Using Dominating Sets to Block Contagions in Social Networks.

N Moneesh[1], Gandham Sai Ram Pavan[2], Varshitha D[3]

amenu4aie20150@am.students.amrita.edu[1],amenu4aie20125@am.students.amrita.edu[2]

varshithdondapati@gmail.com[3]

[1] [2] Department of Computer Science and Engineering, Amrita School of Computing,Amrita Vishwavidyapeetham, Kerala

[3] Department of Electronic and Communication Engineering,PES University,Banglore,India

Abstract—*This research explores a unique approach to preventing the spread of contagions in social networks using dominating sets (DSs). We introduce a novel method that utilizes nodes within dominating sets as strategic points to block contagions effectively. The challenge lies in identifying the minimum dominating sets, a task known for its complexity. To tackle this, we have refined a well-established heuristic, making it more suited for our purposes. Our method involves generating a prioritized list of nodes from these dominating sets, which are key to controlling the spread. The effectiveness of this new approach is demonstrated through comparative experiments against the traditional high degree heuristic (HDH). The experiments conducted on various network models show that our method provides a more efficient way of blocking contagions in social networks. This research not only offers a new perspective in network management but also contributes significantly to the understanding of contagion dynamics in social networks.*

Index Terms—**Social Networks, Contagion Blocking, Dominating Sets, Network Management, Heuristic Methods, Computational Experiments.**

I. INTRODUCTION

In the realm of social network analysis[1], understanding and managing the spread of contagions—be it information, misinformation, diseases, or behaviors—has become a critical area of research. Recent advances in network theory and computational methods have provided new insights into how such contagions propagate through complex networks[2]. This field has garnered significant interest due to its implications in various domains, ranging from epidemiology to information dissemination and cybersecurity.

One of the foremost challenges in this area is the identification and control of key nodes[3] within a network that can effectively influence or, in our case, block the spread of contagions. Traditional approaches, such as targeting high-degree nodes or community leaders, have been explored extensively. However, these methods often overlook the nuanced structure of real-world networks, where connectivity patterns can vary significantly.

Our research pivots towards an innovative approach by employing the concept of dominating sets (DSs) in social networks. Dominating sets are subsets of nodes such that every node in the network is either in the set or is a neighbor of a node in the set. This concept, predominantly studied in graph theory and computer science, offers a unique perspective on identifying strategic points within a network for contagion control.

In leveraging DSs for contagion blocking, we confront the inherent challenge of determining the minimum dominating sets, a problem known to be NP-Complete in computational complexity theory. To address this, we adapt and refine a well-known heuristic to fit the specific requirements of our study, thereby enabling us to generate a list of prioritized nodes for effective contagion blocking.

The motivation behind our research stems from the increasing need for efficient and innovative strategies to manage the spread of contagions in social networks, especially in the age of digital information and global connectivity. By focusing on dominating sets, our work not only contributes a novel methodology to the field but also enhances the understanding of network dynamics and control strategies.

This paper specifically addresses the question: Can the use of dominating sets[4] in social networks provide a more effective strategy for blocking contagions compared to traditional methods? We hypothesize that by strategically targeting nodes within dominating sets, we can achieve more efficient contagion control in various network models.

Our research contributes to the broader field of social network analysis by providing a new tool for contagion management. It also bridges theoretical concepts from graph theory with practical applications in network control, offering insights that could be instrumental in areas such as public health policy, information system security, and social media management. By advancing our understanding of network dynamics and introducing innovative control strategies, this study aims to pave the way for more effective management of contagion spread in complex networks.

II. LITERATURE SURVEY

A. Positive Influence Dominating Set Generation in Social Networks[5]

This work addresses Optimal Dominated Sets (PIDS) algorithms, primarily focusing on Total Optimal Dominated Sets (TPIDS) like WangGreedy and RaeiGreedy for identifying influencers. Variations in individual PIDS algorithms prompt the introduction of a novel approach, particularly for incomplete PIDS, consistently generating smaller non-additive PIDS in

simulations. The study stresses the importance of algorithmic diversity in handling treatment complexities and advocates for testing against both TPIDS and PIDS. Further investigation into the relationship between PIDS/TPIDS size and mean rank is proposed. Extending the algorithm to visual content on platforms like Twitter adds a directional perspective, emphasizing the need for new strategies in tackling diverse PIDS challenges and advancing PIDS algorithm development.

