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Research Article

The Analysis of Epidemic Network Model with Infectious Force in Latent and Infected Period

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We discuss the epidemic network model with infectious force in latent and infected period. We obtain the basic reproduction number and analyze the globally dynamic behaviors of the disease-free equilibrium when the basic reproduction number is less than one. The effects of various immunization schemes are studied. Finally, the final sizes relation is derived for the network epidemic model. The derivation depends on an explicit formula for the basic reproduction number of network of disease transmission models.

1. Introduction

Disease spreading has been the subject of intense research since long time ago. With the advent of modern society, fast transportation systems have changed human habits, and some diseases that just a few years ago would have produced local outbreaks are nowadays a global threat for public health systems. A recent example is given by influenza A(H1N1). In order to understand the mechanism of diseases spreading and other similar processes, such as rumors spreading, networks of movie actor collaboration and science collaboration, WWW, and the Internet, it is of great significance to inspect the effect of complex networks features on disease spreading. Therefore, it is of utmost importance to carefully take into account as much details as possible of the structural properties of the network on which the infection dynamics occurs. And in the general case, the epidemic system can be represented as a network where nodes stand for individuals and an edge connecting two nodes denotes the interaction between individuals. The degree k of a node is the number of its neighbors, that is, the number of links adjacent to the node.

In the past, researchers mainly focused the disease transmission study on the conventional networks [1, 2] such as lattices, regular tree, and ER random graph. Since late 1990s, scientists have presented a series of statistical complex topological characteristics [3–6] such as the small-world (SW) phenomenon [7] and scale-free (SF) property [8] by investigating many real networks. On scale-free networks, it was assumed that the larger the node degree, the greater the infectivity of the node, and the infectivity is just equal to the node degree. Under such an assumption, for instance, Pastor-Satorras et al. concluded that the epidemic threshold $\lambda_c = 0$ for heterogenous networks with sufficiently large size [9]. Subsequently, the studies of dynamical processes on complex networks also have attracted lots of interests with various subjects [10–15], and as one of the typical dynamical processes built on complex networks, epidemic spreading has been investigating intensively once more. The susceptible-infected-susceptible (SIS) [10, 11], susceptible-infected-recovered (SIR) [16, 17], and susceptible-infected (SI) [18–20] models on complex networks have been extensively studied recently.

In this paper, we will establish the susceptible-exposed-asymptomatically infected, symptomatically infected-recovered(SEAIR) epidemic model on a network. We provide a detailed analytical of the SEAIR model on complex networks. The remainder of this paper presents our model and results. In the next section, we describe the epidemic model on networks with infectious force in latent and infected period. The subsequent section is devoted to determine the stability of the disease-free equilibrium. In Section 4, we consider two models of immunization. In Section 5, we derive the final sizes relation of the network epidemic models.

2. Model and Parameters

We propose a SEIAR model by classifying the population as susceptible (S), exposed (E), asymptomatically infected (A), symptomatically infected (I), and removed/immune (R), for example, the spreading process of H1N1. The asymptomatic infected compartment contains those who fail to show noticeable symptoms or with light flu-like symptoms but are not identified, and are able to spread the H1N1 infection. We also assume that a susceptible individual becomes infected if in contact with an exposed, asymptomatically or symptomatically infective individual. Then the susceptible enters the exposed class E of those in the latent period. After the latent period, the individual enters the class I or A of infectives, who are infectious in the sense that they are capable of transmitting the infection. When the infectious period ends, the individual enters the recovered class R. We assume that a removed individual will never become susceptible or infected again. In our model, new births, natural deaths and migrations are ignored. The flow diagram of the individuals is depicted in Figure 1.

