Diffusion of resources and their impact on epidemic spreading in multilayer networks with simplicial complexes

Qingyi Sun [a], Zhishuang Wang [b], Dawei Zhao [c,*], Chengyi Xia [d,*], Matjaž Perc [e,f,g,h]

[a] *Tianjin Key Laboratory of Intelligence Computing and Novel Software Technology, Tianjin University of Technology, Tianjin 300384, China*
[b] *Faculty of Intelligence Manufacture, Wuyi University, Jiangmen 529020, China*
[c] *Shandong Provincial Key Laboratory of Computer Networks, Shandong Computer Science Center (National Supercomputer Center in Jinan), Qilu University of Technology (Shandong Academy of Sciences), Jinan 250014, China*
[d] *School of Control Science and Engineering, Tiangong University, Tianjin 300387, China*
[e] *Faculty of Natural Sciences and Mathematics, University of Maribor, Koroška cesta 160, 2000 Maribor, Slovenia*
[f] *Department of Medical Research, China Medical University Hospital, China Medical University, Taichung 404332, Taiwan*
[g] *Alma Mater Europaea, Slovenska ulica 17, 2000 Maribor, Slovenia*
[h] *Complexity Science Hub Vienna, Josefstädterstraße 39, 1080 Vienna, Austria*

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ABSTRACT

Recent studies have shown that personal resources have a significant impact on the dynamics of epidemic spreading. In previous studies, the main way for individuals to be able to obtain resources was through pairwise interactions. However, the human relationship network is often characterized also by group interactions, not just by pairwise interactions. To study the impact of resource diffusion on disease propagation in such higher-order networks, we therefore propose a multilayer network model, where the upper-layer network represents a resource network composed of random simplicial complexes to transmit resources, while the lower-layer network represents the network of physical contacts where the disease can spread. We derive the outbreak threshold expression for the epidemic by means of the micro Markov chain method, which reveals that the diffusion of resources may substantially change the epidemic threshold. We also show that the final fractions of infected individuals obtained via the micro Markov chain method and the classical Monte Carlo method are very similar, thus confirming that the model can predict well the epidemic spreading within the networked population. Finally, through extensive simulations, we show also that increasing the spread of resources on 2-simplexes can suppress the epidemic spreading and outbreaks, thus outlining possibilities for novel containment strategies.

1. Introduction

Epidemic spreading is an important topic in complex systems theory. In recent years, with the emerging infectious diseases, such as SARS [1], Ebola virus [2], and COVID-19 [3–6], infectious diseases pose a serious threat to human health and economic development. In previous studies on epidemic transmission, researcher main focus on some factors, such as individual birth rate [7], immunity to disease [8,9], government's epidemic prevention policy [10,11], individual acceptance of vaccines [12], awareness of disease prevention [13–23], and resources required for epidemic prevention [24,25] and so on.

During the outbreaks, related resources are critical to restrain the propagation of the disease, such as medical resources, living resources, etc. For example, [26] studied how resource allocation can be more effective in suppressing the spread of disease when resources are limited, and [27] found that the resources had a threshold, and the part

exceeding the threshold would have a counter-effect of suppressing the spread of the disease. Them examine the impact of resources on disease transmission and mainly focus on how investments in public resources affect disease transmission.

However, in real life, public resources are usually finite, especially during the spread of the epidemic. Due to the limited public resources, individuals often get resources by different ways, which through their own social networks or from their neighbors [28–30]. Therefore, the interaction between personal resources and epidemiological dynamics is crucial [31]. At present, most of the research on personal resources involve the pairwise interaction resources of nodes [32], ignoring the high-order relationship hidden inside the population. In addition to directly interacting with neighbors to obtain resources, individuals can also get resources through their own small groups. Meanwhile, in the

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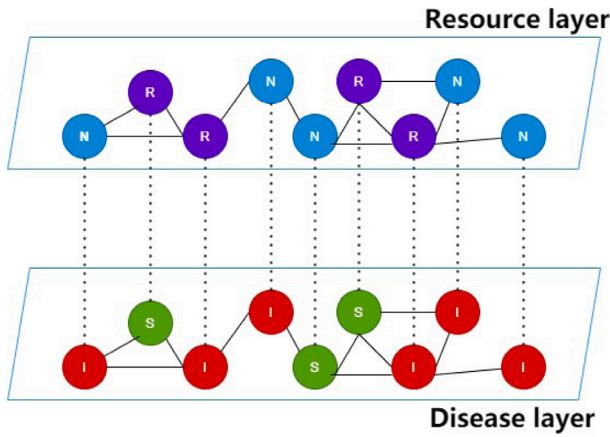

Fig. 1. Schematic representation of two-layered network model, the upper layer network is resource layer, which describes the transmission of resources, the lower layer network is disease layer, which describes the spread of epidemics. The dashed line between the resource and disease layers represents the nodes are a one-to-one mapping relationship. Resource layer network and disease layer network are undirected and weightlessin.

Fig. 2. The transition pattern between N and R states on the upper layer. The panel (a) shows the nodes get resources by pairwise interaction from his neighbors that have resources(R-type) with λ becomes R state. The panel (b) represents the node is in a 2-simplex and can get resources by pairwise interaction with λ and by 2-simplex with λ^* becomes R state. The panel (c) represents that a node in state R may consume resources to state N with probability δ at each time step.

real word scenarios, social networks are often beyond the pair interactions [33–36], and each individual has his own circle or small group. When you belong to a group, persons around you have resources, then your probability of getting resources within this group will be greatly improved. For instance, during the epidemics of COVID-19 in Shanghai, in addition to exchanging resources directly with neighbors, individuals will also appoint a "team leader" in the corresponding floor or community to purchase resources, and then exchange resources within this small group [37]. In this way, the probability of individuals getting resources in a small group will be greatly improved compared with that exchanging resources between a pair of neighbors. Thus, in order to better study this phenomenon of resource diffusion, we introduce the simplex complex into the diffusion of networked resources.

