A Stochastic Model of Multivirus Dynamics

Shouhuai Xu, Wenlian Lu, and Zhenxin Zhan

Abstract—Understanding the spreading dynamics of computer viruses (worms, attacks) is an important research problem, and has received much attention from the communities of both computer security and statistical physics. However, previous studies have mainly focused on single-virus spreading dynamics. In this paper, we study multivirus spreading dynamics, where multiple viruses attempt to infect computers while possibly combating each other because, for example, they are controlled by multiple botmasters. Specifically, we propose and analyze a general model (and its two special cases) of multivirus spreading dynamics in arbitrary networks (i.e., we do not make any restriction on network topologies), where the viruses may or may not coreside on computers. Our model offers analytical results for addressing questions such as: What are the sufficient conditions (also known as epidemic thresholds) under which the multiple viruses will die out? What if some viruses can “rob” others? What characteristics does the multivirus epidemic dynamics exhibit when the viruses are (approximately) equally powerful? The analytical results make a fundamental connection between two types of factors: defense capability and network connectivity. This allows us to draw various insights that can be used to guide security defense.

Index Terms—Multiple virus dynamics, epidemic dynamics, epidemic threshold, complex networks, complex systems, cyber warfare model.

1 INTRODUCTION

To solve the problem of computer viruses (malware, worms, or bots), we need a set of approaches, ranging from legislation to technology. One technological approach, we call the dynamical systems approach, aims to understand the attack(-defense) dynamics so as to offer insights and guidance for defense from a whole-system perspective (i.e., by addressing macroscopic questions). This approach is complementary to the well-established approaches such as access control and cryptography. Despite the attention that has been paid by communities including computer security and statistical physics, existing studies mainly focused on single-virus spreading dynamics. In this paper, we study multivirus spreading dynamics, where multiple viruses may be controlled by multiple attackers and thus may combat against each other. We have witnessed incidents of this type. For example, the Welchia worm tried to “kill” the Blaster worm by deleting the Msblant.exe file created by W32.Blaster.Worm [26]. Although such incidents are not exactly as full-fledged and sophisticated as the virus combats investigated in the paper, they can be seen as a prelude to (some of) the investigated scenarios that may soon become reality. As such, we need to investigate and understand the consequences of fighting viruses so as to get prepared by enhancing our body of knowledge.

1.1 Our Contributions

For multivirus spreading dynamics, there are two scenarios: the viruses spread independent of each other and thus the dynamics can be understood as a trivial extension of the single-virus dynamics; the viruses spread nonindependently and may further fight against each other. The present paper focuses on the latter scenario and its two special cases: 1) the viruses can coreside on computers, and 2) the viruses do not coreside on computers because the viruses can “rob” each other. Specifically, we make the following contributions.

First, we propose a novel continuous-time nonlinear dynamical system model for the spreading of multiple viruses in arbitrary networks (because any topology would be possible in practice). The general model is difficult to analyze, but we manage to present general sufficient conditions (also known as epidemic thresholds) under which all viruses will die out (one applies regardless of the degree of initial infection, and the other applies when the initial infection is light). We also present simplified versions of these sufficient conditions so as to make them easier to use.

Second, in order to gain deeper results, we further consider the aforementioned two special cases of the general model. While the special cases naturally inherit the sufficient conditions in the general model (which become more succinct in the special cases though), we additionally obtain the following results. In the special case, where multiple viruses do not coreside on computers, we investigate the combat between the viruses, namely that some viruses can “rob” other viruses (e.g., botmasters rob each other’s bots). We analytically answer: 1) Under what conditions the weak viruses (i.e., viruses that can be robbed by, but cannot rob, others) will die out? 2) What are the outcomes when the viruses are (approximately) equally powerful? In the special case where multiple viruses may coreside on computers, we analytically answer: 1) Under what conditions some viruses will
die out? 2) What are the outcomes when the viruses are (approximately) equally powerful in the setting of two viruses (the setting of three or more viruses is left as an open problem)? Finally, we conduct a simulation study, under the same model assumptions, to confirm the analytical results offered by the model.

Third, the analytical results make a fundamental connection between two types of factors: the defense capability and the connectivity of the network (via the largest eigenvalue of its adjacency matrix). Therefore, the analytical results not only deepen our understanding of multivirus spreading dynamics, but also offer insights and guidance for defense (e.g., how to tune the parameters by adjusting the defense mechanisms and/or how to tune a network so as to kill all or some of the viruses). The analytical results are often “succinct” (i.e., simple expressions of the parameters) enough to allow us to draw further insights by comparing them.

1.2 Related Work

There are mainly two approaches to understanding security properties from a whole-system perspective: epidemic-like and attack-graph-like. This paper falls into the epidemic-like approach.

**Epidemic-like approach.** This approach aims to characterize, among other things, sufficient conditions (epidemic thresholds) under which the spreading will die out. The study of computer virus dynamics was started by Kephart and White [19], [20], who adopted/adapted some homogeneous biological epidemic models [22], [21], [3], [2], [15]. Recent studies investigated heterogeneous models (see, e.g., [35], [4], [25], [30], [31], [29], [10]), which are interesting not only for their own sake but also because of their practical potential (because any topology is possible). These studies were mainly conducted by the statistical physics community with an emphasis on power law networks (see, e.g., [25], [30], [31], [29]). Very recently, computer scientists investigated spreading in arbitrary networks [34], [13], [10] (rather than just power law topologies). This paper moves a significant step beyond them by considering multiple viruses spreading in arbitrary networks, where the viruses may combat against each other as well.

**Attack-graph-like approach.** In an attack graph, a node is the state of a network and an arc depicts a step in an attack that exploits vulnerabilities uncovered by vulnerability scanners (cf. [33], [18], [1] and their follow-ons). This approach aims to identify, among other things, 1) attack paths between a starting node or a set of starting nodes and some target node, and 2) guidance for security hardening [27], [24]. Recently, Bursztein and Goubault-Larrecq [8], [7], [6] introduced the novel concept of anticipation game, which aims to introduce game theory into attack graphs so as to prove that a safety property holds and further to answer questions about strategic objectives (e.g., what is the most effective patching strategy?).

**On the relationship between the two approaches.** At the current stage of our knowledge, the two approaches are incompatible. Here, we discuss some informal observations, while pointing out that it is an important future work to precisely characterize the relationship (e.g., how can we unify them into a more general framework?). First, the two approaches share some common goals. 1) Both approaches take a whole-system perspective, rather than a component perspective. For example, the vulnerabilities used in the attack-graph-like approach can be used as an input for constructing the system graph used in the epidemic-like approach. 2) Both approaches are useful for “what if” analysis as we show in this paper. Second, the two approaches can answer different kinds of questions under different premises. 1) Attack-graph-like approach often assumes known vulnerabilities that can be obtained using scanners, and thus cannot deal with zero-day exploits. Epidemic-like approach in principle can accommodate zero-day exploits, perhaps with the help of domain expert knowledge. 2) Attack-graph-like approach suffers from the state explosion problem [1], [11]; whereas, epidemic-like models can handle very large networks (e.g., hundreds of millions of nodes). 3) Epidemic-like approach can make a fundamental connection between the defense capability and the network connectivity. We do not know how to accommodate network connectivity into the attack-graph-like approach.

**Outline.** In Section 2, we present and explore a general model of multivirus dynamics. We investigate in Section 3 the special case that the viruses may fight against each other and do not coresize on computers, and in Section 4 the special case that the viruses may coresize on computers. In Section 5, we draw further insights from the analytical results. In Section 6, we report our simulation study. We conclude the paper in Section 7 with open problems.

2 General Multivirus Dynamics Model

2.1 The Master Equation

**Parameters.** Let \( \mathcal{I} \) denote a set of viruses with \( |\mathcal{I}| \geq 2 \). Suppose viruses spread according to a finite network \( G = (V, E) \), where \( V = \{1, 2, \ldots, n\} \) is the set of nodes or vertices and \( E \) is the set of edges or arcs. We call \( G \) the system graph, and denote by \( A = [a_{uv}] \) its adjacency matrix, where \( a_{uv} = 0 \) and for all \( v \neq u, a_{uu} = 1 \) if and only if \((u, v) \in E\). This representation accommodates, and thus our results equally apply to, both directed and undirected graphs.

A system graph abstracts a networked system. A vertex in a system graph my represent a computer with some vulnerabilities, and an edge or arc captures that the exploitation of one vulnerability or the compromise of one computer could lead to the exploitation/compromise of another. A system graph may be obtained, for example, by combining the output of vulnerability scanners and systems configurations (in a fashion similar to [12], [28], [33], [18], [1], [11]), by analyzing the firewall isolation/filtering rules (e.g., which computer is allowed to directly access which other computers), or by using the concept of dependency graphs in a fashion similar to [6]. It is worthwhile to point out that our goal is to investigate the dynamics without making any assumption about the system graph, which certainly exists and can be arbitrary in practice.

The following table summarizes the main parameters and notations used throughout the paper.
for the case of \( \frac{1}{\alpha} \) and "infectious" interchangeably. Each node belongs to one of the following states: secure, vulnerable, and infected. We consider a continuous-time Markov chain (CTMC) with \( \lambda_1, \ldots, \lambda_m \) as the maximum number of time steps in state \( i \), and \( \sum_{i=1}^{m} \lambda_i \) as the geometrically distinct eigenvalues of adjacency matrix \( A \) with \( \lambda_i \) being the largest (in modulus) eigenvalue. The set of multiple viruses \( \mathcal{V} \) is the real part of \( a \) complex number \( z \). The set of eigenvalues of a square matrix \( M \) is the geometrically distinct eigenvalues of adjacency matrix \( A \).

