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An Optimization Model for Epidemic Mitigation and Some Theoretical and Applied Generalizations

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ABSTRACT

In this paper, we present a binary-linear optimization model to prevent the spread of an infectious disease in a community. The model is based on the remotion of some connections in a contact network in order to separate infected nodes from the others. By using this model we find an exact optimal solution and determine not only the minimum number of deleted links but also their exact positions. The formulation of the model is insensitive to the number of edges in a graph and can be used (with complete or local information) to measure the resistance of a network before and after an infectious spreads. Also, we propose some related models as generalizations: quarantining problem including resource constraints (time, budget, etc.), maximum rescued nodesminimum deleted links problem and minimum removed links problem finding a prespecified number of nodes with weakest connections.

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1 Abstract continued

These quarantining problems can be used in other fields, specially in graph theory. For this reason, three applications have been appended: generalized minimum cut problem, finding an isolation with no single node, and partitioning problem.

2 Introduction

The dynamics of infectious diseases spread (such as influenza, smallpox, HIV, SARS, etc.) and the efficacy of intervention strategies depend deeply on the underlying host contact network. The importance of network structure has been explored in various papers [5,6,7,11,14] where network structures are considered as indispensable tools to model infectious disease that provide insights to prevent the spread of disease between communities. For example, Hartvigsen et al. found that vaccinating hosts preferentially with high clustering coefficients results in twice the number of hosts infected as random vaccinations than their strategy targeting highest degree hosts [10]. Miller and Hyman compared vaccination strategies based on random vaccination (no information) to complete information about a realistic social network and showed that vaccinating those people with the most unvaccinated contacts is more effective than a vaccination strategy based on node degree [8].

As an abstract common idea in such these studies, communities are considered as a contact network and analyzed with emphasis on the understanding of their structures for preventing the spread of disease. However, these strategies are very different from one another in prevention measures, initial limitations or relaxations in problem definition, the construction of an abstraction through a mathematical model and solution techniques to find an optimum.

In some methods such as vaccination approaches, network structure stays unchanged. In contrast, we follow in this paper methods preventing the spread of disease by changing contact patterns [3,4,10,13,15]. These methods solve a problem of link removal and are applicable in situations in which prevention is interpreted as a cut in a network (reducing or cutting contacts with infected elements). For example, the prevention of the spread of infectious diseases such as HIV, tuberculosis or SARS for which there is no vaccine.

Based on some specific applications or requirements, different initial assumptions may be considered for a model. Some methods consider the nodes of a network as clusters of communities, hotels, cities or individuals [8,9,10,12,18,19] or may only act on locally available network information [16]. In this paper, nodes represent individuals and a model is presented to cover situations with both local and global network information. Among the papers that have studied the preventing techniques of the spread of an infection, only a few ones have investigated link isolation or link removal methods [3,4,10,13,15,17]. Some papers in this category studied the network structure problem before the spread of an infection. Omic et al. proposed a link isolation strategy based on the quarantining of susceptible clusters and studied empirically the influence of clustering on robustness against epidemics in real-world and artificial networks [19]. Authors in [12] investigated a quarantining problem to maximize the speed at which the virus is eliminated. For this purpose, they solved some related problems by Lagrange multipliers technique. Marcelino and Kaiser [4] examined the effects of flight cancellation ranked by edge centrality to decrease the spread of disease in an airline network. On the other hand, Enns et al. studied the problem of link elimination after the spread of infection. They converted the problem into a non-convex quadratically constrained quadratic program and then relaxed it to a convex optimization one via a semidefinite relaxation. Using this semidefinite program, they found a lower bound on the objective function of the original problem by a randomization method [5]. Another method in the field of optimization theory was used by Carlyle [11] who developed an integer programming problem to find an optimal quarantining based on the suspected infection status of individuals. This model did not incorporate resource constraints and emphasized on geographically feasible partitions.

In this paper, we study the structure of a contact network and propose a preventing method to control an infectious disease spreading through the network. The general idea of the method is based on the deletion of some links (or edges) such that all of infected nodes are isolated and the cardinality of the set of susceptible nodes connected to infected ones is minimized [14]. For this purpose, we present a new optimization model and utilize it firstly to a network under assumptions considered in [14] where the infection state of nodes is initially known and the number of removable links is bounded from above. The formulation of this problem (referred to the primary problem, in this paper) is formed as a linear programming problem in which some variables are binary. The number of these difficile variables in the formulation is as many as the number of nodes in the network. The number of such these variables is advantageously not dependent on the amount of density in a graph. Actually, this invariance property causes the model to be insensitive to the number of links as problem data. Furthermore, although some difficulties arise computationally from binary variables, the preceding link invariant as well as the linear structure of the model, enables us to apply desirably well-known methods in the field of integer programming such as interior point algorithms or powerful combined approaches such as simplex implementation together with a special cutting plane technique [6]. Besides the computational aspects, the model finds an exact solution and characterizes the position of links that should be eliminated for an optimal quarantining.

