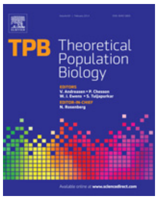
Theoretical Population Biology 106 (2015) 83–93

Contents lists available at ScienceDirect

Theoretical Population Biology

journal homepage: www.elsevier.com/locate/tpb



On the impact of epidemic severity on network immunization algorithms

Bita Shams, Mohammad Khansari *

University of Tehran, Faculty of New Sciences and Technologies, Amir Abad, North Kargar Street, Tehran, 1439957131, Iran

HIGHLIGHTS

- Interaction of the immunization algorithms, epidemic trials and network structure is investigated.
- Immunization algorithms are applied to various real and model networks.
- Degree-based immunization algorithms are more efficient in mitigation of weak epidemics.
- Network largest component size is a vital element in spreading of severe epidemics.

ARTICLE INFO

Article history:
Received 30 April 2014
Available online 23 October 2015

Keywords:
Complex networks
Immunization algorithms
Epidemic model
Infection rate
Graph

ABSTRACT

There has been much recent interest in the prevention and mitigation of epidemics spreading through contact networks of host populations. Here, we investigate how the severity of epidemics, measured by its infection rate, influences the efficiency of well-known vaccination strategies. In order to assess the impact of severity, we simulate the SIR model at different infection rates on various real and model immunized networks. An extensive analysis of our simulation results reveals that immunization algorithms, which efficiently reduce the nodes' average degree, are more effective in the mitigation of weak and slow epidemics, whereas vaccination strategies that fragment networks to small components, are more successful in suppressing severe epidemics.

1. Introduction

A range of infectious disease outbreaks has been reported in the last decades. Influenza outbreaks have occurred in large public gatherings such as the 2002 winter Olympics in the USA, 2008 Olympics in Beijing, and the 2009 music festivals in Belgium (Chowell et al., 2012). A large number of Toronto residents got infected during an outbreak of the severe acute respiratory syndrome (SARS) in 2003 (Svoboda et al., 2004). In 2010, measles outbreaks of various sizes occurred in a majority of European Union countries (Steffens et al., 2010). Severe outbreaks of infectious diseases do not only have great impacts on social life and healthcare, but they also affect the economy through productivity degradation and high cost of treatment (Hadidjojo and Cheong, 2011). Hence, it is crucial to develop an effective strategy to prevent and control epidemic spreading through the population.

Some of the traditional epidemic intervention procedures such as quarantine involve weakening or cutting the relationships (Hadidjojo and Cheong, 2011). Vaccination is another strategy which not only protects immunized people, but also indirectly protects their friends by breaking transmission chains and reducing risk of infection (Cornforth et al., 2011). From an economical perspective, mass vaccination (i.e. vaccinating the entire population) is not always feasible because of high cost and limitation of vaccination units (Chen et al., 2008; Restrepo et al., 2006; Schneider et al., 2011). Therefore, an efficient immunization policy is required to minimize immunization costs as well as the number of infected individuals.

The study of mathematical models for epidemic has a long history reaching back to 1920s when Kermack and Kendrick established the first birth–death model of epidemic spreading (Lewis, 2009). By the end of the twentieth century, a variety of models had been proposed to more accurately represent epidemics dynamic. However, the majority neglect population variability in age, sex, contact rate, individual behavior, spatial patterning, etc. (Hartvigsen et al., 2007; Lewis, 2009; Miller and Hyman, 2007; Reluga, 2010; Ventresca and Aleman, 2013). Therefore, a series

---

* Corresponding author.
E-mail addresses: shams.bita@ut.ac.ir (B. Shams), m.khansari@ut.ac.ir (M. Khansari).

http://dx.doi.org/10.1016/j.tpb.2015.10.007
0040-5809/

of deterministic and stochastic compartmental models has been proposed to capture the heterogeneity in contact patterns (Ferguson et al., 2003; Keeling et al., 1997; Lefevre and Picard, 1989; Meyers, 2006; Yorke et al., 1989). Network epidemic is a recent advancement in epidemiology taking into account heterogeneous social structures of real population (Cai et al., 2014; Lewis, 2009; Meyers, 2006; Ventresca and Aleman, 2013).

Network epidemic studies dynamics of epidemic spreading through contact networks of host populations. A contact network is an undirected graph where nodes represent individuals and edges represent the relationship between pairs of individuals (Salathé and Jones, 2010; Youssef and Scoglio, 2011). Due to faster dynamics of epidemics than changes in host populations, a static snapshot of contact networks is commonly considered in the literature (Christley et al., 2005; Eubank et al., 2004; Ferrari et al., 2006; Kitchovitch and Liò, 2011; Schneider et al., 2012; Youssef and Scoglio, 2011). A great deal of research has been carried out both on network modeling of epidemic spreading (Eubank et al., 2004) and on finding the relations between network structure and epidemic parameters (Ames et al., 2011; Chakrabarti and Faloutsos, 2003; Chakrabarti et al., 2008; Youssef and Scoglio, 2011). The results have provided major insights into the development of new immunization strategies. A large number of immunization algorithms have been proposed based on immunizing hubs (i.e. the nodes with highest degree) in networks (Cohen et al., 2003; Dezső and Barabási, 2002; Gallos et al., 2007; Gao et al., 2011; Gómez-Gardeñes et al., 2006; Hu and Tang, 2012; Pastor-Satorras and Vespignani, 2002). The community structure of real networks has made it possible to immunize intercommunal individuals who play an important role in infectious propagation among different communities (Hébert-Dufresne et al., 2013; Masuda, 2009; Salathé and Jones, 2010; Yamada and Yoshida, 2012; Yoshida and Yamada, 2012). There is another group of immunization schemes that attempts to raise the epidemic threshold by reduction of largest eigenvalue of network adjacency matrix (Chakrabarti and Faloutsos, 2003; Chakrabarti et al., 2008; Peng et al., 2010). Recently, several other immunization approaches have been put forward that focus on reducing the size of the largest connected component (i.e. set of vertices that are reachable from each other) of the network of non-immunized nodes in order to reduce worst-case epidemic size (Schneider et al., 2012, 2011; Shams and Khansari, 2013).

