# Modeling Malware Propagation in Networks

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## Abstract

The paper proposes to study spreading characteristics of malware using a stochastic model, based on the Interactive Markov Chains, that belongs to the special case called "influence model." We generalize influence model so that the status of a node and the influences a node exerts from neighbors depend on the current status of the node and the statuses of its neighbors. Such generalized model is flexible enough to model various phenomena including spreading of failures in power grid, malwere propagation in computer networks, and spreading of ideas in social networks.

As a particular example we discuss the spreading of e-mail viruses through a network. Although we have focused on the propagation of e-mail viruses, the approach proposed here is general enough to be adapted to describe other malware propagation. Our model is numerically and analytically tractable. We consider three stochastic models: susceptible-infective-removed (SIR), susceptible-infective-immune (SIM), and susceptible-infective-immune-susceptible (SIMS). For SIMS model and arbitrary network topology closed expressions for average number of infected and immune nodes when time goes to infinity are found. We show that epidemic threshold for SIMS model does not depend on the network topology.

*Key words:* malware propagation, computer viruses, stochastic models, malicious software, susceptible-infective-immune model

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## 1. Introduction

Protecting a computer system from malicious attacks is a key challenge to network security and management. Malware (short for malicious software) is designed specially for either damaging or disrupting a computer system. The terminology covers over an entire gamut of hostile softwares including viruses, Trojan Horses, and network worms [1, 2].

Several approaches have been proposed to model and simulate malware spreading in complex networks with different topologies. An epidemiological model, which is suitable to analyze virus spreading in random graphs, was presented in [3]. In Ref. [4] a model for virus propagation in arbitrary topologies was proposed and epidemic threshold of virus infection was obtained. The authors proved that, under reasonable approximations, the epidemic threshold for a network is closely related to the largest eigenvalue of its adjacency matrix [4]. The spread of Code Red, taking into consideration of the human countermeasures and the worms impact on Internet infrastructure, was modeled in [5]. The propagation of active worms employing random scanning for investigating the spread of localized-scanning worms was studied in [6]. Epidemiological model for investigating the requirements for containing the self-propagation worm with random target selection was applied in [7]. In Ref. [8] the authors addressed the question of what topological properties of the graph determine the persistence of epidemics. In Ref. [9] the authors developed an analytic framework for modeling the dynamics of malware propagation in networks of smart phones that specifically accounts for the mobile nature of these devices. The focus of work in Ref. [10] is on modeling the spread of topological malwares, which is important for understanding their potential damages, and for developing countermeasures to protect the network infrastructure. The authors of Ref. [11] modeled the spread of malware in decentralized, Gnutella type of peer-to-peer networks. In the article [12], the author considered the effects of Internet worms on persistently unpatched hosts and hosts for which vulnerabilities are refreshed. The focus of Ref. [13] was on spreading dynamics of malware that can replicate itself on other nodes in a network of wireless sensing devices.

This paper proposes to study the behavior of malware, including their spreading characteristics. To this purpose we build a stochastic model based on Influence Model that provides a probabilistic analysis of the system. Although we have focused on the propagation of e-mail viruses, the approach is general enough to be adapted to describe other kinds of malware. The concept of interactions on networks is not new, and has appeared in various forms in a variety of fields. The influence model [14] differs from other previous models of interactions (such as stochastic Ising model, cellular automata, infinite particle system, voter model, interactive Markov chain) in several ways, two most important are (1) each site (node) may contain an arbitrary (finite) local chain and (2) the network may have an arbitrary (finite) graph and influence structure. The influence model [14, 15, 16] is a simple (and mathematically tractable) model of random, dynamical interactions on networks. It consists of a network of nodes, each with a status that evolves over time. The evolution of the status at a node is according to an internal Markov chain, but with transition probabilities that depend on, not only the current status of that node, but also on the statuses of the neighboring nodes.

Our work is an extension of the work by Garetto et. al. [17] in several directions. First, we generalize the influence model so that the status of a node and the influences a node exerts from neighbors depend on the current status of the node and the statuses of its neighbors. Second, we build a model for malware spreading, which is analytically and numerically tractable. Third, we consider three stochastic models: susceptible-infective-removed (known as a SIR model), susceptible-infective-immune (SIM model), and susceptible-infective-immune-susceptible (SIMS model). Finally, we study in detail the spreading of malware using the SIMS model for arbitrary network topology. The rest of the paper is organized as follows: we describe the influence model and its generalization in Section 2. In Section 3 we propose our model and study its properties. Section 4 is devoted tot the analysis of the SIMS model; in particular, we show under what condition the spreading of the viruses dies out in the network. Finally, we conclude the paper in Section 5.

## 2. Influence model and its generalizations

### *2.1. Binary Influence Model*

The influence model is suggested in [14] as a model of random, dynamical interactions on networks. We refer the reader to [14] for a full account of the model and its properties; here we give a brief description of the model. Define the directed graph of a $N \times N$ matrix $G$, denoted by $\Gamma(G)$, as the directed graph on nodes 1 to $N$, where a directed edge from $i$ to $j$, denoted by $(i, j)$, exists if and only if $g_{ij} \neq 0$. The edge weight given by $g_{ij}$ and is the amount of influence that node $j$ exerts on node $i$. Consider a graph with $N$ nodes, referred to as sites; each site has a *status* value that varies over time as it is 'influenced' by the neighbors. Assume that we are given an $N \times N$ matrix $D = [d_{ij}]$ $(d_{ij} \geq 0)$, where $d_{ij}$ is defined as $d_{ij} = g_{ij} / \sum_j^N g_{ij}$. Then $D$ is a stochastic matrix, that is $\sum_j d_{ij} = 1$ for each $i$. The graph $\Gamma(D^T)$ will be called the *network influence graph.* An edge $(i, j)$ exists on this graph if the status of $j$ can be influenced by the status of $i$. The weight on edge $(i, j)$ can be interpreted as the amount of influence that $i$ exerts on $j$ relative to the total amount of influence that $j$ receives. The total amount of influence received by any site is equal to the sum of incoming edge weights, which is 1, because $D$ is stochastic matrix.