A natural generalization is resulted directly from the primary problem in a way that the other resource constraints are also similarly included. Precisely, we associate time as well as a cost coefficient with each link and define two additional upper bounds on the total time and the total budget spent on a link breaking process.

Apart from these formulations, the number of removed links may be considered in many situations as another impressive parameter interfering in the quality of an optimum. Actually, an optimal isolation with the most number of rescued nodes for an infection, may be obtained, on the other hand, by the most number of removed connections as well. However, it may be prefered to decrease this number of disconnected relationships for several reasons such as some limitations on operating time, invested budget, the remotion possibility of some links or the amount of network's connectivity. By considering this new factor, we present a generalized model that can be used to measure the resistance

of networks to the spread of a disease both after and before an infection agent is introduced. In this model, the number of removable links is no longer treated only as a crisp constraint. Instead it also serves as a variable in the objective function of the problem. According to this strategy, the number of removed links is minimized, while the number of rescued nodes is as large as possible. The robustness of a given network before the extent of infection is assessed by an additional constraint on the number of nodes that will be likely infected. In doing so, the model finds the best reaction of a network confronting an infection whose least amount has been already specified.

In fact, this formulation permits us to characterize the infection state of some nodes or that of all nodes (the case in which the robustness is measured after an infection spreads) beforehand.

Finally, none of the preceding generalization increases the number of binary variables; in fact, the structure of the models makes it simply possible in any case to analyze the reaction of a given network to the changing of the infection state of nodes. We list our contribution briefly as follows:

- We investigate a social network with individuals as nodes and human connections as links. If some nodes are infected, then this infection can spread by the connections. So, a natural way is to delete some connections and isolate the infected nodes from the others. At first, we present a mathematical model for this problem (problem (1)).
- (2) Problem (1) is converted into an integer-linear problem (problem (4)).
- (3) We modify problem (4) and obtain a new integer-linear problem (problem (3)) having the least number of binary variables.
- (4) The optimal solution of problem (1) is derived from that of problem (3).
- (5) Some generalizations, applied and theoretical aspects of problem (3) are presented.

In section 3, we formulate the primary problem as a linear programming model including some binary variables. This model solves the problem of link removal to control a spreading disease. In section 4, a developed model has been proposed to optimize both the number of rescued nodes and the number of removed links, simultaneously. This generalization can be used to characterize the robustness of networks after or before the spreading of an infection. Section 5 presents some corollaries of the preceding models, particularly in graph theory. At last, numerical examples have been provided to illustrate the models.

3 Primary Problem

Consider a network G = (N, E) consisting of a set N of n nodes (|N| = n) whose elements (nodes) have been numbered from 1 to n and a set E of m edges (|E| = m). We refer to

an edge joining the node pair i and j as $\{i, j\}$. Also, we represent a cut of the network by the notation $[N_1, N_2]$ in which $N_2 = N - N_1$. Here, neither N_1 nor N_2 is empty, and each edge $\{i, j\} \in [N_1, N_2]$ has one endpoint in N_1 and the other endpoint in N_2 . Let $\bar{N} \subseteq N$ denote the set of infected nodes and k_0 be a preassumed scalar denoting the upper bound of removable edges. According to the assumptions, an optimization problem (henceforth called the primary problem) is to find a cut $[N_1, N_2]$ of network G such that $\bar{N} \subseteq N_1$ and $|N_1|$ is minimum. Equivalently, we would like to separate a network into two parts (including probably several components) in such a way that:

- (i) All infected nodes belong to the same part.
- (ii) The number of other nodes (initially uninfected nodes) not belonging to this part (rescued nodes) is maximized (identically, the number of susceptible nodes staying connected to infected ones is minimized).
- (iii) The number of deleted links does not exceed a given upper bound.

We associate with each node $i \in N$ a variable x_i whose value is equal to one, if node i belongs to the part to which the infected nodes belong and equal to zero, otherwise. Our model is then formulated as follows:

$$\min \sum_{i=1}^{n} x_{i}$$

$$\sum_{\{i,j\}\in E} |x_{i} - x_{j}| \leq k_{0}, \quad i = 1, 2, \cdots, n-1$$

$$x_{i} \in \{0, 1\} \quad \text{for } i = 1, 2, \cdots, n$$

$$x_{i} = 1, \quad i \in \bar{N}$$
(1)

