Robust Structural Balance in Signed Networks Using a Multiobjective Evolutionary Algorithm

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Abstract—The aim of network structural balance is to find proper partitions of nodes that guarantee equilibrium in the system, which has attracted considerable attention in recent decades. Most of existing studies focus on reducing imbalanced components in complex networks without considering the tolerance of these balanced networks against attacks and failures. However, as indicated by some recent studies, the robustness of structurally balanced networks is also important in real applications, which should be emphasized in balancing processes. Currently, it remains challenging to define suitable robustness measures for signed networks, and few performance enhancement strategies have been designed. In this paper, two measures are designed to numerically evaluate the robustness of structurally balanced networks. Furthermore, the simultaneous enhancement on these two measures is modeled as a multiobjective optimization problem, and a multiobjective evolutionary

algorithm, MOEA/D-RSB, is developed to successfully solve this problem. Experiments on synthetic and real-world networks demonstrate the good performance of MOEA/D-RSB in finding robust balanced candidates. In addition, the features of partitions with different robustness performances are analyzed to show the impact of different balancing strategies on network robustness. The obtained results are valuable in dealing with some problems arising in social and natural dynamics.

I. Introduction

he complex network, which exists widely in nature, society, and infrastructures, plays a crucial role in daily life. With an intuitive representation of relations among nodal members, network models provide an effective method to analyze the dynamics and discipline of complex systems [1], [2]. In such an age of information and technology, the utilization of social media network platforms,

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such as Facebook, Twitter, and WeChat, boosts the application of network theory in modern society [3]. Focusing on the interaction status between members in a network, friendly or hostile relationships can be found in a number of networked systems [4], [5], and the analysis of multiple relations is quite valuable in many

areas, including bioinformatics and sociology. Signed networks provide a direct reflection of these relations through diverse types of links, which have been greatly emphasized recently [6], [7].

Briefly, links in a signed network are labeled with attributive information between the attached nodes, but links in plain networks do not maintain such information. An illustrative example of a signed network can be found in Fig. 1. Given a network with multiple relationships, the excavation of attributive information is an important process to equilibrate components in the whole system and build a balanced status. Several properties of signed networks have been found and summarized to resolve this problem, such as the community structure [2], [6], [8] and the structural balance [4], [5], [9], [10]. In terms of allocating communities, the partitions of nodes reflect their potential functional clusters, and the equilibrium is expected to be held within communities. Currently, the design of effective and efficient methods to allocate members in different types of networked systems is still a challenge. In [10], the structural balance theory was proposed based on the relational phenotype presented in the social psychology field [10] and extended into a generalized version by the graph theory [11]. As defined in [11], a network is generally balanced if it can be separated into several clusters, where nodes are positively connected inside clusters and negatively connected with those in other clusters. This theory explains the features of balanced structures, which reflects the origin of conflicts in social networks.

On the basis of the balance theory, a great stream of literature has investigated how to compute the imbalance of networked systems and transform them into balanced ones. Ma et al. designed a weight-based measure to numerically evaluate the cost for balance transformation [12]. Under the guidance of this measure, a memetic algorithm has also been developed to search for a nodal cluster allocation with a lower transformation cost. Considering that nodes may also have attribute assignments in some circumstances, Du et al. indicated that the proper sign change of both nodes and edges can make a fully signed network become balanced [5]. They also extended the work on reversing the structural balance efficiently through changing node attributes [13]. In addition, the structural balance has been applied in some other fields such as sign prediction [14] as well. These studies further reveal the evolution process of imbalanced systems and may help to alleviate some intractable social dilemmas, such as religious conflicts and psychological bias. On the other hand, regarding a networked system, the invulnerability or robustness of its structure is extremely important. Networks, which are exposed to

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> complicated environments, may suffer from attacks and errors, thus leading to great losses for human beings [15]-[17]. As a result, great effort has been devoted to defining network robustness and designing corresponding enhancement strategies. Several robustness measures have been proposed in [18]-[20]. A variety of optimizing strategies, such as evolutionary computation [16], heuristic searching [18], and information disturbance [19], were designed and successfully solved the network robustness enhancement task.

> However, for the signed network that gives an intuitive representation of multiple relations arising in sociology and biology, most existing work focused on the balance transformation problem. Few studies have investigated the robustness of the structure-balanced network. Generally, the equilibrium exists inter- and intra-clusters in a balanced network, and the maintenance of such a status is decisive to its functionality. In detail, the cooperative or friendly connections inside clusters are necessary to guarantee the affiliation relation. Meanwhile, since criticism and competition are indispensable in building a healthy social environment, competitive or hostile connections between clusters are also inevitable in a system. From a global view, these connections represent interactions between different members and are vital for sustaining the equilibrium. Once structural failures occur, especially under intentional attacks, these connections tend to become damaged and impact the balance of networks. Therefore, a method that mitigates the negative influence of losing balance-related connections on the whole system or enhances the robustness of balanced networks against potential structural perturbations is important. The robustness of signed networks has broad values in some related fields including social dynamical analysis [20], [21] and ecosystems protection [22]. Meanwhile, communities can be found in a balanced signed network [4], [6], [9], and these closely connected clusters may represent collaborations or alliances among nodes. The resistance of communities against structural failures is meaningful to the whole system

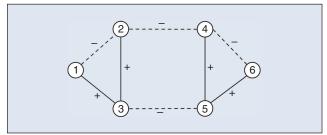


FIGURE 1 An illustrative signed network. The solid links represent positive correlations between nodes, and the dashed links represent negative correlations between nodes.

[23], [24]. Considering these potential application scenarios, this article aims to examine the design of robustness evaluation metrics for structurally balanced networks.

Therefore, we manage to evaluate the robustness of balanced networks from the perspective of structural information. To the best of our knowledge, this is the first attempt to numerically define the robustness of balanced networks. Two measures are designed to estimate the inter-cluster robustness and the intra-cluster robustness, respectively. Then, the correlation between these two measures was verified through experiments. Furthermore, to reach the goal of robust structural balance (RSB) in signed networks, a multiobjective evolutionary algorithm based on MOEA/D [25], termed MOEA/D-RSB, was developed to search for a series of cluster candidates and optimize both of the robustness measures. The experimental results on synthetic and real-world network data validate the effectiveness of MOEA/D-RSB.

