

A Memetic Algorithm for Finding Robust and Influential Seeds for Networks under Cascading Failures

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Abstract. How to select a set of nodes with the strongest information spreading capability from a complex network is known as the influence maximization problem. Existing research has mostly focused on structurally stable networks, and the impact of network structural changes on the influence diffusion process is yet to be explored. Simultaneously, network systems are inevitably subject to disturbances or even structural damage during operation, such as cascading failures. To address the robust influence maximization (RIM) problem under cascading failures, this paper investigates the RIM problem caused by link attacks leading to cascading failures. A numerical metric is designed to comprehensively assess the robust influence performance of seeds. For the RIM problem, a memetic algorithm with an ecological niche strategy, termed MA-RIM_{CF-Link}, is designed to find seeds with stable influence, and experiments on synthetic and practical networks validate the competitiveness and effectiveness.

Keywords: complex networks, cascading failure, robustness, influence maximization

1 Introduction

In the past decade, there has been substantial emphasis on the Influence Maximization (IM) problem. This problem involves a network, G , where a propagation model defines how nodes interact within G . Additionally, a constant, K , is employed to specify the desired scale of the seed set, determining the maximal influence range. The significance of IM is evident in various applications, ranging from product marketing to opinion spreading [1].

Kempe *et al.* [2] initially characterized the IM problem as a combinatorial optimization problem, highlighting its NP -hard complexity. They proposed a greedy algorithm, leveraging the Monte Carlo process for influence assessment. While straightforward, this algorithm poses a computational challenge, particularly in its application to large-

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scale networks. Lee *et al.* [3] introduced a rapid evaluation method by considering only potential nodes within the 2-hop radius of seeds.

In the realm of optimization, the IM problem can be cast as selecting an optimal seed set from the network based on specific evaluation criteria. Various optimization solvers offer potential avenues for addressing this challenge. Heuristic-based search algorithms like the hill-climbing algorithm [2] and simulation annealing [4] have been employed for IM problem resolution, albeit with suboptimal search efficiency. Simultaneously, the structural characteristics embedded in networks, such as degree, betweenness coefficient, and association structure [5,6], can offer valuable insights for seed selection. However, these features often grapple with overlapping regions, limiting their performance. Moreover, population-based search methods have been applied to the IM problem with successful outcomes. These include the discrete particle swarm algorithm [7], the Memetic algorithm [8], and the multi-objective algorithm.

Previous studies have predominantly focused on scenarios where the network structure remains static, assuming that the influence propagation media, represented by nodes and links, remain undisturbed throughout the propagation process [9-11]. However, in practical physical network systems, structural perturbations are inevitable due to internal factors, external environmental interferences, and, in some instances, malicious attacks and sabotage. Such disruptions, whether targeting nodes or links, can significantly impact or even paralyze network functionality.

Within the domain of network robustness, there is a growing emphasis on exploring various attack scenarios and analyzing their impact [12-14]. The development of robustness evaluation metrics has furthered our understanding and ability to enhance network resilience. Among the factors contributing to network damage, cascading failures emerge as a prominent failure mode, occurring when specific nodes or links in the network fail, triggering the successive failure of interconnected components, ultimately resulting in the collapse of the entire network [15]. Despite initial forays into the Robust Influence Maximization (RIM) problem considering structural changes, comprehensive investigations remain limited. For instance, while some scholars explored the RIM problem under nodal malicious attacks, others delved into the problem under cascading failures caused by node-based attacks [16-18]. However, cascading failures can also result from link-based attacks, which are often less surveilled and can be paralyzed at a lower cost. Addressing cascading failures caused by link-based attacks involves studying how to assess and determine seeds with robust influential ability throughout the entire system, posing open questions in need of further exploration.

Addressing the limitations of prior research, this work introduces a population-based algorithm, MA-RIM_{CF-Link}, to tackle the IM problem under cascading failures, considering changes in network structure. Utilizing insights from previous studies, a metric is formulated to assess the seed set's influence performance under cascade attacks, guiding the optimization process. The performance and feasibility of MA-RIM_{CF-Link} are demonstrated on both synthetic and practical networks. The Contributions of the work are summarized as follows. 1. The paper investigates the problem of robust influence maximization under cascading failures caused by link failures. It proposes suitable metrics to assess the robustness of seed nodes in this scenario; 2. An effective algorithm is

proposed for finding optimal nodes, validated through experiments on both synthetic and real network data, demonstrating the effectiveness and efficiency.

