The Comprehensive Influence of Network Structure, Heterogeneity and Dynamic Behavior on Network Virus Propagation

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ABSTRACT

There are two shortcomings in current research on network virus propagation. One is that all virus propagation models assume that the virus can only spread by infecting neighbor nodes. The other is that infection rate is set by a single factor, ignoring important structural information and behavior information of the network. To address these problems, we take the static structure characteristics of the network, dynamic behavior, and heterogeneity into account, and analyze the impact of the three elements on the infection rate. In the actual process of virus propagation, it is not always preferred to infect neighbor nodes. Through our research, we found that the network based on the three elements hides a propagation mechanism with wormhole effect. There is a hidden effective distance between any two nodes. When the susceptible nodes have a shorter effective distance from the source of infection, the infection rate will increase. The node with a shorter effective distance from the source of infection will be preferentially infected. The 'jumping' virus propagation with wormhole effect is presented on the whole network. Based on the classic SIR model, we propose the SIR-SHB model.

CCS CONCEPTS

• **Computing methodologiesModeling and simulation**; • **Simulation types and techniquesAgent / discrete models.**;

KEYWORDS

Cyber security, Virus propagation, Dynamic behavior, Heterogeneous network, Network structure

1 INTRODUCTION

As people rely more and more on the Internet for their daily life, it is crucial to understand the potential threats of the Internet, and Internet viruses are a major threat to network security. At the end of the last century, researchers found that biological epidemics and network virus spread have significant similarity, and applied epidemic models to network virus spread. In the last two decades, a number of researchers had migrated the biological epidemiological model, such as Susceptible-Infected-Susceptible (SIS) and Susceptible-Infected-Recovered (SIR), to the network virus propagation [1–6]. The network structure hides important information, and traditional models only consider some characteristics of network topology, such as degree distribution. It is difficult for these models to reveal the influence of network structure on the epidemic of virus. An effective way to overcome this difficulty is to build an epidemic model that captures the state of all nodes in the network, and this node-based model can make full use of the characteristics of network topology. Thus, researchers can use these models to further analyze the impact of network topology on virus prevalence. The network structure has a significant influence on the propagation of the virus, Mukul Gupta et al.[7] proposed a novel method that computes the ranking scores of the nodes in the network and considered the influence of other nodes simultaneously

when forming the set of top-N influential nodes, and used network structures to identify a set of nodes that are most influential. Sahneh and Scoglio[8] established a node-based Susceptibility-Alerting-Infection-Susceptibility (SAIS) model by introducing an alerting compartment into the continuous-time node-based SIS model. Youssef M et al.[9-12] analyzed the influence of important information contained in complex network structure on virus propagation. Theoretical analysis of these epidemiological models based on structural features suggests that the maximum eigenvalue of the network's adjacencies plays a key role in determining the prevalence of the virus.

Most existing epidemic models are established based on the homogeneous assumption of propagation network, the network of all nodes have the same infection rate and recovery rate. However, the important levels, functions, and other attributes of the nodes of the network are generally different in real networks. Most of real networks are heterogeneous rather than homogeneous. Mieghem and Omic[13] proposed a SIS model based on heterogeneous nodes, Khanafer et al.[14] analyzed the dynamic properties of the model. It is expected that by analyzing such models, patches can be allocated to each node in the network in a more cost-effective manner[15–18]. More than ten years ago, researchers successively paid attention to the important influence of dynamic behavior on virus propagation. Based on these classic bioepidemic models, many extant models with state transitions among nodes[19–22] were proposed to study the dynamic characteristics of network worms. In the dynamic process of virus propagation, statistical data and the mode of propagation will change constantly, Tie Li et al.[23] proposed a new incremental learning model which can be used for complicated dynamical scenarios. These studies help reveal the dynamic behavior of network worms and provide effective theoretical guidance for later network managers to protect network security.

All these models assume that the spread of viruses can only be through the topological neighbors, but this is obviously inconsistent with the actual spread of Internet viruses. There are many factors that affect the infection rate, and the models mentioned above are not fully studied in this area. Generally speaking, there are two main questions about virus propagation:

(1) How to determine the infection rate of virus propagation?

(2) How to accurately model the virus propagation process in a complex network?

