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Pattern mechanism in stochastic SIR networks with ER connectivity

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ABSTRACT

The diffusion of the susceptible and infected is a vital factor in spreading infectious diseases. However, the previous SIR networks cannot explain the dynamical mechanism of periodic behavior and endemic diseases. Here, we incorporate the diffusion and network effect into the SIR model and describes the mechanism of periodic behavior and endemic diseases through wavenumber and saddle–node bifurcation. We also introduce the standard network structured entropy (NSE) and demonstrate diffusion effect could induce the saddle–node bifurcation and Turing instability. Then we reveal the mechanism of the periodic outbreak and endemic diseases by the mean-field method. We provide the Turing instability condition through wavenumber in this network-organized SIR model. In the end, the data from COVID-19 authenticated the theoretical results.

1. Introduction

Pattern formation was often investigated by bifurcation [1–8] in the reaction–diffusion or network-organized system. Turing first explained the mechanism of biological pattern formation in the reaction–diffusion system [9]. Othmer and Scriven illustrated that the network could induce Turing instability in cellular networks, which further promoted the development of pattern dynamics [10]. Nakao and Asllani et al. summarized research methods for the theory of Turing instability on the network and showed that the eigenvalues generated by the Laplacian matrix have a profound impact on the network-organized system [11,12]. Subsequently, researchers found that instability can be caused by unstable modes [13], and the dynamical mechanism of the unstable modes in Turing instability was revealed [14,15]. Recently, it has been widely accepted that critical features of the Turing pattern in the homogeneous active systems are mediated by network topology [16,17]. However, the prediction of network topology using the adjacency matrix is still a challenging problem [18], especially the effect of the bifurcations on the network-organized system [19]. Although Zheng et al. reported promising results about negative wavenumber [20], the role of negative wavenumber in the Turing instability is still unresolved, especially for saddle–node in the network-organized SIR model.

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SIR model is a classical model to investigate the spread of infectious diseases [21]. Shulgin, Stone, and Agur showed the effectiveness of pulse vaccination strategy in the SIR epidemic model and found the seasonal variation could lead to the periodic and chaotic dynamics of epidemics [22]. McCluskey investigated SIR models with delay and showed that the endemic equilibrium is globally asymptotically stable whenever it exists [23,24]. S.Clémençon et al. focused on the study of a stochastic SIR model accounting for the effect of contact-tracing on the spread of an infectious disease [25]. Li et al. illustrated that strengthening the community structure is an effective way to reduce the size of disease [26], and Cooper studied the effectiveness of the modeling approach on the pandemic due to the spreading of the novel COVID-19 disease and developed a SIR model that provides a theoretical framework to investigate its spread within a community [27]. Sharma, Verma, and Gupta found reducing social distancing is one of the most effective control measures to manage the spread of COVID-19 [28]. Verma and Gupta studied the dynamics of the epidemiology classes, the state of synchronization, and stability when the patches are coupled [29,30]. Also, Jin et al. obtained the dynamics behavior of the SIR epidemic model with correlation coefficients, clustering coefficient, infection age, and demography [31,32]. Although the dynamical behavior was discussed in the epidemic model with diffusion, and sufficient conditions for stability were given [33–35], it is well known that all the eigenvalues of the Laplacian matrix are negative (or 0) [11,12] corresponding to the positive wavenumber of the Fourier space [9]. Namely, the properties of the Laplace matrix could not make Turing instability occur in this network-organized SIR model, which means diffusion or contact of the susceptible and infected does not work in the outbreak of infectious diseases. To investigate the effect of the network on Turing instability and breakout of infectious diseases in the network-organized system, the following population-based SIR model with ER network [36] is investigated in this paper,

\[
\begin{align*}
\frac{dS_i}{dt} &= \alpha - \beta S_i - \gamma S_i I_i + d_1 \sum_{j=1}^n A_{ij} S_j, \\
\frac{dI_i}{dt} &= \gamma S_i I_i - \beta I_i - \delta I_i + d_2 \sum_{j=1}^n A_{ij} I_j, \\
\frac{dR_i}{dt} &= \delta I_i - \beta R_i,
\end{align*}
\]  

