Data Min Knowl Disc (2015) 29:423–465
DOI 10.1007/s10618-014-0351-4

Inhibiting diffusion of complex contagions in social networks: theoretical and experimental results

Chris J. Kuhlman · V. S. Anil Kumar · Madhav V. Marathe · S. S. Ravi · Daniel J. Rosenkrantz

Received: 26 February 2013 / Accepted: 22 April 2014 / Published online: 14 May 2014

Abstract We consider the problem of inhibiting undesirable contagions (e.g. rumors, spread of mob behavior) in social networks. Much of the work in this context has been carried out under the 1-threshold model, where diffusion occurs when a node has just one neighbor with the contagion. We study the problem of inhibiting more complex contagions in social networks where nodes may have thresholds larger than 1. The goal is to minimize the propagation of the contagion by removing a small number of nodes (called **critical nodes**) from the network. We study several versions of this problem and prove that, in general, they cannot even be efficiently approximated to within any factor $\rho \geq 1$, unless **P** = **NP**. We develop efficient and practical heuristics for these problems and carry out an experimental study of their performance on three well known social networks, namely `epinions`, `wikipedia` and `slashdot`. Our results show that these heuristics perform significantly better than five other known methods. We also establish an efficiently computable upper bound on the number of nodes to which a contagion can spread and evaluate this bound on many real and synthetic networks.

Keywords Complex contagions · Blocking · Social networks

Responsible editor: Tina Eliassi-Rad

C. J. Kuhlman (✉) · V. S. Anil Kumar · M. V. Marathe
Virginia Bioinformatics Institute, Virginia Tech, Blacksburg, VA 24061, USA
e-mail: ckuhlman@vbi.vt.edu

S. S. Ravi · D. J. Rosenkrantz
Department of Computer Science, University at Albany–SUNY, 1400 Washington Avenue, Albany, NY 12222, USA

1 Introduction and motivation

Analyzing social networks has become an important topic in the data mining community (Richardson and Domingos 2002; Domingos and Richardson 2001; Kempe et al. 2003, 2005; Chakrabarti et al. 2008; Tantipathananandh et al. 2007; Anderson et al. 2012). Many researchers have studied diffusion processes in social networks. Some examples are the propagation of favorite photographs in a Flickr network (Cha et al. 2008), the spread of information (Gruhl et al. 2004; Kossinets et al. 2008) via Internet communication, the effects of online purchase recommendations (Leskovec et al. 2007), formation of online communities (Shi et al. 2009), hashtag propagation in Twitter (Romero et al. 2011), and virus propagation between computers (Pastor-Satorras and Vespignani 2001). In some instances, models of diffusion are combined with data mining to predict social phenomena; e.g., product marketing (Domingos and Richardson 2001; Richardson and Domingos 2002), trust propagation (Guha et al. 2004), and epidemics through social contacts (Martin et al. 2011). Furthermore, coupled processes of network and dynamics evolutions are studied with comparisons against experimental data (Centola et al. 2007; Centola 2010); see Vespignani (2012) for an overview.

Here, we are interested in a particular class of diffusion, that of **complex contagions**. As stated in Centola and Macy (2007), "Complex contagions require social affirmation from multiple sources." That is, a person acquires a complex social contagion through interaction with $t > 1$ other individuals, as opposed to only a single individual (i.e., $t = 1$). The latter is called a **simple contagion**, perhaps the most notable of which are disease propagation (Pastor-Satorras and Vespignani 2001; Longini et al. 2005) and computer virus transmission (Jin et al. 2009).

The idea of complex contagions dates back to at least the 1960s as described in (Granovetter 1978; Schelling 1978), and more current studies are referenced in (Centola and Macy 2007; Barash et al. 2012; Barash 2011). Such phenomena, according to these researchers, include diffusion of innovations, spread of rumors and worker strikes, educational attainment, fashion trends, and growth of social movements. For example, in strikes, mob violence, and political upheavals, individuals can be reluctant to participate for fear of reprisals to themselves and their families. It is safer for one to wait for a critical mass of one's acquaintances to commit before committing oneself. These models are concerned with the onset of a behavior and thus focus on the transition from non-participating to participating. Like many epidemic models, they use only one active or contagious state. A notable exception is the threshold model of Melnik et al. (2013) which uses two such states, with different strengths of contagion associated with them. Here, we use a contagion model with one active state.

Crucially, recent data mining analyses and experiments have provided evidence for complex contagion dynamics on appropriate social networks. Examples include online DVD purchases (Leskovec et al. 2007), teenage smoking initiation (Harris 2008; Kuhlman et al. 2011), spread of health-related information (Centola 2010), joining LiveJournal (Kleinberg 2007), and recruitment of people to join Facebook (Ugander et al. 2012).

The threshold model that we employ in this work has been used by many social scientists (e.g., Granovetter 1978; Watts 2002; Centola and Macy 2007) to understand social behaviors. It is argued in (Watts 2002) that threshold dynamics may be used in several situations where more detailed human reasoning is precluded. In a recent study (Gonzalez-Bailon et al. 2011), joining a protest in Spain in 2011 was analyzed through Twitter messages. In that study, deterministic thresholds[1] were used to explain the onset of user involvement in the protest.

Another motivation for our work is from recent quantitative work (Centola and Macy 2007; Centola 2009) showing that simple contagions and complex contagions can differ significantly in behavior. It is well known (Granovetter 1973) that weak edges play a dominant role in spreading a simple contagion between clusters within a population, thereby dictating whether a contagion will reach a large segment of a population. However, for complex contagions, this effect is greatly diminished (Centola and Macy 2007). Another difference between simple and complex contagions, discussed in (Centola 2009), is the following: scale-free (SF) communication graphs (i.e., those with power-law degree distributions) show high tolerance for random node failures (i.e., diffusion can still reach the majority of nodes when nodes are removed randomly from the network) for simple contagions, but have low tolerance to random failures for complex contagions.

Additional differences between simple and complex contagions are presented in this paper, where the focus is on the problem of finding agents (called critical nodes) in a population that will thwart the spread of complex contagions. In particular, our theoretical results (presented in Sect. 4) show that one variant of this problem can be solved efficiently for simple contagions, while it is computationally intractable for complex contagions. Furthermore, we show experimentally that several effective heuristics (Habiba et al. 2008; Bonacich 1972; Kleinberg 1999; Tong et al. 2010) for determining critical nodes for simple contagions perform poorly in stopping complex contagions. Thus, our results point out some fundamental differences between simple and complex contagions with respect to diffusion.

Computing effective sets of critical nodes is important because it has wide applicability in several domains of network dynamics. Examples include thwarting the spread of sensitive information that has been leaked (Chakrabarti et al. 2008), disrupting communication of adversaries (Arulselvan et al. 2009), marketing to counteract the advertising of a competing product (Richardson and Domingos 2002; Domingos and Richardson 2001), calming a mob (Granovetter 1978), or changing people's opinions (Dreyer and Roberts 2009). Indeed, contagion dynamics with critical nodes have been used in several domains, including peer influence in youth behavior, repression of social movements, opinion dynamics, and social isolation in epidemiology (Albert et al. 2000; Mobilia 2003; Mobilia et al. 2007; Kawachi 2008; Centola 2009; Siegel 2010; Salathe and Jones 2010; Acemoglu and Ozdaglar 2011; Yildiz et al. 2011). But these studies overwhelmingly use simple contagion dynamics and/or simple heuristics for determining critical nodes (e.g. using high degree nodes). For complex contagions, we provide diffusion blocking methods that are

[1] That work uses relative thresholds, whereas we use absolute thresholds (see Sect. 2.3 for definitions). Since these threshold values differ only by a scaling factor, our results readily extend to relative thresholds.

far better than such methods. More generally, inhibiting diffusion is one aspect of a broader goal of *controlling* diffusion in complex networks as advocated in (Liu et al. 2011).

Another aspect of our work complements previous studies of contagion blocking. Many previous works (Albert et al. 2000; Barash 2011; Habiba et al. 2008; Centola 2009; Tong et al. 2010) assume that the seed set—the set of nodes initially possessing a contagion—is unknown and a single set of critical nodes is selected to halt diffusion from any seed set. Here, we study the contagion blocking problem assuming that the seed set is known. We compare our methods' results with those from several others, and demonstrate the improved performance that can be realized with this extra information.

Following (Granovetter 1978; Schelling 1978; Watts 2002; Centola and Macy 2007), we utilize a two-state system where nodes in state 0 (1) do not (do) possess the contagion. A node transitions from state 0 to state 1 if the number of its neighbors in state 1 is at least a specified threshold t. Nodes may *not* transition back to state 0 from state 1 (Macy 1991; Kempe et al. 2003; Siegel 2009; Gonzalez-Bailon et al. 2011; Ugander et al. 2012). Critical nodes are initially in state 0, and remain in state 0 throughout the diffusion process, regardless of the states of their neighbors, and thereby retard contagion propagation.

Overview of contributions We formulate several variants of the problem of finding a smallest critical set and prove that, in general, they cannot even be efficiently approximated to within any factor $\rho \geq 1$, unless **P** = **NP**. These results motivate the development and evaluation of two practical heuristics for finding critical sets. We compare our methods against five state-of-the-art methods and demonstrate that our methods are much more effective in blocking diffusion of complex contagions. We also provide a detailed set of blocking results to understand the range of applicability and the limitations of our methods. Finally, using thousands of networks, we critically evaluate a method to bound the maximum possible (MP) spread size (i.e., the maximum number of nodes to which a contagion can spread) in a network, which is useful in quantifying the effectiveness of blocking schemes. (A detailed summary of results is provided in Sect. 3.1.)

Paper organization Section 2 describes the model employed in this work and develops problem formulations. Section 3 contains a summary of our main results and related work. Theoretical results are provided in Sect. 4. Our two heuristics are described in Sect. 5. Section 6 contains experimental results on blocking, including the experimental setup, comparisons against five state-of-the-art blocking methods, and further results over a larger parameter space. We present in Sect. 7 theoretical and experimental results for maximum spread sizes of complex contagions in social networks. Conclusions and future work constitute Sect. 8.

This paper combines and extends the results in a conference paper (Kuhlman et al. 2010b) and a workshop paper (Kuhlman et al. 2010a). The former contains preliminary versions of the results in Sect. 4 through 6, while the latter contains a preliminary version of the results in Sect. 7.

2 Dynamical system model and problem formulation

2.1 System model and associated definitions

We model the propagation of complex contagions over a social network using discrete dynamical systems (Barrett et al. 2006, 2007). We begin with the necessary definitions.

Let $\mathbb{B}$ denote the Boolean domain {0,1}. A **Synchronous Dynamical System** (SyDS) $\mathcal{S}$ over $\mathbb{B}$ is specified as a pair $\mathcal{S} = (G, \mathcal{F})$, where

(a) $G(V, E)$, an undirected graph with a set V of n nodes and a set E of m edges, represents the underlying social network over which the contagion propagates, and
(b) $\mathcal{F} = \{f_1, f_2, \ldots, f_n\}$ is a collection of functions, with f_i denoting the **local transition function** associated with node v_i, $1 \le i \le n$.

Each function f_i specifies the local interaction between node v_i and its neighbors in G. To provide additional details regarding these functions, we note that each node of G has a state value from $\mathbb{B}$. To encompass various types of social contagions described in Sect. 1, nodes in state 0 (1) are said to be **unaffected** (**affected**). Thus, in the case of information flow, for example, an affected node has received the information and will pass it on. It is assumed that once a node reaches the state 1, it cannot return to state 0. We refer to a discrete dynamical system with this property as a **ratcheted dynamical system**. (Other names such as "progressive systems" (Kleinberg 2007) and "irreversible systems" (Dreyer and Roberts 2009) have also been used.)

We can now formally describe the local transition functions. The inputs to function f_i are the state of v_i and those of the neighbors of v_i in G; function f_i maps each combination of inputs to a value in $\mathbb{B}$. For the propagation of contagions in social networks, it is natural to model each function f_i $(1 \le i \le n)$ as a t_i**-threshold function** (Eubank et al. 2006; Chakrabarti et al. 2008; Dreyer and Roberts 2009; Centola et al. 2006; Centola and Macy 2007; Kempe et al. 2003; Kleinberg 2007) for an appropriate nonnegative integer t_i. Such a threshold function (taking into account the ratcheted nature of the dynamical system) is defined as follows.

(a) If the state of v_i is 1, then the value of f_i is 1, regardless of the values of the other inputs to f_i.
(b) If the state of v_i is 0, then the value of f_i is 1 if at least t_i of the inputs are 1; otherwise, the value of f_i is 0.

A **configuration** $\mathcal{C}$ of a SyDS at any time is an n-vector $(s_1, s_2, \ldots, s_n)$, where $s_i \in \mathbb{B}$ is the value of the state of node v_i $(1 \le i \le n)$. A single SyDS transition from one configuration to another can be expressed by the following pseudocode.

```
for each node $v_i$ do in parallel
  (i) Compute the value of $f_i$. Let $s_i'$ denote this value.
  (ii) Update the state of $v_i$ to $s_i'$.
end for
```

Thus, in a SyDS, nodes update their state *synchronously*. Other update disciplines (e.g. sequential updates) for discrete dynamical systems have also been considered in the literature (Barrett et al. 2006, 2007).

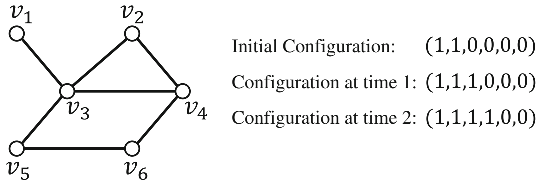

v_1
v_2
v_3
v_4
v_5
v_6
Initial Configuration: (1,1,0,0,0,0)
Configuration at time 1: (1,1,1,0,0,0)
Configuration at time 2: (1,1,1,1,0,0)

Fig. 1 An example of a synchronous dynamical system. Each configuration has the form $(s_1, s_2, s_3, s_4, s_5, s_6)$ where s_i is the state of node v_i, $(1 \leq i \leq 6)$. The configuration at time 2 is a fixed point

If a SyDS has a transition from configuration $\mathcal{C}$ to configuration $\mathcal{C}'$, we say that $\mathcal{C}'$ is the **successor** of $\mathcal{C}$ and that $\mathcal{C}$ is a **predecessor** of $\mathcal{C}'$. A configuration $\mathcal{C}$ is called a **fixed point** if the successor of $\mathcal{C}$ is $\mathcal{C}$ itself.

Example Consider the graph shown in Fig. 1. Suppose the local interaction function at each node is the 2-threshold function. Initially, v_1 and v_2 are in state 1 and all other nodes are in state 0. During the first time step, the state of node v_3 changes to 1 since two of its neighbors (namely v_1 and v_2) are in state 1; the states of other nodes remain the same. In the second time step, the state of node v_4 changes to 1 since two of its neighbors (namely v_2 and v_3) are in state 1; again the states of the other nodes remain the same. The resulting configuration (1, 1, 1, 1, 0, 0) is a fixed point for this system.

The SyDS in the above example reached a fixed point. This is not a coincidence. The following simple result shows that every ratcheted dynamical system over $\mathbb{B}$ reaches a fixed point.

Proposition 1 *Every ratcheted discrete dynamical system over* $\mathbb{B}$ *reaches a fixed point in at most n transitions, where n is the number of nodes in the underlying graph.*

Proof Consider any ratcheted dynamical system $\mathcal{S}$ over $\mathbb{B}$. In any transition of $\mathcal{S}$ from one configuration to another, nodes can only change from 0 to 1 (but not from 1 to 0). Thus, after at most n transitions where nodes change from 0 to 1, there can be no more state changes, i.e., $\mathcal{S}$ reaches a fixed point. □

In the context of opinion propagation, reaching a fixed point means that everyone has formed an unalterable opinion, and hence will not change their mind.