In this paper, similar to the coupling interaction between information diffusion and disease spread, we propose a new two-layered network model to investigate the role of 2-simplex higher-order structure in the interactions between resource and epidemics. This model contains two layers: the resource layer and the disease layer. Among them, the resource layer is obtained by random simplex complexes and represents the transmission of resources, while the disease layer is built on two different networks: random and scale free networks, which describes the spread of an epidemic within a population. Through extensive simulations, it is found that the steady-state density of infected nodes obtained by Micro Markov Chain (MMC) closely matches that obtained by Monte Carlo (MC), at the same time, it is also indicated that with the introduction of 2-simplex in the resource layer, the propagation rate of resources increases, and the proportion of nodes that own resources in the resource layer increases, reducing the density of infected nodes in the disease layer. The results suggest that networks constructed from random simplex complexes at the resource layer have a potential impact on the spread dynamics of the entire network.

The rest of the paper is organized as follows. In Section 2, we first introduce the two-layer network model and derive the probability transition equation, and then utilize MMC to analyze the outbreak threshold. Then, we present the theoretical and simulation results obtained by MMC and MC in Section 3. Finally, we conclude this paper with some promising outlooks in Section 4.
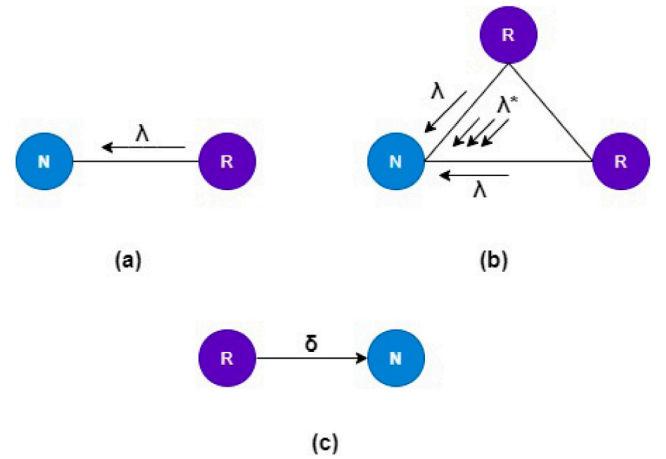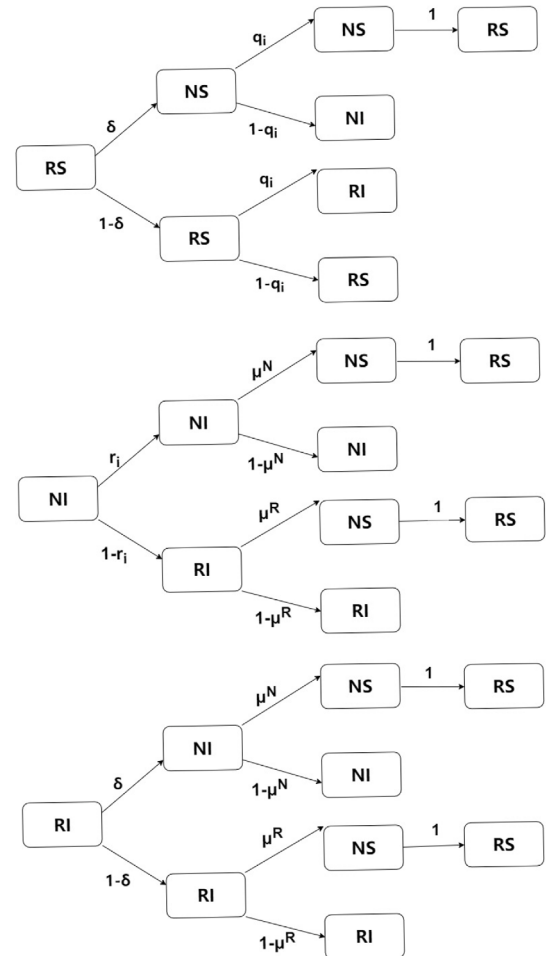