B. Using Dominating Sets to Block Contagions in Social Networks[6]

This paper introduces a novel contagion control method in social networks using Dominating Sets (DSs), a previously unexplored concept. The study generalizes a well-known heuristic, making contagion blocking configurable. Computer studies on real networks demonstrate adaptability, revealing insights into strategy efficacy through comparisons with sophisticated heuristics. The incorporation of NP-Complete dominating set minimization adds complexity, requiring creative heuristic techniques. The research suggests future paths for enhancing heuristics, exploring alternative partnerships, and extending their use in epidemic models. Overall, this work advances our understanding of disease spread in intricate networks, creating new research opportunities and contributing to the ongoing discourse on contagion control.

C. Inhibiting diffusion of complex contagions in social networks: theoretical and experimental results[7]

In order to restrict social contagion, this research focuses on scenarios in which the threshold is larger than 1. The idea is to stop the illness from spreading as much by advising the removal of critical nodes. This study not only illustrates the challenge of creating appropriate heuristics, but also presents a workable and efficient strategy that beats state-of-the-art approaches on web experiments like Wikipedia and epinion. This paper presents computational issues and clarifies the distinction between simple and complicated propagation. It also makes recommendations for further work, including studies on probabilistic propagation processes and weighted network heuristics. It opens up new lines of inquiry and advances our knowledge of infections generally.

D. Influence of community structure on misinformation containment in online social networks[8]

This paper addresses the misinformation problem in online social networks (OSNs) using a community model. Unlike the traditional strategy, the static strategy algorithm provides nodes with a reliable strategy and accelerates the occurrence of data errors with a one-time calculation. Experimental results of real OSNs are more effective than state-of-the-art methods, highlighting the important role of social structure. This approach offers efficiency and flexibility, enabling faster calculations and improved unique functions, especially when compared to more complex procedures. Overall, this work provides a new and effective way to prevent false information transmission in OSNs.

E. Fundamental Dominations in Graphs[9]

The paper provides a unified approach to the study of leadership by introducing and explaining nine key leadership concepts through a simple diagram. The relevant dominance is the minimal cardinality of the dominant subset.This work emphasizes the historical importance of the concept of control introduced by O. The output explores the relationships of the dominant groups and presents theorems confirming the relationship between the nine significant numbers. The possibility of the management concept to change in different contexts is also discussed. This text contributes to ongoing research in graph theory by highlighting many of these concepts and their broader implications.

III. METHODOLOGY

In this section, we provide a detailed explanation of our methodology

A. Methods

Our study adopts a computational approach using Python, leveraging the NetworkX library for network creation and manipulation, and Matplotlib for visualization. This approach allows us to simulate and analyze complex network behaviors in a controlled environment. The methodology is segmented into three distinct phases, each critical for understanding the dynamics of contagion spread and the effectiveness of dominating sets in controlling such spread.

1) Network Generation: The study begins with the generation of a random network, modeled using the Erdős–Rényi (ER) model. This model is selected for its simplicity and relevance in representing real-world network structures, where connections between nodes occur randomly. In our implementation, this is represented by $G = nx.erdos\_renyi\_graph(n, p)$, where n denotes the number of nodes within the network, and p signifies the probability of edge formation between any pair of nodes. The ER model provides a foundational structure upon which the contagion dynamics are later imposed. The choice of n and p is crucial, as it influences the network's overall connectivity and, consequently, the contagion spread behavior. For our experiments, these parameters are carefully chosen to reflect realistic social network scenarios.