2.2 Problem formulation

For simplicity, statements of problems and results in this paper use terminology from the context of information propagation in social networks, such as that for social unrest. It is straightforward to interpret the results for other contagions.

Suppose we have a social network in which some nodes are initially affected. In the absence of any action to contain the unrest, it may spread to a large part of the population. Decision-makers must decide on suitable actions (interventions) to inhibit information spread, such as quarantining a subset of people. Usually, there are resource constraints or societal pressures to keep the number of isolated people to a minimum (e.g., quarantining too many people may fuel unrest or it may be difficult to apprehend particular individuals). Thus, the problem formulation must take into account both information containment and appropriate resource constraints.

We assume that only people who are as yet unaffected can be quarantined. Under the dynamical system model, quarantining a person is represented by removing the corresponding node (and all the edges incident on that node) from the graph. Equivalently, removing a node v corresponds to changing the local transition function at v so that v's state remains 0 for all combinations of input values. The goal of isolation is to minimize the number of new affected nodes that occur over time until the system reaches a fixed point (when no additional nodes can be affected). We use the term **critical set** to refer to the set of nodes removed from the graph to reduce the number of newly affected nodes. Resource constraints can be modeled as a budget constraint on the size of the critical set. We can now provide a precise statement of the problem of finding critical sets. (This problem was first formulated in (Eubank et al. 2006) for the case where each node computes a 1-threshold function.)

2.2.1 *Smallest critical set to minimize the number of new affected nodes (SCS-MNA)*

Given A social network represented by the SyDS $\mathcal{S} = (G(V, E), \mathcal{F})$ over $\mathbb{B}$, with each function $f \in \mathcal{F}$ being a threshold function; the set I of nodes which are initially in state 1 (the elements of I are called **seed nodes**); an upper bound β on the size of the critical set.
Requirement A critical set $C \subseteq V - I$ such that $|C| \leq \beta$ and among all subsets of $V - I$ of size at most β, the removal of C from G leads to the smallest number of new affected nodes.

An alternative formulation, where the objective is to maximize the number of nodes who are not affected, can also be considered. We use the name “Smallest Critical Set to Maximize Unaffected Nodes” for this problem and abbreviate it as SCS-MUN. To maintain the complementary relationship between the minimization (SCS-MNA) and maximization (SCS-MUN) versions, we assume that critical nodes are not included in the set of unaffected nodes in the formulation of SCS-MUN. With that assumption, any optimal solution for SCS-MUN is also an optimal solution for SCS-MNA. Our results in Sect. 4 provide an indication of the difficulties in obtaining provably good approximation algorithms for either version of the problem. So, our focus is on obtaining heuristics that work well in practice.

We also consider the problem of finding critical sets in a related context. Let $\mathcal{S} = (G(V, E), \mathcal{F})$ be a SyDS and let $I \subseteq V$ denote the set of seed nodes. We say that a node $v \in V - I$ is **salvageable** if there is a critical set $C \subseteq V - (I \cup \{v\})$ whose removal ensures that v remains in state 0 when the modified SyDS (i.e., the SyDS obtained by removing C) reaches a fixed point. Otherwise, v is called an **unsalvageable** node. Thus, in any SyDS, only salvageable nodes can possibly be saved from becoming affected.

Example Consider the 2-threshold SyDS shown in Fig. 1. Node v_4 in that figure is salvageable since removal of v_3 ensures that v_4 won't be affected. Nodes v_5 and v_6 are salvageable since they are not affected even when no nodes are removed from the system. However, node v_3 is not salvageable since it has two neighbors (v_1 and v_2) who are initially affected.

We now formulate a problem whose goal is to find a smallest critical set that saves all salvageable nodes.

2.2.2 *Smallest critical set to save all salvageable nodes (SCS-SASN)*

Given A social network represented by the SyDS $\mathcal{S} = (G(V, E), \mathcal{F})$ over $\mathbb{B}$, with each function $f \in \mathcal{F}$ being a threshold function; the set I of seed nodes which are initially in state 1.
Requirement A critical set $C \subseteq V - I$ of minimum cardinality whose removal ensures that all salvageable nodes are saved from being affected.

As will be shown in Sect. 4, the complexity of the SCS-SASN problem for simple contagions is significantly different from that for complex contagions.

2.3 Types of thresholds

In the above discussion, the threshold (also called the **absolute threshold**) of each node was specified as a non-negative integer. A **homogeneous threshold** SyDS is one where all the nodes of a SyDS have the same threshold t, for some integer $t \geq 0$. A **heterogeneous threshold** SyDS is one where nodes may have different thresholds. Researchers (e.g. Centola and Macy 2007) have also considered **relative thresholds**, where the threshold value of a node is a non-negative fraction of the number of neighbors of the node. (Here, each node is considered a neighbor of itself.) Similar to absolute thresholds, one can also consider homogeneous and heterogeneous relative thresholds. We refer to these variants as the "t-threshold variants." Most of our theoretical results (Sect. 4) are presented in terms of absolute thresholds. Extensions of these results to the other t-threshold variants are straightforward, as outlined in the Appendix.

2.4 Additional terminology

Here, we present some terminology used in the later sections of this paper. The term "t-threshold system" is used to denote a SyDS with a homogeneous absolute threshold $t \geq 0$ (thus, the value of t is the same for all nodes of the system).

We also need some terminology with respect to approximation algorithms for optimization problems (Garey and Johnson 1979). For any $\rho \geq 1$, a ρ-**approximation** for an optimization problem is an efficient algorithm that produces a solution which is within a factor of ρ of the optimal value for all instances of the problem. Such an approximation algorithm is also said to provide a **performance guarantee** of ρ. Clearly, the smaller the value of ρ, the better is the performance of the approximation algorithm.

The following terms are used in describing simulation results and the behavior of the heuristics that produce critical sets. The **spread size** is the number (or fraction) of

Table 1 Acronyms used in this paper

Acronym	Expansion
BCH	Betweenness centrality critical node heuristic
CBH	Covering based heuristic
ECH	Eigenvalue centrality critical node heuristic
ED	Exponential decay
ER	Erdős–Renyi
HCH	High degree critical node heuristic
HITS	Hyperlink-induced topic search
MSC	Minimum set cover
MVC	Minimum vertex cover
PBH	Potential based heuristic
RCH	Random critical node heuristic
SCS-MNA	Smallest critical set to minimize the number of new affected nodes
SCS-MUN	Smallest critical set to maximize the number of unaffected nodes
SCS-SASN	Smallest critical set to save all salvageable nodes
SF	Scale free
SMC	Set multicover
SyDS	Synchronous dynamical system

nodes in the affected state; the **final spread size** is the value at the end of a diffusion instance. A **cascade** occurs when diffusion starts from a set of seed nodes and the final fractional or absolute spread size is large relative to the number of nodes that can possibly be affected. **Halt** means that the chosen set of critical nodes will stop the diffusion process, thus preventing a cascade. A **delay** means that the chosen set of critical nodes will increase the time at which the peak number of newly affected nodes occurs, but will not necessarily halt diffusion. Finally, Table 1 provides acronyms and Table 2 lists variables used throughout this document.

3 Summary of results and related work

3.1 Summary of results

Section 2 presented the formulations of the problems studied in this paper. The following is a summary of our main results.

(a) We show that for any $t \geq 2$ and any $\rho \geq 1$, it is **NP**-hard to obtain a ρ-approximation for either the SCS-MNA problem or the SCS-MUN problem for t-threshold systems. (The result holds even when ρ is a function of the form n^{δ}, where $\delta < 1$ is a constant and n is the number of nodes in the underlying network).

(b) We show that the problem of saving all salvageable nodes (SCS-SASN) can be solved in linear time for 1-threshold systems and that the required critical set is unique. In contrast, we show that the problem is **NP**-hard for t-threshold systems

Table 2 Variables used in this paper

Symbol	Meaning
f	Local transition function
m	Number of edges in a graph
n	Number of nodes in a graph
n_s	Number of seed nodes in a simulation
s_i	State of node v_i
t	Threshold
$\mathbb{B}$	Boolean state set {0, 1}
C	Critical set of nodes used to block contagion spread
$\mathcal{C}, \mathcal{C}'$	Configurations of a synchronous dynamical system
E	Set of edges in a graph G
$\mathcal{F}$	Set of local transition functions
G	Graph or network
I	Seed node set (i.e., set of nodes that are initially in state 1 in a simulation)
$L_G(t)$	The size, in terms of nodes, of the largest connected component of a maximal t-core of a graph
$\mathcal{S}$	Synchronous dynamical system
T	An upper bound on time
V	Set of nodes in a graph G
β	Budget on the size of the critical set

for any $t \geq 2$. We present an approximation algorithm for this problem with a performance guarantee of $\rho < 1 + \ln(s)$, where s is the number of salvageable nodes in the system. We also show that the performance guarantee cannot be improved significantly, unless **P** = **NP**.

(c) We develop two intuitively appealing heuristics, designated covering-based heuristic (CBH) and potential-based heuristic (PBH), for the SCS-MNA problem, and carry out an experimental study of their performance on three social networks, namely `epinions`, `wikipedia` and `slashdot`. We compare our schemes against five known methods for determining critical nodes (representing a range of blocking methods): random assignment, high-degree nodes, nodes of high betweenness centrality (Freeman 1976), nodes of high eigenvector centrality (Bonacich 1972), which can also be computed for undirected graphs using the hyperlink-induced topic search (HITS) algorithm (Kleinberg 1999), and maximum eigenvalue drop (also called NetShield) (Tong et al. 2010). We show that our methods are far more effective in blocking complex contagions.

(d) We establish an upper bound on the spread size for diffusion in t-threshold systems, for $t \geq 1$. Interestingly, this upper bound estimates a dynamic quantity (maximum spread size) using an easily computable static parameter of the network. We show experimentally that this upper bound is achievable for several values of t for real social networks. We also evaluate the effectiveness of the bound for a large number of synthetic networks.

Our heuristics can be used with heterogeneous thresholds. They can also be extended for use under more general transition criteria for nodes (e.g. generalized contagion models of Dodds and Watts 2005) and with probabilistic diffusion (where a node transitions from 0 to 1 with probability p when its threshold is met). Finally, our methods can also be extended for use in time-varying networks where the edges of the network and transition criteria change in a repeatable pattern (e.g., to reflect daytime and night-time interactions as in Prakash et al. 2010).

3.2 Related work

Work on finding critical sets has been almost exclusively confined to simple contagions (i.e., 1-threshold systems). Critical nodes are called "blockers" in (Habiba et al. 2008); they examine dynamic networks and use a probabilistic diffusion model with threshold = 1. They utilize graph metrics such as degree, diameter, and betweenness centrality (adapted to time-varying networks) to identify critical nodes. Anshelevich et al. (2009) also study dynamic networks and threshold-1 behavior. They use newly affected nodes to specify a predefined number of new blocking nodes per time step as deterministic diffusion emanates from a single seed node.

Many sophisticated methods for blocking simple contagions involve eigenvalue (and eigenvector) computations. Eigenvector centrality (Bonacich 1972) is used to rank nodes from best blocker to worst blocker in decreasing order of the magnitude of their eigenvector components for the dominant eigenvalue (e.g., Habiba et al. 2008; Tong et al. 2010). HITS (Kleinberg 1999) is another eigenvector-based approach for identifying blocking nodes when applied to undirected graphs. PageRank (Page et al. 1999) of a node v is closely aligned with eigenvector centrality, and was also studied in (Habiba et al. 2008; Tong et al. 2010). Initially in (Wang et al. 2003), and later in (Ganesh et al. 2005; Chakrabarti et al. 2008), a blocking scheme based on eigenvalues of the adjacency matrix of the underlying graph is discussed. A drawback of this method is that it is not practical for large networks, since it requires a large number of eigenvalue computations. To overcome this drawback, an efficient eigenvector-based heuristic has recently been proposed and evaluated on three social networks in (Tong et al. 2010).

A variety of network-based candidate measures for identifying critical nodes for simple contagions are described in (Borgatti 2006); however, the applications are confined to small networks. The effectiveness of removing nodes at random and removing high degree nodes has been studied in (Holme 2004; Albert et al. 2000; Crucitti et al. 2004; Cohen et al. 2003; Madar et al. 2004; Dezso and Barabasi 2002; Briesemeister et al. 2003). An approximation algorithm for the problem of minimizing the number of new affected nodes for simple contagions is presented in (Eubank et al. 2006).

Moving now to complex contagions, we are aware of only one work on inhibiting diffusion, and that is for 2-threshold systems. Centola (2009) examined how removal of nodes from 10,000-node synthetic exponential and power law (i.e., SF) graphs affects the diffusion of complex contagions. His motivation was to determine how resilient a network is to random and targeted node removal schemes; the former scheme removes nodes uniformly randomly while the latter removes high degree nodes. His work differs from ours in that it is focused on observing the spread size under the two node removal schemes rather than on stopping diffusion. While the results in (Centola 2009) show that the targeted method works well in inhibiting diffusion in some synthetic networks, we show herein that this method does not work well for realistic social networks, for $t = 2, 3$, and 5.

Although we limit ourselves to static networks, our methods can be applied to time-varying networks if the network modifications are deterministic in time. As motivated in (Prakash et al. 2010), this is a reasonable first approximation of people's regular, repeatable behavior and is used extensively in epidemiological modeling (e.g., Barrett et al. 2008; Perumalla and Seal 2010). Our methods can also be used without modification for probabilistic diffusion where below the threshold t, the probability of node transition is zero, and at or above the threshold, a node v transitions with probability p_v.

4 Theoretical results for the critical set problems

4.1 Overview and a preliminary lemma

In this section, we first establish complexity results for finding critical sets. We also present results that show a significant difference between 1-threshold systems and t-threshold systems where $t \geq 2$. Most of the results in this section are for homogeneous thresholds; extensions of the results to heterogeneous and relative thresholds are outlined in the Appendix.

Lemma 1 *Given a SyDS $\mathcal{S} = (G(V, E), \mathcal{F})$, the set $I \subseteq V$ of initially affected (i.e., seed) nodes and a critical set $C \subseteq V - I$, the number of new affected nodes in the system that results when C is removed from V can be computed in $O(|V| + |E|)$ time.*

Proof Recall that the removal of C is equivalent to changing the local transition function f_v of each node $v \in C$ to the function that remains 0 for all inputs. Since the resulting SyDS $\mathcal{S}_1$ is also a ratcheted SyDS, by Proposition 1, it reaches a fixed point in at most $n = |V|$ steps. The fact that each local transition function is a threshold function can be exploited to find all the nodes that are affected over the time steps in $O(|V| + |E|)$ time.

The idea is to have for each node $v \in V$, a counter c_v that stores the number of neighbors of v that are currently affected. To begin with, for each unaffected node, the counter is initialized to 0. In time step 1, for each node $w \in I$, the counter for each unaffected neighbor x of w is incremented. If the count for x reaches its threshold, then x is added to a list L of nodes which will contain all the nodes that are affected at time step 1. At the next time step, the above procedure is repeated using the nodes in L (instead of the nodes in I). This method can be carried out for each subsequent time step until the system reaches a fixed point (i.e., until the list of newly affected nodes becomes empty). It can be seen that for each node v of G, this method explores the adjacency list of v just once through all the time steps. So, the total time spent in the computation is $O(\sum_{v \in V} \text{degree}(v)) = O(|E|)$. The initialization of the counters and the final step to output the newly affected nodes take $O(|V|)$ time. Therefore, the total time is $O(|V| + |E|)$. □

4.2 Complexity results

As mentioned earlier, the SCS-MNA problem was shown to be NP-complete in (Eubank et al. 2006) for the case when each node has a 1-threshold function. We now extend that result to show that even obtaining a ρ-approximate solution is **NP**-hard for systems in which each node computes the t-threshold function for any $t \geq 2$.