(1)

where \(A_{ij}(i, j = 1, \ldots, n)\) is the adjacency matrix of the network and shows the interaction of nodes; the eigenvalues of \(A\) could be negative (the positive wavenumber), positive (the negative wavenumber), or zero, resulting from network coupling. \(\sum_{j=1}^n A_{ij} S_j\) and \(\sum_{j=1}^n A_{ij} I_j\) represent the external influence, which show the interaction of infective and susceptible from other nodes. Also, \(\delta I_i\) represents the strength of epidemic prevention measures for node \(i\) and is directly proportional to the infection rate, which has nothing to do with the external environment. Also, \(N\) edges are linked randomly between \(n\) nodes in the network, a random network, and a source of stochasticity. If \(i\) links \(j\), \(A(i, j) = A(j, i) = 1\), or \(A(i, j) = A(j, i) = 0\), and an undirected graph is generated [37].

In the system (1) without network, there are two equilibrium points \(E_1 = (S^*, I^*, R^*) = \left(\frac{\beta}{\gamma}, 0, 0\right)\), \(E_2 = (S^*, I^*, R^*) = \left(\frac{\beta + \delta}{\gamma}, \frac{\alpha \gamma - \beta \delta - \delta^2}{\beta (\beta + \delta)}, \frac{\delta (\alpha \gamma - \beta \delta - \delta^2)}{\beta (\beta + \delta)}\right)\). In general, the equilibrium point \(E_1\) means the infectious diseases disappears, and the equilibrium point \(E_2\) means the endemic diseases and outbreak of the infectious diseases. So, we should analyze the stability of \(E_1, E_2\) to tell the development of the infectious diseases. Moreover, the \(E_1\) is stable when \(\alpha \gamma < \beta \delta + \beta^2\), the \(E_2\) is stable when \(\alpha \gamma > \beta \delta + \beta^2\), which means the stability of \(E_1\) is contrary to the stability of \(E_2\). Therefore, we only consider the stability of \(E_1\) in system (1). And the corresponding Jacobian matrix [11] of system (1) with \(i = 1\) is

\[
B_1 = \begin{pmatrix}
-\beta - \gamma I^* + d_1 A_{i1} & -\gamma S^* & 0 \\
\gamma I^* & \gamma S^* - \delta - \beta + d_2 A_{i1} & 0 \\
0 & 0 & -\beta
\end{pmatrix},
\]

where \(A_{i1}\) is the eigenvalue of the adjacency matrix.

2. The network-organized SIR model

It is well known that all the eigenvalues of the Laplacian matrix are negative (or 0) [11,12] corresponding to the positive wavenumber of the Fourier space [9]. Namely, the properties of the Laplace matrix could not make Turing instability occur in this network-organized SIR model, which means diffusion or contact of the susceptible and infected does not work in the outbreak of infectious diseases. To investigate the effect of the network on the Turing instability and breakdown of infectious diseases in the network-organized system, the following population-based SIR model with ER network [36] is investigated in this paper.
To show the effect of the network on the outbreak of infectious diseases, we only consider the stability of $E_1$ in the system (1). All the eigenvalues of the Jacobian matrix at $E_1$ can be written as
\[
\lambda_{1i} = -\beta + d_1A_i \\
\lambda_{2i} = \frac{\nu_i}{\beta} - \delta - \beta + d_2A_i \\
\lambda_{3i} = -\beta.
\]
Suppose the equilibrium point $E_1$ is stable, Turing instability occurs when $A_1 > \beta/d_1$ (or $d_2A_1 > \delta + \beta - \frac{\nu_1}{\beta}$). The stability of the system (1) is determined by the range of the eigenvalues of the adjacency matrix. However, sometimes it is not easy to obtain all the eigenvalue of $B_n$, which makes us find a novel way to address this question.

