Social Models and Algorithms for Optimization of Contact Immunity of Oral Polio Vaccine

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Abstract. Oral polio vaccine (OPV) can produce contact immunity and help protect more individuals than the vaccinated from polio. To better capture the utilization of OPV's contact immunity, we model the community as a social network, and formulate the task of maximizing the contact immunity effect as an optimization problem on graphs, which is to find a sequence of vertices to be "vaccinated" to maximize the total number of "infected" vertices. Furthermore, we consider the restriction imported by immune deficient individuals, and study related problems. We present polynomial-time algorithms for these problems on trees, and show the intractability of problems on general graphs.

Keywords: epidemic model, social network, graph theory, parameterized complexity

1 Introduction

Polio, a common name for poliomyelitis, is an acute, viral, and highly infectious disease, transmitted by person-to-person spread mainly through the faecal-oral route or by a common vehicle, such as contaminated water or food, and multiplies in the intestine [2]. Individuals infected by polio can exhibit a range of symptoms if the virus enters the blood circulation [5]. When poliovirus enters the central nervous system, it can infect and destroy motor neurons, leading to muscle weakness and acute flaccid paralysis. Polio mainly affects children under 5 years of age, which is the reason that polio was called infantile paralysis. The paralysis caused by polio is usually in legs and irreversible, which makes many polio survivors disabled for life [9]. In fact, before the use of vaccine, polio was the most common cause of permanent disability.

This paper studies epidemics of polio, which started to appear in the late 19th century and became one of the most dreaded childhood diseases in the 20th century. Like most diseases caused by virus infection, there was hardly any cure for polio. In 1949, Jonas Salk made an effective polio vaccine [7] and the Global Polio Eradication Initiative was launched in 1988, since when polio cases have decreased by over 99%. In this initial victory of the battle against polio, polio vaccine plays a crucial role. There are 2 safe and effective vaccines for polio, the inactivated polio vaccine (IPV) which is injected and the oral polio

vaccine (OPV) which is given by mouth. IPV consists of inactivated poliovirus, while OPV consists of live, attenuated poliovirus. Therefore IPV carries no risk of vaccine-associated polio paralysis, but induces very low levels of immunity in the intestine; OPV also produces a local immune response in the intestine and can limit the replication of the wild poliovirus inside the intestine [1], but the live attenuated virus in OPV can cause paralysis, in extremely rare cases. When a person immunized with IPV is infected with wild poliovirus, the virus can still multiply inside the intestines and be shed in the faeces, risking continued circulation, which does not happen in the case of OPV. There are more advantages of OPV over IPV in terms of expenses and length of immunity [6].

In addition, there is yet another fact that makes OPV even more important in combating polio. For several weeks after vaccination of OPV, the attenuated virus replicates in the intestine, and is excreted in the faeces. Then the virus can be transmitted to others in close contact, making them immuned. This means that immunization with OPV can result in the immunization of people who have not been directly vaccinated, especially in areas where hygiene and sanitation are poor [4]. We call this phenomenon *contact immunity*.

Although human benefit from vaccines made form attenuated virus, for people with congenital or acquired immune deficiency, the attenuated virus in OPV can cause severe complications [3]. Immune deficient people are more common in recent years, as the Acquired Immune Deficiency Syndrome (AIDS) spreads, and application of immunosuppressor increases, in organ transplantations or cure for some autoimmune diseases. Therefore, when vaccinate OPV to a community, it is necessary to avoid vaccinating immune deficient individuals.

In this paper, we study how to take advantage of contact immunity, so that limited OPV can be applied to a community containing immune deficient patients, to give as much protection to the population as possible, while not infecting immune deficient individuals. By modeling the community as a social network, we formulate the task into an optimization problem on graphs, and propose efficient algorithms.

2 Preliminaries

2.1 Definitions and Notations

Graphs. Unless otherwise mentioned, a graph G in this paper is a simple, finite, and undirected graph with vertex set $V(G)$ and edge set $E(G)$. We usually use n to denote $|V(G)|$ and m to denote $|E(G)|$. A graph is *connected* if for any two vertices of the graph there exists a path connecting them. If a graph is disconnected, we refer to each maximal connected induced subgraph as a *connected component* of the graph.