The significance of this paper is to explore a more realistic mode of virus propagation and make theoretical contributions to the accurate defense of virus propagation. In order to solve these problems, our main contributions are as follows:

(1) We comprehensively analyzed the static structure characteristics, heterogeneity, and dynamic behavior analysis of the network's impact on the infection rate.

(2) We proposed the SIR-SHB model, which revealed the effective distance hidden in the network, and analyzed the 'jumping' mode of virus propagation mechanism with wormhole effect.

The rest of this article is organized as follows: Section 2 describes the frame structure of the paper, and analyzes the influences of the static structure characteristics, heterogeneity, and dynamic behavior of the network on the spread of the virus. Section 3 explains the hidden mechanism based on SHB (Structure-Heterogeneity-Behavior), revealing the effective distance in the network and the

'jumping' mode of virus propagation. Section 4 is the experimental simulation analysis, which analyzes the impact of heterogeneity and the importance of nodes on the spread of the virus. Section 5 is the conclusion.

2 GENERAL FRAMEWORK

2.1 Problem Definition

In the classic SIR model, individuals are divided into three categories: susceptible individuals, infected individuals, and recovered individuals. A susceptible individual is not infected, but easily infected; an infected individual means that the individual has been infected and has the ability to infect susceptible individuals; a recovered individual has no ability to infect, and will not be infected again. Assuming that α is the infection rate, β is the recovery rate, s(t), i(t) and r(t) respectively represent the density of individuals in the susceptible state, infected state, and recovered state at time t, and satisfies the condition of s(t) + i(t) + r(t) = 1, the propagation dynamics equation of the SIR model can be expressed as a system of differential equations as follows.

$$\begin{cases} \frac{ds(t)}{dt} = -\alpha i(t)s(t) \\ \frac{di(t)}{dt} = \alpha i(t)s(t) - \beta i(t) \\ \frac{dr(t)}{dt} = \beta i(t) \end{cases} \tag{1}$$

The previous SIR model considered a single factor when setting the infection rate, ignoring important structural information and dynamic behavior information in the network. In order to solve the single-factor problem, we comprehensively considered the static structure characteristics, dynamic behavior and heterogeneity of the network, and analyzed the impact of these three factors on the infection rate. We can describe the dynamic infection rate on a graph by a differential equation system:

$$\alpha(t) = f(X(t), S, H, M(t), t) \tag{2}$$

Where $\alpha(t) \in \mathbb{R}^{n \times n}$ represents the dynamic infection rate matrix of a dynamic system consisting of n linked nodes at time t∈[0,∞). X(t) ∈ $\mathbb{R}^n$ represents the node state of a dynamic system consisting of n linked nodes at time t, nodes are divided into three states, namely susceptible nodes, infected nodes, and recovery nodes respectively. $S = (D, C, B)$ is the network structure characteristic capturing how nodes are important relatively, D represents degree centrality of nodes, C represents closeness centrality of nodes, B represents betweenness centrality of nodes. $H = (V, E)$ is the heterogeneity of networks, V represents heterogeneity of nodes. For example, in computer network, switches and routers are heterogeneous nodes compared to computers. E represents the heterogeneity of edges, and the communication connection is a physical connection, the interactive connection is a virtual connection, and the communication connection is a heterogeneous edge relative to an interactive connection. M(t) ∈ $\mathbb{R}^{n \times n}$ represents the flows matrix at time t. X(0) = X_0 is the initial states of this system at time t = 0. The function $f: \mathbb{R}^{n \times n} \rightarrow \mathbb{R}^{n \times n}$ governs the dynamic infection rate of change of dynamics on the graph.

2.2 The Influence of Static Characteristics of Network Structure on Virus Propagation

In this paper, three common indexes (degree centrality, betweenness centrality and closeness centrality) are selected from many static geometric characteristics of network structure to discuss the influence of static characteristics of network structure on the propagation process. The following will briefly introduce the basic concepts of degree centrality, betweenness centrality and proximity centrality.

The degree of nodes is the simplest and most important parameter to characterize the characteristics of nodes, and the edge directly connected to the node v_i is more important locally. Degree centrality is the most direct measurement index to describe the centrality of nodes in network analysis, and the degree centrality below is expressed by $C_D(v_i)$. When a node has a large degree centrality, the node is more important in the network, and the degree centrality mainly depicts the local influence of a node. From a local perspective, if the degree centrality of the infected node is greater, the probability of infecting a nearby susceptible node at the next moment will also be higher.