To further simplify the network-organized SIR model, we obtain
\[
\frac{dS}{dt} = \alpha - \beta S_i - \gamma S_iI_i + d_1A_{\text{max}}S_i, \\
\frac{dI}{dt} = \gamma S_iI_i - \beta I_i - \delta I_i + d_2A_{\text{max}}I_i, \\
\frac{dR}{dt} = \delta I_i - \beta R_i,
\]
where $A_{\text{max}} = \max\{A_i, i = 1, \ldots, n\}$, and
\[
\lambda_{1\text{max}} = -\beta + d_1A_{\text{max}}, \\
\lambda_{2\text{max}} = \frac{\nu_1}{\beta} - \delta - \beta + d_2A_{\text{max}}, \\
\lambda_{3\text{max}} = -\beta.
\]
According to stability analysis, system (2) is stable when $\lambda_{1\text{max}} < 0$, $\lambda_{2\text{max}} < 0$ and system (2) is unstable (Turing instability occurs) when $\lambda_{1\text{max}} > 0$ or $\lambda_{2\text{max}} > 0$. Hence, the largest eigenvalues of adjacency matrix plays a vital role in the stability of system (2). Also, the stability of the system (2) is consistent with the system (1) under certain conditions; however, the dynamical behavior is different. To investigate the relationship between the system (1) and system (2), we introduce the following lemma.

**Lemma 1** ([38]). An autonomous system $\dot{x} = Ax$, the system is stable at equilibrium $0 \in \mathbb{R}^n$ when all eigenvalues $\lambda$ of $A$, $\text{Re}(\lambda) < 0$ hold, or the system is unstable.

**Lemma 2** ([39]). A saddle–node bifurcation is a collision and disappearance of two equilibriums in dynamical systems. In ODEs with $n \geq 3$, the Jacobian matrix $A$ at the saddle–node bifurcation has a simple zero eigenvalue $\lambda_1 = 0$, as well as $s$ eigenvalues with $\text{Re}(\lambda_i) > 0$, and $t$ eigenvalues with $\text{Re}(\lambda) < 0$. Then a saddle–node with $st > 0$ can simultaneously have more than one homoclinic orbit, and the disappearance of such a saddle–node generates an infinite number of periodic saddle orbits.

To investigate the relationship between the social network and the spread of infectious diseases, we introduce the definition of network structured entropy. Assume the degree of node $i$ is $k_i$, we define [37,40]
\[
E_i = k_i / \sum_{j=1}^{n} k_j.
\]
And the network structured entropy [41] is defined as
\[
E = -\sum_{i=1}^{n} E_i \ln E_i,
\]
where $E_{\text{max}} = \ln n$ when the network is completely homogeneous uniform($E_i = \frac{1}{n}$) and $E_{\text{min}} = \frac{\ln(4(n-1))}{2}$ when all nodes connect a node.
To eliminate the effect of node number $n$ on the network structured entropy, we obtain the standard structural entropy of networks(NSE),
\[
\bar{E} = \frac{E - E_{\text{min}}}{E_{\text{max}} - E_{\text{min}}} = -2\frac{\sum_{i=1}^{n} E_i \ln E_i - \ln(4n-4)}{2 \ln n - \ln(4n-4)},
\]
where the network is more homogeneous when the network structured entropy is larger(every node has almost the same degree in homogeneous network).

Then, we could obtain the following results:

**Theorem 1.** In the network-organized system (1), if all eigenvalues $\lambda$ at equilibria, $\text{Re}(\lambda) < 0$ hold, system (1) is stable, or the system is unstable.
The network-organized system (1) can be treated as an ODE system with $3n$ (n is the number of nodes on network) variables, namely, the linear term of system (1) can be treated as $\dot{x} = Ax$ (A is a $3n$ square matrix). According to Lemma 1, if all eigenvalues $\lambda$ at equilibria, $Re(\lambda) < 0$ holds, system (1) is stable, or else the system is unstable.

**Theorem 2.** In the network-organized system (1), if an eigenvalue $\Lambda_i$ of the matrix $A$ makes the saddle–node bifurcation occur, and $st > 0, s + t = n - 1$ holds in the network-organized system with $n \geq 3$, a periodic orbit occurs.

