HPU2 Journal of Sciences:
Natural Sciences and Technology

journal homepage: https://sj.hpu2.edu.vn

Article type: Research article

Spreading dynamic of a fractional network-based siqr epidemic model with fuzzy transmission rate

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Abstract

For better understanding the influence of heterogeneity of complex networks and quarantine treatment on epidemic spreading, we present a study on a fractional network-based epidemic model with fuzzy transmission. Based on the next-generation method, we determine an important threshold value of the epidemiology theory, say $\Re_0$. Then, we indicate that $\Re_0$ significantly depends on the topology structure of the network and malware load. Next, we prove that the threshold value $\Re_0$ not only determines the unique existence of endemic equilibrium E_* but also ensures the clean of malware programs on the network.

Keywords: Fractional network-based SIQR epidemic model, fuzzy transmission, basic reproduction number, disease-free equilibrium, endemic equilibrium, asymptotic stability.

1. Introduction

In classical model, when the population is small and well-mixed, the rate of disease-causing contacts is often supposed to be equal. This assumption makes the model's evaluation more simply and tractable. However, it is un-realistic when the population is sufficiently large. Therefore, many researchers have used mathematical network-based models to study the epidemic disease spreading in complex networks such as the Internet, Facebook, Instagram, social networks, sensor networks and biological chain networks, etc., in which the connectability of different node is certainly un-similar and of course, the infections of malware programs to these nodes are also not the same. Recently, various epidemic models with network-based settings have been analyzed for better understanding the dynamical behavior of epidemic diseases. Indeed, the paper [21] is known as a meaning pioneer work in this topic with a detailed study on both analytical and numerical perspectives for a network-based SIS epidemic model on scale-free network. The most important contribution of this work is the finding of a threshold value for which the epidemic is absent and the corresponding dynamical behavior. In [9], Huo et. al. proposed a three-compartmental epidemic model with susceptible, infected and recovered states to describe the virus infection on scale-free network. Firstly, the basic reproduction number $\Re_0$ was evaluated to study some characteristic properties of the proposed model. After that, by establishing an

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https://doi.org/10.56764/hpu2.jos.2022.1.1.21-41.

Received date: 23-8-2022 ; Revised date: 26-8-2022 ; Accepted date: 30-8-2022

appropriate Lyapunov function, the authors proved the importance of the number $\mathfrak{R}_0$ in the study of asymptotic behavior of endemic equilibrium. In [14], Li et. al. introduced an SIRS epidemic model to describe the virus propagation on heterogeneous network. This work proved that the presence or absence of the disease on network completely depends on the value of $\mathfrak{R}_0$, i.e., the virus-free equilibrium is globally asymptotically stable if $\mathfrak{R}_0 < 1$, while if $\mathfrak{R}_0 > 1$ then it is unstable. However, the contribution of this work has just simulated the widespread phenomena of virus, but, in reality, the further treatments such as vaccination or quarantine also need to be discussed in the model. On the other hand, For investigating the influence of heterogeneity of the complex networks and quarantine strategy on epidemic spreading, Li et. al. [15] proposed a network-based SIQRS epidemic model and found out that the threshold value $\mathfrak{R}_0$ significantly depends on the topology of complex networks and quarantine rate. Furthermore, this work also presented the epidemic permanence and the local asymptotic stability of disease-free equilibrium. The flexibility and memory property of the network's environment are also factors that need to be taken into consideration when modeling real-world phenomena on the complex heterogeneous network. This is the reason why in this work, we consider a network-based SIQRS epidemic model with fractional derivative instead of classical integer derivative as in [15]. Numerous studies have proved that fractional calculus has a considerable advantage and superiority when modeling many non-local phenomena and memory processes. Beside the rapid popularization of fractional calculus, the study of fractional dynamical systems has achieved a lot of noticeable results in sciences and engineering, see [6,7,9]. The stability theory of fractional differential equations is also an important branch in the quanlitative theory of fractional differential equations. Recently, Cong et al. [3] fully introduced Lyapunov's first method for the study of fractional differential equations. In addition, with the introduction of Lyapunov function method (see [12]), the stability analysis of fractional differential systems by Lyapunov's second method has attracted more and more attentions. However, to the best of our knowledge, the construction of an appropriate fractional Lyapunov function subject to a fractional differential equations is quite complicated and requires several strict assumptions. In fact, this theory is still in the first stage of development and needs more further studies. Some valuable references in fractional Lyapunov function can be found in [2, 12, 13, 19, 22]. For the better modeling and data-fitting, fractional calculus has been also applied to study the fractional epidemiology theory and applications. However, to the best of our knowledge, there have only a few studies on network-based epidemic models with fractional-order. Some of them can be found in [8,20].

Since the nature of almost natural phenomena is vagueness and uncertainty, the mathematical modeling of real-world epidemic diseases must always accept the presence of uncertainties. However, to our best knowledge, there have been very few studies considering the environmental uncertainty in any epidemic model. It is well-known in many biological models that the epidemic disease occurs only if the viral load reaches a certain threshold and obviously, the concept of viral amount is quite difficult to express by exact or certain value. This leads to the use of fuzzy set theory initiated by Zadeh [23] to get the better modeling of epidemic diseases in realistic situations. Despite of the tremendous potential in the modeling of epidemic models, the uses of fuzzy sets in epidemiology theory are not frequent. Some noticeable applications of fuzzy sets in epidemic models can be found in Dong et. al. [6,7], Mondal et. al. [16], Nandi et. al. [18].

Motivated by aforesaid, this work is devoted to present a detailed study on a fractional network-based four compartmental epidemic model with fuzzy transmission. The main contributions of this work can be highlighted as follows:

(i) Formulate a fractional epidemic model in the form of mean-field reaction rate equations, namely fractional network-based $SIQR$ epidemic model, for describing and analyzing the malware spreading on complex heterogeneous network with quarantine treatment.

(ii) Since the fact that disease infection often occurs only if the malware load on the network exceeds a certain threshold value and reaches a saturation level at certain malware load, we propose to introduce the fuzzy membership function into the transmission rate.