Fig. 3. Transition probability trees for 3 states(RS, NI, RI). People will not be infected with probability $q_i(t)$. $r_i(t)$ represents nodes that cannot obtain resources from his neighbors nodes that have resources. Individuals who have resources may consume them with probability δ. Infected individuals who have resources may recover with probability μ^R. Infected nodes who do not have resources may recover with probability μ^N. We assume that if the individuals are not be infected and do not have resources, the individuals will generate resources and become RS.
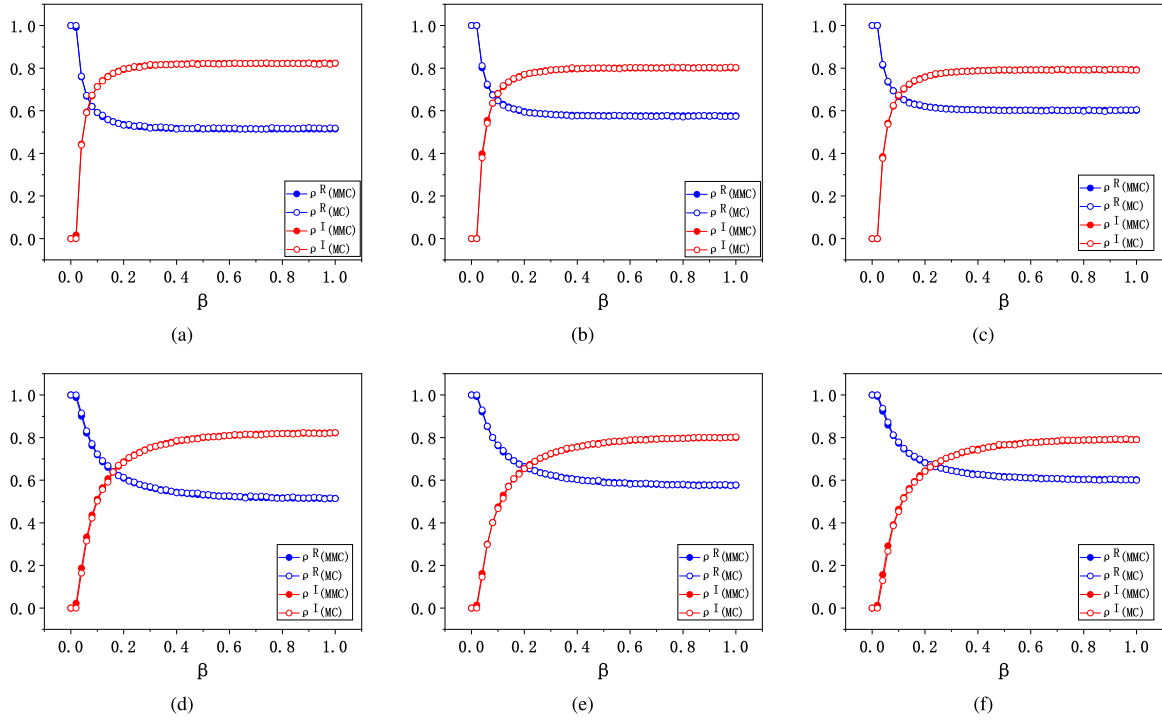
Fig. 4. Proportion of the final fractions of infected individuals and R-type ones as the function of β. Panels (a), (b), and (c) are obtained by ER-random network in the lower layer. Panels (d), (e), and (f) are obtained by scale free network in the lower network. The open circles represent the results obtained by MC, the full circles represent the results obtained by MMCA. Panels (a) and (d), $\lambda_\delta = 0$. Panels (b) and (e), $\lambda_\delta = 3.2$. Panels (c) and (f), $\lambda_\delta = 6.4$. The value of λ is set to be 0.15.

2. Methods and models

2.1. Simplicial complexes

In this paper, beyond the traditional binary interactions, we introduce simplicial complexes [37] characterizing the higher-order properties into the coupling model of resources and epidemics. So as to better understand the proposed model, let us first introduce the basic concept related with simplicial complexes. In simple terms, k-simplex is a set of $k + 1$ nodes in the network, and these $k + 1$ nodes are connected to each other. For example, 0-simplex represents one node, which does not link with any other nodes; 1-simplex represents that there are two nodes connected to each other, which also represents links in the network; 2-simplex represents triangles in the network, 3-simplex represents a tetrahedron in a network, and so on. Combining simplex of different orders, we call it a simplicial complexes. When $k > 1$, k-simplex represents the higher-order structure of the network.

2.2. Two-layered coupling network model of resources and epidemics

In this study, we propose a novel two-layer disease transmission model to study the coupled transmission of epidemics and resources. Among them, lower layer represents spread of disease, and the traditional SIS (Susceptible–Infected–Susceptible) model is adopted here. The upper layer depicts the process through which individuals get resources, likewise it is called the RNR (Resourced-No-resourced-Resourced) model. However, different from previous studies, we introduce a higher-order network into the upper resource layer, that is, we do not only consider resource exchange via pairwise interactions, but also consider the extra way that individuals can get resources through simplicial complexes. Each node in the upper and lower layers has a one-to-one correspondence, which means that the state of each node is jointly determined by resources and diseases. We assume that the upper and lower layers of the network are un-directed and un-weighted, and the model is illustrated in Fig. 1.

Here, in the lower network, which is the disease layer, we use the SIS disease propagation model to describe the spread of the disease. Each node in the lower layer has two states: infected (I) and susceptible (S). In the disease layer, each S node will be infected by its neighbors with probability β, which neighbors are at the I state. At the same time, the node in state I may revert from state I to state S with probability μ.

In the resource layer, nodes may be at two different states: no-resourced (N) and resourced (R) states of epidemics. The nodes in the N-type can obtain resources in two ways, through pairwise interactions with the probability of λ and through 2-simplex with the probability of λ^* and then become the R-type one. R-type nodes may consume resources and enter the state N with the probability of δ, and the process of nodes getting and consuming resources can be observed in Fig. 2.

It is worth mentioning that the status of the upper-layer node may affect the recovery at the disease layer nodes. If the upper-layer node is in the R state, it means that the node is at resource state, and the lower-layer disease can be easily recovered through resources, and the upper layer node is at the N state, which means that has no resources to recover. We use μ^R to represent the recovery probability of R-type node, μ^N to represent the recovery probability of N-type node, $\mu^N = \xi\mu^R (0 \leq \xi \leq 1)$, which indicates that the N-type node has a lower recovery probability than the R-type node. Nodes with more resources are easier to recover, which is also in line with the actual situation. If $\xi = 0$, infected nodes will not recover without resources.

Taking together, the states on both layers will be divided into three categories: RI, RS, and NI. Note that NS state is neglected here since we assume that the upper node will automatically obtain the resources once the corresponding lower-layer node is susceptible, that is, by NS state change to RS state.

