

An *SIQS* Epidemic Model on the Specific Networks

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Abstract: The population structure is one of causes of infectious epidemics. The research, therefore, aims to study and construct specific heterogeneous networks. Also, the purpose of the study is to discuss their main characteristics, as well as touch on an impact of various network properties on disease spread through *SIQS* model. In this study, the basic reproductive number is derived in order to analyze the model stability. The networks have been constructed for three types under conditions of initial infected population connections, namely, the randomly initial infected, selectively initial infected with the highest number of links, and selectively initial infected with the lowest number of links. The results show an influence of the specific networks and a quarantined rate on dynamics and size of the infected epidemics. The outbreak has spread rapidly on the network in which the initially infected population has the highest number of connections. The increasing rate of quarantine has significantly reduced the number of infections. The practical applications of the study will be useful in controlling the spread of the disease for networks that the risk population are identified.

Keywords: network, infective disease, mathematical modelling, basic reproductive number, stability analysis.

1. Introduction

Epidemics of an infectious disease are caused by a direct contact (person-to-person). After the contact, the rapid spread of infectious diseases will be spread to a large number of people in a given population within a short period of time. Therefore, population structure is the main factor causing and controlling epidemics, especially, the structure of the risk population that is able to spread the infectious disease. Consequently, epidemics mathematics model has played an important role as a tool to analyze and diagnose the epidemics. As to implement a defensive measure, the model was constructed to manage a control of the epidemics and limit its side effects.

According to some previous studies, the continuous networks were studied. Eames et al. [1] constructed a variety of mathematics models: mean-field model and pair-wise model, to study the spread of sexually transmitted on the networks. Keeling et al. [2] studied and summarized epidemics models and networks. They revealed various relationships of mathematics' models and networks as to show an importance of the network structure regarding role and an understanding of the epidemiological process. Salathe et al. [3] constructed a community structure for studying its effects on epidemics. The results showed that the community structure of population not only affects the outbreak but also can prevent the spread of diseases. Dongmin et al. [4] developed a hetero-

geneous network for explaining dynamics of influenza transmission. Some of the findings illustrated that a social network degree is a critical factor determining the size of an epidemic.

This study, therefore, aims to study and construct the specific heterogeneous networks with the assumption of knowing the infected population or the risk group that has the potential to be the intermediary for the infectious outbreak. Besides, the study aims to focus on the impact of the networks on the epidemics. The analysis of numerical solutions of mathematical models, showing the number of people infected, and the epidemics period were included in this paper.

2. Methodology

The development of mathematical models is a part of a process for producing tools or methods as to understand the epidemics' actions. This current study aims to develop a specific network of a population group and present numerical studies for the infection spread from the *SIQS* simulation model of the created specific networks.

2.1 *SIQS* model

SIQS model is an epidemic model representing the infectious diseases that cause our body to be partly able to recover or unable to create immunity. As a result, the population that once recovered from the disease can return to be infectious. Thus, reducing the chance of infection is a means to help reduce or delay the epidemics. Detention or isolation of patients from the normal population is one of the key factors in reducing the spread of the disease. The population in this model has divided into 3 groups: normal population or risk group (Susceptible) represented with *S*, the infected population (Infected) represented with *I* and the infected population that has been isolated (Quarantined) represented with *Q*. The relationship of the population in each group can be shown in Figure 1 [5].

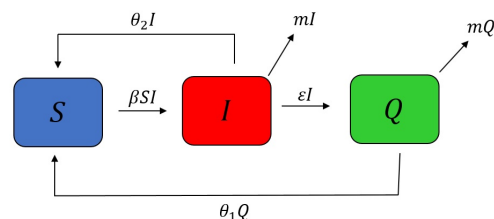


Figure 1. Schematic diagram of *SIQS* mathematical Model

The hypothesis of the model is presented as follows,

- The infected population are able to spread the infection to others.
- The infected population that have been quarantined are not able to spread the infection to others.
- Rate values do not be the negative numbers as can be defined and shown in Table 1.

Table 1. Parameter definitions

| Parameter | Definition |
|---------------|----------------------|
| β | Transmission rate |
| ε | Quarantine rate |
| θ_1 | Recovery rate of Q |
| θ_2 | Recovery rate of I |
| m | Disease mortality |

From Figure 1, the parameter definitions can be presented in a system of differential equations. To be clarified, the system of differential equations presents the number of populations from each group that has changed over time. The rates that affect the increase in the population were formed as the positive signs. Meanwhile, the rates that cause the decline of the population were transformed to the negative signs as shown in equation Eq. (1)

$$\begin{aligned}\dot{S} &= -\beta SI + \theta_2 I + \theta_1 Q, \\ \dot{I} &= \beta SI - (\theta_2 + \varepsilon + m)I \\ \dot{Q} &= \varepsilon I - (\theta_1 + m)Q\end{aligned}\quad (1)$$

2.2 Stability of an SIQS model

In order to find an equilibrium point of the model, setting up an equation is needed. After solving the equation, the equilibrium point is formed as an equation as follows:

$$E^0 = (S, I, Q) = (S^0, 0, 0)$$

The mathematical formulation of SIQS model problem is completed by non-negative initial conditions.