(iii) Based on the next-generation method, we analytically compute the basic reproduction number $\mathfrak{R}_0$, that is an important threshold value in epidemiology theory. This quantity plays a key role in not only the existence of endemic equilibrium E_* but also the local asymptotic behavior of malware-free equilibrium E_0.

(iv) By using the linearization method, we give a criteria for the local asymptotic stability of disease-free equilibrium E_0 based on the $4n \times 4n-$Jacobi matrix's eigenvalues that are related to the basic reproduction number $\mathfrak{R}_0$. Next, by applying direct estimations and fractional contracttion principle, we can conclude that the attractivity of the equilibrium E_0 depends upon a threshold value $\mathfrak{R}_0$.

The structure of this work is given as follows:

2. Materials and methods or Experiments

2.1. Model Formulation

In this paper, we propose to use Barabási-Albert scale-free network [1] to describe for the heterogeneity of malware spreading on complex networks. Assume that when the network attains the scale-free stationary state, the probability distribution that a randomly given node has degree k follows the power-law $\mathbb{P}(k) = mk^{-3}$. In addition, assume that the number of divided groups $n = 100$ and from $\sum_{k=1}^{n} \mathbb{P}(k) = 1,$ we get $m = 0.8319$. Moreover, the network structure 's parameter $\langle k \rangle$ is computed by MatLab program: $\langle k \rangle = \sum_{k=1}^{n} mk^{-2} \approx 1.3601.$ In addition, the other used parameters are given as follows:

$$A = 0.12, \quad d = 0.1, \quad \omega = 0.5, \quad \gamma = 0.15, \quad r = 0.3.$$

2.1.1. The formulation of the fractional network-based $SIQR$ epidemic model

Since the nature of complex network is heterogeneous, it is well-known that the total population can't be well-mixed and the rate of disease-causing contacts is varied depending upon the node's connectivity. Indeed, based on the number of connected links a node has per unit time, we classify the total population into *n* groups and assume that nodes in a same group share the same dynamical property. Denote $S_k(t)$, $I_k(t)$, $Q_k(t)$ and $R_k(t)$ by the densities of susceptible, infectious, quarantined and recovered nodes with degree k at time t, respectively for $k = 1, 2, ..., n$ and denote $T_k(t)$ by the total number of nodes with degree k at time t. The flowchart of SIQR epidemic model in th k^{th}- group is given in Figure 1.

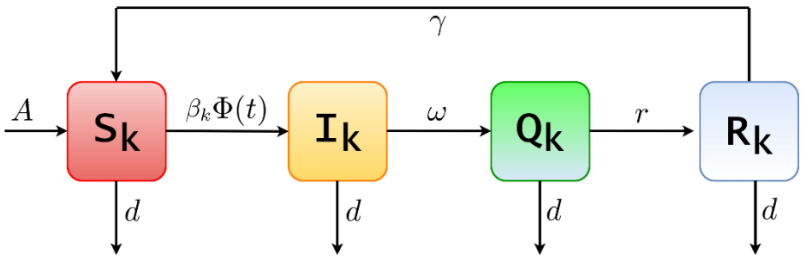

Figure 1. The flowchart of malware propagation among four compartments: Susceptible, Infectious, Quarantine, Recovered

In this work, we present a study on the network-based epidemic model governed by the following fractional mean-field reaction rate equation:

$$\begin{cases} {}_0^C D_t^q S_k(t) = A - \beta_k S_k(t)\Phi(t) - dS_k(t) + \gamma R_k(t) \\ {}_0^C D_t^q I_k(t) = \beta_k S_k(t)\Phi(t) - (\omega + d) I_k(t) \\ {}_0^C D_t^q Q_k(t) = \omega I_k(t) - (r + d) Q_k(t) \\ {}_0^C D_t^q R_k(t) = r Q_k(t) - (\gamma + d) R_k(t) \end{cases} \quad (1)$$

where the notation ${}_0^C D_t^q(.)$ denotes for the Caputo fractional derivative of order $q \in 0,1$ of state function (see [10], pp. 92), $\beta_k(v)$ is the degree-dependent fuzzy transmission rate, γ is the rate of being susceptible from the recovered state, ω is the quarantine rate of infectious nodes and r, d, A are the recovered rate, the natural death rate, the natural birth rate, respectively. Futhermore, since the un-correlation of node's connectivity on the network is taken into account, the probability that a given link is connected to an infectious node can be expressed by the following function

$$\Phi(t) = \frac{1}{\langle k \rangle} \sum_{i=1}^{n} i\mathbb{P}(i) I_i(t)$$

where $\langle k \rangle = \sum_{i=1}^{n} i\mathbb{P}(i)$ is known as the mean degree of the network.

2.1.2. The fuzzy transmission

In this work, assume that the degree-dependent transmission rate of k^{th} - group is $\beta_k = k\beta \leq k$. Moreover, with the aim of taking into consideraion the heterogeneity of complex network, the transmission paramrter β is proposed to express as a funcition of available malware programs. In particular, we use the following fuzzy set to describe this parameter.

$$\beta(v) = \begin{cases} 0 & if \ v \leq v_0 \\ \beta \dfrac{v - v_0}{v_1 - v_0} & if \ v_0 < v \leq v_1 \\ \beta & if \ v_1 < v \leq v_{max}. \end{cases}$$

It can be seen that the malware propagation always has a lower threshold value v_0, under which the chance of transmission is negligible. In addition, there exists an upper threshold value, say v_1,

beyond which the transmission rate reaches the maximum value $\beta(v) = \beta$. When the malware load is in the range v_o, v_1, the transmission rate $\beta(v)$ is an increasing linear function of malware load v. In addition, assume that the amount of malware load has an upper bound $v_{\max}$. Note that the values of $v_0, v_1, v_{\max}$ would depend upon both environmental characteristics and nature of malware programs, that is reasonable for the choice of fuzzy membership function. Furthermore, in order to express the concept "malware load", it seems suitable to use linguistic variables. For instance, based on three above threshold values, we classify the malware load into three classes corresponding to linguistic terms "LOW (A_l)", "MEDIUM (A_m)" and "HIGH (A_h)". In addition, in each classification, we use fuzzy numbers to express the malware load (see Figure 2). This approach can be found in [16,18].

