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POWER CONTAMINATION AND DOMINATION ON THE GRID

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Summary. The contamination game of a grid graph $G(n,m)$ is a dynamic variant of the domination, similar to the power domination. This standard is introduced by Haynes, Hedetniemi and Henning in 2002, which is initially defined as a basic domination for a set of vertices S in a graph G, and then a propagation of this domination in all vertices of G, while starting with S. On the other hand, the contamination phenomena in $G(n,m)$ is interpreted by an evolutionary automaton cellular, which aims to propagate viruses according to a given propagation rules. In this paper, we define a mathematical self-playing game called a contamination game based on the power domination, in which, we identify the minimum number of contaminant cells for $G(n,m)$, called the contamination number and denoted $\gamma\left(G(n,m)\right)$.

1 INTRODUCTION

Electric power systems need to be monitored in real-time. One way to achieve this task is to place phase measurement units at selected locations in the system. The power system monitoring problem is a combinatorial optimization problem that consists of minimizing the number of measurement devices to be put in an electric power system. The power system monitoring problem has been formulated as a graph theory domination problem by Haynes, Hedetniemi, Hedetniemi, and Henning in [1]. This problem is of somehow different flavor than standard domination type problems, since putting a phase measurement unit into a vertex of a graph can have global effects. For instance, if an electric power system can be modeled by a path, then a single measurement unit suffices to monitor the system no matter how long is the path.

Let $\boldsymbol{G} = (\boldsymbol{V}, \boldsymbol{E})$ be a connected graph. For a vertex $\boldsymbol{v}$ of $\boldsymbol{G}$, let $\boldsymbol{N}(\boldsymbol{v})$ denote the open neighbor-hood of $\boldsymbol{v}$, and for a subset $\boldsymbol{S} \subset \boldsymbol{V}$ let $\boldsymbol{N}(\boldsymbol{S}) = (\bigcup_{\boldsymbol{v}\in\boldsymbol{S}} \boldsymbol{N}(\boldsymbol{v})) \setminus \boldsymbol{S}$. We denote by $\boldsymbol{M}(\boldsymbol{S})$ the set monitored by $\boldsymbol{S}$, defined algorithmically as follows [2]:

Algorithm 1 Construction of a monitored set $\boldsymbol{M}(\boldsymbol{S})$
Input: Graph $G = (V, E)$ and $S \subset V$. Output: $\boldsymbol{M}(\boldsymbol{S})$ the monitored set by $\boldsymbol{S}$.
1: Initiate $M(S) \leftarrow S \cup N(S)$; 2: While there exists $v \in M(S)$ such that $N(v) \cap \left(V \setminus M(S)\right) = \{w\}$ do 3: $M(S) \leftarrow M(S) \cup \{w\}$; 4: EndWhile; 5: Return $\boldsymbol{M}(\boldsymbol{S})$;

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The set $\boldsymbol{S}$ is called a power dominating set of $\boldsymbol{G}$ if $\boldsymbol{M}(\boldsymbol{S}) = \boldsymbol{V}$ and the power domination number, denoted by $\boldsymbol{\gamma_\pi}(\boldsymbol{G})$, is the minimum cardinality of a power dominating set.

Various papers have addressed the power domination number, in which they essentially concentrate on its algorithmic point of view (see [3], [4], [5], [6], [7] and [8]). This problem is proven to be NP-complete even when restricted to bipartite graphs, chordal graphs, planar graphs, circle graphs and split graphs [9]. In contrast, the problem can be solved in polynomial time for trees and interval graphs [10]. Dorfling and Henning obtained closed formulas for the power domination numbers of grid graphs [11]. This result is in striking contrast with the fact that a determination of such formulas for the usual domination number of grid graphs is an open problem [1]. Now, a natural description of a grid is a cartesian product of two paths. However, there exist other graph products such as the strong, the direct, and the lexicographic product [1]. Hence, it is natural to ask whether the power domination number can also be determined for these products of paths.

In this paper we introduce a new variant of domination characterized as a virus-contamination in grid graph $\boldsymbol{G}(\boldsymbol{n},\boldsymbol{m})$, which is defined in two steps:

(1) Local domination for a few cells of $\boldsymbol{G}(\boldsymbol{n},\boldsymbol{m})$.