The following table summarizes the main notations used in the general model (Section 2) and their simplified versions (if applicable) used in its special cases (Sections 3 and 4). The derivation of (2.1), we assumed that the infection probabilities at time \( t \) may or may not be equal to \( \frac{1}{\alpha} \) if \( \alpha \) is not infected (i.e., secure or vulnerable), and thus \( \frac{1}{\alpha} \) belongs to one of the following states: secure, vulnerable, and infected. We consider a continuous-time Markov chain (CTMC) with \( \lambda_1, \ldots, \lambda_m \) as the maximum number of time steps in state \( i \), and \( \sum_{i=1}^{m} \lambda_i \) as the geometrically distinct eigenvalues of adjacency matrix \( A \) with \( \lambda_i \) being the largest (in modulus) eigenvalue.

The state transition diagram. We consider a continuous-time model. At any time \( t \), a node \( v \) is in one of the following \( m \) states: 1, \ldots, \( m-1 \), and \( m \). The vertices of a state transition diagram are the aforementioned states 1, \ldots, \( m \). To simplify presentation, we define:

- **Infection-map** \( \mathcal{I} \): \( (j, k, l) \in \mathcal{I} \) is the transition of node \( v \)'s state from \( j \) to \( l \) because of its neighboring nodes \( u \) in state \( k \), where \( \{u, v\} \in \mathcal{E} \). The transition probability at time \( t \) is

\[
\delta_{j,k,l}(t) = 1 - \prod_{(u,v) \in \mathcal{E}} \left( 1 - \delta_{j,k,l}(t) \right),
\]

where \( \delta_{j,k,l} \) is the probability/capability of a single-k-infected neighbor \( u \) causing that \( v \)'s state changes from \( j \) to \( l \). Note that possibly \( \delta_{j,k,l} = 0 \) (e.g., when \( k = m \)) and thus \( \delta_{j,k,l}(t) = 0 \). Note also that in the derivation of (2.1), we assumed that the infection events and the curing events are independent.

- **Recovery-map** \( \mathcal{R} \): \( (j, k, l) \in \mathcal{R} \) is the transition of node \( v \)'s state from \( j \) to \( l \) because of the curing of viruses belonging to \( k \). Because an infected node may become susceptible again, our model is a susceptible-infectious-susceptible (SIS) one.

The master equation. We are concerned with \( \delta_{j,k,l}(t) \), the probability that a node \( v \)'s state transforms from \( j \) to \( l \) at time \( t \) as

\[
\mathbf{P}^i_j(t) = \begin{cases} \beta_{j,k}, & (j, k, l) \in \mathcal{R}, \\ \delta_{j,k,l}(t), & (j, k, l) \in \mathcal{I}. \end{cases}
\]

Because an infected node may become susceptible again, our model is a susceptible-infectious-susceptible (SIS) one.

2.2 Preliminaries

We will need the following lemmas, whose notations may be treated as independent of the main body of the paper. Lemmas 1 and 2 are available from standard textbooks, but may be less known when compared with Gershgorin’s disc theorem [16], the Perron-Frobenius theorem [5], and Gronwall’s inequality [14], which will be used in our analysis as well.

**Lemma 1 (Theorem 2.5.3, pp. 114, [17])**. Let \( C = (c_{ij}) \in \mathbb{R}^{n \times n} \) be a nonsingular matrix with \( c_{ij} \leq 0, i,j = 1, \ldots, n, \) and \( i \neq j \). Then the following statements are equivalent.
• $C$ is an $M$-matrix, meaning that all elements of $C^{-1}$ are nonnegative.
• The real part of every eigenvalue of $C$ is positive.
• There is a positive definite diagonal matrix $P$ such that $PC^{-1}$ is strictly column (or row) diagonally dominant.
• There is a positive definite diagonal matrix $Q$ such that $QC + C^{-1}Q$ is positive definite.

**Lemma 2 (Theorem 4.2, pp. 100, [14]).** System $\frac{d}{dt} \mathbf{x}(t) = B\mathbf{z}(t)$, with $\mathbf{x}(t) \in \mathbb{R}^n$ and $B \in \mathbb{R}^{n \times n}$, is asymptotically exponentially stable if and only if the real part of every eigenvalue of $B$ is negative.

**Lemma 3.** Consider a vector variable $u(t) = [u_1, \ldots, u_n(t)]^\top \in \mathbb{R}^n$ satisfying
\[
\frac{d}{dt} x_i(t) \leq \sum_{j=1}^n c_{ij} x_j(t), \forall i = 1, \ldots, n, t \geq 0,
\]
where $c_{ij} \geq 0$ for all $i \neq j$. Furthermore, consider the following comparison system:
\[
\frac{d}{dt} y_i(t) = \sum_{j=1}^n c_{ij} y_j(t), \quad \forall i = 1, \ldots, n, t \geq 0.
\]
If $x_i(0) \leq y_i(0)$ for all $i = 1, \ldots, n$, then $x_i(t) \leq y_i(t)$ holds for all $i = 1, \ldots, n$ and $t \geq 0$.

**Proof.** Let $t_0$ be the index of the component which satisfies $x_i(t) = v_i(t)$ for the first time, denoted by $t_0$. We have
\[
\left. \frac{d}{dt}(x_i(t) - y_i(t)) \right|_{t=t_0} = c_{ii}(t_0) - y_i(t_0) + \sum_{j \neq i} c_{ij}(t_0)(x_j(t_0) - y_j(t_0)) \leq 0,
\]
owing to $x_j(t) \leq y_j(t)$ for all $j \neq i$. This implies that $x_i(t) - y_i(t)$ does not strictly increases at $t = t_0$, which proves the lemma. □

### 2.3 General Sufficient Conditions for the Dying Out of All Viruses

**Theorem 4 (A general sufficient condition for all viruses to die out regardless of the degree of initial infection).** Let $\lambda_1$ be the largest (in modulus) eigenvalue of the adjacency matrix $A$ of the system graph $G = (V, E)$. Let $H = [a_{kj}]$, where $k, j \in \{1, \ldots, m - 1\}$ and
\[
a_{kj} = \sum_{l} \mathbf{1}_{(l, k)}(\text{possibly some } a_{kj}'s \text{ equal to zero}).
\]
Let $B = [b_{kj}]$, where $k, j \in \{1, \ldots, m - 1\}$ and
\[
b_{kj} = \beta_{kj}(\text{possibly some } b_{kj}'s \text{ equal to zero}).
\]
Let $\mathbf{b} = \text{diag}[b_1, \ldots, b_{m-1}]$, where $B' = \text{diag}[b_1, \ldots, b_{m-1}]$, where $b_j = \sum_{k,l} \mathbf{1}_{(k,l)}(\text{for } j \in \{1, \ldots, m - 1\})$. If
\[
\max\{\Re(\xi) : \xi \in \lambda(\lambda_1 H + B - B')\} < 0,
\]
all viruses will die out no matter how many nodes are initially infected with whichever viruses.

**Proof.** First, we show that it can be derived from condition (2.3) that
\[
\max\{\Re(\xi) : \xi \in \lambda(\lambda_1 H + B - B')\} < 0.
\]
The Perron-Frobenius theorem [5] says that $\lambda_1$ is a real number. Using the first and second items in Lemma 1, (2.3) implies that $-\lambda_1 H - B - B'$ is an $M$-matrix and that there is a positive definite diagonal matrix $D = \text{diag}[d_1, \ldots, d_m]$ such that $D(\lambda_1 H + B - B'D^{-1})$ is strictly diagonal dominant thanks to the third item of Lemma 1. Therefore, $D(\lambda_1 H + B - B'D^{-1})$ is strictly diagonal dominant for every $w \in \lambda(A)$. This leads to (2.4) according to Lemma 1 again.

Second, from (2.1) and (2.2), we have for $v \in V$ and $j \in \{1, \ldots, m - 1\}$:
\[
\frac{d}{dt} x_{ij}(t) = \sum_{l \in V_k} a_{vl} \mathbf{a}_{kj} x_{ik}(t) + \sum_{k} b_{kij} x_{ik}(t) - b_{jv} x_{ij}(t),
\]
with $x_{ij}(0) = i_{ij}(0)$ for $v \in V$ and $j \in \{1, \ldots, m - 1\}$. Note that $x_{ij}(t) = x_{ij}(t)$ for all $t \geq 0$.

Now, we define the following comparison system:
\[
\frac{d}{dt} x_{ij}(t) = \sum_{v \in V_k} a_{vl} \mathbf{a}_{kj} x_{ik}(t) + \sum_{k} b_{kij} x_{ik}(t) - b_{jv} x_{ij}(t),
\]
with $x_{ij}(0) = i_{ij}(0)$ for $v \in V$ and $j \in \{1, \ldots, m - 1\}$. Let $\bar{\lambda}_1, \bar{\lambda}_2, \ldots, \bar{\lambda}_H$ be the geometrically distinct eigenvalues of $A$. Let $A = S^{-1}JS$ be the adjacency matrix $A$'s Jordan decomposition, where $J$ is its Jordan canonical form and in block-diagonal form
\[
J = \begin{bmatrix}
J_1 & & \\
& \ddots & \\
& & J_H
\end{bmatrix},
\]
and
\[
\bar{\lambda}_h 1 0 \cdots 0 \\
0 \bar{\lambda}_h 1 \cdots 0 \\
\vdots & \vdots & \ddots & \vdots \\
0 0 0 \cdots \bar{\lambda}_h
\end{bmatrix}
\]
for $1 \leq h \leq H$.