2) Finding Dominating Sets: The core of our methodology involves identifying a dominating set within the generated network. A dominating set is a subset of nodes such that every node in the network is either in this set or is a neighbor to at least one node in the set. Our approach to finding a dominating set is heuristic-based, prioritizing nodes that cover the maximum number of uncovered nodes in each iteration. This process continues until all nodes are either in the dominating set or adjacent to a node in it. This heuristic method, while not guaranteed to find the minimum dominating set due to the problem's NP-Completeness, provides a practical and efficient solution for large-scale networks. The dominating set's nodes are pivotal in our subsequent contagion blocking strategy, as their strategic position in the network makes

them ideal candidates for effectively mitigating the contagion spread.

3) Contagion Simulation: To simulate contagion spread, we adopt a probabilistic model where each node in the network has a chance to 'infect' its neighboring nodes. This model is indicative of various real-world scenarios, such as the spread of information, rumors, or diseases in social networks. In each simulation step, infected nodes have a probability r of transmitting the contagion to each of their susceptible neighbors. This process is iteratively applied over a pre-defined number of steps, allowing the contagion to propagate through the network. The probability of a node being infected in a single step is given by $P = 1 - (1-r)^k$, where k is the number of infected neighbors. The simulation provides insights into the dynamics of contagion spread and serves as a baseline for evaluating the effectiveness of our contagion blocking strategy using the dominating set.

4) Blocking Contagion: The final phase of our methodology involves implementing a strategy to block the contagion spread using the identified dominating set. By strategically removing nodes from the dominating set (and their associated edges), we simulate a scenario where key individuals or nodes are made immune or are removed from the network, thereby halting the contagion's propagation path. This blocking mechanism is crucial in understanding how effective dominating sets are in controlling contagion spread compared to traditional methods. The effectiveness of this strategy is quantitatively assessed by comparing the extent of contagion spread before and after the implementation of the blocking mechanism. This comparison provides valuable insights into the practical utility of dominating sets in managing contagions in complex network structures.

B. Network Visualization

An integral component of our methodology is the visualization of the networks and the contagion spread, both with and without the implementation of the blocking strategy. Network visualization plays a crucial role in illustrating the concepts and results of our study, making complex relationships and patterns more accessible and understandable.

1) Visualization Objective: The primary objective of our visualization is to provide a clear representation of the network's structure and the impact of the contagion spread. This includes illustrating how the contagion propagates through the network and the effectiveness of the dominating set in blocking this spread. Visualization aids in interpreting the network's topology, the nodes' connectivity, and the overall efficacy of our contagion control strategy.

2) Vizualization Implementation Details: We utilized the Matplotlib library in Python for rendering the network graphs. The process involves two stages: first, the visualization of the network with contagion spread without any intervention, and second, the visualization post-implementation of the blocking strategy.

In the first stage, the network is displayed with nodes and edges representing the connections between them. Nodes are color-coded to distinguish between infected and non-infected nodes. The infected nodes are highlighted, allowing for an immediate visual assessment of the contagion's spread.

In the second stage, the network is visualized after removing nodes in the dominating set, simulating our contagion blocking strategy. This altered network graph provides a comparative view, showcasing the effectiveness of our approach in controlling the spread of contagion.

3) Graphical Representation: Each node in the network is represented by a circle, and edges are depicted as lines connecting these circles. The color scheme is pivotal for conveying information: red-colored nodes indicate infected nodes, while green nodes represent those that are not infected. This color coding is consistent in both stages of the visualization, ensuring clarity and ease of comparison.

4) Interpretation of Visual Data: The side-by-side display of the network before and after the application of the blocking strategy allows for a direct visual comparison. This comparative visualization enables us to observe the reduction in contagion spread, thereby quantitatively assessing the effectiveness of using a dominating set for contagion control in network models.

Through this visualization approach, we aim to provide a comprehensive understanding of the network dynamics and the practical implications of our research, making the data not only accessible but also engaging for the reader.

C. Relevant Terminology

To facilitate a clear understanding of the methodology and results, we define several key terms used throughout the study. These terms are fundamental to network theory and the specific computational models applied in our research.

