An Effective Resistance based Genetic Algorithm for Community Detection

Clara Pizzuti[a] and Annalisa Socievole[b]

National Research Council of Italy (CNR), Institute for High Performance Computing and Networking (ICAR),
Via Pietro Bucci, 8-9C, 87036 Rende (CS), Italy

Keywords: Community Detection, Genetic Algorithm, Effective Resistance, Moore-Penrose Pseudoinverse.

Abstract: This work presents a new approach based on genetic algorithms (GAs) and the concept of effective resistance for detecting communities within an undirected graph. The method considers the equivalent electric network of the input graph, where edges are weighted with their effective resistance, a measure of electrical resistance between nodes, whose square root has been shown to be a Euclidean metric. The algorithm computes the similarity between nodes by using the effective resistance values and generates a weighted and sparse graph by adopting a thresholding sparsification strategy based on the nearest neighbors of each node. Experiments over synthetic and real-world networks demonstrate the effectiveness of our approach when compared to other benchmark methods.

1 INTRODUCTION

The community detection problem in complex networks plays a fundamental role in several fields, including telecommunications, sociology, physics, and biology. Many real-world systems, in fact, can be represented through networks where nodes correspond to the objects of the system and edges model the relationships between such objects. The task of finding communities in networks has attracted a lot of attention in the last years since the presence of communities indicates the existence of group organization which could be interesting to uncover for a better understanding of the system.

The problem of finding a community structure can be generally formalized as an optimization problem where a criterion function, catching the intuitive concept of group, is defined and optimized. To date, many community detection algorithms, based on different approaches, such as consensus clustering, spectral methods, statistical inference-based, optimization-based, dynamics-based methods, have been proposed (Fortunato and Hric, 2016).

Real-world networks generally have a very high density of edges and, often, their edges are weighted (Barrat et al., 2004). As observed in (Yan et al., 2018), analyzing these networks with computational methods is very hard, thus preprocessing techniques need to be applied in order to reduce the number of connections and make the problem tractable.

An approach to eliminate edges is *graph sparsification* (Tumminello et al., 2005; Radicchi et al., 2011; Spielman and Srivastava, 1996). In particular, (Spielman and Srivastava, 1996) proposed to build a sparse graph H from the original one G by including in H edges of G with a probability proportional to their effective resistance.

The effective resistance (Klein and Randić, 1993; Ghosh et al., 2008) of an edge is equal to the probability that the edge appears in a random spanning tree of G (Doyle and Snell, 1989), and it was proven to be proportional to the commute-time between its endpoints (Chandra et al., 1996). Moreover, (Klein and Randić, 1993) showed that the square root of the effective resistance between any couple of nodes (i,j) is a Euclidean metric, in particular it measures the distance between nodes i and j. Thus, the computation of the effective resistance for each edge of G provides a distance matrix between each couple of nodes of G.

In this paper, given a network $G=(V,E)$, where V is the set of nodes and E of edges, we propose an evolutionary algorithm to detect communities by exploiting the concept of effective resistance. The main idea is to apply a *Genetic Algorithm (GA)* (Goldberg, 1989) to find communities on the weighted graph

[a] https://orcid.org/0000-0001-7297-7126
[b] https://orcid.org/0000-0001-5420-9959

Pizzuti, C. and Socievole, A.
An Effective Resistance based Genetic Algorithm for Community Detection.
DOI: 10.5220/0010644300003063
In *Proceedings of the 13th International Joint Conference on Computational Intelligence (IJCCI 2021)*, pages 28-36
ISBN: 978-989-758-534-0; ISSN: 2184-3236

$G' = (V, W)$ obtained from G by computing the effective resistance of all the node pairs of G. G' has the same set V of nodes of G, while the set W of edges consists of the effective resistance between any couple of nodes (i, j) of V. However, the adjacency matrix Ω corresponding to G' is a full matrix, thus a sparsification procedure is necessary to reduce the number of edges and make clear the original network structure.

The simplest way to obtain a sparse graph is the weight thresholding (Yan et al., 2018), i.e. removing the edges whose weight is above a fixed threshold. Deleting as many edges as possible without altering the original system is a key point.

Our approach considers for each node i only a fixed number nn of the most similar nodes and removes from Ω all the edges between i and the nodes not included in this set of nn nearest neighbors to obtain a sparse weighted adjacency matrix $\widetilde{\Omega}$. We therefore run the GA over the sparsified weighted adjacency matrix $\widetilde{\Omega}$ by evolving a population of individuals and minimizing the concept of *modularity* of a partition, the most popular quality function of community structure introduced by Girvan and Newman (Girvan and Newman, 2002).