The *r-ball of v* for the center $v \in V$ and the radius $r \in \mathbb{N}$, denoted by $B(v, r)$, is defined as $B(v, r) = \{x \mid d(v, x) \leq r, x \in V\}$, and $B(v, 0) = \{v\}$. When $u \in B(v, r)$, we also say that u is *covered* by $B(v, r)$. When $B(v_1, r_1) \cap B(v_2, r_2) \neq \emptyset$, we say that the 2 balls are *joint*.

Social Network. A *social network* is a social structure made up of a set of social actors, such as individuals, and a set of the dyadic ties between these actors. A social network can be modeled as a *social graph* $G = (V, E)$, where V is a finite set of vertices, and $E \subseteq V \times V$ is the set of edges connecting pairs of vertices. A vertex in G represents an individual in the social network, while an edge connecting u and v represents the relationship between individuals u and v. In this paper, we use the terms social network and social graph interchangably, and corresponding elements of social network and social graph interchangably for convenience and simplicity.

Parameterized Complexity. A *paramerized problem* $\mathcal{Q}$ is a subset of $\Sigma^* \times \mathbb{N}$ for some finite alphabet Σ. The second component is called the *parameter*. The problem $\mathcal{Q}$ is *fixed-parameter tractable* (FPT) if it admits an algorithm deciding whether $(I, k) \in \mathcal{Q}$ in time $f(k) \cdot |I|^{O(1)}$, where $|I|$ is the size of I and f is a computable function depending only on k.

To prove the intractability of a parameterized problem $\mathcal{Q}'$, we usually present an FPT reduction from a known W[t]-hard problem $\mathcal{Q}$ to $\mathcal{Q}'$. An *FPT reduction* from a problem $\mathcal{Q}$ to a problem $\mathcal{Q}'$ is a function that maps (I, k) to (I', k') such that (a) $(I, k) \in \mathcal{Q} \Leftrightarrow (I', k') \in \mathcal{Q}'$, (b) the function is computable in time $g(k) \cdot (|I| + k)^{O(1)}$ for some function g, and (c) $k' \leq h(k)$ for some function h.

2.2 Models

In this section, we introduce the epidemic model of OPV's contact immunity.

We model the social network of a community as a social graph $G = (V, E)$. In the context of contagion spreading, that two individuals are related means that virus can be transmitted directly from one to the other in daily-life contact. We model the relationship as an undirected edge $e = uv$, since the contact between u and v is basically undirected and symmetric.

There are some properties of OPV, or attenuated poliovirus, when it develops contact immunity. When an individual v is vaccinated with OPV, v gets immunity against polio, and gains infectivity at the same time. Because of the attenuated poliovirus spreaded by v, all individuals that are neighbors of v in the social graph get infected with high probability, and therefore get immuned. Note that OPV's are usually vaccinated multiple times to ensure immunity, and the vaccine used on an already vaccinated individual is called a *booster vaccine*. Booster vaccination leads to longer and stronger infectiousness, since the virus inhabits in intestine for longer time and reproduces more. Also, like the cases of most infectious viruses, the farther v is from infectious individuals, in the sense of either space or social network, the less possible he or she gets infected.

To model the spreading of attenuated poliovirus in a better way, we try to retain its properties, then reduce and simplify the real situation. There are 3 states of vertices in G. The *susceptible* are those who are susceptible to polio, whose set is denoted by P; the *infected* are those who get infected by attenuated poliovirus, whose set is denoted by I; and among the infected, the *infectious* are those who are active in spreading the attenuated virus, whose set is denote by

F, so $F \subseteq I$. Infectious individuals will infect their neighbors. When an individual turns infected, he or her will not be susceptible again; when an individual becomes infectious, he or her will stay infectious, in sufficiently long time.