Theorem 1 *Assuming that the bound β on the size of the critical set cannot be violated, for any $\rho \geq 1$ and any $t \geq 2$, there is no polynomial time ρ-approximation algorithm for the SCS-MNA problem for t-threshold systems, unless* **P** = **NP**.

Proof Suppose $\mathcal{A}$ is a ρ-approximation algorithm for the SCS-MNA problem for t-threshold systems for some $\rho \geq 1$ and $t \geq 2$. We will show that $\mathcal{A}$ can be used to efficiently solve the **Minimum Vertex Cover** (MVC) decision problem (Garey and Johnson 1979): Given an undirected graph $G(V, E)$ and an integer k, is there a subset V' of V such that $|V'| \leq k$ and for each edge $\{u, v\} \in E$, at least one of u and v is in V'?

Let $G = (V, E)$ be the given graph for the vertex cover problem, with $n = |V|$ and $m = |E|$. We construct a SyDS $\mathcal{S} = (H(V_H, E_H), \mathcal{F})$ as follows. The vertex set V_H consists of three pairwise disjoint groups of nodes denoted by X, Y and Z. The set $X = \{x_1, x_2, \ldots, x_t\}$ consists of t nodes all of which are initially 1. The set $Y = \{y_1, y_2, \ldots, y_n\}$ contains a node for each member of V. Let $\alpha = \lceil \rho(n-k) \rceil + k + 1$. The set $Z = \{z_1, z_2, \ldots, z_{\alpha m}\}$ contains a total of αm nodes, with α nodes corresponding to each edge of G. All the nodes in $Y \cup Z$ are initially 0. The edges in E_H are as follows.

(a) Each node in Y is adjacent to each node in X.
(b) Each node in Z is adjacent to the first $t-2$ nodes (i.e., nodes $x_1, \ldots, x_{t-2}$) of X.
(c) Let g_j denote the group of α nodes corresponding to edge $e_j \in E$; each node of g_j is adjacent to the two nodes in Y which correspond to the end points of the edge $e_j \in E$, $1 \leq j \leq m$.

The local transition function at each node of $\mathcal{S}$ is the t-threshold function. The value of β (the upper bound on the critical set size) is set to k. This completes the construction of the SCS-MNA instance. Obviously, the construction can be done in polynomial time.

Suppose G has a vertex cover $V' = \{v_{i_1}, v_{i_2}, \ldots, v_{i_k}\}$ of size k. It can be verified that when the critical set $C = \{y_{i_1}, y_{i_2}, \ldots, y_{i_k}\}$ is removed, only the $n-k$ nodes in $Y - C$ are affected; that is, the number of new affected nodes is $n-k$. Since Algorithm $\mathcal{A}$ provides a performance guarantee of ρ, the critical set output by $\mathcal{A}$ in this case leads to at most $\rho(n-k)$ new affected nodes.

Now suppose that a minimum vertex cover for G has $k+1$ or more nodes. We claim that no matter which subset of k (or fewer) nodes from $Y \cup Z$ is chosen as the critical set, the number of newly affected nodes is at least $\rho(n-k)+1$. To see this, note that any critical set can use at most k nodes of Y. Since any minimum vertex cover for G has $k+1$ or more nodes, no matter which subset of k nodes from V is chosen, at least one edge $e_j = \{v_p, v_q\}$ remains uncovered (i.e., neither v_p nor v_q is in the chosen set). As a consequence, no matter which subset of k nodes from Y is chosen, there is at least one group g_j of α nodes in Z such that for each node $z \in g_j$, the two nodes in Y, say y_p and y_q, that are adjacent to z are not in the critical set. Thus, y_p and y_q will become affected and consequently all nodes in group g_j become affected. Since g_j contains $\alpha = \lceil \rho(n-k) \rceil + k + 1$ nodes, even if C includes k nodes from g_j, at least $\lceil \rho(n-k) \rceil + 1$ nodes of g_j will become affected. Thus, when the minimum vertex cover for G is of size $k+1$ or more, the number of newly affected nodes is *strictly greater than* $\rho(n-k)$.

Now, suppose we execute $\mathcal{A}$ on the resulting SCS-MNA instance and obtain a critical set C. From the above argument, G has a vertex cover of size at most k if and only if the number of new affected nodes that result from the removal of C is at most $\rho(n-k)$. From Lemma 1, the number of new affected nodes after the removal of a critical set can be found in polynomial time. Thus, using $\mathcal{A}$, we have a polynomial time algorithm for the MVC problem, contradicting the assumption that **P** $\neq$ **NP**. □

We note that, in the above proof, the factor ρ need not be a constant; it may be a function of the form n^δ, where $\delta < 1$ is a constant and n is the number of nodes of the graph in the MVC instance.

We now present a result similar to that of Theorem 1 for the maximization version of the problem (SCS-MUN).

Theorem 2 *Assuming that the bound β on the size of the critical set cannot be violated, for any $\rho \geq 1$ and any $t \geq 2$, there is no polynomial time ρ-approximation algorithm for the SCS-MUN problem for t-threshold systems, unless* **P** = **NP**.

Proof Assume that $\mathcal{A}$ is a ρ-approximation algorithm for the SCS-MUN problem. We prove the result by a reduction from the Minimum Vertex Cover problem, similar to the one used to prove Theorem 1. The modifications are as follows.

(a) In addition to the sets of nodes X, Y and Z, we have another set of nodes $W = \{w_1, w_2, \ldots, w_h\}$, where $h = \lceil (\rho - 1)|Z| \rceil$.
(b) Each node in W is adjacent to the first $t-1$ nodes in X and all nodes in Z.

Now, if G has a vertex cover of size k, then by choosing the corresponding nodes of Y, all the nodes in $Z \cup W$ can be saved from becoming affected. Recall from Sect. 2.2 that the chosen critical nodes are not included in the set of unaffected nodes. Thus, in this case, the number of unaffected nodes is $|Z| + \lceil (\rho - 1)|Z| \rceil \geq \rho|Z|$. Since $\mathcal{A}$ is a ρ-approximation algorithm, it must produce a critical set of size k such that the number of nodes which are not affected is at least $|Z|$.

If every vertex cover for G has $k+1$ or more nodes, then no matter which subset of k (or fewer) nodes is chosen from Y, at least one node of Z will become affected. Consequently, all the nodes in W (which are not in the critical set) will also become affected. Therefore, no matter which critical set of size k is chosen, the number of unaffected nodes is at most $|Z| - 1$.

Thus, using $\mathcal{A}$, we can obtain a polynomial time algorithm for the MVC problem, contradicting the assumption that **P** $\neq$ **NP**. □

4.3 Critical sets for saving all salvageable nodes

Recall from Sect. 2.2 that a node v of a SyDS is salvageable if there is a critical set whose removal ensures that v will not be affected. The problem of finding optimal critical sets to save all salvageable nodes, denoted by SCS-SASN, was also formulated in that section. We now present results for SCS-SASN that show a significant difference between 1-threshold systems and t-threshold systems where $t \geq 2$.

Theorem 3 *Let $\mathcal{S} = (G(V, E), \mathcal{F})$ be a 1-threshold SyDS. The SCS-SASN problem for $\mathcal{S}$ can be solved in $O(|V| + |E|)$ time. Moreover, the solution is unique.*

Proof Call a given unsalvageable node of G a **fringe** node if it has at least one neighbor that is salvageable. We now argue that the set of all fringe nodes in G is the smallest critical set whose removal ensures that all salvageable nodes are saved from being affected.

First, observe that for a 1-threshold system, a given node is salvageable iff its initial state is 0 and the initial states of all its neighbors are also 0 (thus, determining whether a node v is salvageable can be done in time $O(\text{degree}(v))$ time, where the degree is the number of edges incident on v). It can be seen that removing all the fringe nodes saves all salvageable nodes. Further, this is the smallest critical set since if any fringe node is not removed, all of its salvageable neighbors would become affected. Thus, there is a unique smallest critical set for the system.

As mentioned above, determining whether a node v is salvageable can be done in $O(\text{degree}(v))$ time. Therefore, the time to identify all salvageable nodes is $O(\sum_{v \in V} \text{degree}(v)) = O(|E|)$. The set of fringe nodes consists of those nodes that are initially 0, have at least one neighbor that is initially 1, and have at least one neighbor that is salvageable. Thus, once all salvageable nodes have been identified, determining all the fringe nodes can also be done in $O(|E|)$ time. Outputting the fringe nodes takes $O(|V|)$ time. Thus, the set of all fringe nodes can be found and output in $O(|V| + |E|)$ time. □

The next set of results concerns the SCS-SASN problem for t-threshold systems, where $t \geq 2$.

Theorem 4 *(a) For any integer $t \geq 2$, the SCS-SASN problem is* **NP**-*hard for t-threshold systems.*

(b) There is an integer t such that for t-threshold systems, there is no polynomial time approximation algorithm for the SCS-SASN problem with a performance guarantee of $(1 - \epsilon) \ln(|Z|)$ for any $\epsilon > 0$, where Z is the set of salvageable nodes in the system, unless **P** = **NP**.

Proof of Part (a) This result can be shown by a simple modification to the reduction from Minimum Vertex Cover to the SCS-MNA problem given in the proof of Theorem 1. The modification is that the set Z contains only $m = |E|$ nodes, one corresponding to each edge of G. In the resulting SyDS, the salvageable nodes are those in the set Z. Nodes in the set Y are unsalvageable (each of them has t neighbors who are initially affected). It can be verified that G has a vertex cover of size at most

k iff there is a subset C of Y, with $|C| \leq k$, whose removal saves all the nodes of Z from becoming affected. □

Proof of Part (b) We use a reduction from the **Minimum Set Cover** (MSC) problem (Garey and Johnson 1979): Given a universal set $U = \{u_1, u_2, \ldots, u_n\}$ and a collection $C = \{C_1, C_2, \ldots, C_m\}$ of subsets of U, find a minimum cardinality subcollection C' of C such that the union of the sets in C' is equal to U. We will use the fact that the MSC problem cannot be approximated to within the factor $(1 - \epsilon)\ln(|U|)$ for any $\epsilon > 0$, unless **P** = **NP** (Raz and Safra 1997).

Given an instance of the MSC problem, let q denote the maximum number of occurrences of an element of U in the sets in C. We construct an instance of the SCS-SASN problem as follows. The node set of the underlying graph of the SyDS consists of three pairwise disjoint sets X, Y and Z, where $X = \{x_1, x_2, \ldots, x_q\}$ is the set of initially affected nodes, $Y = \{y_1, y_2, \ldots, y_m\}$ is in one-to-one correspondence with the collection C and $Z = \{z_1, z_2, \ldots, z_n\}$ is in one-to-one correspondence with the set U. Thus, the initial states of the nodes in X are 1 while those of the nodes in $Y \cup Z$ are 0. The edges of the underlying graph are as follows.

(a) Each node in X is adjacent to every node in Y.
(b) Consider each element $u_i \in U$ and suppose u_i appears in sets $C_{i_1}, C_{i_2}, \ldots, C_{i_r}$, for some $r \leq q$; then, node z_i is joined to the first $q - r$ nodes of X and the r nodes $y_{i_1}, y_{i_2}, \ldots, y_{i_r}$ of Y.

The threshold for each node is set to q. Thus, the constructed SyDS is a q-threshold system.

It can be seen that none of the nodes in Y is salvageable while all the nodes in Z are salvageable. Thus, every critical set must be a subset of Y. It can also be verified that any critical set of size α corresponds to a solution to the MSC problem with α subsets from C and vice versa. It follows that if there is an approximation algorithm for the SCS-SASN problem with a performance guarantee of $(1 - \epsilon)\ln(|Z|)$ for the SCS-SASN problem, where $\epsilon > 0$, then, since $|Z| = |U|$, there is an approximation algorithm with a performance guarantee of $(1 - \epsilon)\ln(|U|)$ for the MSC problem. The result of Part (b) follows with $t = q$. □

We now discuss an approximation algorithm for the SCS-SASN problem with a performance guarantee of H_s, where s is the number of salvageable nodes in the system and $H_s = \sum_{i=1}^{s}(1/i)$ is the s^{th} **Harmonic Number**. Since $H_s < 1 + \ln(s)$, this algorithm shows that the lower bound result of Part (b) of Theorem 4 is nearly tight. Moreover, our approximation algorithm is valid even when nodes have different thresholds (i.e., for systems with heterogeneous thresholds).

The idea is to reduce the SCS-SASN problem to a more general form of the MSC problem, called the set multicover (SMC) problem (Vazirani 2001). Like the MSC problem, the input to the SMC problem consists of the set U and the collection C of subsets of U. In addition, for each element $u \in U$, a coverage requirement $\sigma_u \in \mathbb{Z}^+$ is also given, and the goal of the SMC problem is to pick a minimum cardinality subcollection C' of C such that for each element $u \in U$, there are at least σ_u subsets in C' that contain u. An approximation algorithm with a performance guarantee of H_p, where $p = |U|$, is known for the SMC problem (Vazirani 2001). This fact is used

Input: A SyDS with underlying graph $G(V, E)$, a threshold $t_i \geq 0$ for each node $v_i \in V$, the set $I \subseteq V$ of initially affected nodes.

Output: A critical set $Q \subseteq V - I$ such that removal of Q ensures that none of the salvageable nodes is affected.

Steps:

1. Let $Y = \{v_i \in V \ : \ v_i$ is adjacent to t_i or more nodes in $I\}$. (**Note:** Y is the set of nodes that *cannot* be salvaged. The algorithm returns a critical set $Q \subseteq Y$.)
2. Let $Z = V - (I \cup Y)$. (**Note:** Z is the set of salvageable nodes.)
3. Construct an instance of the Set Multicover (SMC) problem as follows.
   (a) Let $U = Z$. For each node $v_i \in Z$, suppose v_i is adjacent to p_i nodes of I and q_i nodes of Y. Then, the coverage requirement σ_i for v_i is given by
   $\sigma_i = \max\{0, \ p_i + q_i - t_i + 1\}$.
   (b) For each node $v_j \in Y$, create the set $C_j = \{v_i \in Z \ : \ \sigma_i > 0$ and $\{v_i, v_j\} \in E\}$, $1 \leq j \leq |Y|$. (**Note:** Nodes with coverage requirement ≤ 0 cannot get affected since their thresholds are too high. So, they need not be considered in creating the SMC instance.)
4. Use the known approximation algorithm with a performance guarantee of H_p, where $p = |U|$, to find a solution to the SMC problem instance constructed in Step 3.
5. If the solution obtained in Step 4 is the set $C' = \{C_{j_1}, C_{j_2}, \ldots, C_{j_r}\}$, then output $Q = \{v_{j_1}, v_{j_2}, \ldots, v_{j_r}\}$ as the critical set.

Fig. 2 An approximation algorithm for the SCS-SASN problem

in our approximation algorithm for the SCS-SASN problem shown in Fig. 2. It can be seen that the approximation algorithm runs in polynomial time. We now prove its correctness and its performance guarantee.

Theorem 5 *The critical set Q produced by the algorithm in Fig. 2 ensures that none of the salvageable nodes is affected. Also, $|Q| \leq |Q^*| H_s$, where Q^* is an optimal critical set and s is the number of salvageable nodes in the system.*

Proof We first observe that the set Z constructed in Step 2 of the algorithm contains all the salvageable nodes. The reason is that no node in Y is salvageable since for each node $v \in Y$, the number of initially affected neighbors is at least the threshold of v. Moreover, by removing all the nodes in Y, we can ensure that none of the nodes in Z is affected.