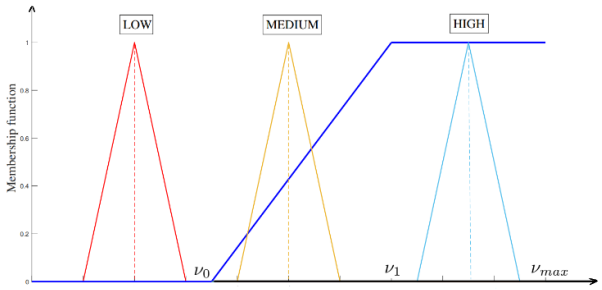

Figure 2. The membership function of fuzzy transmission rate σ and longuistic variables of the amount of malware program

2.1.3. The positiveness of the network-based SIQR epidemic model

We assume that the initial conditions of the network-based epidemic model (1) satisfy

$$S_k(0) > 0, \quad I_k(0) \geq 0, \quad Q_k(0) \geq 0, \quad R_k(0) \geq 0, \quad k = 1, 2, ..., n. \tag{1}$$

It can be verified that solution of Cauchy problem (1) - (2) is defined for all $t > 0$ and $k = 1, ..., n$ (see Appendix for more details). From the view point of epidemiology, we only need to focus on the positiveness and positively invariant set of solution. For simplicity, we denote

$$\tilde{x}(t) = \left(S_1(t), I_1(t), Q_1(t), R_1(t), ..., S_n(t), I_n(t), Q_n(t), R_n(t)\right)^{\mathrm{T}}$$

$$\Pi^+ = \left\{ \tilde{x}(t) \in \mathbb{R}_+^{4n} : S_k(t) + I_k(t) + Q_k(t) + R_k(t) \leq \frac{\mathrm{A}}{d}, k = \overline{1, n} \right\}.$$

Due to the presence of epidemic disease on network, we assume that $\Phi(t) > 0$ for each $t \geq 0$.

Theorem 2.1. *Assume that the initial condition* (2) *belongs to* Π^+. *Then, for each* $t > 0$, *the solution* $\tilde{x}\ t$ *of Cauchy problem* $(1) - (2)$ *belongs to* Π^+.

Proof. We assume by contrary that there exists a time $t_* > 0$ such that $S_k(t_*) = 0$, $S_k(t) > 0$ for all $0 \leq t < t_*$ and $S_k(t) < 0$ if $t > t_*$. Then, our proof is proceeded in two following cases:

Case 1: If the function $I_k(t)$ is non-negative for all $t \geq 0$ then by applying the fractional comparison principle (see Lemma 10, [13]), the differential inqualities

${}_0^C D_t^q Q_k(t) = \omega I_k(t) - (r+d)Q_k(t) \geq -(r+d)Q_k(t),$

which implies that $Q_k(t) \geq Q_k(0)\mathbb{E}_q(-(r+d)t^q) \geq 0.$ Similarly, we have $R_k(t) \geq 0$ for all $t \geq 0$. Therefore, at $t = t_*$, we have ${}_0^C D_t^q S_k(t)\Big|_{t=t_*} = A + \gamma R_k(t_*) > 0$. By using Lemma 2.8, it implies that the function $S_k(t_*) > 0$, which contradicts to our assumption.

Case 2: Assume that there exists a time $t_0 > 0$ such that $I_k(t_0) = 0$, $I_k(t) > 0$ for all $t \in [0, t_0)$ and $I_k(t) < 0$ for all $t > t_0$. We have if $t_0 > t_*$ then by doing similar arguments as in Case 1, we can prove that the functions $Q_k(t)$, $R_k(t)$ are all non-negative on $[0, \mathrm{t}_0]$ and $S_k(t_*) > 0$, which leads to the contradiction. If $t_0 \leq t_*$ then we have $S(t) > 0$ for all $t \in [0, t_0]$. As a result, the differential inequality ${}_0^C D_t^q I_k(t) = \beta_k(v)S_k(t)\Phi(t) - (\omega + d)I_k(t) > -(\omega + \mathrm{d})\,\mathrm{I}_k(t)$ implies that $I_k(t) > 0$ for all $t \in [0, t_0]$, that is a contradiction. Finally, we can conclude that $S_k(t) > 0$ for all $t \geq 0$. Similarly, we can also prove that $I_k(t)$, $Q_k(t)$ and $R_k(t)$ are all non-negative for each $t \geq 0$ and $k = \overline{1,n}$.

According to the assumption $\tilde{x}(0) \in \Pi^+$, we have $T_k(0) = S_k(0) + I_k(0) + Q_k(0) + \mathrm{R}_k(0) \leq \dfrac{A}{d}$. By summing up all fractional differential equations of the system (1), we immediately obtain

$${}_0^C D_t^q T_k(t) = A - dT_k(t). \tag{2}$$

Then, by using Example 4.9 in [10] and Lemma 2.7 in Appendix for $q_1 = q,\ q_2 = 1$ and $x = -\mu t^q$, the general solution of the fractional differential equation (3) is given by

$$T_k(t) = T_k(0)\mathbb{E}_q(-dt^q) + \mathrm{A}t^q\,\mathbb{E}_{q,q+1}(-dt^q) = T_k(0)\mathbb{E}_q(-dt^q) + \frac{A}{d}[1 - \mathbb{E}_{q,1}(-dt^q)].$$

Since $0 \leq \mathbb{E}_q(-dt^q) \leq 1$ for all $t \geq 0$, we have $T_k(t) \leq \dfrac{A}{d}\mathbb{E}_q(-dt^q) + \dfrac{A}{d}[1 - \mathbb{E}_{q,1}(-dt^q)] = \dfrac{A}{d}$,

which means that Π^+ is a positively invariant set for the epidemic model (1).