In contrast to classical compartment models, we consider the whole population and their contacts in networks, each person in a community can be regarded as a vertex in the network, and each contact between two individuals is represented as an edge (line) connecting their vertices. The number of edges emanating from a vertex, that is, the number of contacts a person has, is called the degree of the vertex. We classify the population into groups based on the number of contacts the individual can make per unit of time. The densities of susceptible, exposed, asymptomatically infected, symptomatically infected,vaccinated and recovered nodes of degree k at time t, denoted by $S_k(t)$, $E_k(t)$,

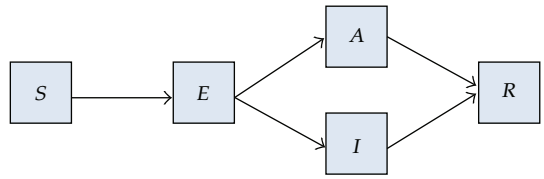

Figure 1: Flow diagram.

$A_k(t)$, $I_k(t)$, and $R_k(t)$ respectively. Clearly, these variables obey the normalization condition:

$$S_k(t) + E_k(t) + A_k(t) + I_k(t) + R_k(t) = 1, \tag{2.1}$$

$k = 1, 2, \ldots, n$, n is the maximum number of contact each individual can make. Therefore the network model with infectious force in latent and infected period follow

$$\begin{aligned}
\frac{dS_k(t)}{dt} &= -\lambda_1 k S_k(t)\Theta^E(t) - \lambda_2 k S_k(t)\Theta^A(t) - \lambda_3 k S_k(t)\Theta^I(t),\\
\frac{dE_k(t)}{dt} &= \lambda_1 k S_k(t)\Theta^E(t) + \lambda_2 k S_k(t)\Theta^A(t) + \lambda_3 k S_k(t)\Theta^I(t) - \delta E_k(t),\\
\frac{dA_k(t)}{dt} &= q\delta E_k(t) - \alpha_1 A_k(t),\\
\frac{dI_k(t)}{dt} &= (1-q)\delta E_k(t) - \alpha_2 I_k(t),\\
\frac{dR_k(t)}{dt} &= \alpha_1 A_k(t) + \alpha_2 I_k(t),
\end{aligned} \tag{2.2}$$

where $\Theta^f(t) = (1/\langle k\rangle)\sum_k kP(k)f_k(t)$, $f = E, A, I$, $\langle k\rangle = \sum_k kP(k)$. The factor $\Theta(t)$ represents the probability that any given link points to an infected node. It is assumed that all parameters are positive constants and summarized in the following list:

λ_1, λ_2, λ_3: transmission coefficient between communities S_k and E_i, A_i, I_i, $i = 1, 2, \ldots, n$;

δ: the transfer rate between the exposed and the infectious;

q, $1 - q$: rate of becoming asymptomatically infected and symptomatically infected;

α_1, α_2: recovery rate of asymptomatically infected and symptomatically infected.

The mathematical formulation of the epidemic problem is completed given initial conditions such as $S_k(0) \simeq 1$, $I_k(0) \simeq 0$, $E_k(0) = A_k(0) = R_k(0) = 0$.

3. Global Stability of the Model and Basic Reproduction Number

In this section, we will show the basic reproduction number R_0 and the global stability of the disease-free equilibrium. Following van den Driessche and Watmough [21], we note that only compartments E_k, A_k, and I_k are involved in the calculation of R_0. At the disease-free equilibrium $P^0(1,0,0,0,0,\ldots,1,0,0,0,0)$, the rate of appearance of new infections F and the rate of transfer of individuals out of the two compartments V are given by

$$F = \left(F_{ij}^{n\times n}\right)_{3\times 3}, \tag{3.1}$$

where $F_{21}^{n\times n}$, $F_{22}^{n\times n}$, $F_{23}^{n\times n}$, $F_{31}^{n\times n}$, $F_{32}^{n\times n}$, and $F_{33}^{n\times n}$ are zero matrices, $F_{11}^{n\times n} = (\lambda_1/\langle k\rangle)T^{n\times n}$, $F_{12}^{n\times n} = (\lambda_2/\langle k\rangle)T^{n\times n}$, and $F_{13}^{n\times n} = (\lambda_3/\langle k\rangle)T^{n\times n}$, where