The objective function sets the values of x_i 's equal to zero as many as possible and maximizes consequently the number of rescued nodes. According to the first constraint, only links connecting an infected node to an uninfected one are calculated by the inequality (the summation is taken over indices i < j to consider each edge $\{i, j\} \in E$ once). Also, links indicate in general only connections between nodes. Based on this, the existence of several links between two nodes gives no more information and we can show such these parallel arcs with one link between that nodes. Nevertheless, if parallel arcs are meaningful in an application, we encounter some notational difficulties. Actually, this difficulty is merely notational and can be easily handled by various methods such as: using an appropriate data structure or replacing parallel arcs with one weighted link (see Corollary 3.5). In agreement with the purpose of the primary problem and the definition of upper bound k_0 , other links (those joining two infected or two uninfected nodes) are not considered in the formulation. Binary variables $x_i(i = 1, \dots, n)$ are as many as the number of nodes and an infected node i can be easily characterized in the beginning by defining the value of x_i equal to one. By this treatment, we can analyze a given network

with different positions of its infected nodes simply by changing the values of x_i 's from one to zero or vice versa. According to the preceding statements, we have the following theorem.

Theorem 1. The optimal feasible solution of problem (1) is the feasible optimum to the primary problem.

Proof. Let $N_1 = \{i : x_i = 1\}$ for an optimal feasible solution of problem (1). Obviously, $\overline{N} \subseteq N_1$ and $[N_1, N - N_1]$ is a cut (condition (i)). Since $|x_i - x_j| = 1$ iff $x_i \neq x_j$, then each edge in the cut is calculated by inequality constraint in (1) and vice versa. Thus, this inequality satisfies condition (ii). Condition (ii) is attained from the definition of the objective function.

Obviously, vector $\mathbf{1}^t = [1, 1, \dots, 1]_{1 \times n}$ is always a feasible solution of problem (1) and introduces a trivial isolation (as large as a whole network) in which all of nodes are infected. Therefore, we consider justifiably only isolations (as the feasible quarantinings of the primary problem) in which there exists at least one $i \in N - \overline{N}$ such that $x_i = 0$. The following lemma gives a feasibility criterion to the primary problem in terms of the optimum of problem (1).

Lemma 3.1. The primary problem has no feasible quarantinings iff vector $\mathbf{1}$ is the unique optimum of problem (1).

In order to linearize problem (1), firstly we consider the following substitutions for each $\{i, j\} \in E$ such that i < j:

$$P_{ij} + N_{ij} = Y_{ij}$$

$$P_{ij} - N_{ij} = x_i - x_j$$

$$Y_{ij} \le 1$$

$$P_{ij}, N_{ij}, Y_{ij} \ge 0$$
(2)

By these substitutions, the linear-binary formulation of the primary problem is stated as (see Remark 3.2):

$$\min \sum_{i=1}^{n} x_{i}$$

$$\sum_{\{i,j\}\in E} Y_{ij} \le k_{0}, \quad i = 1, 2, \cdots, n-1 \quad (3)$$

$$\bar{X} \begin{cases} P_{ij} + N_{ij} = Y_{ij}, \{i, j\} \in E \text{ and } i < j \\ P_{ij} - N_{ij} = x_{i} - x_{j}, \{i, j\} \in E \text{ and } i < j \\ Y_{ij} \le 1, \{i, j\} \in E \text{ and } i < j \\ P_{ij}, N_{ij}, Y_{ij} \ge 0, \{i, j\} \in E \text{ and } i < j \\ x_{i} \in \{0, 1\}, \quad i = 1, 2, \cdots, n \end{cases}$$

$$x_i = 1$$
, $i \in N$

For brevity, we show the set of vectors (x, Y, P, N) satisfying the constraints above except the first and the last constraints by the notation \bar{X} .

Remark 3.2. Consider problem (3) with additional constraints $P_{ij}, N_{ij} \in \{0, 1\}$ for $\{i, j\} \in E$, *i.e.*

$$\min \sum_{i=1}^{n} x_{i}$$

$$\sum_{\{i,j\}\in E} Y_{ij} \le k_{0}, \quad i = 1, 2, \cdots, n-1 \quad (4)$$

$$(x, Y, P, N) \in \bar{X}$$

$$x_{i} = 1, i \in \bar{N}$$

$$P_{ij}, N_{ij} \in \{0, 1\}, \{i, j\} \in E$$

where $x^t = (x_i)_{1 \times n}$, $Y^t = (Y_{ij})_{1 \times m}$, $P^t = (P_{ij})_{1 \times m}$ and $N^t = (N_{ij})_{1 \times m}$. The integrality constraints on variables P_{ij} and N_{ij} imply $Y_{ij} = |x_i - x_j|$ for each $\{i, j\} \in E$. Therefore, the feasible regions of two problems (1) and (4) are obviously the same and these problems are consequently equivalent. If the integrality requirement on P_{ij} 's and N_{ij} 's is dropped, problem (3) is attained with the fewer binary variables. Nevertheless, Theorem 2 below shows that an optimal solution of problem (3) is (or can be converted into) an optimum of problem (4) and hence that of problem (1).