Based on existing studies, several improvements have been made in MOEA/D-RSB to solve the RSB problem. First, different from the random population generation strategy in [4], [12], [26], an objective-directed initialization strategy has been designed to generate potential candidates for following search operators, which contributes to the convergence of the algorithm. Furthermore, the neighbors of individuals for making the crossover are determined based on weight vectors, which are relatively independent of the genetic information in MOEA/D [25]. However, the neighbors are selected based on the chromosome information in MOEA/ D-RSB, i.e., the partition of nodes, and individuals with larger partition differences tend to be chosen as neighbors. This operation improves the efficiency of the crossover operator. Moreover, many existing studies [5], [12], [26], [27] only considered the partition information of nodes in local learning procedures, whereas in MOEA/D-RSB, a two-step local search operation has been designed to perform the local refinements based on the partition information of both nodes and clusters. This operator further improves the search ability of MOEA/D-RSB.

Our contributions to the complex network field are summarized as follows. First, different from the existing robustness measures in [18]–[20], we intend to evaluate the robustness of signed networks in two separate processes. The stabilities of both friendly and hostile clusters are considered to reflect the overall robustness of the system. Then, traditional structural balance methods [4], [12] have been shown to be less effective on enhancing the robustness of signed networks, and the designed MOEA/D-RSB shows competitive performance in solving this problem. Finally, a series of candidates with different balance emphases can be obtained in the optimization process; these candidates may provide possible solutions to the dilemmas indicated in [20]–[22].

The rest of this paper is organized as follows: the related work on the structural balance and robustness evaluation is reviewed in Section II. The design of two robustness metrics for structural balance and their correlational study are shown in Section III. Section IV depicts the details of the proposed algorithm MOEA/D-RSB, and the corresponding experimental results are reported in Section V. Finally, Section VI summarizes the work in this paper.

II. Related Work

A signed network can be represented as a graph $G = (\mathbf{V}, \mathbf{E})$, where $\mathbf{V} = \{1, 2, ..., N\}$ is the set of N vertices and $\mathbf{E} = \{e_{ij} \mid i, j \in \mathbf{V}\}$ is the set of M links. The value of e_{ij} can be either +1 or -1. $e_{ij} = +1$ denotes a positive relationship between nodes i and j, and $e_{ij} = -1$ denotes a negative relationship. A cluster partition $S = \{s_1, s_2, ..., s_N\}$ is expected to be generated during the balancing process, where $s_i = k \in [1, N]$ (i = 1, 2, ..., N) represents the partition of node i in the network.

A. Structural Balance of Signed Networks

In [10], the definition of structural balance was given as follows: "A general signed network is balanced when all of its triangles have an even number of negative edges." This triangle theory explains the origin of imbalance in social networks and lays the basis for structural balance. Following this definition, an energy function was proposed in [28] to evaluate the imbalance in complete signed networks through recording the number of imbalanced edges. Furthermore, considering that complete signed networks only have two clusters, which are not common in reality, an improved version of energy function h was designed in [12] to deal with general networks, defined as follows:

$$h = \sum_{i,j \in \mathbf{V} \text{ and } i \neq j} \frac{1 - e_{ij} \Theta\left(s_i, s_j\right)}{2} \tag{1}$$

where $e_{ij} \in \{+1, -1\}$ is the sign of this edge, $\Theta(s_i, s_j)$ is a sign function whose value is 1 when $s_i = s_j$, or -1 when $s_i \neq s_j$. s_i is the cluster assignment of node i, and the range for s_i is [1, N].

In essence, h records the number of negative intra-cluster edges and the number of positive inter-cluster edges, and it can be expressed as follows [12]:

$$h = \sum_{i,j \in \mathbf{V} \text{ and } s_i \neq s_j} \left[\frac{1 - e_{ij} \Theta(s_i, s_j)}{2} \right]$$

$$+ \sum_{m,n \in \mathbf{V} \text{ and } s_m = s_n} \left[\frac{1 - e_{mn} \Theta(s_m, s_n)}{2} \right]$$

$$= \sum_{i,j \in \mathbf{V} \text{ and } s_i \neq s_j} \left| e_{ij}^+ \right| / 2 + \sum_{m,n \in \mathbf{V} \text{ and } s_m = s_n} \left| e_{mn}^- \right| / 2$$
(2)

where e_{ij}^{\dagger} denotes the set of positive edges inter-clusters, and e_{mn}^{\dagger} denotes that of negative edges intra-cluster.

Based on the aforementioned structural balance metrics, a variety of optimization techniques have been devoted to search for rational cluster partitions in networks. Combined with community allocation information, some community-related methods show celerity in finding possible cluster candidates with similar attributes [6], [29]. These methods mainly take the global structural information into account and can output the

results in a short time; however, they are easy to trap in local optima [26] because little concern is given to local features of the network. Methods based on evolutionary computation, which can divide networks with more rationality, are widely applied in solving the structural balance problem. Some single objective [5], [12], [27] optimization algorithms have been designed to search for the best partition from arbitrary initializations. With better utilization of structural information, such methods have shown good results in balancing networks. Furthermore, some multiobjective optimization algorithms [4], [26] have been proved to be effective, and more balancing choices for a specific network can be provided, which contribute to further analyses on balanced networks. In addition, another way to reduce the imbalance in networks is to attribute signs from different layers [29], [30]; this multiplex information compression strategy may help in the design of topologies and the prediction of dynamical changes.