The remainder is structured as follows: Section 2 introduces the IM and cascading failure. Section 2.3 design a metric for assessing the level of robust influence. Section 3 provides details on the MA-RIM_{CF-Link}. Section 4 conducts experiments on synthetic and practical networks, validating the performance and feasibility of MA-RIM_{CF-Link}. Finally, in Section 5, we draw conclusions and engage in a discussion.

2 Related Work

A network can be modeled as a graph $G = \{\mathbf{V}, \mathbf{E}\}$, where $\mathbf{V} = \{1, 2, \dots, N\}$ denotes the N nodes in the network and $\mathbf{E} = \{e_{ij} \mid i, j \in \mathbf{V} \text{ and } i \neq j\}$ denotes the links between different nodes in the network.

2.1 The Influence Maximization problem

The essence of the IM problem lies in the selection of K nodes from network G to create a seed set S . In the context of the IM problem, two primary challenges emerge: effectively modeling the influence diffusion and assessing the spread range of influence.

Within the diffusion model, crucial elements governing propagation behavior encompass activation probability, link weight, and network multiplicity. A classic model, the independent cascade (IC) model [2], stands out. In this model, activated nodes disseminate influence to their inactivated neighbors through links at each time step. The activation probability (p) is predetermined for each attempt, and successfully activated nodes transition to an active state. If an inactivated node is influenced by multiple activated nodes, each attempt is independent. This process continues until no more nodes become activated, with nodes existing in either activated or inactivated states. The Weight Cascade (WC) model [19] is introduced for weighted networks, where activation probability p is no fixed and determined by the link weight (w_{ij}).

Once the propagation mechanism is identified, the subsequent challenge involves evaluating the performance of the seed set S . The influence level, denoted as $\sigma(S)$, represents the cumulative total of all nodes activated during the propagation process. Traditionally, this is determined through Monte Carlo simulation, a direct but computationally demanding approach, especially for larger networks. To address this, an efficient method relying on hop information [3] has been proposed to approximate the influence performance of S . This method estimates the influence scope within the 2-hop range of the seed nodes and is defined as follows,

$$\hat{\sigma}(S) = \sum_{s \in S} \hat{\sigma}\{s\} - \sum_{s \in S} \sum_{c \in C_s \cap S} p(s, c)(\sigma_c^1 - p(c, s)) - \chi \quad (1)$$

Where $\sigma(s)$ represents the 2-hop influence of seed s . C_s is the connected neighbors set of seed s , $p(i, j)$ is the activation probability between node i and j , and $\sigma_1 c$ is the 1-hop range of node c . χ denotes the duplicated influence generated by activated nodes, as

$$\chi = \sum_{s \in S} \sum_{c \in C/S} \sum_{d \in C \cap S/\{s\}} p(s, c) p(c, d) \quad (1)$$

In the context of the IM problem, the calculation of seed set influence often presupposes a fully connected network, which is an idealized scenario. Nevertheless, practical environments are characterized by networks vulnerable to external disruptions, including potential malicious attacks, resulting in network incompleteness. The RIM problem is concerned with selecting K nodes from a network to achieve optimal influence performance, even in the presence of structural damages to the network [17,18]. Notably, Wang *et al.* [8] tackled the RIM problem under network structural disruptions and introduced a metric for assessing the robust information capability of seeds.

2.2 The Cascading Failure Model

In the context of cascading failures, when certain edges in the network fail, the disturbance tends to propagate to adjacent components [20]. The detailed process of cascading failures is outlined as follows.

Step 1: The number of failures t as 0. The initial load is correlated with the degree of the linked nodes. where k_i, k_j is the degree of node i, j , and α is a coefficient. The capacity of each edge in the network is calculated according to its load, as $C_{ij} = \beta * L_{0ij}$, where β is the tolerance parameter.

Step 2: t is updated to $t + 1$. The edge with the highest load in the network is selected as the failure edge.