Theorem 2. Suppose that (x, Y, P, N) is an optimal solution of problem (3), where $x^t = (x_i)_{1 \times n}$, $Y^t = (Y_{ij})_{1 \times m}$, $P^t = (P_{ij})_{1 \times m}$ and $N^t = (N_{ij})_{1 \times m}$. If (x^*, Y^*, P^*, N^*) is defined as follows:

 $x_{ij}^* = x_{ij}$

$$P_{ij}^* = \begin{cases} P_{ij} & P_{ij} \neq N_{ij} \\ 0 & P_{ij} = N_{ij} \end{cases}$$
$$N_{ij}^* = \begin{cases} N_{ij} & P_{ij} \neq N_{ij} \\ 0 & P_{ij} = N_{ij} \end{cases}$$
$$Y_{ij}^* = P_{ij}^* + N_{ij}^*$$

for each $\{i, j\} \in E$ with i < j, then

- (a) $Y_{ij}^* = |x_i^* x_j^*|$, for each $\{i, j\} \in E$ with i < j.
- (b) (x^*, Y^*, P^*, N^*) is an optimal solution of problem (1).

Proof. (a) Let $x_i = 0$ and $x_j = 1$. Then, $P_{ij} - N_{ij} = -1$. Since $P_{ij} + N_{ij} = Y_{ij} \leq 1$, $P_{ij} \geq 0$ and $N_{ij} \geq 0$, we have $P_{ij} = 0$ and $N_{ij} = 1$. Hence, $P_{ij}^* = 0$ and $N_{ij}^* = 1$ that implies $Y_{ij}^* = P_{ij}^* + N_{ij}^* = |x_i^* - x_j^*| = 1$ (the proof is similar when $x_i = 1$ and $x_j = 0$). Otherwise, let $x_i = x_j = 0$. Then, $P_{ij} - N_{ij} = 0$. In this case, since $P_{ij} + N_{ij} = Y_{ij} \leq 1$, we have $P_{ij} = N_{ij} \leq 0.5$. However, $P_{ij}^* = N_{ij}^* = 0$ that means $Y_{ij}^* = |x_i^* - x_j^*| = 0$ (the proof is similar when $x_i = x_j = 1$).

(b) At first, we prove that (x^*, Y^*, P^*, N^*) is an optimal solution for problem (3). If $x_i - x_j = 0$, then $P_{ij} = N_{ij}$ and we have by our definition $P_{ij}^* = N_{ij}^* = 0$. In this case, $0 \le Y_{ij}^* = P_{ij}^* + N_{ij}^* \le P_{ij} + N_{ij} = Y_{ij} \le 1$ and $\sum_{\{i,j\}\in E} Y_{ij}^* \le \sum_{\{i,j\}\in E} Y_{ij} \le k_0$. However, since

 $x_i^* = x_i$, it is easy to see that (x^*, Y^*, P^*, N^*) satisfies all the constraints of problem (3) (otherwise, if $x_i - x_j \neq 0$, then the feasibility of (x^*, Y^*, P^*, N^*) is trivially obtained where $P_{ij}^* = P_{ij}, N_{ij}^* = N_{ij}$, and $x_i^* = x_i$). Moreover, since the objective function possesses only variables x_i and also $x_i^* = x_i$, thus the values of objective function for (x, Y, P, N) and (x^*, Y^*, P^*, N^*) are equal. Therefore, (x^*, Y^*, P^*, N^*) is an optimal solution for problem (3).

On the other hand, we have $P_{ij}^*, N_{ij}^* \in \{0, 1\}$ and $Y_{ij}^* = |x_i^* - x_j^*|$ (part (a)) that mean (x^*, Y^*, P^*, N^*) is a feasible solution for problem (4). Now, since the feasible region of problem (4) is the subset of that of problem (3), thus (x^*, Y^*, P^*, N^*) must be also an optimal solution for problem (4). Now, the result follows from Remark 3.2.

Corollary 3.3. Regarding the proof above, i.e., part (a), we can obtain vector Y^* more simply which is as follows:

$$Y_{ij}^* = \begin{cases} 0 & P_{ij} \in (0, 0.5] & (or N_{ij} \in (0, 0.5]) \\ 1 & P_{ij} \in \{0, 1\} & (or N_{ij} \in \{0, 1\}) \end{cases}$$

Corollary 3.4. By the definition, vector Y^* characterizes the positions of broken links. If $Y_{ij}^* = 1$, then $\{i, j\}$ is deleted by the model.

