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RESEARCH ARTICLE

Evolutionary Approach for Detecting Significant Edges in Social and Communication Networks

VASILY LUBASHEVSKIY[1] AND IHOR LUBASHEVSKY[2]
[1]Institute for International Strategy, Tokyo International University, Kawagoe 350-1197, Japan
[2]HSE Tikhonov Moscow Institute of Electronics and Mathematics, 123458 Moscow, Russia

Corresponding author: Vasily Lubashevskiy (vubashe@tiu.ac.jp)

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ABSTRACT Detection of significant edges maintaining the connectivity in complex networks is essential in many applications such as attack vulnerability analysis, the spread of epidemic diseases, and information spreading patterns discovery. There are many existing methods enabling us to evaluate the criticality ranking of links in networks, which are based on straightforward algorithms and topological features of analyzed graphs. In this paper, we offer another perspective on the problem and propose a novel approach, to be called the Evolutionary Approach (EA), that is based on a genetic-like algorithm and turns directly to an integral criterion of decomposition efficiency instead of network topology. Like all the genetic algorithms, EA is grounded on the iterative enhancement of randomly generated solutions via reproduction, cross-over, and mutation processes. The EA-efficiency is illustrated via decomposing three real-world benchmark networks by using the proposed method, the acknowledged Link Entropy (LE) method, and the most recent Improved Link Entropy (ILE) method. The comparison of the obtained results demonstrates that the EA-efficiency exceeds the ILE-efficiency for 5.7%–28.1% depending on the network complexity, with respect to the LE-efficiency the increase is approximately two-fold. Besides, the temporal aspects of ordering the network edges according to their significance using solely EA or in its combination with LE and ILE are discussed.

INDEX TERMS Complex networks, critical edges, evolutionary approach, improved link entropy, link entropy.

I. INTRODUCTION

Modern life depends crucially on the reliable functioning of many complex networks [1], [2], [3]. For example, transportation and communication systems [4], [5], [6], [7], power supply [8], [9], [10] are networks of complex structure, protein-DNA biological systems [11], [12], [13], social [14], [15], political [16], and even adolescent romantic networks [17], [18] have also complex structure. Thereby, the stability of complex networks has attracted much attention during the last decades.

Nowadays, there have emerged a variety of research directions in this field. For example, one of them is devoted to the resilience of networks whose nodes can be destroyed. In this case, detecting nodes that make the functioning of a network in question highly vulnerable is of prime importance [3], [19], [20], [21], [22], [23]. Another one is related to the development of networks and their optimization focused on link prediction and connection planning [24], [25], [26], [27]. Our research belongs to the direction of network science that is aimed at elucidating the resilience of networks whose links can be destroyed. In the given case, detecting links whose role is crucial in maintaining the network connectivity becomes one of the main issues in this scope [15], [28], [29], [30], [31], [32], [33].

Within the graph representation of real-world networks, numerous investigations have been focused on determining edges (links) whose role is critical in data transmission and maintaining connectivity. The results have shown that the proper quantification of the edge significance and the subsequent modification of the system topology can substantially enhance the robustness of the network and make it more reliable and efficient against targeted edge attacks [34]. The matter is that the loss of even a few connections on a network can cascade, resulting in the total collapse of the system. To elucidate this type of collapse, a significant number of researches

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have been devoted to the infrastructure risks related to edge failures [6], [35], [36]. In some sense, the opposite problem is the efficient decomposition of a network by cutting the minimal number of links. In particular, based on the actual data from South Korea, it has been demonstrated that by removing the most significant links of social networks, the spread of a contagious disease can be depressed due to a significant decrease in the infection network [37].

As far as particular algorithms that describe the efficient decomposition of networks based on determining the edge significance are concerned, we may note the following. Dealing with community structure in social and biological networks, Girvan & Newman [12] used the *betweenness centrality of edges*. Later, focusing on social networks, Meo et al. [38] employed the *k-path centrality* to measure edge significance. In the case of weighted network, Wang and Chen [39] proposed a method based on the*degree product* to characterize cascading-failure-induced disasters in nature. Chen et al. [40] turned to the *bridgeness* to quantify the edge significance in maintaining the network connectivity; this index is determined explicitly by the local information of the network topology. Finally, there have been developed a family of novel methods based on the probability distributions divergence, namely, *link entropy* (LE) by Qian et al. [28], *deep link entropy* (DLE) by Ozaydin and Ozaydin [31], and the *improved link entropy* (ILE) by Lubashevskiy et al. [33] demonstrated their high efficiency.

The efficiency of these methods has been compared numerically for artificial and real networks [28], [30], [31]. The decrease rate in the size R_{gc} of the largest connected component (normalized to the total number of nodes R_{gc}) caused by removing the most significant edges has been employed as the corresponding efficiency criterion. Indeed, the better the method of detecting edge criticality and, consequently, the more suitable the link ranking, the faster the decrease in R_{gc} caused by removing the edges ordered downward according to their significance [15], [28], [30], [31], [32], [33].

