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CONTAMINATION NUMBER OF THE KING'S GRAPH

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Abstract There are several ways in which viruses can spread at the cellular level within biological tissues. Some viruses can infect neighboring cells by binding to specific receptors on their surface while remaining suspended in the interstitial fluid between cells. In this study, we investigate a theoretical model based on graphs to understand viral contamination. This model is closely related to the well-known power dominating set problems in graphs. To be specific, we define a contaminating set of vertices in a graph G based on a predetermined system of vertex contamination. A set S of vertices is considered a contaminating set of G if, by following the contamination system starting with the affected vertices in S, all vertices in the graph can be contaminated. The contaminating number of a graph, denoted by $\gamma_c(G)$, is the minimum cardinality of a contaminating set for that graph. In this paper, our focus is on studying the contaminating number of $n \times m$ King graphs, which we represent as $\gamma_c(P_n \boxtimes P_m)$.

1 Introduction

The challenge of monitoring power systems involves a form of combinatorial optimization that requires minimizing the number of measuring devices needed to oversee the system's performance. Unlike standard domination problems [1, 4, 7], where adding a unit to a vertex only affects its local region, in this case, the effects can be felt globally. For example, if a power system is represented as a path, a single measuring unit can monitor the entire system, regardless of its length. The power system monitoring problem has been formulated as a graph theory domination problem by Haynes, Hedetniemi, Hedetniemi, and Henning [5].

Consider a connected graph $G = (V, E)$. For any vertex v in G, the open neighborhood of v denoted as $N(v)$ represents the set of neighbors of v excluding v itself, and for a subset S of V let $N(S) = (\cup_{v \in S} N(v)) \setminus S$. The set monitored by S, denoted as $M(S)$, is defined algorithmically as follows [6]:

Algorithm 1 Construction of a monitored set $M(S)$

Input: Graph $G = (V, E)$, and $S \subset V$

Output: $M(S)$: the set monitored by S

```
Initiate $M(S) \leftarrow S \cup N(S)$;
While there exists $v \in M(S)$ such that $N(v) \cap (V \backslash M(S)) = \{w\}$ do
    $M(S) \leftarrow M(S) \cup \{w\}$;
EndWhile;
Return $M(S)$;
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The power domination number, denoted by $\gamma_\pi(G)$, is defined as the minimum cardinality of a power dominating set S in a graph G such that $M(S) = V$. Several studies have focused on the algorithmic aspects of this problem, showing that it is NP-complete even in restricted classes of graphs such as bipartite, chordal, planar, circle, and split graphs [2]. However, for trees and interval graphs, the problem can be solved in polynomial time [2, 6]. Dorfling and Henning have obtained closed formulas for the power domination numbers of grid graphs [3], which is in contrast with the fact that determining such formulas for the usual domination number of grid graphs is still an open problem [5]. Although a grid is commonly described as a cartesian product of two paths, there are other graph products such as the strong, direct, and lexicographic product [5]. Therefore, it is natural to ask whether the power domination number can be determined for these types of path products as well.

A King's graph is a graph that represents all the legal moves that a king chess piece can make on a chessboard. Each vertex in the graph corresponds to a square on the chessboard, and each edge represents a valid move. Specifically, an $n \times m$ king's graph represents an $n \times m$ chessboard, and it can be constructed by creating a map graph from the chessboard's squares. This involves creating a vertex for each square and connecting two vertices with an edge if their corresponding squares share a common edge or corner as shown in Figure 1. Alternatively, it can be generated as the strong product of two path graphs $P_n \boxtimes P_m$.