A comparison with a baseline genetic algorithm optimizing modularity and running on the original graph G, along with two of the best-known community detection methods *Louvain* (Blondel et al., 2008) and *Infomap* (Rosvall and Bergstrom, 2008) shows that the proposed algorithm obtains results better than the contestant methods both over synthetically generated and real-world networks.

The paper is organized as follows. The next section describes some measures proposed for computing node similarity and how these measures are used for the community detection task. Section 3 recalls the concept of effective resistance, defines the community detection problem we tackle and describes our method. Section 4 describes the datasets used and the experiments performed to validate the proposed algorithm. Finally, Section 5 concludes the paper and discusses the future directions.

2 RELATED WORK

Distances and similarity measures between the nodes of a graph are widely used in data analysis and especially in clustering tasks. Many measures have been proposed so far including the widely investigated Shortest Path distance (Dijkstra et al., 1959), the Resistance (Klein and Randić, 1993), the logarithmic Walk measure, the Forest measure related to Resistance, and many others (Deza and Deza, 2009) (Avrachenkov et al., 2017).

In their pioneering work, Klein and Randic (Klein and Randić, 1993) proposed the use of the *effective resistance*, also named *resistance distance*, between two nodes as a meaningful distance measure. Indeed, it has been shown that this measure is a Euclidean distance.

The close link between the effective resistance and the commute-time of a random walker on a graph has been studied in (Chandra et al., 1996). Moreover, the relationship between the Laplacian matrix of the graph and the commute-time was investigated in (Saerens et al., 2004). For this reason, the effective resistance is also named *commute-time distance*.

In (Avrachenkov et al., 2019), a set of similarity measures on graphs based on three fundamental graph matrices, the adjacency matrix, the Laplacian matrix, and the stochastic Markov matrix are analytically studied and compared. For each measure, the work investigates if it is (a) a kernel, (b) a proximity measure, and (c) a transitional measure.

In (Yen et al., 2007), the commute-time kernel is used for clustering the nodes of a weighted undirected graph. The method is based on a two-step procedure that initially computes the sigmoid commute-time kernel matrix from the adjacency matrix of the graph, providing a similarity measure between nodes, and then, clusters the nodes by exploiting a kernel-based k-means or fuzzy k-means on the obtained kernel matrix. The proposed methodology combining commute-time kernel and kernel clustering outperforms standard k-means, as well as spectral clustering, on a difficult graph clustering problem.

A comprehensive study on graph nodes clustering with the sigmoid commute-time kernel can be found in (Yen et al., 2009). In (Sommer et al., 2016), six different distance measures are transformed into kernels and tested on kernel k-means and a weighted version of it. A comparison with the Louvain method shows the effectiveness of the distance-based algorithms.

The impact of network topology on the efficiency of proximity measures for community detection is investigated in (Aynulin, 2019). Specifically, the work checks wether the advantage of using one measure is kept for different network topologies. The authors showed that there are measures behaving well for most topologies.

In the next section the concept of effective resistance metric is recalled and how it is exploited for detecting effective community structure is described.

3 COMMUNITY DETECTION BASED ON EFFECTIVE RESISTANCE

In this section, we first introduce the concept of effective resistance as distance metric and then describe the proposed method.

3.1 Effective Resistance

Klein and Randic, in their seminal work (Klein and Randić, 1993), proposed the theory of resistive electrical networks to define a new distance function between vertices. They suggested that if fixed resistors are assigned to the edge of a connected graph, the effective resistance between couples of nodes is a graphical distance.

Given an undirected and connected graph $G = (V,E)$, an *equivalent electric network* can be associated with G by weighting each edge $(i,j) \in E$ with positive weights w_{ij} representing the conductance, i.e. the inverse of the electrical resistance ω_{ij} of a resistor, so that $\omega_{ij} = \frac{1}{w_{ij}}$ *ohm* (Klein and Randić, 1993). As described in (Klein and Randić, 1993; Van Mieghem et al., 2017), for any edge of the graph G, a distance function can be defined as follows.

The *effective resistance* ω_{ij} between any pair of nodes i and j is defined as the voltage developed between i and j when a unit current is injected at node i and is withdrawn at node j. The corresponding $N \times N$ matrix including all the ω_{ij} between each node pair i and j is denoted Ω.

