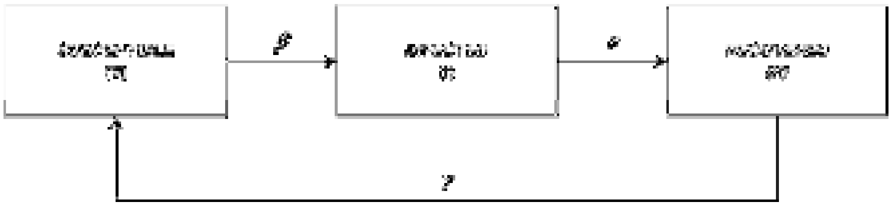

Figure 1. Diagram pattern of the SIRS epidemic model

According to Koepke et al., (2016), the CTMC SIRS epidemic model is the transition probability of individuals in the susceptible, infected, and recovered groups at time to t. SIRS epidemic model have population assumptions N constant with three random variables $S(t)$, $I(t)$, and $R(t)$, so that the total population is $N = S\ (t) + I(t) + R(t)$. The number of individuals in the susceptible, infected, and recovered groups at each time t are $S(t) = s$, $I(t) = i$, and $R(t) = r$. Therefore, based on Koepke et al., (2016), CTMC SIRS epidemic model can be written in equation (2).

$$\begin{aligned} P_{(s+j,i+k,r+l),(s,i,r)}(\Delta t) &= \{\beta \frac{i}{N} s\Delta t + o(\Delta t)\ (j,k,l) = (-1,1,0)\ \varepsilon i\Delta t + o(\Delta t)\ (j,k,l) \\ &= (0,-1,1)\ \gamma r\Delta t + o(\Delta t)\ (j,k,l) \\ &= (1,0,-1)\ 1 - \left[\beta \frac{i}{N} s + \varepsilon i + \gamma r\right] \Delta t + o(\Delta t)\ (j,k,l) = (0,0,0)\ o(\Delta t)\ lainnya \end{aligned} \tag{2}$$

c. CTMC SIQRS epidemic model

SIQRS epidemic model is a modification of the SIRS epidemic model with the quarantine phase (Fatimatuzzahroh et al., 2021). The main cause of disease outbreaks in a population is due to contact between infected individuals who have not carried out quarantine and susceptible individuals (Agustianingsih et al., 2020). Therefore, the SIRS epidemic model emerged with the quarantine assumption called the SIQRS epidemic model. The pattern of disease spread in the SIQRS epidemic model is not much different from the SIRS epidemic model. The difference lies in the way infected individuals recover. In the SIQRS epidemic model, infected individuals can recover from the disease in two ways, through the quarantine phase or without going through the quarantine phase. The assumptions from the SIRS epidemic model are used in this model, but there are two additional assumptions as follows:.

1. Infected individuals can recover in two ways, by going through the quarantine phase or without going through the quarantine phase.
2. Infected individuals who quarantine cannot infect susceptible individuals.

The population in the SIQRS epidemic model is categorized into four groups including susceptible group (S), infected group (I), quarantined group (Q), and recovered group (R). The spread of disease in the SIQRS epidemic model occurs if there is transmission of individuals from the susceptible to the infected group with a contact rate of β, from the infected to the recovered group with a natural recovery rate of ε, from the infected to the quarantined group with a quarantine rate of δ, from the quarantined to the recovered group with a recovery rate with quarantine of α, and from the recovered to the susceptible group with a contact rate of γ. The pattern diagram of the SIQRS epidemic model is shown in Figure 2.

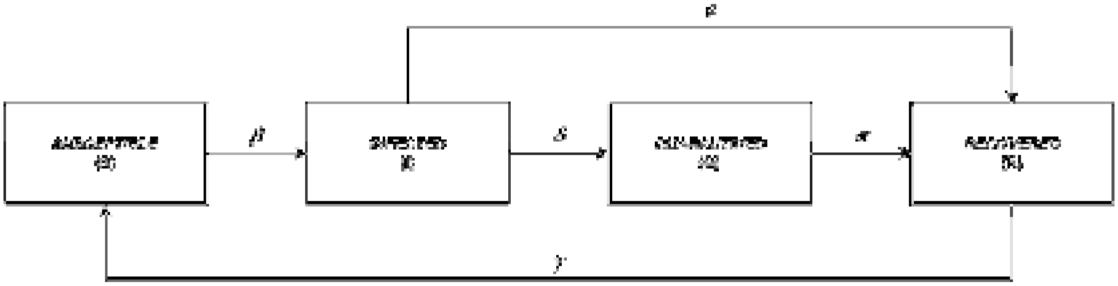

Figure 2. Diagram pattern of the SIQRS epidemic model

The CTMC SIQRS epidemic model is the transition probability of individuals in the susceptible, infected, quarantined and recovered groups over time t. SIQRS epidemic model have population assumptions N constant with four random variables $S(t), I(t), Q(t)$and $R(t)$, so that the total population is $N = S\ (t) + I(t) + Q(t) + R(t)$. The number of individuals in the susceptible , infected , quarantined and recovered groups at each time t is $S(t) = s$, $I(t) = i$, $Q(t) = q$, and $R(t) = r$. The joint probability function of $S(t), I(t), Q(t)$ and $R(t)$ can be written in equation (3).