B. Network Robustness and Robustness Measures

For a networked system, the resistance against attacks and errors is one of the most important functionalities. There has been much progress in evaluating the robustness of networks from different types of structural perspectives. Focusing on the connection matrix of networks, the eigenvalue of Laplacian matrices presents the impact of topological changes on the connectivity [31]. The graph theory is another method to understand the functionality of networks. The critical removal fraction of nodes (links) to make a network malfunction was designed in [17] based on the percolation threshold. Considering that a complete disintegration is unusual in real scenarios, the literature [18] pointed out that the robustness measure should be feasible when part of a network maintains its integrity after being attacked, and a measure R has been designed to record the change of the largest connected component under nodal failures. The extension of R into link-based attacks was proposed in [32], i.e., R_l . The details of R and R_l can be found in the Supplementary Materials.¹

These numerical measures, on one hand, can work as comparison criteria in selecting better networks. On the other hand, they can provide the guidance for optimization processes. Faced with the robustness enhancement challenge in modern networked systems, much attention has been paid to designing valid techniques for optimizing networks. One possible method is to adjust the properties of networks with purpose to improve their performances, which has been shown to be effective in some recent studies [19], [33]. Another popular method is to rewire the topology of networks and search for better connection types. In [18], a greedy algorithm was proposed to mitigate the damage caused by malicious attacks on networks. Population-based search strategies were later emphasized to further promote optimization results. For example, a multiagent genetic algorithm was designed in [34] to improve the tolerance of networks against cascading failures and malicious attacks. Several

¹Supplementary materials are available at https://www.researchgate.net/publication/336363660 multiobjective optimization algorithms have been developed to deal with multiple performance improvement tasks on networks, and a trade-off optimization was reached between different robustness measures [16], [35], [36]. A series of potential solutions can be generated in the optimizing process.

III. The Robustness of Structural-Balanced Networks

As indicated in [19]-[21], the resistance against potential damages of balanced networks is of significance in realistic scenarios, but the design of proper measures remains to be solved. Traditionally, the robustness of common networked systems is defined as the ability to withstand structural failures [16], [18], [32]. However, these existing measures cannot be directly applied to evaluate the robustness of signed networks. First, the links in signed networks are labeled with correlative relation information between the attached nodes. Those cooperative (friendly) connections inside clusters and competitive (hostile) connections between clusters tend to sustain the equilibrium of the whole system, and these two types of links can be analyzed independently [26] to reflect the overall performance of a balanced network. The measures in Eqs. (S1) and (S2) of the Supplementary Materials only consider the structural connection information, and these measures are incomplete to handle signed networks where both the connection information and attributive information can be found. Second, distinct cluster partitions can be detected in balanced networks, and cooperative links are expected to be located intra clusters, while those competitive ones are expected to be located inter cluster. Those imbalanced links, i.e., competitive intracluster connections and cooperative inter-cluster connections, should not be considered as contributive to networks' functionality, because they are superfluous for balancing networks. Moreover, for a specific signed network, too many imbalanced links are adverse to the normal function of the system, and a well-balanced network should maintain fewer imbalanced links. Existing measures omit the differences in links and may not give a good description of the stability of balanced networks. Based on these concerns, the direct utilization of existing robustness measures on signed networks seems to be careless.

Considering the features of signed networks, both the connectivity and the balancing status are important to the integrity of this system. As shown in [26], independent dispositions on intra-cluster and inter-cluster balanced links can analyze the balance status of a given signed network. Meanwhile, the linkbased structural destruction has been proven to be effective in influencing the connectivity [32] and the functional distribution [24] of a system. Based on these related studies, the robustness of structural-balanced networks can be divided into two parts, namely, the intra-cluster part and inter-cluster part, and the integrity of the network can be evaluated separately.

In terms of the intra-cluster robustness, those negative or hostile links located inside clusters should be omitted. These links are redundant in the expected condition (fully positive

Both the connectivity and the balance status of signed networks should be considered in the robustness evaluation process.

inside the cluster) and contribute little to the connectivity. Then, all the positive or friendly links inside clusters are selected and sorted in the order of a certain importance measure. The edge degree [32] is used here to evaluate the importance. After obtaining the rank of these valid links, the signs of links are neglected to transform the network into a plain one. Then, these edges are removed in order and the fraction of the largest connected component is recorded. The cumulative value is the output of this robustness metric. The details of the measure are defined as follows:

$$R_{\text{intra}} = \frac{1}{M} \sum_{e \in \mathbf{E}_{\text{posi}}} s(e) \tag{3}$$

where M is the total number of links in the network, and \mathbf{E}_{posi} is the set of positive links located inside clusters, and the links are ranked according to their importance. Here, the importance of an edge e_{ii} can be defined by multiplying the degree of attached nodes, i.e., edge degree [32] as degree (i) \times degree (j). s(e) is the fraction of the largest connected component after edge e is removed. It should be noted is that all the negative links inside clusters are removed before the evaluation process. 1/M is the normalization factor to make networks with different sizes of positive/negative links comparable.

This measure evaluates the tolerance of balanced networks when losing cooperative connections inside clusters while keeping the competitive connections steady. The total number of links is taken as the normalization factor. In this way, more balanced positive links, which represent a potentially better balance status, tend to result in a higher robustness value, and both the connectivity and balancing status are considered in the evaluation process. At the same time, clusters with denser structures are estimated to perform better in the evaluation process, which can resist more failures inside groups. Such groups may also show good performance in biological competitions and social activities [9], [11], [22].

For the inter-cluster robustness, the positive or friendly links between different clusters should be removed first. Considering these links are taken as redundant in the expected condition (fully negative between clusters), they make little sense to the connectivity of inter-clusters. Then, all the negative or hostile links between clusters are selected and sorted in the order based on the same importance measure in R_{intra} . Then, the network is transformed into a plain one, and the fractions of the largest connected component in the process of removing these ordered links are recorded. The details of the measure are defined as follows:

$$R_{\text{inter}} = \frac{1}{M} \sum_{e \in \mathbf{F}_{\text{norm}}} s(e) \tag{4}$$

where \mathbf{E}_{nega} is the set of negative links located between clusters, where links here are ranked according to their importance, i.e., the edge degree. M and s(e) are the same as those in Eq. (3). Also, all the positive links between clusters are removed before the evaluation process.

1/M is the normalization factor.