In the present work, we put forward another principle of quantifying the edge significance. Accepting that the higher efficiency of the edge significance detection, the stronger drop in the value of R_{gc}, we turn to an integral criterion grounded on the dependence $R_{gc}(\rho)$, where ρ is the relative amount of removed edges. In this way, we gain the ability to treat the network destruction as a problem of optimizing the process of link removal. A certain genetic-like algorithm to be called the Evolutionary approach (EA) is proposed to tackle this optimization problem. To examine the efficiency of the proposed approach, three standard benchmark real-world networks are decomposed employing the EA, LE, and ILE methods. The choice of the LE and ILE algorithms as competitive methods is caused by that their comparison with algorithms turning to the other acknowledged indices of the edge significance (betweenness centrality, degree product, bridgeness, diffusion importance, topological overlap, and k-path edge centrality) has demonstrated the superiority of LE [28] and its descendant, ILE [33].

By the present paper, we want to attract the attention of the scientific community, dealing with network stability and security, to the genetic type algorithms as a promising approach. We expect our work to encourage the development of alternative methods, enhancing the plurality of perspectives. The prospects of the EA-development, especially in combination with straightforward algorithms, are outlined in the Discussion (Sec. V).

II. ALGORITHM EFFICIENCY MEASURE

Algorithms of network decomposition via removing the most significant edges may be categorized as the local-type algorithms. Indeed, within these algorithms the network edges with the highest significance are removed step-by-step in the descending order. At each step the network connectivity is gradually destroyed, leading to the emergence of mutually disconnected components whose number also gradually increases. Moreover, after removing one edge, the significance of the remaining edges can be re-evaluated because the resulting networks has changed.

The efficiency of these algorithms is often evaluated by plotting the size R_{gc} of the largest connected component *vs* the relative amount of removed edges ρ [28], [30], [31]. Here, to make it possible to compare the decomposition of networks different in size, two normalizations are typically used. First, the size of connected components is normalized to the total number of nodes. Second, the amount of the removed edges is normalized to the number of edges m in the original network. Thereby, at the initial step ($\rho = 0$) the value $R_{gc} = 1$ (the original network is assumed to be a connected graph), respectively, at the final stage of network decomposition, when $\rho \to 1$, the value $R_{gc} \to 0$.

The popularity of the $R_{gc}(\rho)$-criterion is due to its clarity—the sharper the decrease in the value of R_{gc} as ρ increases, the higher the significance of the removed edges. When for two algorithms A_1 and A_2 applied to decomposing the same network, the corresponding dependencies $R_{gc:1}(\rho)$ and $R_{gc:2}(\rho)$ are such that, e.g., $R_{gc:1}(\rho) < R_{gc:2}(\rho)$ for any $\rho > 0$, the $R_{gc}(\rho)$-criterion enables one to order the two algorithms unambiguously according to their efficiency, namely, $A_1 \succ A_2$. Otherwise, i.e., when, e.g., there is a value ρ_b of the relative number of removed edges such that $R_{gc:1}(\rho) < R_{gc:2}(\rho)$ for $\rho < \rho_b$ and $R_{gc:1}(\rho) > R_{gc:2}(\rho)$ for $\rho > \rho_b$, a more sophisticated criterion is required for comparing decomposition algorithms in efficiency.

In the present work we turn to an integral criterion based on the $R_{gc}(\rho)$-dependence which considers the contributions of all the steps in network decomposition equipollent. Namely, if the $R_{gc}(\rho)$-dependence were a continuous function of the continuous argument $\rho \in [0, 1]$, the area S_{rgc} under the curve $R_{gc}(\rho)$ could be used to specify the efficiency of network decomposition. This type of criterion actually focuses the main attention on the general features of network topology rather than on particular details of the network structure at its micro-level. Since the network decomposition is represented by a sequence of discrete values $\{\rho_i\}$ (for $i \in [0, m]$) with the

same spacing $1/m$, i.e., $\rho_{i+1} - \rho_i = 1/m$ for $\forall i$, we introduce the desired value S_{rgc} as

$$S_{rgc} = \frac{1}{m} \sum_{i=0}^{m} R_{gc}(\rho_i), \tag{1}$$

which is just a discrete approximation of the hypothetical continuous integral of $R_{gc}(\rho)$ over the region $0 < \rho < 1$. Employing the value S_{rgc} as a quantitative measure, we accept that the smaller the value S_{rgc}, the more efficient the network decomposition. Below we will refer to the quantity S_{rgc} also as to the area under the curve $R_{gc}(\rho)$.