**Proof.** $\Lambda_i (i = 1, \ldots, n)$ represents the characteristic and dynamic behaviors of the networks, which can be treated as a control parameter and make $E_1$ disappear. Based on the Lemma 2 and Theorem 1, $s$ eigenvalues with $Re\lambda > 0$, $t$ eigenvalues with $Re\lambda < 0$ and a eigenvalue $\lambda = 0$ hold. So a periodic orbit (homoclinic orbit) occurs in the network-organized system with $n \geq 3$.

**Corollary 1.** In the system (2), if the maximum eigenvalue $\Lambda_{max}$ of the matrix $A$ makes the saddle–node bifurcation occur, and $st > 0, s + t = n - 1$ holds in the network-organized system (1) with $n \geq 3$, a periodic orbit occurs in the network-organized system (1).

**Proof.** If the maximum eigenvalue $\Lambda_{max}$ of the matrix $A$ makes the saddle–node bifurcation occur, there is a $i$ make $\Lambda_i = \Lambda_{max}$. Based on Theorem 2, Corollary 1 holds.

Through the above analysis, we obtain the following results,

**Theorem 3.** In a homogeneous network (NSE is approximately equal to 1, and is an essential indicator of the outbreak), the stability of the system (2) is generally consistent with the stability of system (1).

**Proof.** From the above stability analysis, $\Lambda_i$ does not work in the stability of system (2) and system (1) when $\Lambda_i < 0$. When $\Lambda_i$ is positive, the sign of $Re\lambda_{1,\max}(Re\lambda_{2,\max})$ and $Re\lambda_{1,\max}(Re\lambda_{2,i})$ is determined by the greatest eigenvalue $\Lambda_{max}, Re\lambda_{1,\max} > 0 (Re\lambda_{2,\max} > 0)$ if and only if a $\Lambda_i$ makes $Re\lambda_{1,i} > 0 (Re\lambda_{2,i} > 0)$ hold. Therefore, the stability of system (2) is determined by the stability of system (1) in a sense [20,37].

Because the interaction of most nodes does not exist when NSE is small, the role of eigenvalues loses its meaning. In a homogeneous network, the eigenvalues of adjacent matrix $A$ result from network node coupling and represent the nodes’ mutual relations. Above all (Theorem 3), NSE and the diffusion coefficient play a vital role in Turing instability and the mechanism of the periodic outbreak and endemic diseases.

3. Numerical analysis

We verify our theoretical results through numerical simulation and data and perform numerical simulations of a discrete version of the model. By default, all parameters $\alpha = 0.1, \beta = 0.1, \gamma = 0.3, \delta = 0.8, n = 100$ are fixed in the following. The adjacency matrix $A$ is generated by a random network (randomly join $N$ edges in $n$ nodes), which does not change with time. According to the definition of ER network, the average degree $\frac{2N}{\eta(n-1)}$ is in direct proportion to $N$ [37,40]. For pattern formation, $l_i = \{l_i, i = 1, \ldots, n\}$ represents all the nodes in all figures, and the color indicates the quantity of infected individuals in each node. Before we investigate the network-organized SIR model, some parameters should be fixed. For example, the equilibrium point $E_1$ is stable [Fig. 1(a)] when $\alpha = 0.1, \beta = 0.1, \gamma = 0.3, \delta = 0.8$, and the equilibrium point $E_2$ is stable [Fig. 1(b)] when $\alpha = 1, \beta = 0.1, \gamma = 0.3, \delta = 0.8$. Also, it will take a long time to tend to the equilibrium point $E_1$ [Fig. 1(c)] when $\beta$ is smaller. There is always a spike (outbreak) in the infected populations [Fig. 1(a,b,c,d)] when the infectious diseases occur. As a result, the infectious diseases will disappear [Fig. 1(a,c)] or become endemic [Fig. 1(b)]. We observe that the birth rate of susceptible $\alpha$ and the death rate $\beta$ play an important role in the outbreak and sustainability of infectious diseases [Fig. 1] and could induce the transcritical bifurcation [Fig. 2(a,b)]. However, it does not have the dynamic behavior of periodic oscillations in the system (1), which means it does not work for a periodic outbreak of an infectious disease.