Different from R_{intra} , this measure focuses on the tolerance of balanced networks against losing competitive connections between clusters. Meanwhile, the cooperative connections keep unchanged. Similarly, the total number of links acts as the normalization factor, which means that more balanced negative links make for better results. This measure also considers both the connectivity and balancing status in the evaluation process. Meanwhile, if a partition receives enough attention in building competition between clusters, this structural balancing candidate is likely to achieve a good evaluation result. In some realistic scenarios, the competition between system members is essential to the equilibrium, and a coordinating relational distribution contributes to the good performance in evolutionary games [35], [36] and natural competitions [9].

The two measures supplement to each other, and both of them are necessary to evaluate the overall robustness of a structural-balanced network. Both the connectivity and the balance status of signed networks are considered. The adopted accumulation mechanism, as in [24], [32], guarantees valid records regarding the connectivity of networks. The independent analyses of the inter-cluster and intra-cluster links, as in [26], obtain their balance status. Different partitions have different impacts on the robustness of signed networks, because the number of positive links between clusters and that of negative links inside clusters may vary. This phenomenon may cause differences in the network structure for the robustness evaluation processes. As an example, two possible partitions and corresponding network structures for the robustness evaluation on the toy network in Fig. 1 are given in Fig. 2. The partition in Fig. 2(a) concentrates on reducing the number of positive links between clusters, and that in Fig. 2(b) focuses on reducing the number of negative links inside clusters. To achieve the goal of balancing the structure, two different partitions can be found in the figure, and these partitions cause structural differences in the robustness evaluation process, which reveals the effect of partition strategies on the robustness of signed networks. The overall characteristics of signed networks are considered when evaluating their robustness. These measures evaluate the performance of a certain cluster partition in numerical form, which can further guide the optimization procedure.

The negatively correlative relation between these two robustness measures has been validated on LFR networks [37] through experiments, and the details can be found in the Supplementary Materials, including Algorithm S1, Fig. S1 and Table S1. A simultaneous enhancement is difficult to achieve for the two measures. Single-objective optimization techniques seem to be less efficient for optimizing the robustness of balanced networks because only one result can be obtained in a search round and only one measure can be maximized. Therefore, a multiobjective optimization method is more suitable to consider both of the measures and deal with the multiobjective optimization problem (MOP) between R_{inter} and Rintra. Meanwhile, a series of different candidates in the solution space can be generated to provide diversified solutions to the MOP.

IV. MOEA/D-RSB

The evolutionary algorithms (EAs) have been proved to be effective in solving different types of MOPs in past decades [4], [16], [25], [26], [35], [36]. A multiobjective EA is developed based on the framework of MOEA/D [25] in this study to optimize R_{inter} and R_{intra} of the signed networks simultaneously, termed MOEA/D-RSB. In this algorithm, each chromosome C_i in the population represents a certain cluster partition in the form of an integer vector with N dimensions (N is the number of nodes in the network) as $C_i = \{c_{i1}, c_{i2}, ..., c_{iN}\}$, where c_{ii} is the cluster allocation of node j in the network. In this way, nodes are divided into several partitions, and those with the same value in the chromosome are in the same cluster. The details of the algorithm are given in this section.

Generally, a randomly initialized population is suggested when utilizing EAs to solve optimization problems [25]. However, we focus on an MOP related to network structures, which is different from numerical optimization problems in [25]. Specifically, the coding method should properly represent network structures, and more information is maintained compared with numerical optimization problems. As shown in [18], [35], even networks with a small size can manifest numerous structural varieties; therefore, the optimization of networks tends to have a larger solution space. Meanwhile, considering that the evaluation process of proposed robustness measures is relatively computationally costly, the simple random population initialization seems to be deficient for the enhancement task and contributes little to the convergence of the whole search process. Therefore, a problem-directed initial strategy is necessary for solving the designed MOP.

A. Initialization

Intuitively, as indicated in [26], a cluster partition that guarantees more negative links and less positive links between clusters can lead to a better tolerance against inter-cluster collapses in the network; similarly, a partition that allocates more positive links and less negative links inside clusters makes for the resistance toward intra-cluster failures. In this way, a population, which is composed of diversified partition candidates emphasizing different strategies for reducing imbalanced links, can provide potentially good solutions to both of the robustness measures. Another advantage of this initialization strategy is that it can be easily guided by the subparts in Eq. (2) at a low cost, which is helpful to reduce the computational cost of MOEA/D-RSB. This initial population provides better initial points for the following multiobjective optimization process, and similar operations can be found in [16], [35], [36] to solve different MOPs in networks.

Based on Eq. (2), the two separate objectives in the initialization operator are defined as follows:

Min
$$h^{+} = \sum_{i,j \in \mathbf{V} \text{ and } s_{i} \neq s_{j}} |e_{ij}^{+}|/2$$
 (5)
Min $h^{-} = \sum_{m,n \in \mathbf{V} \text{ and } s_{m} = s_{n}} |e_{mn}^{-}|/2$ (6)

$$\operatorname{Min} h^{-} = \sum_{m,n \in \mathbf{V} \text{ and } s_{m} = s_{n}} \left| e_{mn}^{-} \right| / 2 \tag{6}$$

where h^+ represents the number of positive links between clusters, and h^- represents the number of negative links inside clusters. In the initialization process, search operations are implemented taking h^+ or h^- as the objectives to generate cluster candidates. In addition, some randomly generated candidates are also necessary to further promote the diversity of the initial population. The details of the initialization operator are given in Algorithm S2 of the Supplementary Materials.

B. Genetic Operator

In solving the MOP between R_{inter} and R_{intra} , some genetic operators are necessary to generate more potential candidates and search for better solutions in the local area.