We now argue that the set Q produced by the algorithm is indeed a critical set; that is, the removal of Q ensures that none of the nodes in Z is affected. To see this, consider any node $v_i \in Z$ and let p_i and q_i denote the number of neighbors of v_i in I and Y respectively. The coverage requirement for v_i was chosen as $\sigma_i = \max\{0, \ p_i + q_i - t_i + 1\}$. If $\sigma_i = 0$, then $p_i + q_i \leq t_i - 1$, and therefore, v_i cannot be affected. If $\sigma_i \geq 1$, then the number of neighbors of v_i after removing all the nodes in Q is at most $p_i + q_i - \sigma_i$ which is at most $t_i - 1$ by the definition of σ_i. Hence, v_i will not get affected. □

To prove the performance guarantee, we have the following claim.

Claim 1 *Any critical set of size α corresponds to a solution to the SMC problem with α sets and vice versa.*

Proof of Claim 1 Consider any critical set $Q' = \{v_{j_1}, v_{j_2}, \ldots, v_{j_\alpha}\}$ of size α. We argue that the corresponding collection $C' = \{C_{j_1}, C_{j_2}, \ldots, C_{j_\alpha}\}$ of sets is a solution to the SMC problem. Since Q' is a critical set, for any node $v_i \in Z$, after the removal of Q', the number of neighbors of v_i in $I \cup (Y - Q)$ is at most $t_i - 1$. Using this fact, it can be verified that each node $v_i \in Z$ is covered at least σ_i times by C'. In other words, C' is a solution to the SMC problem. The proof that any solution to SMC problem with α sets corresponds to a critical set of size α is similar, and this establishes Claim 1.

To establish the performance guarantee, let Q^* be an optimal critical set. Thus, by the above claim, there is a solution to the SMC problem with at most $|Q^*|$ sets. Since the approximation algorithm for the SMC problem provides a performance guarantee of H_s, where $s = |U| = |Z|$, the size of the solution to the SMC problem obtained in Step 4 of the algorithm is at most $|Q^*|H_s$. Since the approximation algorithm produces a critical set whose size is exactly the number of sets in the approximate solution to the SMC problem, we have $|Q| \le |Q^*|H_s$. □

5 Heuristics for finding small critical sets

5.1 Overview

The complexity results presented in Sect. 4 point out the difficulty of developing heuristics with provably good performance guarantees for the SCS-MNA and SCS-MUN problems. So, we focus on the development of heuristics that work well in practice for one of these problems, namely SCS-MNA. In this section, we present two such heuristics. The first heuristic uses a greedy set cover computation. The second heuristic relies on a potential function, which provides an indication of a node's ability to affect other nodes. Experimental evaluation of these heuristics on several social networks is discussed in Sect. 6.

5.2 Covering-based heuristic (CBH)

Given a SyDS $\mathcal{S} = (G(V, E), \mathcal{F})$ and the set $I \subseteq V$ of nodes whose initial state is 1, one can compute the set $S_i \subseteq V$ of nodes that change to state 1 at the i^{th} time step, $1 \le i \le T$, for some suitable $T \le |V|$, which can be taken as the time to reach a fixed point (this can be done efficiently as explained in the proof of Lemma 1). The CBH, whose details appear in Fig. 3, chooses a critical set C as a subset of S_i for some suitable i. The intuitive reason for doing this is that each node v in S_{i+1} has at least one neighbor w in S_i (otherwise, v would have changed to 1 in an earlier time step). Therefore, if a suitable subset of S_i can be chosen as critical so that none of the nodes in S_{i+1} changes to 1 during the $(i+1)^{\text{st}}$ time step, the contagion cannot spread beyond S_i. Consistent with the goal of the SCS-MNA problem, we seek to halt the diffusion process as early as possible in Step 2 of Fig. 3. There are two means by which this can be accomplished at each time i: Step 2(i)(a) which checks whether S_i can itself serve as a critical set (i.e., $|S_i| \le \beta$) and Step 2(i)(e) which checks whether the covering procedure discussed below produces a suitable critical set from S_i.

```
Input: A SyDS $\mathcal{S} = (G(V, E), \mathcal{F})$, the set $I \subseteq V$ of nodes whose initial state is 1, the upper bound $\beta$ on the size of the critical set and the number of simulation steps $T \leq |V|$.
Output: A critical set $C \subseteq V - I$ whose removal leads to a small number of new affected nodes.
Steps of the heuristic:
1. Simulate the system for $T$ time steps and determine sets $S_1$, $S_2$, ..., $S_T$, where $S_i$ is the set of newly affected nodes at time $i$, $1 \leq i \leq T$.
2. Comment: This step uses a greedy covering procedure.
    (i) for $i = 1$ to $T - 1$ do
        (a) if $|S_i| \leq \beta$, then output critical set $C = S_i$ and stop.
        (b) For each node $v_j \in S_i$, construct the set $\Gamma_j$ which consists of all the neighbors of $v_j$ in $S_{i+1}$. Let $\Gamma$ denote the collection of all the sets constructed. (We have $|\Gamma| > \beta$.) The coverage requirement for each node $v_k$ of $S_{i+1}$ is $n_k - t_k + 1$, where $n_k$ is the number of affected neighbors of $v_k$ at times $\leq i$, and $t_k$ is the threshold of $v_k$. (An explanation for this choice of coverage requirement is provided in Section 5.2.)
        (c) Use a greedy approach to find a subcollection $\Gamma'$ of $\Gamma$ containing at most $\beta$ sets that satisfies the coverage requirement for as many elements of $S_{i+1}$ as possible.
        (d) Let the critical set $C_i$ consist of the nodes of $S_i$ corresponding to the elements of $\Gamma'$.
        (e) if all nodes in $S_{i+1}$ are covered appropriately then output $C = C_i$ and stop.
        (f) Let $R_i \subseteq S_{i+1}$ be the set of nodes whose coverage requirement is not met by $\Gamma'$.
    (ii) Among all the critical sets $C_i$ constructed in Step 2(i)(c), output the earliest $C_i$ such that $|R_i|$ is minimum.
```

Fig. 3 Details of the CBH

In general, when nodes have thresholds ≥ 2, the problem of choosing at most β nodes from S_i to prevent a maximum number of nodes in S_{i+1} from changing to 1 corresponds to the SMC problem mentioned in Sect. 4. Step 2(i)(b) constructs an instance of SMC, where each set Γ_j in the collection Γ corresponds to a node v_j of S_i. The elements to be covered are the nodes in S_{i+1}. The coverage requirement for each node $v_k \in S_{i+1}$ is determined as follows. Suppose v_k has threshold t_k and has n_k affected neighbors in $S_1 \cup S_2 \cup \ldots \cup S_i$. Since $v_k \in S_{i+1}$ is affected in time step $i + 1$ in the absence of any critical nodes, we have $n_k \geq t_k$. Thus, to prevent v_k from getting affected, at least $n_k - (t_k - 1) = n_k - t_k + 1$ nodes from S_i must be chosen as critical nodes. In the SMC formulation, this number corresponds to the coverage requirement for node v_k.

Since SMC is **NP**-hard, a greedy approach is used (Step 2(i)(c)) for this covering problem (Vazirani 2001). This approach iterates over the sets of Γ; in each iteration, the chosen set from Γ corresponds to a node v_j from S_i that contributes to saving the largest number of nodes in S_{i+1} from becoming affected. That is, v_j is the node that has the greatest number of edges in $G(V, E)$ to nodes in S_{i+1} that are still affected (ties are broken arbitrarily). Thus, the subcollection Γ' produced by Step 2(i)(c) corresponds to a subset of S_i.

If the conditions in Steps 2(i)(a) and 2(i)(e) are not satisfied for any T, $1 \leq i \leq T-1$, then a solution that has the smallest number of nodes whose coverage requirement is not met is chosen as the output. We now establish the running time of CBH.

Proposition 2 *Let $G(V, E)$ denote the underlying graph of the given SyDS $\mathcal{S}$. The running time of CBH is $O(|V||E|)$.*

Proof Consider the description of CBH in Fig. 3. Using Lemma 1, Step 1 can be implemented to run in $O(|V|+|E|)$ time. In each iteration of Step 2(i), it can be seen that the dominant part of the running time is due to the greedy heuristic for SMC. This heuristic can be implemented to run in $O(\sigma)$ time, where σ is the sum of the sizes of the given sets (Vazirani 2001). In CBH, since the set constructed for any node v is of size at most degree(v), the sum of the sizes of all the sets is at most $\sum_{v \in V}$ degree$(v) = |E|$. Thus, each execution of the greedy heuristic runs in $O(|E|)$ time. Since Step 2(i) runs the greedy set cover heuristic $T-1$ times, the running time of that step is $O(T|E|)$. Since $T \leq |V|$, the worst-case running time of CBH is $O(|V||E|)$. □

5.3 Potential-based heuristic

Here, we provide the details of the PBH. The idea is to assign a potential to each node v depending on how early v is affected and how many nodes it can affect later. Nodes with larger potential values are more desirable for inclusion in the critical set. While the CBH chooses a critical set from one of the S_i sets, the potential based approach may select nodes in a more global fashion from the whole graph.

We assume that set S_i of newly affected nodes at time i has been computed for each i, $1 \leq i \leq T$, where T is the time at which the system reaches a fixed point. For any node $x \in S_i$, let $N_{i+1}[x]$ denote the set of nodes in S_{i+1} which are adjacent to x in G. The potential $P[x]$ of a node x is computed as follows.

- For each node x in S_T, $P[x] = 0$. (**Justification** Since there is no diffusion beyond level T, it is useless to have nodes from S_T in the critical set).
- For each node x in level S_i, $1 \leq i \leq T-1$,

$$P[x] = (T-i)^2 \left[|N_{i+1}[x]| + \sum_{y \in N_{i+1}[x]} P[y] \right] \qquad (1)$$

(**Justification** The term $(T-i)^2$ decreases as i increases. Thus, the term enables us to assign higher potentials to nodes that are affected earlier. The term $|N_{i+1}[x]|$ is included in the expression for potential so that nodes which have a large number of neighbors in the next level become desirable candidates for inclusion in the critical set.)

The steps of the PBH are shown in Fig. 4. Steps 1, 2 and 3 compute the potentials for all the nodes in $S_1 \cup S_2 \cup \ldots \cup S_T$ in a bottom-up fashion. Step 4 indicates how the critical set is chosen. We now establish the running time of PBH.

Input: A SyDS $\mathcal{S} = (G(V, E), \mathcal{F})$, the set $I \subseteq V$ of nodes whose initial state is 1, and the upper bound β on the size of the critical set.

Output: A critical set $C \subseteq V - I$ whose removal leads to a small number of new affected nodes.

Steps of the heuristic: (The description below uses some notation presented in the main text.)

```
1. Simulate the system $\mathcal{S}$ and determine sets $S_1$, $S_2$, ..., $S_T$, where $T$ is the time step
   at which $\mathcal{S}$ reaches a fixed point and $S_i$ is the set of newly affected nodes at time $i$,
   $1 \le i \le T$.
2. for each node $x \in S_T$ do
       $P[x] = 0$.
3. for $i = T - 1$ downto 1 do
       for each node $x \in S_i$ do
           (a) Find $N_{i+1}[x]$ and let $P[x] = |N_{i+1}[x]|$.
           (b) for each node $y \in N_{i+1}[x]$ do
                   $P[x] = P[x] + P[y]$
           (d) Set $P[x] = (T - i)^2 P[x]$.
4. Let the critical set $C$ contain $\beta$ nodes with the highest potentials among all the nodes.
   (Break ties arbitrarily.) Output $C$.
```

Fig. 4 Details of the PBH

Proposition 3 *Let $G(V, E)$ denote the underlying graph of the given SyDS $\mathcal{S}$. The running time of PBH is $O(|V| + |E|)$.*

Proof Consider the description of PBH in Fig. 4. From Lemma 1, Step 1 can be implemented to run in $O(|V| + |E|)$ time. Step 2 runs in $O(|V|)$ time. In Step 3, the potential for each node v is computed by examining the neighbors of v. Thus, for any node v, the time used to compute v's potential is $O(\text{degree}(v))$. Hence, the time used to compute the potentials of all the nodes is $O(\sum_{v \in V} \text{degree}(v)) = O(|E|)$. Step 4 can be carried out in $O(|V|)$ time since the β^{th} largest potential value can be computed in $O(|V|)$ time using the well known linear time selection algorithm (Cormen et al. 2001). Hence, the overall running time of PBH is $O(|V| + |E|)$. □

The next section presents a simple example to illustrate similarities and differences between the behaviors of PBH and CBH.

5.4 Comparison of critical node heuristics

We compare behaviors of the two critical node heuristics PBH and CBH with respect to how they block $t = 2$ diffusion on the graph of Fig. 5 when the two nodes A and B are the seed nodes. We note that this graph could be embedded in a larger graph. Also, we have chosen the edges among the nodes to be somewhat regular for expository reasons. However, there are many edge sets among this set of nodes that will give the same behavior as that discussed below. Furthermore, many additional edges can be introduced without affecting the spread size.

In the absence of critical nodes, the contagion will propagate throughout the network. In particular, nodes G and H are affected by nodes C and D, and hence nodes L, M, N, and P are all affected through the nodes C and D. We consider two cases

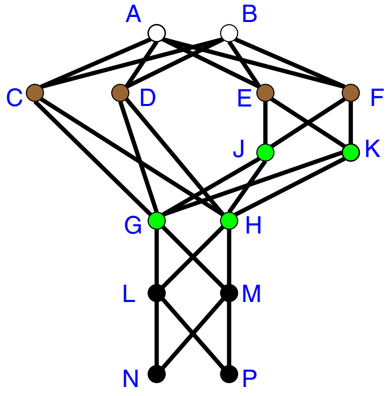


Fig. 5 Example graph where threshold-2 diffusion starts from the two seed nodes A and B. Without critical nodes, the *four brown nodes* (C, D, E and F) are affected at time $i = 1$ and the *four green nodes* (G, H, J and K) are affected at $i = 2$ (Color figure online)

of critical nodes: one in which CBH performs much better than PBH and a second case where the two methods perform comparably. We now consider the case where the number of blocking nodes is $\beta = 2$ and demonstrate that CBH performs far better than PBH.

For CBH, we start with the nodes (in green) that are affected at time $i = 2$. The candidate nodes that may be specified as critical are the four brown nodes, namely C, D, E and F. If either of C or D is not affected at $i = 1$, then neither G nor H can be affected at $i = 2$ (because their thresholds are 2). Similarly, if either E or F is not affected at $i = 1$, then neither J nor K can be affected at $i = 2$, and the contagion is halted in that direction. Thus, CBH will select one of $\{C, D\}$ and one of $\{E, F\}$ as critical nodes (ties are broken arbitrarily) and the final spread size is four nodes: the two seeds and whichever two of the four brown nodes are not set critical.

For PBH, we note that potentials are computed first for the nodes that are affected last, and the computations proceed backwards to the seed nodes. Starting from nodes N and P, whose potentials are zero, the potentials of nodes will increase as one moves up toward the seed nodes. Thus, the nodes with the largest potential, and hence the nodes that will form the set critical, are C and D. The resulting spread size is 12 since all nodes except C and D will be affected.

Now, for the second case, suppose instead that β is increased from 2 to 4. The critical sets for CBH and PBH are, respectively, $\{C, D, E, F\}$ and $\{C, D, G, H\}$ and the final spread sizes are 2 and 6. Thus, with four critical nodes, the difference in spread sizes between the two heuristics is cut in half (from a difference of 8 when $\beta = 2$, to a difference of 4 when $\beta = 4$).

In Sect. 6.4 (Fig. 12) we discuss parameter settings which show significant differences between the blocking performances of PBH and CBH for realistic social networks.