We first discuss in more detail the *binary influence model.* For the binary influence model, the status of the site $i$ is represented by 0 or 1. The values 0 or 1 may represent any two different statuses such as ‘on’ vs. ‘off’, ‘healthy’ vs. ‘sick’, or ‘normal’ vs. ‘failed’. Let $\mathbf{p}_i^T(k) = [p_i^0(k)\ \ p_i^1(k)]$ be 2-dimensional probability vector of node $i$ at time $k$. $p_i^0(k)$ and $p_i^1(k)$ are the probabilities that node $i$ at time $k$ is in status ON and OFF, respectively. Further, let $\mathbf{s}_i^T(k) = \left[s_j^0(k)\ \ s_j^1(k)\right]$ be 2-dimensional status vector of node $i$ at time $k$. The status vector can only have one element equal to 1; the other element is equal to 0. If $s_j^0(k) = 1$ then the node $i$ is in status ON, if $s_j^1(k) = 1$ then the node $i$ is in status OFF. Let $d_{ij} = g_{ij} / \sum_{j=1}^{N} g_{ij}$ be the normalized influence that node $j$ exerts on node $i$, $\sum_j d_{ij} = 1$.

Let $A_{ij}$ be a $2 \times 2$ Markov transition matrix of the interactions of statuses of nodes $i$ and $j$,

$$A_{ij} = \begin{bmatrix} a_{ij}^{00} & a_{ij}^{01} \\ a_{ij}^{10} & a_{ij}^{11} \end{bmatrix} \tag{1}$$

$a_{ij}^{00} = Prob[s_i^0(k) = 1 | s_j^0(k-1) = 1]$ and $a_{ij}^{01}$ are the probabilities that node $i$ in the next time step will go to status ON and OFF, respectively, if node’s $j$ current status is ON. $a_{ij}^{10}$ and $a_{ij}^{11}$ are the probabilities that node $i$ in the next time step will go to status ON and OFF, respectively, if node’s $j$ current status is OFF.

The evolution equations of the influence model are defined as:

$$\begin{aligned} \mathbf{p}_i^T(k+1) &= \sum_{j=1}^{N} d_{ij} \mathbf{s}_j^T(k) A_{ij}, & (2) \\ \mathbf{s}_i^T(k+1) &= Bernoulli[\mathbf{p}_i^T(k+1)], & (3) \end{aligned}$$

The operation $Bernoulli[\cdot]$ can be thought of as flipping $N$ independent coins, at each time step, to realize the two entries of $[s_i^0(k)\ \ s_i^1(k)]$, where the probability of the $i$-th coin turning up heads (status ON) is $p_i^0(k)$. Note that in the interactions between nodes $i$ and $j$, the status if node $i$ in the next time step depends only on the status of node $j$ in the previous time step, i.e. the status of node $i$ in the next time step does not depend on its own current status. This is a limitation of the influence model.

### *2.2. Binary status dependent influence model*

We present now a binary status dependent influence model, in which node's status, at the next time step, depends on its own current status. For this model, we replace Eq. (2) of the binary influence model with the following equation:

$$\mathbf{p}_i^T(k+1) = d_{ii}\mathbf{s}_i^T(k)A_{ii} + \sum_{j=1,j\neq i}^{N} d_{ij}\mathbf{s}_i^T(k)\begin{bmatrix} \mathbf{s}_j^T(k)A_{ij}^0 \\ \mathbf{s}_j^T(k)A_{ij}^1 \end{bmatrix} \tag{4}$$

In this model the interactions of statuses between nodes $i$ and $j$ are described by two Markov transition matrices:

$$A_{ij}^0 = \begin{bmatrix} \alpha_{ij}^{00} & \alpha_{ij}^{01} \\ \alpha_{ij}^{10} & \alpha_{ij}^{11} \end{bmatrix},$$

and

$$A_{ij}^1 = \begin{bmatrix} \beta_{ij}^{00} & \beta_{ij}^{01} \\ \beta_{ij}^{10} & \beta_{ij}^{11} \end{bmatrix}.$$

$A_{ij}^0$ is the Markov transition matrix of interactions between nodes $i$ and $j$ when node $i$ is in status ON, and $A_{ij}^1$ is the Markov transition matrix of interactions of statuses between nodes $i$ and $j$ when node $i$ is in status OFF.

**Proposition 1.** *If $A_{ij}^0 = A_{ij}^1 = A_{ij}$, then Eq. (4) reduces to Eq. (2).*

Proof. Let $\mathbf{e}$ is all ones column vector with number of ones as the number of statuses of a node. Note that $\mathbf{s}_j^T(k)\mathbf{e} = 1$.

$$\begin{aligned} \mathbf{p}_i^T(k+1) &= d_{ii}\mathbf{s}_i^T(k)A_{ii} + \sum_{j=1,j\neq i}^{N} d_{ij}\mathbf{s}_i^T(k)\begin{bmatrix} \mathbf{s}_j^T(k)A_{ij} \\ \mathbf{s}_j^T(k)A_{ij} \end{bmatrix} \\ &= d_{ii}\mathbf{s}_i^T(k)A_{ii} + \sum_{j=1,j\neq i}^{N} d_{ij}\mathbf{s}_i^T(k)\mathbf{e}\mathbf{s}_j^T(k)A_{ij} \\ &= d_{ii}\mathbf{s}_i^T(k)A_{ii} + \sum_{j=1,j\neq i}^{N} d_{ij}\mathbf{s}_j^T(k)A_{ij} = \sum_{j=1}^{N} d_{ij}\mathbf{s}_j^T(k)A_{ij} \end{aligned}$$

■

### *2.3. Binary status-and-influence dependent influence model*

We now present a novel status-and-influence dependent influence model. In this model, the influence that node $j$ exerts on node $i$ depends on the current statuses of nodes $i$. Let $d_{ij}^0$ be the normalized influence that node $j$ exerts on node $i$ when node $i$ is in status ON. In a similar way, $d_{ij}^1$ is the normalized influence that node $j$ exerts on node $i$ when node $i$ is in status OFF. For this model, the evolution equation is defined as

$$\mathbf{p}_i^T(k+1) = \mathbf{s}_j^T(k)\mathrm{diag}(d_{ii}^0, d_{ii}^1)A_{ii} + \sum_{j=1,j\neq i}^{N} \mathbf{s}_i^T(k) \begin{bmatrix} d_{ij}^0\mathbf{s}_j^T(k)A_{ij}^0 \\ d_{ij}^1\mathbf{s}_j^T(k)A_{ij}^1 \end{bmatrix}, \qquad (5)$$

where $d_{ij}^0 = g_{ij}^0 / \sum_{j=1}^N g_{ij}^0$ and $d_{ij}^1 = g_{ij}^1 / \sum_{j=1}^N g_{ij}^1$ and, $g_{ij}^0$ and $g_{ij}^1$ are the total amount of influence that node $j$ exerts on node $i$ when node $i$ is in status 0 and 1, respectively. The operator $\mathrm{diag}(\cdot)$, makes a diagonal matrix from a vector.