Closeness centrality reflects the closeness between one node and other nodes in the network, which is one of the indicators to measure the centrality of nodes. When the distance between node v_i and other nodes is short, the value of the closeness centrality of node v_i is high. If the value of the close centrality of node v_i is high, it indicates that the distance from other nodes to node v_i is as short as possible, the closeness centrality of nodes is proportional to its importance in the network. When the infected nodes have a higher value of closeness centrality, the probability of the virus spreading to the whole network will increase. The closeness centrality below is represented by $C_D(v_i)$.

Betweenness centrality is a measure of graph centrality based on the shortest path. The betweenness of a node is the number of shortest paths passing through the node in a network. For each pair of nodes in a connected graph, there is at least one shortest path between the pair of nodes, which minimizes the number of edges the path passes. When the infected nodes have a higher value of betweenness centrality, the probability of the virus spreading to the whole network will increase. The betweenness centrality below is represented by $C_B(v_i)$.

The static characteristics of the network structure have a direct impact on the spread of the virus. The more important the infected node is, the higher the probability of other susceptible nodes being infected, and the faster the virus spreads. In order to show the position of nodes in different network topologies more intuitively, Figure 1 shows two special network structures. Figure 1(a) shows the concept of closeness centrality, the node v_6 has the largest degree and its degree value is 6. However, starting from node v_3 or node v_4 to any node v_i is shorter than the path from other nodes to node v_i. Starting from node v_3 or node v_4, it can reach other nodes at the fastest speed. Therefore, no matter from the perspective of virus attack or virus defense, node v_3 and node v_4 are more important than node v_6. As shown in Figure 1(b), the network structure is divided into two parts, which are connected by key node v_7, so that the two local areas can communicate with each other. Node v_2 and node v_8 have the largest degree, and the degree

(a) The Schematic Diagram of Closeness Centrality

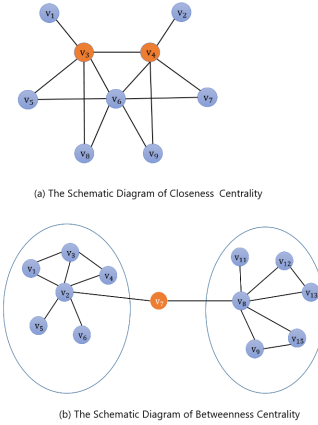(b) The Schematic Diagram of Betweenness Centrality

Figure 1: The Schematic Diagram of the Role of Network Nodes.

value is both 6. Even if the degree value of node v_7 is 2, which is the lowest degree value in the entire network, but it plays a key role in the connection of the entire network. From the perspective of virus defense, node v_7 is the most important in the entire network. This paper considers integrating three indicators into one composite index to describe the importance of nodes. The calculation formulas of $C_D(v_i)$, $C_C(v_i)$, $C_B(v_i)$ and comprehensive index $C_S(v_i)$ of nodes are as follows:

$$C_D(v_i) = \frac{k_i}{N-1} \qquad (3)$$

$$C_C(v_i) = (N-1) / \sum_{\substack{j=1 \\ j \neq i}}^{N} d_{ij} \qquad (4)$$

$$C_B(v_i) = \sum_{s \neq i \neq t} \frac{n_{st}^i}{g_{st}} \qquad (5)$$

$$C_S(v_i) = 2\frac{C_D(v_i)}{\sum_1^n C_D(v_i)} + 4\frac{C_C(v_i)}{\sum_1^n C_C(v_i)} + 4\frac{C_B(v_i)}{\sum_1^n B(v_i)} \qquad (6)$$

where k_i is the degree value of the node v_i, N is the total number of nodes in the graph, $N-1$ is the maximum possible degree of the node v_i, d_{ij} is the distance from the node v_i to the node v_j, g_{st} is the number of the shortest path connecting the node v_s to the node v_t, and n_{st}^i represents the number of shortest paths connecting node v_s and node v_t through node v_i. After normalizing degree centrality, closeness centrality, and betweenness centrality, we assign appropriate weights to obtain comprehensive index $C_S(v_i)$.

2.3 The Influence of Network Dynamic Behavior on Virus Propagation

In the classic SIR model, the infected node infects its neighbors with the same probability per unit time, but this is not the case in actual network virus propagation. For example, in the Internet network, even if there is a communication connection between two hosts and they are neighbors, but they do not have packet propagation, then there will be no virus propagation. In the Internet network,

the value of communication traffic can represent the active degree of dynamic behavior between hosts. In the transportation network, the traffic flow can represent the active degree of dynamic behavior between cities. In social networks, the closeness of contact between people indicates the active level of user behavior.