$$P_{(s,i,q,r)}(t) = P[S(t) = s, I(t) = i, Q(t) = q, R(t) = r] \tag{3}$$

The movement of individuals from one group to another at time t causes a change in state which is called a transition. The change in the number of susceptible individuals in the time interval Δt is *j.* The change in the number of infected individuals in the time interval Δt is *k*. The change in the number of quarantined individuals in the time interval Δt is *l*. The change in the number of recovered individuals in the time interval Δt is *m*. Therefore, the transition probability of state *s* to state *s* + *j,* from state *i* to state *i* + *k,* from state *q* to state *q* + *l*, from state *r* to state *r* + *m* in the time interval Δt can be written in equation (4)

$$\begin{aligned} P_{(s+j,i+k,q+l,r+m),(s,i,q,r)}(\Delta t) &= P\{(S(t+\Delta t), I(t+\Delta t), Q(t+\Delta t), R(t+\Delta t)) \\ &= (s+j, i+k, q+l, r+m) | (S(t), I(t), Q(R), R(t) = (s,i,q,r)\} \end{aligned} \tag{4}$$

The change in state (s, i, q, r) become state $(s-1, i+1, q, r)$ shows that there is a transition of one individual from the susceptible to the infected group. The contact rate or transmission rate from the susceptible to the infected group is β and *s* is the number of susceptible individuals. If i is the number of infected individuals in population *N,* then the probability that the number of individuals in the infected group who can make contact with individuals in the susceptible group is equal to $\frac{i}{N}$. Therefore, the transition probability of state (s, i, q, r) become state $(s-1, i+1, q, r)$ can be written in equation (5).

$$P_{(s-1,i+1,q,r),(s,i,q,r)}(\Delta t) = \beta \frac{i}{N} s\Delta t + o(\Delta t) \tag{5}$$

The change in state (s,i,q,r) become state $(s,i-1,q+1,r)$ shows that there is a transition of one individual from the infected to the quarantined group. This is caused by infected individuals who are quarantined to prevent interactions with susceptible individuals. The quarantine rate from the infected to the quarantined group is δ and the number of infected individuals is i, then the transition probability of the state (s,i,q,r) become state $(s,i-1,q+1,r)$ can be written in equation (6).

$$P_{(s,i-1,q+1,r),(s,i,q,r)}(\Delta t) = \delta i\Delta t + o(\Delta t) \tag{6}$$

The change in state (s,i,q,r) become state $(s,i-1,q,r+1)$ shows that one individual moves from the infected to the recovered group. This is caused by individuals who have recovered from an illness naturally without going through a quarantine phase. The natural recovery rate from the infected group to the recovered group is $\varepsilon$and the number of individuals in the infected group is i , then the transition probability of the state (s,i,q,r) become state $(s,i-1,q,r+1)$ can be written in equation (7).

$$P_{(s,i-1,q,r+1),(s,i,q,r)}(\Delta t) = \varepsilon i\Delta t + o(\Delta t) \tag{7}$$

The change in state (s,i,q,r) become state $(s,i,q-1,r+1)$ shows that there is a transition of one individual from the quarantined to the recovered group. This is caused by individuals who have recovered from an illness after going through the quarantine phase. The recovery rate with quarantine from the quarantined group to the recovered group is α and the number of quarantined individuals is q, then the probability of transition from state (s,i,q,r) become state $(s,i,q-1,r+1)$ can be written in equation (8).

$$P_{(s,i-1,q,r+1),(s,i,q,r)}(\Delta t) = \alpha q\Delta t + o(\Delta t) \tag{8}$$

The SIQRS epidemic model assumes that recovered individuals have temporary immunity, so that they can become susceptible individuals again. The change in state (s,i,q,r) become state $(s+1,i,q,r-1)$ shows that one individual moves from the recovered to the susceptible group. The rate of recovered individuals become susceptible individuals is γ and the number of individuals in the recovered group is r, then the transition probability of the state (s,i,q,r) become state $(s+1,i,q,r-1)$ can be written in equation (9).