**Proposition 2.** *When $d_{ij}^0 = d_{ij}^1 = d_{ij}$, and $A_{ij}^0 = A_{ij}^1 = A_{ij}$ then Eq. (5) reduces to Eq. (4).*

Noting that $\mathrm{diag}(d_{ii}, d_{ii}) = d_{ii}\mathbf{I}$, where $\mathbf{I}$ is the identity matrix, the proof is the same as for the status dependent binary model.

### *2.4. General status-and-influence dependent Influence Model*

We now discuss general influence model: each site in the general influence model is allowed to have different Markov chain. The model allows also an arbitrarily connected structure of sites defined by a weighted directed graph $D$, in which $d_{ij}$ is the weight associated to the edge directed from $i$ to $j$ ($d_{ij}$ is equal to zero if no edge exists from $i$ to $j$). Each weight $d_{ij}$ takes a value in the interval $[0, 1]$, and represents the amount of influence that $i$ exerts on $j$ relative to the total amount of influence that $j$ receives, which is normalized to one: $\sum_j d_{ij} = 1$. Let $M_i$ be the order of the local Markov chain at the site $i$ for $1 \leq i \leq N$, where $N$ is the number of sites (nodes). At time $k$, the status of site $i$ is represented by a length-$M_i$ status vector, an indicator vector containing a single 1 in the position corresponding to the present status, and 0 everywhere else:

$$\mathbf{s}_i(k) = [s_i^1(k) \;\; s_i^2(k) \;\; \ldots s_i^{M_i}(k)]^T,$$

where $s_i^n(k) = 1$ if only if the status of the site $i$ at time $k$ is $n$, $1 \leq n \leq M_i$. Let

$$\mathbf{p}_i(k) = [p_i^1(k) \;\; p_i^2(k) \;\; \ldots p_i^{M_i}(k)]^T$$

be the probability mass-function (PMF) of the site $i$ at time $k$. The transition matrix $A_{ij}$ (which has a number of rows equal to the number of statuses in $j$ and a number of columns equal to the number of statuses in $i$) completely specifies the way in which site $j$ influences site $i$. In the influence model the evolution of each site is constrained to take the multi-linear form

$$\begin{aligned} \mathbf{p}_i^T(k+1) &= \sum_{j=1}^{N} d_{ij}\mathbf{s}_j^T(k)A_{ij} && (6) \\ \mathbf{s}_i^T(k+1) &= MultiRealize[\mathbf{p}_i^T(k+1)], && (7) \end{aligned}$$

where $MultiRealize[\cdot]$ performs a random realization for each element of the vector $\mathbf{p}_i^T(k+1)$ in the same manner as in a binary influence model.

We now generalize the influence model one step further to general status-and-influence dependent influence model. Let $\left\{A_{ij}^{m_i}\right\}_{m_i=1}^{M_i}$ be $M_i$ Markov transition matrices that describe the interactions between node $i$ with $M_i$ statuses and node $j$ with $M_j$ statuses. These matrices are all $M_j \times M_i$, i.e. matrices with $M_j$ rows and $M_i$ columns. The $(m_j, m_i)$ element of the $A_{ij}^{k_i}$ matrix is the probability that in the next time step node $i$ will be in status $m_i$ if its current status is $k_i$. Let $d_{ij}^{m_i}$ be the influences that node $j$ exerts on node $i$, when node $i$ is in a status $m_i$.

The general status-and-influence dependent influence model is described when Eq (6) is replaced by the following equation:

$$\mathbf{p}_i^T(k+1) = \mathbf{s}_i^T(k)\mathrm{diag}(d_{ii}^0, d_{ii}^2, \ldots, d_{ii}^{M-1})A_{ii} + \mathbf{s}_i^T(k) \begin{bmatrix} \sum_{j=1, j\neq i}^{N} d_{ij}^1 \mathbf{s}_j^T(k) A_{ij}^1 \\ \sum_{j=1, j\neq i}^{N} d_{ij}^2 \mathbf{s}_j^T(k) A_{ij}^2 \\ \vdots \\ \sum_{j=1, j\neq i}^{N} d_{ij}^{M_i} \mathbf{s}_j^T(k) A_{ij}^{M_i} \end{bmatrix} \tag{8}$$

where $d_{ij}^{m_i} = g_{ij}^{m_i} / \sum_{i=1}^{N} g_{ij}^{m_i}$ and $g_{ij}^{m_i}$ is the total amount of influence that node $j$ exerts on node $i$ when node $i$ is in status $m_i$.

**Proposition 3.** *Each $p_i^l(k+1)$, $l = 1, \ldots M_i$, is a valid probability.*

Proof. First, we notice that $p_i^l(k+1) \geq 0$ because $A_{ij}^l$, $d_{ij}^l$, and $\mathbf{s}_j^T(k)$ are nonnegative, and $\mathbf{p}_i^T(k+1)\mathbf{e} = 1$.

Since,

$$\begin{aligned}
\mathbf{p}_i^T(k+1)\mathbf{e} &= \mathbf{s}_i^T(k)\mathrm{diag}(d_{ii}^0, d_{ii}^2, \ldots, d_{ii}^{M-1})A_{ii}\mathbf{e} \\
&+ \mathbf{s}_i^T(k)\begin{bmatrix} \sum_{j=1,j\neq i}^N d_{ij}^1 \mathbf{s}_j^T(k)A_{ij}^1\mathbf{e} \\ \sum_{j=1,j\neq i}^N d_{ij}^2 \mathbf{s}_j^T(k)A_{ij}^2\mathbf{e} \\ \vdots \\ \sum_{j=1,j\neq i}^N d_{ij}^{M_i} \mathbf{s}_j^T(k)A_{ij}^{M_i}\mathbf{e} \end{bmatrix} \\
&= \mathbf{s}_i^T(k)\mathrm{diag}(d_{ii}^0, d_{ii}^2, \ldots, d_{ii}^{M-1})\mathbf{e} + \mathbf{s}_i^T(k)\begin{bmatrix} \sum_{j=1,j\neq i}^N d_{ij}^1 \mathbf{s}_j^T(k)\mathbf{e} \\ \sum_{j=1,j\neq i}^N d_{ij}^2 \mathbf{s}_j^T(k)\mathbf{e} \\ \vdots \\ \sum_{j=1,j\neq i}^N d_{ij}^{M_i} \mathbf{s}_j^T(k)\mathbf{e} \end{bmatrix} \\
&= \mathbf{s}_i^T(k)[d_{ii}^0, d_{ii}^2, \ldots, d_{ii}^{M-1}]^T + \mathbf{s}_i^T(k)\begin{bmatrix} \sum_{j=1,j\neq i}^N d_{ij}^1 \\ \sum_{j=1,j\neq i}^N d_{ij}^2 \\ \vdots \\ \sum_{j=1,j\neq i}^N d_{ij}^{M_i} \end{bmatrix} \\
&= \mathbf{s}_i^T(k)[d_{ii}^0, d_{ii}^2, \ldots, d_{ii}^{M-1}]^T + \mathbf{s}_i^T(k)\begin{bmatrix} 1-d_{ii}^1 \\ 1-d_{ii}^2 \\ \vdots \\ 1-d_{ij}^{M_i} \end{bmatrix} = 1
\end{aligned} \tag{9}$$

