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Methods for removing links in a network to minimize the spread of infections

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ABSTRACT

Minimizing the spread of infections is a challenging problem, and it is the subject matter in many different fields such as epidemiology and cyber-security. In this paper, we investigate link removal as an intervention strategy and study the relative effectiveness of different link removal methods in minimizing the spread of infections in a network. With that in mind, we develop four connectivity-based network interdiction models and formulate these models as mixed integer linear programs. The first model minimizes the number of connections between infected and susceptible nodes; the second the number of susceptible nodes having one or more connections with infected nodes; the third the total number of paths between infected and susceptible nodes; and the fourth the total weight of the paths between infected and susceptible nodes. We also propose heuristic algorithms to solve the models. The network interdiction models act as link removal methods, i.e., each return a solution consisting of a set of links to remove in the network. We compare the effectiveness of these four methods with the effectiveness of an existing link removal method [25], a method based on link betweenness centrality [18], and random link removal method. Our results show that complete isolation of susceptible nodes from infected nodes is the most effective method in reducing the average number of new infections (reduce occurrence) under most scenarios, and the relative effectiveness of the complete isolation method increases with transmission probability. In contrast, removing the highest probability transmission paths is the most effective method in increasing the average time to infect half of the susceptible nodes (reduce speed) under most scenarios, and the relative effectiveness of this method decreases with transmission probability.

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1. Introduction

The spread of harmful infections are common in real life networks: infectious diseases spread through social and transportation networks, computer viruses and malware spread in computer networks, and propaganda and rumors spread in online social networks. Minimizing the spread of these infections is very important because they can cause significant economic and social damage. Worldwide, infectious diseases cause over 10 million deaths each year, accounting for 23% of the total disease related deaths [53]. In the well-known influenza pandemic of 1918, 30 to 50 million people are estimated to have died [22]. According to Sanger [41], 1000 to 1500 centrifuges of an Iranian nuclear power plant were destroyed by spreading a computer worm called Stuxnet. Lethal worms and viruses such as Stuxnet can easily fall in the hands of terrorist organizations and rogue nations.

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The simplest and traditional way of modeling spread of infections assumes that the population as a homogeneous mix of individuals and then compartmentalizes them based on their infection status. Although this simple compartmental framework has been extended to include some upper level host heterogeneities such as contact patterns among age groups, differing spatial structure, inclusion of individual contact structure is a fairly recent phenomenon [4]. The maturation of network science is enabling researchers to find limitations in the homogeneous mixing assumption and discover the value of network modeling [33,37,38,52]. It is indeed important to capture the underlying network because the ability of networks to maintain connectivity when subjected to selective or random removal of nodes or links depends on the particular network topology [2,23]. Connectivity is a popular measure for networks, and it represents the ability of a network's nodes to communicate with one another, thereby, facilitating the spread of infections. Connectivity is applicable to infection control because removing the nodes and links in reducing the connectivity of a network is analogous to immunization of individuals and preventing contacts in reducing the spread of

infections. In one of the earlier studies that applied network modeling, Satorras and Vespignani [42] showed that the tolerance of scale-free networks [5] against random node or link removal does not allow a homogeneous approximation of connectivity in infectious disease spread modeling and results in overestimation of the epidemic threshold. Pastor-Satorras and Vespignani [38] even found the absence of an epidemic threshold in scale-free networks. Epidemic threshold as defined by [38] is the minimum value of the effective reproduction rate $\left(\frac{\text{Infection rate}}{\text{Recovery rate}}\right)$ for which the infection spreads and turns into an epidemic; otherwise, infection dies out. The implication of the work by Satorras and Vespignani [42] is that even in networks with very small average connectivity, epidemics can occur, and to find the most influential set of individuals to immunize or quarantine, one must consider the underlying network topology, irrespective of whether the topology resembles a scale-free, random [19], small-world [52], or some other type of network. Immunizing or quarantining randomly based on homogeneous mixing assumption does not ensure effective reduction of the connectivity of the network, thereby, not preventing the spread of infections effectively.

It is possible to reduce the connectivity of a network and consequently minimize or slow down the spread of infections in the network by interdicting the network in two ways: removing links and removing nodes. Tong et al. [47] and Kimura et al. [25] proposed heuristic algorithms to minimize spread in a network by removing a subset of links. Enns et al. [18] proposed a network interdiction model with a non-linear programming formulation that minimizes the number of nodes at risk of infection. He et al. [20] proposed a model that removes a set of both links and nodes to minimize the total cost composed of the cost of infection and the cost of preventing infection. Their model can also be used as a node and link removal method to minimize spread by accounting for the cost of prevention in a budget constraint. Koch et al. [26] analyzed the behavior of basic reproduction number as defined originally by Newman [37] with respect to link removal and proposed a new definition for basic reproduction number. Yang et al. [54] proposed a method to control a special type of spread known as the traffic-driven outbreak by removing links using different link ranking metrics. Chung et al. [10] studied the efficacy of several centrality based link removal strategies on the spread of infectious diseases through the global airline network. Kuhlman et al. [27] proposed approximate algorithms for link removal to minimize complex (threshold-based) contagion.

