Improving time bounds for the contact process on finite graphs using k-dominating sets

Zachary Adams

April 5, 2020

1 Introduction

The contact process is a two compartment model of epidemic growth that separates an afflicted population into susceptible and infected individuals. Infected individuals pass the disease to the neighbours at a constant rate, and each individual is cured at some individual cure rate. This model is useful for studying diseases like the flu and the common cold, where infected individuals often survive the disease, but remain susceptible to infection after being cured. Whereas many compartmental models make the assumption of a homogeneously mixed population when addressing the dynamics of disease, the contact process leverages the tools of graph theory in order to relax this assumption.

The version of the contact process I studied is a continuous time Markov process whose state space is an undirected graph. At any instant in time, the nodes of the graph are either sick or healthy with some collection of vertices is infected when the process begins. Sick vertices infect their neighbours at poisson rate β and are cured independently at poisson rate c_i which is peculiar to each node. Each node may represent an individual, or a community that is susceptible to a disease, and each edge a pair that are frequently in contact. Naturally, it is of interest to understand efficient ways to allocate medicine so that all nodes are cured in a certain amount of time. To put it simply, what is the quickest, cheapest way to kill a disease.

Classically, the contact process is studied on infinite graphs such as $\mathbb{Z}^d$ or infinite trees, where the cure rate is set to 1 for each vertex. By setting the cure rate to 1, we can see the infection rate as $\frac{\beta}{c}$. An interesting first question is whether or not the disease can survive forever on such a graph. This depends on the infection parameter β as well as the structure of the graph. While infinite graphs are of some interest, the contact process is also studied on finite graphs. While the question of the disease dying out on an infinite graph depends on β, on a finite graph, it is guaranteed that the disease will die

off in finite time. Given this result the obvious next questions are: (a) how quickly will the disease die off given some infection parameter and cure rate, and (b) Is it possible to differentiate the distribution of cure to protect some vertices more or less than others. Answers to these questions come from Borgs, Chayes, Ganesh and Saberi [1] who proved that by taking the cure rate to be equal to the degree, then for $\beta < 1$ the disease will die off in $O(\log(n))$ time. Further, they show that this result is essentially optimal for certain types of graphs, in particular, for certain expander graphs.

In this paper we try to improve on prior analysis, using the structure of the graph to better understand how quickly the disease will die out given a distribution of medicine that is proportional to the degree of each vertex. Can we say that a disease will die off more or less quickly given information about the currently infected set of vertices? In fact, we will prove that the disease will decay more quickly if the disease contains a dominating set.

In this paper, I first review the construction of this model and give statements and proofs of previous results. In the third section, I present my results on the decay rate of infected vertices where infected sets contain dominating sets, and also give some results regarding the existence of certain dominating sets in graphs. I conclude with questions for further study.

2 The Model

Let G be an undirected graph of order n. The contact process on G, $CP(T, \beta, \vec{\sigma}, G)$, is a continuous time Markov process with an initially infected set $T \subset V(G)$ parametrized by a constant infection rate $\beta \in [0, 1)$, a vector $\vec{\sigma} = (c_1, c_2, ..., c_n)$ where c_i is the cure rate at vertex v_i. For every vertex v_i, there is an associated $x_i(t) \in \{0, 1\}$ that indicates the infection state of v_i at time t, where $x_i = 1$ if v_i is infected and $x_i = 0$ if v_i is not infected. Thus the entire process can be characterized by the state vector $\vec{x}(t) = (x_1(t), \ldots, x_i(t), \ldots, x_n(t))$. We say that the process has ended, or that the disease has been eradicated, when all vertices are healthy i.e. $\vec{x} = \vec{0}$.

The contact process has two transition events, the spread and the cure events. An infected vertex spreads the disease to its neighbours at rate β, and each vertex v_i is cured at rate c_i. Both events are continuous time Markov processes, that is, the state of the process doesn't depend on history, it is without memory. The waiting time between such events is given by an exponentially distributed random variable X, that is, the random variable X has probability density function $-\lambda e^{-\lambda t}$ for some parameter lambda.

Additionally, the $n \times n$ real symmetric matrix A, is the adjacency matrix of the graph G and is defined $A = [a_{ij}]$ where $a_{ij} = 1$ if $(i, j) \in E(G)$ and 0 otherwise.