As defined in [25], T_n neighbors for each individual in the population should be determined for conducting genetic operators. The selection of neighbors is based on the closeness of the weight vectors. In MOEA/D-RSB, we mainly focus on searching for partitions that promote the robustness of signed networks, and the chromosome information for each individual is a specific partition for all the nodes in the network instead of numerical coding information as in [25]. As shown in [12], [26], the information exchange between individuals with a larger partition difference may contribute to

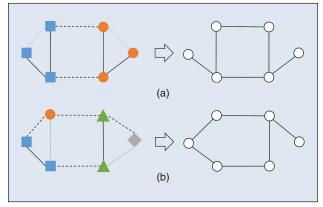


FIGURE 2 Two possible partitions and corresponding network structures for robustness evaluation of the network given in Figure 1. In the figure, nodes allocated into different clusters are labeled in different shapes and colors, and those imbalanced links (positive links between clusters and negative ones inside clusters) are marked in grey. In the robustness evaluation process, imbalanced links, which are redundant to the structural balance, should be removed from the network. Structural differences can be found in the two network structures for robustness evaluation. We can see a close impact of nodal partitions on the robustness of signed networks. (a) A possible partition and its network structure for robustness evaluation. (b) Another scenario for robustness evaluation.

The network-related optimization shows high complexity, which further influences algorithm design processes.

better optimization results. The normalized mutual information (NMI) [38] is implemented here to evaluate the partition difference between two individuals. A larger NMI indicates that the difference between these two individuals is more evident. For each individual in the population, the NMI values between its partition and all other individuals are evaluated first; then, T_n individuals with larger NMI values are selected as neighbors in this evolutionary iteration. Since the partition difference between individuals may change in the evolutionary process, the T_n neighbors of each individual are updated in each iteration instead of keeping them the same. In this way, the following crossover operator, which aims at exchanging genetic information, is more likely to be conducted between individuals with a larger partition difference to improve the search ability.

The crossover operator is designed to exchange partition information of two selected individuals in the population and generate more candidates. The two-way crossover has shown good performance in swapping cluster information [12], [26], which works as follows. For two chromosomes $C_a = \{C_{a1}, C_{a2}, ..., C_{aN}\}$ and $C_b = \{C_{b1}, C_{b2}, ..., C_{bN}\}$, a node n is selected randomly and the cluster information of all the nodes in C_a that have the same cluster with n will be exchanged into C_b , and vice versa. Then, one chromosome is chosen randomly as the output of this operator. An example of

Algorithm 1 MOEA/D-RSB

- Generate Ω chromosomes following the operations in Algorithm S2 to initialize the population, $t \leftarrow 1$;
- Update z with current optimal solutions for each objec-Step 2: tive; set $EP \leftarrow \emptyset$;
- For each individual Indi, evaluate the partition difference Step 3: between Indi's partition and all other individuals' partitions by NMI and find the T_n neighbors of Ind_i with larger partition difference;
- Step 4: (1) Select two individuals Ind_k and Ind_l randomly from the T_n neighbors of each individual Ind_{ii} and conduct the crossover operator to generate a new solution y;
 - (2) Mutate y through the mutation operator to produce a better candidate y';
 - (3) Try to update z with y'; search in T_n neighbors of Ind_i , if the Tchebycheff distance condition is met, update this neighbor with y';
 - (4) Update **EP** with y': remove all solutions dominated by y', add y' into **EP** if no solution in **EP** dominates y';
- Step 5: $t \leftarrow t + 1$;
- Step 6: If t > Maxgen, then output **EP**; otherwise, go to Step 3.

this crossover operator can be found in Fig. S2 of the Supplementary Materials.

A mutation operator is also needed in [25] to achieve problem-specific improvement of individuals in the population. A two-step local search strategy is designed here to seek better

partitions based on the current cluster information. First, one of the two robustness measures, namely, R_{inter} and R_{intra} , is chosen randomly with the same probability to guide the search process. Then, in the first step of this operator, the neighborbased search is implemented. Every node in the network tries to replace its cluster allocation with the allocation of connected neighbors, and the one that makes the largest improvement, as evaluated by the robustness measure, is employed. This step focuses on the neighborhood connection information of each node in the network, and the best cluster partition in the individual's local area is kept in the chromosomes. In the second step of this operator, the cluster-based search is implemented. A randomly selected cluster intends to merge with the connected ones, all the nodes in this cluster are allocated into one of those neighboring clusters, and the partition that makes the largest robustness improvement is preserved here. This step focuses on the macroscopic partition in the network, and some clusters, especially those with small sizes, are likely to merge with other connected clusters. This may contribute to reducing imbalanced links in the individual and improving the robustness. The details of this mutation operator are shown in Algorithm S3 of the Supplementary Materials.

C. The Framework of MOEA/D-RSB

MOEA/D-RSB contains the following procedures. First, for each individual in the population, T_n individuals with larger partition difference are selected as neighbors for conducting the crossover operator. For an individual Indi, if none of the other individuals can perform better in terms of both of the two objectives than Indi, Indi is considered as a non-dominated solution. An external population (EP) is implemented to preserve all the non-dominated candidates generated in the multioptimization process. Then, best-found solutions in terms of each objective are stored in a set z.

In the searching process, the crossover operation is implemented on each individual Ind, after obtaining the initial population; a new solution y is generated here. Afterwards, the mutation operation is made on y to obtain a problem-specific improvement and generate y'. If y' achieves the best solution in the current population, z is updated with y'. At the same time, for each neighbor n_i of Ind_i , if γ' reaches a better Tchebycheff distance [25] than n_i , the chromosome of n_i is updated with y'. At the end of a generation, the non-dominated solutions in the current population are found and preserved in **EP**, and **EP** is the output of MOEA/D-RSB when the search time reaches a predefined criterion Maxgen, and each solution in **EP** places different emphases on R_{inter} or R_{intra}. The details of MOEA/D-RSB are summarized in Algorithm 1.A flowchart like that in [39], [40] is given in Fig. S3 of the Supplementary Materials to show the calculation process of the algorithm.

