

Broadcast Networks based on the Virus Evolutionary Algorithm

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Abstract—An optimization algorithm for virus evolution is to research the spread process of a computer or biological virus in network system. The objective of the algorithm is mainly to control the speed of the virus evolution with limited network resource and to study how users can be infected in the network. A dynamical probabilistic system on a connected graph is adopted to model the virus evolution. A traditional virus evolution model needs to solve a non-convex optimization problem taking the spectral radius function of a nonnegative matrix as an optimization objective in the description of virus evolution model. On this basis, two novel approximation algorithms are proposed in this paper. Based on continuous convex approximation, the first one is a suboptimal with rapid speed. The second one can adopt branch-and-bound techniques to achieve a global optimal solution, which use some key inequalities of nonnegative matrix. Comparing with traditional virus evolution model, the simulation experiment shows that the improved algorithm can reach the global optimum in the process of virus evolution and has fast convergence capability in different network conditions.

Index Terms—Virus Evolution; Minimum Spectral Radius; Non-Negative Matrix Theory; Branch-And-Bound; Dynamical Probabilistic System; Non-Convex Optimization

I. INTRODUCTION

The results of Perron and Frobenius concerning spectral properties of matrices with nonnegative elements have become an important tool in the study of iterative methods for linear equations in \mathbb{R}^n . These results have been generalized in various ways; for example, Krein, Rutman and Schaefer for general extensions to infinite-dimensional spaces and further references. Simple proofs of the Perron-Frobenius results for matrices can be found in Varga and Householder. These proofs, however, do not appear to carry over to the case of linear mappings on a finite-dimensional space which are nonnegative under a general partial ordering on the space. For this case, it is necessary either to emulate the infinite-dimensional proofs by using the Brouwer fixed point theorem or to depend heavily on the spectral theory of finite-dimensional linear maps and the Jordan form of a matrix and Vandergraft.

Virus evolution is a spread process of a computer or biological virus in network system. How to estimate and control the spread of virus is an important issue in the research of information physical system or medical epidemiology. A dynamical probabilistic system on a connected graph is adopted to model the virus evolution, so how to control the process to apply to systems control theory is analyzed. Generally, the stability of the evolution process is decided by the network connectivity and any virus-related parameters, such as propagation models, incident rates and so on. Therefore, how virus spread in bio-systems or information physical networks and how they can be controlled is a complicated stochastic nonlinear control problem. Network resources have to be used within the constraints of more practical constraints, such as the main protective measures in practical use, the limited capacity. Thereby, parameters need to be applied to research and analysis of statistical optimization solution in dynamical probabilistic system.

In the existing literature, a typical propagation model divides nodes in the network into three basic types: 1) impressionable: the node is healthy, but is easily infected; 2) infected: the node can infect others; 3) recuperative: the node was infected, but is cured for now. Based on the different combination of three basic types, different virus models can be considered. When network connectivity (graph theory) is considered by virus model, a threshold value of virus is used to evaluate the situation of virus evolution. That is to say different threshold criteria and their relationship with graph structures can be analyzed. In addition, based on the specific threshold in specific network, such as the network related closely to the spectral radius of the topological matrix, it also is analyzed. Some researches propose different optimization algorithms under different assumptions, such as minimizing a general cumulative cost and representing the optimal dynamic repair strategies under the isotropy assumption that all nodes have same contact rate. With the prosperity and development of mobile computation, especially the increase of mobile devices with Bluetooth, analyzing the virus threshold plays an important role in mobile ad-hoc networks. In order to find the source of a computer virus in a network, inference technique can be

adopted. Furthermore, some papers also research the basic spread model which is for characterizing a mobile phone virus outbreak. In these related works, the network topology is a fundamental property to control virus diffusion.

The research introducing formally a deterministic standard virus to control algorithm is the most noticeable. And the research is to minimize the spectral radius of the network topology matrix (including the virus spreading rate) under a given amount of network resources. However, the algorithm has some limitations in the actual application; for example, it is assumed that the interaction overview diagram of the virus evolution must be symmetric or diagonal symmetric matrix. These assumptions can be relaxed to expand its application range. For different nodes in the network may generate different levels of immunization, it may be more useful to generalize the virus topological structure including a directed asymmetric interactive diagrams.

The proposed algorithm in this paper adopts deterministic finite optimization theory to study how to control the virus evolution and optimize the rate of virus evolution under a limited network resource sets. Inspired by the literature [9], a deterministic virus evolution control framework is studied, which solve a non-convex optimization problem under the restraint of control variables, on basis of minimizing a spectral radius function. Firstly, as we all know, the optimal solution of the spectral radius minimization problem is located at the border of the constraint set. Then, feasible suboptimal solution of the spectral radius minimization problem is obtained by using continuous convex approximation based on geometric programming. Key tools in non-negative matrix theory, such as the Perron-Frobenius theorem and the Friedland-Karlin inequalities, are finally adopted to find bounds of the branch-and-bound method. Therefore, an algorithm that can compute the global optimal solution of the spectral radius minimization problem is proposed.

