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The propagation-weighted priority immunization strategy based on propagation tree

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ABSTRACT

In this paper, we constructed the virus propagation tree for any infected node through improving the k-shell decomposition method. Supposing we determine the position of infected nodes, the root node of the propagation tree is an infected node and its children nodes are susceptible nodes. The virus can be diffused from the bottom to top along with the tree. Based on the analysis of the virus propagation tree, a propagation-weighted priority immunization strategy was proposed to vaccinate the influential nodes(the nodes are the several nodes of the most risky in the high-risk node and it is convenient for us to immune). The mathematical proof and the computer simulation on scale-free network are given. The results show that the propagation-weighted priority immunization is effective to prevent the virus from diffusing.

1. Introduction

At the present stage, the major object of study is the huge network system in the complex network, and the relationship of the links in the network is intricacy. What's more, a great deal of studies showed that the topology structure and the statistical characteristics are closely related to the propagation behavior in the network. In recent years, the study of evaluation about the propagation influence of the node attracted a lot of attention in the network [1–12]. For example, the Hub node in the computer network, the key point in the electric power network, and the key figure in the scientific research cooperation network, they all play the particular role in their own networks.

It is a very meaningful work to find out the key node by analyzing the topology structure of the network and the link relations between nodes in the network [13] . The key node can be controled to affect the state of the rest of nodes in the network. For instance, the information released by the "big V" user who has tens of millions fans can spread to the whole network more quickly. In 2010, the k-shell decomposition method [14] proposed by Kitsak et al. is used to divide the network and find out the core network of the complex network or the key node which called weighed node. The k-shell decomposition method is a method used to partition a network into hierarchically ordered sub-structures [15] and it is a kind of coarse classification method for the importance of the node, but the distinguish is not obvious. The importance of a node can be denoted by the changing distance after removing the node. In 2015, Liu et al. do the further analysis [16]about the k-shell decomposition method, and they pointed out that the node which has high-impact connected well with the k-nuclear network and the edge node in the propagation of the network. For any edge, they also proposed that how to get the number of the edge's outward extending edges by the both end nodes of the edge, they use the number to define the importance of the edge in the propagation.

Finding the high-propagation-impact nodes has important guiding significance to control the propagation of the virus. By the way of immuning the high-propagation-weighted nodes, the spread of the virus in the network will be influenced. Obviously, the k-shell decomposition method and the related research has obtained the certain proof, but it is not realistic to use k-shell decomposition method to find out the propagation-weighted node in the population network. Because of the huge population network and the unstability of the internal connection, it's hard to describe the topology structure of the population network accurately. But it is not equivalent that the method of identity propagation-impact node is invalid. The propagation of the virus has known by us is like this. Firstly, the propagation of the virus is unidirectional, and it can only spread the virus to the susceptible population from the infection source, Secondly, the infection source produced by the virus usually spread the virus to the adjacency nodes. Then, it will gradually diffuse into the population. Therefore, when the location of infection source was located, we can mark the propagation-weighted node from the adjacent node of the infection source.

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The “acquaintance immunization” is designed about vaccinating the acquaintance of the node [17], but we cannot find all acquaintances accurately. And the high risk immunization strategy is to vaccinate the direct neighbor nodes of infected nodes [18–20], but we need to immuned a larger number of nodes. Because these immune strategy exist drawback, so a better immune strategy - the weighted priority immunization strategy was put forward by us.

The rest of the paper is organized as follows: in Section 2, we analyzed and summarized the view produced by the k-shell decomposition method and the literature [16], the algorithm of constructing virus propagation tree was designed and proposed, and then the weighted priority immunization strategy was proposed. In Section 3, the theoretical analysis and computer simulations are given. Finally, conclusions are given in Section 4.

2. The K-shell decomposition method and the propagation-weighted priority immunization strategy

2.1. K-shell decomposition method and related research

In 2010, the k-shell decomposition method proposed by Kitsak et al. is used to divide the network and then find out the core network of the complex network and the key node. The article pointed out that the most influential node is not the node which always has the maximum degree, but the node which located at the heart of the network. The core node can be obtained by k - shell decomposition algorithm. The k-shell decomposition starts from the 1–shell decomposition [14]. First, removing the node whose degree is 1 and the edge connected with the node, after the removal, the network may re-appear the node whose degree is 1, repeat the above operation until the network doesn’t have the nodes whose degree is 1. The above operation is equivalent to shell the outermost layer of the network, the deleted nodes and the edges between the deleted nodes are called the 1-shell, the rest of nodes and the edges between the rest of nodes are called 1-nuclear. In the 1- nuclear network, the degree of the node is 2 at least. In a similar way, the k-shell ($k \geq 1$) can be further decomposed until each node is divided into the correspond k-shell. We need to pay attention to: after the each shell operation, we will get a k-nuclear network. In a sense, the k-nuclear network can be considered as the core network of the complex network, the node can be considered as the core node or the weighted node. In 2015, Liu et al[16]., do the further analysis about the k - shell decomposition method. After the k-shell decomposition, we can get the k-nuclear network and we find the k-nuclear network’s node will have relatively strong coupling. But if in the original network, it exists the local coupling phenomenon between some nodes, the local coupling network will stay in the core network, it resulted in the presence of the pseudo core node in the core network, the k-shell decomposition method performs badly to the network with local coupling network [21], and pointed out that the real core node not only connects with the core node well, but also connected with the edge node well.