- Reproduction number of the model

The basic reproduction number for infectious diseases (Reproduction number: R_0) is important for creating guidelines as to control the epidemics. From Next Generation method [6] let $x = (S, I, Q)^T$, an equation will be formed in a Matrix as presented in Eq. (1)

$$\begin{aligned}\frac{dx}{dt} &= F_i - V_i \quad \text{when } F_i = \begin{bmatrix} \beta SI \\ 0 \end{bmatrix}, \\ V_i &= \begin{bmatrix} (\theta_2 + \varepsilon + m)I \\ -\varepsilon I + (\theta_1 + m)Q \end{bmatrix}.\end{aligned}$$

Jacobian Matrix at Disease-free equilibrium (E^0) is

$$F = DF_i(E^0) = \begin{bmatrix} \beta S & 0 \\ 0 & 0 \end{bmatrix}$$

and

$$V = DV_i(E^0) = \begin{bmatrix} \theta_1 + \varepsilon + m & 0 \\ -\varepsilon & \theta_2 + m \end{bmatrix}.$$

So, the reproduction number is

$$R_0 = \rho(FV^{-1}) = \frac{\beta S^0}{\theta_2 + \varepsilon + m}. \quad (2)$$

The reproduction number is an indicator of the average number of secondary cases in which one case would produce in a completely susceptible population. When $R_0 < 1$ the epidemic is reduced or there is no epidemic. On the other hand, when $R_0 > 1$, the disease is likely to come back again. Due to the average number of consecutive infections from each patient, there is an adequate increase in number to cause an epidemic again.

Theorem 1: If $R_0 < 1$, E^0 is locally asymptotically stable, but if $R_0 > 1$, E^0 is unstable.

2.3 Specific networks

One cause of infectious epidemics is from the direct contact (person- to- person). The network structure of the population is, therefore, an important factor in the study of the possibility of diseases transmission. A chance of getting infected with normal population or risk population groups is from the contact or connection to infected populations. The chance occurred with the rate of transmission of the disease and the number of infected populations that are connected, as shown in Figure 2.

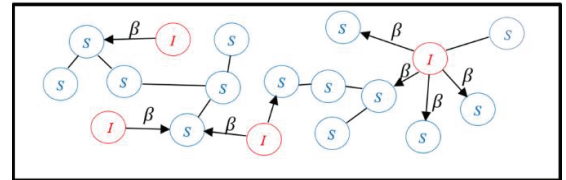


Figure 2. An example of the epidemic network where I is infectious person, S is susceptible person and β is a transmission rate

The current study aims to study and construct 3 types of heterogeneous networks under the condition of initial populations, or node that are infected populations. The created heterogeneous networks will be clarified as follows,

- Network type 1, using a non-specific random method.
- Network type 2, using a specific method. Setting the node that has the highest number of connections or links as the initial infected population. Randomly repeating with the same conditions until the number of infected people reaches the desired number.
- Network type 3, using a specific method. Setting the node that has the least number of connections or links as the initial infected population. Randomly repeat with the same conditions until the number of infected people reaches the desired number.

Algorithm for constructing specific networks

- **Step 1:** Generating heterogeneous network by using Erdős-Rényi network [7].
 - Set up total node = N
 - average degree = $\langle k \rangle$
 - link probability $p = \langle k \rangle / (N - 1)$
 - Create a random network with probability p
 - matrix $G(i,j) = 0$
 - $G(i,j) = 1$ for node i link to node j under a condition $\text{rand}(1) < p$
- **Step 2:** Searching the nodes which have the maximum or minimum link
 - Check sum degree of each node
 - if $G(i,j) \geq 1$ then $\text{dn}(i) = \text{dn}(i) + 1$
 - Find nodes which have maximum or minimum link
 - Node_max = max(dn) or Node_min = min(dn)
- **Step 3:** Setting the initial I node with constraint max or min
 - Set up the number of initial I node = I_0
 - Set up status of all nodes by status $S = 0$ and status $I = 1$
 - status = zeros($N, 1$)
 - while strat_I < I_0
 - start_I = find(dn == Node_max) or start_I = find(dn == Node_min)
 - startnodes = [startnodes, start_I]
 - then
 - status(startnodes(1 : I_0)) = 1

According to algorithm principle, the constructed network contains average degree $\langle k \rangle = p(N - 1)$. Besides, degree distribution will be accordance with the principle of Poisson distribution.

$$p(k) = \langle k \rangle^k \frac{e^{-\langle k \rangle}}{k!}, \quad (3)$$

when k represents the number of connections of each population.