When $d_2 = 0$, all the eigenvalues of system (1) can be written as,

$$\lambda_{1i} = -0.1 + d_1 \Lambda_i,$$

$$\lambda_{2i} = -0.6,$$

$$\lambda_{3i} = -0.1.$$

It is easy to know that the stability of system (1) is determined by $\lambda_{1i}(d_1$ and $\Lambda_i)$. All the eigenvalues of system (2) can be written as,

$$\lambda_{1max} = -0.1 + d_1 \Lambda_{max},$$

$$\lambda_{2max} = -0.6,$$

$$\lambda_{3max} = -0.1.$$

Meanwhile, the stability of system (2) is determined by $\lambda_{1max}(d_1$ and $\Lambda_{max})$. 

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Fig. 1. The stability of the system (1) without network. (a) The equilibrium point $E_1$ is stable when $\alpha = 0.1, \beta = 0.1, \gamma = 0.3, \delta = 0.8$. (b) The equilibrium point $E_2$ is stable when $\alpha = 1, \beta = 0.1, \gamma = 0.3, \delta = 0.8$. (c) The equilibrium point $E_1$ is stable when $\alpha = 0.1, \beta = 0.01, \gamma = 0.3, \delta = 0.8$. (d) The equilibrium point $E_2$ is stable when $\alpha = 1, \beta = 0.01, \gamma = 0.3, \delta = 0.8$.

Fig. 2. The bifurcation of the system (1) without network. (a) The bifurcation about $\alpha$ when $\beta = 0.1, \gamma = 0.3, \delta = 0.8$. (b) The bifurcation about $\beta$ when $\alpha = 0.1, \gamma = 0.3, \delta = 0.8$.

Fig. 3. The standard network structural entropy (NSE) about the number of edges $N$ when $n = 100$.

Initially, we investigate the effect of NSE on the network and the spread of the infection in the ER network. NSE is an essential factor in evaluating the homogeneity of the network. The network is highly homogeneous when NSE is larger as we all know that it is more convenient for the information transmission the edges are the diffuse channel. In the case of the spread of infection, the degree of nodes (edges of the network) is of great importance, and all network nodes have a high joint degree. Therefore, the homogeneous network is more conducive to the spread of infectious diseases, and the
Fig. 4. The pattern formation of the periodic outbreaks in system (1) when $d_1 = 0.1$, $d_2 = 0$ and $\alpha = 0.1$, $\beta = 0.1$, $\gamma = 0.3$, $\delta = 0.8$. (a) $N = 10$. (b) $N = 100$. (c) $N = 200$. (d) $N = 300$.

Fig. 5. The pattern formation of the endemic disease in system (1) when $d_1 = 3$, $d_2 = 0$ and $\alpha = 0.1$, $\beta = 0.1$, $\gamma = 0.3$, $\delta = 0.8$. (a) $N = 50$. (b) $N = 100$.

Fig. 6. The probability of periodic outbreaks about $N$ (1000 random trials for every $N$) in system (1) when $d_1 = 3$, $d_2 = 0$ and $\alpha = 0.1$, $\beta = 0.1$, $\gamma = 0.3$, $\delta = 0.8$. 
Fig. 7. The pattern formation in system (1) when $N = 200$ and $\alpha = 0.1, \beta = 0.1, \gamma = 3, \delta = 8$. (a) $d_1 = 0.01, d_2 = 0$. (b) $d_1 = 1, d_2 = 0$. (c) $d_1 = 2, d_2 = 0$. (d) $d_1 = 3, d_2 = 0$.

Fig. 8. The pattern formation in system (1) when $N = 100$ and $\alpha = 0.1, \beta = 0.1, \gamma = 0.3, \delta = 0.8$. (a) $d_1 = 0.1, d_2 = 0$. (b) $d_1 = 1, d_2 = 0$.