For example, it is assumed that the node i is an infected node. If node j has many outward extending nodes (the outward extending nodes are the nodes can be contacted with the node j and can’t be connected with the node i), and the node i can contact with many new nodes through node j, thus the edge between the node i and the node j is important for node i. On the other hand, if the node i can contact with the node j’s other neighbor nodes directly, and thus the edge between the node i and the node j is less important.

The direction from the infected node to the health node only needs to be considered for the propagation of the virus. Can we reserve some edges to make the network topology clear? For the study, we define d_{ij} denotes the shortest transmission distance between the node i and the node j, and the number of the shortest path between two nodes have three situations: non-exist, single, and multiple. But the shortest distance between two nodes is fixed. And $\{d_{i*} = \psi\}$ can be defined to represent the collection of the nodes which can call it m, the distance between m and the node i is ψ. Motivated by k-shell decomposition method and the research advance in core-periphery structure, a way to simplify the edges was proposed in the network.

2.2. Construct virus propagation tree and design weighted priority immunization strategy

In the real life, the population network is extremely complex, it is difficult for us to obtain the topology structure information, and it is not easy to find out the core network and the key nodes in the network directly. On the other hand, the propagation of the virus is not random, the infection source produced by the virus usually spread the virus to the node which contacts with the virus, and then gradually diffused into the population. Therefore, if we confirm the infection source’s location, we can mark the propagation-weighted node from the adjacent node of the infection source. It increases the practicability of the research greatly.

If we study the propagation of the virus in the complex network, a basic premise is that the propagation of the virus is unidirectional, it can only spread the virus from the infection source to the susceptible population. Supposing we determine the position of infected nodes, considering the propagation characteristic of the infected node, the whole network can be seen as a unidirectional network from the infected node point to the other nodes.

In Fig. 1.(a), we treated the red a1 node as the infected node. In the process of propagation, firstly, it will infect its neighbor node, the node b1, b2, b3, b4, b5, and then, the protection for its neighbor nodes is the key step to control the outward propagation of the node a1. In the high risk immunization strategies, the neighbor nodes of a1 are called high-risk node, the high risk immunization strategies is to immune the high-risk node undifferentiated. But in the real life, it is very difficult to find the high-risk node for us accurately, if the network has more infected nodes, the cost of high-risk immunization strategy is very large. It is difficult to immune all the high-risk node, so it is necessary to analysis the propagation-weighted of the high-risk node. From the point of degree’s value to look, the degree’s value of the node b1, b2, b3, b4, b5 is almost equally. In the meantime, it exists the local coupling phenomenon between the node a1, b2, b4, b5. After a simple decomposition of the k-shell, the node a1, b2, b4, b5 will remain in the core network, and we will also treat them as the core nodes, but the reality is not like this. Before analysis the propagation-weighted of the node b1, b2, b3, b4, b5, first, we assume the node b1, b2, b3, b4, b5 have been infected, as shown in Fig. 1.(a), it is clearly to see, when the node b1, b3 are infected,the node b1, b3 will further spread virus outwardly. In contrast, the other nodes such as the node b2, b4, b5, the influence they produced is small relatively. Meanwhile, we can see that the degree value of the node b1, b2, b3, b4, b5 is almost equally. But the number of the outward extending nodes connected with the node b2, b4, b5 which passed by node a1 is 0. For the node b1, b3, the number of the outward extending nodes is 3 and 2 respectively. According to the above analysis, we may get the outward extending nodes (connected with the node b1 which passed by node a1) is the node c1, c2, c3. But for the node b2, the outward extending nodes are null.

Based on the above analysis, we can get the conclusion: the more the number of the outward extending nodes, the greater the propagation-impact for the neighbor node of the infected node. In a similar way, we can do the similar analysis for the two-step neighbor node (The distance from the source of infection to the two-step neighbor node is 2) to find high-impact-propagation