We assume that, before the vaccination, all individuals in the social network are susceptible to polio, i.e., $P = V$, since we can just remove from the social network those individuals who are already immune to polio, because they scarcely involve in the process of attenuated poliovirus spreading. Suppose we vaccinate people one by one, and there's enough time for contact immunity to take effect. Suppose there are k doses of OPV, denote the *sequence of k vaccinations* by $S_k = (s_1, s_2, \ldots, s_k)$, where $s_i \in V$ for $1 \leq i \leq k$. Note that the same individuals can appear in S for multiple times.

When s_1 is vaccinated, s_1 becomes infected and infectious, and the neighbor set of s_1, $N(s_1)$, become infected because of s_1. The induced subgraph of the closed neighbor set of s_1, $N[s_1]$, is a connected component, which we call an *infected component*, denoted by $IC(v)$, where v is any vertex in this component. The corresponding sets are updated once the status of vertices changes. In this case, vertices in $N[s_1]$ are removed from P and contained in I, and s_1 is contained in F. When s_i, $1 < i \leq k$ is vaccinated, 2 different situations may occur. If $s_i \in I$, meaning that this is a booster vaccination. We simplify the effect of booster vaccination, such that it makes all vertices in $IC(s_i) - F$ infectious, and $\cup_{v \in IC(s_i)} N(v) - IC(s_i)$ infected, then $IC(s_i)$ is updated to be $\cup_{v \in IC(s_i)} N[v]$. If $s_i \notin I$, then s_i becomes infectious, $N[s_i]$ become infected, and $IC(s_i)$ is generated to be $N[s_i]$. Infected components grow indepenently and don't interfere each other. When all vacinations finish, all individuals in I get infected by attenuated poliovirus, and therefore immuned to polio in some level, while infectious individuals in F get strengthened immunity because of booster vaccines.

There are some variants of the model. Sometimes some individuals need the immunity to polio more than others. For example, children under 5 years old, or people living nearby water polluted by virus are more susceptible. In these cases, a *demand index (DI)* is introduced, $DI(v)$ quantifies how pressing v needs the immunity. v's demand is met if and only if v is in F after vaccinations, and the $benefit$ of a vaccination is defined as the sum of $DI(v)$'s where v is newly added to F after the vaccination.

In other cases, some individuals must get strengthened immunity, while some individuals should avoid vaccination, like immune deficient individuals. We define the set of individuals who must get strengthened immunity as *target set*, denoted by S, and define the set of individuals who must not get vaccinated or indirectly strengthened as *restriction set*, denoted by R. It should be ensured that $S \subseteq F$ and $R \cap F = \emptyset$ after vaccinations.

As in many papers that study models of propagation in social network, it's a very common method to simplify the complicated social graph, which is usually a general graph, into a tree. In this paper, we study problems both on general graphs and on trees.

With these models, we want to optimize the effect of contact immunity of OPV on the community, with limited doses of OPV, by making a plan of vaccinations. We propose problems as follows.

2.3 Problems

Five parameterized problems are studied in this paper, where the number k of vaccinations is considered as the parameter.

*Problem 1 (*Maximum Contact Immunity (M-CI)*).* For an undirected graph $G = (V, E)$, and $k \in \mathbb{Z}^+$, find a sequence of k vaccinations S_k on G to maximize $|I|$.

*Problem 2 (*Maximum Benefit of Contact Immunity (MB-CI)*).* For a vertex weighted graph $G = (V, E; \omega)$, where $\omega : V \to \mathbb{R}^+ \cup \{0\}$, and $k \in \mathbb{Z}^+$, find a sequence of k vaccinations S_k on G to maximize the sum of benefit of vaccinations.

*Problem 3 (*Specific Targeting Contact Immunity (ST-CI)*).* For an undirected graph $G = (V, E)$, a set of targets $S \subseteq V$, and $k \in \mathbb{Z}^+$, find a sequence of k vaccinations S_k on G, such that $S \subseteq F$.

*Problem 4 (*Maximum Benefit of Restricted Contact Immunity (MB-RCI)*).* For a vertex weighted graph $G = (V, E; \omega)$, where $\omega : V \to \mathbb{R}^+ \cup \{0\}$, a set of restricted vertices $R \subseteq V$, and $k \in \mathbb{Z}^+$, find a sequence of k vaccinations S_k on G to maximize the sum of benefit of vaccinations, and $R \cap F = \emptyset$.