It is worthy of noting that, first, a similar integral criterion is used to quantify recovery processes of large-scale disasters within the theory of resilience [41], [42], [43]. Second, as it must, the given integral criterion leads to the same conclusion about the superiority of one of two algorithms A_1 and A_2 specifying the edge significance in the former case noted above. However, in the latter case, when two "curves" $R_{gc:1}(\rho)$ and $R_{gc:2}(\rho)$ outpace each other at different stages of the graph decomposition, it also enables one to compare the related algorithms. Third, this integral criterion has also a clear meaning in its application to quantifying the efficiency of the global-type algorithms dealing with the sequences of edge removing as whole entities, i.e., without turning to the significance of individual edges. The evolutionary approach to be constructed below is rooted in genetic algorithms and exemplifies this type methods of network decomposition. Its comparison with link-entropy algorithms will be based on the given integral criterion.

III. METHODS

The present section is devoted to the description of three methods to be compared. The first one is the Link Entropy (LE) developed by Qian et al. [28] and demonstrating high efficiency. The second one is the most recent method, the Improved Link Entropy (ILE) developed by Lubashevskiy et al. [33]. The third one is the Evolutionary Approach (EA) proposed in the given paper. To elucidate their comparison, let us outline them separately.

A. LINK ENTROPY

The construction of the edge significance within LE is divided into two consecutive stages. First, it is detecting the communities belonging to a given network and finding the community membership of the network nodes, i.e., the probability that a given node belongs to a given community. Second, the use of the obtained probability distribution to rank edge importance via the information entropy combined with the Jensen-Shannon divergence.

In what follows, any network in issue will be identified with an undirected, unweighted graph $G = (V, E)$, where V is a set of n nodes and E is a set of m edges. By definition, the adjacency matrix $\mathbf{A}$ of the graph G comprises the elements $a_{ij} = 1$, if there is an edge between nodes i and j or when $i = j$, otherwise, $a_{ij} = 0$.

For detecting the communities forming a given network let us follow the method proposed by Qian et al. [28]. Namely, the pairwise community interaction "hidden" in the adjacency matrix $\mathbf{A}$ is assumed to be "influenced by an unobserved expectation network $\widehat{\mathbf{A}}$, where $\widehat{a}_{ij}$ is an observed variable which denotes the probability of existing a connection between nodes i and j" [28]. The probability that node i belongs to community k is specified by x_{ik}, correspondingly, the expected edge $\widehat{a}_{ij}$ is defined as

$$\widehat{a}_{ij} = \sum_{k=1}^{K} x_{ik} x_{jk} \tag{2}$$

or in the matrix form

$$\widehat{\mathbf{A}} = \mathbf{X}\mathbf{X}^T. \tag{3}$$

Were the matrix $\mathbf{A}$ positive-definite, the Cholesky factorization [44], [45] could be used to find $\mathbf{X}$ (e.g., employing the NumPy library, Python), however, in the general case, the matrix $\mathbf{A}$ is nonnegative-definite only. So we turn to the Nonnegative Matrix Factorization (NMF) [46], [47] for detecting the communities. Namely, the construction of the matrix $\mathbf{X}$ is reduced to the minimization problem

$$\min_{X \geq 0} ||\mathbf{A} - \mathbf{X}\mathbf{X}^T||^2, \tag{4}$$

which can be solved using the multiplicative update rule for x_{ik} according to the gradient descent method introduced by Wang et al. [48]

$$x_{ik} \leftarrow x_{ik} \left(\frac{1}{2} + \frac{(\mathbf{A}\mathbf{X})_{ik}}{(2\mathbf{X}\mathbf{X}^T\mathbf{X})_{ik}} \right). \tag{5}$$

At the final step, each row of the matrix $\mathbf{X}$ is normalized such that the row elements admit interpretation as the probabilistic clustering partition. In other words, this normalization allows us to regard each x_{ik} as the probability of node i belonging to community k. The iterative process described by equation (5) starts from the random positive matrix $\mathbf{X}$, each element of which is not less than 0. Iteration (5) is repeated typically thousand times when the outcome, $\mathbf{X}$, becomes stable within a certain accuracy of the iteration procedure.

The obtained probability distribution in the clustering partition allows us to attribute the link entropy (LE) to each individual edge connecting nodes i and j using the following equation:

$$LE_{ij} = \frac{\left(H(\mathbf{X}_i) + H(\mathbf{X}_j)\right) + 2 \cdot JSD(\mathbf{X}_i||\mathbf{X}_j)}{4}. \tag{6}$$

Here $H(\mathbf{X}_i)$ is the information entropy calculated as

$$H(\mathbf{X}_i) = -\sum_{k=1}^{K} x_{ik} \log(x_{ik}), \tag{7}$$

and $JSD(\mathbf{X}_i||\mathbf{X}_j)$ is the Jensen–Shannon divergence for $\mathbf{M}_{ij} = (\mathbf{X}_i + \mathbf{X}_j)/2$ specified by the expression

$$JSD(\mathbf{X}_i||\mathbf{X}_j) = \frac{D\left(\mathbf{X}_i||\mathbf{M}_{ij}\right) + D\left(\mathbf{X}_j||\mathbf{M}_{ij}\right)}{2} \tag{8}$$

with

$$D(\mathbf{X}_i||\mathbf{M}_{ij}) = \sum_{k=1}^{K}\left[x_{ik}\log\left(\frac{x_{ik}}{m_k}\right)\right]. \tag{9}$$

The obtained set of LE values enables us to judge about the significance of edges: the larger the LE value, the more critical the link from the perspective of network integrity and connectivity.