$$T^{n\times n} = \begin{pmatrix} P(1) & 2P(2) & \cdots & nP(n) \\ 2P(1) & 2^2P(2) & \cdots & 2nP(n) \\ \vdots & \vdots & & \vdots \\ nP(1) & 2nP(2) & \cdots & n^2P(n) \end{pmatrix}, \tag{3.2}$$

and $V = (V_{ij}^{n\times n})_{3\times 3}$, where $V_{12}^{n\times n}$, $V_{13}^{n\times n}$, $V_{23}^{n\times n}$, and $V_{32}^{n\times n}$ are zero matrices,

$$V_{11}^{n\times n} = \begin{pmatrix} \delta & 0 & \cdots & 0 \\ 0 & \delta & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \delta \end{pmatrix}, \quad V_{21}^{n\times n} = \begin{pmatrix} -q\delta & 0 & \cdots & 0 \\ 0 & -q\delta & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & -q\delta \end{pmatrix}, \quad V_{22}^{n\times n} = \begin{pmatrix} \alpha_1 & 0 & \cdots & 0 \\ 0 & \alpha_1 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \alpha_1 \end{pmatrix},$$

$$V_{31}^{n\times n} = \begin{pmatrix} -(1-q)\delta & 0 & \cdots & 0 \\ 0 & -(1-q)\delta & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & -(1-q)\delta \end{pmatrix}, \quad V_{33}^{n\times n} = \begin{pmatrix} \alpha_2 & 0 & \cdots & 0 \\ 0 & \alpha_2 & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \alpha_2 \end{pmatrix}. \tag{3.3}$$

According to the concepts of next generation matrix and the basic reproduction number presented in [21], then, the reproduction number $R_0 = \rho(FV^{-1})$ for (2.2), where ρ represents the spectral radius of the matrix.

To determine the spectral radius of FV^{-1}, we first represent the inverse of V by the following matrix $V^{-1} = (V_{ij}^{-1^{n\times n}})_{3\times 3}$, where $V_{12}^{-1^{n\times n}}$, $V_{13}^{-1^{n\times n}}$, $V_{23}^{-1^{n\times n}}$, $V_{32}^{-1^{n\times n}}$ are zero matrices,

$$V_{11}^{-1^{n\times n}} = \begin{pmatrix} \frac{1}{\delta} & 0 & \cdots & 0 \\ 0 & \frac{1}{\delta} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \frac{1}{\delta} \end{pmatrix}, \quad V_{21}^{-1^{n\times n}} = \begin{pmatrix} \frac{q}{\alpha_1} & 0 & \cdots & 0 \\ 0 & \frac{q}{\alpha_1} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \frac{q}{\alpha_1} \end{pmatrix}, \quad V_{22}^{-1^{n\times n}} = \begin{pmatrix} \frac{1}{\alpha_1} & 0 & \cdots & 0 \\ 0 & \frac{1}{\alpha_1} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \frac{1}{\alpha_1} \end{pmatrix},$$

$$V_{31}^{-1^{n\times n}} = \begin{pmatrix} \frac{1-q}{\alpha_2} & 0 & \cdots & 0 \\ 0 & \frac{1-q}{\alpha_2} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \frac{1-q}{\alpha_2} \end{pmatrix}, \quad V_{33}^{-1^{n\times n}} = \begin{pmatrix} \frac{1}{\alpha_2} & 0 & \cdots & 0 \\ 0 & \frac{1}{\alpha_2} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \frac{1}{\alpha_2} \end{pmatrix}. \tag{3.4}$$

Let $C = FV^{-1}$, we have $C = (C_{ij}^{n\times n})_{3\times 3}$, where $C_{21}^{n\times n}$, $C_{22}^{n\times n}$, $C_{23}^{n\times n}$, $C_{31}^{n\times n}$, $C_{32}^{n\times n}$, and $C_{33}^{n\times n}$ are zero matrices, $C_{11}^{n\times n} = (1/\langle k\rangle)[\lambda_1/\delta + \lambda_2 q/\alpha_1 + \lambda_3(1-q)/\alpha_2]T^{n\times n}$, $C_{12}^{n\times n} = (\lambda_1/\alpha_1\langle k\rangle)T^{n\times n}$, $C_{13}^{n\times n} = (\lambda_2/\alpha_2\langle k\rangle)T^{n\times n}$.