*Problem 5 (*Specific Targeting Restricted Contact Immunity (ST-RCI)*).* For an undirected graph $G = (V, E)$, a set of restricted vertices $R \subseteq V$, a set of targets $S \subseteq V$, and $k \in \mathbb{Z}^+$, find a sequence of k vaccinations S_k on G, such that $S \subseteq F$, and $R \cap F = \emptyset$.

2.4 Overview

Our results for above problems are listed in Table 1.

	M-CI	MB-CI	ST-CI	MB-RCI	ST-RCI
Tree	P	P	P	P	P
General graph	Unknown	Unknown	Unknown	W[2]-hard	W[2]-hard

Table 1. Results of computational complexities

3 Polynomial-Time Algorithms

For a sequence of k vaccinations in a graph G, let C be the set of vaccinees of k vaccinations. The effect of these k vaccinations can be considered as a collection of $|C|$ balls: for each ball $B(v, r)$, the center $v \in C$ and the radius r equals the number of vaccinations on v or $IC(v)$. Moreover, for any collection of balls where every pair of balls has even depth of intersection, we can infer a sequence of vaccinations producing those balls. Thus, we have the following lemma.

Lemma 1. *A collection of balls is equivalent to a sequence of vaccinations.*

To find the optimum solutions of problems with no restriction set, say M-CI, MB-CI and ST-CI, we have the following lemma.

Lemma 2. *There is an optimum solution for* M-CI *(*MB-CI*,* ST-CI*) having the property that no mergence of infected components happens, i.e., all balls in this solution are disjoint.*

Proof. Suppose that in a optimum solution of M-CI (MB-CI, ST-CI), there exist two balls, $B(v_1, r_1)$ and $B(v_2, r_2)$, covering a vertex u, so $u \in B(v_1, r_1) \cap B(v_2, r_2)$. Therefore $d(v_1, u) \leq r_1$ and $d(v_2, u) \leq r_2$. By connecting the shortest path between v_1 and u with the shortest path between u and v_2, we have a path P between v_1 and v_2, whose length is at most $r_1 + r_2$. We can find a vertex w on P satisfying that $d(v_1, w) \leq r_2$ and $d(v_2, w) \leq r_1$. Since $B(v_1, r_1) \cup B(v_2, r_2) \subseteq B(w, r_1 + r_2)$, all vertices covered by $B(v_1, r_1)$ or $B(v_2, r_2)$ can also be covered by a single ball $B(w, r_1 + r_2)$. Therefore we can replace these two joint balls by the new ball, which also yields an optimum solution. By repeating this procedure, we can obtain an optimum solution without any joint balls. □

The above lemma implies that our algorithm for M-CI can be simplified into finding a collection of disjoint balls, the sum of whose radiuses is equal to k, to cover a maximum number of vertices in G. We now present a polynomial-time algorithm for M-CI on trees.

Theorem 1. M-CI *and* MB-CI *can be solved in* $O(k^2n^2)$ *time when input graph is a tree.*

Proof. Given an instance $I = (G, k)$, where G is a tree. We make G into a rooted tree by arbitrarily choosing a vertex r as the root.

For every $v \in V(G)$, we denote by $Tr(v)$ the set of vertices in the subtree rooted by v, and define $C_l(v) = \{x \mid d(v, x) = l, x \in V(G) \cap Tr(v)\}$, for $l \geq 0$. Therefore $B(v, l) \cap Tr(v) = \sum_{i=0}^{l} C_i(v)$.

For any vertex $v \in V(G)$ and any non-negative integers l and t, we define the following notations.

$T_0(v, t) :=$ maximum number of vertices covered by any ball in the subproblem on $Tr(v)$ with the parameter t, in the case that v is not covered by any ball;

$T_1(v,l,t) :=$ maximum number of vertices covered by any ball in the subproblem on $Tr(v)$ with the parameter t, in the case that v is covered, and any vertices outside the subtree whose distance from v is at most l can also be covered by these balls;

$M(v,t) := \max\{T_0(v,t), T_1(v,0,t)\}$;

$N(v,u,l,t) := \max_{k_0+k_1+\cdots+k_p=t}\{T_1(u,l+1,k_0) - |B(u,l-1)\cap Tr(u)| + \sum_{j=1}^{p} M(w_j,k_j)\}$, where $u \in C_1(v)$, $k_0 \geq l+1$, and $\{w_1,\ldots,w_p\} = C_{l+1}(v)\backslash C_l(u)$.