(2) Propagation on all cells of $\boldsymbol{G}(\boldsymbol{n},\boldsymbol{m})$ according to a given initial contamination rules.

2 POWER CONTAMINATION ON THE GRID

Let $\boldsymbol{G}(\boldsymbol{n},\boldsymbol{m}) = (\boldsymbol{V},\boldsymbol{E})$ be a grid graph, and $\boldsymbol{S} \subset \boldsymbol{V}$. The set $\boldsymbol{S}$ is said to be a contaminating set if a full contamination of $\boldsymbol{G}(\boldsymbol{n},\boldsymbol{m})$ can be achieved from $\boldsymbol{G}(\boldsymbol{n},\boldsymbol{m})$ and the power contamination number $\boldsymbol{\gamma_c}\big(\boldsymbol{G}(\boldsymbol{n},\boldsymbol{m})\big)$is the minimum cardinality of a power contaminating set. In the following, we will illustrate the problem as a self-playing game, in order to deal with the problem of contamination in $\boldsymbol{G}(\boldsymbol{n},\boldsymbol{m})$.

For a vertex $\boldsymbol{v}$ of $\boldsymbol{G}(\boldsymbol{n},\boldsymbol{m})$, let $\boldsymbol{M}(\boldsymbol{v})$ and $\boldsymbol{VN}(\boldsymbol{v})$ denote, respectively, Moore neighborhood (see Fig.1(a)) and Von Neumann neighborhood (see Fig.1(b)) of $\boldsymbol{v}$, extended to the cells at the edge of $\boldsymbol{G}(\boldsymbol{n},\boldsymbol{m})$.

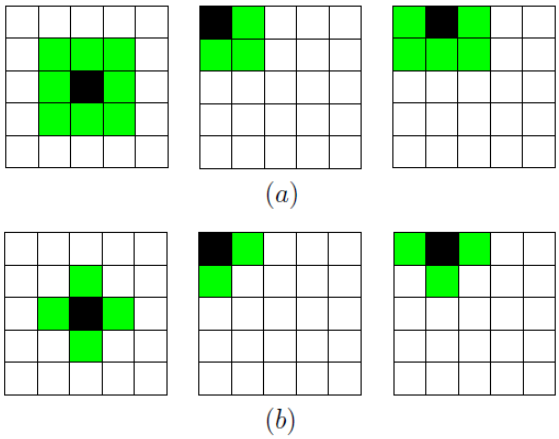

Figure 1: Moore and Von Newmann neighborhoods of the black cell.

2.1 Contamination rules in $G(n, m)$

The contamination game of $G(n, m)$ can be seen as a cellular automaton, or a model where each state leads automatically to the next state from predefined rules. This game takes place on $G(n, m)$, whose cells are considered by analogy as living cells, which can take two different states "sick" or "healthy". At each step, the state of any cell is determined by the state of its eight neighbors, in regards to a given initial contamination rules. The goal of this game is to find the minimum number of initial contaminated cells $\gamma_c(G(n, m))$, such that the entire grid is contaminated. This kind of contamination can be seen as an evolutionary cellular automaton, which models an epidemiological phenomenon, illustrating the propagation of viruses in living cells.

The space of states is a two-dimensional grid of sick or healthy living cells. The chosen transition rule depends on the number and position of the contaminated living neighboring cells that surround a cell, it corresponds to Moore neighborhood.

A cell v is contaminated by two sick cells v_1 and v_2 if one of the following conditions is fulfilled:

(i) $v_1, v_2 \in VN(v)$,

(ii) $v_1, v_2 \notin VN(v)$ and $M(v_1) \cap M(v_2) = \{v\}$.

The possible configurations which satisfy these conditions are given in Fig.2.

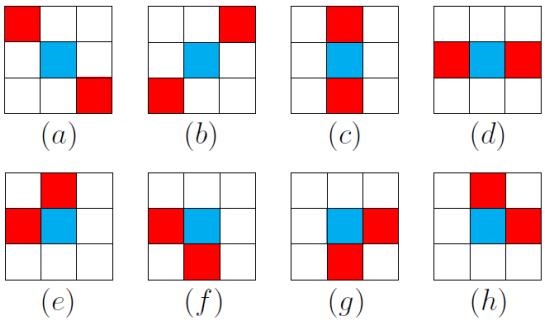

Figure 2: The contamination rules of the blue cell.