the proof is completed. ■

**Proposition 4.** *Assume that: (i)* $d_{ij}^1 = d_{ij}^2 = \ldots d_{ij}^{M_i} = d_{ij}$ *, and (ii)* $A_{ij}^1 = \ldots = A_{ij}^{M_i} = A_{ij}$*. Then Eq. (8) reduces to Eq. (6).*

The proof is the same as for the binary model.

### *2.5. Properties of the model*

The model developed in the previous section (equations (8) and (7)) is a stochastic model based on the Interactive Markov Chains (IMC) framework. Because of the exponential growth in the number of states, large IMCs are extremely difficult to solve numerically, even for a few tens of nodes, so that it is necessary to resort to discrete event simulations. However, our model belongs to the special case of IMC called “influence model”, which provides a particular but tractable representation of dynamic interactions on networks. In a similar way as for the original influence model (which is status independent model), for our model it is possible to obtain the marginal status probabilities of each site by means of a transition matrix whose dimension is equal only to the sum of the dimensions of the local chains. Therefore, our model is computationally equivalent to the original influence model.

The state variable of node $i$, $s_i^l(k+1)$, is a binary random variable (RV) that describes the state $l$ of node $i$. This RV is conditionally independent of all other state variables of all nodes $j = 1, \ldots, N$ and $j \neq i$ at time $k+1$ given all nodes state variables at time $k$. Let us define a state vector for all states of all nodes as: $\mathbf{s}(k) = [\mathbf{s}_1(k)^T \ \ \mathbf{s}_2(k)^T \ \ \ldots \ \ \mathbf{s}_N(k)^T]^T$, and a probability state vector, equivalently, as $\mathbf{p}(k) = [\mathbf{p}_1(k)^T \ \ \mathbf{p}_2(k)^T \ \ \ldots \ \ \mathbf{p}_N(k)^T]^T$. Then the conditional independence can be mathematically formulated as:

$$P\left[\bigcap_{i=1}^{N} s_i^l \middle| \mathbf{s}(k)\right] = \prod_{i=1}^{N} P[s_i^l(k+1)|\mathbf{s}(k)], \tag{10}$$

where $P(\cdot)$ is the probability operator. Thus the conditional expectation of intersection of statuses $s_i^{l_1}(k+1)$ and $s_j^{l_2}(k+1)$, given $\mathbf{s}(k)$ is a product of expectations:

$$\begin{aligned} & E[s_i^{l_1}(k+1) \cap s_j^{l_2}(k+1)|\mathbf{s}(k)] \\ = \ & E[s_i^{l_1}(k+1)|\mathbf{s}(k)]E[s_i^{l_2}(k+1)|\mathbf{s}(k)] \end{aligned} \tag{11}$$

where $E[\cdot]$ is the expectation.

One can compute the status probabilities of node $i$ at time step $t = k+1$ by knowing only the status probabilities of all nodes at time step $t = 0$. Indeed, from

$$E[\mathbf{s}_i(k+1)|\mathbf{s}(k)] = Prob[\mathbf{s}_i(k) = \mathbf{e}_i] = \mathbf{p}_i(k+1)\{\mathbf{s}(k)\}$$

which actually is equation (8), it follows that the probability vector of node $i$ at time step $k+1$ depends on only the elements of vector $\mathbf{s}(k)$. Equivalently,

$$E[\mathbf{s}(k+1)|\mathbf{s}(k)] = Prob[\mathbf{s}(k) = \mathbf{e}] = \mathbf{p}(k+1)\{\mathbf{s}(k)\}$$

and the probability vector of all nodes at time step $k+1$ depends on only the elements of the vector $\mathbf{s}(k)$

Taking the expectation again, now on $\mathbf{s}(k)$ we obtain

$$\begin{aligned} &E\left[E[\mathbf{s}(k+1)|\mathbf{s}(k)]|\mathbf{s}(k-1)\right] = E\left[\mathbf{p}(k+1)\{\mathbf{s}(k)\}|\mathbf{s}(k-1)\right] \\ &= \mathbf{p}(k+1)\{E[\mathbf{s}(k)|\mathbf{s}(k-1)]\} = \mathbf{p}(k+1)\{\mathbf{p}(k)\{\mathbf{s}(k-1)\}\} \end{aligned}$$

where we have used the property (11) to show that

$$E[\mathbf{p}(k+1)\{\mathbf{s}(k)\}|\mathbf{s}(k-1)] = \mathbf{p}(k+1)\{E[\mathbf{s}(k)|\mathbf{s}(k-1)]\}.$$

Taking the expectation $k+1$ times we finally obtain $\mathbf{p}(k+1)$ as a function of $\mathbf{s}(0)$:

$$E[E\ldots E[\mathbf{s}(1)|\mathbf{s}(0)]]\ldots] \quad = \quad \mathbf{p}(k+1)\{\mathbf{p}(k)\{\ldots\mathbf{p}(1)\{\mathbf{s}(0)\}\ldots\}\}.$$

We now present the algorithm for computing the influence probabilities. Let $\mathbf{s}_i(0)$ for $i = 1, \ldots, N$ be the status vectors for all nodes at time step $t = 0$. Let $F_i\{\cdot\}$ is the function that describes the relations between $\mathbf{p}_i(k)$ and $\{\mathbf{s}_1(k-1), \ldots, \mathbf{s}_N(k-1)\}$, i.e. the function in Eq. (8). Then the probability vectors $\mathbf{p}_i(k)$ for $i = 1, \ldots, N$ at time step $t = k$ are:

```
For $t = 1, \ldots, k$
  For $i = 1, \ldots, N$
    $\mathbf{p}_i(t) = F_i\{\mathbf{s}_1(0), \ldots, \mathbf{s}_N(0)\}$
  end
  For $i = 1, \ldots, N$
    $\mathbf{s}_i(0) = \mathbf{p}_i(t)$
  end
end
```

(12)

The algorithm (12) is the mathematical algorithm for computing the probabilities in both models: original influence model Eq. (6)–(7) and our model Eq. (8)–(7), the only difference being that one can write Eq. (6) in more compact form as a matrix equation, see [14].