Step 3: The load of the failed link e_{st} is propagated to all linked links, and the load carried by adjacent links is denoted as

$$\Delta L_{sm} = L_{st} / \left(\sum_{p \in \Gamma_s} L_{sp} + \sum_{q \in \Gamma_t} L_{qt} \right) \quad (2)$$

where Γ_s and Γ_t represent the sets of the neighboring nodes of nodes s and t . If the link e_{sm} receives the additional load that causes its total load to exceed its capacity, then the link is considered as under failure, becoming a failure link, and continue to propagate its load to the neighboring components.

Step 4: The failure process gets terminated if the network is totally collapsed, otherwise the process returns Step 2.

2.3 The Performance Metric

The spread of information between nodes doesn't depend on the integrity of entire system. Instead, it propagates influence through connections between nodes within localized regions. Even seeds within compromised network subcomponents can have an impact, activating more nodes. Considering eq. (1) as references, a metric named R_{SL-cf} is proposed to evaluate the robust information of seeds under cascading failures, as

$$R_{SL-cf} = \frac{1}{M \times Per} \sum_{p=1}^{M \times Per} \hat{\sigma}(S | p) \quad (3)$$

where $M \times Per$ is the total number of cascading failures occurred, and $\hat{\sigma}(S | p)$ is the influence level of seed set S after the p -th cascading failure.

3 MA-RIM_{CF-Link}

3.1 The Framework.

Drawing on the established MA framework, MA-RIM_{CF-Link} combines both population-based and individual-based exploration strategies, integrating a local search operator to enhance search capabilities. Borrowing from the principles of niche memetic algorithm [17], the niche strategy is employed to cluster individuals with similar characteristics, facilitating the exploitation of more individual information.

The execution of MA-RIM_{CF-Link} follows a structured process. Initially, the initialization operator generates NP individuals with an expectation of a random distribution. The population is then divided into clusters, acting as mating pools, taking into account the performance of these individuals. Subsequently, the crossover operator is employed within and among mating pools, expanding the population with NP new individuals. The mutation operator introduces stochastic elements into these new individuals. The population deduplication operation eliminates duplicate individuals, and the population alignment operation generates new individuals to fill vacant regions. The local search operator is applied to attain local optimal solutions using existing optimal information. After each iteration, the selection operator picks superior individuals for the next generation and updates the mating pool. The algorithm concludes and produces the best seed set as the optimal solution upon reaching the termination condition. The framework of MA-RIM_{CF-Link} is outlined in **Algorithm 1**.

Algorithm 1: MA-RIM_{CF-Link}

Input:

G : Inputted network; K : Size of seed set;
 NP : Size of initial population; $NicheSize$: Size of niche;
 p_c : Crossover probability; p_m : Mutation probability;
 p_l : Local search probability; $MaxGen$: Maximal genetic iterations;

Output:

S^* : The best-find seed set;

$P_0 = \{S_1, S_2, \dots, S_K\} \leftarrow Initialization(G, K, NP);$ $g \leftarrow 0;$

While $g < MaxGen$

 Generate the *MatingPool* with the *Partition*($P_g, NicheSize$);

 Generate the offspring population \mathbf{P} with the crossover operator
 ($p_c, MatingPool$);

 Update \mathbf{P} with the mutation operator (p_m, \mathbf{P});

 Update \mathbf{P} with the local search operator (p_l, \mathbf{P});

 Get the \mathbf{P}_{g+1} with the selection operator ($\mathbf{P}, MatingPool$);

 Update the S^* ; $g = g + 1;$

end while

Output the S^* ;

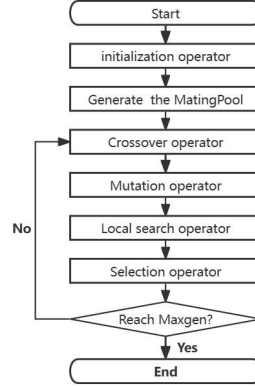


Fig. 1. The main flowchart of MA-RIM_{CF-Link}

3.2 The genetic operators

Initialization and the population partition strategy.