The following algorithm illustrates the contamination and spread process which yield the contaminated set S, according to the contamination rules:

Algorithm 2 Construction of a contaminated set $C(S)$

Input: Graph $G = (V, E)$ and $S \subset V$.
Output: $C(S)$ the subset of vertices contaminated by S.

1: Initiate $C(S) \leftarrow S$;
2: While there exists $v \in V \setminus C(S)$ such that (i) and (ii) are satisfied do
3: $C(S) \leftarrow C(S) \cup \{v\}$;
4: EndWhile;
5: Return $C(S)$;

2.2 Mathematical model

Let $x_{ij}^{(k)}$ be the decision variable at the step k,

$$x_{ij}^{(k)} = \begin{cases} 1 & \text{if the cell } (i,j) \text{ is contaminated in step } k; \\ 0 & else. \end{cases}$$

The goal of this game is to find the minimum number of contaminating cells $\gamma_c\big(G(n,m)\big)$ at the step 0, so that the entire grid is contaminated after k_0 steps, according to Algorithm 2.

The objective is the following:

$$Min(Z) = \sum_{i=1}^{n}\sum_{j=1}^{m} x_{ij}^{(0)} \quad \overset{(k_0 \text{ steps})}{\rightsquigarrow} \quad \sum_{i=1}^{n}\sum_{j=1}^{m} x_{ij}^{(k_0)} = nm,$$

according to the contamination rules presented above, which are written as follows:

$$k \longrightarrow k+1 \begin{cases} x_{ij}^{(k)} x_{i+2,j+2}^{(k)} \leq x_{i+1,j+1}^{(k+1)}, \ \forall i = 1, n-2, \forall j = 1, m-1 & \big(Fig.2(a)\big); \\ x_{ij}^{(k)} x_{i+2,j-2}^{(k)} \leq x_{i+1,j-1}^{(k+1)}, \ \forall i = 1, n-2, \forall j = 1, m-1 & \big(Fig.2(b)\big); \\ x_{ij}^{(k)} x_{i+2,j}^{(k)} \leq x_{i+1,j}^{(k+1)}, \ \forall i = 1, n-2, \forall j = 1, m & \big(Fig.2(c)\big); \\ x_{ij}^{(k)} x_{i,j+2}^{(k)} \leq x_{i,j+1}^{(k+1)}, \ \forall i = 1, n, \forall j = 1, m-2 & \big(Fig.2(d)\big); \\ x_{ij}^{(k)} x_{i+1,j-1}^{(k)} \leq x_{i+1,j}^{(k+1)}, \ \forall i = 1, n-1, \forall j = 1, m & \big(Fig.2(e)\big); \\ x_{ij}^{(k)} x_{i+1,j+1}^{(k)} \leq x_{i,j+1}^{(k+1)}, \ \forall i = 1, n-1, \forall j = 1, m-1 & \big(Fig.2(f)\big); \\ x_{ij}^{(k)} x_{i+1,j-1}^{(k)} \leq x_{i,j-1}^{(k+1)}, \ \forall i = 1, n-1, \forall j = 1, m-1 & \big(Fig.2(g)\big); \\ x_{ij}^{(k)} x_{i+1,j+1}^{(k)} \leq x_{i+1,j}^{(k+1)}, \ \forall i = 1, n-1, \forall j = 1, m-1 & \big(Fig.2(h)\big); \\ x_{ij}^{(k)} \in \{0,1\}. \end{cases}$$

3 CONTAMINATION ON STRONG PRODUCT OF TWO PATHS

A natural representation of a grid $\boldsymbol{G(n,m)}$ is as the strong product of two paths $\boldsymbol{P_n \boxtimes P_m}$, such that (see Fig.3):

(1) each cell of $\boldsymbol{G(n,m)}$ is represented by a vertex $\boldsymbol{v}$ in $\boldsymbol{P_n \boxtimes P_m}$,

(2) the neighboring between two cells in $\boldsymbol{G(n,m)}$ is represented by an edge in $\boldsymbol{P_n \boxtimes P_m}$.