## 3. Modeling malware spreading

### *3.1. Preliminaries*

There is a substantial literature on the SIR models in epidemiology, starting with the work of Kermack and McKendrick [18]. A commonly used approach in early work was to approximate a stochastic model by a deterministic one in a large population (law of large numbers) limit. Here we discuss two stochastic models of viruses spreading.

### *3.1.1. Stochastic Reed-Frost model*

Consider a closed population of $N$ individuals, connected by a neighborhood structure which is represented by an undirected, unweighted graph $G = (V, E)$ with node set $V$ and edge set $E$. One of the earliest stochastic SIR models studied in depth, because of its analytical tractability, is the Reed-Frost model. Each node can be in one of three possibly states, susceptible (S), infective (I) or removed (R). Let A denote the adjacency matrix of the undirected graph $G$, i.e., $a_{ij} = 1$ if $(i, j) \in E$ and $a_{ij} = 0$ otherwise. Each node that is infected at the beginning of a time slot attempts to infect each of its neighbors; each infection attempt is successful with probability $\beta$ independent of other infection attempts. Each infected node is removed at the end of the time slot. Therefore, the the probability that a susceptible node $i$ becomes infected at the end of time slot $k$ is given by:

$$p_i^I(k+1) = 1 - \prod_{j=1}^{N}(1 - \beta a_{ij} s_j^I(k)) \tag{13}$$

where $s_j^I(k)$ denotes the indicator that node $j$ is infected at the beginning of time slot $k$.

### *3.1.2. Garetto-Gong-Towsley model*

Garetto, Gong, and Towsley recently proposed a model for e-mail viruses spreading [17]. As in the previous example, consider a closed population of $N$ individuals, connected by a neighborhood structure which is represented by an undirected, weighted graph $G = (V, E)$ with node set $V$ and edge set $E$. Each node can be in one of three possibly states, susceptible (S), infective (I) or immune (M). We assume that the weighted matrix $D = (d_{ij})$ is stochastic. The model equations are:

$$\begin{array}{rcl} p_j^S(k+1) & = & 1 - p_j^I(k+1) - p_j^R(k+1) \\ p_j^I(k+1) & = & p_j^I(k) + \sum_{i=1}^{N} c_j d_{ij} p_{ij}^{IS}(k) \\ p_j^M(k+1) & = & p_j^M(k) + \sum_{i=1}^{N} (1 - c_j) d_{ij} p_{ij}^{IS}(k), \end{array} \tag{14}$$

where $d_{ij}$ are the edge weights, $c_j$ is the click probability of site $j$ and $p_{ij}^{IS}(k)$ is the joint probability that at time step $k$, the site $i$ is infected, while the site $j$ is still susceptible. Sum of all incoming edge weights into a node is one. This can be interpreted as follows: the edge weight $d_{ij}$ represents the probability that during a time step a user checks if any message has been delivered from source $j$ to destination $i$. If the sum of all edge weights is smaller then one than a self loop is added in order to reach the value of one. Note that the edge associated with a node is just the probability of reading the message, not yet deciding what to do with its content. A click probability $c_{ij}$ is introduced that user $i$ will open the attachment sent from user $j$. This means that user $i$ with probability $1 - c_{ij}$ once an for all will block that attachment sent from user $j$. The decision of opening the attachment will not occur if new copies of the virus are received. The system (14) is not numerically tractable, since the joint probabilities $p_{ij}^{IS}$ are unknown, and there does not appear to exist an easy way to compute them exactly.

*3.2. SIM Model*

In this subsection we show that SIM model (or Garetto-Gong-Towsley model) belongs to the class of status-and-influence dependent influence model discussed in the section 2. The SIM model presented in [17] assumes that when a node reaches status infected or immune it stays in that status forever. With the status-and-influence dependent influence model we can build a model that fulfills this assumption. The general influence model equation are:

$$\mathbf{p}_i^T(k+1) = \mathbf{s}_i^T(k)\mathrm{diag}(d_{ii}^S, d_{ii}^I, d_{ii}^M)A_{ii} + \mathbf{s}_i^T(k) \begin{bmatrix} \sum_{j=1, j\neq i}^N d_{ij}^S \mathbf{s}_j^T(k) A_{ij}^S \\ \sum_{j=1, j\neq i}^N d_{ij}^I \mathbf{s}_j^T(k) A_{ij}^I \\ \sum_{j=1, j\neq i}^N d_{ij}^M \mathbf{s}_j^T(k) A_{ij}^M \end{bmatrix} \tag{15}$$

By setting $d_{ij}^I = d_{ij}^M = 0$ for $j \neq i$ and $d_{ii}^I = d_{ii}^M = 1$ and $\sum_{j=1, j\neq i}^N d_{ij}^S = 1$ and $d_{ii}^S = 0$ we get:

$$\mathbf{p}_i^T(k+1) = \mathbf{s}_i^T(k)\mathrm{diag}(0,1,1)A_{ii} + \mathbf{s}_i^T(k) \begin{bmatrix} \sum_{j=1, j\neq i}^N d_{ij}^S \mathbf{s}_j^T(k) A_{ij}^S \\ \mathbf{0}^T \\ \mathbf{0}^T \end{bmatrix} \tag{16}$$

where $\mathbf{0}$ is a column vector with 3 elements.