The rest of this paper is organized as follows. In Section two, the system model is introduced and the virus evolution problem is formulated. A fast continuous convex approximation algorithm is proposed to solve sub-optimally the problem in Section three. In Section four, a branch-and-bound algorithm is proposed to compute the global optimal solution, which use some key inequalities in nonnegative matrix theory. The performance of our proposed algorithms is compared by numerical evaluation in Section five. The conclusion of this paper is in Section six. The following notation is used in our paper. Column vectors and matrices are denoted by boldfaced lowercase and uppercase, respectively; $\rho(A)$ denotes the Perron-Frobenius eigenvalue of a nonnegative matrix A ; $\mathbf{x}(A)$ and $\mathbf{y}(A)$ denote the right and left eigenvectors of A associated with $\rho(A)$; \mathbf{I} is the identity matrix. For a given vector $\mathbf{x} = (x_1, \dots, x_L)^T$, $\text{diag}(\mathbf{x})$ is a diagonal matrix $\text{diag}(x_1, \dots, x_L)$.

II. SYSTEM MODEL

Virus evolution process is actually a transformation of two nodes state in a broadcast network from infected node to impressionable node. Therefore, state transfer graph can be adopted to show the process. In the contact network model, state transition between nodes is mutual. In order to describe the recovery procedure of the node exactly, a recuperative probability between infected node and impressionable node is introduced.

L users are given in broadcast network, where a virus spreads from infected users to impressionable users. This section mainly review two linear models based on discrete time, namely, the multi-group model and the contact network model. Let F represent the transmission coefficient matrix, where F_{ij} denote the infectious ratio of the i th group node to the j th group node in the multi-group model, or denotes the ratio the i th node infects the j th node in the contact network model.

$\delta = (\delta_1, \dots, \delta_L)^T$ is a recovery vector, where element δ_i denotes the recuperative probability of the infected node. The impressionable-infected model of the i th node is shown in Figure 1. Then, a next generation matrix G is constructed, which denotes the type conversion of nodes at each discrete time slot. Regarding different parameters as control variables in the next generation matrix, the rate of the virus evolution can be controlled. Thus, the optimization problem of minimizing the spectral radius in the next generation matrix is formulated.

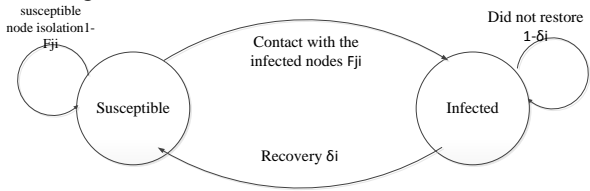


Figure 1. The impressionable-infected model of the i th node

A. Multi-group Model

The multi-group model with N groups is introduced, and the number of nodes in i th group is n_i (which implies $\sum_{i=1}^N n_i = L$). At this point, an infected node does not recover. Let us assume the average infectious time of a node in the i th group is τ_i , so the number $\eta_i(t+1)$ of infectious nodes of the i th group at $(t+1)$ th generation can be described as following equation:

$$\frac{\eta_i(t+1)}{n_i} = \tau_i \left(F_{ii} \frac{\eta_i(t)}{n_i} + \sum_{j \neq i} F_{ij} \frac{\eta_j(t)}{n_j} \right) \quad (1)$$

We notice that the node can be not only infected by node in the same group, but also infected by node from other group. In order to control the virus spreading rate, the following variables are introduced:

$$\hat{F}_{ij} = \frac{1}{\xi_i} F_{ij}, \xi_i \in (0, 1], i, j = 1, \dots, N$$

where ξ resizes the transmission coefficient matrix and decreases the virus evolution rate in the whole network, namely, isolate the infected nodes.

TABLE I. SUMMARY OF THE NEXT GENERATION MATRIX FOR VIRUS EVOLUTION

$\mathbf{G}(\mathbf{s})$	\mathbf{s}	Problem parameters
$\text{diag}(\mathbf{s})\mathbf{B}$	ξ	$\mathbf{B} = \hat{\tau}\text{diag}(\omega)(\hat{\mathbf{F}}^d + \text{diag}(\phi)\bar{\mathbf{F}})$
	ω	$\mathbf{B} = \hat{\tau}\text{diag}(\xi)(\hat{\mathbf{F}}^d + \text{diag}(\phi)\bar{\mathbf{F}})$
$\text{diag}(\mathbf{d}) + \text{diag}(\mathbf{s})\mathbf{B}$	ϕ	$\text{diag}(\mathbf{d}) = \hat{\tau}\text{diag}(\omega)\text{diag}(\xi)\hat{\mathbf{F}}^d$ $\mathbf{B} = \hat{\tau}\text{diag}(\omega)\text{diag}(\xi)\bar{\mathbf{F}}$
	β	$\mathbf{d} = \mathbf{1} - \delta, \mathbf{B} = \bar{\mathbf{F}}$
$\text{diag}(\mathbf{s}) + \mathbf{B}$	$\mathbf{1} - \delta$	$\mathbf{B} = \text{diag}(\beta)\bar{\mathbf{F}}$