Motivated by the phenomena that this model abstracts, the thrust of the research on the contact process is identifying conditions the ensure the end of a disease. That is, what are the conditions on β and $\vec{c}$ such that $\vec{x}(t) = \vec{0}$ for some $t < \infty$. From here, the next step is to consider the most efficient distribution of $\vec{C}$, and the longest time t where $\vec{x}(t) = \vec{0}$.

If the graph on which the contact process occurs is infinite, and if all vertices are cured at the same rate 1, then for values of β below a certain threshold, the disease will die off in finite time. In the case of infinite homogeneous trees (that is trees where every vertex has the same degree), there are certain phase transitions of β for which Pemantle [4] established bounds. His study was primarily concerned with bounding the values of β for which the contact process will live forever, or die out in finite time. He conjectures that there is a single critical value of β such that the contact process dies out for infection parameters less than β and will live forever for values greater than β. While he is unable to prove such a result, he defines four phase transitions, and is able to bound these values based on the number of neighbours of each vertex of the tree. Namely, he is able to bound the smallest infection rate such that the disease can persist forever, λ_1 by,

$$\frac{1}{n} \leq \lambda_1 < \frac{1}{n-1} \tag{1}$$

where $n+1$ is the degree of each vertex.

While a disease may linger forever on an infinite graph, in the case of finite graphs it is certain that the disease will die out in finite time. In particular, if each vertex of a graph is given medicine so that it is cured at rate 1 then with probability 1, the disease will be eradicated in finite time.

Proposition: For a contact process on a finite graph parametrized by infection rate β and a positive cure rate at every vertex, the contact process will die off in finite time with probability 1.

Proof: Suppose that G is a finite graph and let p be the probability that every vertex has a cure event and that no edge has a spread event in time $[0, 1]$. In this case, the disease will be eradicated. Note that $p > 0$ as it is the product of finitely many events which occur with positive probability. Now, consider that the probability that the disease lasts until time t is less than or equal to $(1-p)^t$ and so the probability that the disease lingers forever on the graph is less than or equal to $\lim_{t\to\infty}(1-p)^t = 0$. Thus the disease will be eradicated in finite time. $\square$

Since a disease will eventually die off on a finite graph for any homogeneous distribution of medicine, it is reasonable to consider whether there are more efficient distributions of medicine that still ensure the eradication of a disease in finite time. Borgs, Chayes, Ganesh and Saberi [1] explore this question. They first considered a standard practice in epidemiology known as contact tracing. Contact tracing is

the process of finding the infected individuals and inoculating their neighbours. In the contact process, this is modeled by setting the cure rate for each vertex x that is adjacent to an infected vertex, to $c_x = c + c' d_x^*(t)$ for specific values of c_x , c and with $d_x^*(t)$ equal to the number of infected vertices adjacent to x at time t. They find that for a star graph, and for a finite amount of medicine available for distribution, contact tracing is only effective if the center is not infected and if the number of infected leaves is $o(\frac{c}{\beta})$. If the center is infected and if the number of infected vertices is more than $o(\frac{c}{\beta})$ then contact tracing cannot prevent a disease with a long survival time even if the amount of medicine is growing like $\beta n^{4/3-o(n)}$.

So given that contact tracing is ineffective under many circumstances, Borgs, Chayes, Ganesh, and Saberi [1] find that by distributing medicine proportionally to the degree of each vertex, the disease will die off in $O(\log(n))$ time where n is the order of the graph. The idea behind this result is that it is possible to give more important vertices more medicine, and giving less important vertices less medicine, the distribution is more efficient and still guarantees the end of a disease in some finite time.

Theorem: [1] Consider the contact process on a graph G parametrized by β and by $\vec{c} = (c_1, ..., c_n)$. If the cure rate at each vertex v_i is $c_i > \beta d_i + \delta$ for $\delta > 0$ then with probability $1 - \epsilon$ all vertices are healthy at time t for all $t > \frac{1}{\delta}(\log(n)) + \log(X(0)) + \log(\frac{1}{\epsilon}))$.

Proof (adapted from [2]): First, define a random variable $X(t) = \|\vec{x(t)}\|_1$, the number of infected vertices at time t or the mass of the infection. Next consider $\frac{d}{dt}\mathbb{E}[X(t)]$. The positive contribution to this rate is the βd_i for each infected vertex v_i . Furthermore the negative contribution to the rate the cure rate at each vertex. From these observations, I claim, $\frac{d}{dt}\mathbb{E}[X(t)] \leq \vec{x}(\beta A - Diag(\vec{c}))$, where A is the adjacency matrix and $Diag(\vec{c})$ is the diagonal matrix with diagonal entries from $\vec{c}$.