2.2. The basic reproduction number $\mathfrak{R}_0$ and equilibrium points

2.2.1. The basic reproduction number $\mathfrak{R}_0$

Firstly, it should be noted that equilibrium points of the fractional network-based SIQR epidemic model (1) is stationary points of the following system

$$\begin{cases} S_k + I_k + Q_k + R_k = \dfrac{A}{d} \\ \beta_k(v)S_k\Phi - (\omega + d)\,\mathrm{I}_k = 0 \\ \omega I_k - (r+d)Q_k = 0 \\ rQ_k - (\gamma + d)R_k = 0. \end{cases} \tag{3}$$

The disease-free equilibrium is a stationary point of the system (4), where $I_k = 0$ for all $k = \overline{1,n}.$ Thus, we can find that the epidemic model (1) admits a disease-free equilibrium E_0 given by

$$\mathrm{E}_0 = \underbrace{(A/d, 0, 0, 0, ..., A/d, 0, 0, 0)}_{4n}.$$

Now, our aim is to find a threshold value which plays a key role in the investigation of local asymptotic behavior of the epidemic model (1). This value is called basic reproduction number and denoted by $\Re_0$. To do this, we will apply the next-generation matrix method introduced in Diekmann [4]. The rate matrix *F* of new infection's appearance can be given by

$$F = \frac{A}{d\langle k\rangle}\begin{bmatrix} \beta_1(v)1\mathbb{P}(1) & \beta_1(v)2\mathbb{P}(2) & ... & \beta_1(v)\,\mathrm{n}\,\mathbb{P}(\mathrm{n}) \\ \beta_2(v)1\mathbb{P}(1) & \beta_2(v)2\mathbb{P}(2) & ... & \beta_2(v)\,\mathrm{n}\,\mathbb{P}(\mathrm{n}) \\ \vdots & \vdots & \ddots & \vdots \\ \beta_n(v)1\mathbb{P}(1) & \beta_n(v)2\mathbb{P}(2) & \cdots & \beta_n(v)\,\mathrm{n}\,\mathbb{P}(\mathrm{n}) \end{bmatrix} = \frac{A}{d\langle k\rangle}\begin{bmatrix} \beta_1(v) \\ \beta_2(v) \\ \vdots \\ \beta_n(v) \end{bmatrix}\begin{bmatrix} \mathbb{P}(1) & 2\mathbb{P}(2) & \cdots & n\mathbb{P}(n) \end{bmatrix}$$

and the transition matrix V of infected states is $V = (\omega + \mathrm{d})Id_n$, where Id_n is the $n \times n$ identity matrix. Finally, the basic reproduction number $\Re_0$ is given by $\Re_0 = \dfrac{A\langle k\beta_k\rangle}{d(\omega+d)\langle k\rangle}$, in which the notation $\langle k\beta_k\rangle = \sum_{k=1}^{n}\beta_k(v)k\mathbb{P}(k)$ is the network structure's parameter.

2.2.2. The sensitivity analysis of the threshold value $\Re_0$

Now, we will discuss how different parameters contribute to the change of $\Re_0$. According to Nakul et. al. [17], the sensitivity index of a quantity X depending on a parameter λ can be determined by $\Upsilon_\lambda^{\mathrm{X}} = \dfrac{\partial \mathrm{X}}{\partial \lambda}\times\dfrac{\lambda}{\mathrm{X}}$. By the definition of $\Re_0$ this quantity depends on some model's parameters such as $\omega, \mathrm{d}, \mathrm{A}, \beta(v)$ and the parameter of network structure. Therefore, by direct computations, we obtain

$$\Upsilon_{\beta(v)}^{\Re_0} = 1 \qquad \Upsilon_{A}^{\Re_0} = 1 \qquad \Upsilon_{\langle k^2\rangle/\langle k\rangle}^{\Re_0} = 1 \qquad \Upsilon_{\omega}^{\Re_0} = -\frac{\omega}{\omega+d} \qquad \Upsilon_{d}^{\Re_0} = -\frac{(\omega+2d)}{\omega+d}.$$

Remark 2.1. Here, we can conclude that the basic reproduction number $\Re_0$ is the most sensitive with the death rate *d* and the increase of quarantine rate ω will reduce the value of $\Re_0$. In addition, it will experience a 10% increase of the value $\Re_0$ if we increase the parameter $\beta(v)$ by a same percentage. Similarly, we also have the value of $\Re_0$ increases with the increase of structure parameter $\langle k^2\rangle/\langle k\rangle$, which means that the epidemic disease could be controlled if the value $\langle k^2\rangle/\langle k\rangle$ is decreasing, whereas the higher value of $\langle k^2\rangle/\langle k\rangle$ could follow that more efforts must be done to eliminate malicious objects on the network.

2.2.3. The influence of the fuzzy transmission rate to $\Re_0$

Since $\beta_k(v) = k\beta(v)$, the quantity $\Re_0$ can be known as a function of malware load v. Now, we will discuss the influence of malware load to the value of $\Re_0$. We will consider three cases of malware

load w.r.t. the linguistic meanings "LOW", "MEDIUM" and "HIGH".

Case I. If the malware load is "LOW", i.e., the fuzzy number $A_l = (\nu_c - \varepsilon, \nu_c, \nu_c + \varepsilon)$ satisfies $\nu_c + \varepsilon < \nu_0$, then the transmission rate $\beta_k(\nu) = 0.$ In addition, it is clear that the basic reproduction number $\mathfrak{R}_0$ then becomes zero, which means that the epidemic disease is absent on the network. This case can be understood that the disease is not enough to cause the infection or malware programs attacked to some nodes that have less importance with the network.

Case II. If the malware load is "MEDIUM", i.e., the fuzzy number $A_m = (\nu_c - \varepsilon, \nu_c, \nu_c + \varepsilon)$ satisfies $\nu_c - \varepsilon \geq \nu_0$ and $\nu_c + \varepsilon < \nu_1$, then the transmission rate $\beta_k(\nu)$ is known as a linear function w.r.t. malware load ν. As a result, the basic reproduction number $\mathfrak{R}_0 := \mathfrak{R}_0(\tau)$, given by

$$\mathfrak{R}_0(\tau) = \frac{A\beta\langle k^2\rangle}{d(\omega+d)\langle k\rangle}\frac{\nu-\nu_0}{\nu_1-\nu_0},$$

is an increasing function w.r.t. malware load ν, which leads to a fact that the higher malware load is, the bigger value basic reproduction number $\mathfrak{R}_0$ gets, where $\langle k^2\rangle = \sum_{i=1}^{n} i^2 \mathbb{P}(\mathrm{i})$.