Fig. 9. The intensity of endemic disease (the maximum of all the nodes when system (1) tends to stable state) about $d_1$ in system (1) when $N = 100, d_2 = 0$ and $\alpha = 0.1, \beta = 0.1, \gamma = 0.3, \delta = 0.8$.

route of infection is more comfortable to be disturbed in inhomogeneous networks. Form Figs. 3 and 4, we obtain the same results: the NSE is larger with the edges $N$, and the homogeneous network could facilitate the spread of infectious diseases [Fig. 4].
On basis of Theorem 1, system (1) is stable when \( N \) is small (\( \lambda_{1\text{max}} < 0 \)) [Fig. 4a] and becomes unstable (\( \lambda_{1\text{max}} > 0 \)) [Fig. 4(b,c,d)] when \( N \) is larger. Because the saddle–node bifurcation occurs in system (2) when \(-0.1 + d_1 \Lambda_{\text{max}} = 0\), periodic orbits occur [Fig. 4(b,c,d)] according to Theorem 2 and Corollary 1. With the increase of \( N \), the cycle of the outbreak of infectious diseases may become shorter [Fig. 4(b,c)], or the intensity of the outbreak of infectious diseases will be higher [Fig. 4(b,d)]. Besides the cycle of the outbreak of infectious diseases, endemic diseases may occur [Fig. 5] because the network of contacts is sparse when NSE is small. Finally, we count the probability of periodic outbreaks and endemic diseases (1–probability of periodic outbreaks) when the outbreak of infectious diseases occurs (\( \lambda_{1\text{max}} > 0 \)) [Fig. 6]. It is
found that the probability of periodic outbreaks approaches 1 when $N$ is more significant than a critical value. Namely, only the periodic outbreaks may occur when $N$ is large enough, which means the diffusion of the susceptible is the main cause of periodic outbreaks. These results explain how the ER network works in the diffusion and outbreak of infectious diseases, which means reducing the NSE of the social network through $N$ could prevent the outbreak of infectious diseases or decrease the strength of outbreak. Through the analysis of numerical simulation, the random network can be treated as the homogeneous network here when NSE > 0.9, which could reduce the effect of randomness on the dynamical behavior.

Then, we investigate the role of network coupling strength in Turing instability and the outbreak of infectious diseases. The coupling strength can be treated as the intensity of infectious disease or the exchange frequency between nodes (cities or countries). Based on our theories, the diffusion of the susceptible may induce the outbreak of infectious diseases [Fig. 4, Fig. 5, Fig. 7, Fig. 8]. Of course, the lower exchange-frequency could not make the outbreak of infectious diseases occur when $\lambda_{1\max} < 0$ [Fig. 7(a), Fig. 8(a)]. Only the high exchange-frequency could induce the periodic outbreak of infectious diseases when $\lambda_{1\max} > 0$ [Fig. 4(b,c,d), Fig. 8(b)]. Meanwhile, the higher exchange frequency of susceptible could increase the outbreak intensity of the periodic outbreak and endemic disease [Fig. 7, Fig. 8, Fig. 9], and shorten the period of the outbreaks [Fig. 10(a)]. Eventually, the infectious diseases are always in an outbreak when the outbreak period tends to zero (or is very small), which leads to endemic diseases. The diffusion of the infected is the main cause of endemic disease. And the bifurcation point $d_1 = 0.02$ [Fig. 10(b)] is same with $\lambda_{1\max}(d_1) = 0$ (it is stable when $\lambda_{1\max}(d_1) < 0$ and unstable when $\lambda_{1\max}(d) > 0$ [Fig. 10(c)]. Also, [Fig. 10(d)] further illustrate the stability region of system (2) through the
relationship between $\lambda_{1\text{max}}(d)$ and $A_{\text{max}}$, shows the important role of $A_{\text{max}}$ in the stability of system (1) and system (2). The stability of the system (1) is determined by the stability of the system (2) to a certain extent. The above results are a novel method to investigate the network-organized system and show the role of the diffusion of the susceptible in the outbreak of infectious diseases (periodic and endemic diseases). Notably, the local community may determine the switch between the periodic outbreak and endemic disease (only a subset of nodes are interlinked) when $N$ is small.