There are two facts that are key to this proof. First, if X is an exponentially distributed waiting time with rate λ, then

$$\mathbb{P}(X < h) = \int_0^h \lambda e^{-\lambda x} dx = \lambda h + O_{h\to 0}(h^2). \tag{2}$$

Furthermore, If X and Y are independent exponentially distributed waiting times with rates λ_1, λ_2 then

$$\mathbb{P}(X, Y < h) = \int_0^h \int_0^h \lambda^2 e^{-\lambda(x+y)} dy dx = O_{h\to 0}(h^2). \tag{3}$$

Armed with these two facts, I can compute the derivative using the definition which says that

$$\frac{d}{dt}\mathbb{E}[\vec{x}(t)] = \lim_{h\to 0} \frac{\mathbb{E}[\vec{x}(t) - \vec{x}(t+h)]}{h} \tag{4}$$

if it exists. To execute the computation, consider the conditional expectation $\mathbb{E}[\vec{x}(t) - \vec{x}(t+h)|\vec{x}(t)]$. Equation 2 implies that the probability of two independent events (whether two of the same kind of

event, or one spread and one cure event) happening is $O_{h\to 0}(h^2)$. Yet, the probability of a spread event from vertex v_i and v_j in time interval $(t, t+h)$ is $\beta x_i(t)h + O_{h\to 0}(h^2)$ and the probability of a cure event at vertex v_j occurring in time interval $(t, t+h)$ is $x_i(t)c_i h + O_{h\to 0}(h^2)$. Using the linearity of expectation, and the tower property of conditional expectation, we have,

$$\mathbb{E}[\vec{x}(t) - \vec{x}(t+h)|\vec{x}(t)] \leq \vec{x}(t)(\beta A - diag(\vec{c}) + O(h^2) \tag{5}$$

as vertices can't be reinfected. The h cancels, and $O(h^2)$ goes to 0 with h, hence we have

$$\frac{d}{dt}\mathbb{E}[\vec{x}(t)] \leq \mathbb{E}[\vec{x}(t)(\beta A - diag(\vec{c}))]. \tag{6}$$

Thus, By solving this matrix differential equation with initial condition $\mathbb{E}[x(\vec{0}) = \vec{x}(0)$, we have that

$$\mathbb{E}[\vec{x}(t)] = \vec{x}(0)e^{t(\beta A - diag(\vec{c})} \tag{7}$$

Define $Q = \beta A - diag(\vec{C})$. Using the Gershgorin Circle Theorem, We see that the eigenvalues of Q lie in the interval,

$$[-c_i - \beta d_v, -c_i + \beta d_v] \tag{8}$$

Thus every eigenvalue of Q is greater than δ. Thus we have that for λ the largest eigenvalue of Q

$$\begin{aligned}
\mathbb{E}[\|\vec{x}(t)\|_1] &= \|\vec{x}(0)e^{Qt}\|_1 \\
&\leq \sqrt{n}\|\vec{x}(0)e^{Qt}\|_2 \\
&\leq \sqrt{n}\|\vec{x}(0)\|_2\|e^{Qt}\|_2 \\
&\leq \sqrt{n}\|\vec{x}(0)\|_1\|e^{\lambda t} \\
&\leq \sqrt{n}X(0)e^{-\delta t},
\end{aligned}$$

and so by Markov's inequality, we have that $\mathbb{P}(X(t) > 0) < \epsilon$ when $t > \frac{1}{\delta}(\log(n)) + \log(X(0)) + \log(\frac{1}{\epsilon}))$.
□

This result shows that it is possible to distribute medicine differentially and still ensure the end of a disease. At this stage, it is natural to ask whether it is actually necessary to protect each vertex, or if it is possible to protect some and not others. Using PageRank vectors Chung, Horn and Tsiatas [3] showed that it is possible to contain an infection by protecting some collection of vertices that contains the infected set. Briefly, PageRank, is in some sense of way to count the number of paths between vertices, and thereby measure the "connectedness" of certain components in a graph. Fomrally, it is defined on a graph G with a seed vector $\vec{s}$ and some parameter α. PageRank is defined recursively as

$$pr(\alpha, \vec{s}) = \alpha\vec{s} + (1-\alpha)pr(\alpha, \vec{s})W, \tag{9}$$

where W is $D^{-1}A$ or the inverse of the diagonal degree matrix times the adjacency matrix. This recursion relation can be solved explicitly giving,

$$pr(\alpha, \vec{s}) = \alpha \sum_{0}^{\infty} (1-\alpha)^i \vec{s} W^i. \tag{10}$$