B. IMPROVED LINK ENTROPY

The Improved Link Entropy is the second benchmark method used in the present paper. The process of graph decomposition by the ILE method is very similar to the LE but has two significant distinctions: an update on the link entropy values and an update on the number of communities.

When the LE approach is applied, the entropy of all the links is assessed only once. However, after any link of the graph is removed, the resulting modified graph cannot be considered to have the same topological features. It leads to the necessity of entropy recalculation for each of the remaining links at every step of network deconstruction.

The same logic is applied to the number of communities assigned to the network while finding the matrix $\mathbf{X}$ (see equations 2–4). At the first step, the number of communities may be assigned according to reality (the actual number of communities in the social network) or just assumed for some other reasons. But after any link is removed and the graph is modified, the number of communities must be a subject of re-evaluation. Community detection is an individual direction in network science [49], [50] and is not the subject of the present work. In developing the ILE approach [33], three community detection methods proposed by Louvain [51], Leiden [52], and Walktrap [53] were compared. The Louvain as well as Leiden methods demonstrated the best efficiency in applying to the network decomposition with comparably similar results. In the present work, the Leiden approach is selected to be used within the ILE method.

C. EVOLUTIONARY APPROACH

An Evolutionary Approach (EA) proposed in the present work is an adaptation of the genetic algorithm which is widely known as a powerful tool for optimization and search problems. The EA operates with a set of synthetic chromosomes that are strings of numbers representing the order of edges E according to which the edges are removed from the graph G, the network under consideration. Put differently, each chromosome $C(x_1, x_2, \ldots, x_m)$ consists of a unique combination of integers $\{x_i\}$ from 1 to m without repetition, where m is the number of edges in the network. Each individual chromosome is a trial solution to the given problem of graph decomposition and specifies the order of edge removal. Namely, the edge with index x_1 is removed first, then the edge with x_2 is removed, finally, the edge with x_m is removed, finishing the network decomposition. Table 1 illustrates, in particular, the chromosome structure.

TABLE 1. Illustration of the chromosome structure and the cross-over process. By way of example, the first two lines show sequences of genes of two candidate solutions (Parent 1 and Parent 2). According to Parent 1, the order of link removal is 1, 2, . . . , 8. For Parent 2 this order is 8, 1, . . ., 4. The cross-over procedure for Parents 1 and 2 is illustrated by lines 3-5 and 6-8. In Parent 1 a set of genes (x_5–x_7 shown in bold) is selected randomly for the injection into Parent 2. First the genes matching the selected set is removed from Parent 2 (shown in gray). Then the remaining genes of Parent 2 are aligned in such a way that the injecting set from Parent 1 be positioned as in Parent 1. It specifies the gene structure of Child 1. Child 2 is generated in the same way, by injecting a selected set of genes from Parent 2 to Parent 1. Child 1 and Child 2 are passed as candidate solutions to the next generation.

$C(x_1, x_2, \ldots, x_8)$	x_1	x_2	x_3	x_4	x_5	x_6	x_7	x_8
Parent 1	1	2	3	4	5	6	7	8
Parent 2	8	1	7	2	6	3	5	4
Parent 1	1	2	3	4	**[5**	**6**	**7]**	8
Parent 2	8	1	7	2	6	3	5	4
Child 1	8	1	2	3	**[5**	**6**	**7]**	4
Parent 2	8	**[1**	**7**	**2]**	6	3	5	4
Parent 1	1	2	3	4	5	6	7	8
Child 2	3	**[1**	**7**	**2]**	4	5	6	8

Initially, the set of 500 chromosomes created randomly to be the source for the EA iterative process not changing the total number chromosomes. At each step of the iterative process the chromosomes are converted into the chromosomes of the next generation via **reproduction**, **cross-over**, **mutation** and **invasion** processes.

1) SELECTION

It is a phase of the iteration when chromosomes are chosen as candidates from the current generation for the later breeding process. Every candidate is assessed via the objective function S_{rgc} (Exp. 1) and the list of candidates is rewritten in ascending order; the smaller the value S_{rgc}, the better the fitting of the candidate.

2) REPRODUCTION

The best 10% of candidates are copied into the next generation with no modification of their genes. The reproduction of the best candidates is implemented in order to avoid potential degradation of the generation because the **cross-over**, **mutation** and **invasion** give a chance but do not guarantee the improvement at the next step of evolution.

3) CROSS-OVER

The best 20% of candidates are selected to pass their genes to the new generation. For this purpose, each selected candidate is coupled with another randomly chosen chromosome. After that, from each member of a couple, a portion of its genes is singled out again from the random position and injected into the same position of the partnering chromosome. In the resulting sequence, the repeated elements are removed to prevent gene duplicates. The proportion of a chromosome for the cross-over procedure is chosen to be 20% in the frame of the current numerical experiment. As a result, each couple of chromosomes gives rise to two new candidates, their children, which are included into the new generation. Table 1 illustrates the cross-over process using a simple example.