The population-based optimization algorithm necessitates an initialization operation to create the initial population, denoted as P_0 , based on the input network G . For each individual P_i in P_0 , K nodes are randomly chosen as seeds from the network G , constituting the gene information of that particular individual. The validity of these nodes and no duplicates seeds is crucial, denoted as $P_i = \{s_1, s_2, \dots, s_K\}$, where s_m and s_n (m and n within $[0, K-1]$) are distinct. Following the initialization operator, NP individuals with random characteristics are generated, establishing the initial population.

Implementing the population partition strategy involves regrouping individuals into mating pools based on their fitness. Individuals within a population are categorized into niches based on their fitness, with the tendency for similar individuals to be placed in the same niche, which has a fixed size. The strategy is detailed as follows: the individual with the highest fitness is chosen from the ungrouped individuals to lead niche $Niche_i$. Subsequently, individuals with the highest similarity are selected from the remaining pool to join $Niche_i$ in descending order of similarity until the niche reaches its predefined size, $NicheSize$. This process repeats until all individuals are allocated to their respective niches. Given the discrete nature of genes in an individual and their order insignificance to fitness, seed intersection among individuals is used for similarity assessment, denoted as $similarity(P_i, P_j) = (P_i \cap P_j) / K$.

Crossover operator and Mutation operator.

The crossover operator facilitates the exchange of partial gene segments in two individuals, while the mutation operator introduces genes at randomly-selected positions.

The specific process of crossover is outlined as follows: treating the seeds as a chromosome, with the K nodes in the seeds representing the K gene segments on the chromosome. Two chromosomes, denoted as $x = \{x_1, x_2, \dots, x_K\}$ and $y = \{y_1, y_2, \dots, y_K\}$, are

randomly selected. A crossover point, pos ($1 \leq pos \leq K$), is then randomly chosen. The gene fragment before the crossover point remains unchanged, while genes after the crossover point (including the crossover point) swap positions. If the exchanged gene duplicates existing genes, new genes are randomly generated at the duplicated gene's position for no repeated genes on chromosome. Final chromosomes are $x' = \{x_1, x_2, \dots, x_{pos-1}, y_{pos}, y_{pos+1}, \dots, y_K\}$ and $y' = \{y_1, y_2, \dots, y_{pos-1}, x_{pos}, x_{pos+1}, \dots, x_K\}$.

The mutation operator is executed as follows: a chromosome $x = \{x_1, x_2, \dots, x_K\}$ is randomly chosen, and a mutation point, pos ($1 \leq pos \leq K$), is randomly generated. The gene x_{pos} at the original mutation point is replaced by the newly generated gene y , ensuring that the new gene does not duplicate any existing genes on the chromosome. This results in a mutated chromosome, $x' = \{x_1, x_2, \dots, x_{pos-1}, y, x_{pos+1}, \dots, x_K\}$.

The local search operator.

The local search operator is deployed to explore the local neighborhoods of individuals, enhancing the overall performance of the population. While a larger neighborhood space for local search enhances overall algorithm optimization, it also comes at the cost of increased computational resources. To strike a balance between optimization and computational efficiency, this work confines the local search neighborhood to the 2-hop domain. Specifically, it iteratively searches for neighboring nodes of a given node, and with a low probability, explores the 2-hop neighborhood.

The selection operator.

Advantageous genetic traits are more likely to persist in the next generation, thereby enhancing the overall competitiveness of the population. The roulette wheel selection strategy is chosen, where an individual's fitness serves as the selection criterion. Each individual has a certain probability of entering the next population through this process, ensuring population diversity. However, this simple principle also introduces the risk of discarding the optimal individual. To mitigate this, the optimal individual is preserved by elite retention to prevent degradation.

Complexity analysis.

The MA-RIM_{CF-Link} algorithm consists of two main parts: initialization phase and genetic iteration phase. The initialization phase is responsible for generating candidate seeds and is executed only once, with a complexity of $O(N)$. On the other hand, the genetic iteration phase needs to be repeated. The complexity of each iteration is analyzed as follows: in the crossover operator, generating a new individual from two individuals has a complexity of $O(P \times K)$. In the mutation operator, iterating through each individual has a complexity of $O(P \times K)$. In the global search operator, each individual has the opportunity to update genes with a complexity of $O(P \times K \times \langle k \rangle)$. In the local search operator, iterating through the search domain of individuals, where the network's average degree is $\langle k \rangle$, has a complexity of $O(T \times P \times K \times \langle k \rangle)$. In the selection operator, the complexity is $O(P)$. The entire genetic iteration process needs to be repeated $MaxGen$ times, resulting in a complexity upper limit of $O(MaxGen \times P \times K \times \langle k \rangle)$.