Table 3 Selected characteristics of three realistic social networks (Richardson et al. 2003; Leskovec et al. 2008, 2010)

Network	Number of nodes	Number of edges	Average degree	Average clustering coefficient	Number of connected components	Size of largest component
`Epinions`	75879	405740	10.7	0.138	2	75877
`Slashdot`	77360	469180	12.1	0.0555	1	77360
`Wikipedia`	7115	100762	28.3	0.141	1	7115

6 Blocking experiments and results

6.1 Overview

We first describe the social networks used for testing. Next, we compare the blocking performance of our heuristics with those of five known heuristics. When then provide further results from an experimental evaluation of our methods to illustrate additional aspects of blocking. Our results provide answers for the SCS-MNA problem. We also provide timing data for our heuristics to emphasize the tradeoff between execution speed and quality of critical sets.

6.2 Networks and generation of seed nodes

Table 3 provides selected features of the three social networks used in this study (we refer to these as "realistic social networks," since they were produced by mining real social datasets). We assume that all edges are undirected to accentuate diffusion and thereby test the heuristics more stringently. Average degree and average clustering coefficient vary by more than a factor of 2 across the networks. Power law degree distributions for the three networks are shown in Fig. 6a. While we use mined networks to investigate realistic structures, other works (e.g., Barash 2011) look at the effects of stylized structures on contagion processes without blocking nodes.

A **k-core** of a graph is a subgraph in which each node has a degree of at least k (Seidman 1983). A k-core is **maximal** if there is no larger subgraph (in terms of number of nodes) which is also a k-core.[2] Figure 6b provides maximal k-core sizes for the three networks. The number of nodes in each maximal k-core must be non-increasing as k increases. We will be particularly interested in $k = 2, 3, 5$, and 20 in this paper, and for each of these values, the maximal k-core forms one connected component (although in general, a k-core need not consist of only one component).

All our diffusion experiments use the following method of generating seed sets. For a given value of number n_s of seeds, 100 sets of seed nodes are determined from each network to provide a range of cases for testing the heuristics. Each set of seed nodes is taken from a 20-core; thus, each seed node has a degree of at least 20. Choosing seed

[2] A precise formal definition of maximal core is given in Sect. 7.1.

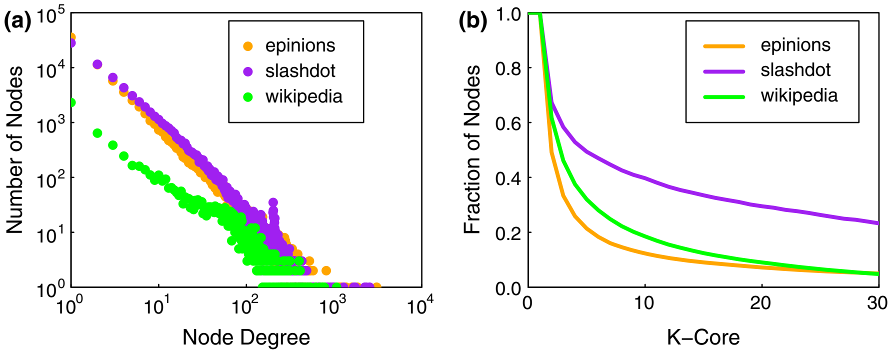


Fig. 6 **a** Degree distributions and **b** k-core sizes for the three networks of this study

nodes from the 20-core provides a good compromise between selecting high-degree nodes, and having a sufficiently large pool of nodes to choose from so that there is no duplication of seed node sets. Moreover, each set of seed nodes forms a connected subgraph, which fosters diffusion. Thus, the test cases utilize two means (namely, seeding of high-degree nodes and ensuring that they form a connected subgraph) to foster diffusion and hence tax the heuristics.

Barash et al. (2012) demonstrate that there are conditions under which complex contagions will not spread in stylized graphs; as mentioned earlier, they do not consider critical nodes. Since our goal is to study the effectiveness of critical nodes in blocking diffusion, we seek to generate widespread diffusion in the absence of critical nodes, even for small seed sets. Then, the number of affected nodes when including critical nodes indicates the effectiveness of a blocking method in inhibiting contagion spread.

6.3 Comparisons of CBH and PBH with other blocking methods

We now turn to evaluating the heuristics in halting and delaying diffusion by first comparing our heuristics with five other heuristics: (1) randomly setting nodes critical (RCH), (2) setting high-degree nodes critical (HCH), (3) setting critical the nodes with greatest betweenness centrality (BCH), (4) setting critical nodes with greatest eigenvector centrality (ECH), which for undirected graphs is the same as the HITS method (Kleinberg 1999), and (5) the maximum eigenvalue drop method called NetShield (Tong et al. 2010). As mentioned earlier, methods referred to in items (2) through (5) above were proposed in the literature for blocking simple contagions. The random choice method (RCH) serves as a baseline. In the remainder of this section, the above five approaches are referred to collectively as *other blocking methods*.

Our experimental procedure is as follows. We consider the three networks (`epinions`, `slashdot` and `wikipedia`) discussed in Sect. 6.2 and set the threshold value $t = 2$. We use two values (namely, 2 and 3) for the number n_s of seed nodes. For each value of n_s, 100 sets of seed nodes are generated from the 20-core of the corresponding social network. The budget β on the number of blocking nodes is set to

500. We chose the values of n_s and β to give the blocking methods a good opportunity to succeed since the value of β/n_s is reasonably large (250 and 166.7 respectively for $n_s = 2$ and 3). For each combination of social network, value of n_s and blocking method with $\beta = 500$, we ran 100 diffusion instances (one corresponding to each seed set) and recorded the number of nodes in the affected state (state 1). The seed sets are the same for each blocking method. For each set of 100 diffusion instances, we provide the average number of affected nodes.

We also provide, in the last column of the following tables, the ratio of average number of affected nodes to the maximum possible (MP) number of nodes that can be affected. This ratio is crucial because for complex contagions, graph structure itself can retard contagion propagation, and a blocking method should not be given credit for a seemingly smaller spread size when the effect is due to the graph structure. For example, 47 % of epinions nodes (i.e., 35755 nodes) have degree 1. With $t = 2$ diffusion, it is impossible for these nodes to become affected (unless they are seed nodes) because they cannot have two neighbors in state 1. Thus, one upper bound on the maximum spread size for $t = 2$ contagion in epinions is 40124 (= 75879 − 35755) nodes. In fact, a tighter upper bound is the size of the largest connected component of the 2-core, which for epinions is 37300 nodes (a general result, from which this bound for epinions follows, will be established in Sect. 7). Thus, with no blocking nodes, the MP spread size in epinions for $t = 2$ diffusion is 37300. To illustrate why this MP spread size is important, suppose a method that uses blocking nodes allows a spread size of 30000 on the epinions network. Here, one might conclude (erroneously) that the blocking method is effective because only a fraction $30000/75879 \approx 0.4$ of all the nodes are affected. In actuality, the method is not effective because a fraction $30000/37300 \approx 0.8$ of all the nodes that the contagion can reach in the absence of blocking nodes are affected, even though blocking nodes are used. Therefore, the values in the final column of the following tables normalize the average spread size (computed over 100 diffusion instances via simulation) by the theoretical MP spread size. This ratio assists in the interpretation of the reported spread size.

Our experimental results for epinions, slashdot, and wikipedia, are given in Tables 4 through 9, where each table contains data for one network and one seed set size. Our findings can be summarized as follows.

1. For all three networks, CBH and PBH perform well in blocking diffusion, allowing almost no spreading for any diffusion instance. Over the conditions of all tables, PBH permits widespread contagion propagation for only one diffusion instance; CBH permits no widespread diffusion. The random choice method RCH allows the greatest fractions of affected nodes for all three networks (the reason for the poor performance by RCH is that nodes of degree 1 account for between 35 and 50 % of nodes in these networks. RCH has a good chance of choosing such nodes as critical nodes even though other nodes which are better suited to block the complex contagion are available).
2. For the epinions network (Tables 4, 5), HCH, BCH, ECH/HITS and NetShield permit average spread sizes between 18809 and 27119 nodes. For slashdot (Tables 6, 7), the range in numbers of affected nodes is 12440 to 31882 nodes,

Table 4 Performance of blocking methods for epinions ($t = 2$ and $\beta = 500$) with two seed nodes

Blocking method	Average number of nodes affected with blocking	Ratio of (average affected) to (MP number affected)
CBH	2.0	5.4×10^{-5}
PBH	2.0	5.4×10^{-5}
Random (RCH)	32373.0	0.87
High degree (HCH)	20627.7	0.55
Betweenness centrality (BCH)	18809.3	0.50
Eigenvector centrality (ECH/HITS)	22105.1	0.59
NetShield	20929.2	0.56

The maximum number of nodes that can be affected from $t = 2$ diffusion for epinions is 37300

Table 5 Performance of blocking methods for epinions ($t = 2$ and $\beta = 500$) with three seed nodes

Blocking method	Average number of nodes affected with blocking	Ratio of (average affected) to (MP number affected)
CBH	3.0	8.0×10^{-5}
PBH	306.1	8.2×10^{-3}
Random (RCH)	34437.7	0.92
High degree (HCH)	25712.3	0.69
Betweenness centrality (BCH)	25896.2	0.69
Eigenvector centrality (ECH/HITS)	26585.5	0.71
NetShield	27119.1	0.73

The maximum number of nodes that can be affected from $t = 2$ diffusion for epinions is 37300

while for wikipedia (Tables 8, 9), the range in numbers of affected nodes across other methods is 1877 to 3185 nodes. For all three networks, when the number of seed nodes increases to $n_s = 3$, contagion spreading significantly increases. These results suggest that in the three networks, complex contagions are often able to circumvent the nodes of high degree or high centrality and find alternate paths to reach many nodes.

3. Average numbers of affected nodes for PBH and CBH are two orders of magnitude less, and in most cases are three to four orders of magnitude less, than those for the five other methods. These results highlight the improved blocking performance that can be realized by using the additional information provided by the seed node sets.
4. It is also useful to compare the performance of the other blocking methods. The high degree heuristic performs just as well as—in some cases better than—the more sophisticated methods in blocking complex contagions. This result provides an interesting contrast with the findings in Tong et al. (2010) for simple contagions, where NetShield was shown to have the best performance.

Table 6 Performance of blocking methods for `slashdot` ($t = 2$ and $\beta = 500$) and two seed nodes

Blocking method	Average number of nodes affected with blocking	Ratio of (average affected) to (MP number affected)
CBH	2.0	4.2×10^{-5}
PBH	2.0	4.2×10^{-5}
Random (RCH)	27523.7	0.58
High degree (HCH)	15453.7	0.32
Betweenness centrality (BCH)	15990.9	0.33
Eigenvector centrality (ECH/HITS)	13425.1	0.28
NetShield	12440.7	0.26

The maximum number of nodes that can be affected from $t = 2$ diffusion for `slashdot` is 47760

Table 7 Performance of blocking methods for `slashdot` ($t = 2$ and $\beta = 500$) and three seed nodes

Blocking method	Average number of nodes affected with blocking	Ratio of (average affected) to (MP number affected)
CBH	3.0	6.3×10^{-5}
PBH	3.1	6.5×10^{-5}
Random (RCH)	43569.8	0.91
High degree (HCH)	23586.5	0.49
Betweenness centrality (BCH)	27183.4	0.57
Eigenvector centrality (ECH/HITS)	31882.1	0.67
NetShield	26952.7	0.56

The maximum number of nodes that can be affected from $t = 2$ diffusion for `slashdot` is 47760

5. The results also show that *all* five of the other methods are more effective in blocking complex contagions in `slashdot` than in `epinions` and `wikipedia`. We believe that this is related to the average clustering coefficients (C_{ave}) of the networks. As can be seen from Table 3 (Sect. 6.2), the `slashdot` network has the smallest C_{ave} among the three networks. For complex contagions, where multiple affected neighbors are required to propagate a contagion, the clustering coefficient is potentially an important factor in determining a network's ability to spread contagions. The C_{ave} values for `epinions` and `wikipedia` are somewhat more typical of social networks, while that for `slashdot` is smaller (Newman and Park 2003). These results suggest that networks with smaller C_{ave} can still spread complex contagions, but blocking their progression is easier.

We end this section by noting that the other blocking methods are sensitive to the number of seed nodes: an increase in numbers n_s of seed nodes from 2 to 3 significantly decreases the effectiveness of these methods. We will see this sensitivity to n_s in CBH and PBH as well in Sect. 6.4; however, in our methods, this sensitivity is pushed further out to larger values of n_s.

Table 8 Performance of blocking methods for `wikipedia` ($t = 2$ and $\beta = 500$) and two seed nodes

Blocking method	Average number of nodes affected with blocking	Ratio of (average affected) to (MP number affected)
CBH	2.0	4.2×10^{-4}
PBH	2.0	4.2×10^{-4}
Random (RCH)	4187.3	0.87
High degree (HCH)	1882.8	0.39
Betweenness centrality (BCH)	2337.2	0.49
Eigenvector centrality (ECH/HITS)	1885.6	0.39
NetShield	1876.6	0.39

The maximum number of nodes that can be affected from $t = 2$ diffusion for `wikipedia` is 4786

Table 9 Performance of blocking methods for `wikipedia` ($t = 2$ and $\beta = 500$) and three seed nodes

Blocking method	Average number of nodes affected with blocking	Ratio of (average affected) to (MP number affected)
CBH	3.0	6.3×10^{-4}
PBH	39.2	8.2×10^{-3}
Random (RCH)	4361.3	0.91
High degree (HCH)	3171.6	0.66
Betweenness centrality (BCH)	3171.3	0.66
Eigenvector centrality (ECH/HITS)	3036.7	0.63
NetShield	3185.4	0.67

The maximum number of nodes that can be affected from $t = 2$ diffusion for `wikipedia` is 4786

6.4 Experimental evaluation of CBH and PBH

We carried out a parametric study to experimentally evaluate the performance of PBH and CBH. Table 10 lists the parameters and values used in the parametric study.

The test plan consists of running 100 simulations of diffusion instances (one instance per seed node set) on each of the three networks for all combinations of t, n_s, and β values shown in Table 10. Our simulator outputs for each node v the time at which v is affected. The heuristics use this as input data and calculate one set of β critical nodes for each iteration (i.e., diffusion instance). The simulations are then repeated, but now they include the critical nodes, so that the decrease in the total number of affected nodes caused by a critical set can be quantified. The main results from this full-factorial parametric study are outlined below. For brevity, when results for different networks and combinations of parameter values are similar, only results for one representative network and some specific combinations of parameter values are presented.

For reasons discussed in Sect. 6.3, all results are given as the average number of affected nodes over 100 diffusion instances, divided by the MP number of affected nodes, designated "(Ave. Affected)/(MP Affected)." We also refer to this ratio as

Table 10 Parameters and values of the full-factorial parametric study

Networks	Thresholds (t)	Numbers of seeds (n_s)	Budgets on critical nodes (β)
Epinions, slashdot, wikipedia	2, 3, 5	2, 3, 5, 10, 20	0, 5, 10, 20, 50, 100, 500, 1000

For each network and each combination of parameter values, 100 diffusion instances were run

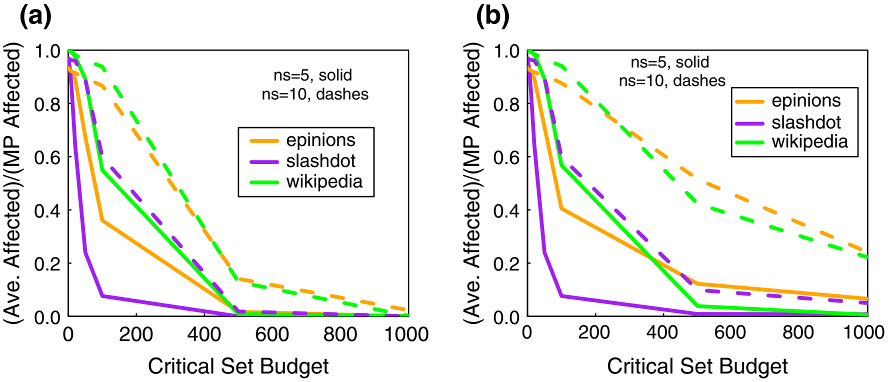


Fig. 7 Comparisons of the **a** CBH and **b** PBH for inhibiting diffusion in all networks, for two seed set sizes and $t = 2$. The ordinate is the average number of affected nodes (counting seed nodes) over 100 diffusion instances divided by the MP number of affected nodes

the **spread fraction**. The denominator is the theoretical upper bound on spread size, derived from Theorem 6 (which is established in Sect. 7).