4) MUTATION

The best 30% of candidates are singled out for the mutation process implemented as follows. At the beginning, 10% of genes are randomly extracted from a chromosome. Then the obtained subset is shuffled, grouped, and injected back into the original chromosome at the random position. The resulting mutated chromosome is passed to the new generation.

5) INVASION

The collection of **reproduction**, **cross-over**, and **mutation** processes enables us to find a good solution but gives a risk of falling into the local optimum. In order to enhance the chance of avoiding it, each new generation includes 20% of randomly generated chromosomes, each of which may be selected during the **cross-over** process as a parent for the further generations.

As a result, each new generation is formed according to the following schema: **10**% is formed by the best 10% solutions from the previous generation; **30**% are the result of mutation of the best 30% chromosomes from the previous generation; **40**% of chromosomes are the outcome of the cross-over; and final **20**% are the result of the invasion.

Formally, there may be an almost limitless number of generations since the **invasion** procedure guarantees the appearance of a new chromosome that may fit better than the best candidate of a previous generation. The iteration of generations is limited only by two factors. First, the Evolutionary approach stops when the generation number 10000 is formed. This breakpoint is set artificially as a parameter of simulation, and the maximal number of generations is big enough to find a good solution. Second, if within 100 generations, best candidate solutions provide the same value of S_{rgc}, the Evolutionary approach stops. Such a long repetition of the best S_{rgc} informs us that we found a local or global optimum, the improvement of which is unlikely.

IV. DATA AND NUMERICAL EXPERIMENT

To assess the efficiency of the Evolutionary Approach and to compare it with the methods based on Link Entropy and Improved Link Entropy, a numerical experiment has been conducted. Three real-world networks that are different in their size, the number of communities, and the number of edges have been selected. These three networks are often used as benchmarks [28], [31], [33], the basic statistics of these networks are shown in Table 2.

TABLE 2. Basic statistics of the three networks. Their structural properties include the number of nodes (N), the number of edges (E), the average degree ($\langle k \rangle$), the maximal degree (k_{max}), the degree heterogeneity (H_k), and the clustering coefficient (C).

Networks	N	E	$\langle k \rangle$	k_{max}	H_k	C
Karate	34	78	4.5882	17	1.6933	0.5706
Dolphins	62	159	5.1290	12	1.3268	0.2590
Football	115	613	10.6609	12	1.0069	0.4032

A. ZACHARY'S KARATE CLUB NETWORK

The Zachary's Karate Club is a well-known network [54], which is often used in testing various methods of network analysis. It consists of 78 edges and 34 nodes, usually considered to have two communities [55], [56] and represents a small size network, the circular layout of which is drawn in Fig. 1 (I).

Numerical simulation of the graph decomposition using all the three methods is illustrated in Fig. 1 (II). This Figure depicts how the size R_{gc} of the largest connected component (normalized to the initial number of nodes) decreases with the relative number ρ of the removed edges for the network decomposition governed by the EA, LA, and ILA algorithms. As seen, for the Zachary's Karate Club network the Evolutionary Approach shows significantly better performance than the conventional Link Entropy algorithm as well as is slightly better in comparison with the Improved Link Entropy algorithm. It is justified by the overall earlier and stronger drop of the $R_{gc}(\rho)$-dependence for the EA.

B. DOLPHINS NETWORK

The Dolphins network [57] is an undirected social network of frequent associations between 62 dolphins in a community living off Doubtful Sound, New Zealand. It has often been used as a benchmark for various studies [28], [31], [33], [58], [59], consists of 62 nodes, 160 links and is usually considered to have six communities, which makes it a representative of a medium size network. The circular layout of the Dolphins' network is shown in Fig. 2 (I).

Figure 2 (II) depicts the deconstruction of this network. As seen, the LE method of the edge significance evaluation results in a slight and graduate decrease of the $R_{gc}(\rho)$-dependence, while the ILE method results in almost no changes in the size R_{gc} of the largest connected component for the first approximately twenty percent of removed edges and with the following sharp drop, which makes the ILE method more efficient than the LE. The EA gives rise to the earlier drop in R_{gc} than the ILE and is characterized by the smaller area S_{rgc} under the curve $R_{gc}(\rho)$. The latter two feature enable us to judge about the superior performance of the EA.

C. AMERICAN COLLEGE FOOTBALL NETWORK

The American College Football network [12] is the network of American football games between Division IA colleges during the regular season in Fall 2000. The football network can be regarded as a representative of big networks: it consists of 115 nodes and 613 edges. There is no consensus on the number of communities in the football network [31], but in the present paper, for the purpose of numerical simulation, the network is assumed to be initially divided by nine communities [60]. The circular layout of the American College Football network is represented by Fig. 3 (I).