In spite of these efforts, a comprehensive analysis on performance of immunization algorithms has never been reported to our knowledge. Although several experiments have been conducted in order to evaluate immunization algorithms (see Table 1), they have significant shortcomings. Firstly, only a small number of efficient immunization algorithms are included (Schneider et al., 2012, 2011). Secondly, experiments are conducted based on a single network (Eames et al., 2009; Miller and Hyman, 2007; Ventresca and Aleman, 2013) or network structure (Hartvigsen et al., 2007). Thirdly, only structural properties are considered (Masuda, 2009; Schneider et al., 2012; Shams and Khansari, 2014; Ventresca and Aleman, 2013). And fourthly, none of these studies has considered the impact of epidemic severity on immunization algorithms (Hartvigsen et al., 2007; Ma et al., 2013; Salathé and Jones, 2010; Shams and Khansari, 2014; Ventresca and Aleman, 2013).

In this paper, we aim to address the question of how immunization algorithms reduce the number of infected individuals with regard to the severity of disease and the structure of the network. In this paper, we express the epidemic severity in terms of its infection rate. To overcome the challenge, we simulate the SIR model with different infection rates on various real and model networks which are immunized by well-known vaccination strategies.

2. Immunization strategies

In the last decade, a number of immunization algorithms have been developed. Here, we explore six immunization strategies including degree immunization, effective degree immunization, betweenness immunization, eigenvector immunization, PageRank immunization, and stochastic hill-climbing immunization which are regarded as the most efficient strategies according to literature (Chen et al., 2008; Gallos et al., 2007; Hartvigsen et al., 2007; Hu and Tang, 2012; Masuda, 2009; Miller and Hyman, 2007; Restrepo et al., 2006; Salathé and Jones, 2010; Schneider et al., 2012, 2011; Ventresca and Aleman, 2013; Vidondo et al., 2012). In addition to these popular approaches, we exploit random immunization as a control means of performance evaluation.

2.1. *Degree immunization*

Degree immunization (DI) algorithm immunizes nodes who have the highest number of interactions in the population (Dezső and Barabási, 2002; Hu and Tang, 2012; Pastor-Satorras and Vespignani, 2002). Since the nodes with higher degree are more likely to spread disease due to their higher connections, vaccinating them reduces the contagion propagation through the population (Ventresca and Aleman, 2013). Furthermore, immunizing hubs quickly reduces network density, which is an important factor in the growth rate of the epidemic (Hadidjojo and Cheong, 2011).

2.2. *Effective degree immunization*

Effective degree immunization (EDI) is a modification of degree immunization which recalculates degree of vertices after immunization (i.e. removal) of highest degree node (Chen et al., 2008; Hu and Tang, 2012; Miller and Hyman, 2007; Schneider et al., 2012). The idea behind this algorithm is that immunization of a node reduces the degree of its neighbors. So, vaccination of nodes based on their degree in initial network is not always the most efficient algorithm. Therefore, it is recommended to immunize nodes based on their effective degree which is their degree in the current network of non-immunized nodes during the immunization procedure (Hu and Tang, 2012). This algorithm is also known as highest degree adaptive immunization in the literature (Chen et al., 2008; Schneider et al., 2012, 2011).

2.3. *Betweenness immunization*

Betweenness immunization (BI) prioritizes nodes for vaccination regarding their betweenness centrality which is the proportion of time a node lies on the shortest path between other nodes (Freeman, 1978). Nodes with high betweenness centrality, so-called bridge nodes, connect different communities of networks (Hébert-Dufresne et al., 2013; Salathé and Jones, 2010). Therefore, their removal via vaccination breaks lots of transmission chains an infection that starts in a quota cannot easily propagate to other parts of the population.

2.4. *Eigenvector immunization*

Eigenvector centrality of a node, the principal eigenvector of the adjacency matrix of network, provides a measure of nodal infectious risk according to the risk level of its neighbors (Bonacich, 1987; Borgatti, 2005). Additionally, it has been proved that eigenvector centrality determines the impact of node removal on decreasing the largest eigenvalue of network adjacency matrix (Masuda, 2009; Restrepo et al., 2006) which is the inverse of epidemic threshold (Chakrabarti and Faloutsos, 2003; Chakrabarti et al., 2008; Masuda, 2009; Peng et al., 2010; Restrepo et al., 2006; Youssef and Scoglio, 2011). Network epidemic threshold is a quantity which determines whether an infection dies out over