2.4 An SIQS model of specific networks

This present study illustrates the dynamics of SIQS model according to equation Eq. (1) by studying and comparing the results of epidemics rates or the number of populations that has changed over time on three types of heterogeneous networks. The solution of equation Eq. (1) can be considered by using Stochastic simulation model. According to the model, the dynamics of the epidemic were valued by the rate of transmission, the rate of detention of infected people, the rate of disease recovery, and the rate of death. The exposure of the normal population to the disease occurs only when there is a connection between the normal population and the infected population. The chance of the disease spread depends on the rate

of the disease transmission and the number of infected populations, having connections. The infected population can be recovered based on the recovery rate. The process of simulating changes in the system is able to occur with an exponential distribution at the rate equal to the sum of all change rates in the system. During each period, only one event occurs by an independent random method for a population change. But it is proportional to the relationship of the rate of each population. In this research, the well-known Gillespie algorithm [8, 9] is the method for implementing SIQS stochastic simulation as follows,

SIQS Stochastic Simulation algorithm,

- **Step 1:** Find the rate of all events
 - S node: a rate of change is equal to β multiplied by total numbers of I node that has a connection.
 - I node: a rate of change is equal to $\theta_2 + \varepsilon + m$
 - Q node: a rate of change is equal to $\theta_1 + m$
- **Step 2:** Selecting the event to happen at random but proportionally to the events' rates relative to each other and then change the status of node_event

From the above procedures, it can be seen that the spread of infection depends on the connections of the infected population. Therefore, the network of the population affected the epidemics. These three networks were considered under the same conditions: total population N , average degree $\langle k \rangle$, and the number of the initial populations from each group that is equivalent. However, to the extent of infected population, node setting was considered from the number of connections in the networks.

3. Results

The present study reveals the numerical results from model SIQS presented in equation Eq. (1). To be clarified, equation Eq. (1) was investigated whether it is a stable model under conditions of the basic reproduction number equation Eq. (2). The data was shown the specific characteristics of the specific network. Besides, the results show the dynamics of the SIQS model on the network.

3.1 Numerical results of SIQS model under the conditions of the basic reproduction number

Based on the experiment, model Eq. (1) was considered based on the basic reproduction number by changing the infection rate. In order to be concordance with the conditions of $R_0 > 1$ and $R_0 < 1$. The infection rate β from 0 to 0.004 was changed while other rates remained constant. The results indicate the numerical solutions of equation Eq. (1), when considering the number of infected people with the disease, the equilibrium point is consistent with the R_0 value. In other words, if $R_0 < 1$, the number of infected people reached E^0 (Converting to zero). On the other hand, if $R_0 > 1$, the number of infected people unconverges to E^0 according to the theorem 1. In addition, the number of infected people vary according to the basic reproduction number. When the R_0

level increases, the number of infected people increases as shown in Figure 3 and also show some numerical solution of Eq. (1) under condition $R_0 < 1$ and $R_0 > 1$ as shown in Figure 4a -4b respectively.

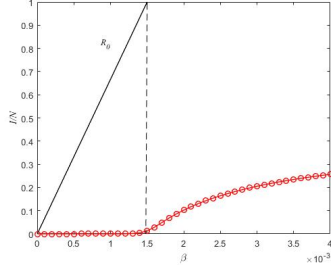


Figure 3. The fraction of infected I/N in the steady state with $N = 100$, $I(0) = 5$, $\theta_1 = 0.07$, $\theta_2 = 0.05$, $m = 0.00001731$, $\varepsilon = 0.1$ and $\beta = 0$ to 0.004

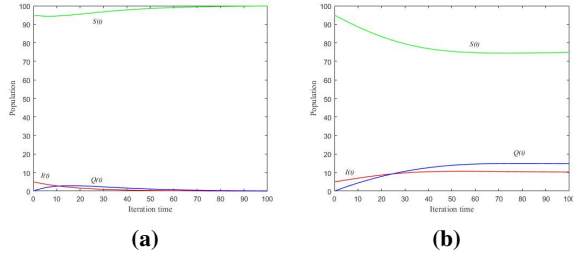


Figure 4. Time evolution of $S(t)$, $I(t)$ and $Q(t)$ with $N = 100$, $I(0) = 5$, $\theta_1 = 0.07$, $\theta_2 = 0.05$, $m = 0.00001731$, $\varepsilon = 0.1$ and (a) and (b) with $\beta = 0.001$ ($R_0 < 1$) and $\beta = 0.002$ ($R_0 > 1$), respectively