The interesting feature is that ω_{ij} is upper bounded by the shortest path distance in a graph (Van Mieghem, 2010). Moreover, the communte-time distance C_{ij} between two nodes i and j, i.e. the expected number of steps needed during a random walk from i to j, is $C_{ij} = u^T\widetilde{A}u\ \omega_{ij}$, where u is the all one vector and $u^T\widetilde{A}u$ is the double of the sum of all the edge weights in the weighted adjacency matrix $\widetilde{A}$ (Chandra et al., 1996).

In (Klein and Randić, 1993), it is shown that the square root $\sqrt{\omega}_{ij}$ of the effective resistance is a Euclidean metric. More precisely, the effective resistance matrix Ω is a distance matrix, in which for any triple of non-negative elements, $\omega_{ii} = 0$, and the triangle inequality, $\omega_{ij} \leq \omega_{ik} + \omega_{kj}$ is satisfied.

Moreover, Ω can be defined (Doyle and Snell, 1989; Klein and Randić, 1993; Van Mieghem, 2010) as

$$\Omega = \zeta u^T + u\zeta^T - 2L^+ \tag{1}$$

where the vector

$$\zeta = \left(L^+_{11}, L^+_{22}, \ldots, L^+_{NN}\right) \tag{2}$$

contains the diagonal elements of the Moore-Penrose *pseudoinverse* matrix L^+ of the weighted Laplacian matrix $\widetilde{L}$ of the graph G.

Recall that, given $\Delta = diag(d_i)$ the $N \times N$ diagonal degree matrix, where $d_i = \sum_{j=1}^{N} a_{ij}$, the Laplacian matrix L of the graph G is defined as the $N \times N$ symmetric matrix $L = \Delta - A$, with elements

$$l_{ij} = \begin{cases} d_i & \text{if } i = j \\ -1 & \text{if the edge } (i,j) \in E \\ 0 & \text{otherwise} \end{cases} \tag{3}$$

The effective resistance between two nodes x and y equals

$$\omega_{xy} = (e_x - e_y)^T L^+ (e_x - e_y) = l^+_{xx} + l^+_{yy} - 2l^+_{xy} \tag{4}$$

where e_k is the basic vector with the m-th component equal to $(e_k)_m = \delta_{mk}$ and δ_{mk} is the Kronecker-delta: $\delta_{mk} = 1$ if $m = k$, otherwise $\delta_{mk} = 0$.

3.2 Problem Definition

Given a graph G, let Ω be the resistance matrix associated with G, nn the number of nearest neighbors to consider, and $\widetilde{\Omega}$ the matrix obtained from Ω with elements

$$\widetilde{\omega}_{xy} = \begin{cases} \omega_{xy} & \text{if } y \text{ is among the } nn \\ & \text{nearest neighbors of } x \\ 0 & \text{otherwise} \end{cases} \tag{5}$$

The community detection problem is defined as: *find a partition $C = \{C_1, \ldots, C_k\}$ of the nodes of G such that the weighted modularity of C is maximized.*

The weighted modularity Q is computed as

$$Q = \frac{1}{2m} \sum_{ij} \left(\widetilde{\omega}_{ij} - \frac{k_i k_j}{2m} \right) \delta(C_i, C_j) \tag{6}$$

where m is the sum of the edge weights, k_i and k_j the sum of the weights of the edges attached to nodes i and j respectively, and δ is the Kronecker function which yields one if i and j are in the same community, i.e. $C_i = C_j$, zero otherwise. Modularity measures the expected number of edges within the communities of a random graph with the same degree distribution.

Basically, we look for a community structure where both intra-community weighted modularity and similarity between nodes is high (thus the overall distance between the nodes of the same community is low).

3.3 Method Description

In this section, a detailed description of the method is given. *OmeGAnet* is a method based on Genetic Algorithms (*GA*) (Goldberg, 1989), an *evolutionary computation* technique which revealed very efficacious for the task of community detection (Pizzuti, 2018).

The algorithm creates a population of individuals (i.e. a network division in communities) that are initially randomly generated, and then evolves the population through variation and selection operators by optimizing the value of the objective function while exploring the search space.

Each individual is represented with the *locus-based* adjacency representation (Park and Song, 1998) for which an individual I is a vector of N genes (i.e. nodes). Each gene can assume a value k from 1 to N. When a value k is assigned to the i-th gene, it means that nodes i and k are connected. A decoding step identifies all the connected components of the graph which correspond to the network division in communities.

As crossover operator, *OmeGAnet* exploits the *uniform crossover* which generates a random binary mask of length equal to the number of nodes. The offspring is then generated by selecting from the first parent the genes where the mask is 0, and from the second parent the genes where the mask is 1.

Finally, the mutation operator randomly assigns the value of a i-th gene to one of its neighbors.