2.3. Analytical results based on MMC

We use $p_i^{RI}(t)$, $p_i^{RS}(t)$, and $p_i^{NI}(t)$ to express the probability that node i become RI, RS and NI states at the time t. Let $q_i(t)$ represent

the probability of node i not being infected by any neighbor, $r_i^1(t)$ is the probability of the node i that no obtained resources through the link(pairwise interaction) from neighbors at time step t, and $r_i^2(t)$, which is represent the probability of node i does not get resources through 2-simplex from neighbors at time t. The probability that a node obtains resources is jointly affected by $r_i^1(t)$ and $r_i^2(t)$, that is, $r_i(t)$. Thus, through these definitions, we can get,

$$
\begin{cases}
q_i(t) = \prod_j (1 - b_{ji}(p_j^{RI}(t) + p_j^{NI}(t))\beta) \\
r_i^1(t) = \prod_j (1 - a_{ji}p_j^R(t)\lambda) \\
r_i^2(t) = \prod_{c_i} (1 - c_{ijk}p_j^R(t)p_k^R(t)\lambda^*) \\
r_i(t) = r_i^1(t)r_i^2(t),
\end{cases} \tag{1}
$$

where $[\alpha_{ij}]$ and $[\beta_{ij}]$ represent the adjacency matrices of the resource and disease layer networks. $p_j^R(t) = p_j^{RI}(t) + p_j^{RS}(t)$, In the equation of $r_i^2(t)$, c_i represents the number of i nodes in the 2-simplex. c_{ijk} represents the nodes of i, j, k located in the same 2-simplex. λ^* represents the probability of the nodes obtain resources from neighbors through 2-simplex, We can see it specific expression,

$$
\lambda^* = \lambda_\delta \delta / k_2, \tag{2}
$$

where λ_δ is the rescaled resource diffusion parameter and k_2 represents the number of this node in 2-simplex. Then, through the above formula, we can deduce the transition probability of each state, and the transition diagram, which can be seen in Fig. 3,

$$
\begin{cases}
p_i^{NI}(t+1) = p_i^{NI}(t)r_i(t)(1 - \mu^N) + p_i^{RS}(t)\delta(1 - q_i(t)) \\
\qquad + p_i^{RI}(t)\delta(1 - \mu^N) \\
p_i^{RS}(t+1) = p_i^{NI}(t)[(1 - r_i(t))\mu^R + r_i(t)\mu^N] \\
\qquad + p_i^{RS}(t)[(1 - \delta)q_i(t) + \delta q_i(t)] \\
\qquad + p_i^{RI}(t)[(1 - \delta)\mu^R + \delta \mu^N] \\
p_i^{RI}(t+1) = p_i^{NI}(t)(1 - r_i(t))(1 - \mu^R) + p_i^{RS}(t)(1 - \delta) \\
\qquad (1 - q_i(t)) + p_i^{RI}(t)(1 - \delta)(1 - \mu^R).
\end{cases} \tag{3}
$$

As $t \to \infty$, the diffusion of resources and the spread of disease, that can get to the stable state, then, the steady states that we can get, and shown as follows.

$$
\begin{cases}
p_i^{RI}(t+1) = p_i^{RI}(t) = p_i^{RI} \\
p_i^{RS}(t+1) = p_i^{RS}(t) = p_i^{RS} \\
p_i^{NS}(t+1) = p_i^{NS}(t) = p_i^{NS}.
\end{cases} \tag{4}
$$

Thus, we can also get the steady state equations of Eq. (3) as follows,

$$
\begin{cases}
p_i^{NI} = p_i^{NI}r_i(1 - \mu^N) + p_i^{RI}\delta(1 - \mu^N) + p_i^{RS}\delta(1 - q_i) \\
p_i^{RS} = p_i^{NI}[(1 - r_i)\mu^R + r_i\mu^N] + p_i^{RS}[(1 - \delta)q_i \\
\qquad + \delta q_i] + p_i^{RI}[(1 - \delta)\mu^R + \delta \mu^N] \\
p_i^{RI} = p_i^{NI}(1 - r_i)(1 - \mu^R) + p_i^{RI}(1 - \delta)(1 - \mu^R). \\
\qquad + p_i^{RS}(1 - \delta)(1 - q_i).
\end{cases} \tag{5}
$$

As is known to all, near epidemic threshold, the proportion of infected individuals at the steady state is close to 0. So we can assume $p_i^I \to 0$, where $p_i^I = p_i^{RI} + p_i^{NI}$, and then we can obtain,

$$
q_i \approx 1 - \beta \sum_j b_{ji}\, p_j^I = 1 - \alpha_i \tag{6}
$$

By substituting Eq. (6) into p_i^{NI} and p_i^{RI} of Eq. (5), we can derive the follow equation,

$$
\begin{cases}
p_i^{NI} = p_i^{NI}r_i(1 - \mu^N) + p_i^{RI}\delta(1 - \mu^N) + p_i^{RS}\delta\alpha_i \\
p_i^{RI} = p_i^{NI}(1 - r_i)(1 - \mu^R) + p_i^{RI}(1 - \delta)(1 - \mu^R) \\
\qquad + p_i^{RS}(1 - \delta)\alpha_i.
\end{cases} \tag{7}
$$

By adding p_i^{NI} and p_i^{RI} of Eq. (7) to get p_i^I, after simplify, we can obtain,

$$
\begin{cases}
p_i^I = -p_i^{NI}r_i\mu^N - p_i^{RI}\delta\mu^N + p_i^{RS}\delta\alpha_i \\
\qquad + p_i^I - p_i^I\mu^R + p_i^{NI}r_i\mu^R + p_i^{RI}\delta\mu^N \\
\qquad + p_i^{RS}(1 - \delta)\alpha_i
\end{cases} \tag{8}
$$