Case III. If the malware load is "HIGH", i.e., the fuzzy number $A_h = (\nu_c - \varepsilon, \nu_c, \nu_c + \varepsilon)$ satisfies $\nu_c - \varepsilon \leq \nu_1$, then the transmission rate $\beta_k(\nu) = k\beta$ is a constant function w.r.t malware load ν**.** Thus, the basic reproduction number $\mathfrak{R}_0$ only depends on parameters and network structure.

2.2.4. The existence and uniqueness of the endemic equilibrium

Next, the following theorem presents an interesting result on the existence and uniqueness of an endemic equilibrium $E_*(EE)$ *of the fractional network-based* $SIQR$ *epidemic model* (1).

Theorem 2.2. *The following assertions are fulfilled:*

(i) If $\mathfrak{R}_0 \leq 1$ *then the epidemic model* (1) *can't have any endemic equilibrium.*

(ii) If $\mathfrak{R}_0 > 1$ *and* $A \leq d\left[1 + \frac{\omega}{(r+d)}\left(1 + \frac{r}{\gamma+d}\right)\right]$ *then the epidemic model* (1) *has exactly a unique endemic equilibrium* $E_* = \left(S_1^*, I_1^*, Q_1^*, R_1^*, ..., S_n^*, I_n^*, Q_n^*, R_n^*\right)$, *where*

$$S_k^* = \frac{\omega+d}{\beta_k(\nu)\Phi^*} I_k^*, \quad Q_k^* = \frac{\omega}{r+d} I_k^*, \quad R_k^* = \frac{r\omega}{(r+d)(\gamma+d)} I_k^*,$$

(iii)
$$I_k^* = \frac{A\beta_k(\nu)\Phi^*}{d\left[\omega + d + \beta_k(\nu)\Phi^* + \frac{\omega\beta_k(\nu)\Phi^*}{r+d}\left(1 + \frac{r}{\gamma+d}\right)\right]} \qquad \Phi^* = \frac{1}{\langle k\rangle}\sum_{i=1}^{n} i\mathbb{P}(i) I_i^*.$$

(iv) *Proof. Firstly, note that at the endemic equilibrium state, the quadruple* $\left(S_k^*, I_k^*, Q_k^*, R_k^*\right)$ satisfies the system (4) and the compartments I_k are nonzero. Thus, the quantity $\Phi = \frac{1}{\langle k\rangle}\sum_{i=1}^{n} i\mathbb{P}(i) I_i$ is also positive. Now, we will express the terms S_k, Q_k and R_k by I_k. In

particular, we have

$$S_k = \frac{\omega + d}{\beta_k(\nu)\Phi} I_k, \quad Q_k = \frac{\omega}{r+d} I_k, \quad R_k = \frac{r\omega}{(r+d)(\gamma+d)} I_k,$$

$$I_k = \frac{\mathrm{A}\beta_k(\nu)\Phi}{d\left[\omega + d + \beta_k(\nu)\Phi + \frac{\omega\beta_k(\nu)\Phi}{r+d}\left(1 + \frac{r}{\gamma+d}\right)\right]}.$$

So, we obtain the following self-consistency equation

$$\Phi = \frac{1}{\langle k \rangle} \sum_{i=1}^{n} \frac{\mathrm{A}\beta_i(\nu) i \mathbb{P}(i)\Phi}{d\left[\omega + d + \beta_i(\nu)\Phi + \frac{\omega\beta_i(\nu)\Phi}{r+d}\left(1 + \frac{r}{\gamma+d}\right)\right]}. \tag{4}$$

Our aim to find a condition for which (5) has a solution $\Phi^* \in (0,1)$. For this aim, we define

$$F(\Phi) = \frac{1}{\langle k \rangle} \sum_{i=1}^{n} \frac{\mathrm{A}\beta_i(\nu) i \mathbb{P}(i)}{d\left[\omega + d + \beta_i(\nu)\Phi + \frac{\omega\beta_i(\nu)\Phi}{r+d}\left(1 + \frac{r}{\gamma+d}\right)\right]}.$$

Here, we can see that the function $F(\Phi)$ is continuous in $[0,1]$ and differentiable on $(0,1)$. In addition, for each $\Phi \in (0,1)$, we have $F(\Phi) < \frac{1}{\langle k \rangle} \sum_{i=1}^{n} \frac{\mathrm{A}\beta_i(\nu) i \mathbb{P}(i)}{d(\omega+d)} = \Re_0$ and $F(\Phi) = \Re_0$ if and only if $\Phi = 0$. Moreover, at $\Phi = 1$, we have

$$F(1) = \frac{1}{\langle k \rangle} \sum_{i=1}^{n} \frac{\mathrm{A}\beta_i(\nu) i \mathbb{P}(i)}{d\left[\omega + d + \beta_i(\nu) + \frac{\omega\beta_i(\nu)}{r+d}\left(1 + \frac{r}{\gamma+d}\right)\right]} < \frac{1}{\langle k \rangle} \sum_{i=1}^{n} \frac{\mathrm{A}\beta_i(\nu) i \mathbb{P}(i)}{d\beta_i(\nu)\left[1 + \frac{\omega}{r+d}\left(1 + \frac{r}{\gamma+d}\right)\right]} \le 1.$$

It is easy to see that a non-trivial solution of the equation $F(\Phi) = 1$ is also a non-trivial solution of (5). In the case $\Re_0 \le 1$, since $F(\Phi) < \Re_0 \le 1$, the equation $F(\Phi) = 0$ has no solution and hence, the first assertion is completed. If $\Re_0 > 1$ then it directly follows that $F(0) > 1$ and hence, by Intermediate Value theorem, the equation $F(\Phi) = 1$ has at least one solution $\Phi \in (0,1)$, which is also a non-trivial solution of (5). Moreover, for each $\Phi \in (0,1)$, we have

$$\frac{d}{d\Phi} F(\Phi) = -\frac{\mathrm{A}}{d\langle k \rangle} \sum_{i=1}^{n} \frac{\beta_i(\nu) i \mathbb{P}(i)\left[\beta_i(\nu) + \frac{\omega\beta_i(\nu)}{r+d}\left(1 + \frac{r}{\gamma+d}\right)\right]}{\left[\omega + d + \beta_i(\nu)\Phi + \frac{\omega\beta_i(\nu)\Phi}{r+d}\left(1 + \frac{r}{\gamma+d}\right)\right]^2}.$$