$$P_{(s+1,i,q,r-1),(s,i,q,r)}(\Delta t) = \gamma r\Delta t + o(\Delta t) \tag{9}$$

When there is no change in state or no individual moves from one group to another, t can be said that state (s,i,q,r) remain become state (s,i,q,r). Therefore, the transition probability of $the\ state(s,i,q,r)$ become $state(s,i,q,r)$ can be written in equation (10).

$$P_{(s,i,q,r),(s,i,q,r)}(\Delta t) = 1 - \left[\beta \frac{i}{N} s + \delta i + \varepsilon i + \alpha q + \gamma r\right] \Delta t + o(\Delta t) \tag{10}$$

The transition of an individual from one state to another occurs within a very small time interval, therefore, only one individual can make the transition at a time. The probability of more than one or equal to two individuals transitioning at one time is very small, approaching zero. Therefore, the probability that there are more than one or equal to two individuals transitioning within the Δt time interval is $o(\Delta t)$ where $\frac{o(\Delta t)}{\Delta t} = 0$. Based on equations (5) – (10), the transition probability of the CTMC SIQRS epidemic model can be written in equation (11).

$$\begin{aligned} P_{(s+j,i+k,q+l,r+m),(s,i,q,r)}(\Delta t) = \{&\beta \frac{i}{N} s\Delta t + o(\Delta t)\ (j,k,l,m) \\ &= (-1,1,0,0)\ \delta i \Delta t + o(\Delta t)\ (j,k,l,m) = (0,-1,1,0)\ \varepsilon i \Delta t + o(\Delta t)\ (j,k,l,m) \\ &= (0,-1,0,1)\ \alpha q \Delta t + o(\Delta t)\ (j,k,l,m) = (0,0,-1,1)\ \gamma r \Delta t + o(\Delta t)\ (j,k,l,m) \\ &= (1,0,0,-1)\ 1 - \left[\beta \frac{i}{N} s + \delta i + \varepsilon i + \alpha q + \gamma r\right] \Delta t + o(\Delta t)\ (j,k,l,m) \\ &= (0,0,0,0)\ o(\Delta t)\ lainnya \end{aligned} \tag{11}$$

d. Interpreting and comparing simulation results of the CTMC SIQRS and SIRS epidemic models on the spread of monkeypox.

Application of the CTMC SIQRS and SIRS epidemic model simulations on the spread of monkeypox using parameters β, ε, δ, and α referring to the Peter et al., (2022). In the research conducted by Peter et al., (2022), parameter values were estimated based on cumulative data on monkeypox cases in Nigeria from January – December 2019. The parameters used based on the research Peter et al., (2022) included $\beta = 61 \times 10^{-6}$, $\varepsilon = 242 \times 10^{-6}$, $\delta = 1369 \times 10^{-6}$and $\alpha = 99 \times 10^{-6}$.

The parameters for the rate of re-infected individuals in the susceptible group (γ) were estimated based on data cases of monkeypox re-infection from Britannica (2024) in four countries, Italy, France, England and Switzerland, where in these four countries there were reinfected cases or repeated infections after the first infection. Two cases occurred in Milan (Raccagni et al., 2023), and one case each occurred in Paris (Zeggagh et al., 2023), London (Golden et al., 2023) and Geneva (Musumeci et al., 2023). These five cases occurred in 2022. The estimated results of the rate of return of individuals in vulnerable groups from the four countries were averaged and a value was obtained $\gamma = 15 \times 10^{-7}$. The population size is assumed to be constant $N = 100$ at the initial values $S(0) = 90$, $I(0) = 10$, $Q(0) = 0$, and $R(0) = 0$. The simulation result of CTMC SIRS on the spread of monkeypox is shown in Figure 3.