Corollary 3.5. Let t_{ij} (or/and b_{ij}) be the time (the budget) that should be consumed for breaking link $\{i, j\}$ and t_0 (or/and b_0) be an upper bound on the admissible total time (total budget) spent by a process of link removing. These additional resource restrictions can be formulated as $\sum_{\{i,j\}\in E} t_{ij}|x_i - x_j| \leq t_0$ and $\sum_{\{i,j\}\in E} b_{ij}|x_i - x_j| \leq b_0$ and similarly linearized as stated in problem (2).

4 Maximum Rescued Nodes - Minimum Deleted Links

In this section, we study an isolating model with regard to the number of both rescued nodes and removed links as well. Firstly, we consider a problem in which only (an estimation for) the lower bound of infection damage is at hand. Our formulation is stated

as:

$$\min \qquad k+M\sum_{i=1}^{n} x_{i}$$

$$\sum_{\{i,j\}\in E} Y_{ij} \leq k, i = 1, 2, \cdots, n-1$$

$$\sum_{i=1}^{n} x_{i} \geq k_{1}$$

$$(x, Y, P, N) \in \bar{X}$$

$$(5)$$

where $k_1 \neq 0$ is a scalar, M is an adequately large positive number and \bar{X} is defined as in (3) (if $k_1 = 0$, zero vector $\mathbf{0}^t = [0, \dots, 0]_{1 \times n}$ is obviously the unique optimum). Variable k denotes the number of deleted links and has a role to play in the objective function. In this model, no nodes are initially infected. Instead, the least number of nodes that will be likely infected has been supposed to be equal to k_1 . The objective of this formulation is to assess the best reaction of a network (to find an isolation with many rescued nodes and a few deleted links) in a case in which only the least amount of an infection damage is known (at least, k_1 nodes will be infected).

Remark 4.1. The primary infection state of nodes can be easily added to the model by setting their values initially equal to one or zero. This case can be interpreted as a solution strategy in which some additional local information about nodes is known. Obviously, the number of initial infected nodes, say \bar{k} , must be less than or equal to k_1 . Specially, if $\bar{k} = k_1$ and $k = k_0$, problem (5) is converted into the primary problem in which optimal quarantining and the robustness of networks are investigated after the extent of an infection.

Remark 4.2. If penalty multiplier M = 1, problem (5) may have alternative optima in terms of the numbers of rescued nodes and deleted links. Figure 1 depicts one example.

Initial infected nodes have been shown in black. According to Remark 4.1, we have $\bar{k} = 3$. Let $k_1 = 4$ and objective function $f(x, k) = k + \sum_{i=1}^{n} x_i$ (M = 1). Since each isolation introduces naturally a set of infected nodes and a set of deleted links, let ${}^{P}N = \{i : x_i = 1\}$ and ${}^{P}Y = \{\{i, j\} \in E : Y_{ij} = 1 \text{ and } i < j\}$ for each isolation ${}^{P}x \in \{0, 1\}^n$. So, for each isolation ${}^{P}x$, we have $f({}^{P}x, {}^{P}k) = {}^{P}k + \sum_{i=1}^{n} {}^{P}x_i = |{}^{P}Y| + |{}^{P}N|$. Hence, problem (4) has four optimal solutions ${}^{1}x, {}^{2}x, {}^{3}x$ and ${}^{4}x$ which are as follows:



Figure 1: A network with three initial infected nodes 1, 2, 3

$$\begin{split} {}^{1}x &= [1,1,1,1,0,0]^{t}: {}^{1}N = \{1,2,3,4\}, \\ {}^{1}Y &= \{\{4,5\},\{4,6\}\}, \\ {}^{1}k &= 2, \ f({}^{1}x,{}^{1}k) = 6 \\ {}^{2}x &= [1,1,1,1,0]^{t}: {}^{2}N = \{1,2,3,4,5\}, \\ {}^{2}Y &= \{\{4,6\}\}, \\ {}^{2}k &= 1, \ f({}^{2}x,{}^{2}k) = 6 \\ {}^{3}x &= [1,1,1,1,0,1]^{t}: {}^{3}N = \{1,2,3,4,6\}, \\ {}^{3}Y &= \{\{4,5\}\}, \\ {}^{3}k &= 1, \ f({}^{3}x,{}^{3}k) = 6 \\ {}^{4}x &= [1,1,1,1,1,1]^{t}: {}^{4}N = \{1,2,3,4,5,6\}, \\ {}^{4}Y &= \emptyset, \\ {}^{4}k &= 0, \ f({}^{4}x,{}^{4}k) = 6 \end{split}$$

Anyway, the theorem below shows that if ${\cal M}$ is a dequately large, such these Pareto-optimal

solutions are converted into the unique optimum.