The steps performed by *OmeGAnet* are the following. It receives in input the graph $G = (V, E)$, the number of nearest neighbors *nn* to consider, and performs the following steps:

1. compute the Laplacian L of G;
2. compute the Moore-Penrose *pseudoinverse* matrix L^+ of L;
3. compute the effective resistance matrix Ω from L^+ as $\omega_{xy} = l^+_{xx} + l^+_{yy} - 2l^+_{xy}$;
4. make Ω a distance matrix by substituting each element as $\omega_{xy} = \sqrt{\omega_{xy}}$;
5. normalize the elements of Ω and make Ω a symmetric matrix $\Omega = 0.5[\frac{\Omega}{max(\Omega)} + (\frac{\Omega}{max(\Omega)})^T]$;
6. generate the sparse similarity weighted matrix $\widetilde{\Omega}$ from Ω by maintaining for each node x only the *nn* entries ω_{xy} having the minimum distance value, i.e the connections with the nodes y having the highest similarity values with x;
7. run the Genetic Algorithm on $\widetilde{\Omega}$ for a number of iterations by using modularity as fitness function to maximize, uniform crossover and neighbor mutation as variation operators;
8. obtain the partition $C = \{C_1, \dots, C_k\}$ corresponding to the solution with the highest fitness value.

Table 1: LFR-128 parameters setting.

Parameter	Value
Number of nodes	128
Node average degree	8
Node maximal degree	9
Exponent for power law creating degree sequence	2
Exponent for power law creating community sizes	1
Mixing parameter μ	[0.1; 0.6]
Maximal community size	40
Minimal community size	20
Average density	0.062

In the next section, we compare *OmeGAnet* with three community detection methods and compare the results they obtain on synthetic and real-world datasets.

4 EXPERIMENTAL EVALUATION

For validating *OmeGAnet*, we performed several simulations using Matlab 2020a and the Global Optimization Toolbox.

Regarding the input parameters to our approach, we experimentally set them by performing a trial and error procedure.

In the following subsections we describe the datasets, the evaluation measures used, the algorithms in comparison and finally the results obtained.

4.1 Datasets

4.1.1 Synthetic Networks

To create synthetic networks with realistic community structures, the Lancichinetti-Fortunato-Radicchi (LFR) benchmark (Lancichinetti et al., 2008) has been used.

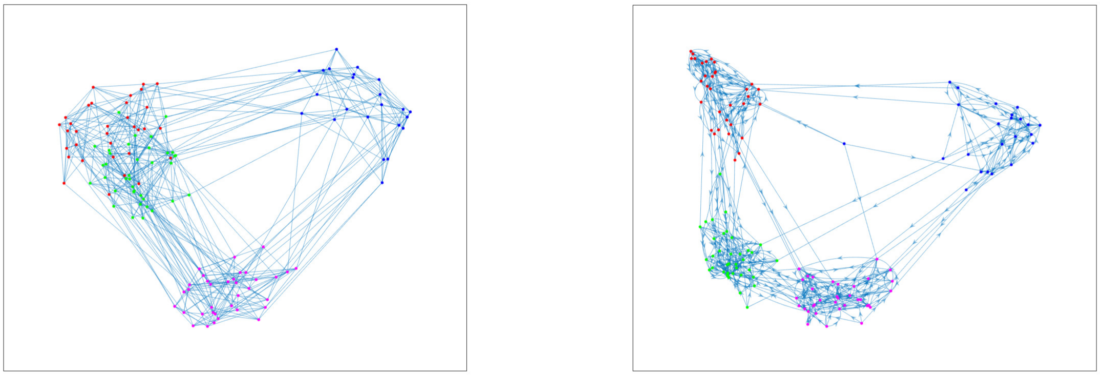
This well-known and widely used network generator is able to control the structure of the communities by properly setting the *mixing parameter* μ. The lower the μ, the clearer the resulting community structure with much more intra-community links than inter-cluster links. On the contrary, when μ has high values, the community structure is not clear.

The parameters used for generating the LFR networks are shown in Table 1. In particular, for each μ value we generated 10 network instances.

4.1.2 Real-world Networks

We considered four real-world networks for which the ground-truth division is known.

- **Zachary Karate Club.** This well-known dataset contains the data of the friendship social network



(a) (b)

Figure 1: (a) A 128-nodes LFR network generated with $\mu = 0.2$ and (b) its reduced graph with $nn = 5$.

of 34 members of a karate club, collected by Wayne Zachary in 1977. The group has been observed for two years, splitting in two communities almost of the same size due to disagreements between the members.