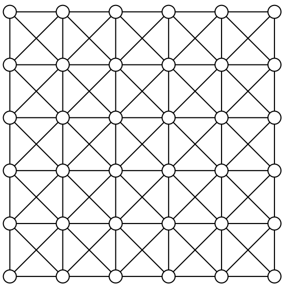
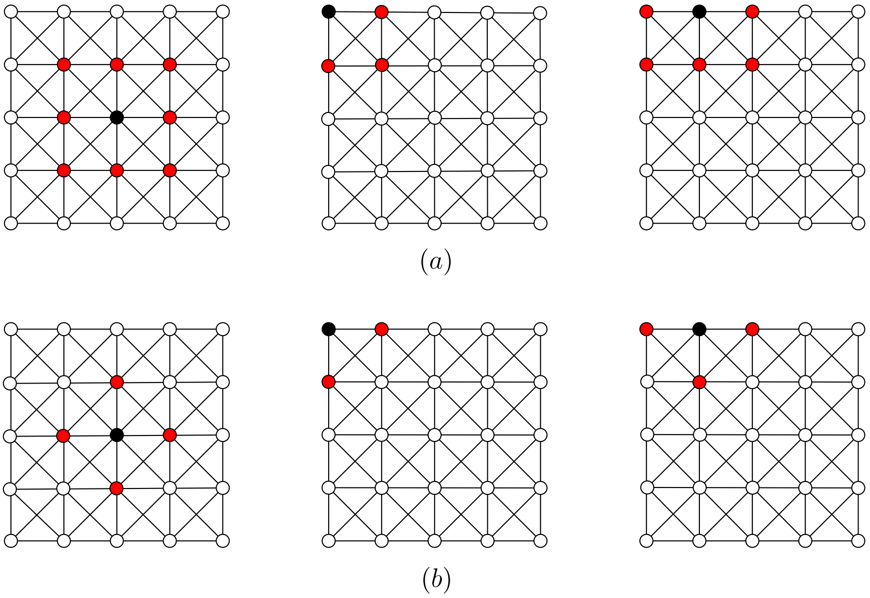


Figure 1. The 6 × 6 king's graph.

This paper presents a novel form of domination called "Viral Contamination", which is applied to the king's graph $P_n \boxtimes P_m$. The viral contamination is defined in two stages: firstly, by establishing local contamination for a small subset of vertices in $P_n \boxtimes P_m$, and secondly, by spreading the contamination to all vertices of $P_n \boxtimes P_m$ using pre-established rules for contamination.

2 The rules of contamination

In this section, we will introduce the topic of viral contamination in the king's graph. The Moore neighborhood and Von Neumann neighborhood of a vertex v in $P_n \boxtimes P_m$ are denoted as $\mathrm{M}(v)$ and $\mathrm{VN}(v)$, respectively, and are illustrated in Figure 2(a) and 2(b). To encompass vertices located on the edge of $P_n \boxtimes P_m$, both neighborhoods are expanded.


(a)

(b)

Figure 2. Moore and Von Newmann neighborhoods of the black vertex.

The contamination game can be viewed as a cellular automaton, which is a model where each state leads automatically to the next state based on predefined rules. The game takes place on $P_n \boxtimes P_m$, where each vertex is analogous to a living cell that can be either "sick" or "healthy". At each step, the state of a vertex is determined by the state of its eight neighbors, based on a given initial contamination rules. The objective of the game is to determine the minimum number of initially infected vertices, denoted as $\gamma_c(P_n \boxtimes P_m)$, required to infect the entire King graph. This form of contamination simulates an epidemiological phenomenon, depicting the transmission of viruses within living cells. The state space consists of a king's graph of sick or healthy living vertices, and the transition rule chosen depends on the number and position of contaminated neighboring living vertices surrounding a vertex, using the Moore or Von Neumann neighborhood.

A vertex v is contaminated by two sick vertices v_1 and v_2 if one of the following conditions is met:

(1) $v_1, v_2 \in \mathrm{VN}(v)$,

(2) $v_1, v_2 \notin \mathrm{VN}(v)$ and $\mathrm{M}(v_1) \cap \mathrm{M}(v_2) = \{v\}\cdot$

The possible configurations which satisfies these conditions are given in Figure 3. Figure 3 shows two vertices highlighted in red, which indicate the initially infected vertices, whereas the black vertex represents a healthy vertex that will eventually become infected and join the infected set.