Now we are ready to compute the eigenvalues of the matrix $C = FV^{-1}$. Obviously, the C and $C_{11}^{n\times n}$ have same spectral radius. Since matrix $C_{11}^{n\times n}$ has rank 1, the spectral radius $\rho(C_{11}^{n\times n})$ is equal to the trace of matrix $C_{11}^{n\times n}$.

Therefore, the basic reproduction number R_0 is

$$R_0 = \left[\frac{\lambda_1}{\delta} + \frac{\lambda_2 q}{\alpha_1} + \frac{\lambda_3(1-q)}{\alpha_2}\right]\frac{\langle k^2\rangle}{\langle k\rangle}. \tag{3.5}$$

In summary, we have the following theorem.

Theorem 3.1. *If $R_0 < 1$, the infection-free equilibrium $P^0(1,0,0,0,0,\ldots,1,0,0,0,0)$ is locally asymptotically stable, and if $R_0 > 1$, the infection-free equilibrium P^0 is unstable, an epidemic ensues.*

Next, we will prove the global asymptotic stability of the infection-free equilibrium.

Theorem 3.2. *If $R_0 < 1$, the infection-free equilibrium $P^0(1,0,0,0,0,\ldots,1,0,0,0,0)$ is global asymptotic stability.*

Proof. Let us consider the Lyapunov function

$$L(t) = \sum_k (a_k S_k(t) + b_k E_k(t) + c_k A_k(t) + d_k I_k(t)), \tag{3.6}$$

where $a_k = 2kP(k)$, $b_k = 3kP(k)$, $c_k = (k/q)P(k)$, and $d_k = (k/(1-q))P(k)$. We now compute the time derivative of $L(t)$ along the solutions of (2.2). It is seen that

$$\begin{aligned}
L'(t) &= -2\sum_k kP(k)\left(\lambda_1 kS_k\Theta^E + \lambda_2 kS_k\Theta^A + \lambda_3 kS_k\Theta^I\right) \\
&\quad + 3\sum_k kP(k)\left(\lambda_1 kS_k\Theta^E + \lambda_2 kS_k\Theta^A + \lambda_3 kS_k\Theta^I - \delta E_k\right) \\
&\quad + \sum_k kP(k)\left(\delta E_k - \frac{\alpha_1}{q}A_k\right) + \sum_k kP(k)\left(\delta E_k - \frac{\alpha_2}{1-q}I_k\right) \\
&= \sum_k kP(k)S_k\left(\lambda_1 k\Theta^E + \lambda_2 k\Theta^A + \lambda_3 k\Theta^I\right) - \sum_k \delta kP(k)E_k \\
&\quad - \sum_k \frac{\alpha_1}{q}kP(k)A_k - \sum_k \frac{\alpha_2}{1-q}kP(k)I_k \\
&\le \sum_k kP(k)\left(\lambda_1 k\Theta^E + \lambda_2 k\Theta^A + \lambda_3 k\Theta^I\right) - \sum_k \delta kP(k)E_k \\
&\quad - \sum_k \frac{\alpha_1}{q}kP(k)A_k - \sum_k \frac{\alpha_2}{1-q}kP(k)I_k \\
&= \left(\lambda_1\Theta^E + \lambda_2\Theta^A + \lambda_3\Theta^I\right)\langle k^2\rangle - \left(\delta\Theta^E + \frac{\alpha_1}{q}\Theta^A + \frac{\alpha_2}{1-q}\Theta^I\right)\langle k\rangle \\
&= \left(\delta\Theta^E + \frac{\alpha_1}{q}\Theta^A + \frac{\alpha_2}{1-q}\Theta^I\right)\langle k\rangle\left(\frac{\lambda_1\Theta^E + \lambda_2\Theta^A + \lambda_3\Theta^I}{\delta\Theta^E + (\alpha_1/q)\Theta^A + (\alpha_2/(1-q))\Theta^I}\frac{\langle k^2\rangle}{\langle k\rangle} - 1\right) \\
&\le \left(\delta\Theta^E + \frac{\alpha_1}{q}\Theta^A + \frac{\alpha_2}{1-q}\Theta^I\right)\langle k\rangle(R_0 - 1) \le 0.
\end{aligned} \tag{3.7}$$