When the node $i$ is in status $S$, if the source node $j$ is in status $S$ than the destination node $i$ will stay in status $S$. If the source node $j$ is in status $I$ than the destination node will go in status $I$ with the click probability $c_{ij}$ and will go in status $M$ with probability $1 - c_{ij}$. If the source node $j$ is in status $M$ than the destination node will stay in status $S$ with probability 1. This means that the destination node $i$ can not be infected or immunized by the source node $j$ when the source node is immune. The transition matrix for the status $S$ , for $i \neq j$, is equal to

$$A_{ij}^S = \begin{bmatrix} 1 & 0 & 0 \\ 0 & c_{ij} & 1 - c_{ij} \\ 1 & 0 & 0 \end{bmatrix}$$

When the node is self influenced it preserves it previous status, meaning that when node is in status $S$, $I$ or $M$ it stays in status $S$, $I$ or $M$, respectively. The Markov chain for $j = i$ is therefor:

$$A_{ii} = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

If we substitute equations for $A_{ii}$, $A_{ij}^S$, we can rewrite the equations as follows:

$$\begin{aligned} p_i^S(k+1) &= s_i^S(k) \textstyle\sum_{j=1,j\neq i}^N d_{ij}(s_j^S(k) + s_j^M(k)) \\ p_i^I(k+1) &= s_j^I(k) + s_i^S(k) \textstyle\sum_{j=1,j\neq i}^N c_{ij} d_{ij} s_j^I(k) \\ p_i^M(k+1) &= s_j^M(k) + s_i^S(k) \textstyle\sum_{j=1,j\neq i}^N (1 - c_{ij}) d_{ij} s_j^I(k), \end{aligned} \tag{17}$$

The last equation reduces to the SIM model. We stress that as a consequence of the Markov property of the influence model, $s_i^I(k)$, $s_i^S(k)$, and $s_i^M(k)$ are independent random variables from all other node status random variables at any time step $k$ conditioned on the previous history of the nodes statuses. Therefore, for example, we have

$$\begin{aligned} P(s_i^I(k) s_j^S(k) | \mathbf{s}(k-1)) &= \\ P(s_i^I(k) | \mathbf{s}(k-1)) P(s_j^S(k) | \mathbf{s}(k-1)). \end{aligned}$$

### *3.3. SIR Model*

Status-and-influence dependent influence model is general enough to model various viruses spreading on networks. For example, choosing properly the parameters of the influence model, we can obtain the following variant of the

SIR model:

$$
\begin{aligned}
p_i^S(k+1) &= 1 - s_i^I(k) - s_i^R(k) - s_i^S(k)\sum_{j=1}^{N}\delta_{ij}d_{ij}s_j^I(k)\\
p_i^I(k+1) &= s_i^S(k)\sum_{j=1}^{N}\delta_{ij}d_{ij}s_j^I(k)\\
p_i^R(k+1) &= s_i^I(k) + s_i^R(k).
\end{aligned}
\tag{18}
$$

As in the original SIR model, here, equation (18), each node can be in one of three possibly states, susceptible (S), infective (I) or removed (R). The edge weight $d_{ij}$ represents the probability that during a time step a user checks if any message has been delivered from source $j$ to destination $i$. We assign a click probability $\delta_{ij}$ that user $i$ will open the attachment sent from user $j$ (and will be infected). Each infected node is removed at the end of the time slot.

## 4. SIMS model

As in the previous SIM example, consider the SIM model with modified Markov matrix $A_{ii}$, set to:

$$
A_{ii} = \begin{bmatrix} 1 & 0 & 0\\ \delta_1 & 1-\delta_1 & 0\\ \delta_1 & 0 & 1-\delta_1 \end{bmatrix},
\tag{19}
$$

we obtain the following model equations:

$$
\begin{array}{lcl}
p_i^S(k+1) &=& s_i^S(k)\sum_{j=1}^{N} d_{ij}(s_j^S(k)+s_j^M(k)) + \delta_1 s_i^I(k) + \delta_2 s_i^M(k)\\
p_i^I(k+1) &=& (1-\delta_1)s_i^I(k) + s_i^S(k)\sum_{j=1}^{N} c d_{ij} s_j^I(k)\\
p_i^M(k+1) &=& (1-\delta_2)s_i^M(k) + s_i^S(k)\sum_{j=1}^{N}(1-c)d_{ij}s_j^I(k),
\end{array}
\tag{20}
$$

where $d_{ij}$ are the edge weights, and $c_j = c$ for all $j$, is the click probability. The nodes in statuses I and M continue to preserve their status at a rate of $1-\delta_1$ and $1-\delta_2$, accordingly, i.e. they convert back to status S with a rate of $\delta_1$ and $\delta_2$, accordingly. Let $X(k) = \sum_{i=1}^{N} s_i^S(k)$, $Y(k) = \sum_{i=1}^{N} s_i^I(k)$, and $Z(k) = \sum_{i=1}^{N} s_i^M(k)$ be the total number of susceptible, infective and immune nodes at time $k$, respectively. Further, let $N_S = \mathbb{E}[X(\infty)]$, $N_I = \mathbb{E}[Y(\infty)]$, and $N_M = \mathbb{E}[Z(\infty)]$. The object of interest is the number of nodes that eventually become infected and immune, $N_I$ and $N_M$, compared to the total number of nodes in the network. We assume that initially only one node is infected.

In terms of probabilities only, Eq. (20) can be rewritten as

$$\begin{aligned} p_i^S(k+1) &= p_i^S(k) \textstyle\sum_{j=1}^N d_{ij}(p_j^S(k) + p_j^M(k)) + \delta_1 p_i^I(k) + \delta_2 p_i^M(k) \\ p_i^I(k+1) &= (1-\delta_1)p_i^I(k) + p_i^S(k) \textstyle\sum_{j=1}^N c d_{ij} p_j^I(k) \\ p_i^M(k+1) &= (1-\delta_2)p_i^M(k) + p_i^S(k) \textstyle\sum_{j=1}^N (1-c) d_{ij} p_j^I(k). \end{aligned} \tag{21}$$

Equivalently $N_S, N_I, N_M$ can be computed using Eq. (21) as $N_S = \sum_{i=1}^N p_i^S(\infty)$, $N_I = \sum_{i=1}^N p_i^I(\infty)$, and $N_M = \sum_{i=1}^N p_i^M(\infty)$. The main result of this section is the following

**Theorem 1.** *Assume that initially (for $k = 0$) at least one node is infected. Then, for $c < \delta_1$*

$$N_S = N, N_I = 0, N_M = 0,$$

*and for $c > \delta_1$,*

$$\begin{aligned} N_S &= \frac{\delta_1}{c} N \\ N_I &= \frac{\delta_2(c-\delta_1)}{\delta_1 + c(\delta_2 - \delta_1)} N \\ N_M &= \frac{\delta_1(1-c)(c-\delta_1)}{c(\delta_1 + c(\delta_2 - \delta_1))} N \end{aligned}$$