The comparison of the network decomposition is shown in Fig. 3 (II) As in the case of the Dolphin network, the LE method gives rise to a gradual decrease of the $R_{gc}(\rho)$-dependence, outpacing the ILE and EA during the first stage of decomposition. The ILE method demonstrates a strong cumulative effect on the graph decomposition. At first, almost 40% of removed edges do not result in any decrease in the

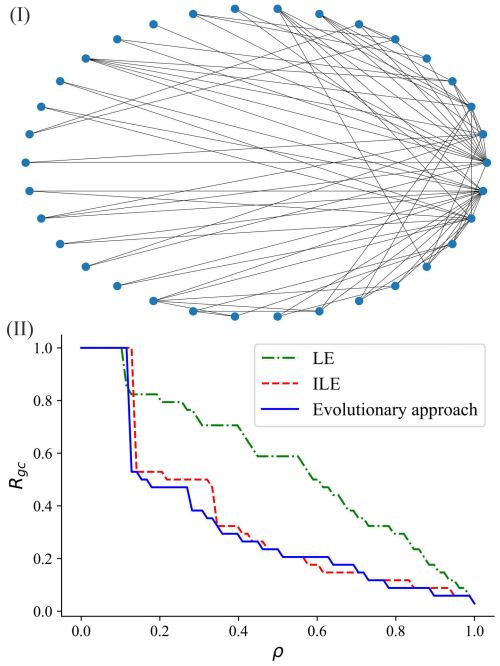

FIGURE 1. (I) The circular layout of the Zachary's Karate Club network [54] and (II) its decomposition within the Evolutionary Approach (EA) (blue solid line), the Link Entropy (LE) method (green dash-dotted line), and the Improved Link Entropy (ILE) method (red dashed). The lines represent the corresponding fraction of nodes R_{gc} belonging to the largest connected component vs the relative amount of removed nodes ρ.

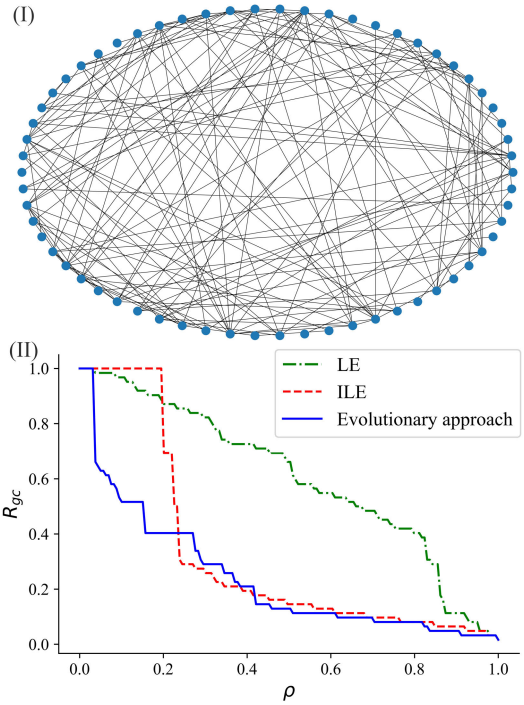

FIGURE 2. (I) The circular layout of the Dolphins network [57] and (II) its decomposition within the Evolutionary Approach (EA) (blue solid line), the Link Entropy (LE) method (green dash-dotted line), and the Improved Link Entropy (ILE) method (red dashed). The lines represent the corresponding fraction of nodes R_{gc} belonging to the largest connected component vs the relative amount of removed nodes ρ.

$R_{gc}(\rho)$-dependence, but then, after removing a few edges, the value R_{gc} drops step-wise from 1 to almost 0.15. The integral area S_{rgc} under the curve $R_{gc}(\rho)$ turns out to be much smaller, confirming that the ILE outperforms the LE method. The network decomposition governed by the EA exhibits a behavior similar to the ILE method outcome, but it prepares the drop of the R_{gc} earlier and results with even smaller area S_{rgc}, outperforming the ILE and LE methods.

V. DISCUSSION

The decomposition of the analyzed three benchmark networks of small, medium and relatively large size—the Zachary's Karate Club network, the Dolphins network, and the American College Football network—clearly demonstrated the proposed Evolutionary Approach to be superior to the conventional methods represented by the Link Entropy algorithms and the improved Link Entropy algorithm. As demonstrated in [28], the LE is superior to the well recognized algorithms, namely, the Edge betweenness centrality, Degree product, Bridgeness, Diffusion importance, Topological overlap in the efficiency of network decomposition. Naturally, the ILE—the improved version of the LE—is superior to the LE [33]. For this reason, in comparing the EA with straightforward algorithms we confine our consideration to the LE and ILE.

The edge removal, according to the queuing obtained by the EA, has exhibited a faster overall drop of the $R_{gc}(\rho)$-dependence and a smaller area S_{rgc} under the curve $R_{gc}(\rho)$, which is summarized in Table 3.