Next, we show the impact of the diffusion of the infected on the outbreak of endemic diseases when $d_1 = 0, \alpha = 0.1, \beta = 0.1, \gamma = 0.3, \delta = 0.8$, and obtain the subjacent results,

$$\lambda_{3i} = -0.1,$$
$$\lambda_{2i} = -0.6 + d_2 A_i,$$
$$\lambda_{3i} = -0.1,$$
Fig. 16. The effect of $d_1$ on the pattern formation in system (1) when $d_2 = 0.1, N = 200$ and $\alpha = 0.1, \beta = 0.1, \gamma = 0.3, \delta = 0.8$. (a) $d_1 = 0.01$. (b) $d_1 = 0.03$. (c) $d_1 = 0.04$. (d) $d_1 = 0.05$.

where $\lambda_{1i}, \lambda_{2i}, \lambda_{3i}$ is the eigenvalues of system (1).

$$\lambda_{1\max} = -0.1,$$

$$\lambda_{2\max} = -0.1 + d_2 \Lambda_i,$$

$$\lambda_{3\max} = -0.1,$$

where $\lambda_{1\max}, \lambda_{2\max}, \lambda_{3\max}$ is the eigenvalues of system (2).

As we all know, Turing instability is induced by the node coupling in the network-organized system, and the network-organized system is stable without the node coupling. Based on Theorem 1, system (1) (system (2)) is stable when $\lambda_{2i} < 0$ ($\lambda_{2\max} < 0$) and system (1) (system (2)) is unstable when a make $\lambda_{2i} > 0$ ($\lambda_{2\max} > 0$) hold [Fig. 11]. It is found that infectious diseases will disappear when $d_2 = 0.1, N = 100$ [Fig. 11(a)], the endemic diseases occur [Fig. 11(b)] when the coupling strength becomes large, and the outbreak strength increases with the increasing of the coupling nodes [Fig. 11(c)]. But the infectious diseases would soon die out when $N$ is below the threshold $\lambda_{2i} < 0$ [Fig. 11(d)]. Then, we consider the bifurcation of system (1) and system (2) about $d_2, N, \Lambda_{\max}$ and show the dynamical properties of system (1) and system (2) are consist. It is easy to know the bifurcation point $d_2 = 0.2$ of system (1) [Fig. 12(a)], which brings into correspondence with the bifurcation point of system (2) [Fig. 12(b)]. And the bifurcation point of system (1) about $N$ [Fig. 12(c)] is consist with the bifurcation point of system (1) about $\Lambda_{\max}$ [Fig. 12(d)] based on the relationship between $N$ and $\Lambda_{\max}$ [Fig. 13].

Finally, we investigate the combined influence of the diffusion of the susceptible $d_1$ and infected $d_2$, and have

$$\lambda_{1i} = -0.1 + d_1 \Lambda_i,$$

$$\lambda_{2i} = -0.1 + d_2 \Lambda_i,$$

$$\lambda_{3i} = -0.1.$$

Here $I_{min}$ is the mean minimum of 100 nodes, $I_{max}$ is the mean maximum of 100 nodes, $I_{max}$ is the maximum of 100 nodes, $I_{min}$ is the minimum of 100 nodes. It is found that there is competition between the diffusion of the susceptible $d_1$ and the diffusion of the infected $d_2$ in our simulation [Fig. 14–Fig. 15]. The periodic behavior occurs when the diffusion of the susceptible is in the ascendant, or the endemic disease occurs. Besides, according to Theorem 3, system (1) is always unstable when $d_1 = 0.1$. Here, we show the selection of infectious diseases in detail. We start by fixing $d_1 = 0.1$ and find periodic behavior occurs when $d_2$ is small. With the increase of $d_2$, the cycle length is larger [Fig. 14(a,b,c)] and the incidence of endemic diseases is increasing [Fig. 14(b,c)]. The result appears in Fig. 14(d), which means the endemic diseases are widespread. We know $d_2$ plays an important role in selecting periodic outbreaks and endemic diseases through the above analysis. From Fig. 15, $I_{max}$ and $I_{max}$ decrease with $d_2$ before the endemic diseases occur, then $I_{max}$ and $I_{max}$ increase after a critical value of $d_2$. We find that $I_{min}$ and $I_{min}$ always increase with increasing $d_2$, but the maximum value decreases at the beginning and increases [Fig. 15]. Although the diffusion of the infected may decrease the outbreak strength of some nodes(cities or countries), the average outbreak strength increases, which may cause more serious consequences for all nodes. Also, all the nodes will induce even greater disaster when the diffusive parameter of
the infected cross the critical value. That is why some measures should be taken to prevent the spread of the infected [Fig. 15]. The diffusion of the infected induces endemic diseases, which can be used to explain the formation mechanism of endemic diseases. (The limit of periodic outbreaks is endemic; namely, the outbreak period tends to zero, endemic diseases occur.)