- **Amazon US Politics Books.** The second dataset contains the data of books co-purchased on Amazon.com by customers during the US political elections in 2004. The network was collected by Krebs and contains 105 nodes and 374 edges. The books were later classified into the three political groups liberal, neutral and conservative by Newman.
- **American College Football.** This dataset contains the network of 115 American football teams extracted from the Fall 2000 regular season games. The teams were linked during a game with a resulting number of 616 edges/games and partitioned in 12 communities.
- **Bottlenose Dolphins.** The last dataset contains the network of 62 Bottlenose dolphins from Doubtful Sound in New Zealand. Linked through 159 edges, the edges represent frequent associations observed between dolphins. Here, the dolphins are partitioned into two communities.

4.2 Evaluation Measure

We evaluate the quality of the solutions by using the *Normalized Mutual Information (NMI)*.

Given two divisions A and B of a network, and C the confusion matrix whose element C_{ij} is the number of nodes of community i of the partition A that are also in the community j of the partition B, the NMI between A and B is defined as:

$$NMI(A,B) = \frac{-2\sum_{i=1}^{c_A}\sum_{j=1}^{c_B} C_{ij} log(C_{ij}n/C_{i.}C_{.j})}{\sum_{i=1}^{c_A} C_{i.} log(C_{i.}/n) + \sum_{j=1}^{c_B} C_{.j} log(C_{.j}/n)} \tag{7}$$

where c_A (c_B) is the number of groups in the partition A (B), $C_{i.}$ ($C_{.j}$) is the sum of the elements of C in row i (column j), and n is the number of nodes. If $A = B$, $NMI(A,B) = 1$. If A and B are completely different, $NMI(A,B) = 0$.

4.3 Algorithms in Comparison

We first compare *OmeGAnet* with a baseline GA-based algorithm, denoted *GA-mod*, adopting the same locus-based representation, initialization, crossover and mutation operators which optimizes the modularity value. In particular, population initialization connects a node with one of its *nn* nearest neighbors, instead of a random neighbor.

We also compare *OmeGAnet* to two benchmarks: *Louvain* (Blondel et al., 2008) and *Infomap* (Rosvall and Bergstrom, 2008).

The *Louvain* method is based on a greedy modularity optimization approach. First, the algorithm identifies small communities by locally optimizing modularity. Then, it builds a new network whose nodes are the communities previously found, and these steps are repeated until a hierarchy of high-modularity communities is obtained.

Infomap exploits the principles of information theory by defining the community detection problem as the problem of finding a description of minimum information of a random walk on the graph. The method maximizes the Minimum Description Length as objective function by quickly providing an approximation of the optimal solution.

Table 2: NMI results for the LFR-128 networks.

	$\mu = 0.1$	$\mu = 0.2$	$\mu = 0.3$	$\mu = 0.4$	$\mu = 0.5$	$\mu = 0.6$
OmeGAnet	1	1	0.8049	0.3308	0.1314	0.0698
GA-mod	1	1	0.6967	0.2988	0.117	0.06
Louvain	0.8793	0.8716	0.5555	0.3228	0.0865	0.055
Infomap	1	1	0.6728	0.2875	0.1162	0.0624

Table 3: Modularity results for the LFR-128 networks.

	$\mu = 0.1$	$\mu = 0.2$	$\mu = 0.3$	$\mu = 0.4$	$\mu = 0.5$	$\mu = 0.6$
OmeGAnet	0.7038	0.5446	0.3983	0.3308	0.2999	0.2854
GA-mod	0.7038	0.5446	0.3908	0.3104	0.3223	0.3035
Louvain	0.6268	0.4661	0.3733	0.314	0.3356	0.3086
Infomap	0.7038	0.5446	0.4101	0.2875	0.3386	0.3289

4.4 Results

The first experiment has been carried out on a pool of synthetic network with 128 nodes.

Figure 1 shows an instance of a network generated with a mixing parameter $\mu = 0.2$. Figure 1 (a) shows the community structure of the ground-truth composed by four communities colored in red, green, magenta and blue. Figure 1 (b), shows the reduced graph with *nn*=5, the value for this parameter able to produce the better results.

It is worth pointing out that, by considering the subset of neighbors having the highest similarity (i.e. the lowest distance), the underlying communities are more visible and the structure is clearer. Here, the few interlinks between communities make, for example, more visible the communities in green and in red. Table 2 shows the NMI results for the LFR-128 networks.

For the genetic algorithms *OmeGAnet* and *GA-mod* we have set maximum number of generations 100, population size 700, *nn*=5, crossover fraction 0.9 and mutation rate 0.1. Each value has been averaged over 10 runs of the method. For communities with clear structure ($\mu = 0.1$ and $\mu = 0.2$), the two genetic algorithms and *Infomap* match the ground-truth correctly identifying the underlying communities.