Furthermore, $L'(t) = 0$ if and only if $E_k = A_k = I_k = 0$. Therefore, by the LaSalle Invariance Principle [22], P^0 is the global asymptotic stability if $R_0 < 1$. □

4. Immunization Strategy

Immunization is very helpful in controlling diseases. In this section, we will discuss various immunization schemes [23–25].

4.1. Uniform Immunization Strategy

Uniform immunization strategy is simplest immunization schemes [23–25], and vaccinates is also a fraction of the population randomly. Immune nodes cannot become infected and, thus, do not transmit the infection to their neighbors. In this case, for a fixed spreading rate, the relevant control parameter is the immunity p $(0 < p < 1)$, defined as the fraction of immune

nodes present in the network. At the mean-field level, the presence of uniform immunity will effectively reduce the spreading rate by a factor $(1-p)$ [23], that is, the probability of finding and infecting a susceptible. By substituting $\lambda_1 \to (1-p)\lambda_1$, $\lambda_2 \to (1-p)\lambda_2$, and $\lambda_3 \to (1-p)\lambda_3$ in the system (2.2), then the system (2.2) becomes

$$\begin{aligned}
\frac{dS_k(t)}{dt} &= -\lambda_1 k(1-p)S_k(t)\Theta^E(t) - \lambda_2 k(1-p)S_k(t)\Theta^A(t) - \lambda_3 k(1-p)S_k(t)\Theta^I(t),\\
\frac{dE_k(t)}{dt} &= \lambda_1 k(1-p)S_k(t)\Theta^E(t) + \lambda_2 k(1-p)S_k(t)\Theta^A(t) + \lambda_3 k(1-p)S_k(t)\Theta^I(t) - \delta E_k(t),\\
\frac{dA_k(t)}{dt} &= q\delta E_k(t) - \alpha_1 A_k(t),\\
\frac{dI_k(t)}{dt} &= (1-q)\delta E_k(t) - \alpha_2 I_k(t),\\
\frac{dR_k(t)}{dt} &= \alpha_1 A_k(t) + \alpha_2 I_k(t).
\end{aligned} \tag{4.1}$$

We obtain that the basic reproduction number is

$$\widetilde{R}_0 = (1-p)R_0. \tag{4.2}$$

If no immunization were done, then $\widetilde{R}_0 = R_0$; when $0 < p < 1$, $\widetilde{R}_0 < R_0$, that is, the immunization scheme is effective; while as $p \to 1$, $\widetilde{R}_0 \to 0$, that is, in the case of a full immunization, it would be impossible for the epidemic to spread in the network.