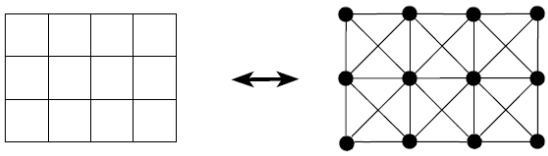

Figure 3: $G(3,4)$ modeled as the strong product of paths.

The number of neighboring of each cell in $G(n,m)$ represents the degree of the corresponding vertex in $P_n \boxtimes P_m$, as shown in Fig.3. This implies that the virus-contamination on $G(n,m)$ is equivalent as on $P_n \boxtimes P_m$.

Fig.4 represents an optimal contamination of $G(3,4)$. The red cells (equivalently the red vertices in $P_3 \boxtimes P_4$) represent the contaminated cells in step 0.

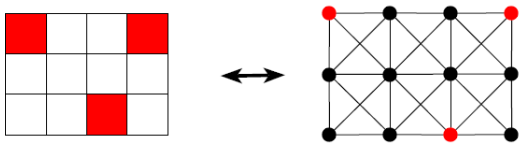

Figure 4: $\gamma_c(G(3,4)) = 3$.

The evolution of the total contamination of the grid $G(3,4)$ is shown in Fig.5.

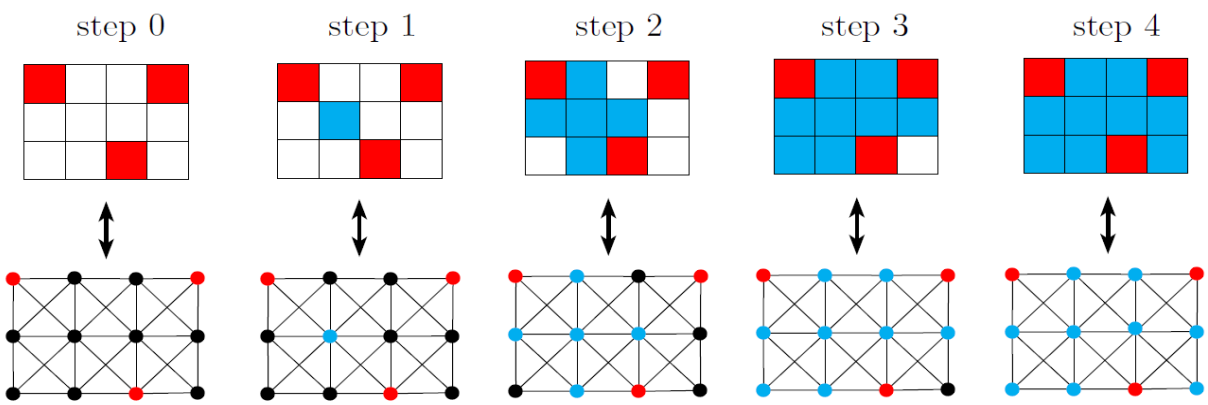

Figure 5: The evolution of the total contamination of $G(3,4)$.

4 MAIN RESULTS

Lemma 4.1. For any positive integer \$m\$, the contamination number of the path $P_m = P_1 \boxtimes P_m$ is:

$$\gamma_c(P_m) = 1 + \left\lfloor \frac{m}{2} \right\rfloor.$$

Proof. Let $v_1, \dots, v_m$, with $d(v_1) = d(v_m) = 1$ and for $i \in \{2, \dots, m-1\}$, $d(v_i) = 2$. In order to have a full contamination of P_m, we should deploy viruses on the extremities of the path, v_1 and v_m, and then we deploy the viruses alternatively on P_m, according to the contamination rule Fig.2(d). Thus, we should deployed $2 + \left\lfloor \frac{m-2}{2} \right\rfloor$ viruses, which implies that $\gamma_c(P_n) = 1 + \left\lfloor \frac{m}{2} \right\rfloor$ (see for instance Fig.6).