Let $Y(t) = SX(t)$. Then (2.5) can be rewritten as
\[
\frac{d}{dt} Y(t) = JY(t)\Theta + Y(t)B - Y(t)B'.
\]
Write $Y(t)$ in row as $Y(t) = [Y_1(t), Y_2(t), \ldots, Y_n(t)]^\top$, where $n = |V|$ and each row $Y_{\ell}(t) \in \mathbb{R}^{m-1}$. Thus, for each $Y_{\ell}(t)$, (2.6) can be component-wisely rewritten as
where \( \xi(t) = 0 \) if \( Y_c(t) \) is an eigenvector of \( A \) and \( \xi(t) = Y_{v+1}(t) \) otherwise. Lemma 2 and (2.4) imply \( \lim_{t \to \infty} Y(t) = 0 \) exponentially if \( \xi(t) = 0 \) for all \( t \geq 0 \). By induction, we can prove \( \lim_{t \to \infty} X(t) = 0 \) for all \( v \). This is equivalent to \( \lim_{t \to \infty} x(t) = 0 \) exponentially. From Lemma 3, we have \( i_{v,j}(t) \leq X_{v,j}(t) \) for all \( v, j \) and \( t \). So, we have \( \lim_{t \to \infty} i_{v,j}(t) = 0 \) exponentially and complete the proof. \( \square \)

Now, we present a corollary that is easier to use.

**Corollary 5** (a simplified sufficient condition for all viruses to die out regardless of the degree of initial infection). If for all \( j \in \{1, \ldots, m-1\} \), it holds that

\[
\lambda_1 < \frac{\sum_{[k]:[k,j]\in R} \beta_{jk} - \sum_{[k]} \beta_{jk}^I}{\sum_{[k]} \beta_{jk}^I}, \tag{2.7}
\]

all viruses will die out no matter how many nodes are initially infected with whichever viruses.

**Proof.** From condition (2.7), we have for all \( j \in \{1, \ldots, m-1\} \)

\[
-b_j^I + \sum_{k} [\lambda_1 a_{jk} + b_{jk}] < 0. \tag{2.8}
\]

Let \( z \) be an arbitrary eigenvalue of matrix \( \lambda_1 \Theta + B - B' \). The Gershgorin disc theorem [16] says \( z + b_j^I - \lambda_1 a_{jj} - b_{jj} \leq \sum_{k} [\lambda_1 a_{jk} + b_{jk}] \), where the right-hand side is less than zero because of condition (2.8), which implies \( \Re(z) < 0 \) for all \( z \in \lambda(\lambda_1 \Theta + B - B') \). Via Theorem 4, we complete the proof. \( \square \)

Theorem 4 and Corollary 5 say that when the parameters satisfy the respective conditions, all viruses will be killed no matter how many nodes are initially infected. Therefore, the conditions may be overdemanding when only some (but not many) nodes are initially infected (i.e., light initial infection). In what follows we give a sufficient condition under which the viruses die out in the case of light initial infection; this sufficient condition is close to being necessary.

**Theorem 6** (a sufficient condition for all viruses to die out in the case of light initial infection). Let \( \Theta = [\tilde{a}_{jk}] \in \mathbb{R}^{m-1,m-1} \), where \( k,j \in \{1, \ldots, m-1\} \) and \( \tilde{a}_{jk} = v_{\text{m.k}}^I \). If

\[
\max \{ \Re(z) : z \in \lambda(\lambda_1 \Theta + B - B') \} < 0, \tag{2.9}
\]

then all viruses will die out; if

\[
\max \{ \Re(z) : z \in \lambda(\lambda_1 \Theta + B - B') \} < 0, \tag{2.10}
\]

then the viruses do not die out.

**Proof.** For \( v \in V \) and \( j \in \{1, \ldots, m-1\} \), consider the following linear system near \( i_{v,m} = 1 \) or equivalently \( i_{v,j} = 0 \) for all \( v \in N \) and \( j = 1, \ldots, m-1 \), by neglecting all terms with order higher than 1

\[
d\frac{d}{dt} x_{v,j}(t) = \sum_{u \in V} a_{uv} \beta_{m,k} x_{u,k}(t) + \sum_{(k,l) : [k,l] \in R} \beta_{jk}^I x_{v,j}(t) - \sum_{(k,l) : [j,k,l] \in R} \beta_{jk}^I x_{j,v,l}(t) = \sum_{u \in V} a_{uv} \tilde{a}_{jk} x_{u,k}(t) + \sum_{k} b_{kJ} x_{u,k}(t) - b_{jk} x_{j,v,l}(t). \tag{2.11}
\]

Let \( X(t) = [x_{v,j}(t)]_{v \in V,j \in \{1, \ldots, m\}} \). Then, (2.11) can be rewritten as

\[
d\frac{d}{dt} X(t) = AX(t) + X(t)B - X(t)B'. \tag{2.12}
\]

Reasoning in a fashion similar to the proof of Theorem 4, we can prove (2.9) is sufficient for the local stability of system (2.2).

Condition (2.10) says that the real part of some eigenvalue of linear system (2.11) is greater than zero. Noticing that (2.11) is the linearization of (2.2) and according to the stable manifold theorem [32], if the linearized system has at least one eigenvalue with a positive real part, then the original system is unstable. Thus, we conclude that the original system (2.2) is unstable surrounding \( i_{v,j} = 0 \) for all \( j \in J \). We complete the proof. \( \square \)

In a similar fashion, we have the following corollary:

**Corollary 7** (a simplified sufficient condition for the viruses to die out when the initial infection is light). If for all \( j \in \{1, \ldots, m-1\} \),

\[
\lambda_1 < \frac{\sum_{[k]:[k,j]\in R} \beta_{jk}^I - \sum_{[k]} \beta_{jk}^I}{\sum_{[k]} \beta_{jk}^I}, \tag{2.13}
\]

then all viruses will die out in the presence of light initial infection.

The above analytical results allow us to draw:

**Insight 8.** The above analytical results, especially Corollaries 5 and 7, can quantitatively guide the deployment/adjustment of defense mechanisms (e.g., decreasing \( \beta_{jk}^I \) by enforcing deeper packet inspection over network edges, and/or increasing \( \beta_{jk}^I \) by deploying more antivirus softwares of different vendors, and/or decreasing \( \lambda_1 \) by disabling/filtering some network edges) so as to satisfy the sufficient conditions and to kill the spreading of all viruses.

### 3 Deeper Results in the Case of Disjoint Spreading

In this section, we consider the special case that the fighting viruses do not coexist on computers, which allows us to simplify some notations. Specifically, we say a node \( v \in V \) is susceptible if \( v \) is not infected, and \( j \)-infected if \( v \) is infected by virus \( j \) where \( j \in J \); these states, respectively, correspond to \( \Theta \)-infected and \( \{j\} \)-infected in the general model. We are still concerned with: \( s_v(t) \), the probability node \( v \in V \) is susceptible at time \( t \), which corresponds to \( i_{v,\emptyset}(t) \) in the general model; \( i_{v,j}(t) \), the probability \( v \in V \) is \( j \)-infected at time \( t \) where \( j \in J \), which corresponds to \( i_{v,j}(t) \) in the general model. The invariant is \( s_v(t) + \sum_{j=1}^J i_{v,j}(t) = 1 \). Other parameters are:
\[
\delta_{v,1}(t) = \beta_{v,1} \left( 1 - \delta_{v,1}(t) - \delta_{v,2}(t) \right)
\]

\[
\delta_{v,2}(t) = \theta_{v,2} \left( 1 - \delta_{v,1}(t) - \delta_{v,2}(t) \right)
\]

\[1 - \delta_{v,1}(t) - \delta_{v,2}(t)\]

**Fig. 2.** A simplified state transition diagram of node \( v \in V \) with \( |J| = 2 \).

- \( \beta_j \): The probability/capability a \( j \)-infected node becomes susceptible at any time, where \( j \in J \). Note that \( \beta_j \) corresponds to \( \beta_{(j),j} \) in the general model. We may call the diagonal matrix \( B = \text{diag} [\beta_1, \ldots, \beta_{|J|}] \) the “cure matrix.”

- \( \gamma_j \): The probability/capability a \( j \)-infected node \( u \) successfully infects a susceptible node \( v \), where \( (u, v) \in E \) and \( j \in J \). Note that \( \gamma_j \) corresponds to \( \vartheta_{(j),j}^{(j)} \) in the general model. We may call the diagonal matrix \( \Gamma = \text{diag} [\gamma_1, \ldots, \gamma_{|J|}] \) the “infection matrix.”

- \( \vartheta_{v,j} \): The probability/capability that virus \( j \) successfully “robs” virus \( \ell \) (i.e., a node \( v \)’s state changes from \( \ell \)-infected to \( j \)-infected), where \( (u, v) \in E \), \( \ell, j \in J \), and \( \ell \neq j \) (i.e., a virus does not rob itself). Note that \( \vartheta_{v,j} \) corresponds to \( \vartheta_{v,j}^{(j)} \) in the general model. We may call \( R = [\vartheta_{v,j}]_{|J| \times |J|} \) the “robbing matrix.”

- \( \delta_{v,j}(t) \): The probability a susceptible node \( v \) becomes \( j \)-infected at time \( t \), with

\[
\delta_{v,j}(t) = 1 - \prod_{(u, v) \in E} \left( 1 - \gamma_{u,v}(t) \right).
\]

Note that \( \delta_{v,j}(t) \) corresponds to \( \delta_{v,j}^{(j)}(t) \) in the general model.

- \( \theta_{v,\ell,j}(t) \): The probability an \( \ell \)-infected \( v \) becomes \( j \)-infected at time \( t \), with

\[
\theta_{v,\ell,j}(t) = 1 - \prod_{(u, v) \in E} \left( 1 - \vartheta_{u,v}(t) \right).
\]

Note that \( \theta_{v,\ell,j}(t) \) corresponds to \( \theta_{v,\ell,j}^{(j)}(t) \) in the general model.