Chung, Horn and Tsiatas proved that if the initially infected set S of size s lies within a set H and if every vertex in H is cured at a rate equal to their degree, Then the probability that the infection ever leaves H is bounded above by

$$\frac{s}{\beta} pr(1-\beta, \frac{\mathbf{1}_S}{s}) \mathbf{1}_{\overline{H}}^* = \frac{s}{\beta} \frac{\mathbf{1}_S}{s} \left[(1-\beta) \sum_{k=0}^{\infty} \beta^k W^k \right]. \tag{11}$$

So there is a way to give medicine only to a certain subset that contains the infected set with some degree of certainty that the disease will end before it leaves H .

A generalization of the contact process proposed by Chung, Horn, and Hughes [2], called the Dynamic Demand model, views demand for a product in the same way as the propagation of a disease, and the supply satisfying a demand as a cure. Their model allows demands for multiple commodities to interact on a network. The proof of the last result is a particular case of their proof of the same result in this more general setting.

3 Results

Previous analyses of the contact process on finite graphs are concerned primarily with efficient distributions of medicine that ensure a disease dies off in some finite time. In this paper, we take this as the starting point for our analysis. We consider the question of how quickly a disease will die off given a distribution strategy. In particular, we are able to improve the time bound from Borgs et.al [1] and Chung, Horn, and Hughes [2] by proving that the decay rate of the disease is greater than guarantee of previous results given certain conditions on the infected set are met.

Previous analysis considered the positive contribution to the number of infected vertices at any given time to be given by β times the adjacency matrix of the graph. This assumes that each infected vertex is infecting each of its neighbours at poisson rate β, which induced a decay rate like $e^{-\beta A - D)t}$ which is controlled by the highest eigenvalue which was negative. However, this is not necessarily the case. If two adjacent vertices are both infected, then these vertices are not infecting each other at all. In fact, if the infected set is large, it is likely that many sick vertices are adjacent to many other sick vertices, and so much of their positive contribution is wasted on infecting their already sick neighbours. So it is easy to see that there is significant over counting, especially if the infected set is large and dense. In these cases, the number of infected vertices will decrease more quickly.

At first glance, it seems a bit counter-intuitive to say that a disease will end more quickly if many people are already infected, but upon closer examination, the reasoning is sound. The key insight is that the spread of the disease is restricted when the number of infected vertices is large. When the majority of the graph is infected, the disease has few places to spread. Perhaps more interesting is that the infected set does not necessarily have to be very large in order for this effect to manifest. By more precisely counting the places an infection can spread, we can more accurately bound the decay rate of the number of infected vertices.

To make this notion more precise, we introduce the language of dominating sets.

Definitions

1. A subset H of $V(G)$ is called dominating in G if every vertex in $G - H$ has a neighbour in H .
2.Let k be a positive integer. A subset H of $V(G)$ is k-dominating, if every vertex of $G - H$ has k neighbours in H.
3. Let H be a subset of $V(G)$,define the diagonal matrix $M_H = [m_i]$ with diagonal entries $m_i = 1$ if $v_i \in V(G)/H$ and $m_i = 0$ if $v_i \in H$.
4. for a positive integer k, $\gamma_k(G)$ is the minimum cardinality of a k-dominating set on G

If we assume that the infected set at time t contains a k-dominating set H, then, as every vertex in H is already infected, we can ignore spread events between elements of H, and only consider spread events that occur between elements of H and elements outside of H, and between elements not in H.

Theorem 1: If for every vertex v_i the cure rate $c_i > \beta d_i - \delta$ and if an infected set at time t has a subset that is k-dominating in the graph, then the disease will decay at a rate greater than $\delta + k\beta$.