We use dynamic programming to compute $\{T_0(v,t), T_1(v,l,t)\}_{(v,l,t)}$, where $v \in V(G), t = 0,1,\ldots,k, l = 0,1,\ldots,t$:

$$T_0(v,t) = \max_{\substack{k_1+\cdots+k_d=t \\ \{v_1,\ldots,v_d\}=C_1(v)}} \sum_{i=1}^{d} M(v_i,k_i) \tag{1}$$

$$T_1(v,l,t) = |B(v,l)\cap Tr(v)| + \max\left\{ \max_{\substack{k_1+\cdots+k_d=t-l \\ \{v_1,\ldots,v_d\}=C_{l+1}(v)}} \sum_{i=1}^{d} M(v_i,k_i), \max_{\substack{i=1,\ldots,d \\ \{v_1,\ldots,v_d\}=C_1(v)}} N(v,v_i,l,t) \right\} \tag{2}$$

In Equation 1, we distribute all t vaccinations among subtrees rooted by v's children $\{v_1,\ldots,v_d\} = C_1(v)$, since v is not covered. The number $M(v_i,k_i)$ denotes the maximum number of vertices covered in $Tr(v_i)$ after k_i vaccinations satisfying that the vertex v is not covered by any balls whose centers are in $Tr(v_i)$. However, if we enumerate all possible allcations of t vaccinations to d subtrees such that $k_1+\cdots+k_d = t$, there will be $O(t^d)$ combinations, making the running time of the algorithm superpolynomial. To reduce the time of computing $T_0(v,t)$, we need another dynamic programming to compute the sequence

$$P(i,j) = \max_{k_1+\cdots+k_i=j} \sum_{l=1}^{i} M(v_l,k_l), 1 \leq i \leq d, 0 \leq j \leq t,$$

according to the fact that

$$P(i,j) = \max_{a+b=j}\{P(i-1,a) + M(v_i,b)\},$$

supposing $P(0,j) = P(i,0) = 0$. Therefore we get $T_0(v,t) = P(d,t)$, and the time for computing $T_0(v,t)$ is $O(d\cdot t^2)$. Similar methods are used multiple times in this paper when we allocate a sum of vaccinations to subtrees and get the maximum sum of some functions on subtrees.

In Equation 2, it is easy to see that any vertex $u \in Tr(v)$ with $d(u,v) \leq l$ must be covered, whose set is $B(v,l)\cap Tr(v)$. There are two cases when v is covered by a ball centered in $Tr(v)$: (i) vertex v is vaccinated for l times, (ii) there exists a child $v_i \in C_1(v)$ such that there is a ball centered in $Tr(v_i)$ that covers v and all vertices with distances $\leq l$ to v. The number $N(v,v_i,l,t)$ denotes the maximum number of vertices in $Tr(v)\backslash B(v,l)$ that can be covered, with other vaccinations allocated properly to subtrees other than $Tr(v_i)$.

Finally, we use $\max\{T_0(r,k), \max_{l=0}^{k} T_1(r,l,k)\}$ to denote the maximum number of vertices covered, i.e., the maximum number of people infected by the attenuated poliovirus. In order to get the sequence of vaccinations, we attach a sequence to every T_0, T_1, M, N, P to keep track of the current sequence of vaccinations and maintain sequences during the dynamic programming.