In this paper, according to the comprehensive index defined by the network structure characteristics, the nodes in the topology are divided into three levels, and the active degree of interaction between nodes is defined according to the three levels, and the node set can be described as $v^c = \{v^1, v^2, v^3\}, v^1, v^2, v^3$ represent the primary, the secondary, and the tertiary level nodes respectively. The calculation formula for the flow from node i to node j is as follows:

$$m_{ij} = g\left(v_i^c, v_j^c\right) \tag{7}$$

the function is an implicit function, and the flow value depends on the specific problem to be solved.

2.4 The Impact of Network Heterogeneity on Virus Propagation

Previous network propagation studies focused on homogeneous networks, but in actual network virus propagation, there may be different types of nodes and edges. In computer networks, routers, switches, and hosts belong to different types of nodes, and communication connections and interactive connections belong to different types of edges. This shows that in actual networks, there are heterogeneous nodes and heterogeneous edges. The heterogeneity of the network has a direct impact on the spread of the virus, for example, in computer virus propagation, the host can be infected, while the probability of switches and routers being infected is 0. Similarly, the communication connection edges in the physical sense and the interactive connection edges in the virtual sense are different types of edges, if both of these edges are in the same network topology, the network is heterogeneous. The following simulation model considers the influence of network heterogeneity on the virus propagation. The calculation formula of heterogeneity coefficient γ_{ij} is as follows:

$$\gamma_{ij} = \begin{cases} 1, & if\ node\ i\ and\ j\ are\ homogeneous \\ 0, & if\ node\ i\ and\ j\ are\ heterogeneous \end{cases} \tag{8}$$

3 THE HIDDEN MECHANISM BASED ON SHB (STRUCTURE-HETEROGENEITY-BEHAVIOR)

In this section, we will focus on the 'jumping' mode of virus propagation mechanism with wormhole effect. Based on the structural characteristics, heterogeneity and behavioral characteristics of the network, we find that there is a hidden effective distance in the network, the effective distance between nodes is inversely proportional to the probability of infection.

The traditional network virus propagation is to give priority to infect neighbor nodes, and the virus spreads from near to far from the source of infection. However, in reality, the virus propagation presents a 'jumping' mode. Network virus propagation is complex, network-driven dynamic process. The multi-scale nature of the network combined with the inherent heterogeneity makes it difficult to develop an intuitive understanding of these processes,

to distinguish relevant factors from peripheral factors, to predict their time course. However, we show that unintelligible 'jumping' propagation mode can be reduced to a surprisingly simple, homogeneous wave propagation mode. If the traditional geographical distance is replaced by a SHB motivated effective distance, the hidden wormhole effect will be easily detected. The probability of infection between two nodes has no obvious relationship with the geographical distance, but has a strong relationship with the effective distance. When the effective distance between nodes is short, the probability of infection will increase.

3.1 The Effective Distance Hidden in the Network

According to the comprehensive index $C_S(v_i)$ of network structure characteristics proposed in section 2, the importance of all nodes in the network can be determined, the level indirectly indicates the importance of the node. The dynamic behavior of the network can be described by a flow matrix, which is M = $(m_{ij})_{n\times n}$, obviously, the diagonal is 0.

In order to better describe the degree of interaction between nodes, the flow information is converted into a jump probability. There is a jump probability p_{ij} $(0 \leq p_{ij} \leq 1)$ between any two nodes. The calculation formula of p_{ij} is as follows:

$$p_{ij} = \frac{m_{ij}}{m_j} \tag{9}$$

$$m_j = \sum_i m_{ij} \tag{10}$$

where m_j represents the total flow of the node j to other nodes, m_{ij} represents the value of flow from node j to node i. Matrix P = $(p_{ij})_{n\times n}$.

The key idea we pursue here is that, despite the structural complexity of the underlying network, the redundancy of connections, and the multiplicity of paths a contagion phenomenon can take, the dynamic process is dominated by a set of most probable trajectories that can be derived from matrix P of the jump probability. Given the jump probability p_{ij}, i.e. the degree of interaction between node i and node j, if node i to node j must pass multistep paths, then the jump probability is accumulated and multiplied. Here, we consider using a logarithmic function to convert the multiplication of probability to additivity of distance.