$\bar{F}_{ij} = \frac{1}{\phi_i} \hat{F}_{ij}, \phi_i \in (0,1], i \neq j, i, j = 1, \dots, N$ Note that $\bar{\mathbf{F}}$

is a nonnegative matrix, $\bar{F}_{ii} = 0$, for all i . So, the contact rate between different groups is decreased, which means that the movement range of nodes is restricted in its own group.

$$\hat{\tau} = \frac{1}{\omega_i}, \omega_i \in (0,1], i = 1, \dots, N$$

The variable ω_i is introduced to control infectious time of nodes in each group. Actually, ω_i can be set to be infinity when anti-virus software is used to prevent the infection.

The next generation matrix for virus evolution can be described as following equation:

$$\mathbf{G} = \hat{\tau}\text{diag}(\omega)\text{diag}(\xi)(\hat{\mathbf{F}}^d + \text{diag}(\phi)\bar{\mathbf{F}}) \quad (2)$$

where $\hat{\mathbf{F}}^d$ is a diagonal matrix and has $\hat{F}_{ii}^d = \hat{F}_{ii}$ for all i .

Next, the contact network model is introduced in section B. Similar to this section, the next generation matrix firstly is established, and then the control variables are introduced to analyze the epidemic evolution.

B. Contact Network Model

A virus spreads by communication of nodes in the contact network model, and movement of nodes do not depend on any group pattern. The probability that the i th node is infected at the $(t+1)$ th time slot is $p_i(t+1)$, which described by in term of $\mathbf{p}(t)$ as following equation:

$$p_i(t+1) = \left(1 - \prod_{j=1}^L (1 - F_{ij} p_j(t))\right) + (1 - \delta_i) p_i(t) \quad (3)$$

where δ_i is recovery rate. We should notice that $\prod_{j=1}^L (1 - F_{ij} p_j(t))$ is the probability that the i th node does not communicate with any infected node, and its

opposite side is the probability that the i th node is infected by at least one infected node.

The another form of Equation (3) can guide and control the immunity of each node (use $F_{ij} = \beta_i \tilde{F}_{ij}$ to denote, where $\beta_i \in [0,1], i \neq j, i, j = 1, \dots, L$), which can

be rewritten as: $p_i(t+1) = \sum_{j=1}^L \beta_i F_{ij} p_j(t) + (1 - \delta_i) p_i(t)$.

The form adopt $1 - \prod_{j=1}^L (1 - F_{ij} p_j(t))$ to well represent $\sum_{j=1}^L F_{ij} p_j(t)$. Therefore, the next generation matrix is described as following equation:

$$\mathbf{G} = \text{diag}(\mathbf{1} - \delta) + \text{diag}(\mathbf{1} + \beta) \quad (4)$$

The virus evolution depends mainly on the recovery rate δ and the immunity β which both can be optimized appropriately.

C. Spectral Radius Minimization Problem

The spectral radius of the next generation matrix, which can be denoted as $\rho(\mathbf{G})$, is a key indicator for characterizing the spreading rate of a virus. the next generation matrix related to a control variable \mathbf{s} is considered and summarized in Table 1, where \mathbf{s} can be ξ , ϕ or ω in Equation (2), and δ or β in Equation (4).

In addition, let us assume that \mathbf{s} is constrained by an upper boundary \mathbf{u} and a lower boundary \mathbf{b} , and $\sum_{i=1}^L s_i$ can not be less than Γ . In order to illustrate the feasibility, these constraints on \mathbf{s} should implicitly satisfy $\Gamma \leq \sum_{i=1}^L u_i$. Thus, minimizing speed of the epidemic evolution can be formulated as following equation:

$$\begin{aligned} \min \quad & \rho(\mathbf{G}(\mathbf{s})) \\ \text{s.t.} \quad & \sum_{i=1}^L s_i \geq \Gamma \\ & \mathbf{b} \leq \mathbf{s} \leq \mathbf{u} \\ \text{var:} \quad & \mathbf{s} \end{aligned} \quad (5)$$

where (5) is non-convex in general (because of the spectral radius objective function), therefore, the problem can hardly be solved.

Lemma 1. Suppose $\mathbf{G}(\mathbf{s})$ is irreducible, so the constraint $\mathbf{1}^T \mathbf{s} \geq \Gamma$ in (5) obtains equality at optimum point, namely, $\mathbf{1}^T \mathbf{s}^* = \Gamma$.