3.2 The specific characteristics of networks

From all of the above review of algorithm, there are three types of networks constructed by starts with setting up the initial value as $N = 1000$ and $\langle k \rangle = 7$, so $p = \langle k \rangle / (N - 1) = 0.007$. And then connects node by using a randomized probabilistic algorithms method, $p = 0.007$. Consequently, Erdős-Rényi network was constructed. The initial value of the infected population is $I(0) = 10$. Finally, the node was examined according to the network conditions required to determine the status of the infected person.

Figure 5 shows examples of all 3 constructed networks considering the total initial population value with the k connection value between 0 and $N - 1$ compared with the Poisson distribution according to equation Eq. (3). It was found that the network has a consistent connection to the algorithm. When considering the initial population that is infected from all three networks by checking the connection values of each node, the results that reach the conditions of the network will be shown in Table 2.

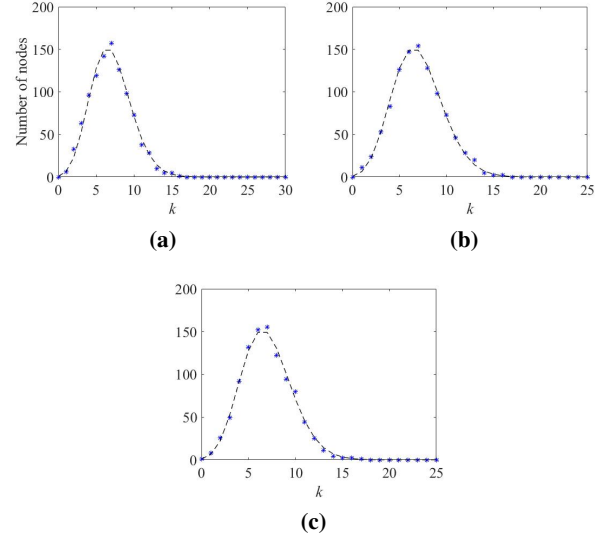


Figure 5. Comparison the degree distribution of networks $N = 1000$ and $\langle k \rangle = 7$ with Poisson distribution (black - - line): network 1 (a), network 2 (b), network 3 (c)

Table 2. Number of a link of an initially infected person which correspond the networks in Figure 5

| Network | I_1 | I_2 | I_3 | I_4 | I_5 | I_6 | I_7 | I_8 | I_9 | I_{10} |
|---------|-------|-------|-------|-------|-------|-------|-------|-------|-------|----------|
| 1 | 6 | 7 | 8 | 10 | 6 | 11 | 7 | 7 | 3 | 4 |
| 2 | 16 | 13 | 16 | 14 | 15 | 14 | 14 | 14 | 12 | 15 |
| 3 | 1 | 2 | 1 | 1 | 1 | 1 | 0 | 1 | 1 | 1 |

3.3 The dynamics of SIQS on networks

This study reveals the numerical results of SIQS model on three networks by considering the effects of epidemics from network structure and the hypothesis of the model.

The initial experiment with defining the initial value of the parameter, $N = 1000$, $\langle k \rangle = 7$, $I(0) = 10$, $Q(0) = 0$, $S(0) = N - I(0) - Q(0)$, $\varepsilon = 0.1$. Then, the researchers solved the solution of equation Eq. (1) according to the principles of the Gillespie algorithm comparing with the three networks as shown in Figure 6(a). At the beginning of the outbreak from the period 0 to 20, the network type 2 took the fastest rate. Networks 1 and 3 took the lower speed of the outbreak rate respectively. At the same time, the number of infected people in network type 2 is greater than network types 1 and 3. During the period of 20 to 30, the number of infected people has decreased until the value reaches the equilibrium point.

Figure 6(b) illustrates the increase of the quarantine process for infected person by adjusting the value of ε to $\varepsilon = 0.2$ on the initial conditions of other parameters at the same value as Figure 6(a). It can be seen that the characteristics of the epidemics spread remained constant. The number of infected people at a time will be the highest on the network type 2 and followed by networks 1 and 3, respectively, with the number of infected people decreasing by more than a half compared to $\varepsilon = 0.1$ in Figure 6(a).