Effect of critical set budget and number of seed nodes on spread fraction Figure 7 compares the spread fraction for CBH and PBH across all three networks for $n_s = 5$ (solid curves) and 10 (dashed curves). As one would expect, for both the methods, given a value for n_s, the spread fraction decreases as the budget β on critical nodes increases. The two plots show how a doubling of the number of seed nodes can produce a six-fold increase in the spread fraction; compare the slashdot data for $\beta = 100$, where increasing the number of seed nodes from 5 to 10 increases the spread fraction from about 0.1 to 0.6. The blocking performance of CBH and PBH are similar for slashdot; however, CBH significantly outperforms PBH for epinions and wikipedia when the number of seed nodes is increased to 10. As mentioned in Sect. 6.3, this behavior can be attributed to the significantly smaller average clustering coefficient of slashdot compared to the other networks.

Effect of threshold and critical set budget on spread fraction The effect of increasing threshold values on the spread fraction is shown in Fig. 8 for the epinions network using CBH for four values of β; the two plots correspond to $n_s = 20$ and 50, respectively. In Fig. 8a, if we use $t = 2$ and $\beta = 1000$ as a baseline case, we see that increasing the threshold from 2 to 3 enables the number of blocking nodes to be reduced by 500 while achieving a slightly lower spread fraction (0.27 vs. 0.22). If the threshold is increased to 5, the number of blocking nodes can be decreased by an order

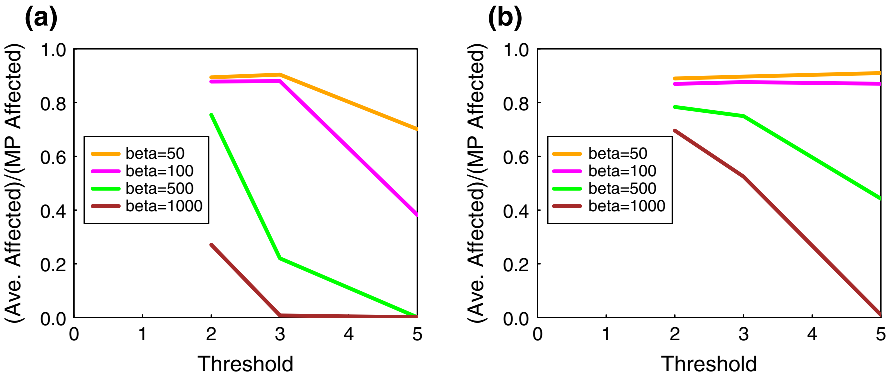


Fig. 8 Effect of threshold on spread fraction in the `epinions` network, with $\beta = 50$, 100, 500 and 1000. CBH is used in both plots, with **a** $n_s = 20$ and **b** $n_s = 50$

of magnitude, from 1000 to 100, with only a 50 % increase in the spread fraction (0.27 vs. 0.38). Thus, increasing the threshold can significantly decrease the critical node budget needed to achieve the same spread fraction. However, by comparing Fig. 8a, b, it is seen that increasing the number of seed nodes from 20 to 50 significantly increases the spread fraction.

Figure 8b also illustrates the benefit of normalizing the average spread size by the size of the seeded component of the t-core. For $\beta = 50$ and 100, as t increases from two to five, the average number of affected nodes decreases from about 32000 for $t = 2$, to 22000 for $t = 3$, to 14000 for $t = 5$. Yet, these decreases are essentially attributable to graph structure, rather than the effectiveness of critical nodes, as indicated by the relatively constant spread fraction for varying threshold.

Effect of critical nodes on the spread size per diffusion instance To this point, parametric study results have focused on the spread fraction, an average quantity over all 100 diffusion instances for a given n_s. Here, we instead examine the character of `slashdot` data for each diffusion instance for $n_s = 10$ in Fig. 9. For each value of β, the (normalized) spread size for each of the 100 diffusion instances is arranged in increasing numerical order and plotted in Fig. 9a for $t = 3$. To explain this figure, consider the plot for $\beta = 10$. The curve makes a steep transition from essentially 0 (i.e., essentially zero diffusion) to 0.95 at 30 % of iterations, indicating that 70 % of iterations produce significant diffusion. Increasing the value of β shifts the curves to the right, that is, reduces the fraction of iterations that produces large spread sizes. The value $\beta = 500$ halts all diffusion. Note that the maximum normalized spread size across all values of β is relatively constant. Because the ordinate value is near 1.0—for instances where the contagion spreads significantly—these data indicate that the number of affected nodes is a very large fraction of the t-core size.

Figure 9b provides similar data, but for $t = 5$. As a result, these curves are shifted to the right compared to those in Fig. 9a. Nonetheless, the transitions from small to large numbers of affected nodes are sharp, and for diffusion instances with large numbers of affected nodes, the numbers are very close to the numbers of nodes in the t-core since

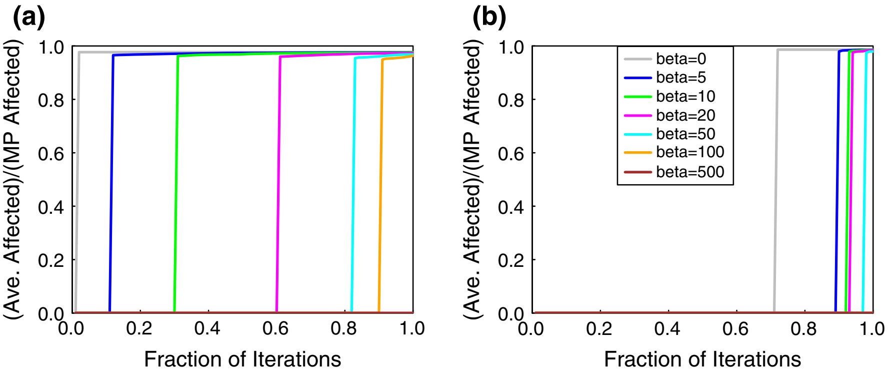
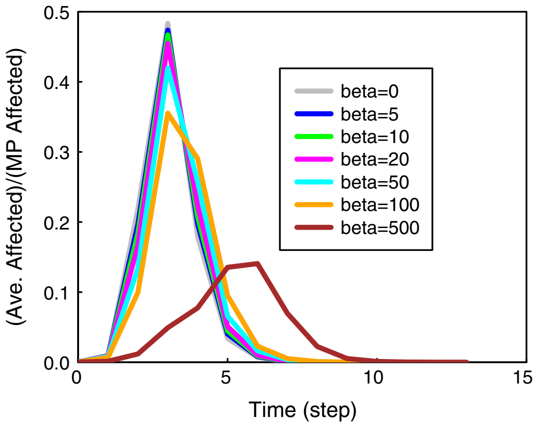


Fig. 9 Final fractions of affected nodes arranged in increasing order for each of the 100 iterations (to generate each *curve*) for the `slashdot` network and CBH heuristic for $n_s = 10$ and **a** $t = 3$ and **b** $t = 5$. The legend is the same in both plots

Fig. 10 Average curves of newly affected nodes for PBH for the case $t = 2$, $n_s = 10$, and different values of β with the `epinions` network



the ordinate values are near 1.0. We also observe that the large ordinate values are essentially independent of β. All data generated in this study possess these features.

Effect of critical set budget in delaying peak spread fraction In Fig. 10, the spread fraction, in terms of *newly* affected nodes at each time step, over the 100 diffusion instances is plotted for different β values. These results are for `epinions` with $t = 2$ and $n_s = 10$ when PBH is used. From the figure, it can be seen that while a budget of $\beta = 500$ does not halt the diffusion, it slows down the diffusion compared to the other budget sizes, moving the time of the peak in the number of newly affected nodes from 3 to 6. In applications such as disease propagation over a population or worm propagation in computer networks, this delay provides additional time for decision-makers to devise appropriate intervention strategies (Cohen et al. 2003; Porras et al. 2004) and could be used analogously for social contagions.

Blocking performance of CBH and PBH with a small number of seed nodes Figure 11 examines the regime of small numbers of seed nodes, and depicts the spread fraction as a function of β for `wikipedia`. A $(1/\beta)$ behavior is observed, so that the spread

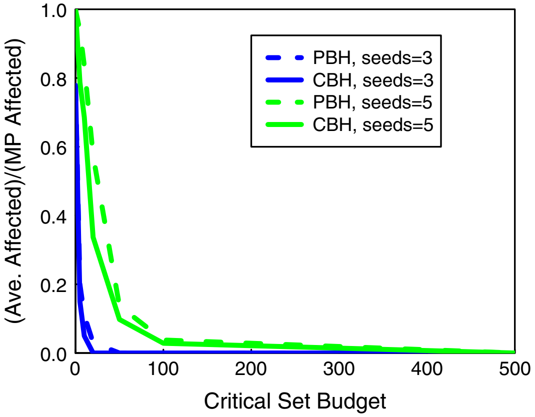


Fig. 11 Comparisons of the CBH and PBH in inhibiting diffusion in the `wikipedia` network for $t = 3$

fraction drops off sharply with increasing budget. However, to completely eliminate all cascades, $\beta = 500$ is required for both heuristics when $n_s = 5$. In most of our experiments, $\beta/n_s \geq 100$ was required to halt all diffusion. However, the $n_s = 3$ curves demonstrate that for very small seed sets and when $n_s = t$, $<$ 100 critical nodes can halt all diffusion, which corresponds to $\beta/n_s < 33$. Further, all of these curves depict more precipitous drops than those in Fig. 7.

Parameter settings that show significant differences between the blocking performances of CBH and PBH Figure 12 provides results showing the greatest differences in performance between the two heuristics in thwarting diffusion. This is done by comparing spread fractions. From Fig. 12, it is seen that for the `epinions` network with $n_s = 10$, the spread fraction under CBH and PBH are respectively 0.14 and 0.52 when β is fixed at 500. A similar difference is seen for the `wikipedia` network with $n_s = 20$.

It can be seen from Fig. 12 that, critically, once a value of n_s produces even a small (~ 0.10) spread fraction for a fixed β, further increases in n_s will result in large increases in spread fraction. For both networks, we observe that $\beta/n_s = 500/3 = 167$ will halt all diffusion. However, the `epinions` data illustrate that for $n_s = 5$ and $\beta = 500$, the ratio of $\beta/n_s = 100$ does not halt all diffusion for either CBH or PBH. Hence, as n_s increases, the ratio β/n_s required to stop all diffusion can be quite large.

Timing profiles for CBH and PBH We now compare the execution times of CBH and PBH. To carry out this study, serial implementations of CBH and PBH were run on a single core (with 2GB of memory) of a system with a 3 GHz Intel Xeon processor. Figure 13 depicts the execution times for each heuristic for $\beta = 5$ as n_s is varied. The two plots are for `epinions` and `wikipedia` respectively, with different curves in the same plot corresponding to the two heuristics and three different threshold values (2, 3 and 5). For the `epinions` network, Fig. 13a, these times translate into a maximum of roughly 1.5 hours for CBH to determine 100 sets of critical nodes, versus less than 5 minutes for PBH. The execution times for `wikipedia` are significantly smaller than those for `epinions` since the former network is smaller in size (by a factor of 10) than the latter. In general, PBH is clearly faster than CBH, and this experimental result is in agreement with the worst-case running time estimates for the

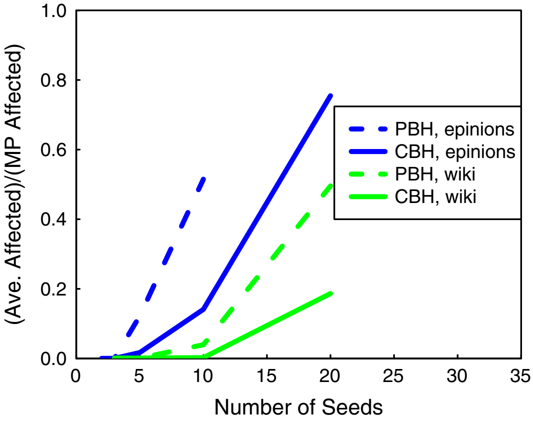


Fig. 12 Comparisons of the CBH and PBH in inhibiting diffusion in the `epinions` with $t = 2$ and `wikipedia` (`wiki`) with $t = 3$. The number β of critical nodes is 500

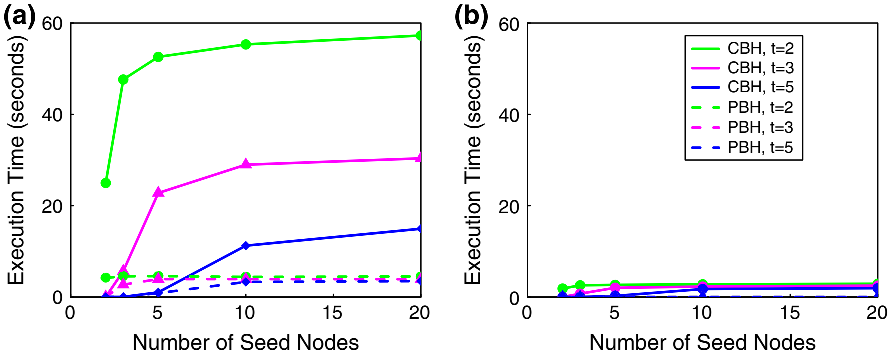


Fig. 13 Times for CBH and PBH to compute one set of critical nodes for $\beta = 5$ as a function of number of seed nodes for three threshold values. Part **a** is for the `epinions` network and Part **b** is for the `wikipedia` network. Times are averages over 100 iterations. The legend is the same for both plots

two methods obtained in Sect. 5. Since CBH is better than PBH in blocking complex contagions, we see a tradeoff between blocking performance and speed of algorithm execution.

7 Comparisons of spread sizes against theoretical upper bound

As demonstrated in Sect. 6.4, it is useful to reason about the effectiveness of a blocking scheme in terms of how many nodes still get affected when using critical nodes, relative to the total number of nodes that could possibly be affected without critical nodes. We now address that issue in a quantitative manner by presenting an upper bound on the spread size of a complex contagion. Our approach uses a *static* network property that is easily computed to provide a bound on system *dynamics*. Furthermore, we provide an extensive experimental evaluation of our bound on many networks and different threshold values.

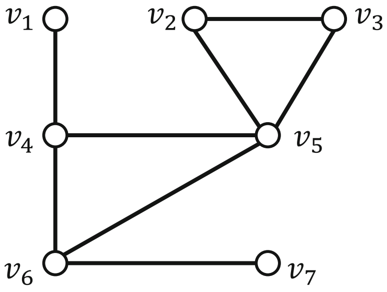


Fig. 14 An example to illustrate the definitions of t-core and maximal t-core

7.1 Theoretical bounds on spread size

Recall that the maximum spread size in a social network is the total number of nodes whose state is 1 at the end of the diffusion process. We assume that the given SyDS is a t-threshold system for some $t \geq 1$; that is, each local transition function is the t-threshold function. We start with a graph theoretic definition, extending (Seidman 1983).