Proof: According to Perron-Frobenius theorem, $\mathbf{G}(\mathbf{s})$ has real spectral radius, and the Perron right and left eigenvectors related with the spectral radius are real and strictly positive. Assume corresponding right and left eigenvectors are \mathbf{x} and \mathbf{y} , respectively, and $\mathbf{x} > \mathbf{0}$, $\mathbf{y} > \mathbf{0}$. According to the eigenvector sensitivity theory, we can get

$\partial \rho(\mathbf{G}(\mathbf{s}))/\partial s_i = \mathbf{y}^T (\partial \rho(\mathbf{G}(\mathbf{s}))/\partial s_i)^T \mathbf{x}$. $\mathbf{G}(\mathbf{s})$ is non-falling by checking the first order derivative of the special cases of $\mathbf{G}(\mathbf{s})$ in Table 1. These derivatives are respectively given as follows:

For $\mathbf{G}(\mathbf{s}) = \text{diag}(\mathbf{s})\mathbf{B}$, we can get

$$\partial \rho(\mathbf{G}(\mathbf{s}))/\partial s_i = \rho(\mathbf{G}(\mathbf{s})) x_i y_i \geq 0$$

For $\mathbf{G}(\mathbf{s}) = \text{diag}(\mathbf{d}) + \text{diag}(\mathbf{s})\mathbf{B}$, we can get

$$\partial \rho(\mathbf{G}(\mathbf{s}))/\partial s_i = x_i \sum_{j=1}^L B_{ji} y_j$$

For $\mathbf{G}(\mathbf{s}) = \text{diag}(\mathbf{s}) + \mathbf{B}$, we can get

$$\partial \rho(\mathbf{G}(\mathbf{s}))/\partial s_i \geq 0$$

Therefore, $\rho(\mathbf{G}(\mathbf{s}))$ is non-falling. Because a feasible \mathbf{s} is selected as small as possible for minimizing $\rho(\mathbf{G}(\mathbf{s}))$, so $\mathbf{1}^T \mathbf{s} \geq \Gamma$ obtains equality at optimum point.

Next, Equation (5) is firstly solved according to successive convex approximation in Section 3. Then, a branch-and-bound method is proposed to calculate the global optimal solution for Equation (5) in Section 4.

III. CONTINUOUS CONVEX APPROXIMATION OPTIMIZATION FOR VIRUS EVOLUTION

A continuous convex approximation technique based on geometric programming (similarly to the compression method in symbolic programming) is proposed to approximate Equation (5).

Algorithm1 (continuous convex approximation)

Select a feasible initial point $\mathbf{s}(0)$

Define $\alpha_l(k) = \frac{s_l(k)}{\sum_{j=1}^L s_j(k)}, l=1, \dots, L$ Use geometric

programming to solve the k th approximation problem:

$$\begin{aligned} \min \quad & \lambda \\ \text{s.t.} \quad & \mathbf{G}(\mathbf{s}) \mathbf{v} \leq \lambda \mathbf{v} \\ & \prod_{l=1}^L \left(\frac{s_l}{\alpha_l(k)} \right)^{\alpha_l(k)} = \Gamma \\ & \mathbf{b} \leq \mathbf{s} \leq \mathbf{u} \\ \text{var:} \quad & \mathbf{s}, \mathbf{v}, \lambda \end{aligned} \quad (6)$$

where the optimal solution is denoted as $\mathbf{s}(k+1)$

Theorem 1: Starting from any feasible initial point $\mathbf{s}(0)$, $\mathbf{s}(k)$ converges to the local optimal solution in Equation (5).

Introducing the auxiliary variables λ and \mathbf{v} , Equation (5) can be rewritten as following equation:

$$\begin{aligned} \min \quad & \lambda \\ \text{s.t.} \quad & \mathbf{G}(\mathbf{s}) \mathbf{v} \leq \lambda \mathbf{v} \\ & \sum_{l=1}^L s_l = \Gamma \\ & \mathbf{b} \leq \mathbf{s} \leq \mathbf{u} \\ \text{var:} \quad & \mathbf{s}, \mathbf{v}, \lambda \end{aligned} \quad (7)$$

However, due to the polynomial equation $\sum_{l=1}^L s_l = \Gamma$ in constraint set, the Equation (7) still cannot be converted into a geometric programming problem. Assume $g(\mathbf{s}) = \sum_{l=1}^L s_l$, a monomial $\tilde{g}(\mathbf{s})$ will make the following equality hold.

$$g(\mathbf{s}) \geq \tilde{g}(\mathbf{s}) = \prod_{l=1}^L \left(\frac{s_l}{\alpha_l} \right)^{\alpha_l} \quad (8)$$

Let $\alpha_l(k) = s_l(k-1)/\sum_{i=1}^L s_i(k-1)$, then $\tilde{g}(\mathbf{s})$ is the best local monomial approximation to $g(\mathbf{s})$ near \mathbf{s} in the sense of first order Taylor approximation. Thus, the continuous convex approximation technique in Equation (6) can be used.