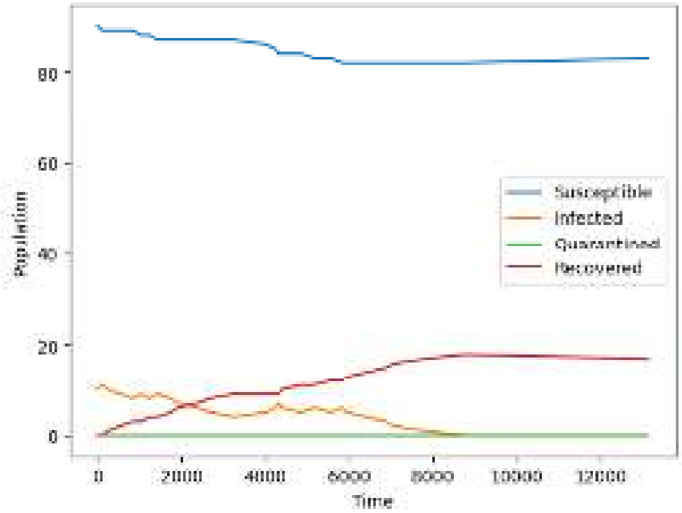

Figure 3. Simulation results of the CTMC SIRS epidemic model

Figure 3. shows that the number of individuals in the infected group decreased slowly over time until it reached the zero line at the time of $t = 8768.42$ day. Meanwhile, the number of individuals in the susceptible group decreased, although not significantly. This is caused by the presence of individuals in the susceptible group who are infected with the disease. On the other hand, the number of individuals in the recovered group has increased slowly since the initial time due to the presence of individuals in the infected group who have recovered from the disease and moved to the recovered group. Therefore, it can be inferred that the monkeypox epidemic ended on $t = 8768.42$ days when there were no infected individuals. Meanwhile, the simulation result of CTMC SIQRS on the spread of monkeypox is shown in Figure 4.

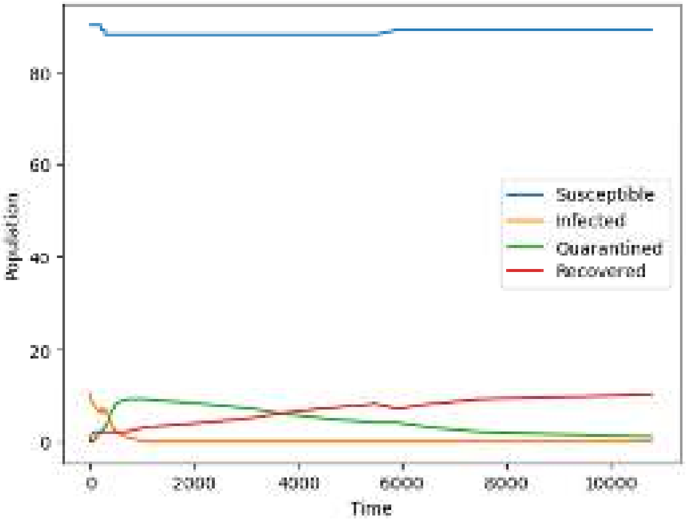

Figure 4. Simulation results of the CTMC SIQRS Epidemic Model

The simulation result in Figure 4 show that the number of susceptible individuals decrease at time $t = 202.18$ and $t = 281.50$ because there is two individual who is infected. At time $t = 5902.81$, the graph increases because there is one individual who loses immunity and becomes susceptible again. After that, the graph of susceptible individual tend to be stable at 89 until the end of the observation time.

The number of individuals in the infected group has decreased significantly since the beginning of time until it reaches zero at $t = 1046.98$ due to the movement of infected individuals to quarantined and recovered groups. There is a little increased over time $t = 202.18$ and $t = 281.50$ because of the movement from the susceptible group to the infected group. Furthermore, the number of infected individuals undergoing quarantine increased at the beginning until it reached a peak at that time $t = 671.25$ and then slowly decreased again until it approached zero because there were individuals who recovered from the disease.

The number of individuals in the recovered group increased slowly from the beginning until $t = 10796.64$, it is because there were individu in the infected and quarantined groups who recovered from monkeypox. Based on the simulation results, it can be concluded that the monkeypox epidemic ended on $t = 1046.98$ days when there were no infected individuals.

From Figure 3 and Figure 4, it can be inferred that the quarantine phase helps accelerate the decline in the number of infected individuals so that the epidemic ends more quickly. In the CTMC SIQRS model the epidemic ends on $t = 1046.98$ days = 2.8 years, while in the CTMC SIRS model the epidemic ends on the $t = 8768.42$ days = 24 years. This is caused by the large rate of quarantine resulting in the movement of individuals from the infected group to the quarantined group. Infected individuals who undergo quarantine are assumed not to have had contact with individuals in the susceptible group, so they cannot transmit the disease.

4. CONCLUSION

In conclusion, it can be inferred that the CTMC SIRS and CTMC SIQRS epidemic models can be denoted in the form of transition probabilities shown in equations (2) and (11). The CTMC SIQRS and SIRS epidemic models can be applied to the spread of monkeypox. In the CTMC SIQRS epidemic model it is concluded that the epidemic ends at $t = 1046.98$ days $= 2.8$ years, whereas in the CTMC SIRS model the epidemic ends at $t = 8768.42$ days $= 24$ years. Quarantine can prevent contact between infected individuals and susceptible individuals so that disease transmission does not occur. Therefore, the number of infected individuals is decreasing and the pandemic will end sooner.

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