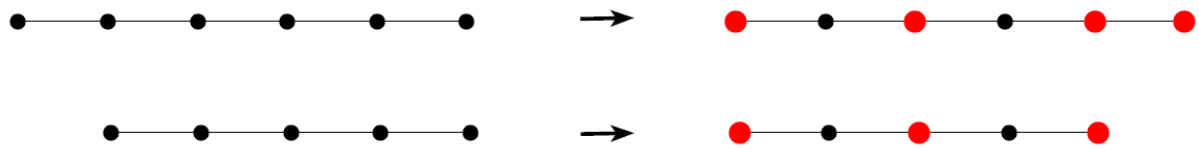

Figure 6: Optimal contamination in P_6 and P_5.

□

Theorem 4.2. Let n, m be two positive integers. Then we have

$$\gamma_c(P_n \boxtimes P_m) \leq \begin{cases} max\left\{\left\lfloor \frac{n}{2} \right\rfloor, \left\lfloor \frac{m}{2} \right\rfloor\right\} + 1 & \text{if } n \text{ and } m \text{ have the same parity,} \\ max\left\{\left\lceil \frac{n}{2} \right\rceil, \left\lceil \frac{m}{2} \right\rceil\right\} + 1 & \text{else.} \end{cases}$$

Proof. Let us first observe that the minimum number of viruses contaminating the grid $G(n, m)$ is the same as $G(m, n)$, simply rotate $G(n, m)$ through $\frac{\pi}{2}$. For this reason, we assume throughout the proof that $m \geq n \geq 1$.

In the following we give a construction of a contaminant set with the given cardinality. We conjecture that the construction is optimal; therefore this upper bound gives the exact value.

If $n = 1$, the contamination is achieved with the given cardinality, using Lemma 1. Suppose that $m \geq n \geq 2$ and set $G = P_n \boxtimes P_m$. In order to have a full contamination, it suffices to decompose G into G_1 and G_2, such that $G_1 = P_n \boxtimes P_n$ and $G_2 = P_n \boxtimes P_{m-n}$. The contamination of G_1 and G_2 induces a full contamination of G. For that, we distinguish fourth cases:

Case 1: n and m are even.

Let P_{n-i}^i be a diagonal of $P_n \boxtimes P_n$ of order i and size $n - i$, such that $i \in \{0, \dots, n-1\}$. The main diagonal P_n^0, which is a path, is fully contaminated using $\frac{n}{2} + 1$ viruses, according to Lemma 1. From the contamination rules defined above, more precisely Fig.2(f) and Fig.2(h), the parallel paths P_{n-i}^1 of size $n - 1$ are fully contaminated. The contamination continues to spread according to the same rules until reaching the last diagonal. Thus we have a full contamination of $G_1 = P_n \boxtimes P_n$.

Now we move to the contamination ofG_2. To contaminate this latter it suffices to alternatively deploy $\frac{m-n}{2}$ viruses on the first path from the top of G, starting by the last vertex according to the contamination rules Fig.2(d) and Fig.2(e). Hence, we get a full contamination of G_2, and then a full contamination of $G = P_n \boxtimes P_m$, using $\frac{m}{2} + 1$ viruses (see Fig.7).

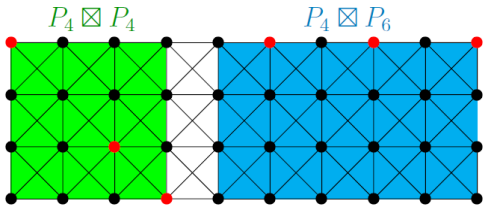

Figure 7: Contamination strategy in $P_4 \boxtimes P_{10}$.

Case 2: n and m are odd.

The contamination of G is done in two steps, as seen in the first case. A full contamination of $P_n \boxtimes P_n$ is attained by deploying alternatively $\left\lceil \frac{n}{2} \right\rceil$+1 viruses on the main diagonal of G_1 using Lemma 1 and the contamination rules Fig2(a), Fig.2 (f) and Fig.2(h). The contamination of G_2 is obtained by deploying alternatively $\frac{m-n}{2}$ viruses on the first path from the top of G, starting by the last vertex according to the contamination rules Fig.2 (d) and Fig.2(e). Hence, we get a full contamination of G_2, and then a full contamination of $G = P_n \boxtimes P_m$, by using $\left\lceil \frac{n}{2} \right\rceil + \frac{m-n}{2} + 1 = \left\lceil \frac{m}{2} \right\rceil + 1$ viruses (see Fig.8).

