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Link removal for the control of stochastically evolving epidemics over networks: A comparison of approaches

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HIGHLIGHTS

- Disease control efforts are often constrained by limited resources.
- Limited resources can be used more effectively by leveraging network information.
- We compare four link removal algorithms to prevent disease spread under a budget.
- Optimal quarantining performs best for large budgets and structured networks.
- Knowing where an outbreak begins is most valuable at moderate budget levels.

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ABSTRACT

For many communicable diseases, knowledge of the underlying contact network through which the disease spreads is essential to determining appropriate control measures. When behavior change is the primary intervention for disease prevention, it is important to understand how to best modify network connectivity using the limited resources available to control disease spread. We describe and compare four algorithms for selecting a limited number of links to remove from a network: two “preventive” approaches (edge centrality, R_0 minimization), where the decision of which links to remove is made prior to any disease outbreak and depends only on the network structure; and two “reactive” approaches (S–I edge centrality, optimal quarantining), where information about the initial disease states of the nodes is incorporated into the decision of which links to remove. We evaluate the performance of these algorithms in minimizing the total number of infections that occur over the course of an acute outbreak of disease. We consider different network structures, including both static and dynamic Erdős–Rényi random networks with varying levels of connectivity, a real-world network of residential hotels connected through injection drug use, and a network exhibiting community structure. We show that reactive approaches outperform preventive approaches in averting infections. Among reactive approaches, removing links in order of S–I edge centrality is favored when the link removal budget is small, while optimal quarantining performs best when the link removal budget is sufficiently large. The budget threshold above which optimal quarantining outperforms the S–I edge centrality algorithm is a function of both network structure (higher for unstructured Erdős–Rényi random networks compared to networks with community structure or the real-world network) and disease infectiousness (lower for highly infectious diseases). We conduct a value-of-information analysis of knowing which nodes are initially infected by comparing the performance improvement achieved by reactive over preventive strategies. We find that such information is most valuable for moderate budget levels, with increasing value as disease spread becomes more likely (due to either increased connectedness of the network or increased infectiousness of the disease).

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1. Introduction

Despite remarkable progress in the past century, infectious diseases continue to cause millions of deaths worldwide every year (Fauci, 2001; Morens et al., 2004; Arias and Murray, 2009). A variety of approaches can be used to prevent such diseases and control their spread, including vaccination, treatment, changing

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risk behaviors, and quarantining. However, implementation of these measures is often constrained by limited budgets, time, and/or personnel, necessitating difficult decisions about how to best allocate these scarce resources to prevent disease spread.

The way in which individuals and populations come into contact with each other influences how a disease spreads as well as which control measures are most effective. These contact patterns can be represented as a contact network, with nodes representing individuals (or groups of individuals) and links representing contacts that have the potential for disease transmission from one node to another. Different aspects of network structure have been demonstrated to influence the severity of an epidemic and the speed and extent of its spread (Ganesh et al., 2005; Chakrabarti et al., 2008; Youssef and Scoglio, 2011; Watts and Strogatz, 1998; Newman and Watts, 1999; Moore and Newman, 2000; Jackson and Rogers, 2007; May and Lloyd, 2001; Pastor-Satorras and Vespignani, 2001, 2002a; Eames, 2008; Miller, 2009; Newman, 2003; House and Keeling, 2011). For example, for the same average number of contacts, an epidemic is more likely to occur in networks with highly heterogeneous contact distributions (Jackson and Rogers, 2007; May and Lloyd, 2001; Pastor-Satorras and Vespignani, 2001, 2002a). This is illustrated in the extreme in the so-called “scale-free” networks, where a small number of highly-connected nodes act as hubs that facilitate rapid, near-unstoppable disease spread (Pastor-Satorras and Vespignani, 2001, 2002a). In contrast, diseases spread more slowly and less diffusely in highly clustered networks (Eames, 2008; Miller, 2009; Newman, 2003; House and Keeling, 2011); though a disease may quickly spread locally within a densely connected cluster, it is less likely to escape the cluster and cause a global outbreak in the network.