The state transition diagram depicted in Fig. 1 is now simplified as Fig. 2.

For a given state transition diagram, we define

\[ N_{in}(j) = \{ \ell : \text{there is an arc from } \{ \ell \} \text{ to } \{ j \} \text{ in the state transition diagram} \}, \]

\[ N_{out}(j) = \{ \ell : \text{there is an arc from } \{ j \} \text{ to } \{ \ell \} \text{ in the state transition diagram} \}. \]

In other words, \( \ell \in N_{in}(j) \) means virus \( j \) can rob virus \( \ell \), and \( \ell \in N_{out}(j) \) means virus \( \ell \) can rob virus \( j \). For example, corresponding to the state transition diagram in Fig. 2, we have \( N_{in}(1) = N_{out}(1) = \{ 2 \} \) and \( N_{in}(2) = N_{out}(2) = \{ 1 \} \) due to the symmetry that the viruses can rob each other. Then, the general master equation (2.2) becomes for \( v \in V \)

\[
\begin{align*}
\frac{d}{dt}s_{v,j}(t) &= \left( -\delta_{v,j}(t) - \sum_{\ell \in J} \theta_{v,\ell,j}(t) \right) i_{v,j}(t) + \left( \sum_{\ell \in J} \beta_{\ell,j} \right) i_{v,j}(t) \\
\frac{d}{dt}i_{v,j}(t) &= \delta_{v,j}(t) s_{v,j}(t) + \sum_{\ell \in N_{in}(j)} \theta_{v,\ell,j}(t) i_{v,\ell}(t) - \left( \beta_{j} + \sum_{\ell \in N_{out}(j)} \theta_{v,\ell,j}(t) \right) i_{v,j}(t), j \in J.
\end{align*}
\]

**3.1 More Succinct Sufficient Conditions for the Dying Out of All Viruses**

Consider the special case where \( 1 = \{ \ell \}, k = \{ k \}, j = \{ j \} \) in the general model. We have \( \beta_{j,j}^{(j)} = \beta_{j,j} \) and \( \beta_{j,k}^{(j)} = 0 \) for all other cases; we have \( \vartheta_{(j),j}^{(j)} = \gamma_{j,j} \), \( \vartheta_{(j),j}^{(j)} = \vartheta_{j,j} \) for \( j \neq m \) and \( j \neq k \), and \( \vartheta_{(j),j}^{(j)} = 0 \) otherwise. The following are special cases of Corollaries 5 and 7, respectively.

**Corollary 9.** (more succinct sufficient condition for all viruses to die out regardless of the degree of initial infection) If for all

\[
j \in J, \lambda_1 < \frac{\beta_j}{\gamma_j + \sum_{\ell \in J} \vartheta_{j,\ell,}^{(j)}}
\]

then all viruses will die out no matter how many nodes are initially infected.

**Corollary 10** (more succinct sufficient condition for all viruses to die out in the case of light initial infection). Suppose some, but not many, nodes are initially infected. If \( \lambda_1 < \frac{\beta_j}{\gamma_j} \) holds \( \forall j = 1, \ldots, |J| \) then the viruses will die out. If \( \exists j \in \{ 1, \ldots, |J| \} \) such that \( \lambda_1 > \frac{\beta_j}{\gamma_j} \) then the viruses do not die out.

Insight 8 is naturally inherited by the above results.

**3.2 What if Some Viruses Are More Powerful than Others?**

Suppose the set of viruses \( J \) can be partitioned into two nonempty sets: \( J_1 \), the set of weaker viruses, and \( J_2 \), the set of stronger viruses, such that in the state transition diagram, there are no arcs starting at any \( \{ \ell \} \), \( \ell \in J_2 \), and arriving at some \( \{ j \}, j \in J_1 \). In other words, a state transition diagram, after omitting the susceptible state, possesses the “weaker-stronger” structure depicted in Fig. 3a. Note the viruses

\[ J_1 \text{: set of viruses that cannot rob viruses belonging to } J_2 \]

\[ J_2 \text{: set of viruses that can rob viruses belonging to } J_1 \]

**Fig. 3.** \( J \) may be partitioned, based on their robbing capabilities, into weaker viruses set \( J_1 \subset J \) and stronger one \( J_2 = J \setminus J_1 \).
belonging to \( J_1 \) may be able to rob each other, but are unable to rob any virus belonging to \( J_2 \). On the other hand, viruses belonging to \( J_2 \) may be able to rob some viruses belonging to \( J_1 \), and may additionally rob other viruses belonging to \( J_2 \) as well.

Although there may be many ways to partition \( J \) while preserving the weaker-stronger structure, we may focus on the partitions where \( |J_1| \) is maximal because the weaker viruses may die before the stronger ones die. However, we should be aware that there may be multiple ways of partitioning while maximizing \( |J_1| \). For example, in the example shown in Fig. 3b with \( J = \{1, 2, 3, 4, 5\} \), virus 5 can be robbed by viruses 1 and 2; virus 1 can be robbed by virus 3; virus 2 can be robbed by virus 4. In this example, there are two ways of partitioning while maximizing \( |J_1|: J_1 = \{1, 2, 3, 5\} \) in one case (within red-color curve) and \( J_1 = \{1, 2, 4, 5\} \) in the other (within blue-color curve). Therefore, we can define

\[
J = \max_{|J'| \subset J: |J'| \leq |J|} \{j \in J: \beta_j, \ell, j' \in J', \ell \in J \setminus J', \{\ell\}\}
\]

pointing to \( \{j'\} \) in the state transition diagram.

The following results concern the fate of the viruses belonging to any \( J_1 \in \mathcal{J} \) of interest.

**Theorem 11 (sufficient condition for the dying out of weaker viruses).** If for all \( j \in J_1 \),

\[
\lambda_1 < \frac{\beta_j}{\gamma_j + \sum_{\ell \in J_1} \vartheta_{\ell j}},
\]

then all viruses belonging to \( J_1 \) will die out regardless of the number of nodes initially infected.

**Proof.** To prove the theorem, we also first prove the following result: If

\[
\max \{\mathcal{R}(z) : z \in \lambda(\Gamma(1 + R_{11}) - B_1)\} < 0,
\]

then all viruses belonging to \( J_1 \) will die out regardless of the degree of initial infection. Since condition (3.2) implies the condition (3.3), we complete the proof.

Now we prove that if condition (3.3) holds, then all viruses belonging to \( J_1 \) will die out regardless of the degree of initial infection. For \( j \in J_1 \), we have

\[
\frac{d}{dt} i_{v,j}(t) = \delta_{v,j}(t)s_j(t) + \sum_{\ell \in N_{w}(j)} \theta_{\ell j}i_{v,\ell}(t) - \left( \beta_j + \sum_{\ell \in N_{w}(j)} \vartheta_{\ell j} \right) i_{v,j}(t)
\]

\[
- \left( \beta_j + \sum_{\ell \in J \setminus J_1} \vartheta_{\ell j} \right) i_{v,j}(t)
\]

\[
- \theta_{\ell j}i_{v,\ell}(t) + \sum_{\ell \in V \setminus \ell \in J_1} \sum_{\ell \in J_1} \vartheta_{\ell j}i_{v,\ell}(t) - \beta j_{v,j}(t)
\]

\[
= \sum_{\ell \in V} \vartheta_{v,j}(t) \gamma_j + \sum_{\ell \in J \setminus J_1} \sum_{\ell \in J_1} \vartheta_{\ell j}i_{v,\ell}(t) - \beta j_{v,j}(t)
\]

because \( \vartheta_{\ell j} = 0 \) for all \( j \in J_1 \) and \( \ell \notin J_1 \) and \( \ell \notin J_1 \). Write the robbing matrix \( R \) as \( R = \left[ R_{10}, R_{11} \right] \), where \( R_{11} \) corresponds to the virus subset \( J_1 \). According to the definition of \( J_1 \), we have \( R_{21} = 0 \). Let \( \Gamma_1 \) and \( B_1 \) be submatrix of \( \Gamma \) and \( B \) corresponding to \( J_1 \), respectively. Consider the following comparison system of \( X_1(t) = [x_{v,j}(t)]_{v \in V, j \in J_1} : \frac{d}{dt} X_1(t) = AX_1(t)(\Gamma_1 + R_{11}) - X_1(t)B_1 \). We have \( i_{v,j}(t) \leq x_{v,j}(t) \) for all \( v \in V, j \in J_1 \), and \( t \geq 0 \) when they take the same initial value, namely \( i_{v,j}(0) = x_{v,j}(0) \), thanks to Lemma 3. Let \( A = S^{-1} AS \) be \( A \)'s Jordan decomposition and \( Y_1 = SX_1 \), we have \( \frac{d}{dt} Y_1 = Y_1(\Gamma_1(1 + R_{11}) - Y_1B_1 \). Reasoning in a fashion similar to the proof of Theorem 4, we can conclude that under condition (3.3), \( \max \{\Re \lambda_j(\Gamma_1 + R_{11}) - B_1)\} < 0 \) for all \( v \in V \). This means \( \lim_{t \to \infty} Y_1(t) = 0 \). Therefore, \( \lim_{t \to \infty} X_1(t) = 0 \) and thus \( \lim_{t \to \infty} i_{v,j}(t) = 0 \) for all \( v \in V \) and \( j \in J_1 \). This completes the proof. \( \square \)

**Theorem 12 (sufficient condition for the dying out of weaker viruses in the case of light initial infection).** If \( \forall j \in J_1, \lambda_j < \frac{\beta_j}{\gamma_j} \), then the viruses belonging to \( J_1 \) will die out in the case of light initial infection with viruses belonging to \( J_1 \).