MOEA/D-RSB contains two main components, i.e., the initialization and evolutionary search. Ω individuals are generated in the initialization, and the robustness evaluation operation needs the computational cost of O(M). The initialization part needs $O(\Omega \cdot N \cdot M)$ in the worst case, where N and M are the numbers of nodes and links, respectively. The evolutionary search is conducted Maxgen times, where the neighbor determination operation, the crossover operator, the mutation operator, and the EP update operation are conducted. Since the robustness evaluation operation is only conducted in the mutation operator, the computational cost of MOEA/D-RSB is mainly determined by the mutation process, which needs $O(N \cdot M)$ basic operations for each individual. Therefore, the computational complexity of MOEA/D-RSB is $O(Maxgen \cdot \Omega \cdot N \cdot M)$.

V. Experimental Results

A. Experiments on Synthetic Networks

The performance of MOEA/D-RSB is validated on synthetic networks first. The parameters in the experiment are set as follows: the size of population Ω as 100, the maximum number of generations Maxgen as 100, the number of neighbors T_n as 10, and the mutation probability p_m as 0.4. Networks with different sizes are generated from the LFR model [37] first, with the average degree being 4, the maximum degree being 20, the exponent for the degree distribution being 3, and the mixing parameter being 0.3. LFR networks with 200, 500, and 1000 nodes are generated. Then, signs are uniformly assigned to the links in the generated networks, and each network has almost half positive links and half negative links.

Several multiobjective algorithms, including NSGA-II [41], MOPSO [42], and SPEA [43], are implemented with designed operators in the experiment, denoted as NSGAII-RSB, MOP-SO-RSB, and SPEA-RSB. Corresponding results are shown in Fig. 3. As shown in the figure, MOEA/D-RSB and NSGAII-RSB can achieve competitive results on all the tested synthetic networks, but MOEA/D-RSB tends to find Pareto fronts with better diversity. An external population has been designed in MOEA/D-RSB to preserve non-dominated solutions found in the search process, which is not considered in NSGAII-RSB. Some previous studies on optimizing networks [35], [36] indicate that such a solution preservation strategy contributes to the search ability of the algorithm. The results in Fig. 3 are consistent with the conclusion. Meanwhile, individuals for conducting the crossover operation are selected based on the partition difference information instead of random selection, which further promotes the search ability of MOEA/D-RSB. In terms of MOPSO-RSB, the results are unsatisfactory, and fewer solutions can be obtained on Pareto fronts. As shown in [26], [27], MOPSO adapts the framework of particle swarm optimization (PSO), and with PSO, it is easy to get trapped in local optima when dealing with optimization tasks on large-scale networks.

Another algorithm, SPEA-RSB, has achieved mediocre results compared with MOEA/D-RSB and NSGAII-RSB.

Furthermore, the hypervolume ratio (HVR) [44], inverted generational distance (IGD) [45], and the stability measure (Stab) [44] of the results on the LFR-200 network are listed in Table I. The results indicate that the proposed algorithm has a

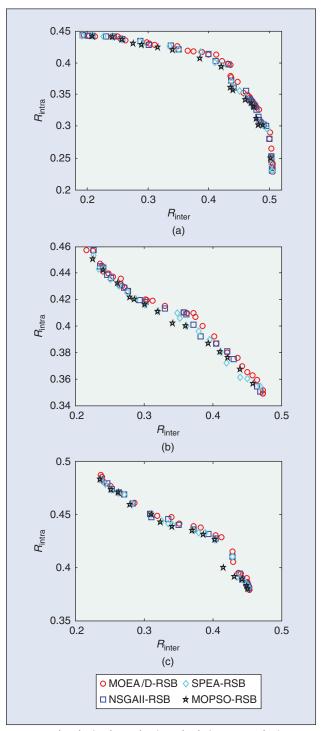


FIGURE 3 The obtained non-dominated solutions on synthetic networks using different multiobjective algorithms. (a) LFR-200 nodes. (b) LFR-500 nodes. (c) LFR-1000 nodes.

TABLE I The averaged HVR values, IGD values, and their standard deviations of obtained results on the LFR-200 network. The results are averaged over ten independent realizations. The integrated Pareto fronts of all the tested algorithms are selected as reference points for evaluating IGD values. A statistical comparison using ANOVA with a significance level of p = 0.05 is also conducted, shown in brackets. the results of MOEA/D-RSB are taken as the baseline, and "+" indicates that the compared algorithm is inferior to MOEA/D-RSB, "-" indicates the compared algorithm outperforms MOEA/D-RSB, while "a" means the two algorithms show no statistically significant difference.

NETWORK	ALGORITHM	HVR	IGD	STAB
LFR-200	MOEA/D-RSB	$0.989 \pm 0.2 \times 10^{-2}$	$0.0021 \pm 0.2 \times 10^{-4}$	$0.0017 \pm 0.3 \times 10^{-6}$
	NSGAII-RSB	$0.978 \pm 0.4 \times 10^{-2}$ (+)	$0.0032 \pm 0.3 \times 10^{-4}$ (+)	$0.0016 \pm 0.2 \times 10^{-6} (\approx)$
	SPEA-RSB	$0.965 \pm 0.9 \times 10^{-3}$ (+)	$0.0055 \pm 0.3 \times 10^{-4}$ (+)	$0.0025 \pm 0.1 \times 10^{-6}$ (+)
	MOPSO-RSB	$0.952 \pm 1.1 \times 10^{-3}$ (+)	$0.0105 \pm 0.7 \times 10^{-4}(+)$	$0.0010 \pm 0.5 \times 10^{-7}$ (-)

steady performance when dealing with synthetic networks with different sizes and always outperforms the other multiobjective algorithms compared in this work. The results on other networks are shown in Table S2 of the Supplementary Materials. The advantage of MOEA/D in solving the robust structural balance problem on signed networks is marked here.

Meanwhile, some multiobjective algorithms have been proposed to find rational partitions in networks, including MOEA/ D-SB [26], MOEA/D-Net [46], and MOGA-Net [47]. The experimental results of these algorithms on the LFR-200 network are shown in Fig. 4. As shown in the figure, most balanced networks obtained by these algorithms perform less robustly compared with those obtained by MOEA/D-RSB. The diversity of the obtained Pareto fronts is also unsatisfactory, and the generated solutions of the other multiobjective algorithms constitute a small part in the whole solution space and are inferior to the results of MOEA/D-RSB. It can be concluded that the robustness of signed networks cannot be guaranteed when balancing their structures; the proposed algorithm is more effective in finding partitions that lead to robust signed networks.