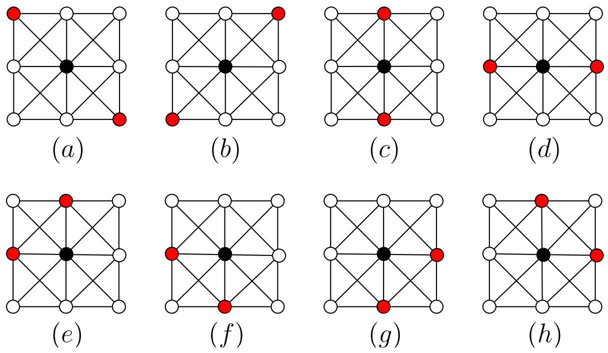


Figure 3. The contamination rules for the black vertex.

The following algorithm illustrates the process of viral contamination and the spread of the virus, which leads to the formation of the contaminated set S, while adhering to the contamination rules.

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

Input: King graph and $S \subset V$

Output: $C(S)$: the set contaminated by S

```
Initialize $C(S) \leftarrow S$;
While $\exists\, v \in V \backslash C(S)$, such that conditions (1) or (2) are satisfied do
    $C(S) \leftarrow C(S) \cup \{v\}$;
End While;
Return $C(S)$.
```

3 Mathematical model for the contamination game: a dynamical system

The contamination game on the $n \times m$ King graph, can be viewed as a dynamic system, where the decision variable at step k is denoted by $x_{ij}^{(k)}$, where:

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

Here, we will adopt the following notation: for any positive integer n, we define $[n]$ as the set $\{1, 2, \ldots, n\}$. Let $P_n \boxtimes P_m$ be the $n \times m$ King graph, where the vertex set V is given by $[n] \times [m] = \{(i,j) \mid 1 \leq i \leq n, 1 \leq j \leq m\}$. The i-th row of $P_n \boxtimes P_m$ represents the set $i \times [m]$, while a column with index j is a set of the form $[n] \times j$. As mentioned earlier, the goal of this game is to determine the minimum number of vertices that must be initially infected at step 0 to infect the entire King graph within k_0 steps, following Algorithm 2.

The objective is the following:

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

according to the contamination rules presented above (see Figure 3), which are written as follows:

$$k \rightsquigarrow k+1 \left\{ \begin{array}{lll}
x_{ij}^{(k)}\ x_{i+2,j+2}^{(k)} \leq x_{i+1,j+1}^{(k+1)}, & \forall i = 1, n-2,\ \forall j = 1, m-2; & (Fig.\ 2(a)) \\
x_{ij}^{(k)}\ x_{i+2,j-2}^{(k)} \leq x_{i+1,j-1}^{(k+1)}, & \forall i = 1, n-1,\ \forall j = 1, m-1; & (Fig.\ 2(b)) \\
x_{ij}^{(k)}\ x_{i+2,j}^{(k)} \leq x_{i+1,j}^{(k+1)}, & \forall i = 1, n-2,\ \forall j = 1, m; & (Fig.\ 2(c)) \\
x_{ij}^{(k)}\ x_{i,j+2}^{(k)} \leq x_{i,j+1}^{(k+1)}, & \forall i = 1, n,\ \forall j = 1, m-2; & (Fig.\ 2(d)) \\
x_{ij}^{(k)}\ x_{i+1,j-1}^{(k)} \leq x_{i+1,j}^{(k+1)}, & \forall i = 1, n-2,\ \forall j = 3, m; & (Fig.\ 2(e)) \\
x_{ij}^{(k)}\ x_{i+1,j+1}^{(k)} \leq x_{i,j+1}^{(k+1)}, & \forall i = 1, n-1,\ \forall j = 2, m; & (Fig.\ 2(f)) \\
x_{ij}^{(k)}\ x_{i+1,j-1}^{(k)} \leq x_{i,j-1}^{(k+1)}, & \forall i = 1, n-1,\ \forall j = 1, m-1; & (Fig.\ 2(g)) \\
x_{ij}^{(k)}\ x_{i+1,j+1}^{(k)} \leq x_{i+1,j}^{(k+1)}, & \forall i = 1, n-1,\ \forall j = 2, m; & (Fig.\ 2(h)) \\
x_{ij}^{(k)} \in \{0, 1\}, & \forall i = 1, n,\ \forall j = 1, m,\ \forall k \in \mathbb{N}. &
\end{array} \right.$$

Figure 4 illustrates an optimal contamination scenario in $P_3 \boxtimes P_4$. The red vertices depict the infected vertices at step 0.