We define the effective distance d_{ij} from node i to a connected node j as:

$$d_{ij} = 1 - \log p_{ij} \geq 1 \tag{11}$$

if there are multiple paths from node to node, the smallest distance among multiple paths is taken as:

$$d_{ij} = \min\{d_1, d_2, \cdot s,\ d_m\} \tag{12}$$

where m represents that there are m paths from node i to node j. The effective distance reflects that few flow between nodes is actually equivalent to a large distance.

3.2 Virus Propagation with 'Jumping' Mode

The effective distance has a negative correlation with the infection probability, the effective distance between nodes is inversely proportional to the probability of infection. Considering that the range
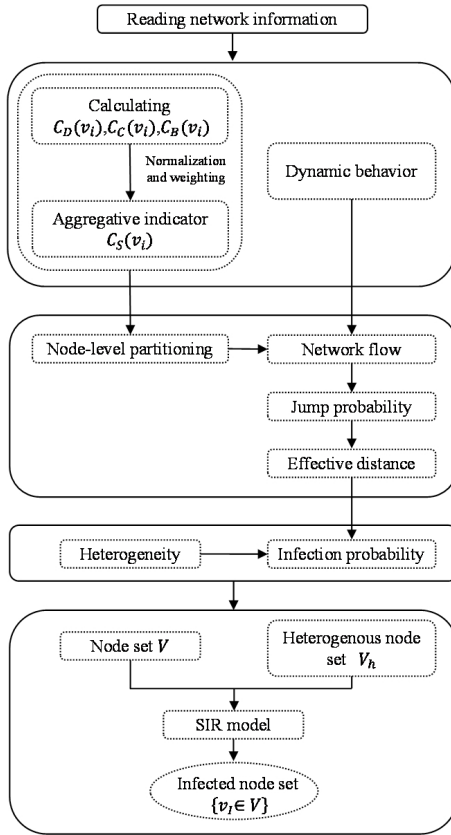
Figure 2: The Algorithm Framework of the 'Jumping' Mode of Virus Propagation.

of infection probability is $0 \leq \alpha_{ij} \leq 1$, we use the sigmoid function to map the effective distance combined with the heterogeneous coefficient to the infection probability matrix $A = (\alpha_{ij})_{n \times n}$, if node i is a heterogeneous node, then the heterogeneous coefficient is 0, and the infection rate is also 0, the calculation formula of α_{ij} is as follows:

$$\alpha_{ij} = \left(1 - \frac{1}{1 + e^{-d_{ij}}}\right)\gamma_{ij} \tag{13}$$

This paper considers the three factors of network structure, heterogeneity, and behavioral characteristics comprehensively, and calculates the difference of infection probability. According to different infection probabilities, network virus propagation presents a 'jumping' infection mode. The algorithmic framework for the 'jumping' mode of virus propagation is shown in Figure 2
We found an actual network topology on The Internet Topology Zoo, with 55 nodes and 74 edges, we conducted a virus propagation simulation experiment on this network topology and compared the traditional mode of infection through neighbor nodes and the 'jumping' mode of virus propagation. We revealed the positive linear relationship between the effective distance and the virus propagation time.

Figure 3 shows the classic SI model, the virus spreads in a way that only infects neighbor nodes, and the virus spreads from near to far over geographical distance. Figure 4 shows the spread of the virus according to different infection probabilities, showing a 'jumping' mode of virus propagation. Figure 5 shows the virus propagation in a heterogeneous network. According to the difference in the probability of infection, the virus propagation of heterogeneous network shows a 'jumping' mode of virus propagation. Figure 6 shows that the actual geographic distance in the network has no obvious relationship with the virus propagation time, that is, it is not necessary to infect nodes with a short geographic distance in cyberspace first, and the effective distance has an obvious positive linear relationship with the virus propagation time. The effective distance from the node to the source of infection is proportional to the time of infection.
Figure 3 shows the initial infection node is the 14th node, blue nodes are susceptible nodes, and red nodes represent the infected node. The traditional virus propagation can only infect neighbor nodes. (a) (b) (c) (d) showed the infection pattern from near to far. Figure 4 indicates the initial infected node is the 14th node, blue nodes represent the susceptible node, red nodes represent the infected node. Taking into account the differences in the probability of infection, (a) (b) (c) (d) (e) (f) presents the 'jumping' mode of virus propagation.
Figure 5 shows that the initial infection node is the 14th node, blue nodes are susceptible nodes, red nodes represent infected nodes, and green nodes represent heterogeneous nodes. It can be seen that heterogeneous nodes will not be infected. For example, a router in a computer network is a heterogeneous node relative to the host, and it is impossible to be infected in actual situations.
Figure 6 indicates the origin of the coordinates indicates that the source of infection is the 14th node, and the geographical distance from other nodes to the source of the infected node has a weak relationship with the time of virus propagation. Figure 7 indicates the effective distance between other nodes and the source of the infected node has an obvious positive linear relationship with the virus propagation time. If the effective distance from the node to the source of infection is short, the virus will arrive quickly.