Theorem 3. Suppose that M = m + 1 in problem (5), where m = |E|. Then, the optimal solution of the problem is unique in terms of the numbers of infected nodes and deleted links.

Proof. By contradiction, suppose that ${}^{1}x$ and ${}^{2}x$ are optimal solutions with different numbers of infected nodes and deleted links. So, we have $f({}^{1}x, {}^{1}k) = f({}^{2}x, {}^{2}k)$. Without loss of generality, let $|{}^{1}N| \leq |{}^{2}N|$ (by the notation ${}^{i}N$ in Remark 4.2).

Firstly, assume that the inequality is strict i.e. $|^1N| < |^2N|$. Since ${}^1k, {}^2k \leq m$ we have:

$$f(^{1}x,^{1}k) = {}^{1}k + (m+1)\sum_{i=1}^{n} x_{i} = {}^{1}k + (m+1)|^{1}N|$$

$$< (m+1)|^{2}N|$$

$$\leq {}^{2}k + (m+1)|^{2}N| = f(^{2}x,^{2}k)$$

that contradicts $f({}^{1}x,{}^{1}k) = f({}^{2}x,{}^{2}k)$. Otherwise, $|{}^{1}N| = |{}^{2}N|$, equality $f({}^{1}x,{}^{1}k) = f({}^{2}x,{}^{2}k)$ implies ${}^{1}k = {}^{2}k$. Hence, ${}^{1}x$ and ${}^{2}x$ have the same number of infected nodes $(|{}^{1}N| = |{}^{2}N|)$ and the same number of deleted links $({}^{1}k = {}^{2}k)$. This contradiction completes the proof.

To apply theorem 3 for the case stated in Remark 4.2, we have m = 6, $f({}^{1}x, {}^{1}k) = 30$, $f({}^{2}x, {}^{2}k) = f({}^{3}x, {}^{3}k) = 36$ and $f({}^{4}x, {}^{4}k) = 42$. Therefore, ${}^{1}x$ is introduced as the unique optimum.

5 Some Related Models

In some situations, it is desirable to find an isolation having or preserving additional properties, for example, an isolation with no single nodes or with a number of infected nodes as close as possible to a certain percentage of the number of all nodes. Conversely, the analysis of some properties in a network leads to an isolation problem. For example, the findings of the weakest relationships in a network show that if they are cut, the network is separated exactly into two components. Induced by problems (3) and (5), three models are proposed to solve the stated examples. These models can also be combined with problems (3) and (5) or with either problem as other generalizations of the primary problem.

5.1 Minimum Removed Links Problem

In this problem, there is an attempt to find a feasible quarantining with the least number of deleted links (regardless of the increase in the number of rescued nodes). This set of links introduces the minimum cut in a graph. The problem is written in the following way:

$$\sum_{\{i,j\}\in E} Y_{ij} \leq k, \ i = 1, 2, \cdots, n-1$$

$$1 \leq \sum_{i=1}^{n} x_i \leq n-1 \qquad (6)$$

$$(x, Y, P, N) \in \bar{X}$$

If we set $\sum_{i=1}^{n} x_i = 1$, problem (6) finds a node having the minimum links (minimum degree) in a graph. Such a node can be interpreted as the weakest node in some applications in view of the connectivity in a contact network. For example, in Figure 2 the weakest node is node 7 with 3 edges (i.e. node 7 has the minimum number of edges in the network). Similarly, if we set $\sum_{i=1}^{n} x_i = 2$, problem (6) finds a 2 nodes-component (a component having only two nodes) with the least number of links with the rest of a network. This component can be also treated as the weakest 2 nodes-component in the network. In Figure 2, 2 nodes-component including nodes 13 and 20 is the weakest 2 nodes-component with 5 connections with the rest of the network. Table 1 shows the weakest k nodes-component and the number of it's connections in the network shown in Figure 2 for $k = 1, 2, \dots, 11$.

Remark 5.1. Inequalities $1 \leq \sum_{i=1}^{n} x_i \leq n-1$ remove vectors $\mathbf{1}_{1\times n}^t$ and $\mathbf{0}_{1\times n}^t$ from the feasible region of problem (6). Hence, each feasible solution has at least one infected node $x_i = 1$ and at least one rescued node $x_j = 0$.

Theorem 5.2 below says that each feasible solution of problem (6) separates a given connected network into exactly two components.

Theorem 5.2. Suppose that (x^*, Y^*, P^*, N^*) is the optimal solution of problem (6) with optimal value k^* and G_1, G_2, \dots, G_l are components of network G = (N, E) that are generated by (x^*, Y^*, P^*, N^*) . Then, l = 2.