**Proof.** Note that for any \( j \in J_1 \), if there exists \( \ell \) with \( \vartheta_{\ell j} > 0 \), then \( \ell \in J_1 \). Considering only the viruses belonging to \( J_1 \) in (3.1), and ignoring the terms of order higher than 2, we obtain for \( j \in J_1 \)

\[
\frac{d}{dt} i_{v,j}(t) = \sum_{u \in V} a_{uv} \gamma_j i_{u,j}(t) s_j(t) + \sum_{u \in V, \ell \notin J_1} \vartheta_{\ell j} a_{uv} i_{v,\ell}(t) i_{u,j}(t)
\]

\[
- \left( \beta_j + \sum_{\ell \notin J_1} \vartheta_{\ell j} \right) i_{v,j}(t)
\]

\[
= \sum_{u \in V} a_{uv} \gamma_j i_{u,j}(t) s_j(t) + \sum_{u \in V, \ell \notin J_1} \vartheta_{\ell j} a_{uv} i_{v,\ell}(t) i_{u,j}(t) - \beta j_{v,j}(t)
\]

Consider the following comparison system for \( j \in J_1 \):

\[
\frac{d}{dt} y_{v,j}(t) = \sum_{u \in V} a_{uv} \gamma_j y_{u,j}(t) - \beta j_{v,j}(t).
\]

Reasoning in a fashion similar to the proof of Theorem 6, we can show that under the given condition \( \lambda_j < \frac{\beta_j}{\gamma_j} \), \( \lim_{t \to \infty} y_{v,j}(t) = 0 \). Therefore, \( i_{v,j}(t) = 0 \) for \( j \in J_1 \) are locally asymptotically stable. We complete the proof. \( \square \)

The above analytical results allow us to draw:

**Insight 13.** When it is impossible to kill all viruses, Theorems 11 and 12 offer guidelines for quantitatively tuning parameters (as mentioned above) to kill the weaker viruses.

Because the weaker-stronger structure is not based on the curing-capabilities, but rather based on the robbing-capabilities, of the viruses, this offers an extra leverage to the defender:

**Insight 14.** Even if we are unable to directly kill the weaker viruses, we may exploit the stronger viruses to help alleviate the weaker viruses when the stronger viruses are actually easier to kill.

### 3.3 What if the Viruses Are (Approximately) Equally Powerful?

Here we address the question: What if the viruses are (approximately) equally powerful?

**Theorem 15 (outcome of viruses being equally powerful).**

Suppose for all \( j, j' \in J \) with \( j \neq j' \), there exist \( \beta, \gamma, \vartheta \) such that \( \beta_j = \beta = \beta_j' \), \( \gamma_j = \gamma_j' = \gamma \), and \( \vartheta_{\ell j} = \vartheta_{\ell j'} = \vartheta \). If

\[
\lambda_j < \frac{\beta}{\gamma + \vartheta}.
\]

then \( \forall v \in V \) and \( j, j' \in J \), \( j \neq j' \), we have \( \lim_{t \to \infty} i_{v,j}(t) = i_{v,j'}(t) = 0 \).
Proof. Note that
\[
\begin{align*}
\frac{d}{dt}i_{v,j}(t) - \frac{d}{dt}i_{v,j}(t) &= (\delta_{v,j}(t) - \delta_{v,j}(t))s_v(t) \\
&+ \sum_{\ell \in J}[\theta_{v,j}(t) - \theta_{v,j}(t)]i_{v,j} - \beta(i_{v,j}(t) - i_{v,j}(t)) \\
&- \sum_{\ell \in J}\theta_{v,j}(t)[i_{v,j}(t) - i_{v,j}(t)].
\end{align*}
\]
Since \(|\delta_{v,j}(t) - \delta_{v,j}(t)| \leq \sum_{u \in V} a_{v,u}|i_{u,j}(t) - i_{u,j}(t)|\gamma\) and \(|\theta_{v,j}(t) - \theta_{v,j}(t)| \leq \sum_{u \in V} a_{v,u}|i_{u,j}(t) - i_{v,j}(t)|\), we have
\[
\frac{d}{dt}[i_{v,j}(t) - i_{v,j}(t)] \leq (\gamma + \theta)\sum_{u \in V} a_{v,u}|i_{u,j}(t) - i_{v,j}(t)| - \beta|i_{v,j}(t) - i_{v,j}(t)|.
\]
Consider the following comparison system: \(\frac{d}{dt}x(t) = [-\beta I_n + (\gamma + \theta)A]x(t),\) where \(I_n\) is the \(n \times n\) identity matrix, and \(A\) is the adjacency matrix. Reasoning in a fashion similar to the proof of Theorem 9, we see that condition (3.4) implies that the comparison system is asymptotically stable, and thus \(\lim_{t \to -\infty}|i_{v,j}(t) - i_{v,j}(t)| = 0 \forall v \in V, \forall j, j' \in J.\)

Theorem 16 (outcome of viruses being approximately equally powerful). Suppose for all \(\ell, j, j', j' \in J\) with \(\ell \neq j\) and \(j' \neq \ell\), there exists some \(\epsilon > 0\) such that \(|\beta_j - \beta_{j'}| \leq \epsilon, |\gamma_j - \gamma_{j'}| \leq \epsilon,\) and \(|\theta_{v,j} - \theta_{v,j'}| \leq \epsilon.\) If
\[
\lambda_1 < \frac{\beta_j}{\gamma_j + \theta_{v,j}},
\]
holds for some \(\ell, j, j' \neq j\), then there exists \(d^*\) independent of \(\epsilon\), such that \(\lim_{t \to -\infty}|i_{v,j}(t) - i_{v,j}(t)| \leq d^* \epsilon\) for all \(v \in V\) and \(j, j' \in J.\)

Proof. Note that, according to (3.1)
\[
\begin{align*}
\frac{d}{dt}i_{v,j}(t) - \frac{d}{dt}i_{v,j}(t) &= (\delta_{v,j}(t) - \delta_{v,j}(t))s_v(t) \\
&+ \sum_{\ell \in J}[\theta_{v,j}(t) - \theta_{v,j}(t)]i_{v,j} - \beta_j(i_{v,j}(t) - i_{v,j}(t)) \\
&- \beta_j(i_{v,j}(t) - i_{v,j}(t)) + (\beta_j - \beta) i_{v,j}(t).
\end{align*}
\]
Note also that
\[
|\delta_{v,j}(t) - \delta_{v,j}(t)| \\
\leq \prod_{(u,v) \in E} (1 - \gamma_j i_{u,j}(t)) - \prod_{(u,v) \in E} (1 - \gamma_j i_{u,j}(t)) \\
+ \prod_{(u,v) \in E} (1 - \gamma_j i_{u,j}(t)) - \prod_{(u,v) \in E} (1 - \gamma_j i_{u,j}(t)) \\
\leq \gamma_j \sum_{u \in V} a_{v,u}|i_{u,j}(t) - i_{u,j}(t)| + \sum_{u \in V} a_{v,u}|\gamma_j - \gamma_j| \\
\leq \gamma_j \sum_{u \in V} a_{v,u}|i_{u,j}(t) - i_{u,j}(t)| + \tilde{d} \epsilon,
\]
where \(\tilde{d}\) is the largest node (in-)degree, namely \(\tilde{d} = \max\{|\{(u,v) \in E\}|\}).\) Similarly
\[
|\theta_{v,j}(t) - \theta_{v,j}(t)| \leq \sum_{u \in V} a_{v,u}\theta_{v,j}(t) - i_{v,j}(t) + \tilde{d} \epsilon.
\]
Therefore, we have
\[
\begin{align*}
\frac{d}{dt}|i_{v,j}(t) - i_{v,j}(t)| &\leq |\delta_{v,j}(t) - \delta_{v,j}(t)| + \sum_{\ell \in J}[\theta_{v,j}(t) - \theta_{v,j}(t)]i_{v,j} - \beta_j(i_{v,j}(t) - i_{v,j}(t)) \\
&- \sum_{\ell \in J}\theta_{v,j}(t)[i_{v,j}(t) - i_{v,j}(t)] - \beta_j[i_{v,j}(t) - i_{v,j}(t)] \\
&+ |\beta_j - \beta_j| \leq (\gamma_j + \theta_{v,j}) \sum_{u \in V} a_{v,u}|i_{u,j}(t) - i_{u,j}(t)| \\
&- \beta_j[i_{v,j}(t) - i_{v,j}(t)] + (|J| + 2)\tilde{d} \epsilon.
\end{align*}
\]
Let \(1 = [1, 1, \ldots, 1]^T.\) Consider the following comparison system:
\[
\frac{d}{dt}x(t) = [-\beta J_n + (\gamma + \theta)A]x(t) + d' \epsilon 1,
\]
for some given \(\epsilon, j \in J, j \neq j',\) and \(d' = \tilde{d}(|J| + 2)\) which is clearly independent of \(\epsilon.\) Let \(W_j = -\beta J_n + (\gamma_j + \theta_{v,j})A.\) From condition (3.5), we see that \(-W_j\) is an \(M\)-matrix, and thus Lemma 1 says that there exists positive definite diagonal matrix \(Z_j\) such that \(Z_j W_j + W_j Z_j\) is negative definite. Let \(\rho_j^n\) and \(\rho_j^m\) be the smallest (in modulus) eigenvalues of \(1/2(Z_j W_j + W_j Z_j)\) and \(Z_j,\) respectively. Then, we have
\[
\begin{align*}
\frac{d}{dt}x(t) &= [2\rho_j^m x(t)]x(t) + d' \epsilon x(t) + (d' \epsilon)^2 n \frac{\epsilon}{\rho_j^m} \\
\leq 2(\rho_j^m + \epsilon) x(t) + (d' \epsilon)^2 n \frac{\epsilon}{\rho_j^m} \\
\leq 2(\rho_j^m + \epsilon) x(t) + (d' \epsilon)^2 n \frac{\epsilon}{\rho_j^m},
\end{align*}
\]
for all \(-\rho_j^m < \epsilon < 0.\) Setting \(\epsilon = -\rho_j^m\) and using Gronwall’s inequality [14], we have
\[
\begin{align*}
x(t) &\leq \exp\left(\frac{2\rho_j^m + \epsilon}{\rho_j^m} t\right) x(0) + \frac{(d' \epsilon)^2 n}{\rho_j^m} \left[1 - \exp\left(\frac{2\rho_j^m + \epsilon}{\rho_j^m} t\right)\right] \\
&\leq \exp\left(\frac{\rho_j^m}{\rho_j^m} t\right) x(0) + \frac{(d' \epsilon)^2 n}{\rho_j^m} \left[1 - \exp\left(\frac{\rho_j^m}{\rho_j^m} t\right)\right].
\end{align*}
\]
Therefore, we have
\[
\lim_{t \to -\infty}\|x(t)\|^2_2 \leq \lim_{t \to -\infty}\|x(t)\|^2_2 \leq (d' \epsilon)^2 n \frac{\rho_j^m}{\rho_j^m}.
\]
One can see that condition (3.5) implies that the comparison system (3.6) satisfies \(\lim_{t \to -\infty}\|x(t)\|^2_2 \leq d^* \epsilon\) for some \(d^*\) independently of \(\epsilon.\) This leads to \(\lim_{t \to -\infty}|i_{v,j}(t) - i_{v,j}(t)| \leq d^* \epsilon\) for all \(v \in Z,\) where \(d^*\) can be estimated as
\[
d^* = \frac{d'}{\rho_j^m} \sqrt{\frac{\rho_j^m}{\rho_j^m}}.
\]
This completes the proof. \(\Box\)