4 EXPERIMENT

This section takes the BA network as an example to study the propagation mode of the new SIR-SHB model through numerical simulation, and the infection rate is calculated by the method proposed in this paper. The parameters selected in the simulation process are as follows: the number of nodes in the network is 1500, the initial time of virus propagation in the network is 0, and the initial infection ways are divided into random infection and deliberate infection.

4.1 The Impact of the Initial Infection Way on The Spread of Network Viruses

According to the SIR-SHB model proposed in this paper, the nodes can be divided into three levels, and the probability matrix of infection can be calculated. The initial infection can be carried out in two ways, the first way is random infections, a node is randomly selected from 1500 nodes as the source of infection; the second way
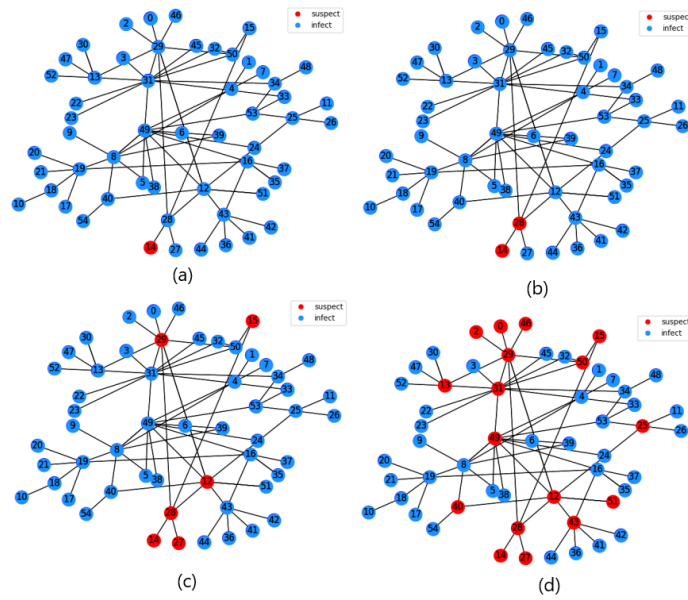
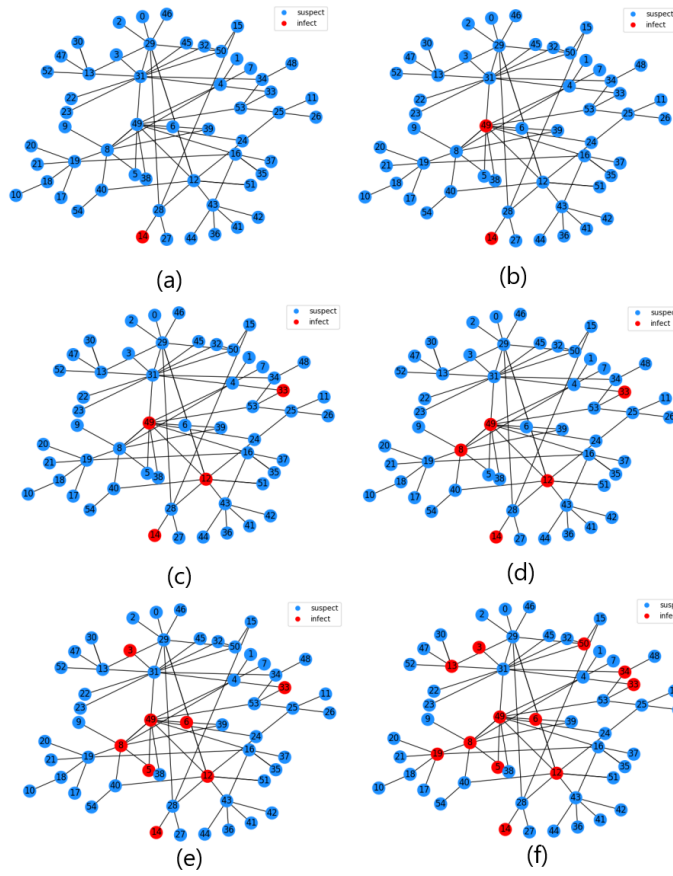**Figure 3: The Local Process of Traditional Virus Propagation by Neighbor Node.**