In addition, the parameter setting and complexity comparison of these algorithms can be found in Table S3 of the

Supplementary Materials. From Table S3, we can see that the complexity of MOEA/D-RSB is higher than that of existing multiobjective algorithms, which were designed to solve the plain balance task without considering the robustness of signed networks. The complexity increasement is mainly caused by the following factors. First, we focus on the robustness of balanced signed networks, which is of high complexity; but the existing algorithms in [26], [46], [47] just focus on reducing of the imbalance in signed networks that can be evaluated cheaply. Furthermore, a two-step local

search procedure has been designed in MOEA/D-RSB for exploiting individual genetic information and improving the robustness level of the whole population. This operator results in a relatively higher computational complexity but contributes to better optimization results. The superiority of MOEA/D-RSB in finding robust balanced partitions validates the good search ability of the algorithm.

A series of partitions can be obtained in the experiments, and each of them has different emphases on R_{inter} and R_{intra} . The selection from these results is an open question; as shown in [16], [35], [36], three solutions are suggested to be sampled from the Pareto front to better represent the performance, including the one located at the rightmost part of the Pareto front which has the highest R_{inter} , the one located at the leftmost part of the Pareto front which has the highest R_{intra} and the one located in the middle of the Pareto front which has a balanced performance between R_{inter} and R_{intra} . The solutions are sampled from the Pareto front obtained by MOEA/D-RSB in Fig. 4 following this method and are labeled as G_p , G_l , and G_m . The robustness values of these sampled solutions are collected and listed in Table II. Meanwhile, the state-of-the-art single-objective optimization method MLMSB [12] for finding balanced network structures has also

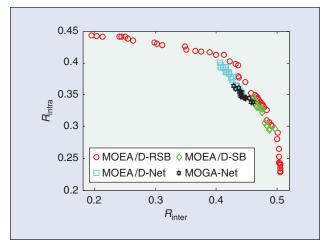


FIGURE 4 Comparisons with the results of other existing multiobjective partition algorithms on the LFR-200 network.

TABLE II The values of R_{inter} and R_{intra} of solutions obtained by different methods. The results are averaged over ten independent realizations. G_{rr} , G_{lr} , and G_{m} are sampled from the nondominated solutions obtained by MOEA/D-RSB.

Network		R _{inter}	R _{intra}
LFR-200	G_r	$0.5039 \pm 4.4 \times 10^{-3}$	$0.1977 \pm 4.7 \times 10^{-3}$
	G_I	0.2051 ± 4.6 × 10 ⁻³	$0.4417 \pm 2.7 \times 10^{-3}$
	G_m	$0.4392 \pm 4.1 \times 10^{-3}$	$0.3762 \pm 4.4 \times 10^{-3}$
	MLMSB-R _{inter}	$0.5045 \pm 4.2 \times 10^{-3}$	$0.1908 \pm 3.8 \times 10^{-3}$
	MLMSB-R _{intra}	$0.2134 \pm 3.5 \times 10^{-3}$	$0.4361 \pm 4.3 \times 10^{-3}$
	MLMSB-h	$0.4401 \pm 4.4 \times 10^{-3}$	$0.3722 \pm 4.4 \times 10^{-3}$

been tested to provide comparisons. In the experiment, we set different optimization objectives for MLMSB as follows: the one aimed at finding partitions with maximum R_{inter} is labeled as MLMSB-R_{inter}, the one aimed at finding partitions with maximum R_{intra} is labeled as MLMSB-

 R_{intra} , and the one aimed at finding balanced robustness between R_{inter} and R_{intra} , which can be approximatively achieved by reducing h defined in Eq. (2), is labeled as MLMSB-h. Corresponding numerical results are given in Table II.

As presented in the table, the proposed algorithm tends to perform stably on networks, and the robustness values of sampled networks only fluctuate in a relatively small range. Compared with the results of MLMSB, G_p , G_l , and G_m extracted from the obtained Pareto front of MOEA/D-RSB show similar robustness levels with the results of MLMSB- R_{inter} , MLMSB-R_{intra}, and MLMSB-h. The search ability of MOEA/ D-RSB is also validated here. In addition, the results obtained by MLMSB-h, which can be taken as a co-optimization process on both R_{inter} and R_{intra} , have performances similar to G_m of MOEA/D-RSB. Only one solution that has mediocre performance on both robustness measures can be obtained in one run of MLMSB, which is of low efficiency. In contrast, the proposed algorithm can provide a series of solutions with different robustness levels of the two measures, demonstrating the higher efficiency of MOEA/D-RSB over the existing single-objective optimization methods in finding robust structural balance solutions. From the results in Figs. 3, 4, and Table II, MOEA/D-RSB is found to be effective in searching for trade-off solutions between the two robustness measures; meanwhile, both the exploration and exploitation performances of the proposed algorithm have been validated. For exploring the solution space, the algorithm can obtain widely distributed results that outperform the existing methods; for exploiting the optimal solutions, considerable results with extreme performances on one of the two measures can also be generated.

Focusing on the cluster partitions of the sampled networks, NMI is taken to estimate the similarity between different partitions, and the corresponding numerical results on LFR networks with 200 nodes are shown in Table III. As it can be seen from the table, evident differences can be found between the cluster partitions of G_p , G_l , and G_m , which are sample networks from three peculiar parts of the Pareto front in Fig. 4. To achieve the optimal condition on a specific objective, the allocations of nodes follow different strategies, and the similarity information in Table III just reflects that fact.