TABLE 3. The integral area S_{rgc} under the curve $R_{gc}(\rho)$, see Exp. (1), for all the three methods applied to decomposing the analyzed benchmark networks.

Methods	Karate	Dolphins	Football
LE	0.56	0.60	0.65
ILE	0.35	0.32	0.37
EA	0.33	0.23	0.28

The superiority of the EA is quite expectable. The matter is that the straightforward algorithms and the EA are based on different paradigms. The straightforward algorithms focus on detecting topological features of networks and attribute special properties to individual edges. The Edge betweenness centrality, Degree product, Bridgeness, Diffusion importance, and Topological overlap together with the LE exemplify these features and properties [28]. Then these properties are used in constructing the sequence of edges that represents the network decomposition regarded as the most efficient. By contrast, the EA ascribes no special property to individual edges and operates directly with the efficiency evaluation criterion being of integral structure and attributed to a given network as a whole entity.

In this sense, the EA should be categorized as a holistic algorithm dealing with properties of a given network ascribed to its macro-level only, i.e., the network treated as a whole entity. For an introduction to the concept of holism and its modern understanding, a reader may be referred to [61] and [62]. So if the optimal decomposition of a given

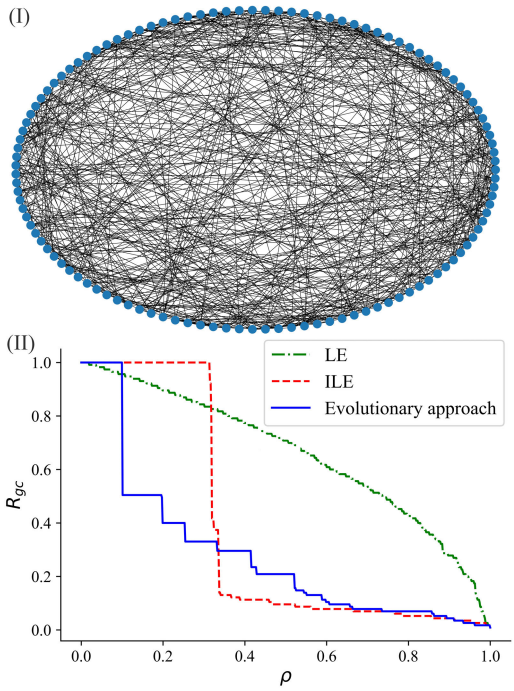

FIGURE 3. (I) The circular layout of the American College Football network [12] and (II) its decomposition within the Evolutionary Approach (EA) (blue solid line), the Link Entropy (LE) method (green dash-dotted line), and the Improved Link Entropy (ILE) method (red dashed). The lines represent the corresponding fraction of nodes R_{gc} belonging to the largest connected component vs the relative amount of removed nodes ρ.

network is its holistic property, only the genetic-type algorithms seem to be able to generate it precisely. In this case, the straightforward algorithms can only approximate it in some way. If the optimal decomposition of this network is reducible in properties to the meso-level or even the micro-level of a network, then the genetic-type and straightforward algorithms may be of the same efficiency.

The EA-generality has a cost, namely, (*i*) the heuristic aspects in the algorithm construction and (*ii*) the running-time problem, which is not independent of each other. The former is reflected in the heuristic choice of the initial set of chromosomes and their number depending on the network topology. For example, highly branching networks similar to the ones analyzed in the present paper and the sexual networks with the long-circle-like structure [18] may require different initiation of the EA-implementation.

As far as the running-time is concerned, let us compare this feature for the considered networks. The running time of the Link Entropy method varies from a few seconds to a few minutes on an ordinary PC, depending on the network size. The corresponding running time of the Improved Link Entropy method varies from a few minutes to an hour. For a similar PC, the running time of the Evolutionary Approach varies from a few hours to a day, depending on the network size. The time consumption of the Evolutionary Approach makes it not the first choice in case of emergency when the network decomposition must be performed as soon as possible. However, if the running time is not a significant factor, the Evolutionary Approach results in a better solution than conventional alternatives.

The combination with the conventional methods can significantly reduce the running time of the Evolutionary Approach. Before initiating the EA, a set of link criticality rankings can be obtained using other methods. This set can be encoded in the form of EA's chromosomes and injected into the initial generation. It will result in a shortcut in the evolutionary process from a not acceptable to a good candidate for a solution, and the EA will improve this candidate to a better one. A potential problem with the given shortcut is that there is a chance of falling to a local minimum and finding good but not the best network decomposition order. However, this problem can be overcome via several parallel EA implementations, each of which uses a unique injected chromosome obtained by different conventional approaches. The development of an approach merging the EA and the straightforward algorithms is a matter of further research.