Definition 1 Let $G(V, E)$ be an undirected graph and let $t \geq 0$ be an integer. A **t-core** of G is an induced subgraph $G'(V', E')$ of G such that each node in G' has a degree of at least t. A t-core $G'(V', E')$ of G is **maximal** if there is no *strict* superset $V'' \supset V'$ of nodes such that the subgraph of G induced on V'' is also a t-core.

Example Consider the graph $G(V, E)$ shown in Fig. 14. The induced subgraph formed on the node set $\{v_4, v_5, v_6\}$ is a 2-core of G. Likewise, the induced subgraph formed on the node set $\{v_2, v_3, v_5\}$ is also 2-core of G. The induced subgraph formed on the node set $\{v_2, v_3, v_4, v_5, v_6\}$ is the maximal 2-core of G.

For any graph G and integer $t \geq 0$, it is easy to see that the maximal t-core is *unique*. In fact, the maximal t-core of G can be constructed efficiently by repeatedly removing nodes whose degree is less than t. The removal process ends when all remaining nodes have degree $\geq t$ (Seidman 1983).

Even if G is connected, the maximal t-core may not be connected. For a graph G and integer $t \geq 0$, we use $L_G(t)$ to denote the number of nodes in a largest connected component of the maximal t-core of G. As will be seen from the results of this section, the parameter $L_G(t)$ can be used to bound the maximum spread size in t-threshold systems. We begin with a simple lemma.

Lemma 2 *Let $G(V, E)$ be an undirected graph. For any $t \geq 0$, a node $v \in V$ is in the maximal t-core of G if and only if node v has at least t neighbors that are also in the maximal t-core.*

Proof Let $G'(V', E')$ denote the maximal t-core of G. If v is in V', then by definition, its degree in G' is $\geq t$; that is, v has at least t neighbors in G'. For the other direction, assume that t of the neighbors of v are in G'. Consider the node removal process that produced G'. This process did not remove any of the t neighbors of v which are in G'. Thus, throughout the removal process, the degree of v was at least t. In other words, v remains in G'. □

We present a result that bounds the maximum spread size in a t-threshold system in terms of the size of the largest connected component of its maximal t-core. In stating this result, we assume that the seed set is of size t. If the seed set has less than t nodes, obviously, there will be no further diffusion in a t-threshold system.

Theorem 6 *Let G be the underlying graph of a t-threshold SyDS, where $t \geq 1$. Let $G'(V', E')$ denote the maximal t-core of G. For any seed set $I \subseteq V'$ with $|I| = t$, the maximum spread size is bounded by $L_G(t)$, the size of a largest connected component of G'. Moreover, for each $t \geq 1$, this bound is achievable.*

Proof We first prove the upper bound. For $t = 1$, the set I contains only one node, say v, and diffusion can lead to new affected nodes only in the connected component that contains v. Thus, the upper bound is trivial for $t = 1$.

So, assume that $t \geq 2$. First, consider the case where the nodes in I are distributed over two or more connected components of the maximal t-core G'. Thus, no node of G' is adjacent to all the nodes in I. In this case, we can prove by contradiction no further diffusion can occur. To see this, consider a node $v \in V$ whose state changes from 0 to 1 in the first time step. Since the threshold is t, node v must be adjacent to all the t nodes of I. Then, by Lemma 2, v will also be in G'. However, this contradicts the previous conclusion that no node in G' is adjacent to all the nodes of I.

Thus, we may assume that all nodes of I are in the same connected component of G'. In such a case, all the newly affected nodes will also be part of that component. Therefore, the spread size is bounded by $L_G(t)$ when $t \geq 2$.

We now argue that this bound is achievable through a simple example. For each $t \geq 1$, let the graph $G(V, E)$ consist of a clique on $t + 1$ nodes. Since the degree of each node of G is t, $L_G(t) = |V|$. Further, choosing any t nodes of the $t + 1$ clique as the seed nodes ensures that all the nodes in V are affected; that is, the maximum spread size is $t + 1 = L_G(t)$. □

The bound given by Theorem 6 enables us to determine that maximum spread sizes such as those in Fig. 9 (Sect. 6.4) are indeed the largest possible spread sizes for a given network and threshold. Also, our approach of computing the size of a largest connected component of a t-core is closely aligned with determining the largest possible spread size for $t = 1$ diffusion by computing the largest connected component of a graph (Albert et al. 2000; Holme 2004).

There are classes of graphs for which the bound given by Theorem 6 is pessimistic. For example, consider an $r \times r$-node lattice graph $G(V, E)$, with $r \gg 2$, where each node is connected to its four neighbors (if they exist) along the four geographic directions (thus, nodes along the boundary have degrees less than 4). Since all nodes have degree ≥ 2, $L_G(2) = |V|$. Yet, it can be seen that for any seed set with $|I| = t = 2$, the MP spread size is $4 \ll L_G(2)$. Thus, it is of interest to experimentally evaluate the effectiveness of the bound for different classes of graphs and values of t. This evaluation is carried out in the next section.

Table 11 Selected characteristics of three synthetic networks

Network	Number of nodes	Number of edges	Average degree	Average clustering coefficient	Number of connected compo-nents	Size of largest component
`er`	99998	500172	10.0	0.000106	1	99998
`sf-01`	100000	499959	10.0	0.000994	1	100000
`sf-02`	100007	568277	11.4	0.0127	1032	97921

7.2 Experimental evaluation of the spread size upper bound

In this section, we use two sets of experiments to carry out an evaluation of the upper bound of Theorem 6 for various synthetic and real social networks. The first set chooses seed nodes from appropriate core subgraphs as used in the proof of Theorem 6. The second set considers a different seeding method and evaluates whether the theoretical bound remains robust. We now discuss the two sets of experiments and results.

Experimental evaluation using core construction Our experimental procedure is as follows. We consider the three real social networks of this study (`slashdot`, `epinions` and `wikipedia`) along with three synthetic networks: two SF networks (`sf-01` and `sf-02`) constructed using two well-known methods (preferential attachment (Barabasi and Albert 1999) and configuration model (Newman 2003), respectively), and an Erdős–Renyi (ER) random graph. The purpose of using synthetic networks in this study is to evaluate whether particular construction methods yield graph structures that affect the upper bound on spread size. Data for the three synthetic graphs are given in Table 11. The average clustering coefficients for the two sf graphs differ by an order of magnitude and these values are also far different from those in Table 3; recall the strong effect of clustering on the results in Sect. 6.3. Although not shown, the degree distributions for the two SF networks are different, even though the average degree is about the same.

We consider three different values of t, namely 2, 3 and 5. We construct the corresponding maximal cores and use Theorem 6 to determine the upper bound on the spread sizes for various graphs. We compare these values against the maximum measured spread sizes from simulations. In these simulations, seed nodes for the three real networks were chosen from their maximal 20-core subgraphs (which are themselves subgraphs of the corresponding 2-cores, 3-cores and 5-cores). Since the average degree of the nodes in the three synthetic graphs is around 10, simulations for the three synthetic networks were done using seed sets from the maximal 10-cores.

Figure 15 provides results for the six networks and three threshold values. There are three data points in the plot for each network, corresponding to $t = 2$, 3, and 5, respectively. For all networks *except* the ER network, the agreement between the experimentally measured spread size (ordinate) and the theoretical bound (abscissa) is excellent, illustrating that in real and synthetic networks, the maximum spread size can be achieved. As just one representative example, consider `wikipedia`. When $n_s = t = 2$, 97 % of simulated diffusion instances achieve the upper bound spread

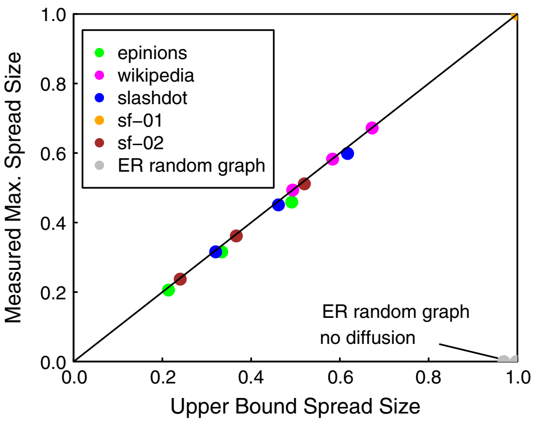


Fig. 15 Comparisons of maximum measured spread sizes from simulations (ordinate values) and upper bound spread sizes from Theorem 6 (abscissa values). The 45° line of perfect agreement is also provided. The data are for the networks of Tables 3 and 11, with thresholds $t = 2, 3$, and 5. Note the data for `sf-01` in the *upper right* hand corner at $(x, y) = (1, 1)$

size. When $n_s = t = 3$ and $n_s = t = 5$, the corresponding percentages are 77 and 35 %, respectively.

The ER random graph data, however, show that the spread size is much smaller than the theoretical maximum. We can explain this behavior as follows. For the 99998-node ER random graph, with an average degree of 10, the probability of having an edge between any pair of nodes is $10/(99998 - 1) \approx 10^{-4}$. It follows that the probability of having two seed nodes each forming an edge with a third node v (so that v will be affected for $t = 2$ diffusion) is roughly 10^{-8}. A simple repetition of this argument shows that ER random graphs with tens of thousands of nodes (or more) and small to moderate degrees will propagate complex contagions with very low probability. Accordingly, the measured spread sizes are nearly zero in Fig. 15, while the theoretical bound is large. These extremes of tight and pessimistic upper bounds motivate our next experiments.

Experimental evaluation using a random seeding and a node removal scheme To understand whether the theoretical upper bound on spread size is robust when the assumptions used in deriving the bound are relaxed, we now consider a second method of seeding. We utilize the *random* seeding method of (Centola and Macy 2007; Centola 2009) where a node v is chosen uniformly at random and the seed set consists of v and all of its neighbors. Since these experiments involve a large number of graphs (as described momentarily), only one threshold value, namely $t = 2$, was used. Thus, the seed node sets are not from the maximal 2-core, as used in Theorem 6.

For this study, we also explored graph structure effects by considering two types of synthetic graphs, namely growth model SF networks and growth model exponential-decay networks, whose degree distributions are often found in real social networks (Centola 2009). These graphs are generated using a combined approach from (Barabasi and Albert 1999) and (Schank and Wagner 2005), producing graphs with $d_{ave} = 4$ and $C_{ave} = 0.24$; using the cited construction procedures enabled us to control both of these properties.

Thirty graph instances of each type are generated, each with 10000 nodes, and these constitute the original graphs. For each of the 30 original instances, six values (namely, 0, 10^{-4}, 10^{-3}, 10^{-2}, 10^{-1} and 2×10^{-1}) of the fraction f of removed nodes are

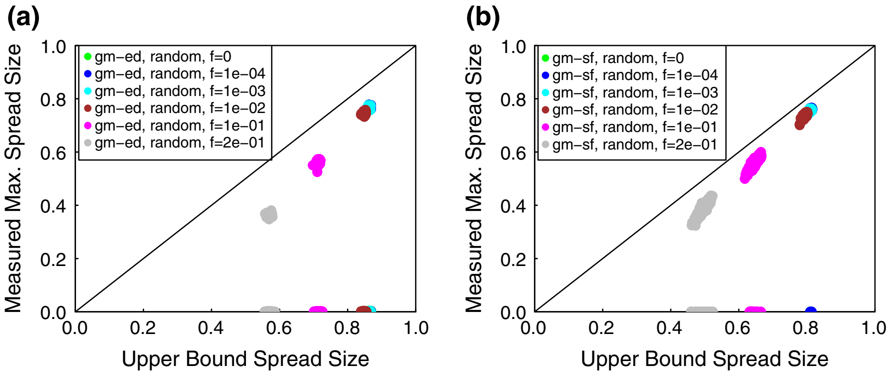


Fig. 16 Comparisons of maximum measured spread sizes from simulations (ordinate values) and upper bound spread sizes from Theorem 6 (abscissa values). The 45° line of perfect agreement is also provided. **a** Data for 3600 graph instances of `gm-ed` networks with different fractions f of nodes removed at random from the 30 original graph instances. **b** Data for 3600 graph instances of `gm-sf` networks with different fractions f of nodes removed at random from the 30 original graph instances

considered. These removed node fractions alter the graph structure and hence provide another means of evaluating graph structure effects on the theoretical upper bound spread size. For each value of f, 20 sets of nodes are removed from each original graph, in turn, resulting in 3600 ($= 30 \cdot 6 \cdot 20$) graph instances. For each graph, the size of the largest connected component of the 2-core is computed. Then, $t = 2$ diffusion is simulated, with 20 seed sets for each graph, to experimentally determine the largest spread size.

Figure 16a contains data for the 3600 growth model exponential-decay (`gm-ed`) networks, and Fig. 16b contains comparable data for 3600 growth model SF (`gm-sf`) networks. With respect to the data in Fig. 16a, over 20 % of the 3600 graph instances produce spread sizes near the line of agreement and 80 % of the graphs produce virtually no diffusion. For the graphs without any removed nodes, 27 % of diffusion instances achieve close to the maximum spread size. However, even a few graphs with 20 % of nodes removed generate spread sizes close to the theoretical limit. With respect to the data in Fig. 16b, over 98 % of the 3600 graph instances produce spread sizes near the line of agreement. For the conditions of this study, the maximum spread size is more readily achieved in `gm-sf` networks. More generally, these results suggest that the bound given by Theorem 6 provides a reasonable indication of the maximum spread size even when the conditions of the theorem are relaxed.

8 Conclusions and future work

We considered the problem of inhibiting the propagation of complex contagions in social networks. We developed analytical formulations for several versions of the problem. We showed that obtaining provably good heuristics for these problems is computationally intractable. We developed two intuitively appealing heuristics for the problem and showed that they perform well on several social networks. Both theoretical and experimental results also demonstrated ways in which simple contagions differ from complex contagions.

There are several directions for future work. First, it is of interest to develop practical heuristics for the critical set problem for complex contagions when there are weights on edges (to model the degree to which a node is influenced by a neighbor). A second research direction is to study the critical set problem for complex contagions when the diffusion process is probabilistic; that is, for each combination of input values, the local transition function at a node gives the probability that the node's state changes to 1. Both analytical and experimental results in that context are of interest. A related avenue is investigation of contagion propagation and inhibition under incomplete information. Experimental studies of contagion blocking are also important to undertake. Although edge deletion, rather than node removal, has been studied (Zhang et al. 2009), we feel there is much more work to be done. Another direction to explore is theoretical models that explain differences in results between the CBH and PBH heuristics. Finally, a challenging research direction is to formulate and study the problem for time-varying networks in which nodes and edges may appear and disappear over time.

Acknowledgments We thank the reviewers for their careful reading of the manuscript and their suggestions and comments. We thank our external collaborators and members of the Network Dynamics and Simulation Science Laboratory (NDSSL) for their suggestions and comments. This work has been partially supported by NSF HSD Grant SES-0729441, NSF PetaApps Grant OCI-0904844, NSF NETS 1201 Grant CNS-0831633, NSF NetSE Grant CNS-1011769, NSF SDCI 1202 Grant OCI-1032677, DTRA R&D Grant HDTRA1-09-1-0017, DTRA Grant HDTRA1-11-1-0016, DTRA 1203 CNIMS Contract HDTRA1-11-D-0016-0001, NIH MIDAS Grant 1205 2U01GM070694-09, NIH MIDAS Grant 3U01FM070694-09S1, NIH MIDAS Grant 2U01GM070694-09, and LLNL Fellowship SubB596713.

Appendix: Results beyond homogeneous thresholds

Many of the results presented in Sect. 4 were for the case of homogeneous absolute thresholds. We now briefly indicate how the results can also be extended to other forms of thresholds defined in Sect. 2.3.