Furthermore, the numbers of balanced and imbalanced links are analyzed to give a direct description of the distributions of positive/negative links in these sampled networks, reported in Table S4 of the Supplementary Materials. As shown in the table, the sampled networks have different distributions of attributive links in the network. The first two columns (P_i and N_b) represent the expected states of structural balance, which means positive links should be located inside clusters and negative ones ought to be located between clusters, and the three

The robustness of signed networks may not be guaranteed in simple balancing processes, and targeted optimization seems to be necessary.

sampled networks present different features in their balanced states. For G_r , inter-cluster connections are important to enhance the performance of R_{inter} , and more inter-cluster negative links (N_b) can reduce the imbalance in the network and improve the invulnerability against losing competitive connections. For G_l , intra-cluster connections dominate the evaluation process of R_{intra} , and more intra-cluster positive links (P_i) guarantee the imbalance to be lessened and promote the tolerance against losing supportive connections. For G_m , which performs similarly to the method that simply reduces h, as in [5], [6], [12], the distribution is mediocre between G_r and G_l . The results here reflect the features of different balance processes in the three sampled networks. On the other hand, in terms of the remaining imbalances in networks, G_m tends to perform the best and shows fewer imbalances. G_r reaches higher R_{inter} but causes more imbalanced links between clusters, and G_l reaches higher R_{intra} but causes more imbalanced links inside clusters. We can see that the robustness of structurally balanced networks can be enhanced at the cost of some balanced links.

B. Experiments on Real-World Networks

The performance of MOEA/D-RSB has also been verified on several real-world networks, including COW [48], EGFR [5], and MIM [49], whose information is depicted in Table S5 of the Supplementary Materials. The obtained non-dominated solutions on these networks are given in Fig. 5, and the results of MOEA/D-SB, MOEA/D-Net and MOGA-Net are also shown to provide comparisons. As shown in the figure, the proposed algorithm is effective in the three tested real-world networks and outperforms the existing methods. Similar to Table II, G_p , G_h , and G_m are extracted from the obtained solutions in Fig. 5, and the robustness values of these solutions and the results of the single-objective optimization method MLMSB- R_{inter} , MLMSB- R_{intra} , and MLMSB-h are listed in Table S6 of the Supplementary Materials. As shown in the table, the results of MOEA/D-RSB reach robustness levels similar to those of the single-objective optimization methods, which reveals the effectiveness of MOEA/D-RSB in finding robust structurally balance partitions in real-world networks.

TABLE III The partition similarity among sampled networks evaluated by NMI. The results are averaged over ten independent realizations.

	G,	G _m	G_I
G_r	1.0	0.667 ± 0.105	0.392 ± 0.079
G_m	0.667 ± 0.105	1.0	0.375 ± 0.082
G_I	0.392 ± 0.079	0.375 ± 0.082	1.0

The robustness of structurally balanced networks can be enhanced at the cost of some balanced links.

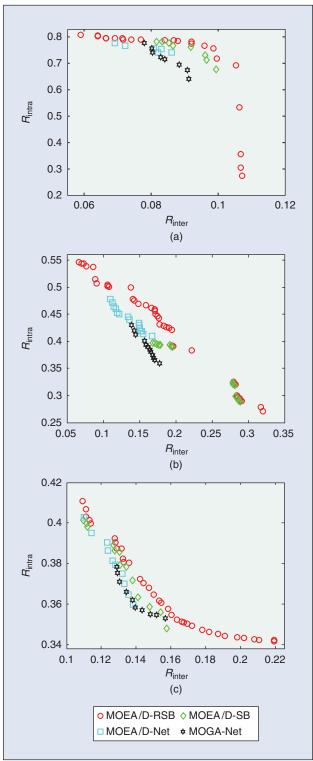


FIGURE 5 The obtained non-dominated solutions of MOEA/D-RSB and several other optimization algorithms on the tested real-world networks. (a) COW. (b) EGFR. (c) MIM.

 G_{r} , G_{m} , and G_{l} are sampled from Fig. 5(a), and their cluster partitions are shown in Fig. S4 of the Supplementary Materials to give an intuitive description of the partition information. As shown in the figure, these

networks have different distributions of balanced links. G_r has more negative links between clusters, G_l has more positive links inside clusters, and G_m reaches a trade-off state between G_r and G_l . The results indicate that solutions located at different parts of the Pareto front have diversified emphases on the balance process, which is closely related to their robustness performances. Meanwhile, these visualized network structures also validate that MOEA/D-RSB can find feasible cluster partitions suitable for different robustness evaluation scenarios.

The results on COW provide potential partition strategies to enhance the stability of social relational networks against possible failures, including cooperation termination between allies (i.e., losing positive links inside clusters) and competitiveness vanishing between competitors (i.e., losing negative links between clusters). Administrators and social members may obtain benefit from the solutions, which can help to select suitable alignment strategies to deal with challenges in social dynamics [20], [21]. The results on EGFR and MIM may help to find meaningful partitions in biological functional networks with better robustness withstanding structural perturbations. A robust allocation of biological members helps to solve problems arising in constructing balanced ecosystems [22]. On the other hand, some existing studies focused on enhancing the robustness of networks through rewiring their topologies [18], [23], [34]-[36], which tend to be costly and difficult to realize in realistic systems [19]. Different from such techniques, the proposed algorithm intends to search for better cluster partitions. In this way, the robustness of systems can be enhanced at a reasonable computational cost, and the application of this method would be less difficult in practical scenarios.

VI. Conclusions

The robustness of structurally balanced networks has potential values in nature and human society. This paper intends to estimate the tolerance of balanced networks, and then enhance their performances. First, two measures have been designed to numerically evaluate the invulnerability of networks after balancing procedures; the simultaneous optimization on both measures has been demonstrated as an MOP through experiments. Furthermore, a multiobjective evolutionary algorithm, MOEA/D-RSB, is developed to solve this MOP by searching for solutions that compromise between the two objectives. The effectiveness of the proposed algorithm has been validated on several networks, and relevant analyses on the results reveal features of the generated solutions. These results may be valuable in solving dilemmas indicated in [20]–[22].

The performance enhancement of different kinds of networked systems is still a challenging problem. Some recent studies [29], [30], [50] indicate the importance and complexity of

networks with multiplex structures. The techniques for promoting the robustness of these networks are worth investigating in the future.

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