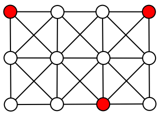


Figure 4. $\gamma_c(P_3 \boxtimes P_4) = 3$.

Figure 5 illustrates the progression of infection across $P_3 \boxtimes P_4$ as time advances.

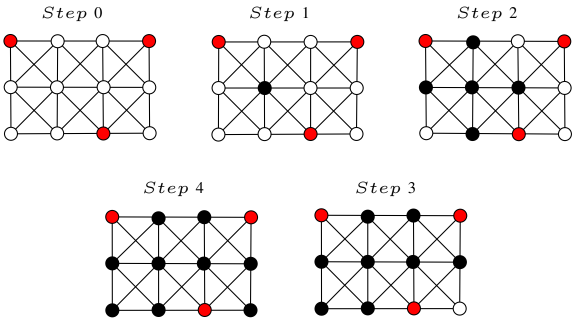


Figure 5. The propagation of the infection on $P_3 \boxtimes P_4$.

4 Main Results

Before presenting the results, we would like to draw attention to the fact that the minimum number of viruses required to infect an $n \times m$ King graph is the same as the minimum number required for an $m \times n$ King graph, which can be achieved by rotating $P_n \boxtimes P_m$ by $\pi/2$. Thus, for convenience, we assume throughout the rest of the article that both n and m are positive integers and $m \geq n$.

Proposition 4.1. *For any positive integer $m \geq 1$, the minimum number of vertices required for initial infection on the path P_m (a $1 \times m$ King graph) is:*

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

Proof. Let $P_m = v_1 \cdots v_m$. The propagation of the virus throughout P_m is clearly achievable solely through the application of rule (d), as depicted in Figure 3. Hence, to minimize the number of virus at state 0, the endpoints of P_m, v_1 and v_m, must be infected first, and for the remaining vertices, the virus deployment should alternate along P_m. Thus, we should deployed $2 + \lfloor \frac{m-2}{2} \rfloor$ viruses, which implies the result (see for instance Figure 6).

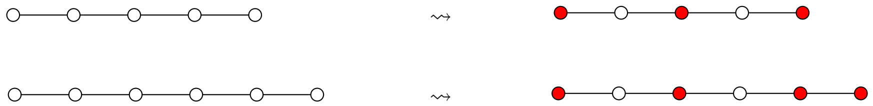


Figure 6. The best way to infect P_5 and P_6 with the minimum number of viruses.

□

Proposition 4.2. *For any positive integer $m \geq 5$, we have:*

$$\gamma_c(P_m) = \gamma_c(P_{m-4}) + 2,$$

where $\gamma_c(P_1) = 1, \gamma_c(P_2) = \gamma_c(P_3) = 2$ and $\gamma_c(P_4) = 3$.