Louvain, on the contrary, achieves only 0.8793 and 0.8716 for $\mu = 0.1$ and $\mu = 0.2$, respectively. As μ increases and the structure of the communities changes becoming less clear, *OmeGAnet* always outperforms all the other contestant methods. From $\mu = 0.3$ to $\mu = 0.6$ the NMI significantly decreases achieving very low values for $\mu = 0.6$.

In Table 3, the modularity values are reported. For $\mu = 0.1$ and $\mu = 0.2$ the modularity value achieved with NMI=1 is 0.7038, as can be observed for *OmeGAnet*, *GA-mod*, and *Infomap*. For $\mu = 0.3$, $\mu = 0.5$ and $\mu = 0.6$ the highest modularity is obtained by *Infomap* while for the other approaches optimizing modularity the highest value is obtained by *OmeGAnet* for $mu = 0.4$.

Table 4: Number of communities for the LFR-128 networks.

	GT	*OmeGAnet*	*GA-mod*	Louvain	Infomap
$\mu = 0.1$	4	4	4	5	4
$\mu = 0.2$	4	4	4	3	4
$\mu = 0.3$	4	4	5	5	7
$\mu = 0.4$	4	4	7	7	9
$\mu = 0.5$	4	4	7	7	6
$\mu = 0.6$	4	4	7	7	9

We point out that our focus is to obtain the highest NMI value for the community partition found and this not always corresponds to the highest modularity value as can be observed.

In Table 4, we finally show the number of communities obtained for a single run of a network. In the second column, the number of classes for the ground- truth (GT) is reported. For each μ the ground-truth is composed by 4 communities. *OmeGAnet* is always able to split the network in 4 groups while the other schemes fragment the communities resulting in a higher number of communities from $\mu = 0.3$ to $\mu = 0.6$. For $\mu = 0.4$, for example, *GA-mod* and *Louvain* find 7 communities, while *Infomap* even 9.

In the second experiment, we tested *OmeGAnet* on the real-world networks described above for which the true number of communities is known.

Table 5 shows the NMI results obtained by setting for the genetic algorithms maximum number of generations 100, population size 500, $nn = 4$, crossover fraction 0.9 and mutation rate 0.1.

In Tables 6 and 7 the modularity and the number of communities are reported. Also for this experiment, the NMI and the modularity values are averaged over 10 runs while the number of communities refers to a single run.

In terms of NMI, *OmeGAnet* outperforms the

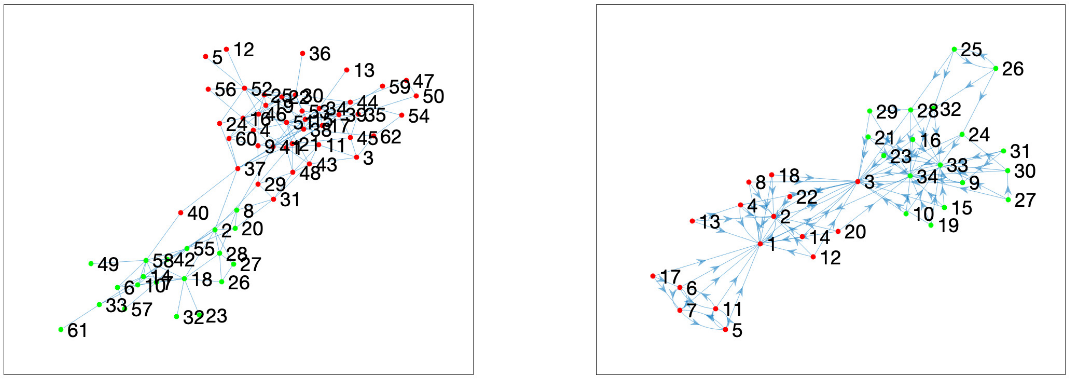


Figure 2: The Zachary Karate Club (a) and its reduced graph with $nn = 4$ (b).