This approximation satisfies the following properties:

For any fixed positive $\mathbf{s}(k)$, $g(\mathbf{s}(k)) = \tilde{g}(\mathbf{s}(k))$

makes any solution in the approximation problem (6) is a feasible point of the original problem (7).

$g(\mathbf{s}(k)) = \tilde{g}(\mathbf{s}(k))$ ensures the solution of each approximation problem makes the object function decrease.

$\nabla g(\mathbf{s}(k)) = \nabla \tilde{g}(\mathbf{s}(k))$ ensures the original problem after the sequences converge satisfies the Karush-Kuhn-Tucker conditions.

Therefore, a series of convex approximation is given Equation (6), and their solution can converge to a stationary point in Equation (5).

Remark: The optimization problem in Step 2 of Algorithm 1 is a geometric programming, which can be solved by an interior point method. The convergence of Algorithm 1 depends on the initial point $\mathbf{s}(0)$. The output of Algorithm 1 is an upper boundary of Equation (5), which provides a convenient for the branch-and-bound method proposed in the next section.

Although the suboptimal solution computed in Algorithm 1 by a continuous convex approximation technique only provides an upper boundary for Equation(5), the global optimal solution can be obtained by a branch-and-bound method that uses Algorithm 1 as a sub-module. An initial vector $\{\mathbf{s} | \mathbf{b} \leq \mathbf{s} \leq \mathbf{u}\}$ is considered, and it can be subdivided iteratively according to the lower boundary of Equation (5). Next, the lower boundary of the situation listed in Table 1 is discussed.

WBCOT needs to solve the following two key issues: 1) when the wireless-based backup connectivity is established; 2) how the wireless-based backup connectivity is established. Therefore, aiming at the above issue, two key technologies (quantization technique and backup connectivity) are adopted and the key indicator of evaluating network survivability and resilience is proposed. To optimize the network connectivity, a wireless-based connectivity optimization technique is presented. The basic principle of this

technique is: use the flexibility of wireless link establishment, construct the backup scheme through the real-time detection and measurement, and try best to guarantee the network connectivity.

For $\mathbf{G}(\mathbf{s}) = \text{diag}(\mathbf{s})\mathbf{B}$, using Friedland-Karlin inequality, we can get

$$\rho(\text{diag}(\mathbf{s})\mathbf{B}) \geq \rho(\mathbf{B}) \prod_{l=1}^L s_l^{x_l(\mathbf{B})y_l(\mathbf{B})}$$

where $\mathbf{x}(\mathbf{B})$ and $\mathbf{y}(\mathbf{B})$ are the Perron right and left eigenvectors of \mathbf{B} , and get $\sum_{l=1}^L x_l(\mathbf{B})y_l(\mathbf{B})$ by normalizing these eigenvectors. Therefore, the optimal value of Equation (5) is the optimal value of the following equality:

$$\begin{aligned} \min \quad & \sum_{l=1}^L x_l(\mathbf{B})y_l(\mathbf{B}) \log s_l \\ \text{s.t.} \quad & \sum_{l=1}^L s_l = \Gamma \\ & \mathbf{b} \leq \mathbf{s} \leq \mathbf{u} \\ \text{var: } & \mathbf{s} \end{aligned} \quad (9)$$

Although the Equation (9) still is a non-convex problem, the objective function used by its convex envelope on the vector constraint set $\{\mathbf{s} | \mathbf{b} \leq \mathbf{s} \leq \mathbf{u}\}$ can obtain the linear programming problem which is similar with Equation (12).

For $\mathbf{G}(\mathbf{s}) = \text{diag}(\mathbf{d}) + \text{diag}(\mathbf{s})\mathbf{B}$, we can get

$$\begin{aligned} \rho(\mathbf{G}(\mathbf{s})) &\geq \rho\left(\left(\min_{l=1,\dots,L} d_l\right)\mathbf{I} + \text{diag}(\mathbf{s})\mathbf{B}\right) \\ &= \rho(\text{diag}(\mathbf{s})\mathbf{B}) + \left(\min_{l=1,\dots,L} d_l\right) \end{aligned}$$

Therefore, the optimal value of the Equation (5) is bounded by the optimal value of the following Equation:

$$\begin{aligned} \min \quad & \rho(\text{diag}(\mathbf{s})\mathbf{B}) + \left(\min_{l=1,\dots,L} d_l\right) \\ \text{s.t.} \quad & \sum_{l=1}^L s_l = \Gamma \\ & \mathbf{b} \leq \mathbf{s} \leq \mathbf{u} \\ \text{var: } & \mathbf{s} \end{aligned} \quad (10)$$

Thus, similar with $\mathbf{G}(\mathbf{s}) = \text{diag}(\mathbf{s})\mathbf{B}$, the convex envelope of the Equation (10) is also obtained by the linear programming in the Equation (12).