Proof. Upon examining $P_m = v_1 \cdots v_m$, it is evident that cells v_1 and v_m each have only one neighboring cell. Consequently, they will never get contaminated during any iteration of the contamination process. Therefore, they must belong to the initial set S. For the purpose of optimization, cells 2 and $m-1$ are not required to be included in the initial set S since v_1 and v_m are already present in it. As a result, there are $m-4$ cells remaining for which we need to decide whether they should be included in S or not. To make this decision, we can solve the problem on the path graph formed by cells $v_3, \ldots, v_{m-2}$ and obtain the value of $\gamma_c(P_{m-4})$. This value represents the minimum cardinality of the contaminating set for this path graph. Consequently, it determines the final result for the given scenario. □

Corollary 4.3. *The generating function of $\gamma_c(P_m)$ is:*

$$f(x) = \frac{x(-x^2 + x + 1)}{(x-1)^2(x+1)}.$$

Proof. Let

$$f(x) = \sum_{m \geq 1} \gamma_c(P_m) x^m.$$

Then

$$x^4 f(x) = \sum_{m \geq 5} \gamma_c(P_{m-4}) x^m.$$

Therefore

$$(1-x^4)f(x) = x+2x^2+2x^3+3x^4+\sum_{m\geq 5}(\gamma_c(P_m)-\gamma_c(P_{m-4}))x^m.$$

By Proposition 4.2, we get

$$f(x) = \frac{x+2x^2+2x^3+3x^4}{1-x^4}+\frac{2x^5}{(1-x)(1-x^4)}.$$

Hence, after simplification, the result yields. □

Theorem 4.4. *Let $m \geq 1$ be a positive integer. Then we have:*

$$\gamma_c(P_m \boxtimes P_m) = \gamma_c(P_m).$$

Proof. To prove our statement, we will use induction for both scenarios where m is even and odd.

Case 1. m even.

Assuming that $m = 2$, the only valid contamination rules for fully infecting $P_2 \boxtimes P_2$ are the (a) or (b) rules illustrated in Figure 3, both of which require at least two viruses to be present diagonally, and so $\gamma_c(P_2 \boxtimes P_2) = \gamma_c(P_2) = 2$. Suppose that all King graph $G' = P_{2k} \boxtimes P_{2k}$, $k \geq 1$, satisfy the statement, then let $G = P_{2k+2} \boxtimes P_{2k+2}$ represented as follows:

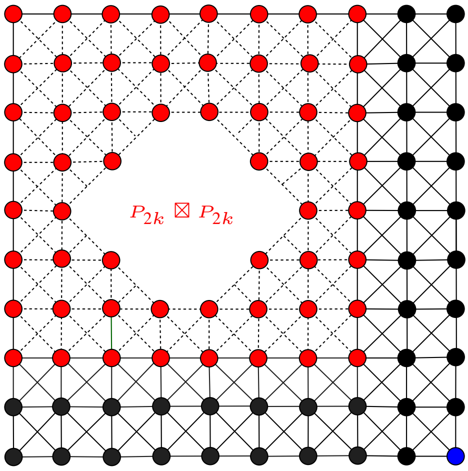


Figure 7. $G = P_{2k+2} \boxtimes P_{2k+2}$.

Applying the induction hypothesis on graph $G' = P_{2k} \boxtimes P_{2k}$ and placing a virus on the vertex of graph G located at the southeast corner (marked in blue), we obtain a total contamination of graph G, following contamination rules (a), (f) and (h) (see Figure 3), with a total number of viruses equal to $\gamma_c(P_{2k})+1$. According to Proposition 4.1, we get:

$$\gamma_c(P_{2k+2} \boxtimes P_{2k+2}) = 2+\left\lfloor\frac{2k}{2}\right\rfloor = 1+\left\lfloor\frac{2k+2}{2}\right\rfloor = \gamma_c(P_{2k+2}).$$

Case 2. m odd.

It is clear that if $m = 1$, we will need only one virus. Similarly, suppose that all King graph

$G' = P_{2k+1} \boxtimes P_{2k+1}$, $k \geq 0$, satisfy the statement, then let $G = P_{2k+3} \boxtimes P_{2k+3}$ represented as follows:

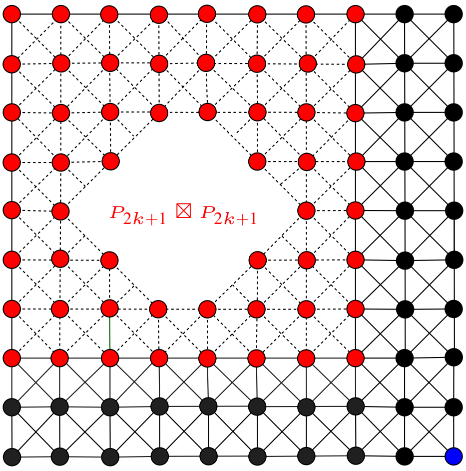


Figure 8. $G = P_{2k+3} \boxtimes P_{2k+3}$.