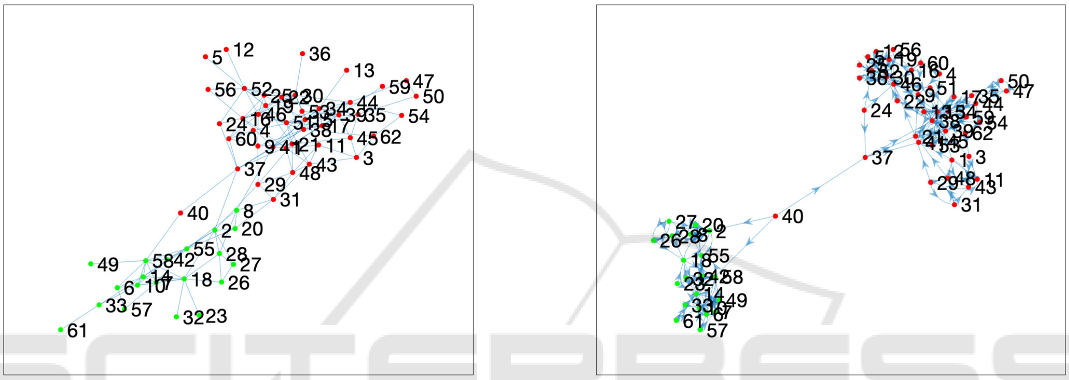


Figure 3: The Bottlenose Dolphins (a) and its reduced graph with $nn = 4$ (b).

other contestant methods also in the real-world networking scenarios considered. For Karate, for example, the two communities are correctly identified while *GA-mod* achieves only 0.5485, *Louvain* 0.5195 and *Infomap* 0.6995 of NMI.

Figure 2 shows the Karate original graph (a) and its reduced version (b) where we can observe that the communities are much more clear than in the original network. Also for the Dolphins dataset, *OmeGAnet* significantly outperforms the other methods.

Figure 3 shows how the reduction of the initial graph better separates the communities. The modularity results, show again that a high modularity does not correspond always to a high NMI. In fact, for Karate, for example, the modularity value giving the ground-truth is the one found by *OmeGAnet*, 0.3715, which is the lowest.

Looking at the number of communities, it is worth pointing out that *OmeGAnet* matches the number of underlying communities in most of the cases. The other algorithms, on the contrary, produce partitions with a higher number of communities. For Dolphins, for example, where the network is divided into two groups, *GA-mod*, *Louvain* and *Infomap* find 4, 10 and 6 communities, respectively.

Table 5: NMI results for the real-world networks with maxGen=100, popSize=500 and nn=4.

	OmeGAnet	*GA-mod*	Louvain	Infomap
Karate	1	0.5485	0.5195	0.6995
Books	0.6313	0.5338	0.4142	0.5369
Football	0.9326	0.9151	0.9269	0.9242
Dolphins	0.8888	0.5749	0.5169	0.5197

Table 6: Modularity results for the real-world networks.

	OmeGAnet	*GA-mod*	Louvain	Infomap
Karate	0.3715	0.4033	0.402	0.402
Books	0.4546	0.4793	0.4833	0.5268
Football	0.5976	0.6008	0.601	0.6005
Dolphins	0.3787	0.5124	0.4952	0.5146

Table 7: Number of communities for the real-world networks.

	GT	*OmeGAnet*	*GA-mod*	Louvain	Infomap
Karate	2	2	4	3	3
Books	3	2	3	8	5
Football	12	12	11	12	12
Dolphins	2	2	4	10	6

5 CONCLUSIONS

We proposed *OmeGAnet*, a new method based on genetic algorithms for dividing the nodes of an undirected and connected graph in communities.

We considered the graph as an electric circuit and computed for each couple of connected nodes the *effective resistance*. We then exploited this distance for weighting the graph and searching communities with high weighted modularity.

By performing several experiments on both synthetic and real-world networks, the results show that the proposed methodology is promising since it clearly outperforms both a standard GA-based algorithm running on the original adjacency matrix of the graph, and the state-of-the-art approaches *Louvain* and *Infomap*.

It is worth pointing out that the choice of the parameter *nn* plays an important role on the performance of *OmeGAnet*. In the current implementation we experimentally set it and found that low values of *nn* allow to obtain good results.

However, more study is necessary to find a general criterion which allows a good setting of this parameter. In fact, the network sparsification is crucial for improving the quality of the community division obtained by the approach.

(Yan et al., 2018) proposed a measure that estimates the variation of spectral properties of the graph when edges are removed. They showed that the structure of real weighted networks is very robust under weight thresholding when edges are removed if their weight is below a threshold value computed with such a measure.

This research line could be a starting point deserving deeper investigation which could be beneficial for determining the minimum number of nearest neighbors to consider when building the sparse similarity weighted matrix $\widetilde{\Omega}$.

REFERENCES

Avrachenkov, K., Chebotarev, P., and Rubanov, D. (2017). Kernels on graphs as proximity measures. In *International workshop on algorithms and models for the web-graph*, pages 27–41. Springer.