Proof: Let $H \subset Supp(\vec{x}(t))$ be k-dominating in G and let M_H be defined as above. Let the random variable $X = \|\vec{x}(t)\|_1$ and consider $\frac{d}{dt}\mathbb{E}(X)$. We begin by noting that an infected vertex infects one of its healthy neighbours at rate β, and so contributes to the total positive growth of X at rate β times the number of neighbours it has that are healthy. Thus, the total positive rate of growth of X is given by

$$\beta \sum_{u \sim v} \mathbf{1}_{u \in Supp(\vec{x}(t))} \mathbf{1}_{v \notin Supp(\vec{x}(t))} = \vec{x}(t)\beta AM \tag{12}$$

where M is a diagonal matrix whose ith entry is $x_i(t)$. Since we have $H \subset Supp(\vec{x}(t))$ we can approximate this rate by $\vec{x}(t)\beta AM_H$. Note that the negative contribution to the rate is still $\vec{x}(t)Diag(\vec{c})$. So we can bound the derivative by

$$\frac{d}{dt}\mathbb{E}(\vec{x}(t)) \leq \vec{x(0)}\,(\beta AM_H - diag(\vec{c})) \tag{13}$$

and so solving this matrix differential equation gives us

$$\mathbb{E}(\vec{x}(t)) \leq \|\vec{x}(0)\|_1 e^{(\beta A M_H - diag(\vec{c}))t}. \tag{14}$$

For $S = \beta A M_H - diag(\vec{c})$ we can use some standard inequalities to bound this equation

$$\begin{aligned}
\mathbb{E}[\|\vec{x}(t)\|_1] &= \|\vec{x}(0)e^{St}\|_1 \\
&\leq \sqrt{n}\|\vec{x}(0)e^{St}\|_2 \\
&\leq \sqrt{n}\|\vec{x}(0)\|_2\|e^{St}\|_2 \\
&\leq \sqrt{n}\|\vec{x}(0)\|_1\|e^{\nu t}
\end{aligned}$$

Where ν is the largest eigenvalue of S.

Now consider the Gershgorin discs of S, $D(a_{ii}, R_i)$. Recall that $R_i = \sum_{i \neq j} |a_{ij}m_j|$, and that $a_{ij}m_j = 1$ if $v_i \sim v_j$ and $v_j \notin H$, and $a_{ij}m_j = 0$ if $v_i \not\sim v_j$ or $v_j \in H$. Because H is k-dominating we have that

$$\sum_{i \neq j} |a_{ij}m_j| \leq \sum_{i \neq j} a_{ij} - k = d_i - k \tag{15}$$

and so by the Gershgorin circle theorem, we have

$$\nu \leq -c_i + \beta \sum_{i \neq j} |a_{ij}m_j| \leq -c_i\beta(d_i - k). \tag{16}$$

Since $c_i > \beta d_i + \delta$, $-c_i + \beta d_i < -\delta$, and so $\nu \leq -\delta - \beta k < -\delta$. Therefore, the decay rate of the number of infected vertices is greater than δ. $\square$

So if the infected set contains a k-dominating set, the disease will die off more quickly than the previous results guaranteed. This raises question about the existence of such k-dominating sets in arbitrary graphs. While we do not prove that k-dominating sets, are common in a graph, we are able to show that certain sets have relatively small extensions that are dominating sets, and 2-dominating sets.

Theorem 2: Every finite graph of order n has a dominating set of size $n\frac{\log(\delta)+1}{\delta+1}$ where δ is the minimum degree of the graph.

Proof: Let G be a graph of order n and let $S \subset V(G)$ be randomly selected with probability p. It follows that $\mathbb{E}[|S|] = np$. If $x \in V(G)$ then $\mathbb{P}(x\text{is not dominated by } S) = (1-p)^{deg(x)+1} \leq (1-p)^{\delta+1}$ where δ is the minimum degree of G . Now, let T be the set of all vertices in G such that 1 of their

neighbours is not dominated by S. Now note that

$$\begin{aligned}\mathbb{E}[|S| + |T|] &\leq np + n(1-p)^{\delta} \\ &= n(p + (1-p)^{\delta}) \\ &\leq n(p + e^{-p\delta}).\end{aligned}$$

If we let $p = \frac{\log(\delta)+1}{\delta+1}$ we have

$$\mathbb{E}[|S| + |T|] \leq n(\frac{\log(\delta)+1}{\delta+1} = n\frac{\log(\delta)+1}{\delta+1} \tag{17}$$

Thus, we have a dominating set $S \cup \{v \in v(G) : v \sim x, \text{ for some } x \in T\}$ of order $n\frac{\log(\delta)+1}{\delta+1}$. $\square$

So we can be sure that dominating sets exist in every graph. This result can be extended to k-dominating sets.