From Figure 6, the numbers of infected people from 3 net-

works are dramatically different according to the initial infected people. It is hypothesized that network type 3 comprises small numbers of initial infected people links, as shown in Table 2 (the lowest). For example, I_7 : there is no connections with other populations, so this person has no chance to spread germs in the system at all. Therefore, the chance of spreading in network type 3 is slower than the chance in network type 1 and network type 2.

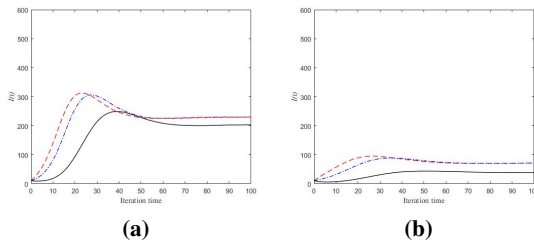


Figure 6. The number of infection prevalence from heterogeneous networks (network 1: blue -.- line, network 2: red -.- line and network 3: black—line). All numerical test use $\beta = 0.06$, $\theta_1 = 0.07$, $\theta_2 = 0.05$, $m = 0.00001731$, $\langle k \rangle = 7$ and simulations are averaged over 50 different network realisations and 50 simulations on each of these. The left and the right panel represent the quarantine rate with $\varepsilon = 0.1$ and $\varepsilon = 0.2$, respectively

Figure 7 is similar to Figure 6. It presents an impact of the additional network structure from creating a network: giving the number of connections in the network by defining $\langle k \rangle = 10$. It has been found that the number of infected people still remained the same with compare to Figure 6, but the number of infected people at a time of all 3 networks has fewer different values.

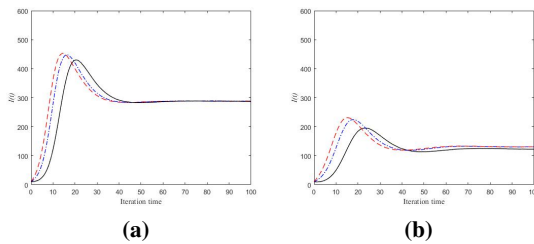


Figure 7. The number of infection prevalence from heterogeneous networks (network 1: blue -.- line, network 2: red -.- line and network 3: black—line). All numerical test use $\beta = 0.06$, $\theta_1 = 0.07$, $\theta_2 = 0.05$, $m = 0.00001731$, $\langle k \rangle = 10$ and simulations are averaged over 50 different network realisations and 50 simulations on each of these. The left and the right panel represent the quarantine rate with $\varepsilon = 0.1$ and $\varepsilon = 0.2$, respectively

4. Discussions and conclusion

This study showed the specific networks' construction as to investigate the spread of epidemics. To the extent of the *SIQS* model, the results showed that the network was constructed in accordance with the Erdős - Rényi network. When the $\langle k \rangle$ value was defined, the number of populations having a

connection value between 0 and $N - 1$ corresponded with Poisson distribution. Networks of type 2 and 3 were defined with the conditions of the infected population: the highest or the lowest number of connections. The experiment's results displayed the concordance between the findings and the constructed networks. Similarly, regarding the numerical results of models Eq. (1) under the basic infectious reproduction level according to the equation Eq. (2), it was found that model Eq. (1) is stable at the equilibrium point, E^0 when $R_0 < 1$. In contrast, when $R_0 > 1$, E^0 is unstable. The numerical results correspond to the theorem 1 as shown in Figure 3 and 4.

The *SIQS* model has been developed under the hypothesis of isolation measures for prevention of infection. The numerical solution of the three network models showed the number of infected people during the outbreak. The comparison of the outbreak showed the networks factors that affect the outbreak. As to clarify, the number of patients which is connected to a large number of networks accelerates the rapid epidemics rates. In contrast, if the infected population has very few connections to the networks, the epidemics rates will arise gradually and the number of patients will fall. Interestingly, it is found that when the $\langle k \rangle$ value is higher, there is no significant effects on the specific networks. The numerical solutions result regarding the $\langle k \rangle$ value is concordance with the results in random networks. Therefore, the possibility of the spread of the disease from all 3 networks is similar, regardless of the number of the initial infected population. From Figure 6, it can be concluded that the results of this experiment will be useful for infection precaution. Besides, it is useful for the population at risk as an intermediary for the spread of diseases. However, networks development or mathematical models' adjustment should be focused as appropriate for a further study. Furthermore, the scope of the study can be expanded. The hypothesis of networks can be more various or related to other perspectives. For instance, specific networks that serves the adjustment of the connections of the infected populations, or the specific networks can be used with a variety of mathematics' models: *SIQR* or *SIER*.

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