4.2. Targeted Immunization

We can use a targeted immunization scheme [25]. We introduce the lower and upper threshold κ_1 and κ_2, such that if $k > \kappa_2$, all nodes with connectivity k are immunized, if $\kappa_1 < k < \kappa_2$, p_k is defined as the fraction of immune individuals, that is, we define the immunization rate σ_k by

$$\sigma_k = \begin{cases} 1, & k > \kappa_2, \\ p_k, & \kappa_1 < k \le \kappa_2, \\ 0, & k \le \kappa_1, \end{cases} \tag{4.3}$$

where $0 < p_k \leq 1$, and $\sum_k \sigma_k P(k) = \overline{\sigma}$. $\overline{\sigma}$ is the average immunization rate. The epidemic model (2.2) becomes

$$\begin{aligned}
\frac{dS_k(t)}{dt} &= -\lambda_1 k(1-\sigma_k)S_k(t)\Theta^E(t) - \lambda_2 k(1-\sigma_k)S_k(t)\Theta^A(t) - \lambda_3 k(1-\sigma_k)S_k(t)\Theta^I(t),\\
\frac{dE_k(t)}{dt} &= \lambda_1 k(1-\sigma_k)S_k(t)\Theta^E(t) + \lambda_2 k(1-\sigma_k)S_k(t)\Theta^A(t) + \lambda_3 k(1-\sigma_k)S_k(t)\Theta^I(t) - \delta E_k(t),\\
\frac{dA_k(t)}{dt} &= q\delta E_k(t) - \alpha_1 A_k(t),\\
\frac{dI_k(t)}{dt} &= (1-q)\delta E_k(t) - \alpha_2 I_k(t),\\
\frac{dR_k(t)}{dt} &= \alpha_1 A_k(t) + \alpha_2 I_k(t).
\end{aligned} \tag{4.4}$$

We obtain that the basic reproduction number is

$$\overline{R}_0 = \left[\frac{\lambda_1}{\delta} + \frac{\lambda_2 q}{\alpha_1} + \frac{\lambda_3(1-q)}{\alpha_2}\right]\frac{\langle k^2(1-\sigma_k)\rangle}{\langle k\rangle}, \tag{4.5}$$

or

$$\overline{R}_0 = R_0 - \left[\frac{\lambda_1}{\delta} + \frac{\lambda_2 q}{\alpha_1} + \frac{\lambda_3(1-q)}{\alpha_2}\right]\frac{\langle k^2\sigma_k\rangle}{\langle k\rangle}. \tag{4.6}$$

5. The Final Sizes Relation

First, we show that the disease will eventually die out, that is, $E_k(\infty) = 0, A_k(\infty) = 0$, and $I_k(\infty) = 0$.

Note that the positive quadrant is invariant, so all solutions of (2.2) lie in the nonnegative, bounded set defined by $S_k(t), E_k(t), A_k(t), I_k(t), R_k(t) \geq 0$ and $S_k(t) + E_k(t) + A_k(t) + I_k(t) + R_k(t) = 1$. Observing that

$$\frac{d}{dt}(S_k(t) + E_k(t)) = -\delta E_k(t), \tag{5.1}$$

we see that $S_k(t) + E_k(t)$ is decreasing whenever $E_k(t) > 0$. However, $S_k(t) + E_k(t)$ is bounded below by 0, hence it has a limit as $t \to \infty$. Because $S_k(t)$ is bounded and decreasing, it has a limit as $t \to \infty$. Therefore, $E_k(t)$ has a limit as $t \to \infty$.

In analyzing the system (2.2) we adopt the conventions that for an arbitrary continuous function $w(t)$ with nonnegative components,

$$w_\infty = \lim_{t\to\infty} w(t), \qquad \overline{w} = \int_0^\infty w(t)dt. \tag{5.2}$$

Integrating (5.1) from 0 to t, we have

$$E_k(t) - E_k(0) + S_k(t) - S_k(0) = -\delta \int_0^t E_k(t)dt. \tag{5.3}$$

Thus,

$$E_k(0) - E_k(\infty) + S_k(0) - S_k(\infty) = \delta \overline{E}_k, \tag{5.4}$$

as $t \to \infty$.