The above analytical results allow us to draw:
Insight 17. When the viruses can rob each other, if the viruses 1) have (approximately) equal attack power and (approximately) equal robbing power and 2) are (approximately) equally defended against, then they will have (approximately) the same fate, no matter how many nodes they initially infect and no matter they will die out or not. Moreover, if they die out, they will die out (asymptotically) at the same time.

4 DEEPER RESULTS IN THE CASE OF NONDISJOINT SPREADING

Now we consider the other special case, where one computer gets incrementally infected (i.e., by one virus after another rather than concurrently) and the viruses on a computer get sequentially (rather than simultaneously) cured. We use capital letters such as $I$ ($I \subseteq J$) to represent states in the state transition diagram, and simplify other parameters as follows:

1. The infection-map $I$ in the general model is now simplified as binary relation $(I,j) \in I$ where $j \in J$ and $j \notin I$, meaning that a node’s state changes from $I$ to $I \cup \{j\}$ because of infection by a $\{j\}$-infected node. We hereby denote the infection probability by $\delta_{I,j}$. The probability of node $v$’s state changes from $I$ to $I \cup \{j\}$ is simplified as

$$P_{v,I,j}(t) = \delta_{I,j}(t) = 1 - \prod_{(u,v) \in E} (1 - \delta_{I,j}u_{\{j\}}(t)).$$

(4.1)

2. The recovery-map $R$ in the general model is simplified as a binary relation $(I,j) \in R$, where $j \in I$, meaning that a node’s state changes from $I$ to $I \setminus \{j\}$ because of curing. We hereby denote the cure probability by $\beta_{I,j}$.

The state transition diagram in Fig. 1 is simplified as the one in Fig. 4. The master equation (2.2) is now simplified as

$$\frac{dI_{v,t}(t)}{dt} = \sum_{(I,j) \in I} \delta_{I,j}I_{v,t}(t) + \sum_{(K,j) \in R} \beta_{I,j}K_{v,t}(t)$$

$$- \sum_{(I,K) \in I} \delta_{I,K}I_{v,t}(t) - \sum_{(I,j) \in R} \beta_{I,j}I_{v,t}(t),$$

(4.2)

where $v \in V$, $I \subseteq J$, and $I \neq \emptyset$.

4.1 More Succinct Sufficient Conditions for the Dying Out of All Viruses

Because the present model is a special case of the general model, we can immediately obtain the following results as corollaries of 5 and 7, respectively.

Corollary 18 (sufficient condition for all viruses to die out regardless of the degree of initial infection). If $\forall I \subseteq J$ where

$$I \neq \emptyset, \lambda_1 < \frac{\sum_{(I,j) \in R} \beta_{I,j} - \sum_{(J,j) \in R, J \subset \{j\}} \beta_{J,j}}{\sum_{(K,j) \in R} \lambda_{K,j}},$$

where $J \subseteq J$ and $j, k \in J$, then all viruses will die out no matter how many nodes are initially infected.

Proof. Note that, according to (4.1) for each $K \in J$ and $k \notin K$, we have

$$\delta_{I,K}K_{v,t}(t) \leq \sum_{w \in V} a_{wv} \theta_{K,w}I_{v,t}(t) \delta_{I,K}(t).$$

Furthermore, for each $K \in I$ and $K \cup \{k\} = I$, we can make the following estimations:
\[ \delta_{v,K}(t)i_{v,K}(t) \leq \sum_{w \in V} a_{uw}\delta_{K,ki_{u,K}(t)}, \quad k \in J, \quad k \neq J. \]

Let \( X(t) = [X_{v,I}(t)] \) with \( v \in V \) and \( I \cap J \neq \emptyset \). Let \( \Gamma = [\gamma_{KI}] \) with \( K, I \in \{L \subseteq J : L \cap J \neq \emptyset\} \), where

\[ \gamma_{KI} = \left\{ \begin{array}{ll} \delta_{I,J}, & K = \{k\} \subseteq I \cap J, (I \setminus \{k\}, k) \in I, \\ 0, & \text{otherwise.} \end{array} \right. \]

Let \( \Delta = [\Delta_{KI}] \) with \( K, I \in \{L \subseteq J : L \cap J \neq \emptyset\} \), where

\[ \Delta_{KI} = \left\{ \begin{array}{ll} \delta_{K,J}, & k \notin J, k \notin K, K \cup \{k\} = I, (K, k) \in I, \\ 0, & \text{otherwise.} \end{array} \right. \]

Consider the following comparison system of the master equation (4.2)

\[ \frac{d}{dt} X(t) = AX(t) + \bar{d}X(t) + X(t)(B - X(t)B'), \]

with \( B = [b_{KI}] \) and \( B' = \text{diag}[b'_I] \), where \( K, I \in \{L \subseteq J : L \cap J \neq \emptyset\} \) and

\[ b_{KI} = \left\{ \begin{array}{ll} \beta_{K,J}, & K = 1 \cup \{j\}, (K, j) \in R, \\ 0, & \text{otherwise,} \end{array} \right. \]

and \( b'_I = \sum_{(I,j) \in R} \beta_{I,J} \).

It can be seen that \( X_{v,I}(t) \geq i_{v,I}(t) \) for all \( t \geq 0, v \in V \), and \( I \cap J \neq \emptyset \) as long as \( X_{v,I}(0) \geq i_{v,I}(0) \). Consider the stability of the following component system:

\[ \frac{d}{dt} y(t) = y(t)[\lambda_1 + \bar{d} + B - B'], \]

with \( y(t) \) being \( n \)-dimensional row vector. Similar to the proof of Corollary 5, we conclude that condition (4.3) implies that the real parts of the eigenvalues of matrix \( \lambda_1 + \bar{d} + B - B' \) are all negative. According to Lemma 2, we have \( \lim_{t \to \infty} y(t) = 0 \). By the same fashion of reasoning as in the proof of Theorem 4, we have \( \lim_{t \to \infty} X(t) = 0 \). According to Lemma 3, we have \( \lim_{t \to \infty} i_{v,I}(t) = 0 \) for all \( I \cap J \neq \emptyset \). This completes the proof.

**Theorem 21** (sufficient condition for the dying out of some viruses that did not infect many nodes initially). For a set of viruses \( J \subset \mathcal{J} \), if for each \( I \) with \( I \cap J \neq \emptyset \)

\[ \sum_{J \setminus (I \cap J)} \beta_{J,J} > \sum_{J \setminus (I \cap J)} \beta_{J,J} + \lambda_1 \]

then all viruses belonging to \( J \) will die out when they did not initially infect many nodes.