Given the importance of network structure to disease spread, it is natural to consider whether and how network information can be used to design more effective disease control interventions. A variety of analyses have shown that interventions that make use of network information outperform those that do not (Pastor-Satorras and Vespignani, 2002b; Eubank et al., 2004; Miller and Hyman, 2007; Hartvigsen et al., 2007; Salathé and Jones, 2010; Marcelino and Kaiser, 2009). For example, Miller and Hyman (2007) compared different vaccination strategies in a simulation model of person-to-person contact in Portland, Oregon. They found that vaccinating individuals with the greatest number of unvaccinated contacts was more effective than random vaccination or vaccinating nodes with the highest number of contacts. Marcelino and Kaiser (2009) investigated flight cancellation as a means of preventing disease spread between cities over the global air travel network. They showed that canceling individual flight routes with the greatest edge centrality (a measure of a link’s importance in maintaining the connectivity of the network) was more effective than simply shutting down airports with the greatest number of flights.

Prior work on how to use network information to target interventions in a population has primarily focused on vaccinating critical nodes in the network to prevent disease spread (Pastor-Satorras and Vespignani, 2002b; Eubank et al., 2004; Miller and Hyman, 2007; Hartvigsen et al., 2007). However, for many diseases, including hepatitis C, HIV, many sexually transmitted infections, and emerging influenza strains, a vaccine does not currently exist and behavior change remains the primary intervention. In such cases, a network-based intervention might instead focus on the *interactions* between nodes that are particularly critical to disease spread.

A number of link removal approaches have been proposed. These can be broadly classified along two dimensions. The first is whether an approach is preventive or reactive. A preventive strategy seeks to modify the network prior to an outbreak to make the network less conducive to disease spread (Marcelino and Kaiser, 2009; Bishop and Shames, 2011), while a reactive strategy assumes that the disease is detected prior to intervention and information about which nodes are initially infected is used to guide how links should be removed to

prevent *further* disease spread (Enns et al., 2012). In general, one would expect reactive strategies to outperform preventive strategies because of the availability of additional information. However, it is unclear under what conditions this additional information is most valuable and when it is unnecessary. The second dimension is whether a strategy is rank-based or optimization-based. Rank-based strategies remove links in order of a link’s “importance” to the network, which may be measured in terms of a link’s betweenness centrality (Girvan and Newman, 2002; Marcelino and Kaiser, 2009), bridgeness (Cheng et al., 2010), or a variety of other metrics (Borgatti and Everett, 2006; De Meo et al., 2012). In contrast, optimization-based strategies consider link removal more holistically and identify a specific set of links to remove, which will change depending on the link removal budget (Bishop and Shames, 2011; Enns et al., 2012). Because there is no closed-form expression for the expected number of infections over the course of a disease outbreak in a contact network, optimization-based strategies must instead be formulated in terms of surrogate objective functions relating to network structure. The characterization of optimization-based strategies has therefore focused on establishing the algorithm’s performance in inducing the desired change in network structure. A systematic evaluation of the impact of optimization-based link removal strategies on the expected number of infections during an outbreak has not yet been done.

In this paper, we compare four approaches to link removal, spanning the four possible combinations of the preventive/reactive and rank-based/optimization-based dimensions. In previous work, we described an optimization-based approach to quarantining infected nodes through link removal under resource constraints and evaluated its performance in separating initially infected and susceptible nodes in a static scenario (Enns et al., 2012). In this paper, we evaluate this optimal quarantining approach and other link removal algorithms as interventions to minimize the expected number of infections over the course of a stochastically evolving epidemic. In contrast to our prior work, where we only considered whether a susceptible node could become infected, not the likelihood of infection, this analysis incorporates the differential risks of infection faced by susceptible nodes based on their position in the network relative to those initially infected as well as the possibility of an outbreak dying out due to random chance.

In Section 2, we outline the link removal problem and describe the four link removal algorithms with their underlying rationale. In Section 3, we simulate acute outbreaks of disease for a variety of disease characteristics and contact network structures (including stochastically evolving networks) and compare the performance of the link removal approaches in terms of the expected final outbreak size as a function of the number of links that can be removed. We evaluate the value of (perfect) surveillance information – that is, the value of knowing which nodes are initially infected – by comparing the relative performance of reactive vs. preventive strategies. We also consider algorithm performance in the case of imperfect surveillance information. Based on the results of these experiments, in Section 4, we conclude with a summary of the network, disease, and budgetary conditions under which different link removal approaches perform best and surveillance information is most valuable.

2. Link removal algorithms

We consider a population of size N interacting through a contact network, represented by an undirected $N \times N$ adjacency matrix, A , where $A_{ij} = 1$ if node i and node j are connected (meaning that individual i can transmit disease to individual j); otherwise, $A_{ij} = 0$. Because we consider the case of an undirected network and symmetric disease transmission, if $A_{ij} = 1$ then $A_{ji} = 1$. We assume that a disease is introduced at time $t=0$, with a small number of

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