Avrachenkov, K., Chebotarev, P., and Rubanov, D. (2019). Similarities on graphs: Kernels versus proximity measures. *European Journal of Combinatorics*, 80:47–56.

Aynulin, R. (2019). Impact of network topology on efficiency of proximity measures for community detection. In *International Conference on Complex Networks and Their Applications*, pages 188–197. Springer.

Barrat, A., Barthelemy, M., Pastor-Satorras, R., and Vespignani, A. (2004). The architecture of complex weighted networks. In *Proc. National Academy of Science*, pages 101,3747.

Blondel, V. D., Guillaume, J.-L., Lambiotte, R., and Lefebvre, E. (2008). Fast unfolding of communities in large networks. *Journal of statistical mechanics: theory and experiment*, 2008(10):P10008.

Chandra, A. K., Raghavan, P., Ruzzo, W. L., Smolensky, R., and Tiwari, P. (1996). The electrical resistance of a graph captures its commute and cover times. *Computational Complexity*, 6(4):312–340.

Deza, M. M. and Deza, E. (2009). Encyclopedia of distances. In *Encyclopedia of distances*, pages 1–583. Springer.

Dijkstra, E. W. et al. (1959). A note on two problems in connexion with graphs. *Numerische mathematik*, 1(1):269–271.

Doyle, P. and Snell, J. (1989). *Random walks and electric networks*. Mathematical Association of America.

Fortunato, S. and Hric, D. (2016). Community detection in networks: A user guide. *Physics reports*, 659:1–44.

Ghosh, A., Boyd, S., and Saberi, A. (2008). Minimizing effective resistance of a graph. *SIAM Rev.*, 50(1):37–66.

Girvan, M. and Newman, M. E. (2002). Community structure in social and biological networks. *Proceedings of the national academy of sciences*, 99(12):7821–7826.

Goldberg, D. E. (1989). Genetic algorithms in search. *Optimization, and MachineLearning*.

Klein, D. J. and Randić, M. (1993). Resistance distance. *Journal of mathematical chemistry*, 12(1):81–95.

Lancichinetti, A., Fortunato, S., and Radicchi, F. (2008). Benchmark graphs for testing community detection algorithms. *Physical review E*, 78(4):046110.

Park, Y. and Song, M. (1998). A genetic algorithm for clustering problems. In *Proceedings of the third annual conference on genetic programming*, volume 1998, pages 568–575.

Pizzuti, C. (2018). Evolutionary computation for community detection in networks: a review. *IEEE Transactions on Evolutionary Computation*, 22(3):464–483.

Radicchi, F., Ramasco, J. J., and Fortunato, S. (2011). Information filtering in complex weighted networks. *Physical Review E*, E83:046101.

Rosvall, M. and Bergstrom, C. T. (2008). Maps of random walks on complex networks reveal community structure. *Proceedings of the National Academy of Sciences*, 105(4):1118–1123.

Saerens, M., Fouss, F., Yen, L., and Dupont, P. (2004). The principal components analysis of a graph, and its relationships to spectral clustering. In *European conference on machine learning*, pages 371–383. Springer.

Sommer, F., Fouss, F., and Saerens, M. (2016). Comparison of graph node distances on clustering tasks. In *International Conference on Artificial Neural Networks*, pages 192–201. Springer.

Spielman, D. A. and Srivastava, N. (1996). Graph sparsification by effective resistances. *Siam Journal on Computing*, (40):1913.

Tumminello, M., Aste, T., Matteo, T. D., , and Mantegna, R. N. (2005). A tool for filtering information in complex systems. In *Proc. National Academy of Science*, pages 102,10421.

Van Mieghem, P. (2010). *Graph spectra for complex networks*. Cambridge University Press.

Van Mieghem, P., Devriendt, K., and Cetinay, H. (2017). Pseudoinverse of the laplacian and best spreader node in a network. *Physical Review E*, 96(3):032311.

Yan, X., Jeub, L. G. S., Flammini, A., Radicchi, F., and Fortunato, S. (2018). Weight thresholding on complex networks. *Physical Review E*, E98:042304.

Yen, L., Fouss, F., Decaestecker, C., Francq, P., and Saerens, M. (2007). Graph nodes clustering based on the commute-time kernel. In *Pacific-Asia Conference on Knowledge Discovery and Data Mining*, pages 1037–1045. Springer.

Yen, L., Fouss, F., Decaestecker, C., Francq, P., and Saerens, M. (2009). Graph nodes clustering with the sigmoid commute-time kernel: A comparative study. *Data &amp; Knowledge Engineering*, 68(3):338–361.