Applying the induction hypothesis on graph $G' = P_{2k+1} \boxtimes P_{2k+1}$ and placing a virus on the vertex of graph G located at the southeast corner (marked in blue), we obtain a total contamination of graph G, following contamination rules (a), (f) and (h) as illustrated in Figure 3, with a total number of viruses equal to $\gamma_c(P_{2k+1}) + 1$. According to Proposition 4.1, we have:

$$\gamma_c(P_{2k+3} \boxtimes P_{2k+3}) = 2 + \left\lfloor \frac{2k+1}{2} \right\rfloor = 1 + \left\lfloor \frac{2k+3}{2} \right\rfloor = \gamma_c(P_{2k+3}).$$

□

Observation 4.5. It can be easily verified that the complete contamination of the graph $P_m \boxtimes P_m$ occurs with the minimum number of viruses placed on the diagonal path P_m (see for instance Figure 9).

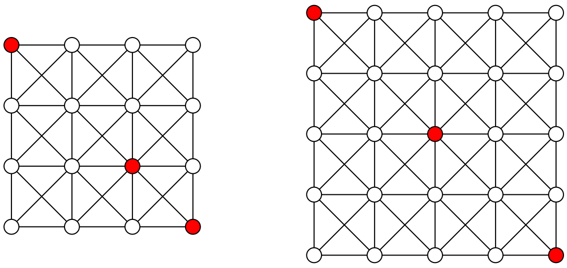


Figure 9. $\gamma_c(P_4 \boxtimes P_4) = \gamma_c(P_5 \boxtimes P_5) = 3$.

The next theorem attempts to provide a generalization of Theorem 4.4.

Theorem 4.6. *Let n, m be two positive integers. Then we have:*

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

Proof. We previously noted that the minimum number of viruses needed to contaminate the King graph $P_n \boxtimes P_m$ is the same as that for $P_m \boxtimes P_n$. This can be accomplished by rotating $P_n \boxtimes P_m$ by $\pi/2$. Hence, for the purpose of this proof, we assume that $m \geq n \geq 1$.

In what follows, we present a construction of a set of viruses that achieves the desired cardinality for contamination. If $n = 1$ the contamination is achieved with the given cardinality using Proposition 4.1. 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^i_{n-i} be a diagonal of $P_n \boxtimes P_n$ of order i and a size $n-i$, such that $i \in \{0, \ldots, n-1\}$. The main diagonal P^0_n which is a path, is fully contaminated using $\frac{n}{2}+1$ according to Proposition 4.1. From the contamination rules defined above, more precisely the rules (f) and (h), the parallel paths P^1_{n-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 $G_1 = P_n \boxtimes P_n$.

We now shift our focus to contaminating G_2. To contaminate this latter it suffices to alternatively deploy $\frac{m-n}{2}$ viruses on the first path from the top of G_2, starting by the last vertex according to the contamination rules (d) and (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 for instance Figure 10).

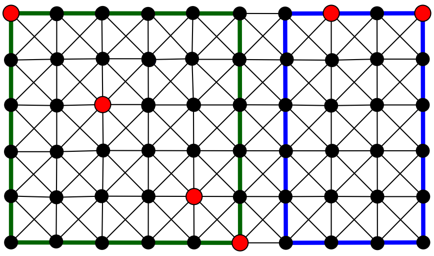


Figure 10. $\gamma_c(P_6 \boxtimes P_{10}) = 6$.

Case 2. n and m are odd.

The virus-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 $\lfloor \frac{n}{2} \rfloor + 1$ viruses on the main diagonal of G_1 using Proposition 4.1 and the contamination rules (a), (f) and (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_2, starting by the last vertex according to the contamination rules (d) and (e). Hence, we get a full contamination of G_2, and then a full contamination of $G = P_n \boxtimes P_m$, by using $\lfloor \frac{n}{2} \rfloor + \frac{m-n}{2} + 1 = \lfloor \frac{m}{2} \rfloor + 1$ viruses (see for instance Figure 11).