In a field related to controlling the spread of infections, other authors have studied the problem of removing nodes in a network in order to maximize the fragmentation of the network, minimizing connectivity [1,3,11,14,44,48,50,49]. This problem is known as the critical node detection problem (CNDP). These studies on the CNDP optimize one or more of the following network fragmentation metrics: (1) the number of connected node pairs (minimize), (2) the largest connected component size (minimize), and (3) the number of connected components (maximize). Although the interdiction models related to CNDP can be used to identify a set of nodes to remove to reduce the spread of infections, they are not expected to reduce spread effectively as they assume that all the nodes to be of the same type rather than dividing the nodes into infectious and susceptible categories. The aforementioned fragmentation metrics also need to be significantly modified before they can be used for interdicting a network to minimize spread; For example, to minimize spread, it is enough to have just two connected components, one with all the infectious nodes and the other with all the susceptible nodes, instead of maximizing the number of connected components.

The field of network vulnerability and robustness analysis [6,9,16,32,34,43,45,21,15] is a closely related field of the critical

node detection problem. The problem analyzed in this field is functionally opposite of the critical node detection problem because in this case, critical components (nodes and links) are those, whose hardening results in maximizing the connectivity of the network. The fragmentation metrics that are minimized in the CNDP are maximized in the robustness problem and vice versa. Moreover, although some of the studies in this field consider cascading failure of components, most of the studies do not consider spreading agents such as infections.

In this paper, we study the problem of detecting a subset of critical links in a network, whose removal minimizes the spread of infections. Therefore, the problem studied in this paper is similar to the critical node detection problem, but it is customized for minimizing spread by removing links instead of nodes. One of the reasons the link removal problem is very important is that link removal allows finer control than node removal. If a node is removed, all of the links connected to the node are automatically removed. In contrast, if a link is removed, only that link is removed. A node can still be removed in this paradigm by removing all of the links connected to it. Therefore, the link removal problem has the potential to provide additional insights into problems that have only been studied under node removal [8,52,7,46,28,40]. Marcelino and Kaiser [29,30] compared several generic edge and node ranking metrics in reducing the global spread of influenza through an airline network. According to their results, link ranking metrics are usually more effective than node ranking metrics. Moreover, in many situations the node removal option is unattractive or not available at all, whereas there is still a way to remove links. For example, it might be very difficult to find and eliminate terrorists in a terrorist network, but there might be a way to block their communication channels, in effect removing links among them. The loss associated with completely shutting down an entire airport might be enormous, but it might be possible to temporarily suspend the flights between two specific airports during a global disease pandemic. However, we should also note that there are cases where node removal is feasible but link removal is not. For example, if the nodes in the network represent individuals and the links represent the interactions between individuals, it may be possible to target specific individuals for vaccination, but preventing specific individual-individual interactions is likely not a feasible strategy.

Although many previous research studied the evolution of an spread of infection with respect to link removal, only a small portion of them studied link removal methods that minimize the spread of infections. The algorithm proposed by Tong et al. [47] is based on the finding that the leading eigenvalue of the network adjacency matrix determines whether a spread will turn into an epidemic [51,39]. They report the effectiveness of their algorithm by showing that it reduces the leading eigenvalue more than other eigenvalues. They also report the effectiveness based on the comparison of the fraction of infected nodes produced by a simulation. However, they do not use information about which nodes are infected and which are not in the link selection mechanism. Also, they do not compare their effectiveness with any existing well-known link removal methods. The algorithm proposed by Kimura et al. [25] is based on bond percolation. The main virtue of the algorithm proposed by Tong et al. [47] and the algorithm along with the speeding mechanism proposed by Kimura et al. [25] is that they are fast. Kimura et al. [25] evaluate the effectiveness of their algorithm in terms of an indirect measure called contamination degree. The model proposed by Enns et al. [18] minimizes connectivity between infectious and susceptible nodes, and later in a subsequent work, Enns et al. [17] compare the effectiveness of the model along with some other link removal approaches. Although Enns et al. [18] present a heuristic procedure, it is unclear if their non-linear programming formulation can

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