Due to the presence of epidemic disease on network, the degree-dependent parameters $\beta_i(\nu)$ are positive for some $i = 1,2,...,n$. Hence, we obtain $\frac{d}{d\Phi} F(\Phi) < 0$, which implies that $F(\Phi)$ is decreasing on $(0,1)$. As a consequence, the self-consistency equation (5) has a unique solution $\Phi^* \in (0,1)$ and this solution will uniquely solve the endemic equilibrium E_*.

2.3. The asymptotic behavior of the disease-free equilibrium E_0

Theorem 2.3. *The disease-free equilibrium* E_0 *is locally asymptotically stable if* $\Re_0 < 1$ *and unstable if otherwise.*

Proof. In order to investigate the local asymptotic stability of the disease-free equilibrium E_0, we will apply the linearization method for the epidemic model (1). For this aim, let us consider Jacobi matrix at the point E_0 subjecting to the epidemic model (1) in the following form

$$\Im_{E_0} = \begin{bmatrix} M_{11} & M_{12} & \cdots & M_{1n} \\ M_{21} & M_{22} & \cdots & M_{2n} \\ \vdots & \vdots & \ddots & \vdots \\ M_{n1} & M_{n2} & \cdots & M_{nn} \end{bmatrix}_{4n\times 4n}$$

where for each $i, j = \overline{1,n}$, the 4×4 - square matrices M_{ii}, M_{ij} are given by

$$M_{ii} = \begin{bmatrix} \frac{\beta_i(v) i \Lambda \mathbb{P}(i)}{d\langle k\rangle} - (\omega + d) & 0 & 0 & 0 \\ -\frac{\beta_i(v) i \Lambda \mathbb{P}(i)}{d\langle k\rangle} & -d & 0 & 0 \\ \omega & 0 & -(r+d) & 0 \\ 0 & 0 & r & -(\gamma + d) \end{bmatrix}, \quad M_{ij} = \begin{bmatrix} \frac{\beta_i(v) j \Lambda \mathbb{P}(i)}{d\langle k\rangle} & 0 & 0 & 0 \\ -\frac{\beta_i(v) j \Lambda \mathbb{P}(i)}{d\langle k\rangle} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}.$$

According to Theorem 5 in [3], the disease-free equilibrium E_0 is locally asymptotically stable if and only if all eigenvalues $\{\lambda_j\}_{j=\overline{1,4n}}$ of Jacobi matrix $\Im_{\mathbb{E}_0}$ satisfy

$$\left|\arg(\lambda_j)\right| > \frac{q\pi}{2}, \qquad j = 1,2,\ldots,4n.$$

Now, by applying the mathematical induction principle, the characteristic polynomial with respect to the matrix $\Im_{\mathbb{E}_0}$ can be given by

$$P(\lambda) = (\lambda + r + d)^n (\lambda + \gamma + d)^n (\lambda + d)^n (\lambda + \omega + d)^{n-1} \left(\lambda + (\omega + d) - \frac{\mathrm{A}}{d\langle k\rangle} \sum_{k=1}^{n} \beta_k(v) k \mathbb{P}(k) \right).$$

It can be easily verified that the characteristic equation $P(\lambda) = 0$ has $4n$ real solutions with multiplicity, in which the negative solutions $\lambda = -(r+d), \lambda = -(\gamma + d), \lambda = -d$ all have the multiplicity n and the negative solution $\lambda = -(\omega + d)$ has the multiplicity $n-1$. The last solution of the characteristic equation $P(\lambda) = 0$ is

$$\lambda = -(\omega + d) + \frac{\mathrm{A}}{d\langle k\rangle} \sum_{k=1}^{n} \beta_k(v) k \mathbb{P}(k) = (\omega + d)(\Re_0 - 1).$$

By using the assumption $\Re_0 < 1$, it follows that the eigenvalues $\{\lambda_j\}_{j=\overline{1,4n}}$ of the Jacobi matrix

$\mathfrak{I}_{\mathbb{E}_0}$ are all negative and hence, $\arg(\lambda_j)=\pi$ for all $j=\overline{1,4n}$. In addition, since $q\in(0,1]$, it implies that $\left|\arg(\lambda_j)\right|=\pi>\frac{q\pi}{2}$ for all $j=\overline{1,4n}$. Therefore, we can conclude that the disease-free equilibrium E_0 is locally asymptotically stable. Otherwise, this equilibrium is unstable.

The rest of this section is to prove the global asymptotic stability of the disease-free equilibrium E_0 of the epidemic model (1)

Theorem 2.4. *If* $\Re_0<1$ *then the disease-free equilibrium* E_0 *is globally asymptotically stable on the region* Π^+, *i.e., the epidemic disease fades out*.