5.2 An Isolation with no Single Nodes

A node is said to be a single node if it has no connections to other nodes. To guarantee that an isolation has no single nodes, constraints $\sum_{j:\{i,j\}\in E}(1-Y_{ij}) \geq 1$, $i = 1, 2, \dots, n$ and $Y_{ij} = Y_{ji}, \forall \{i, j\} \in E$ are considered. These constraints can be added to problems (3), (5) and (6).

Theorem 5.3. Suppose that (x, Y, P, N) is an isolation satisfying constraints $\sum_{j:\{i,j\}\in E} (1 - Y_{ij}) \ge 1, i = 1, 2, \cdots, n$ and $Y_{ij} = Y_{ji}, \forall \{i, j\} \in E$. Then, this isolation has no single nodes.

5.3 Partitioning Problem

Let P be a certain percentage of n = |N|. We would like to find an isolation (with a minimum number of deleted links) in which the number of infected nodes is as close as possible to P. Specially, if $P = \frac{n}{2}$, the problem is to partition a graph by deleting a minimum number of links into two parts (including probably several components) such that the numbers of their elements are as equal as possible to each other. By combining this problem with problem (6), these two parts are converted into two components with approximately the same number of elements. For this purpose, we consider firstly the similar substitutions to (2): $P_0 + N_0 = Y_0, P_0 - N_0 = \sum_{i=1}^n x_i - P$ and $P_0, N_0, Y_0 \ge 0$. The next theorem proves that for an optimal solution of the problem, we have $Y_0 = |\sum_{i=1}^n x_i - P|$.

The problem is formulated as:

$$\min \qquad k + (m+1)Y_0 \\ \sum_{\{i,j\}\in E} Y_{ij} \le k, i = 1, 2, \cdots, n-1 \\ P_0 + N_0 = Y_0 \\ P_0 - N_0 = \sum_{i=1}^n x_i - P \\ P_0, N_0, Y_0 \ge 0 \\ (x, Y, P, N) \in \bar{X}$$

$$(7)$$

where m = |E|. The penalty multiplier of the objective function is equal to m + 1, by similar argument stated in Theorem 3.

Theorem 5.4. Suppose that $(x, Y, P, N, Y_0, P_0, N_0)$ is an optimum of problem (7) with optimal value $k + (m+1)Y_0$. Then, $Y_0 = |\sum_{i=1}^n x_i - P|$.

Proof. At first, suppose that $P_0 > 0$ and $N_0 = 0$. In this case, $P_0 = \sum_{i=1}^n x_i - P > 0$ and $Y_0 = P_0$ that means $Y_0 = |\sum_{i=1}^n x_i - P|$ (other cases in which $P_0 = 0$ and $N_0 > 0$ or $P_0 = N_0 = 0$ are similarly proved). Otherwise, let $P_0, N_0 > 0$. Then, there exists some $\delta > 0$ such that $P_0^* = P_0 - \delta > 0$ and $N_0^* = N_0 - \delta > 0$. So, we have $P_0^* - N_0^* = \sum_{i=1}^n x_i - P$ and $Y_0^* = P_0^* + N_0^* = P_0 + N_0 - 2\delta < Y_0$. Hence, $(x, Y, P, N, Y_0^*, P_0^*, N_0^*)$ is a feasible solution with objective value $k + (m+1)Y_0^* < k + (m+1)Y_0$ that contradicts the optimality of $(x, Y, P, N, Y_0, P_0, N_0)$.

6 Numerical Examples

6.1 Primary Problem or Problem (3)

Assume the following network in which the number of removable links is equal to $k_0 = 13$. Initially infected nodes have been depicted by star.



Figure 2:

Figure 2. shows the optimal solution of problem (3). Infected nodes are illustrated in black and deleted links by dotted lines.

The number of infected nodes = 8The minimum number of deleted links = 13

If we insist on the health of some nodes, say node 5, we set $x_5 = 0$ in the beginning. Then, the solution is attained as depicted in Figure 3.



Figure 3:

The number of infected nodes = 14The minimum number of deleted links = 11

This solution (attained by enforcing the model to rescue node 5) involves an increase in the number of infected nodes from 8 to 14 as a compromise.

Combining Section 5.2 with problem (3), we can find an isolation with no single nodes as is illustrated in Figure 4.



Figure 4:

The minimum number of deleted links = 12

6.2 Maximum Rescued Nodes - Minimum Deleted Links (Problem (5))

Assume problem (5) with M = m + 1 = 48 and $k_1 = 5$. We set k_1 (minimum amount of an infection) equal to the number of initially infected nodes in Figure 2. The solution of problem (5) depicted in Figure 5. which shows the best reaction of the network (compare with the solution in Figure 2.)