The running time of the algorithm can be calculated as follows:

For fixed v, the time for computing $\{T_0(v,t)\}_{(t=0,\ldots,k)}$ is $O(k^2 \cdot |C_1(v)|) = O(k^2 \cdot d(v))$;

For fixed v and l, the computing time of $\{T_1(v,l,t)\}_{(t=0,\ldots,k)}$ is $O(n + (k-l)^2) \cdot |N_{l+1}(v)| + |N_1(v)| \cdot k^2 \cdot |N_{l+1}(v)| = O(n + k^2 \cdot |N_1(v)| \cdot |N_{l+1}(v)|)$;

Thus, for fixed v, the computing time of $\{T_1(v,l,t)\}_{(l=0,\ldots,t,t=0,\ldots,k)}$ is $O(\sum_{l=0}^{k} (n + k^2 \cdot |N_1(v)| \cdot |N_{l+1}(v)|)) = O(kn + k^2 n \cdot |N_(v)1|) = O(k^2 n \cdot d(v))$.

Consequently, the total running time is $O(k^2 n^2)$. □

Note that we can take a simple reduction from ST-CI to MB-CI (or from ST-RCI to MB-RCI) by assigning weight 1 to vertices in target set S and weight 0 to other vertices. Moreover, we can easily reduce MB-CI to MB-RCI (or ST-CI to ST-RCI) by setting the restriction set R to be an empty set. All these reductions take polynomial time and work whenever input graph is a tree or a general graph. We skip the details here. Thus, we have the following lemma.

Lemma 3. ST-CI $\leq_p$ MB-CI, ST-RCI $\leq_p$ MB-RCI, MB-CI $\leq_p$ MB-RCI, *and* ST-CI $\leq_p$ ST-RCI.

By Theorem 1 and Lemma 3, ST-CI on trees is also solvable in polynomial time.

Furthermore, Lemma 2 is not available for problems with restriction set, since we cannot easily replace two joint balls with one single ball when the new single ball may cover vertices in the restriction set. Therefore, the optimum solution of ST-RCI and MB-RCI allows joint balls. Although there are more difficulties introduced, we can also design dynamic programming algorithms to solve ST-RCI and MB-RCI on trees in polynomial time. By applying a dynamic programming for MB-RCI on trees, we have the following theorem.

Theorem 2. MB-RCI *and* ST-RCI *can be solved in* $O(kn^5)$ *time when input graph is a tree.*

Proof. Given an instance $I = (G, k)$, where G is a tree. We arbitrarily choose a vertex r as the root, and the graph G becomes a rooted tree. Denote the distance between v and the nearest restricted vertex in G by $r(v)$, for each vertex $v \in V(G)$. $r(v) = 0$ if v is a restrected vertex. Then the radius of a ball whose center is v should be at most $r(v)$.

For every $v \in V(G), a, b \in \mathbb{Z}, a \geq 0, b \leq a$, consider the subtree rooted by v, we define the function $S(v,a,b)$, which can be computed in linear time:

If $b \geq 0$, $S(v,a,b)$ is defined as the sum of weights of vertices u in subtree, such that $b < d(v,u) \leq a$;

otherwise, $S(v,a,b)$ is defined as (sum of weights of vertices u in subtree, such that $0 \leq d(v,u) \leq a$) + (sum of weights of vertices w outside subtree, such that $d(v,w) \leq \min\{a, |b|-1\}$).

For every $v \in V(G), 0 \leq t \leq k, -n \leq l, h \leq t$, we define $T(v,t,l,h) :=$ the maximum benefit of subproblem on subtree rooted by v with the parameter t, such that:

If $l < 0$, the vertex v is not covered by any ball in the subtree, and the distance between v and the nearest vertex which is covered by some ball in the subtree is exactly $|l|$;

If $l \geq 0$, the vertex v is covered by some ball in the subtree, and the ball spreads outside the subtree by length l;

If $h < 0$, the vertex v is not covered by any ball outside subtree, and the distance between v and the nearest vertex which is covered by some ball outside the subtree is exact $|h|$;

If $h \geq 0$, the vertex v is covered by some ball outside the subtree, and the ball spreads inside subtree by length h.

Now we use dynamic programming to compute $\{T(v,t,l,h)\}_{(v,t,l,h)}$ where $v \in V(G), t \in [0,k], l,h \in [-n,t]$. Assume that the set of children of v is $\{v_1,\ldots,v_d\}$.