Proof. Let $\mathbf{p}^S = [p_1^S p_2^S \dots p_N^S]^T$, $\mathbf{p}^I = [p_1^I p_2^I \dots p_N^I]^T$, and $\mathbf{p}^M = [p_1^M p_2^M \dots p_N^M]^T$, where $p_i^S = p_i^S(\infty)$, $p_i^I = p_i^I(\infty)$, and $p_i^M = p_i^M(\infty)$. We first prove that for $k \to \infty$, $\mathbf{p}^S = p^S\mathbf{e}$, $\mathbf{p}^I = p^I\mathbf{e}$ and $\mathbf{p}^M = p^M\mathbf{e}$. Assuming that $p_i^I > 0$ for all $i$, the following equation

$$p_i^I(k+1) = (1-\delta_1)p_i^I(k) + p_i^S(k) \sum_{j=1}^N c d_{ij} p_j^I(k)$$

by setting $k \to \infty$ can be written in matrix form as

$$\begin{aligned} \mathbf{p}^I &= (1-\delta_1)\mathbf{p}^I + c \times \mathrm{diag}(\mathbf{p}^S)\mathbf{D}\mathbf{p}^I \\ \mathbf{0} &= (\delta_1 \mathbf{I} - c \times \mathrm{diag}(\mathbf{p}^S)\mathbf{D})\mathbf{p}^I. \end{aligned}$$

If we take only the 1-th element of the vector equation we get:

$$\begin{aligned} 0 &= \delta_1 p_1^I - c p_1^S \mathbf{e}^T \mathbf{p}^I \\ 0 &= \delta_1 p_1^I - c p_1^S N_I \end{aligned} \tag{22}$$

where $N_I$ is the average number of infected nodes which is a constant number when $k \to \infty$.

If we now take the second vetor element we obtain:

$$0 = \delta_1 p_2^I - c p_2^S N_I$$

thus

$$(p_1^I - p_2^I) = \frac{cN^I}{\delta_1}(p_1^S - p_2^S) \tag{23}$$

The third equation

$$p_i^M(k+1) = (1-\delta_2)p_i^M(k) + p_i^S(k)\sum_{j=1}^{N}(1-c)d_{ij}p_j^I(k)$$

by setting $k \to \infty$ can be written in matrix form as

$$\mathbf{p}^M = \frac{1-c}{\delta_2} \times \mathrm{diag}(\mathbf{p}^S)\mathbf{D}\mathbf{p}^I$$

If we take only the 1-th element of the vector equation we get:

$$\begin{aligned} p_1^M &= \frac{1-c}{\delta_2} p_1^S \mathbf{e}^T \mathbf{p}^I \\ p_1^M &= \frac{1-c}{\delta_2} p_1^S N_I \end{aligned}$$

If we now take only the 2-th element of the vector equation we obtain:

$$p_2^M = \frac{1-c}{\delta_2} p_2^S N_I$$

Thus

$$\begin{aligned} p_1^M - p_2^M &= \frac{1-c}{\delta_2} N_I (p_1^S - p_2^S) \\ 1 - p_1^S - p_1^I - 1 + p_2^S + p_2^I &= \frac{1-c}{\delta_2} N_I (p_1^S - p_2^S) \\ p_1^I - p_2^I &= -\left(1 + \frac{1-c}{\delta_2} N_I\right)(p_1^S - p_2^S) \end{aligned} \tag{24}$$

From (23) and (24) we get

$$-\left(1+\frac{1-c}{\delta_2}N_I\right)(p_1^S-p_2^S)=\frac{cN^I}{\delta_1}(p_1^S-p_2^S)$$

The equation is satisfied only if $p_1^S = p_2^S$. In a similar fashion, we have $p_i^S = p_j^S$, $p_i^I = p_j^I$, and $p_i^M = p_j^M$.

We now find fixed points of the dynamical system (21). The fixed points of (21) are solutions of the system:

$$\begin{array}{lcl} p^S & = & p^S \sum_{j=1}^N d_{ij}(p^S+p^M)+\delta_1 p^I+\delta_2 p^M \\ p^I & = & (1-\delta_1)p^I + p^S \sum_{j=1}^N c d_{ij} p^I \\ p^M & = & (1-\delta_2)p^M + p^S \sum_{j=1}^N (1-c) d_{ij} p^I, \end{array} \tag{25}$$

which, since $\sum_j d_{ij} = 1$, reduces to

$$\begin{array}{lcl} p^S & = & p^S(p^S+p^M)+\delta_1 p^I+\delta_2 p^M \\ p^I & = & (1-\delta_1)p^I + p^S c p^I \\ p^M & = & (1-\delta_2)p^M + p^S (1-c) p^I, \end{array} \tag{26}$$

Equation (26) for at least one infected node at time zero has two solutions:

$$p^S = 1, p^I = 0, p^M = 0 \tag{27}$$

and

$$\begin{array}{lcl} p^S & = & \dfrac{\delta_1}{c} \\ p^M & = & \dfrac{\delta_1(1-c)(c-\delta_1)}{c(\delta_1+c(\delta_2-\delta_1))} \\ p^I & = & \dfrac{\delta_2(c-\delta_1)}{\delta_1+c(\delta_2-\delta_1)} \end{array} \tag{28}$$

Finally, we study the stability conditions of the fixed points. If we write $x_i = p_i^I$ and $y_i = p_i^M$, since $p_i^S(k)+p_i^I(k)+p_i^M(k) = 1$, Eq. (21) can be rewritten as a dynamical system $F : [0,1]^{2N} \rightarrow [0,1]^{2N}$ defined as

$$\begin{array}{lcl} x_i(k+1) & = & (1-\delta_1)x_i(k) + [1-x_i(k)-y_i(k)]c\sum_{j=1}^N d_{ij}x_j(k) \\ y_i(k+1) & = & (1-\delta_2)y_i(k) + [1-x_i(k)-y_i(k)](1-c)\sum_{j=1}^N d_{ij}x_j(k). \end{array} \tag{29}$$

Jacobian matrix of the system (29) evaluated at the fixed point $(x, y)$ is equal to

$$DF|_{(x,y)} = \left[ \begin{array}{cc} (1-\delta_1 - cx)I_N + (1-x-y)cD & -cxI_N \\ -(1-c)xI_N + (1-x-y)(1-c)D & [1-\delta_2-(1-c)x]I_N \end{array} \right],$$

where $D$ and $I_N$ (identity matrix) are $N \times N$ matrices.