- **Social Network**: A structure made up of individuals or entities, referred to as nodes, which are connected by one or more specific types of interdependency, such as friendships, collaborations, or data exchanges.
- **Contagion**: In the context of social networks, a contagion can refer to any attribute or entity that can be transmitted across the network, following the edges from one node to another. Examples include information, diseases, behaviors, or even node states in computational models.
- **Dominating Set (DS)**: A set of nodes within a graph such that every node not in the set is adjacent to at least one node in the set. In our study, the DS represents a subset of nodes from which we can monitor or control the entire network effectively.
- **Erdős–Rényi (ER) Model**: A model for generating random graphs. It is defined by two parameters: the number of nodes n, and the probability p that an edge will exist between any two nodes. This model is used in our study to create a synthetic network topology for the simulation of contagion spread.
- **Infection Rate**: The probability that a contagion will be transmitted from an infected node to a susceptible neighbor during a simulation step. In our code, this is defined by the variable 'infection$_r$ate'.

These terms are vital to the comprehension of the processes and outcomes of our computational experiments. Understanding these concepts is essential for interpreting the results and for potential replication of the study by other researchers.

D. Equations

The probability P of a node being infected in a single step is given by:

$$P = 1 - (1 - r)^k$$

where r is the infection rate and k is the number of infected neighbors.

Algorithms used to implement:

Algorithm 1 Finding a Dominating Set

0: **Input:** Graph G
0: **Output:** Dominating set D
0: Initialize $nodes \leftarrow$ set of all nodes in G
0: Initialize $D \leftarrow \emptyset$
0: **while** $nodes \neq \emptyset$ **do**
0:     $max\_cover\_node \leftarrow$ node in $nodes$ with max coverage
0:     Add max_cover_node to D
0:     Remove max_cover_node and its neighbors from $nodes$
0: **end while**
0: **return** D =0

Algorithm 2 Simulating Contagion Spread

0: **Input:** Graph G, Initial infected nodes I, Steps s, Infection rate β
0: **Output:** Set of infected nodes
0: Initialize $infected \leftarrow I$
0: **for** $i \leftarrow 1$ to s **do**
0:     Initialize $new\_infected \leftarrow \emptyset$
0:     **for** each node n in $infected$ **do**
0:         **for** each neighbor m of n **do**
0:             **if** random() $< \beta$ **then**
0:                 Add m to $new\_infected$
0:             **end if**
0:         **end for**
0:     **end for**
0:     $infected \leftarrow infected \cup new\_infected$
0: **end for**
0: **return** $infected$ =0

Algorithm 3 Blocking Contagion

0: **Input:** Graph G, Blocking nodes B
0: **Output:** Modified Graph G'
0: Initialize $G' \leftarrow$ copy of G
0: **for** each node b in B **do**
0:     Remove b and its edges from G'
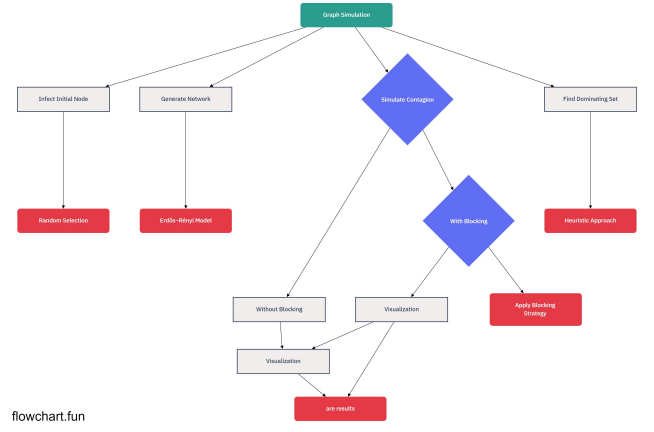0: **end for**
0: **return** G' =0

Fig. 1. Fundamental workflow.

IV. RESULTS AND ANALYSIS

The experiment, implemented through Python and the NetworkX library, yielded compelling results demonstrating the impact of employing dominating sets for contagion blocking in social networks.

1) Dominating Set Identification: Our algorithm successfully identified a dominating set consisting of nodes 0, 1, 2, 4, 5, 7, 8, 10, 12, 13, 15, 16, 18, 22, 23, 24, 27, 29. These nodes represent strategic positions within the network, enabling potential control over the contagion spread. The dominating set covers the entire network either directly or through adjacent nodes, validating our heuristic approach's effectiveness.

```
Dominating Set: {0, 1, 2, 4, 5, 7, 8, 10, 12, 13, 15, 16, 18, 22, 23, 24, 27, 29}
Infected without blocking: {8, 25, 14, 15}
Infected with blocking: {25}
```

Fig. 2. Effective contagion containment in a network using a dominating set-based strategy.