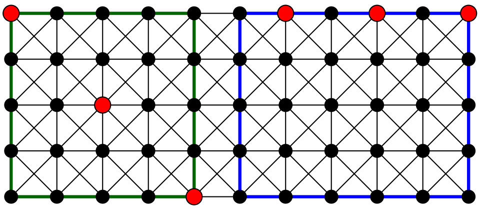


Figure 11. $\gamma_c(P_5 \boxtimes P_{11}) = 6$.

Case 3. n odd and m even.

As seen in the second case, G_1 is fully contaminated by using $\lfloor \frac{n}{2} \rfloor + 1 = \lceil \frac{n}{2} \rceil$. To contaminate G_2 it suffices to alternatively deploy $\lfloor \frac{m-n}{2} \rfloor = \frac{m}{2} - \lceil \frac{n}{2} \rceil$ viruses on the first path from the top of G_2, starting with the second vertex of G_2 then add a virus at the last vertex (see for instance Figure 12). Hence, we have a full contamination of G_2, according to the contamination rules (d) and (e) and then a full contamination of $G = P_n \boxtimes P_m$, using $\lceil \frac{n}{2} \rceil + \lfloor \frac{m-n}{2} \rfloor = \frac{m}{2}$.

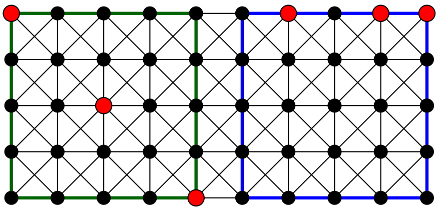


Figure 12. $\gamma_c(P_5 \boxtimes P_{10}) = 6$.

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 $\lceil \frac{m-n}{2} \rceil = \lceil \frac{m}{2} \rceil - \frac{n}{2}$ viruses on the first path from the top of G_2, starting with last vertex (see for instance Figure 13). Hence, we have a full contamination of G_2, according to the contamination rules (d) and (e) and then a full contamination of $G = P_n \boxtimes P_m$, using $\frac{n}{2} + \lceil \frac{m-n}{2} \rceil + 1 = \lceil \frac{m}{2} \rceil + 1$.

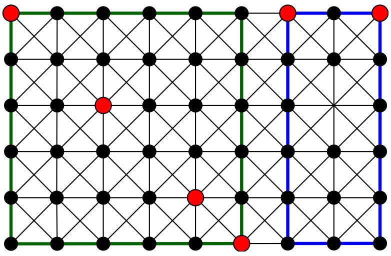


Figure 13. $\gamma_c(P_6 \boxtimes P_9) = 6$.

□

5 Concluding remark

According to Theorem 4.4, the upper bound of Theorem 4.6 is reached when n equals m. Therefore, based on our investigation, we can now propose the following result as a conjecture.

$$\gamma_{cv}(P_n \boxtimes P_m) = \max\left\{\left\lfloor \frac{n}{2} \right\rfloor, \left\lfloor \frac{m}{2} \right\rfloor\right\} + 1.$$

6 Conclusion

In our study, we have introduced a novel parameter named the contamination number $\gamma_c(G)$ within a theoretical graph-based model. This parameter is particularly significant for modeling dynamic biological or social occurrences, such as the contagion game, taking place in King graphs $P_n \boxtimes P_m$. Furthermore, it exhibits a close association with power domination problems in graphs. Our investigation has led to the precise determination of $\gamma_c(G)$ for the King graph $P_n \boxtimes P_n$ and the establishment of an upper bound for the general King graph $P_n \boxtimes P_m$. Additionally, we have formulated a conjecture concerning its exact value. These discoveries play a pivotal role in advancing our understanding of domination phenomena in contagion games and bear practical implications in the realms of computer science and biology.

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