We note that heterogeneous thresholds (absolute and relative) are a special case of the corresponding form of homogeneous thresholds. Therefore, any hardness result that holds for homogeneous thresholds also holds for heterogeneous thresholds. We use this fact several times in the following description. The statements and proofs of all the lemmas and theorems referenced below appear in Sect. 4.

1. Lemma 1 holds for both homogeneous and heterogeneous absolute thresholds. With a minor modification to the proof, the result can be shown to hold for homogeneous and heterogeneous relative thresholds as well. The modification is that when the counter value for a node indicates that the node has reached its relative threshold, the node is added to the list of affected nodes.
2. Theorem 1 holds for homogeneous absolute thresholds and hence for heterogeneous absolute thresholds. To see that it holds for relative thresholds as well, we note that the absolute threshold value t for a node v can be thought of as the relative threshold value of $t/\deg(v)$, where $\deg(v)$ is the number of neighbors of v (includ-

ing v itself). The same approach can be used to show that Theorems 2, 3 and 4 hold for heterogeneous absolute thresholds and both forms of relative thresholds.

3. It was pointed out in Sect. 4 that the approximation algorithm for the SCS-SASN problem actually works for heterogeneous absolute thresholds. Hence, it works for homogeneous absolute thresholds as well. To see that it also works for relative thresholds, we first convert a relative threshold value of τ for a node v to the absolute threshold value $\lceil \tau * \deg(v) \rceil$ and then use the given approximation algorithm.

References

Acemoglu D, Ozdaglar A (2011) Opinion dynamics and learning in social networks. Dyn Games Appl 1:3–49

Albert R, Jeong H, Barabasi A (2000) Error and attack tolerance of complex networks. Nature 406:378–381

Anderson A, Huttenlocher D, Kleinberg J, Leskovec J (2012) Effects of user similarity in social media. In: Proceedings of the 5th ACM symposium on web search and data mining (WSDM 2012).

Anshelevich E, Chakrabarty D, Hate A, Swamy C (2009) Approximation algorithms for the firefighter problem: cuts over time and aubmodularity. In: Proceedings of the conference of the international society for augmentative and alternative communication (ISAAC 2009), pp 974–983

Arulselvan A, Commander CW, Elefteriadou L, Pardalos PM (2009) Detecting critical nodes in sparse graphs. Comput Oper Res 36(7):2193–2200

Barabasi A, Albert R (1999) Emergence of scaling in random networks. Nature 286:509–512

Barash V (2011) The dynamics of social contagion. PhD thesis, Cornell University.

Barash V, Cameron C, Macy M (2012) Critical phenomena in complex contagions. Soc Netw 34:451–461

Barrett C, Bisset K, Eubank S, Feng X, Marathe M (2008) EpiSimdemics: an efficient algorithm for simulating the spread of infectious disease over large realistic social networks. In: Proceedings of the 2008 ACM/IEEE conference on supercomputing.

Barrett CL, Hunt HB, Marathe MV, Ravi SS, Rosenkrantz DJ, Stearns RE (2006) Complexity of reachability problems for finite discrete dynamical systems. J Comput Syst Sci 72(8):1317–1345

Barrett CL, Hunt HB, Marathe MV, Ravi SS, Rosenkrantz DJ, Stearns RE, Thakur M (2007) Predecessor existence problems for finite discrete dynamical systems. Theor Comput Sci 386(1–2):3–37

Bonacich P (1972) Factoring and weighting approaches to status scores and clique identification. J Math Soc 2:113–120

Borgatti SP (2006) Identifying sets of key players in a social network. Comput Math Organiz Theor 12:21–34

Briesemeister L, Lincoln P, Porras P (2003) Epidemic profiles and defense of scale-free networks. In: Proceedings of the 2003 ACM CCS Workshop on Rapid Malcode (WORM 03), pp 67–75

Centola D (2009) Failure in complex social networks. J Math Soc 33:64–68

Centola D (2010) The spread of behavior in an online social network experiment. Science 329:1194–1197

Centola D, Macy M (2007) Complex contagions and the weakness of long ties. Am J Sociol 113(3):702–734

Centola D, Eguiluz V, Macy M (2006) Cascade dynamics of complex propagation. Phys A 374:449–456

Centola D, Gonzlez-Avella JC, Eguluz VM, Miguel MS (2007) Homophily, cultural drift, and the co-evolution of cultural groups. J Conflict Resolut 51:905–929

Cha M, Mislove A, Adams B, Gummadi K (2008) Characterizing social cascades in Flickr. In: Proc. of the first workshop on online social networks (WOSN 08), pp 13–18

Chakrabarti D, Wang Y, Wang C, Leskovec J, Faloutsos C (2008) Epidemic thresholds in real networks. ACM Trans Inf Syst Secur 10(4):1–26

Cohen R, Havlin S, Avraham D (2003) Efficient immunization strategies for computer networks and populations. Phys Rev Lett 91:247

Cormen T, Leiserson CE, Rivest RL, Stein C (2001) Introduction to algorithms. MIT Press, Cambridge

Crucitti P, Latora V, Marchiori M, Rapisarda A (2004) Error and attack tolerance of complex networks. Phys A 340:388–394

Dezso Z, Barabasi A (2002) Halting viruses in scale-free networks. Phys Rev E 65:055

Dodds PS, Watts DJ (2005) A generalized model of social and biological contagion. J Theor Biol 232(4):587–604

Domingos P, Richardson M (2001) Mining the network value of customers. In: Proc. ACM intl. conf. on data mining and knowledge discovery (KDD 2001), pp 57–61

Dreyer P, Roberts F (2009) Irreversible k-Threshold Processes: Graph-Theoretical Threshold Models of the Spread of Disease and Opinion. Discrete Applied Mathematics 157:1615–1627

Eubank S, Kumar VSA, Marathe MV, Srinivasan A, Wang N (2006) Structure of social contact networks and their impact on epidemics. In: Abello J, Cormode G (eds) Discrete methods in epidemiology. DIMACS series in discrete mathematics and theoretical computer science. American Mathematical Society, Providence, pp 179–200

Freeman LC (1976) A set of measures of centrality based on betweenness. Sociometry 40:35–41

Ganesh A, Massoulie L, Towsley D (2005) The effect of network topology on the spread of epidemics. In: Proceedings of the 24th annual joint conference of the IEEE computer and communications societies (INFOCOM 2005), vol 2, pp 1455–1466

Garey MR, Johnson DS (1979) Computers and intractability: a guide to the theory of NP-completeness. W. H. Freeman and Co., San Francisco

Gonzalez-Bailon S, Borge-Holthoefer J, Rivero A, Moreno Y (2011) The dynamics of protest recruitment through an online network. Nature Scientific Reports pp 1–7. doi:10.1038/srep00197

Granovetter M (1973) The strength of weak ties. Am J Sociol 78(6):1360–1380

Granovetter M (1978) Threshold models of collective behavior. Am J Sociol 83(6):1420–1443

Gruhl D, Guha R, Liben-Nowell D, Tomkins A (2004) Information diffusion through blogspace. In: Proc. of the 13th international world wide web conference (WWW 2004), pp 491–501

Guha R, Kumar R, Raghavan P, Tomkins A (2004) Propagation of trust and distrust. In: Proc. of the 13th international world wide web conference (WWW 2004), pp 403–412

Habiba, Yu Y, Berger-Wolf TY, Saia J (2008) Finding spread blockers in dynamic networks. In: The 2nd SNA-KDD Workshop '08 (SNA-KDD 2008)

Harris KM (2008) The National Longitudinal Study of Adolescent Health (Add Health), Waves I and II, 1994–1996; Wave III, 2001–2002 [machine-readable data file and documentation]. Chapel Hill, NC: Carolina Population Center, University of North Carolina at Chapel Hill 2008

Holme P (2004) Efficient local strategies for vaccination and network attack. Europhys Lett 68:908–914

Jin C, Liu J, Deng Q (2009) Network virus propagation model based on effects of removing time and user vigilance. Int J Netw Secur 9:156–163

Kawachi K (2008) Deterministic models for rumor transmission. Nonlinear Anal 9:1989–2028

Kempe D, Kleinberg J, Tardos E (2003) Maximizing the spread of influence through a social network. In: Proc. ACM Intl. Conf. on data mining and knowledge discovery (KDD 2003), pp 137–146

Kempe D, Kleinberg J, Tardos E (2005) Influential nodes in a diffusion model for social networks. In: Proc. Intl. Conf. on automata, languages and programming (ICALP 2005), pp 1127–1138

Kleinberg J (2007) Cascading behavior in networks: algorithmic and economic Issues. In: Nissan N, Roughgarden T, Tardos E, Vazirani V (eds) Algorithmic game theory. Cambridge University Press, New York, pp 613–632

Kleinberg JM (1999) Authoritative sources in a hyperlinked environment. J ACM 46:604–632

Kossinets G, Kleinberg J, Watts D (2008) The structure of information pathways in a social communication network. In: Proc. ACM Intl. Conf. on data mining and knowledge siscovery (KDD 2008)

Kuhlman C, Kumar V, Marathe M, Ravi S, Rosenkrantz D, Swarup S, Tuli G (2011) A bithreshold model of complex contagion and its application to the spread of smoking behavior. In: Proceedings of the workshop on social network mining and analysis (SNA-KDD 2011)

Kuhlman CJ, Kumar VA, Marathe MV, Ravi SS, Rosenkrantz DJ (2010a) Exploiting network structure in enhancing diffusion of complex contagions. In: Proc. workshop on analysis of complex networks (ACNE 2010)

Kuhlman CJ, Kumar VA, Marathe MV, Ravi SS, Rosenkrantz DJ (2010b) Finding critical nodes for inhibiting diffusion of complex contagions in social networks. In: Proceedings of the European conference on machine learning and principles and practice of knowledge discovery in databases (ECML PKDD 2010), pp 111–127

Leskovec J, Adamic LA, Huberman BA (2007) The dynamics of viral marketing. ACM Trans Web 1(1):251–262

Leskovec J, Lang K, Dasgupta A, Mahoney M (2008) Statistical properties of community structure in large social and information networks. In: Proceedings of the 17th international world wide web conference (WWW 2008)

Leskovec J, Huttenlocher D, Kleinberg J (2010) Predicting positive and negative links in online social networks. In: Proceedings of the 19th international world wide web conference (WWW 2010)

Liu YY, Slotine JJ, Barabsi AL (2011) Controllability of complex networks. Nature 473:167–173

Longini IM, Nizam A, Xu S, Ungchusak K, Hanshaoworakul W, Cummings DAT, Halloran ME (2005) Containing pandemic influenza at the source. Science 309:1083–1087

Macy M (1991) Chains of cooperation: threshold effects in collective action. Am Sociol Rev 56(6):730–747

Madar N, Kalisky T, Cohen R, Ben-Avraham D, Havlin S (2004) Immunization and epidemic dynamics in complex networks. Eur Phys J B 38:269–276

Martin G, Marinescu MC, Singh DE, Carretero J (2011) Leveraging social networks for understanding the evolution of epidemics. BMC Syst Biol 5:1–16

Melnik S, Ward JA, Gleeson JP, Porter MA (2013) Multi-stage complex contagion. Chaos 23:013

Mobilia M (2003) Does a single zealot affect an infinite group of voters? Phys Rev Lett 91(2):028701

Mobilia M, Petersen A, Redner S (2007) On the role of zealotry in the voter model. J Stat Mech P08029:1–17

Newman M (2003) The structure and function of complex networks. SIAM Rev 45:167–256

Newman MEJ, Park J (2003) Why social networks are different from other types of networks. Phys Rev E 68:036122

Page L, Brin S, Motwani R, Winograd T (1999) The pagerank citation ranking: Bringing order to the web. Technical Report 1999–66, Stanford InfoLab.

Pastor-Satorras R, Vespignani A (2001) Epidemic spreading in scale-free networks. Phys Rev Lett 86:3200–3203

Perumalla K, Seal S (2010) Reversible parallel discrete-event execution of large-scale epidemic outbreak models. In: Proceedings of the 24th ACM/IEEE/SCS workshop on principles of advanced and distributed simulation (PADS 2010)

Porras P, Briesemeister L, Skinner K, Levitt K, Rowe J, Ting YCA (2004) A hybrid quarantine defense. In: Proceedings of the 2004 ACM CCS Workshop on Rapid Malcode (WORM 04), pp 73–82

Prakash B, Tong H, Valler N, Faloutsos M, Faloutsos C (2010) Virus propagation on time-varying networks: theory and immunization algorithms. In: Proceedings of the 2010 European conference on machine learning and knowledge discovery in databases (ECML PKDD 2010), pp 99–114

Raz R, Safra S (1997) A sub-constant error-probability low-degree test, and a sub-constant error-probability characterization of NP. In: Proc. ACM symp. on theory of computing (STOC 1997), pp 475–484

Richardson M, Domingos P (2002) Mining knowledge-sharing sites for viral marketing. In: Proc. ACM Intl. Conf. on data mining and knowledge discovery (KDD 2002), pp 61–70

Richardson M, Agrawal R, Domingos P (2003) Trust Management for the Semantic Web. In: Proc. of the Second International Semantic Web Conference (ISWC 2003), pp 351–368

Romero D, Meeder B, Kleinberg J (2011) Differences in the mechanics of information diffusion across topics: idioms, political hashtags, and complex contagion on twitter. In: Proceedings of the 20th international world wide web conference (WWW 2011)

Salathe M, Jones J (2010) Dynamics and control of diseases in networks with community structure. PLoS Comput Biol 6:e1000,736-1–e1000,736-11

Schank T, Wagner D (2005) Approximating clustering coefficients and transitivity. J Algorithms Appl 9(2):265–275

Schelling T (1978) Micromotives and macrobehavior. W. W. Norton and Company, New York

Seidman SB (1983) Network structure and minimum degree. Soc Netw 5:269–287

Shi X, Zhu J, Cai R, Zhang L (2009) User grouping behavior in online forums. In: Proceedings of the 15th ACM SIGKDD international conference on knowledge discovery and data mining (KDD 09), pp 777–786

Siegel D (2009) Social networks and collective action. Am J Polit Sci 53:122–138

Siegel D (2010) When does repression work? collective action in social networks. J Polit 73:993–1010

Tantipathananandh C, Berger-Wolf TY, Kempe D (2007) A framework for community identification in dynamic social networks. In: Proc. ACM Intl. Conf. on data mining and knowledge discovery (KDD 2007), pp 717–726

Tong H, Prakash B, Tsourakakis C, Eliassi-Rad T, Faloutsos C, Chau D (2010) On the vulnerability of large graphs. In: Proceedings of the 10th IEEE conference on data mining (ICDM 2010), pp 1091–1096

Ugander J, Backstrom L, Marlow C (2012) Structural diversity in social contagion. Proc Natl Acad Sci 109(9):5962–5966

Vazirani VV (2001) Approximation algorithms. Springer, New York

Vespignani A (2012) Modelling dynamical processes in complex socio-technical systems. Nat Phys 8:32–39

Wang Y, Chakrabarti D, Wang C, Faloutsos C (2003) On the vulnerability of large graphs. In: Proceedings of the 22nd international symposium on reliable distributed systems (RDS 2003), pp 25–34

Watts D (2002) A simple model of global cascades on random networks. Proc Natl Acad Sci 99(9):5766–5771

Yildiz E, Acemoglu D, Ozdaglar A, Saberi A, Scaglione A (2011) Discrete opinion dynamics with stubborn agents. OPRE-2011-01-026.

Zhang HF, Li KZ, Fu XC, Wang BH (2009) An efficient control strategy of epidemic spreading on scale-free networks. Phys Rev Lett 26:068,901-1–068,901-4