1) $l > r(v)$

$$T(v,t,l,h) = 0$$

2) $l \leq 0$

$$T(v,t,l,h) = \max_{k_1+\cdots+k_d=t} \sum_{i=1}^{d} T(v_i,k_i,l+1,h-1)$$

3) $0 < l \leq r(v)$

$$T(v,t,l,h) = \max\{$$
$$S(v,l,h) + \max_{\substack{l_1,\ldots,l_d \leq l,\\ 1\leq j\leq d}} \max_{\substack{k_1,\ldots,k_d\geq 0\\ \Sigma k_j = t-l}} \Sigma_{j=1}^{d} T(v_j,k_j,l_j,\max\{l,h\}-1),$$
$$\max_{\substack{i=1,\ldots,d\\ l_i=l+1}} \max_{\substack{l_1,\ldots,l_d\leq l+1,\\ 1\leq j\leq d}} \max_{\substack{k_1,\ldots,k_d\geq 0, k_i\geq l_i\\ \Sigma k_j = t}} \Sigma_{j=1}^{d} T(v_j,k_j,l_j,\max\{l,h\}-1)$$
$$\}$$

$\max_{l=-n}^{k}\{T(r,k,l,-n)\}$ is the maximum sum of benefit of vaccinations. And the corresponding sequence of vaccinations can be got from dynamic programming similar to the algorithm for M-CI on trees. The running time of this algorithm is $O(kn^5)$.

By Lemma 3, ST-RCI on trees is also solvable in polynomial time. □

4 Intractability

To give a complete picture of complexity of these problems, we show the intractability of ST-RCI and MB-RCI on general graphs. It is still open whether M-CI, MB-CI, and ST-CI are NP-hard when inputs are general graphs.

Theorem 3. ST-RCI *and* MB-RCI *on general graphs are NP-hard and W[2]-hard.*

Proof. We prove it by constructing a polynomial reduction from k-DOMINATING SET to ST-RCI. Given an instance $I = (G, k)$ of DOMINATING SET where $G = (V, E)$ and $V = \{v_1, \ldots, v_n\}$, we construct an instance $I' = (G', S, R, k+1)$ of ST-RCI where $G' = (V', E')$ as following:

$V' := \{r\} \cup \{u\} \cup \{x_1, \ldots, x_n\} \cup \{y_1, \ldots, y_n\} \cup \{r_1, \ldots, r_n\}$;

$E' := \{(r, u)\} \cup \{(u, x_i) \mid 1 \leq i \leq n\} \cup \{(x_i, y_j) \mid (v_i, v_j) \in E\} \cup \{(x_i, y_i) \mid 1 \leq i \leq n\} \cup \{(y_i, r_i) \mid 1 \leq i \leq n\}$;

$S := \{u\} \cup \{y_1, \ldots, y_n\}$;

$R := \{r\} \cup \{r_1, \ldots, r_n\}$.

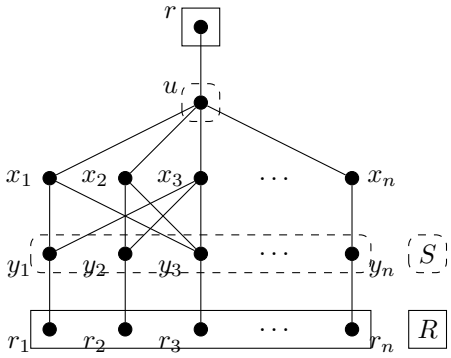

Fig. 1. Construction of ST-RCI instance from k-DOMINATING SET instance.

Due to the restriction set R, there must be only one vaccination on each vertex of $\{u\} \cup \{y_i, \ldots, y_n\}$.

Suppose that G has a k-dominating set $\{v_{i_i}, \ldots, v_{i_k}\}$. It is easy to see that in graph G', the vertices $\{x_{i_1}, \ldots, x_{i_k}\}$ dominate all vertices of $\{y_1, \ldots, y_n\}$. We apply k vaccinations on these vertices $\{x_{i_1}, \ldots, x_{i_k}\}$ one by one. After these vaccinations, the vertices $\{x_{i_1}, \ldots, x_{i_k}\} \cup \{u\} \cup \{y_1, \ldots, y_n\}$ are merged into one infected component. In last step we perform a vaccination on this infected component. The above $k+1$ vaccinations form a solution of I'.