The $\mu^N = \xi\mu^R(0 \leq \xi \leq 1)$, by substituting it into Eq. (8), we can simplify further and get,

$$
p_i^{RS}\alpha_i = p_i^I - p_i^{NI}r_i(1 - \xi) - p_i^{RI}\delta(1 - \xi)\mu^R \tag{9}
$$

Because $p_i^I = p_i^{NI} + p_i^{RI} \ll 1$, we simplify Eq. (9) as follows,

$$
p_i^{RS}\beta \sum_j b_{ji}\, p_j^I = \mu^R p_i^I. \tag{10}
$$

By inserting Eq. (6) into Eq. (10), and because $p_i^I = p_i^{NI} + p_i^{RI} \ll 1$, we can get $p_i^{RS} \approx p_i^R$, so it can be rewritten as follows,

$$
\sum_j (p_i^R b_{ji} - \frac{\mu^R}{\beta}\delta_{ji})p_i^I = 0, \tag{11}
$$

where δ_{ij} is the element of the identity matrix. Noting that the solution of Eq. (11) is an eigenvalue problem for the matrix H whose elements are $h_{ji} = p_i^R b_{ji}$. Then, we can obtain the critical threshold of the proposed model as follows,

$$
\beta_c = \frac{\mu^R}{\Lambda_{\max}(H)}, \tag{12}
$$

where $\Lambda_{\max}(H)$ represents the maximum eigenvalue of matrix H. Then, for the resource layer, we are able to know that the disease outbreak threshold is related to p_i^R by the Eqs. (11) and (12). For the disease layer, by the Eqs. (11) and (12), we can know the μ^R can make an influence on the threshold.

3. Numerical results

Firstly, we depict the evolution of ρ^I and ρ^R, in which ρ^I represents the proportion of infected nodes when the disease spread in the entire disease layer reaches a steady state, ρ^R represents the proportion of nodes with resources when the resource diffusion in the entire resource layer reaches a steady state. The resource layer networks are built by random simplicial complexes [37]. The disease layer networks are constructed by two different networks: ER-random network [38] and scale free network [39]. The resource layer and disease layer nodes are set to be $N = 2000$. The initial value of ρ^I is equal to 1%. $\delta = 0.6$, $\mu^R = 0.4$, $k_1 = 20$, $k_2 = 4$, we herein set $\xi = 0$, (i.e., $\mu^N = 0$, and $\mu = \mu^R$). According to Eq. (2), when $\lambda_\delta = 3.2$, $\lambda^* \approx 0.48$, when $\lambda_\delta = 6.4$, $\lambda^* \approx 0.96$. All experimental results are obtained by averaging over 50 independent runs and the experimental parameters in the text are all defined above.

In order to better check the influence of β on ρ^I and ρ^R, we use two different networks in the lower layer. In Fig. 4, we can see the change of the final results of ρ^I and ρ^R. The resource diffusion rate is set to be 0.15. In panels (a) and (d), $\lambda_\delta = 0$, $\lambda^* = 0$, which means do not introduce the 2-simplex to the resource layer, and the nodes can obtain resources in one way, which through pairwise interactions. we can observe that ρ^I increases with β, ρ^R decreases with β, then both reach a steady state. In panels (b) and (e), $\lambda_\delta = 3.2$, $\lambda^* = 0.48$, the nodes can get resources by 2-simplex, compared with $\lambda_\delta = 0$, we can observe that ρ^I at the stable state is smaller, but ρ^R is bigger, which introducing the 2-simplex interactions in the upper layer, increases the diffusion of resources and then reduce consumption of resources. In panels (c) and (f), $\lambda_\delta = 3.2$, $\lambda^* = 0.96$, compared with $\lambda_\delta = 0$ and $\lambda_\delta = 1.6$, the nodes have higher probability of getting resources by 2-simplex, so ρ^I is more smaller, ρ^R tends to be more bigger, but the change of ρ^I is less obvious than that of ρ^R.

Finally, by introducing 2-simplex interactions, the probability and the way for nodes to get resources are increased, and then reduce
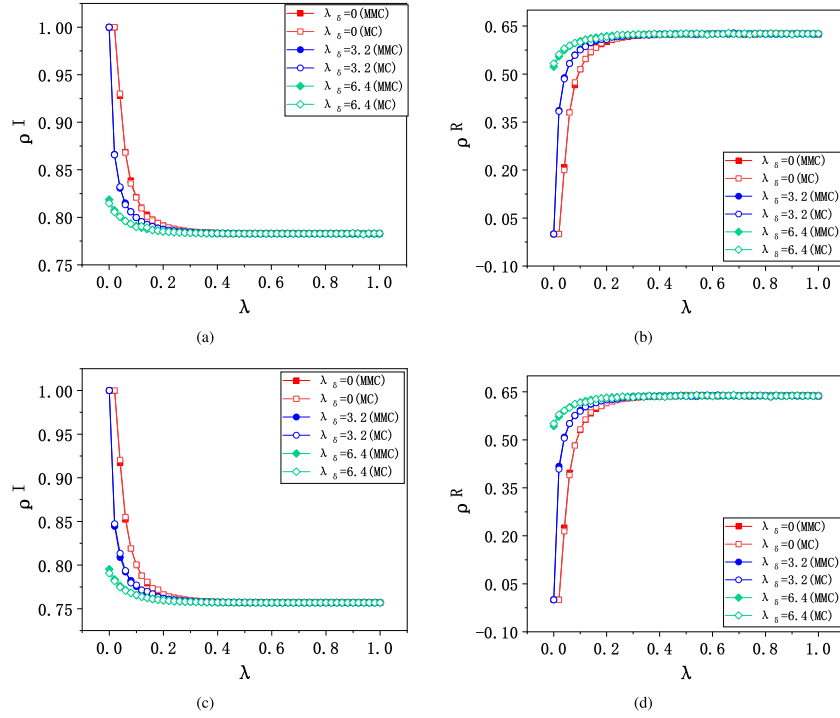
Fig. 5. Proportion of the final fractions of infected individuals and R-type ones with the change of λ. Panels (a), (b), ρ^I and ρ^R are obtained by ER-random network in the lower layer. Panels (c) and (d), ρ^I and ρ^R are obtained by scale free network in the lower network. The open circles represent the results obtained by MC, the full circles represent the results obtained by MMCA. Different color lines represent different results under different values of different λ_δ. The value of the λ_δ is set to be 0, 3.2, and 6.4. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