The left hand side of (5.4) is finite because the components of $S_k(0)$, $S_k(\infty)$, $E_k(0)$ and $E_k(\infty)$ are bounded by the initial total population size. Therefore the right hand side (5.4) is also finite and because δ is positive, $\overline{E}_k < \infty$. Since $E_k(t)$ is a smooth nonnegative function, $E_k(\infty) = 0$ (Similarly $A_k(\infty) = 0, I_k(\infty) = 0$), and

$$\overline{E}_k = \delta^{-1}(S_k(0) - S_k(\infty)) + \delta^{-1}E_k(0). \tag{5.5}$$

Similarly, we can obtain

$$A_k(t) - A_k(0) = q\delta \int_0^t E_k(t)dt - \alpha_1 \int_0^t A_k(t)dt, \tag{5.6}$$

when $t \to \infty$, we have

$$A_k(\infty) - A_k(0) = q\delta \overline{E}_k - \alpha_1 \overline{A}_k. \tag{5.7}$$

Because $A_k(\infty) = 0$ and $\overline{E}_k$ are bound, we have

$$\overline{A}_k = \frac{q\delta \overline{E}_k + A_k(0)}{\alpha_1}. \tag{5.8}$$

For the same reason, we obtain

$$I_k(t) - I_k(0) = (1-q)\delta \int_0^t E_k(t)dt - \alpha_2 \int_0^t I_k(t)dt, \tag{5.9}$$

when $t \to \infty$, we have

$$I_k(\infty) - I_k(0) = (1-q)\delta \overline{E}_k - \alpha_2 \overline{I}_k. \tag{5.10}$$

Because $I_k(\infty) = 0$ and $\overline{E}_k$ are bound, we have

$$\overline{I}_k = \frac{(1-q)\delta \overline{E}_k + I_k(0)}{\alpha_2}. \tag{5.11}$$

Integrating the first equations of (2.2) from 0 to t gives

$$\begin{aligned}\ln\frac{S_k(0)}{S_k(t)} &= \int_0^t \left(\lambda_1 k\Theta^E + \lambda_2 k\Theta^A + \lambda_3 k\Theta^I\right)dt \\ &= \frac{\lambda_1 k}{\langle k\rangle}\sum_k kP(k)\int_0^t E_k(t)dt + \frac{\lambda_2 k}{\langle k\rangle}\sum_k kP(k)\int_0^t A_k(t)dt + \frac{\lambda_3 k}{\langle k\rangle}\sum_k kP(k)\int_0^t I_k(t)dt.\end{aligned} \tag{5.12}$$

When $t \to \infty$, we have

$$\begin{aligned}\ln\frac{S_k(0)}{S_k(\infty)} &= \frac{\lambda_1 k}{\langle k\rangle}\sum_k kP(k)\overline{E}_k + \frac{\lambda_2 k}{\langle k\rangle}\sum_k kP(k)\overline{A_k} + \frac{\lambda_3 k}{\langle k\rangle}\sum_k kP(k)\overline{I_k} \\ &= \frac{\lambda_1 k}{\langle k\rangle}\sum_k kP(k)\overline{E}_k + \frac{\lambda_2 k}{\langle k\rangle}\sum_k kP(k)\frac{q\delta\overline{E}_k + A_k(0)}{\alpha_1} + \frac{\lambda_3 k}{\langle k\rangle}\sum_k kP(k)\frac{(1-q)\delta\overline{E}_k + I_k(0)}{\alpha_2} \\ &= \frac{\lambda_1 k}{\langle k\rangle}\sum_k kP(k)\overline{E}_k + \frac{\lambda_2 k}{\alpha_1\langle k\rangle}\sum_k kP(k)\left(q\delta\overline{E}_k + A_k(0)\right) \\ &\quad + \frac{\lambda_3 k}{\alpha_2\langle k\rangle}\sum_k kP(k)\left((1-q)\delta\overline{E}_k + I_k(0)\right) \\ &= \frac{\lambda_1 k}{\delta\langle k\rangle}\sum_k kP(k)(S_k(0) - S_k(\infty) + E_k(0)) + \frac{\lambda_2 k}{\alpha_1\langle k\rangle}\sum_k kP(k) \\ &\quad \times \left(q\delta\left(\delta^{-1}(S_k(0) - S_k(\infty)) + \delta^{-1}E_k(0)\right) + A_k(0)\right) \\ &\quad + \frac{\lambda_3 k}{\alpha_2\langle k\rangle}\sum_k kP(k)\left((1-q)\delta\left(\delta^{-1}(S_k(0) - S_k(\infty)) + \delta^{-1}E_k(0)\right) + I_k(0)\right) \\ &= \frac{\lambda_1 k}{\delta\langle k\rangle}\sum_k kP(k)(S_k(0) - S_k(\infty) + E_k(0)) \\ &\quad + \frac{\lambda_2 k}{\alpha_1\langle k\rangle}\sum_k kP(k)\left(q(S_k(0) - S_k(\infty) + E_k(0)) + A_k(0)\right) \\ &\quad + \frac{\lambda_3 k}{\alpha_2\langle k\rangle}\sum_k kP(k)\left((1-q)(S_k(0) - S_k(\infty) + E_k(0)) + I_k(0)\right) \\ &= \left[\frac{\lambda_1}{\delta} + \frac{\lambda_2 q}{\alpha_1} + \frac{\lambda_3(1-q)}{\alpha_2}\right]\frac{k}{\langle k\rangle}\sum_k kP(k)(S_k(0) - S_k(\infty) + E_k(0)) \\ &\quad + \frac{\lambda_2 k}{\alpha_1\langle k\rangle}\sum_k kP(k)A_k(0) + \frac{\lambda_3 k}{\alpha_2\langle k\rangle}\sum_k kP(k)I_k(0)\end{aligned}$$