On the other side, suppose that I' has a $(k+1)$-size solution. Since vertex u is in targeting set, we may assume that the l-th vaccination is originated from u, where $1 \leq l \leq k+1$. We also assume that the first $l-1$ vaccinations are originated from vertices $\{x_{i_1}, \ldots, x_{i_p}\} \cup \{y_{j_1}, \ldots, y_{j_q}\}$, where $p + q = l - 1$. Let $\{y_{a_1}, \ldots, y_{a_s}\}$ be a subset of vertices in $\{y_1, \ldots, y_n\}$ that are dominated by $\{x_{i_1}, \ldots, x_{i_p}\}$. Then after the first $l-1$ steps, the vertices $\{x_{i_1}, \ldots, x_{i_p}\} \cup \{u\} \cup \{y_{k_1}, \ldots, y_{k_s}\}$ are merged into one infected component, and the l-th vaccination is performed on this infected component. Let $\{y_{b_1}, \ldots, y_{b_t}\} = \{y_1, \ldots, y_n\} - (\{y_{j_1}, \ldots, y_{j_q}\} \cup \{y_{a_1}, \ldots, y_{a_s}\})$ be the set of remaining specific vertices in G'

after l vaccinations, where $t + q + s = n$. Note that in the next $(k + 1 - l)$ steps we can only perform vaccinations on vertices in $\{y_{b_1}, \ldots, y_{b_t}\}$, since other components become restricted, implying that $t \leq k + 1 - l$. It is clear that vertices in $\{x_{i_1}, \ldots, x_{i_p}\} \cup \{x_{j_1}, \ldots, x_{j_q}\} \cup \{x_{b_1}, \ldots, x_{b_t}\}$ dominate all vertices in $\{y_{a_1}, \ldots, y_{a_s}\} \cup \{y_{j_1}, \ldots, y_{j_q}\} \cup \{y_{b_1}, \ldots, y_{b_t}\} = \{y_1, \ldots, y_n\}$, and the total size is $p + q + t = l - 1 + t \leq k$. Thus, the original graph G has a dominating set of size at most k.

We have completed the proof of NP-hardness. Note that the above reduction is indeed an FPT reduction, and k-Dominating Set is W[2]-hard in the literature. Therefore, ST-RCI on general graphs is W[2]-hard. and thus is very unlikely to be FPT.

By Lemma 3, MB-RCI on general graphs is also NP-hard and W[2]-hard. □

5 Conclusion

In this paper, we have overviewed the history of people fighting polio and introduced oral polio vaccines (OPV). The contact immunity is an important property of OPV that is very important in helping eliminate polio thoroughly. And we have modeled the contact immunity of OPV into models on social graphs, and proposed 5 problems, including Maximum Contact Immunity, Maximum Benefit of Contact Immunity, Specific Targeting Contact Immunity, Maximum Benefit of Restricted Contact Immunity, and Specific Targeting Restricted Contact Immunity. We have studied these problems both on general graphs and on trees.

We have designed polynomial-time algorithms based on dynamic programming for all 5 problems on trees, and have proved the intractability for Maximum Benefit of Restricted Contact Immunity and Specific Targeting Restricted Contact Immunity on general graphs. With these algorithms, we can possibly help improving the effect of OPV in certain circumstances, especially when the supply of vaccines is limited, or the community contains a proportion of immune deficient individuals.

However, we still have some future work to do. For problems Maximum Contact Immunity, Maximum Benefit of Contact Immunity, and Specific Targeting Contact Immunity on general graphs, we haven't found polynomial-time algorithms, neither have we proved their intractabilities.

Furthermore, there may be variant models. For example, we can introduce IPV into the model. As IPV contains no live virus, it is basically safe for even immune deficient people. Moreover, when applying POV to an epidemic area of polio, the normal poliovirus and attenuated poliovirus may compete when transmitting in the social network. Such variant models can also induce problems that have practical significance.

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