2) Contagion Spread Without Blocking: Prior to implementing our blocking strategy, the contagion initiated from a single infected node rapidly spread to four additional nodes 8, 25, 14, 15. The visualization highlights the infected nodes in red, clearly depicting the contagion's reach within the network. This rapid spread underscores the vulnerability of networked systems to contagion and the importance of strategic intervention.

3) Contagion Spread With Blocking: After removing the nodes in the dominating set, the simulation revealed a starkly different outcome. The contagion was notably contained, with only one node 25 becoming infected after the blocking strategy was implemented. The effectiveness of the strategy is evident in the comparative visualization, which shows a substantial reduction in the number of red nodes (infected) within the network.
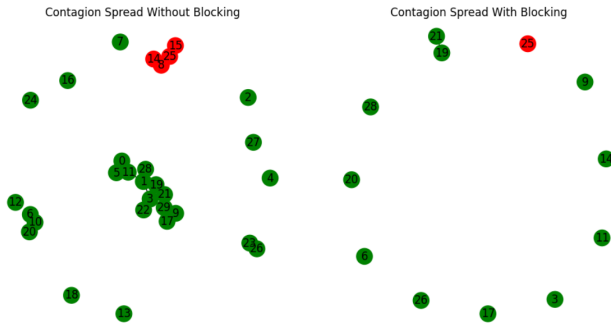
Fig. 3. Contrast in network contagion with and without a dominating set intervention.

Analysis: The results underscore the effectiveness of using dominating sets as a method for controlling contagion spread within a network. The significant reduction in infection spread from four nodes to just one post-blocking is indicative of the potential of this strategy. The visualization provides a clear and intuitive understanding of the network's transformation, facilitating immediate grasp of the strategy's impact.

The dominating set's role is crucial in this context; by removing these nodes, we effectively eliminate key transmission pathways, which could represent critical individuals in a social network or important connections in a communication network.

V. Future Work

The potential for future work stemming from this study is vast and multidimensional. One immediate avenue is to refine the heuristic for identifying dominating sets, exploring optimization algorithms that can cater to specific network characteristics and constraints. Integrating machine learning techniques could also offer adaptive solutions to dynamic networks where contagion patterns evolve over time. Moreover, testing the proposed strategy on empirical data from real-world social networks would validate its practicality and effectiveness in various scenarios, such as viral marketing, public health interventions, and the spread of information or misinformation. Additionally, expanding the study to encompass multi-layered networks and networks with community structures could uncover new insights into complex contagion phenomena. The ultimate goal is to develop robust, scalable strategies that can be deployed in diverse and evolving networked environments.

VI. Conclusion

The research conducted presents a novel approach to mitigating contagion spread within social networks by leveraging the properties of dominating sets. The study's findings offer a promising avenue for enhancing contagion control strategies, which is particularly pertinent in the age of rapid information dissemination and interconnected social systems. Our computational experiments, underpinned by the Erdős–Rényi model, have demonstrated that a dominating set can serve as an effective mechanism for blocking contagions. The heuristic method

employed to identify the dominating set proved to be efficient and effective, as evidenced by the significant reduction in the spread of contagion when the blocking strategy was applied. The visualization of the contagion process, both with and without the implementation of the dominating set strategy, provided clear and intuitive insights into the benefits of this approach.

While the results are encouraging, the scope of the study is subject to the limitations of the model used and the heuristic nature of the dominating set approximation. Future work may expand upon these initial findings by exploring more sophisticated algorithms for dominating set identification and by applying the methodology to more complex and varied network structures. Additionally, real-world validation of the proposed strategy would be an essential step to ascertain its practical applicability and effectiveness in different contexts, such as epidemiology, information security, and beyond.