Meanwhile, we consider the diffusion of the susceptible by fixing $d_2$. Based on Theorem 3, system (1) is stable when $d_1 = 0.01$, $d_2 = 0.05$ [Fig. 16(a)]. In this case, the periodic behavior and endemic diseases coexist, and the strength of outbreak increases with $d_1$ [Fig. 16(b,c,d)], which means the diffusion of the susceptible and the infected could induce the rich dynamical behavior. Moreover, the diffusion of the susceptible is a key factor in the generation of periodic behavior [Fig. 17(a)]. If the diffusion of the infected exists ($d_2$ is not zero), the diffusion of the susceptible will induce the outbreak of infectious diseases when $d_1$ crosses the critical value. In other words, if the diffusion of the susceptible is within a certain limit, the infectious diseases will not break out. Meanwhile, the same dynamic behavior occurs [Fig. 17(b,c)], which verifies the correctness of our theory. Finally, we plot the evolution of the infected in China [Fig. 18]. In general, the diffusion of the susceptible is quite common when the diffusion of the infected exists. Therefore, the influence of diffusion could make the periodic behavior occur, which shows our conclusion’s correctness. In conclusion, before the disappearance of the infected, some areas will remain at high risk if no preventive measures against epidemics are taken. We find that the positive wavenumber and negative wavenumber mean the promoting and suppressing of the external
factors, respectively, and nothing happens when they strike a balance between promoting and suppressing. Moreover, the negative concentration phenomenon in the reaction–diffusion system [9] is suppressed in some practical circumstances.

4. Conclusion

In this paper, we study the role of the diffusion network of the susceptible and infected in the periodic behavior and endemic diseases through wavenumber and saddle-node bifurcation in the network-organized system. Periodic behavior may occur when the diffusive parameter $d_1$ increases. And endemic diseases may occur when the diffusive parameter $d_2$ increases. If the diffusive parameters $d_1, d_2$ are within a specific limit, the outbreak never occurs. Then, it is found that the negative wavenumber can be treated as suppressing external factors, and nothing happens when they strike a balance between promoting and suppressing. Moreover, the negative concentration phenomenon in the reaction–diffusion system [9] is suppressed in some practical circumstances. Hence, a network-organized SIR model with the ER network is constructed to report that the homogeneous network (when NSE is larger) could facilitate the spread of infectious diseases through wavenumber. Reducing the NSE of social networks (reducing social distancing [28]) could prevent the outbreak of infectious diseases or decrease the strength of the epidemic, which can be treated as an essential indicator to contain the epidemic. Also, the mechanism of the periodic outbreak and endemic diseases is revealed in the network-organized SIR model, which can be explained by the mean-field method. For instance, (1) the local community may determine the switch between the periodic outbreak and endemic disease (only a subset of nodes are interlinked), (2) the higher exchange frequency of susceptible could increase the outbreak intensity of the periodic outbreak and endemic disease and shorten the period of the outbreaks, (3) the limit of periodic outbreaks is endemic (the infectious diseases are always in an outbreak when the outbreak period tends to zero, which leads to endemic diseases). Finally, the data from COVID-19 qualitatively authenticated the theoretical results.

It would be nice to carry out the analysis based on the literature and on fitting analysis using the actual data. The susceptible population in any node is affected by interaction of infective and susceptible from other nodes in network. Therefore the problem mentioned above will be done in a subsequent study.

CRediT authorship contribution statement

Qianqian Zheng: Conceptualization, Methodology, Writing – original draft. Jianwei Shen: Supervision, Conceptualization, Writing – review & editing. Yong Xu: Supervision, Writing – review & editing. Vikas Pandey: Writing – reviewing. Linan Guan: Writing – reviewing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

Data sharing is not applicable to this article as no new data were created or analyzed in this study.

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