4 Experimental Results.

The experimental evaluation employs synthetic networks, specifically Scale-Free (SF), Erdős-Rényi (ER), and Watts-Strogatz (WS) networks. These synthetic networks are created with sizes of $N=200$ and $N=500$, average degree $\langle k \rangle = 4$. The outcomes of experiments conducted with algorithms are presented in [4] and [16].

Table 1. R_{SL-cf} of optimal seed sets are acquired for synthetic networks comprising 200 nodes, and the results represent averages over 5 independent realizations. Employing the results from MA-RIM_{CF-Link} as a benchmark. Symbols like "-" signify that the compared algorithm is less effective than MA-RIM_{CF-Link}, "+" indicates that the compared algorithm surpasses MA-RIM_{CF-Link}, and "≈" denotes that the two algorithms exhibit no significant difference.

Network	K	MA-RIM _{CF-Link}	GA	MA	SA
SF	10	11.09	11.09(≈)	11.09(≈)	10.85(-)
	20	21.72	21.69(≈)	21.71(≈)	21.37(-)
	30	32.11	31.98(-)	32.06(-)	31.62(-)
ER	10	10.89	10.89(≈)	10.89(≈)	10.81(-)
	20	21.68	21.63(-)	21.66(≈)	21.42(-)
	30	32.36	32.28(-)	32.32(-)	31.95(-)
WS	10	10.55	10.55(≈)	10.55(≈)	10.48(-)
	20	21.03	20.95(-)	21.00(≈)	20.83(-)
	30	31.46	31.36(-)	31.41(-)	31.18(-)

Table 2. Similar experiments are conducted on networks with $N=500$.

Network	K	MA-RIM _{CF-Link}	GA	MA	SA
SF	10	11.81	11.81(≈)	11.81(≈)	11.01(-)
	20	22.95	22.75(-)	22.94(≈)	21.64(-)
	30	33.77	33.14(-)	33.72(-)	31.80(-)
ER	10	12.14	12.11(-)	12.14(≈)	11.95(-)
	20	24.06	23.92(-)	24.04(≈)	23.56(-)
	30	35.83	35.65(-)	35.78(-)	34.93(-)
WS	10	10.60	10.59(≈)	10.60(≈)	10.48(-)
	20	21.14	21.10(-)	21.12(≈)	20.96(-)
	30	31.63	31.56(-)	31.59(-)	31.32(-)

From the presented numerical outcomes, it is evident that the seed sets derived from MA-RIM_{CF-Link} exhibit superior R_{SL-cf} values in comparison to other algorithms. These seed sets demonstrate sustained information propagation capabilities, even in the face of cascading failures within the network. Notably, SA [4] lags considerably behind

other population-based optimization algorithms. In scenarios where K is small, such as $K=10$, all algorithms can secure commendable optimal solutions. This stems from the fact that nodes with robust information dissemination capabilities have higher degrees in networks, enabling algorithms to swiftly obtain better solutions in such cases. However, as K increases, the pool of high-degree nodes becomes insufficient for the set size, the differences among algorithms become more pronounced.

To begin with, GA exhibits notably inferior performance on SF and ER networks compared to other methods. This can be rationalized by the fact that SF networks adhere to a power-law degree distribution, concentrating most link connections in a small number of nodes. GA, relying solely on random search, struggles to extract valuable information from these critical nodes, especially when the majority of nodes have minimal connections. Similarly, ER networks present similar challenges due to their uniform degree distributions, making it difficult for GA, operating within limited computational resources, to attain the global optimal solution.

Contrastingly, the performance differences among the remaining three algorithms are less pronounced in terms of R_{SL-cf} . However, the distinctions become more apparent in the iteration process, as will be elucidated later. It's noteworthy that even in complex scenarios, MA-RIM_{CF-Link} consistently outperforms other solvers. The results presented in **Fig. 2** and **Fig. 3** underscore that MA-RIM_{CF-Link} achieves substantial and consistent optimization outcomes across various types of synthetic networks, demonstrating its versatility in handling networks with different properties.