Figure 5:

The number of infected nodes = 5The minimum number of deleted links = 5

k	Nodes	Number of
		connections
1	7	3
2	13,20	5
3	4,10,16	5
4	4,9,10,16	6
5	$4,\!9,\!10,\!15,\!16$	5
6	1,5,6,11,17,18	6
7	1,5,6,11,12,17,18	6
8	1,5,6,11,12,13,17,18	6
9	1,5,6,11,12,13,17,18,19	6
10	$1,5,6,\overline{11,12,13,17,18,19,20}$	5
11	2, 3, 4, 7, 8, 9, 10, 14, 15, 16, 21	5

Table 1:

6.3 Minimum Removed Links Problem (generalized minimum cut)

Table 1 shows the weakest k nodes-component and the number of it's connections in the network shown in Figure 2 for $k = 1, 2, \dots, 11$. This table is the result of problem (6) where we set $\sum_{i=1}^{n} x_i = k, \ k = 1, 2, \dots, 11$.

6.4 Partitioning Problem (Problem (7))

Assume problem (7) with $P = \frac{n}{2} = 10.5$. Therefore, the target is to separate the network by deleting minimum links into two parts whose number of nodes are as equal as possible. The solution is shown in Figure 6. in which deleted links are marked by dotted lines.



Figure 6:

The minimum number of deleted links = 5

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References

- [1] A. Aspremont, S. Boyd, Relaxations and randomized methods for nonconvex QCQPs, EE364b Course Notes, Stanford University (2003). http://www.stanford.edu/class/ee3920/relaxations. pdf.
- [2] M. S. Bazarra, J. J. Jarvis, H. D. Sherali, Linear programming and network flows, Third Edition, Published Online: 15 AUG 2011.
- [3] K. Carlyle, Optimizing quarantine regions through graph theory and simulation, Master's thesis, Kansas State University, 2009.
- [4] E. A. Enns, J. J. Mounzer, M. L. Brandeau, Optimal Link Removal for Epidemic Mitigation: A two-way partitioning approach, Elsevier, Mathematical Bioscience, (2012).
- [5] E. Eubank, H. Guclu, V. Kumar, M. Marathe, A. Srinivasan, Z. Toroczkai, N. Wang, Modelling disease outbreaks in realistic urban social networks, Nature 429 (2004) 180.
- [6] G. Hartvigsen, J. Dresch, A. Macula, C. Leary, Network structure, and vaccination strategy and effort interact to affect the dynamics of influenza epidemics, J. Theor. Biol. 246 (2007) 205.
- [7] T. House, G. Davies, L. Danon, M. J. Keeling, A Motif-Based Approach to Network Epidemics. B Math Biol 71: 1693-1706 (2009).
- [8] L. Hufnagel, D. Brockmann, T. Geisel, Forecast and control of epidemics in a globalized world, PNAS 101 (2004) 15124.
- [9] R. Kao, L. Danon, D. Green, I. Kiss, Demographic structure and pathogen dynamics on the network of livestock movements in Great Britain, Proc. R. Soc. B 273 (2006) 1999.
- [10] J. Marcelino, M. Kaiser, Reducing influenza spreading over the airline network, PLoS Curr. Infl. (2009) RRN 1005.
- [11] J. Miller, J. Hyman Effective vaccination strategies for realistic social networks, Physica A 386 (2007) 780.

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- [12] J. C. Miller, Spread of infectious disease through clustered populations, J Roy Soc Interface 6: 1121-1134.
- [13] J. Omic, J. Hernandez, P. Van Mieghem, Network protection against worms and cascading failures using modularity partitioning, in: 22nd International Teletraffic Conference (ITC), Amsterdam, September 7-9, 2010, pp. 1-8.
- [14] R. Pastor-Satorras, A. Vespignani, Immunization of complex networks, Phys. Pev. E 65 (2002) 1.
- [15] S. Roy, A. Saberi, Network design problems for controlling virus spread, in: 46th IEEE Conference on Decision and Control, New Orleans, December 12-14, 2007, pp. 3925-32.
- [16] M. Salathe, J. Jones, Dynamics and control of diseases in networks with community structure, PLoS Comput. Biol. 6 (2010) e 1000736.
- [17] Y. Wang, D. Chakrabarti, C. Wang, C. Faloutsos, Epidemic Spreading in Real Networks: An Eigenvalue Viewpoint, in Proceeding of 22nd International Symposium on Reliable Distributed Systems, Florence, Italy, October, 2003.
- [18] J. Wylie, L. Shah, A. Jolly, Incorporating geographic settings into a social network analysis of injection drug use and bloodborne pathogen prevalence, Health Place 13 (2007) 617.
- [19] Y. Youm, M. Mackesy-Amiti, C. Williams, L. Ouellet, Identifying hidden sexual bridging communities in Chicago, J. Urban Health 86 (2009) 107.