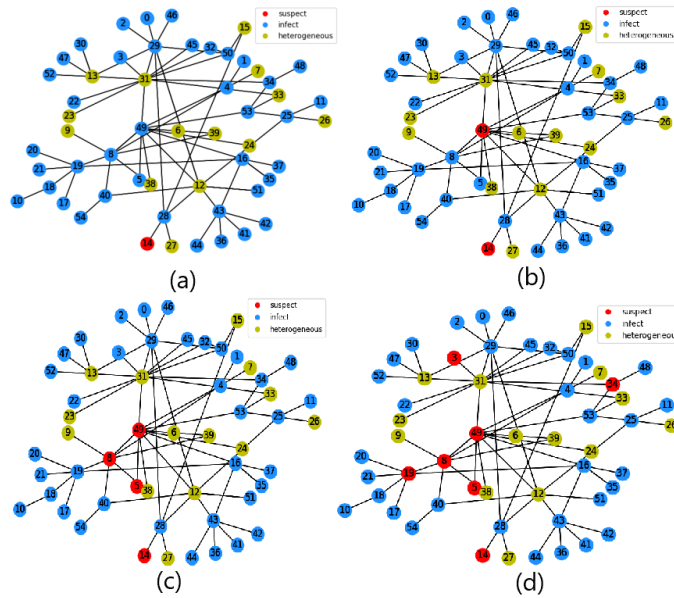**Figure 4: The Local Process of the 'Jumping' Mode of Virus Propagation.**

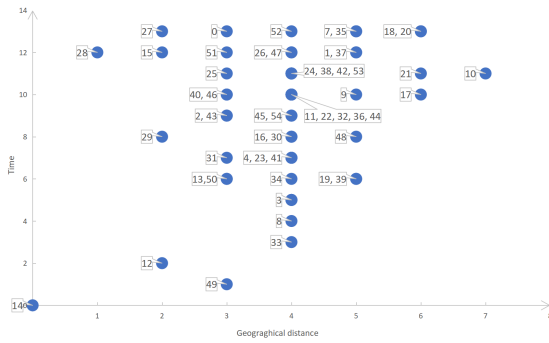**Figure 5: The Local Process of the 'Jumping' Mode of Virus Propagation in Heterogeneous Network.**

Figure 6: The Relationship between Geographical Distance and Propagation Time.
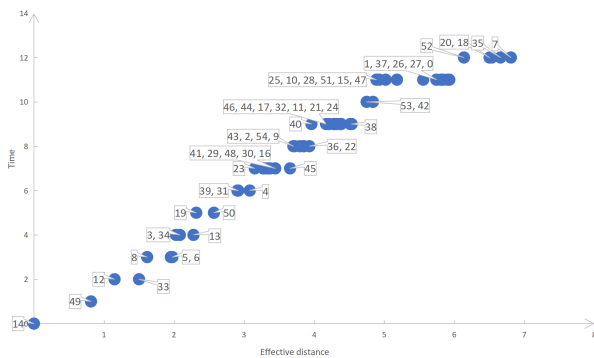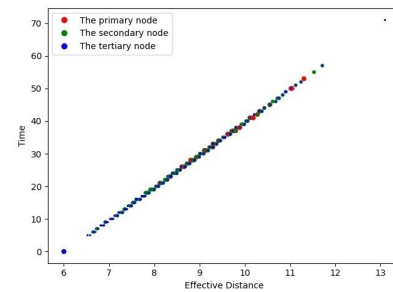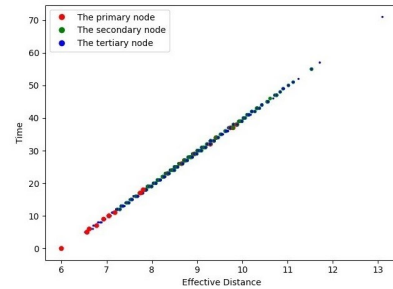

Figure 7: The Relationship between Effective Distance and Propagation Time.