Fig. 6. Proportion of the final results of infected individuals and individuals that have resources with the change of δ. Panels (a), (b), ρ^I and ρ^R are obtained by ER-random network in the lower layer. Panels (c) and (d), ρ^I and ρ^R are obtained by scale free network in the lower network. The open circles represent the results obtained by MC, the full circles represent the results obtained by MMCA. Different color lines represent different results under different values of different λ_δ. The value of the λ_δ is set to be 0, 3.2 and 6.4. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)
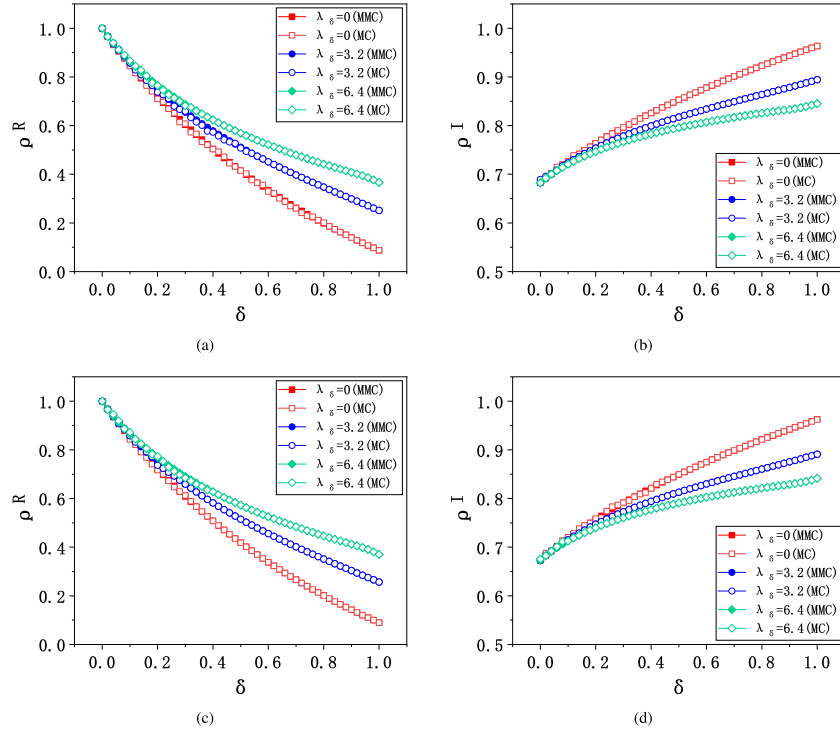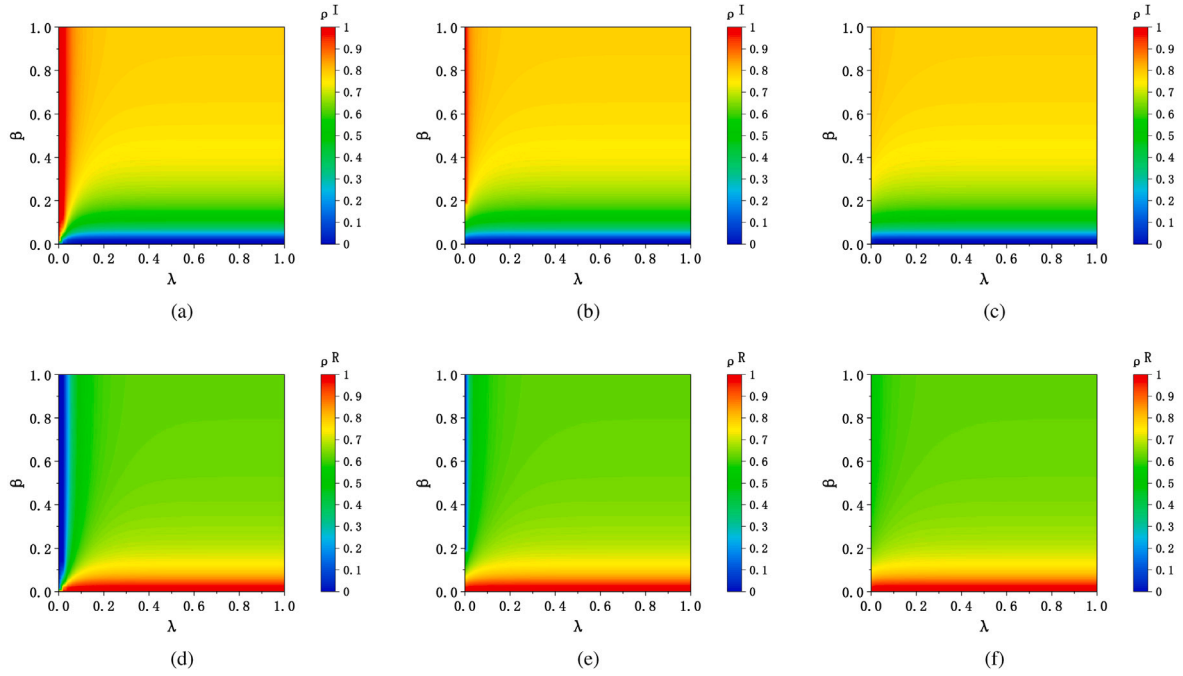
Fig. 7. Proportion of the final results of infected individuals and R-type ones with the change of β and λ. All the results are obtained by MMCA. The lower network is obtained by SF network. Panels (a), (b) and (c) are the results of ρ^I. Panels (d), (e) and (f) are the results of ρ^R. Panels (a) and (d), $\lambda_\delta = 0$. Panels (b) and (e), $\lambda_\delta = 3.2$. Panels (c) and (f), $\lambda_\delta = 6.4$.