**Proof.** Note that a linearization of the master equation (4.2) near \( i_{v,I}(0) = 0 \) for all \( v \in V \) and \( I \cap J \neq \emptyset \), neglecting all terms with order higher than 1, leads to

\[ \frac{d}{dt} i_{v,J}(t) - \frac{d}{dt} i_{v,J}(t) = \left[ 1 - \prod_{(u,v) \in E} \left( 1 - \vartheta_{v,1}^2 i_{u,v}(t) \right) \right] \]

\[ - \left[ 1 - \prod_{(u,v) \in E} \left( 1 - \vartheta_{v,1}^2 i_{u,v}(t) \right) \right] \]

\[ i_{v,J}(t) - \beta_{v,J} \left( i_{v,J}(t) - i_{v,J}(t) \right) \]

\[ \left[ 1 - \prod_{(u,v) \in E} \left( 1 - \vartheta_{v,1}^2 i_{u,v}(t) \right) \right] i_{v,J}(t) \]

\[ \left[ 1 - \prod_{(u,v) \in E} \left( 1 - \vartheta_{v,1}^2 i_{u,v}(t) \right) \right] i_{v,J}(t). \]
Noting
\[
\left| \left( 1 - \prod_{(u,v) \in E} (1 - \vartheta_{1,1} i_{u,(1)}(t)) \right) \right|
\]
\[
\leq \sum_{u \in V} a_{uv} i_{u,(1)}(t) - i_{u,(2)}(t) |\vartheta_{1,1},
\]
and
\[
- \left[ \left( 1 - \prod_{(u,v) \in E} (1 - \vartheta_{1,2} i_{u,(2)}(t)) \right) i_{c,(1)}(t) \right]
\]
\[
- \left( 1 - \prod_{(u,v) \in E} (1 - \vartheta_{1,2} i_{u,(1)}(t)) \right) i_{c,(2)}(t) \right]
\]
\[
\leq - \left( 1 - \prod_{(u,v) \in E} (1 - \vartheta_{1,2} i_{u,(2)}(t)) \right) (i_{c,(1)}(t) - i_{c,(2)}(t))
\]
\[
+ \left( 1 - \prod_{(u,v) \in E} (1 - \vartheta_{1,2} i_{u,(1)}(t)) \right) i_{c,(2)}(t)
\]
\[
- \left( 1 - \prod_{(u,v) \in E} (1 - \vartheta_{1,2} i_{u,(1)}(t)) \right) i_{c,(1)}(t)
\]
\[
\leq - \left( 1 - \prod_{(u,v) \in E} (1 - \vartheta_{1,2} i_{u,(2)}(t)) \right) (i_{c,(1)}(t) - i_{c,(2)}(t))
\]
\[
+ \sum_{u \in V} a_{uv} i_{u,(1)}(t) - i_{u,(2)}(t) |\vartheta_{1,2},
\]
we have
\[
\frac{d}{dt} |i_{c,(1)}(t) - i_{c,(2)}(t)| \leq -\beta_{1,1} |i_{c,(1)}(t) - i_{c,(2)}(t)|
\]
\[
+ \sum_{u \in V} a_{uv} i_{u,(1)}(t) - i_{u,(2)}(t) |\vartheta_{1,1} + \vartheta_{1,2}|
\]
Consider a comparison system
\[
\frac{d}{dt} z_v(t) = -\beta_{1,1} z_v(t) + \sum_{u \in V} a_{uv} z_u(t) |\vartheta_{1,1} + \vartheta_{1,2}|
\]
One can see that \(z_v(t) \geq |i_{c,(1)}(t) - i_{c,(2)}(t)|\) holds for all \(t \geq 0\) and \(v \in N\) as long as \(z_v(0) \geq |i_{c,(1)}(0) - i_{c,(2)}(0)|\).

The given condition implies that the real parts of all eigenvalues of \(-\beta_{1,1} I_n + (\vartheta_{1,2} + \vartheta_{1,1}) A\) are negative. According to Lemma 2, \(\lim_{t \to \infty} z_v(t) = 0\) for all \(v \in V\). This implies \(\lim_{t \to \infty} |i_{c,(1)}(t) - i_{c,(2)}(t)| = 0\) for all \(v \in V\).

The proof is completed. \(\square\)

**Theorem 24 (outcome of viruses being approximately equally powerful).** Suppose there is \(\epsilon > 0\) such that
\[
|\vartheta_{1,1} - \vartheta_{1,2}| \leq \epsilon, \quad |\vartheta_{1,2} - \vartheta_{1,1}| \leq \epsilon, \quad |\beta_{1,1} - \beta_{1,2}| \leq \epsilon, \quad and \quad |\beta_{2,1} - \beta_{1,2}| \leq \epsilon.
\]

If \(\lambda_1 < \frac{\beta_{1,1}}{\beta_{1,1} + \lambda_2} \), then \(\lim_{t \to \infty} |i_{c,(1)}(t) - i_{c,(2)}(t)| \leq d' \epsilon\) for some \(d' > 0\) independent of \(\epsilon\) and all \(v \in V\).
we have
\[
\frac{d}{dt} |v,1(t) - v,2(t)| \leq -\beta_{1,1}|v,1(t) - v,2(t)| \\
+ \sum_{u \in V} a_{vu} |v,1(t) - v,2(t)| (\delta_{1,1} + \delta_{1,2}) + d^t
\]
where \(d^t = 2\tilde{d} + 3\). Via Lemma 1, the given condition implies \(-\beta_{1,1}I_n + (\delta_{1,1} + \delta_{1,2})A\) is an M-matrix. The theorem can be proved in the same fashion as in the proof of Theorem 16.

The above analytical results allow us to draw:

**Insight 25.** If two viruses have (approximately) equal infection power and are (approximately) equally defended against, then they will have (approximately) the same fate, no matter how many nodes they initially infect and no matter they will die out or not. Moreover, if they die out, they will die out (asymptotically) at the same time.

### 5 Further Insights Offered by the Theoretical Results

First, by comparing Corollary 5 and Corollary 7, we draw:

**Insight 26.** The (reactive) countermeasures, which are sufficient for killing the spreading of multiple viruses when some (but not many) nodes are initially infected, might not be sufficient for killing the spreading of multiple viruses when many nodes are initially infected. Therefore, preventive/proactive defense and rapid attack detection/response are always very valuable.

Second, consider a special case of the model investigated in Section 3, namely that the viruses spread disjointly but without being able to rob each other, meaning \(\delta_{1,2} = 0\) for \(\ell, j \in J\). Then, the state transition diagram in Fig. 1 is now simplified as Fig. 5a, and the sufficient condition given in Corollary 9 becomes \(\lambda_1 < \min_{\ell \in J} \frac{\beta_{1,1}}{\beta_{1,2}}\). One the other hand, recall the sufficient condition (due to [10]) for the dying out of a single virus spreading in an arbitrary network is \(\lambda_1 < \frac{\beta_{1,1}}{\beta_{1,2}}\). As a trivial extension, this means that when multiple viruses spread independently over the same network, the sufficient condition for virus \(j\) to die out is \(\lambda_1 < \frac{\beta_{1,1}}{\beta_{1,2}}\). For the case of two viruses, the state transition diagram is Fig. 5b. Also considering Corollaries 10 and 18, the above discussion leads to:

**Insight 27.** The (reactive) countermeasures, which are sufficient for killing the independent spreading of viruses when some nodes are initially infected, are 1) sufficient for killing the disjoint spreading of viruses when some nodes are initially infected, 2) probably not sufficient for killing the disjoint spreading of viruses when many nodes are initially infected, and 3) probably not sufficient for killing the nondisjoint spreading of viruses under certain circumstances (e.g., if \(\beta_{1,1} - \beta_{1,2,1} = 0\) or \(\beta_{1,2} - \lambda_1 = 0\) when there are two viruses).

The above 1) and 2) characterize the power disjoint versus independent spreading in terms of the tolerable number of initially infected nodes. It may seem counterintuitive, but is actually reasonable because the sufficient condition deals with the dying out of viruses, and nothing else (e.g., what happens when the viruses do not die out). Note that there is no contradiction between this statement and Insight 14, where we claimed that the stronger viruses could be exploited to alleviate (but not kill) the weaker viruses that are actually harder for the defender to kill directly.

Third, by considering Theorems 11 and 12, and further Corollaries 9 and 10, we draw:

**Insight 28.** When some viruses can be robbed by, but cannot rob, the others, it is easier to kill these weak viruses when they initially infected some nodes than when they initially infected many nodes. Moreover, weak viruses may be killed without strong viruses being killed.

The above insight cannot be directly applied to the case where the viruses spread nondisjointly and do not rob each other. Still, by comparing Theorems 20 and 21, we draw:

**Insight 29.** When the viruses do not rob each other and spread nondisjointly (but not independently), it is easier to kill a subset of viruses when they initially infected some nodes than when they initially infected many nodes.

### 6 Simulation Study

We use simulation (under the same model assumption) to confirm the analytical results in the disjoint spreading model (Section 3) because of its simplicity. We consider three examples of \(G = (V, E)\): Erdos-Renyi random graph, regular graph, and power law graph. In each case, we have \(|V| = 2,000\). The random graph has average node degree 6.001 and \(\lambda_1 = 7.1424\). The regular graph has node degree 6 and \(\lambda_1 = 6\). The power law graph, which is generated using Brite [23], has average node degree 5.994 and \(\lambda_1 = 11.6514\). The graphs have approximately the same average degree because we want to observe, as a side product, whether there is any difference caused by topology. We simulated two settings with \(|J| = 2\) and \(|J| = 3\); in what follows we only report the results corresponding to \(|J| = 2\) because of space limitation (|J| = 3 exhibits similar outcomes though).
Other parameters will be specified below. To represent the dynamics, we plot the number of nodes infected by virus $j \in J$ at time $t$ based on the average of 20 independent simulation runs.

### 6.1 Simulation Study for Verifying the Sufficient Conditions for the Dying Out of Viruses

**Simulation confirmation of Corollary 9.** We let each virus initially infect 400 or 20 percent randomly selected nodes. For each topology, we use the following three parameter set scenarios: 1) $(\beta_1, \gamma_1, \vartheta_{12}) = (0.1, 0.0005, 0.001)$ and $(\beta_2, \gamma_2, \vartheta_{21}) = (0.1, 0.00045, 0.002)$; 2) $(\beta_1, \gamma_1, \vartheta_{12}) = (0.2, 0.0025, 0.001)$ and $(\beta_2, \gamma_2, \vartheta_{21}) = (0.15, 0.002, 0.002)$; 3) $(\beta_1, \gamma_1, \vartheta_{12}) = (0.2, 0.0005, 0.001)$ and $(\beta_2, \gamma_2, \vartheta_{21}) = (0.3, 0.0045, 0.005)$. In each parameter scenario, the sufficient condition stated in Corollary 9 is satisfied, and thus the analytical result says that the two viruses will die out regardless of the degree of initial infection.