In conclusion, this research enhances our understanding of network dynamics and introduces a viable method for contagion control that could have significant implications for public health, cybersecurity, and information systems management. It opens up new directions for research and development in social network analysis and contagion mitigation strategies.

References

[1] C. Haythornthwaite, "Social network analysis: An approach and technique for the study of information exchange," Library Information Science Research, vol. 18, no. 4, pp. 323–342, Sep. 1996, doi: https://doi.org/10.1016/s0740-8188(96)90003-1.

[2] "Key Nodes Selection in Controlling Complex Networks via Convex Optimization — IEEE Journals Magazine — IEEE Xplore," ieeexplore.ieee.org. https://ieeexplore.ieee.org/abstract/document/8606422 (accessed Nov. 24, 2023).

[3] Kuhlman, Chris Tuli, Gaurav Swarup, Samarth Marathe, Madhav Ravi, S.. (2013). Blocking Simple and Complex Contagion By Edge Removal. Proceedings - IEEE International Conference on Data Mining, ICDM. 10.1109/ICDM.2013.47.

[4] Sampathkumar, E. Latha, L.. (1994). Set domination in graphs. Journal of Graph Theory. 18. 489 - 495. 10.1002/jgt.3190180507.

[5] A. Dhawan, M. Rink, and A. Dhawan, "Positive Influence Dominating Set generation in social networks," 2015. Accessed: Nov. 24, 2023. [Online].

[6] "Using Dominating Sets to Block Contagions in Social Networks — IEEE Conference Publication — IEEE Xplore," ieeexplore.ieee.org. https://ieeexplore.ieee.org/document/10068610 (accessed Nov. 24, 2023).

[7] C. J. Kuhlman, S. Anil, M. V. Marathe, S. S. Ravi, and D. J. Rosenkrantz, "Inhibiting diffusion of complex contagions in social networks: theoretical and experimental results," Data Mining and Knowledge Discovery, vol. 29, no. 2, pp. 423–465, May 2014, doi: https://doi.org/10.1007/s10618-014-0351-4.

[8] A. K. Ghoshal, N. Das, and S. Das, "Influence of community structure on misinformation containment in online social networks," Knowledge-Based Systems, vol. 213, p. 106693, Feb. 2021, doi: https://doi.org/10.1016/j.knosys.2020.106693.

[9] T. W. Haynes, S. T. Hedetniemi, and P. J. Slater, Fundamentals of Domination in Graphs. Marcel Dekker, 1998.

[10] A. K. Abdul Gafur and S. W. Saputro, "On Locating-Dominating Set of Regular Graphs," Journal of Mathematics, vol. 2021, pp. 1–6, Sep. 2021, doi: https://doi.org/10.1155/2021/8147514.

[11] [1]K. Kayathri and M. Phil, "A STUDY ON DOMINATING SETS," 2019. Accessed: Nov. 24, 2023. [Online]. Available: https://tcarts.in/research/research/kok.pdf

[12] S. Shukla and V. Thakur, "Issue 3 www.jetir.org (ISSN-2349-5162)," JETIR2003225 Journal of Emerging Technologies and Innovative Research, vol. 7, 2020, Accessed: Apr. 05, 2022. [Online]. Available: https://www.jetir.org/papers/JETIR2003225.pdf

[13] [T. Sabarwal and J. Higgins, "Control and Spread of Contagion in Networks," SSRN Electronic Journal, 2021, doi: https://doi.org/10.2139/ssrn.3831245.

[14] J. Tsai, T. H. Nguyen, and M. Tambe, "Security Games for Controlling Contagion," Proceedings of the AAAI Conference on Artificial Intelligence, vol. 26, no. 1, pp. 1464–1470, Sep. 2021, doi: https://doi.org/10.1609/aaai.v26i1.8249.

[15] H. L. Carscadden, C. J. Kuhlman, M. V. Marathe, S. S. Ravi, and D. J. Rosenkrantz, "Techniques for blocking the propagation of two simultaneous contagions over networks using a graph dynamical systems framework," Network Science, vol. 10, no. 3, pp. 234–260, Aug. 2022, doi: https://doi.org/10.1017/nws.2022.18.