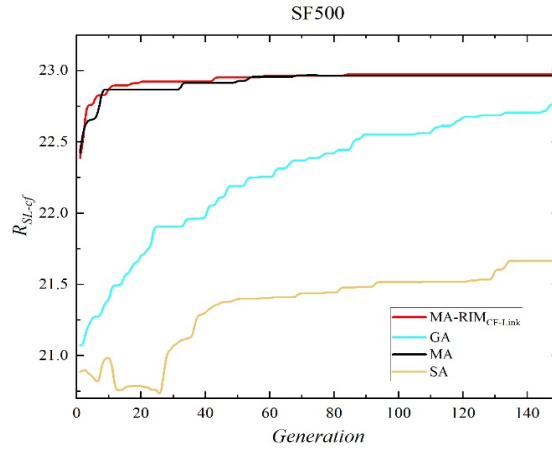


Fig. 2. The convergence curves for R_{SL-cf} of optimal seed set in population.

Additionally, we compared the convergence process of the algorithms, i.e., the variation in the fitness of the best individual in each generation under the guidance of the four optimization algorithms. As shown in **Fig. 2.**, taking the SF network with 500 nodes as an example, it is evident that the optimization performance of the SA algorithm is the poorest. This is because, during the optimization process, SA only compares the quality between two solutions, while the other algorithms are population-based. In

each iteration, they identify the optimal solution from a given population size. Secondly, GA is notably inferior to MA, mainly because GA lacks a local search operator. The local search operator is used to explore the optimal solution within a certain range, significantly enhancing population performance. Finally, it can be observed that the optimization performance of MA and MA-RIM_{CF-Link} is essentially the same, but MA converges faster than MA, reaching the peak with fewer iterations.

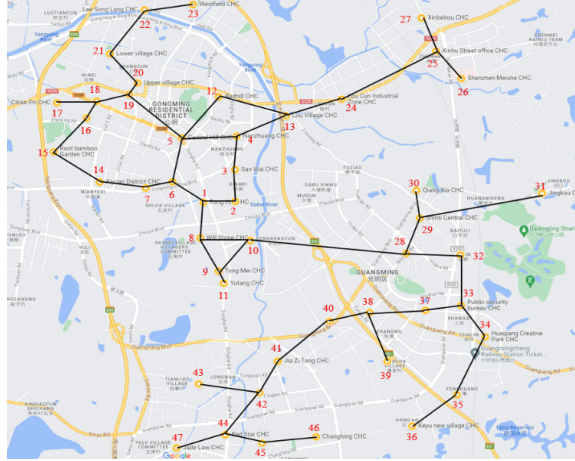


Fig. 3. Healthcare network in *Guangming* District, Shenzhen, consisting of 47 nodes and 50 edges.

We conducted experiments on the collected data, as shown in **Fig. 3.**, which is the distribution map of community health service centers in *Guangming* District, Shenzhen. We selected 5 seed nodes from this network. GA, MA, and MA-RIM_{CF-Link} selected the same nodes (1, 19, 28, 33, 42). These nodes form a core part of the community structure, indicating the effectiveness of the proposed algorithm. For instance, in the event of a significant infectious disease outbreak, these community healthcare centers can consistently and stably radiate their influence.

5 Conclusions

This study addresses the challenge of robust influence maximization in the presence of cascading failures. We introduce a comprehensive metric, R_{SL-cf} , to evaluate the robust influence capability of a given seed set. Using this metric, the seed determination problem is formulated as an optimization task, and we propose a Memetic Algorithm with niche strategy, denoted as MA-RIM_{CF-Link}, to identify robust and influential seeds. The efficacy and efficiency of the proposed algorithm are assessed through comparisons with existing approaches. MA-RIM_{CF-Link} exhibits superior optimization results and convergence capabilities compared to other methods, demonstrating scalability and generality.

In the context of robust influence maximization against structural failures, cascading failures represent only one form of damage. Investigating other types of failure modes and even the interplay of multiple failure modes holds significance for practical applications [12]. Additionally, relying solely on single-layer networks might not adequately capture the dynamics of intricate systems. Therefore, extending the study to multiplex networks is a promising avenue for further investigation [8].

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