Fig. 6 plots (partially) the simulation results, and shows that the three graphs demonstrate similar phenomenon. For example, both viruses spreading over the regular graph die out at about the 1,000th/4,000th/12,000th step in parameter scenarios 1)/2)/3), respectively.

**Simulation confirmation of Corollary 10.** We let each virus initially infect 75 or 3.75 percent randomly selected nodes. For each topology, we consider three parameter scenarios: 1) $(\beta_1, \gamma_1, \vartheta_{12}) = (0.6, 0.5, 0.1)$ and $(\beta_2, \gamma_2, \vartheta_{21}) = (0.6, 0.048, 0.2)$; 2) $(\beta_1, \gamma_1, \vartheta_{12}) = (0.5, 0.3, 0.1)$ and $(\beta_2, \gamma_2, \vartheta_{21}) = (0.5, 0.034, 0.2)$; 3) $(\beta_1, \gamma_1, \vartheta_{12}) = (0.3, 0.1, 0.1)$ and $(\beta_2, \gamma_2, \vartheta_{21}) = (0.3, 0.024, 0.1)$. In every parameter set scenario of every case, the sufficient condition is slightly violated and the viruses may not die out. Fig. 8 plots (partially) the simulation results, which show that in every scenario of every case, the viruses do not die out.

In summary, our simulation confirms Corollaries 9 and 10. As a side-product, our simulation study suggests that it seems more difficult to kill all the viruses in regular and random networks than in power law networks. It is interesting to prove this analytically.

### 6.2 Simulation Study for Verifying the Outcome when Some Viruses Are More Powerful

**Simulation confirmation of Theorem 11.** We let virus 1 initially infect 320 or 16 percent randomly selected nodes, and virus 2 initially infect 1,280 or 64 percent randomly selected nodes. Fig. 9 plots the dynamics of the two viruses with respect to the following three parameter scenarios in each case of system graph topologies: 1) $(\beta_1, \gamma_1, \vartheta_{12}) = (0.4, 0.02, 0.2)$ and $(\beta_2, \gamma_2, \vartheta_{21}) = (0.001, 1.0, 0.0)$; 2) $(\beta_1, \gamma_1, \vartheta_{12}) = (0.6, 0.02, 0.3)$ and $(\beta_2, \gamma_2, \vartheta_{21}) = (0.002, 1.0, 0.0)$;
3) \((\beta_1, \gamma_1, \vartheta_{1,2}) = (0.7, 0.030, 0.4)\) and \((\beta_2, \gamma_2, \vartheta_{2,1}) = (0.002, 1.0, 0.0)\). Note that in each parameter set scenario, virus 1 is the weaker one (i.e., \(\gamma_1 = \{1\}\)) and virus 2 is the stronger one, and the parameters corresponding to virus 1 satisfy the sufficient condition in Theorem 11, which means that virus 1, but not necessarily virus 2, will die out. Note also that we intentionally select the parameters for virus 2 so that the sufficient condition in Corollary 9 is violated; otherwise, virus 2 is bound to die out as well.

**Simulation confirmation of Theorem 12.** We let virus 1 initially infect 80 or 4 percent randomly selected nodes, and virus 2 initially infect 320 or 16 percent randomly selected nodes. Fig. 10 plots (partially) the dynamics of two viruses with the following three parameter scenarios in each case of system graph topologies: 1) \((\beta_1, \gamma_1, \vartheta_{1,2}) = (0.3, 0.021, 0.1)\) and \((\beta_2, \gamma_2, \vartheta_{2,1}) = (0.008, 1.0, 0.0)\); 2) \((\beta_1, \gamma_1, \vartheta_{1,2}) = (0.4, 0.032, 0.4)\) and \((\beta_2, \gamma_2, \vartheta_{2,1}) = (0.009, 1.0, 0.0)\); 3) \((\beta_1, \gamma_1, \vartheta_{1,2}) = (0.6, 0.042, 0.4)\) and \((\beta_2, \gamma_2, \vartheta_{2,1}) = (0.015, 1.0, 0.0)\). In each parameter scenario, virus 1 is the weaker one and virus 2 is the stronger one, and the parameters corresponding to virus 1 satisfy the sufficient condition in Theorem 12, which means that virus 1, but not necessarily virus 2, will die out. With respect to the parameter scenarios 1)/2)/3), simulation shows that in the random graph, the weaker virus dies out at about the 1,500th/2,400th/12,000th step, respectively; in the regular graph, the weaker virus dies out at about the 1,300th/2,300th/11,400th step, respectively; in the power law graph, the weaker virus dies out at about the 800th/1,100th/3,900th step, respectively.

In summary, our simulation study confirms the sufficient conditions given in Theorems 11 and 12, under which the weaker, but not necessarily the stronger, viruses die out.
Fig. 11. Simulation confirmation of Theorem 15 with two viruses.

### 6.3 Simulation Study for Verifying the Outcome of Viruses Being Equally Powerful

Fig. 11 plots (partially) the dynamics of two viruses with three parameter scenarios: 1) \((\beta_1, \gamma_1, \vartheta_{1,2}) = (0.2, 0.0018, 0.002)\) and \((\beta_2, \gamma_2, \vartheta_{2,1}) = (0.2, 0.0018, 0.002)\); 2) \((\beta_1, \gamma_1, \vartheta_{1,2}) = (0.4, 0.0022, 0.002)\) and \((\beta_2, \gamma_2, \vartheta_{2,1}) = (0.4, 0.0022, 0.002)\); 3) \((\beta_1, \gamma_1, \vartheta_{1,2}) = (0.6, 0.0036, 0.002)\) and \((\beta_2, \gamma_2, \vartheta_{2,1}) = (0.6, 0.0036, 0.002)\). All the parameter scenarios satisfy the sufficient condition in Corollary 9, meaning that the two viruses will die out, and the sufficient condition in Theorem 15, meaning that the two viruses will exhibit the same dynamics. We let each of them initially infect 400 or 20 percent randomly selected nodes. Fig. 11 demonstrates that for each graph in each of the parameter scenario, the two viruses exhibit almost identical dynamics.

Fig. 12 plots (partially) the dynamics of two viruses with the following three parameter scenarios: 1) \((\beta_1, \gamma_1, \vartheta_{1,2}) = (0.4, 0.005, 0.02)\) and \((\beta_2, \gamma_2, \vartheta_{2,1}) = (0.4, 0.005, 0.02)\); 2) \((\beta_1, \gamma_1, \vartheta_{1,2}) = (0.6, 0.0075, 0.03)\) and \((\beta_2, \gamma_2, \vartheta_{2,1}) = (0.6, 0.0075, 0.03)\); 3) \((\beta_1, \gamma_1, \vartheta_{1,2}) = (0.8, 0.01, 0.04)\) and \((\beta_2, \gamma_2, \vartheta_{2,1}) = (0.8, 0.01, 0.04)\). All of the three parameter sets do not satisfy the sufficient condition in Corollary 9, meaning that the two viruses may not die out, but satisfy the sufficient condition in Theorem 15, meaning that the two viruses will exhibit the same dynamics. We let each of them initially infect 400 or 20 percent randomly selected nodes. Fig. 12 demonstrates that for each graph in each of the parameter scenario, the two viruses exhibit quite identical dynamics. The small, but sometimes noticeable difference is attributed to the fact that the curves are based on the average of 20 runs and the viruses dying out very slow (in which case oscillation is possible).

In summary, our simulation study confirms the analytical result of Theorem 15, namely that if the viruses are equally powerful, then they will eventually exhibit the same dynamics. In particular, if they are to die out, they will die out at the same time.

### 7 CONCLUSION

We introduced a general model of multivirus spreading dynamics, where the viruses may combat against each other. We presented analytical results in the general model, including sufficient conditions under which the viruses die out when many or some nodes are initially infected, and deeper results for two special cases of the general model. The analytical results made a fundamental connection between the defense capability and the connectivity of the network (via the largest eigenvalue of its adjacency matrix), and allowed us to draw various insights that can be used to guide security defense.

This paper brings a range of new problems for future research. In addition to those mentioned in the body of the paper, we offer: When we state the degree of initial infection, we used the qualitative term “light initial infection,” but can we quantify it? What are the necessary conditions under which the viruses will die out? What are the complete dynamics characteristics when (some or all of) the viruses do not die out?

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Shouhui Xu received the PhD degree in computer science from Fudan University, China. He is an associate professor in the Department of Computer Science, University of Texas at San Antonio. His research interests include cryptography and cyber security modeling and analysis. More information about his research can be found at www.cs.utsa.edu/.

Wenlian Lu received the BS degree in mathematics and the PhD degree in applied mathematics from Fudan University in 2000 and 2005, respectively. He is an associate professor in the School of Mathematical Sciences and a senior member of the Center for Computational Systems Biology, Fudan University, China. He was a postdoctoral researcher in the Max Planck Institute for Mathematics, Leipzig, Germany, from 2005 to 2007. His current research interests include neural networks, nonlinear dynamical systems, and complex systems.

Zhenxin Zhan received the MS degree in computer science from the Huazhong University of Science and Technology, China, in 2008. He is currently working toward the PhD degree in the Department of Computer Science, University of Texas at San Antonio. His primary research interests are in cyber attack detection and malware analysis.

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