For $\mathbf{G}(\mathbf{s}) = \text{diag}(\mathbf{s}) + \mathbf{B}$, a inequality in nonnegative matrix theory firstly viewed.

$$\frac{\rho(\mathbf{D})}{\rho(\mathbf{A})} \geq \prod_{l=1}^L \prod_{j=1}^L \left(\frac{D_{lj}}{A_{lj}} \right)^{\frac{A_{lj}x_l(\mathbf{A})y_l(\mathbf{A})}{\rho(\mathbf{A})}}$$

where \mathbf{A} and \mathbf{D} are irreducible nonnegative matrices. Let us assume $\mathbf{A} = \mathbf{B}$, $\mathbf{D} = \text{diag}(\mathbf{s}) + \mathbf{B}$, we can get

$$\rho(\mathbf{G}(\mathbf{s})) \geq \rho(\mathbf{B}) \prod_{l=1}^L \left(\frac{s_l + B_{ll}}{B_{ll}} \right)^{\frac{B_{ll}x_l(\mathbf{B})y_l(\mathbf{B})}{\rho(\mathbf{B})}}$$

Similarly, the optimal value of the Equation (5) is bounded by the optimal value of the following optimization problem:

$$\begin{aligned} \min \quad & \sum_{l=1}^L B_{ll}x_l(\mathbf{B})y_l(\mathbf{B}) \log(s_l + B_{ll}) \\ \text{s.t.} \quad & \sum_{l=1}^L s_l = \Gamma \\ & \mathbf{b} \leq \mathbf{s} \leq \mathbf{u} \\ \text{var: } & \mathbf{s} \end{aligned}$$

Similar with $G(s) = \text{diag}(s)\mathbf{B}$, the objective function in Equation (11) used by its convex envelope on the vector constraint set $\{\mathbf{s} | \mathbf{b} \leq \mathbf{s} \leq \mathbf{u}\}$ can displace the linear programming problem which is similar with Equation (13).

Borrowing the above inequalities idea in the spectral radius and using the branch-and-bound method, the following algorithm is proposed to solve optimization problem (5) in Equation (5).

Algorithm2 (global optimization algorithm)

Initialization

Set $k = 0$, $\mathcal{Q} = \{\Omega_0\}$, where, Ω_0 is initial rectangular set $[\mathbf{b}, \mathbf{u}]$.

The lower boundary $L_0 = V_l(\Omega_0)$ of Equation (5) is obtain by solving the following linear programming.

$G(\mathbf{s}) = \text{diag}(\mathbf{s})\mathbf{B}$ or $G(\mathbf{s}) = \text{diag}(\mathbf{d}) + \text{diag}(\mathbf{s})\mathbf{B}$

$$\begin{aligned} \min \quad & \sum_{l=1}^L \frac{\log u_l - \log b_l}{u_l - b_l} x_l(\mathbf{B})y_l(\mathbf{B})s_l \\ \text{s.t.} \quad & \sum_{l=1}^L s_l = \Gamma \\ & \mathbf{b} \leq \mathbf{s} \leq \mathbf{u} \\ \text{var: } & \mathbf{s} \end{aligned} \quad (12)$$

$\mathbf{G}(\mathbf{s}) = \text{diag}(\mathbf{s}) + \mathbf{B}$

$$\begin{aligned} \min \quad & \sum_{l=1}^L \frac{\log \frac{u_l + B_{ll}}{b_l + B_{ll}}}{u_l - b_l} B_{ll}x_l(\mathbf{B})y_l(\mathbf{B})s_l \\ \text{s.t.} \quad & \sum_{l=1}^L s_l = \Gamma \\ & \mathbf{b} \leq \mathbf{s} \leq \mathbf{u} \\ \text{var: } & \mathbf{s} \end{aligned} \quad (13)$$

Solving the Equation (5) in Algorithm 1, the upper boundary $U_0 = V_u(\Omega_0)$ can be obtained.

Stop Criterion

If $U_k - L_k < \varepsilon$, then stop;

else go to the next step

2) Branch

Select a rectangular set $\bar{\Omega} = \mathcal{Q}_k$ that satisfies $V_l(\bar{\Omega}) = L_k$. $\bar{\Omega}$ is

divided into Ω_I and Ω_{II} along the longest edge, and we can get

$$\mathcal{Q}_{k+1} = (\mathcal{Q}_k - \{\bar{\Omega}\}) \cup \{\Omega_I, \Omega_{II}\}$$

Update $L_{k+1} = \min_{\Omega \in \mathcal{Q}_{k+1}} V_l(\Omega)$ and $U_{k+1} = \min_{\Omega \in \mathcal{Q}_{k+1}} V_u(\Omega)$.