Theorem 3 : Every graph G of finite order n has 2-dominating set of order

$$n\left(2\frac{\log(\delta)+1}{\delta}\right) \tag{18}$$

Proof: Let $S \subset V(G)$ be chosen randomly with probability p, then the quantity $\mathbb{E}[|S|] = np$. Further
$\mathbb{P}$(x is not adjacent to any vertex in S) $= (1-p)^{deg(x)} \leq (1-p)^{\delta}$
$\mathbb{P}$(x is adjacent to a unique vertex in S) $= pdeg(x)(1-p)^{deg(x)-1} \leq p\delta(1-p)^{\delta-1}$ Let $T_0 = \{x \in G$:x not dominated by S$\}$ and Let $T_1 = \{x \in G$: x is dominated by S but not 2-dominated by S$\}$. If we construct a set that contains S and also contains 1 neighbour of every vertex in T_1 and 2 neighbours of every vertex T_0, we will have constructed a 2-dominating subset of G. The size of such a set is

$$\mathbb{E}[|S| + |T_1| + 2|T_0|] \leq np + n(1-p)^{\delta} + n(p\delta(1-p)^{\delta} \leq n(p + e^{-\delta p} + p\delta e^{-\delta p}) \tag{19}$$

and if $p = \frac{\log(\delta}{\delta}$, we have

$$\mathbb{E}[|S| + |T_1| + 2|T_0|] \leq n(\frac{2\log(\delta)+1}{\delta}). \tag{20}$$

so the order of this set is bounded above by $n(\frac{2\log(\delta)+1}{\delta})$ $\square$.

Though the case of k-dominating sets is significantly more complicated, there is at least one clear proposition.

Proposition: Suppose that G is a graph and $D \subset V(G)$ is k-dominating. If δ_D is the minimum degree of $G - D$ then $k \leq \delta_D$

Proof: Suppose that $k > \delta_D$ and let $v \in G - D$ be of minimum degree. Then v has k neighbours and

is adjacent to at least $\delta_D > k$ vertices in D. This is a contradiction as v is adjacent to more vertices than its degree. $\square$

While the k dominating case is more complicated, is not intractable. Rauterbach and Volkman give an upper bound for the $\gamma_k(G)$ for an arbitrary G, generalizing the result from Theorem 3. They find that

Theorem: [5] For a graph G or order n and minimum degree δ, if $2k \leq \frac{\delta+1}{\log(\delta=1)}$ then $\gamma_k(G) \leq \frac{n}{\delta+1}\left(k\log(\delta+1) + \sum_{i=0}^{k-1} \frac{1}{i!(\delta+1)^{k-1-i}}\right)$.
The proof of this bound is constructive, and so demonstrates that by adding to a random graph, i neighbours of vertices that are adjacent to $k-i$ vertices in the random grpah, we get a k-dominating set of this size in a similar way to Theorems 2 and 3. Thus we know that there are many sets of vertices with small extensions that are k-dominating.

4 Conclusion

While we have shown that the decay rate the number of infected vertices is greater than previous bounds when the infected set contains some dominating set, there is no way to guarantee that such infected sets are common. However, the existence of certain dominating sets in a graph, and certain sets with small extensions that dominate the graph is guaranteed under certain circumstances. If sets with dominating extensions are common, and are likely to exist inside of large infected sets, this result would significantly improve previous bounds on the time that a disease can persist on a graph.

References

[1] Christian Borgs, Jennifer Chayes, Ayalvadi Ganesh, and Amin Saberi. How to distribute antidote to control epidemics. *Random Structures Algorithms*, 37(2):204–222, 2010.

[2] Fan Chung, Paul Horn, and Jacob Hughes. Multicommodity allocation for dynamic demands using PageRank vectors. *Internet Math.*, 10(1-2), 2014.

[3] Fan Chung, Paul Horn, and Alexander Tsiatas. Distributing antidote using PageRank vectors. *Internet Math.*, 6(2):237–254 (2010), 2009.

[4] Robin Pemantle. The contact process on trees. *Ann. Probab.*, 20(4):2089–2116, 1992.

[5] Dieter Rautenbach and Lutz Volkmann. New bounds on the k-domination number and the k-tuple domination number. *Appl. Math. Lett.*, 20(1):98–102, 2007.