consumption of overall resources. However, the impact of 2-simplex on ρ^R is more obvious than that of ρ^I. We can see that the above experimental results obtained by MMC and MC have small errors and can be perfectly matched, indicating that our proposed resource-disease model can achieve correct predictions.

Next, we focus on the impact of resources on disease transmission, that is, the resource transmission rate(λ) and resource consumption rate(λ) in the resource layer. Fig. 5 is the final results of ρ^I and ρ^R with the change of λ. In panels (a) and (b) of Fig. 5, the disease layer is obtained by ER-random network. but in panels (c) and (d), is obtained by scale free network. Three different colored lines represent different results under different values of λ_δ. Specifically, ρ^I decreases with λ and ρ^R increases with λ. For ρ^I in panels (a) and (c), we can observe that a smaller λ can dramatically reduce ρ^I, then, ρ^I reach the stable state when $\lambda \simeq 0.3$. When λ is small, we can observe that ρ^I decreases rapidly with the increases of λ_δ, and then reaches a stable state, especially when $\lambda_\delta = 6.4$, when $\lambda = 0$, the value of ρ^I is much smaller. Then, ρ^I decreases faster. The reason is even if $\lambda = 0$, nodes can also get resources by 2-simplex interaction to recover. When the upper layer does not introduce 2-simplex, resources can only transmit through pairwise interactions among nodes. When λ is small, the spread of resource is weak. After 2-simplex interactions are introduced, we find that λ^* increases with the increase of λ_δ, which means that as λ^* increases, it can help the propagation of resources on the higher-order network, which is referred to as 2-simplex, so that can the propagation of resources in the resource layer can be promoted. Then, the resourceful nodes can recover faster, so that can quickly reduce the risk of infected individuals and reach the stable state. But when λ is large($\lambda > 0.3$), the infected nodes will not decrease with the increase of λ_δ. The reason can be that when λ reaching a value ($\lambda \simeq 0.3$), the resources in the entire resource layer reach saturation state, it means ρ^R reaches the stable state, When λ is small, increasing λ_δ, the resources can quickly spread and then reach a stable state, but the final density of resource nodes will not be affected.

In Fig. 6, we present the impact of δ on the epidemic and resource spread, in panels (a) and (b), the lower layer network is obtained by ER-random network, but in panels (c) and (d), is obtained by scale free

network. Three different colored lines represent different results under different value of λ_δ. For ρ^I in panels (b) and (d), we can observe that ρ^I increases with δ increases. The reason is that as δ increases, resources are consumed. The nodes that be infected have no resources to recover, and then cause ρ^I rising quickly. With the increase of λ_δ, the probability of the node getting resources increases, and then the rate of resource consumption is slowed down. After that, the nodes have resources to recover, and inhibiting the spread of the disease. For ρ^R panels (a) and (c), we can observe that ρ^R decreases as δ increases. By introducing 2-simplex, with λ_δ being increased, the propagation of resources is promoted in the resource layer, thus the rate of resource consumption is slowed down.