Proof. Let $\tilde{x}(t)=\left(S_1(t),I_1(t),Q_1(t),R_1(t),...,S_n(t),I_n(t),Q_n(t),R_n(t)\right)^{\mathrm{T}}$ denote for the non-negative solution of the fractional network-based $SIQR$ epidemic model (1). It suffices to prove that the disease-free equilibrium E_0 is attractive, i.e., $\lim\limits_{t\to\infty}x(t)=E_0$. Then, for each $k=\overline{1,n}$ and $t>0$, since $0\le S_k(t)+I_k(t)+Q_k(t)+R_k(t)\le\frac{A}{d}$, it implies that

$$\begin{cases}0<S_k(t)\le\dfrac{A}{d}\\ R_k(t)=\dfrac{A}{d}-S_k(t)-I_k(t)-Q_k(t)\le\dfrac{A}{d}-S_k(t).\end{cases}$$

From the first differential of (1), we have

$$\begin{aligned}{}_0^C D_t^q S_k(t)&=A-\beta_k(\nu)S_k(t)\Phi(t)-dS_k(t)+\gamma R_k(t)\\&\le A-dS_k(t)+\gamma\left(\frac{A}{d}-S_k(t)\right)\\&=\frac{A(\gamma+d)}{d}-(\gamma+d)S_k(t).\end{aligned}$$

Consider the auxiliary fractional differential systems ${}_0^C D_t^q S_k(t)=\frac{A(\gamma+d)}{d}-(\gamma+d)S_k(t)$. We can see that this fractional differential equation admits a unique equilibrium $S_k^0=\frac{A}{d}$, which is globally asymptotically stable. Then, by using fractional comparison principle (see Lemma 10 in [13]), it follows that for any $\varepsilon>0$, it is true that $S_k(t)\le S_k^0+\varepsilon$ for all t sufficiently large. Thus, for all t sufficiently large, the second equation of (1) implies

$${}_0^C D_t^q I_k(t)\le\beta_k(\nu)\left(S_k^0+\varepsilon\right)\Phi(t)-(\omega+d)I_k(t)=\beta_k(\nu)\left(\frac{A}{d}+\varepsilon\right)\Phi(t)-(\omega+d)I_k(t)$$

And

$$
\begin{aligned}
{}_0^C D_t^q \Phi(t) &\le \frac{1}{\langle k \rangle} \sum_{k=1}^{n} k\mathbb{P}(k) \left[\beta_k(\nu) \left(\frac{A}{d} + \varepsilon \right) \Phi(t) - (\omega + d) I_k(t) \right] \\
&= \frac{1}{\langle k \rangle} \sum_{k=1}^{n} k\mathbb{P}(k) \beta_k(\nu) \left(\frac{A}{d} + \varepsilon \right) \Phi(t) - (\omega + d) \Phi(t) \\
&= (\omega + d) \Phi(t) \left\{ \frac{A}{d(\omega + d)\langle k \rangle} \sum_{k=1}^{n} k\mathbb{P}(k) \beta_k(\nu) - 1 + \frac{\varepsilon}{(\omega + d)\langle k \rangle} \sum_{k=1}^{n} k\mathbb{P}(k) \beta_k(\nu) \right\} \\
&= (\omega + d) \Phi(t) \left\{ \Re_0 - 1 + \frac{\varepsilon \langle k\beta_k \rangle}{(\omega + d)\langle k \rangle} \right\}.
\end{aligned}
$$

Since the assumption $\Re_0 < 1$, we can choose $\varepsilon > 0$ small enough such that $\Re_0 + \dfrac{\varepsilon \langle k\beta_k \rangle}{(\omega + d)\langle k \rangle} < 1.$

In addition, since the assumption that the disease is present on the network, we have $\Phi(0) > 0$. Hence, by using fractional comparison principle, we receive

$$
0 \le \Phi(t) \le \Phi(0) \mathbb{E}_q \left(-(\omega + d) \left(1 - \Re_0 - \frac{\varepsilon \langle k\beta_k \rangle}{(\omega + d)\langle k \rangle} \right) t^q \right),
$$

which implies that $\lim_{t \to \infty} \Phi(t) = 0$ (see Theorem 4.6 in [5], pp. 72). By definition of the function $\Phi(t)$ and the non-negativity of $I_k(t)$, we deduce that $\lim_{t \to \infty} I_k(t) = 0$, that means for any $\varepsilon > 0$, there exists $T_0 > 0$ such that $I_k(t) < \varepsilon$ for all $t \ge T_0$ and for each $k = 1, 2, \ldots, n$. Then, for all $t \ge T_0$, the third fractional differential equation of (1) implies that we have

$$
{}_0^C D_t^q Q_k(t) = \omega I_k(t) - (r + d) Q_k(t) < \omega\varepsilon - (r + d) Q_k(t).
$$

By doing similar arguments as in solving the fractional differential equation (3), we directly obtain $Q_k(t) < \dfrac{\omega\varepsilon}{r + d}$. Next, for all $t \ge T_0$, we also have

$$
\begin{aligned}
{}_0^C D_t^q S_k(t) &= A - S_k(t)\left(d + \beta_k(\nu)\Phi(t)\right) + \gamma \left(\frac{A}{d} - S_k(t) - Q_k(t) - I_k(t) \right) \\
&> A - S_k(t)\left(\gamma + d + \beta_k(\nu)\Phi(t)\right) + \frac{\gamma A}{d} - \gamma \left(\varepsilon + \frac{\omega\varepsilon}{r + d} \right) \\
&= \frac{A(\gamma + d)}{d} - \varepsilon \left(\gamma + \frac{\omega\gamma}{r + d} \right) - S_k(t)\left(\gamma + d + \beta_k(\nu)\varepsilon\right).
\end{aligned}
$$

Thus, we directly get that $S_k(t) > \dfrac{1}{\left(\gamma + d + \beta_k(\nu)\varepsilon\right)} \left[\dfrac{A(\gamma + d)}{d} - \varepsilon \left(\gamma + \dfrac{\omega\gamma}{r + d} \right) \right]$ for all $t \ge T_0$.

Next, by letting $\varepsilon \to 0$, we immediately obtain $\lim_{t \to \infty} S_k(t) = \dfrac{A}{d}$ and $\lim_{t \to \infty} Q_k(t) = 0$. Finally, since the fact that $0 < S_k(t) + I_k(t) + Q_k(t) + R_k(t) \le \dfrac{A}{d}$ and $\lim_{t \to \infty} \left(S_k(t) + I_k(t) + Q_k(t) \right) = \dfrac{A}{d}$, it yields

$$\lim_{t\to\infty} R_k(t) = 0.$$

Therefore, the proof is completed.

2.4. Appendix

In the following, we briefly recall a framework of fractional calculus and fractional differential equations, see [5] for more details.