(a) The way of infection randomly

(b) The way of infection deliberately

Figure 8: The Influence of Initial Infection Way on Propagation.

is deliberate infections, the node with the largest comprehensive index of network structure characteristics is selected as the source of infection. The experimental results are shown in Figure 8, the red node, blue node, and black node represent the first-level node, the second-level node, and the third-level node, respectively.

Figure 8 (a) indicates that if we adopt the way of infecting the primary source randomly, the importance of the node has no obvious relationship with the infection time.

Figure 8 (b) indicates that if we adopt the way of deliberately infecting the initial source, that is, the most important node is infected first, the first-level nodes are concentrated in the early stage being infected, and the second-level and third-level nodes are evenly distributed throughout the infection process.

According to the idea proposed in this paper, there is a short distance between the primary-level node and the initial infection, if we adopt the way of infecting the initial source deliberately, the virus will arrive at these nodes firstly. If we adopt the way of infecting primary source randomly, since the secondary nodes and the tertiary nodes account for the majority, the initial source of infection is most likely to be a low-ranking node, so the three types of nodes are evenly distributed throughout the virus propagation process, which is consistent with the theoretical analysis results of this paper.

4.2 The Impact of Heterogeneity on the Spread of Network Viruses

In order to study the influence of network heterogeneity on virus propagation, we set a heterogeneous ratio of 0.1 in the BA network. During the virus infection process, we compared the changes of the number of infected nodes between homogeneous network and heterogeneous network over time.

Figure 9 shows the number of infected nodes at time t in the BA network. The maximum number of infections in the heterogeneous network is less than the maximum number of infections in the homogeneous network. The infection curve of the heterogeneous network is always below the infection curve of the homogeneous network. Obviously, viruses spread faster and on a larger scale in homogeneous networks. Increasing the heterogeneous ratio can reduce the possibility of virus outbreaks. As time evolves, the number of infected nodes tends to zero in the final entire network, that is, the spread of network viruses is completely controlled, which is consistent with the theoretical analysis results.

In summary, the spread of viruses in the network is affected by the initial infection way (or by the importance of the source of infection). If the global information of the network can be grasped
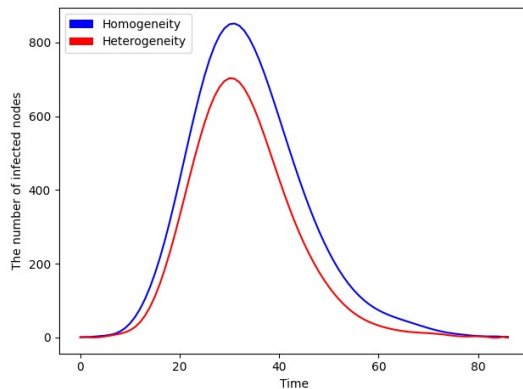
in advance, targeted immunization measures can be taken, such as increasing the heterogeneous ratio, and adopting immunization measures for key nodes, which can effectively reduce the scale and speed of virus propagation.

5 CONCLUSION

Based on the traditional SIR model, this paper proposes the SIR-SHB model, and analyzes the impact of the network, dynamic behavior, and heterogeneity on virus propagation, and reveals the effective distance and the 'jumping' mode of virus propagation mechanism with wormhole effect. The mechanism is of great value for understanding the internal factors of the virus propagation mechanism and topological evolution. We also explored how the importance of the initial source of infection and the heterogeneity of the network affect propagation behavior. The main research results of this paper are as follows:

(1) By analyzing the static structure characteristics of the network, dynamic behavior, heterogeneity comprehensively, we can get the effective distance in the network, and the different infection probabilities, so as to predict the set of infected nodes in the next stage.

(2) Increasing the heterogeneous ratio can effectively reduce the spread speed and scale of network virus.

(3) If an important node is deliberately selected as the source of infection, other important nodes in the network will also be infected at an early stage.

In the future, we will consider dynamically adjusting the network structure, use the SIR-SHB model to analyze important nodes, and take precautionary measures to further test the practical application value of the model.

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Figure 9: Infection Number Curve.

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