The Evolutionary Approach possesses the general value for studies devoted to edge criticality detection, enabling the creation of a database of ''optimal'' solutions for the benchmark networks. It, maybe, will take time to analyze all the benchmark networks and to collect all the results, but the result can hardly be overvalued. Indeed, *first*, typically newly developed methods are compared with the existing ones via simultaneous decomposition of the same networks. The algorithm complexity and the running time also are often used in evaluating new methods. The database of ''optimal'' solutions to the benchmark networks shall make it possible to introduce a new metric quantifying the distance between a proposed solution and the ''optimal'' solution found by the EA. *Second*, the obtained ''optimal'' solutions can stimulate the development of essentially new methods for studying network resilience. Optimal sequences of edge removals may be analyzed from the perspective of detecting such *topological* features of networks that per se underpin or even specify an efficient link removal. It may result in discovering new efficient, straightforward algorithms for edge criticality detection or a mixture of existing methods switching from one to another depending on the topology of the initial and remained graphs.

The proposed Evolutionary Approach can be adapted to other problems of network science. *First*, a similar principle can be used for detecting critical and influential nodes using such metrics as the final affected scale, which reflects the final spreading capacity of initial nodes and the average shortest path length between nodes in the initial infection set [3]. *Second*, the EA optimization criterion—the minimization of S_{rgc}—can be replaced by something else. By way of example, the minimization problem can be formulated as to find a sequence of edge removal maintaining the connectivity of the network as long as possible, which can proceed in a hidden way for an external observer. Then, after preparation, removing a few edges should give rise to the deepest fall of R_{gc}, which illustrates military sabotage of the network. Another example is the minimization of S_{rgc} within the first

10–50–100 edges removed without the requirement of completing network decomposition.

VI. CONCLUSION

Identifying critical links in complex networks is an interesting and challenging issue in network science. Various straightforward algorithms have been proposed to cope with it. In this paper, we have offered to look at the problem from another perspective and presented an evolutionary approach for detecting significant edges. It is based on an optimization technique applied to the efficiency assessment of graph decomposition that turns to a certain *integral criterion*. The numerical results of decomposing three real-world standard benchmark networks have shown that the developed Evolutionary Approach (EA) outperforms the efficient Link Entropy method as well as the most recent Improved Link Entropy method (ILE), exhibiting the highest efficiency among the straightforward algorithms. For the analyzed benchmark networks, it has been demonstrated that the EA-efficiency in the link criticality detection exceeds for 5.7–28.1% the ILE-efficiency depending on the network complexity. The significant limitation of the proposed EA is the running time, which makes it not the first option if the edge criticality should be assessed within a short period. We have discussed how the running time could be reduced by combining the EA with any other conventional, straightforward algorithms.

There are still many challenging issues reflecting various aspects of significant edge detection and whose solution can be enhanced by the developed EA. In particular, employing the EA to generate the optimal decomposition sequences for the main benchmark networks, the obtained results could be used to assess the relative efficiency of existing methods or to construct new straightforward algorithms. The further improvement of EA may be related to (*i*) optimization of the number of generations and chromosomes in them depending on the topological features of analyzed networks and (*ii*) inclusion into consideration also the identification of influential nodes.

The proposed EA is global in nature, i.e., it operates with networks in issue as whole entities, and in its framework, no properties are attributed to individual edges. By contrast, straightforward algorithms directly deal with individual edges and their properties. The demonstrated superiority of the EA allows us to pose the question of whether the optimization of network decomposition is a problem belonging to the global level of network topology. If so, the related problem concerns a straightforward algorithm giving the best approximation of the strictly optimal decomposition sequence.

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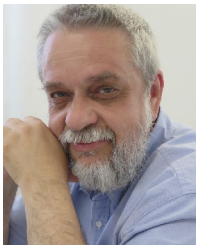
VASILY LUBASHEVSKIY received the M.S. degree in radiophysics and electronics from MIREA Russian Technological University, in 2011, and the Ph.D. degree in engineering from The University of Tokyo, in 2014. From 2014 to 2016, he was with the Resilience Engineering Research Center, The University of Tokyo, as a Project Researcher. From 2016 to 2019, he was with the Regional Environmental Renovation Section, National Institute for Environmental Studies, as a Project Associate. In 2019, he joined the Tokyo International University as an Assistant Professor. His research interests include resilience engineering, complex systems, human behavior modeling, information spreading, and data mining.



IHOR LUBASHEVSKY received the M.S. degree and the Ph.D. degree in physics of semiconductors from the Moscow Institute of Physics and Technology, in 1978 and 1980, respectively, and the Doctor of Science degree (Habilitation in physics and mathematics) in synergetics from Lomonosov Moscow State University, in 1993. After graduation, his research mainly concerned self-organization phenomena, including human behavior and cognition. From 1981 to 2010, he was with the Prokhorov General Physics Institute, Russian Academy of Sciences, as a Lead Research Fellow and a Professor in radioengineering, electronics, and automation with the Moscow Technical University. From 2010 to 2021, he was with the University of Aizu, Aizuwakamatsu, Japan, as a Professor. Since 2021, he has been with the Higher School of Economics, Tikhonov Moscow Institute of Electronics and Mathematics, National Research University, as a Professor. He has authored over a 100 academic papers and six monographs.