We have studied the effects of β, λ, and δ on the spread of the disease alone. However, in the actual situation, the influencing factors of the disease are not single, but compound. So, we consider the combined effects of influencing factors on disease transmission. Fig. 7 shows the proportion of the final results of ρ^I and ρ^R with the change of λ and β with different λ_δ. In Fig. 7, the panels (a), (b) and (c) are heat map of ρ^I of influence of β and λ. In panel (a), $\lambda_\delta = 0$, it means the individuals that not have resources can only get resources from neighbors through link(pairwise interaction). We can observe that when λ is small($\lambda < 0.03$), the disease will break out with small $\beta(\beta \simeq 0.05)$, then the disease can quickly spread to the whole lower layer network. As the increasing of λ_δ, as shown in panels (b) and (c), we can see, when λ is small, the dynamic is difficult to break out and bigger β helps to spread to the whole lower layer network. The reason is nodes can also get resources by 2-simplex when λ is small. Thus, introducing the 2-simple into the upper layer, can increase the probability of nodes getting resources, especially when λ is small. By the way, it can affect both the dynamic outbreak. In Fig. 7, the panels (d), (e) and (f) are heat map of ρ^R of influence of β and λ. When $\lambda_\delta = 0$, it means the individuals that not have resources can only get resources from neighbors through link(pairwise interaction), and when λ is small, as increasing of β, even when β is small, the resources in the upper layer will still be consumed rapidly. After introducing 2-simplex, nodes can get resources through 2-simplex interactions. With the increase of λ_δ, the probability of nodes getting resources grows. Even when λ is small, the resources in the
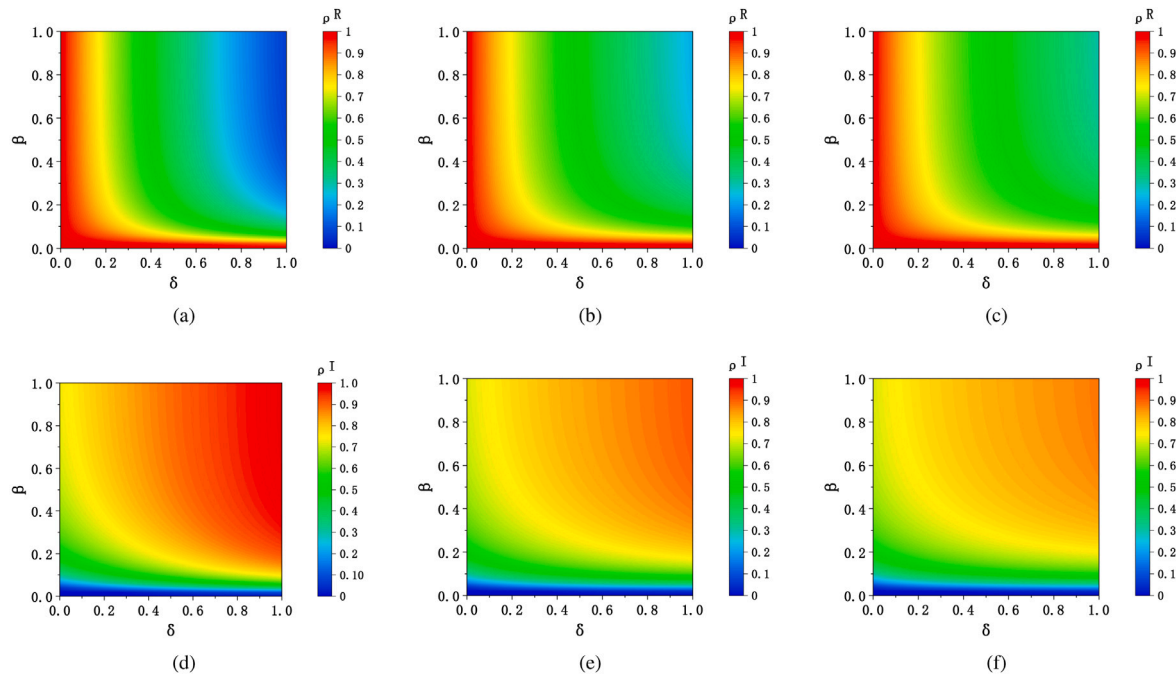
Fig. 8. Proportion of the final results of infected individuals and R-type ones with the change of β and δ. All the panels are obtained by SF network in the lower layer network. Panels (a), (b) and (c) are the results of ρ^R. Panels (d), (e) and (f) are the results of ρ^I. Panels (a) and (d), $\lambda_\delta = 0$. Panels (b) and (e), $\lambda_\delta = 3.2$. Panels (c) and (f), $\lambda_\delta = 6.4$.

entire upper network will not be consumed rapidly with the increase of β.

Fig. 8 shows the heat map of ρ^I and ρ^R with respect to both δ and β with different λ_δ. In Fig. 8, panels (a), (b) and (c) denote the heat map of ρ^R of the influence of β and λ, panels (d), (e) and (f) depict the heat map of ρ^I of the influence of β and λ. In panels (a) and (d), the $\lambda_\delta = 0$, in panels (b) and (e), the $\lambda_\delta = 3.2$, in panels (c) and (f), the $\lambda_\delta = 6.4$. For ρ^R in panel (a), when $\lambda_\delta = 0$, resources can only get by pairwise interaction among nodes. With δ and β being increased, the resources will be consumed completely, the infected nodes will have no resources to recover, which indirectly leads to the increase of ρ^I, as shown in panel (d). When introducing the 2-simplex, nodes can get resources by 2-simplex, as λ_δ increasing, even if β and δ are bigger, resources will not be consumed completely, as shown in panels (b) and (c), which causes infected nodes to have resources and then recover, and thus ρ^I becoming smaller, as shown in panels (e) and (f).

4. Conclusions

In summary, we propose a new two-layer network model: RNR-SIS model, where the upper resource layer network is constructed by random simplicial complexes, and the lower disease layer network adopts two different networks: ER network and SF network. After the introduction of 2-simplex into the resource layer, we study the effect of resources on disease transmission. We obtain the outbreak threshold of the disease spreading through MMC, and then by comparing the experimental results, it is found that the experimental results of MMC and MC have a smaller error and a higher degree of matching, which shows that our proposed model can predict the coupling of resources and diseases well.

Then, through the experimental results, the following conclusions can be obtained: first, when the resource transmission(λ) rate is low, increasing the resource diffusion on the 2-simplex(λ^*) can suppress disease outbreak; Second, when the value of resource diffusion is small, but the value of disease spread is big, increasing the resource diffusion on the 2-simplex can promote the resource diffusion on the whole resource layer, and the individuals can get resources and use them to recover, thus can reduce the density of infected individuals; Third,

for resource dissemination, we also found that when the probability of nodes obtaining resources is very low and the probability of consuming resources is very high, this is not conducive to suppressing the spread of diseases; At last, we find resources have a saturation value. Before reaching the saturation value, resources can more effectively inhibit the spread and outbreak of diseases.

Based on the above experimental results and theoretical predictions, it can be observed that the current outcome has a great inspiration for us to devise the epidemic prevention strategy. Meanwhile, the related conclusions can assist us to deeply understand the role of limited resources during disease transmission, and then enable the public health governments and the population to effectively distribute these limited resources when facing the possible epidemics in the future.

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

No data was used for the research described in the article.

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