The fixed point $(x = 0, y = 0)$ exists for all values of the parameters. The Jacobian matrix evaluated at this fixed point is

$$DF|_{(0,0)} = \left[ \begin{array}{cc} (1-\delta_1)I + cD & 0_N \\ (1-c)D & (1-\delta_2)I_N \end{array} \right].$$

The fixed point $(0, 0)$ is stable when

$$1 - \delta_1 + c < 1.$$

The last equation reduces to

$$c < \delta_1$$

Since $p^S \leq 1$, the fixed point $(x = p^I, y = p^M)$ exists only when $c > \delta_1$ (the case $c = \delta_1$ reduces to $p^S = 1, p^I = 0, p^M = 0$). After tedious but straightforward calculation, it easy to see that this fixed point is stable for all values of the parameters $0 < \delta_1 < 1$, $0 < \delta_2 < 1$, and $\delta_1 < c < 1$.

The proof of the theorem is completed. ■

**Remark 1.** *If $\delta_1 = \delta_2 = 0$, SIMS model reduces to SIM model. For the SIM model the only stable fixed point is $p^S = 0, p^I = c, p^M = 1 - c$, so that the total number of infected and immune nodes is $N_I = cN$ and $N_M = (1 - c)N$ respectively.*

**Remark 2.** *In the SIMS model, the number of infected (or immune) nodes exhibits a sharp threshold: as $c$ is increased, it suddenly jumps from zero to a non-zero fraction of $N$, the number of nodes in the system. The epidemic threshold for SIMS model does not depend on graph topology: this is a simple consequence of the fact that in our model the graph is described not with a adjacency matrix, but with a stochastic matrix, for which the largest eigenvalue is always 1. The effect of the second eigenvalue and the eigenvector that corresponds to the eigenvalue 1 to the spreading dynamics will be discussed in a separate paper.*

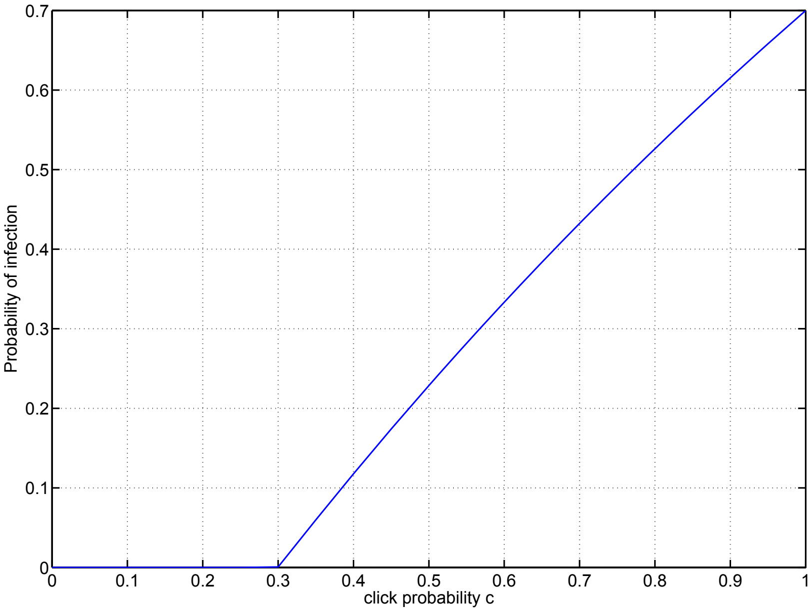

Figure 1: Probability of infection VS click probability when $\delta_1$=0.3

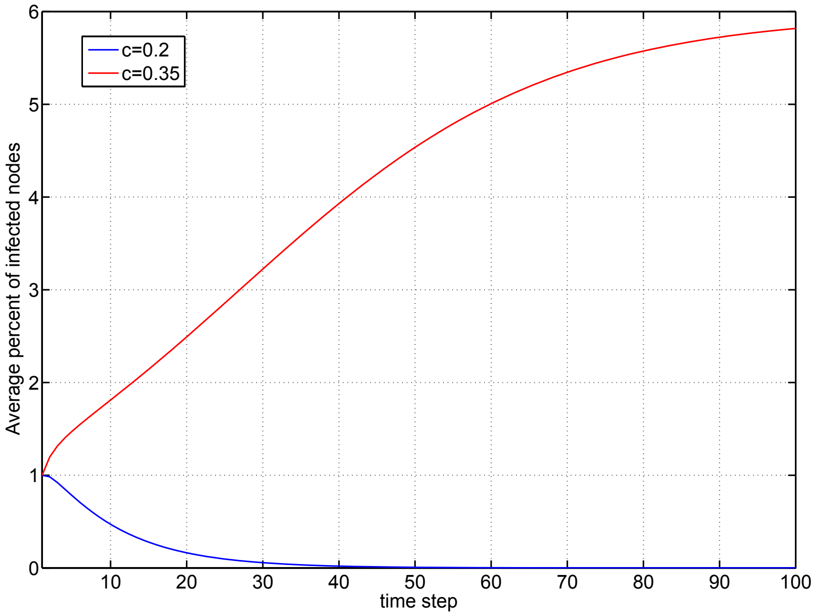

Figure 2: Average percentage of infected nodes VS time step when $\delta_1$=0.3

## 5. Conclusions

The influence model is a simple (and mathematically tractable) model of random, dynamical interactions on networks. It consists of a network of nodes, each with a status that evolves over time. The evolution of the status at a node is according to an internal Markov chain, but with transition probabilities that depend not only on the current status of that node, but also on the statuses of the neighboring nodes. For influence model, each site (node) may contain an arbitrary (finite) local chain and the network may have an arbitrary (finite) graph and influence structure. In this paper we have generalized influence model so that the status of a node and the influences a node exerts from neighbors depend on the current status of the node and the statuses of its neighbors. Such generalized model is flexible enough to model various phenomena including spreading of failures in power grid, malwere propagation in computer networks, and spreading of ideas in social networks.

As a particular example we have discussed the spreading of malware through a network. We considered three stochastic models: susceptible-infective-removed (SIR), susceptible-infective-immune (SIM), and susceptible-infective-immune-susceptible (SIMS). For SIMS model and arbitrary network topology, we found analytical expressions for the epidemic threshold, the number of infected, and the number of immune nodes.

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