Trim

Remove all Ω from \mathcal{Q}_{k+1} , which satisfy $V_l(\Omega) > U_{k+1}$

Set $k = k + 1$, go to step 2

Theorem 2: Starting from any feasible initial rectangular Ω_0 , Algorithm2 converges to the global optimal solution in Equation (5).

Proof: The lower boundary of Equation (5) is obtained by solving the relaxed linear programming problem, and the upper boundary of Equation (5) is got by Algorithm 1 under the situation of the three types of $\mathbf{G}(\mathbf{s})$. Then, based on the upper boundary and lower boundary, Algorithm 2 stop when the found suboptimal point is ε -suboptimal, which complete the proof.

Remark 2: Algorithm 1 runs to Step 2 in an inner loop of Algorithm 2, which provide the upper boundary for Equation (5). L_k includes the child nodes of all the leaves in a binary tree. At the last two steps of Algorithm 2, namely, branch and trim, a global lower boundary on the optimal value of Equation (5) is obtained by minimizing $\rho(\mathbf{G}(\mathbf{s}))$ over all the lower boundary. When b_l is equal to 0 for some l , let $b_l = \varepsilon$ make Algorithm I run smoothly, where ε is positive value as small as possible, and $\varepsilon \rightarrow 0$. Given a ε , the algorithm stop when $U_k - L_k < \varepsilon$.

IV. THE EXPERIMENT AND SIMULATION

In this section, the numerical experiments results are provided to demonstrate the performance of Algorithm 1 in Section 3 and Algorithm 2 in Section 4.

Examples are known in which the fixed point set of Ω_0 , the set of all recurrent points, are not convex sets. For both of the previously cited examples failing to be convex, the action is still the restriction to Ω_0 of an affine map. Here is an example in which the asymptotic action is not affine.

Example 1: $G(\mathbf{s}) = \text{diag}(\mathbf{s})B$ is firstly considered, where B is the symmetric matrix given by:

$$\mathbf{B} = \begin{bmatrix} 0.620 & 0.310 & 0.124 \\ 0.310 & 0.620 & 0.310 \\ 0.124 & 0.310 & 0.620 \end{bmatrix}$$

Let $\Gamma = 2.3$, $[\mathbf{b}, \mathbf{u}] = [\mathbf{0}, \mathbf{1}]$, $\mathbf{0}$ and $\mathbf{1}$ are the vector of all zeroes and the vector of all ones, respectively. The first three iterations in the binary tree of Algorithm 2 are shown in Figure 2.

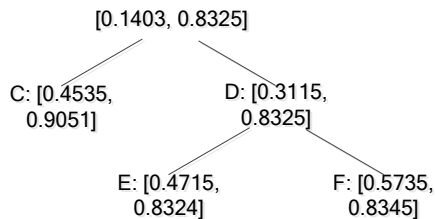
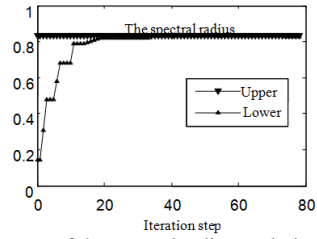


Figure 2. The first three iterations in the binary tree

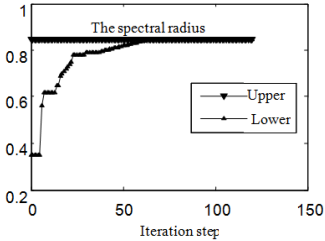
A rectangular set $[\varepsilon, 1]^3$ is used, where $\varepsilon = 0.001$. The upper and lower boundary can be obtained from the

Step 1 of Algorithm 2. In the root node, $L_0 = 0.1403$, $U_0 = 0.8325$. Then, the rectangular set is divided into the two sets C and D (C is $s_1 \in [\varepsilon, (\varepsilon+1)/2]$, D is the set $s_1 \in [(\varepsilon+1)/2, 1]$, $s_2 \in [\varepsilon, 1]$, $s_3 \in [\varepsilon, 1]$). Then, there are $L_1 = 0.3115$ and $U_1 = 0.8325$. The set is divided into the two parts so as to get the bottom children nodes E and F in the third level of binary tree (E is set $s_1 \in [(\varepsilon+1)/2, 1]$, $s_2 \in [\varepsilon, (\varepsilon+1)/2]$, $s_3 \in [\varepsilon, 1]$; F is set $s_1 \in [(\varepsilon+1)/2, 1]$, $s_2 \in [(\varepsilon+1)/2, 1]$, $s_3 \in [\varepsilon, 1]$). Then, get $L_2 = 0.4535$, $U_2 = 0.8324$.