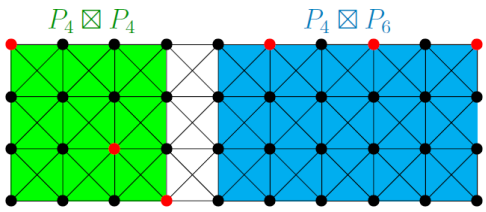

Figure 8: Contamination of $P_3 \boxtimes P_9$.

Case 3: n odd and m even.

As seen in the second case, G_1 is fully contaminated by using $\left\lceil \frac{n}{2} \right\rceil + 1 = \left\lceil \frac{n}{2} \right\rceil$+1 viruses. To contaminate G_2 it suffices to alternatively deploy $\left\lceil \frac{m-n}{2} \right\rceil = \frac{m}{2} - \left\lceil \frac{n}{2} \right\rceil$ viruses on the first path from the top of G, starting with the second vertex of G_2 then add a virus at the last vertex (see Fig.9). Hence, we have a full contamination of G_2, according to the contamination rules Fig.2(d) and Fig.2(e) and then a full contamination of $G = P_n \boxtimes P_m$, using $\left\lceil \frac{n}{2} \right\rceil + \left\lceil \frac{m-n}{2} \right\rceil + 1 = \frac{m}{2} + 1$.

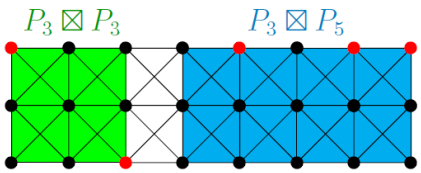

Figure 9: Contamination of $P_3 \boxtimes P_8$.

Case 4: n even and m odd.

The graph G_1 is fully contaminated by using $\frac{n}{2} + 1$, as seen in the first case. To contaminate G_2 it suffice to alternatively deploy $\left\lceil \frac{m-n}{2} \right\rceil = \left\lceil \frac{m}{2} \right\rceil - \frac{n}{2}$ viruses on the first path from the top of G, starting with the second vertex of G_2 then add a virus at the last vertex (see Fig.10). Hence, we have a full contamination of G_2, according to the contamination rules Fig.2 (d) and Fig.2(e) and then a full

contamination of $G = P_n \boxtimes P_m$, using $\frac{n}{2} + \left\lceil \frac{m-n}{2} \right\rceil + 1 = \left\lfloor \frac{m}{2} \right\rfloor + 1$.

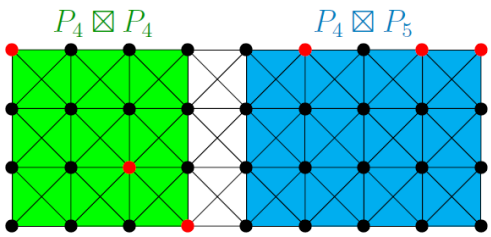

Figure 10: Contamination of $P_4 \boxtimes P_9$.

□

As a consequence of the above theorem, we can give the following Corollary.

Corollary 4.3. For any positive integer n, we have:

$$\gamma_c(P_n \boxtimes P_n) \leq \left\lfloor \frac{n}{2} \right\rfloor + 1.$$

Our investigation therefore puts us in a position to conjecture the following result:

Conjecture. Let n, m be two positive integers. Then we have

$$\gamma_c(P_n \boxtimes P_m) = \begin{cases} max\left\{\left\lfloor \frac{n}{2} \right\rfloor, \left\lfloor \frac{m}{2} \right\rfloor\right\} + 1 & \text{if } n \text{ and } m \text{ have the same parity,} \\ max\left\{\left\lceil \frac{n}{2} \right\rceil, \left\lceil \frac{m}{2} \right\rceil\right\} + 1 & \text{else.} \end{cases}$$

5 CONCLUSION

In this work, we have introduced a new dynamic variant of domination, which has the same principle of unfolding as power domination. This type of domination can be interpreted as a biological phenomenon or an evolutionary social phenomenon, which is called a contamination game and takes place in the grid graph $\boldsymbol{G(n,m)}$. We identified an upper bound for the minimum number of contaminant cells $\boldsymbol{\gamma_c(G(n,m))}$ and conjectured that it gives the exact value.

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