For $q > 0$ and $[a,b] \subset \mathbb{R}$, let $f : [a,b] \to \mathbb{R}$ be a function such that $f \in L^1([a,b])$. Then, the Riemann-Liouville fractional integral operator of order q is defined by

$${}_a\mathrm{I}_t^q f(t) := \frac{1}{\Gamma(q)} \int_a^t (t-s)^{q-1} f(s) ds, \qquad t \in [a,b].$$

Let $m := \lceil q \rceil$ be the smallest integer greater than or equal to q. Then, the Caputo fractional derivative operator of order q of a function $f \in C^m([a,b])$ is defined by

$${}_a^C D_t^q f(t) := \frac{1}{\Gamma(m-q)} \int_a^t (t-s)^{n-q-1} f^{(m)}(s) ds = \left({}_a\mathrm{I}_t^{m-q} D^m f \right)(t), \quad t \in [a,b],$$

where $D^m = \dfrac{d^m}{dx}$ denotes for the m^{th} order derivative. In general, the Caputo fractional derivative for a vector-valued function $f = (f_1, f_2, \ldots, f_n)^{\mathrm{T}}$ is defined component-wise by

$${}_a^C D_t^q f(t) = \left({}_a^C D_t^q f_1(t), {}_a^C D_t^q f_2(t), \ldots, {}_a^C D_t^q f_n(t) \right).$$

Consider the initial value problem for the following fractional differential equations

$${}_a^C D_t^q x(t) = Ax(t) + f(x(t)), \qquad t > 0, \tag{5}$$

subject to the initial conditions

$$x(0) = x_0, \tag{6}$$

where $A \in Mat_{n\times n}(\mathbb{R})$ and $f : \mathbb{R}^n \to \mathbb{R}^n$ is a continuously differentiable function and satisfies Lipschitz condition. According to Corollary 6.9 in [5], it implies the global unique existence of solutions of the initial value problem (6) – (7). As a result, we can rewrite the network-based SIQR epidemic model (1) in the compact form ${}_0^C D_t^q x(t) = \Lambda x(t) + f(x(t)),$ in which

$$x(t) = \left(S_1(t), I_1(t), Q_1(t), R_1(t), ..., S_n(t), I_n(t), Q_n(t), R_n(t) \right)^{\mathrm{T}},$$

$$\Lambda = \begin{bmatrix} -d & 0 & 0 & \gamma \\ 0 & -(\omega+d) & 0 & 0 \\ 0 & \omega & -(r+d) & 0 \\ 0 & 0 & r & -(\gamma+d) \end{bmatrix}_{n\times n}, \quad f\left(x(t)\right) = \begin{bmatrix} A - \beta_k S_k(t)\Phi(t) \\ \beta_k S_k(t)\Phi(t) \\ 0 \\ 0 \end{bmatrix}_{n\times n}.$$

Note that the Jacobi matrix $\dfrac{\partial f\left(x\right)}{\partial x}$ of $f\left(x(t)\right)$ is bounded on Π^+ and hence, by Remark 1.2.1 in [11, pp. 6], we can conclude that $f\left(x(t)\right)$ is Lipschitz on on Π^+, which guuarantees the unique global

existence of solution to the initial value problem (1) – (2).

Let $\varphi:[0,\infty)\times\mathbb{R}^n \to \mathbb{R}^n$ be the solution of the initial value problem (6) – (7). Next, we recall from Definition 7.2 in [5] the notions of stability and asymptotic stability of trivial solution of (6).

Definition 2.5. [5, pp. 157] The trivial solution $x^* \equiv 0$ of the fractional differential equations (6) is said to be

- Stable if for all $\varepsilon > 0$, there exists $\delta = \delta(\varepsilon) > 0$ such that the solution $\varphi(t, x_0)$ of the initial value problem (6) – (7) satisfies $\|\varphi(t, x_0)\| < \varepsilon$ for all $t \geq 0$ whenever $\|x_0\| < \delta$.
- Asymptotically stable if it is stable and there exists some $\gamma > 0$ such that $\lim_{t\to\infty}\|\varphi(t, x_0)\| = 0$ whenever $\|x_0\| < \gamma$ (*attractive*).

Remark 2.6. The trivial solution $x^* \equiv 0$ of the fractional differential equations (6) is said to be globally asymptotically stable if its stability does not depend on the initial condition $x_0 \in \mathbb{R}^n$.

Lemma 2.7. [5, pp. 69] *For each* $q_1, q_2 > 0$, *we have* $\mathbb{E}_{q_1,q_2}(x) = x\mathbb{E}_{q_1,q_2+q_2}(x) + \dfrac{1}{\Gamma(q_2)}$, *where* $\mathbb{E}_{q_1,q_2}(x)$ *is the Mittag – Leffer functions of two parameters* q_1 *and* q_2.

As a consequence of Theorem 1 in [19], we have the following lemma

Lemma 2.8. *Assume that* $q \in (0,1]$ *and the both the function* $\varphi(t)$ *and its Caputo fractional derivative* ${}_0^C D_t^q \varphi(t)$ *belong to the space* $C[a,b]$. *Then we have*

(i) *If* ${}_a^C D_t^q \varphi(t) \geq 0$ *then the function* $\varphi(t) \geq \varphi(a)$.

(ii) *If* ${}_a^C D_t^q \varphi(t) \leq 0$ *then the function* $\varphi(t) \leq \varphi(a)$..

3. Conclusions

In this work, we study the analysis of a fractional network – based SIQR epidemic model with fuzzy transmission to discuss the malware attacking on complex heterogeneous network. To better fitting with real – world scenario, this work also use linguistic variables and funzzy membership function to discuss the influence of malware load in the malware infection on the network. Based on the next – generation matrix, we analytically evaluate the basic reproduction number $\mathfrak{R}_0$, that is an essential threshold value of the epidemiology theory value, and then, investigate the asymptotic stability of malware – free equilibrium and the presence of endemic equilibrium on the network. In some further studies, we are going to answer some other interesting questions on the network – based epidemic model such as condition for the presence of epidemic disease, bifurcation analysis or control problems.

Acknowledgements

This research was also funded by Hanoi Pedagogical University 2 Foudation for Sciences and Technology Development via grant numver C.2020 – SP2 – 06

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