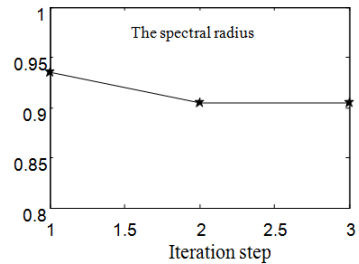
Under such circumstance, the performance of the spectral radius evolution in Algorithm 1 and Algorithm 2 are demonstrated in Figure 3(a) and Figure 3(c), where 3(a) is the performance of Algorithm 1 and 3(c) is the performance of Algorithm 2.



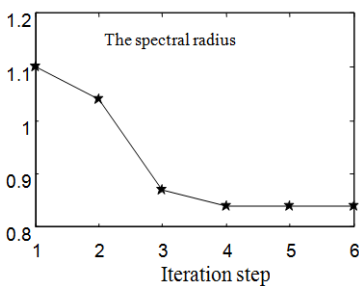
(a) The performance of the spectral radius evolution in Algorithm 1



(b) The performance of the spectral radius evolution in Algorithm 2



(c) Spectral radius evolution in Algorithm 1



(d) Spectral radius evolution in Algorithm 2

Figure 3. The convergence performance

The Figure 3 verify the lower boundary will overlaps with the upper boundary after a set number of iterations so as to prove the convergence. In addition, when

iteration reaches two shown in Figure 3(c), the spectral radius calculated by Algorithm 1 doesn't change. Finally, the optimal spectral radius is $\rho^*=0.8318$, where the corresponding optimal solution is $\mathbf{s}^*=(0.9622, 0.3756, 0.9622)^T$.

Next, $\mathbf{G}(\mathbf{s})=\text{diag}(\mathbf{d})+\mathbf{B}$ is considered, where \mathbf{B} is a nonnegative matrix shown in the following matrix.

$$\mathbf{B} = \begin{bmatrix} 0.000 & 0.124 & 0.124 \\ 0.310 & 0.000 & 0.310 \\ 0.124 & 0.124 & 0.000 \end{bmatrix}$$

Let $\Gamma=1.5$, $[\mathbf{b}, \mathbf{u}]=[\mathbf{0}, \mathbf{1}]$, $\mathbf{0}$ and $\mathbf{1}$ are the vector of all zeroes and the vector of all ones, respectively. Under such circumstance, the performance of the spectral radius evolution in Algorithm 1 and Algorithm 2 are demonstrated in Figure 3(b) and Figure 3(d), where 3(b) is the performance of Algorithm 1 and 3(d) is the performance of Algorithm 2.

The Figure 3 verifies the lower boundary will overlaps with the upper boundary after a set number of iterations so as to prove the convergence. In addition, when iteration reaches four shown in Figure 3(d), the spectral radiuses calculated by Algorithm 1 don't change. Finally, the optimal spectral radius is $\rho^*=0.8441$, where the corresponding optimal solution is $\mathbf{s}^*=(0.525, 0.450, 0.525)^T$.

The remaining statements of the Perron-Frobenius theory can be proven in the standard way. We shall not go into detail here, but rather consider results like those of Section 3 with certain inequalities reversed. An example of such a example is as follows.

Example 2: A test case of Hong Kong SARS include 18 streets in Hong Kong, which can compare three kinds of virus control methods in multi-group model

The model parameters: $f_{ii}=3$, $f_{ij}=0.57$ when street i, j are neighbor. $f_{ij}=0.02$ When street i, j are not neighbor. Under the two circumstances, $\Gamma=3.6667$. In three kinds of virus control methods, comparison results are: 1) isotropy control method allocates the same resource for different streets, which can get $\rho=1.1323$; 2) $\rho=1.0126$ in aeolotropy control method; 3) $\rho=1.0088$ when using Algorithm 2 and $\varepsilon=0.01$. The experiments demonstrate the advantage of using the topology structure of interactive networks by allocating more resources in more important streets. In the experiment, we also have analyzed that the upper boundary obtained by Algorithm 1 reaches a value which is close $\rho=1.0088$ in the first few iterations, and it is obvious that the number of iterations required for convergence is less than 100.

V. CONCLUSIONS

A deterministic virus evolution control framework is proposed in this paper. Based on minimizing a spectral radius function under the constraint of the control

variables, the framework requires to solve a non-convex optimization problem. Firstly, as we all know, the optimal solution of the spectral radius minimization problem is located at the border of the constraint set. Then, feasible suboptimal solution of the spectral radius minimization problem is obtained by using continuous convex approximation based on geometric programming. Key tools in non-negative matrix theory, such as the Perron-Frobenius theorem and Friedland Karlin inequalities, are finally adopted to find boundary of the branch-and-bound method. Therefore, an algorithm that can compute the global optimal solution of the spectral radius minimization problem is proposed. The results of numerical experiment show that our proposed algorithm has faster convergence performance in small and medium-sized networks.

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