$$= R_0 \frac{k}{\langle k^2 \rangle} \sum_k kP(k)(S_k(0) - S_k(\infty) + E_k(0)) + \frac{\lambda_2 k}{\alpha_1 \langle k \rangle} \sum_k kP(k) A_k(0)$$
$$+ \frac{\lambda_3 k}{\alpha_2 \langle k \rangle} \sum_k kP(k) I_k(0). \tag{5.13}$$

If $S_k(0) = S_{k0}$, $I_k(0) = I_{k0}$, and $E_k(0) = A_k(0) = 0$, then the final size relation is

$$\ln \frac{S_{k0}}{S_{k\infty}} = R_0 \frac{k}{\langle k^2 \rangle} \sum_k kP(k)(S_{k0} - S_{k\infty}) + \frac{\lambda_3 k}{\alpha_2 \langle k \rangle} \sum_k kP(k) I_{k0}. \tag{5.14}$$

If $S_k(0) = S_{k0}$, $I_k(0) = I_{k0}$, $E_k(0) = E_{k0}$, and $A_k(0) = A_{k0}$, then the final size relation is

$$\ln \frac{S_{k0}}{S_{k\infty}} = R_0 \frac{k}{\langle k^2 \rangle} \sum_k kP(k)(S_{k0} - S_{k\infty}) + R_0 \frac{k}{\langle k^2 \rangle} \sum_k kP(k) E_{k0}$$
$$+ \frac{\lambda_2 k}{\alpha_1 \langle k \rangle} \sum_k kP(k) A_{k0} + \frac{\lambda_3 k}{\alpha_2 \langle k \rangle} \sum_k kP(k) I_{k0}. \tag{5.15}$$

Therefore, we show that the final size of the susceptible $S(\infty) = N \sum_k P(k) S_{k\infty}$, where N is the whole population size. Similarly, we can obtain the final sizes under various immunization schemes.

6. Conclusions

In this paper, we describe a network epidemic model and calculate the basic reproduction number R_0 and the final sizes relation. The basic reproduction number is the spectral radius of the matrix FV^{-1}. We prove the global asymptotic stability of the disease-free equilibrium when the basic reproduction number is less than 1. The effects of various immunization schemes are studied. Finally, a final size relation is derived for network epidemic models. The derivation depends on an explicit formula for the basic reproduction number of network of disease transmission models.

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