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EVOLUTIONARY COALITION FORMATION IN COMPLEX NETWORKS

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Abstract. An optimal clusterization model is introduced and studied - an approach that combines an evolutionary algorithm by the principles of the physical spin systems. The method is used to investigate the process of coalition formation that appears in complex systems. The numerical experiments show that the proposed hybrid model is able to detect the optimal clusterization in small and large systems by a reasonable cost of complexity (seen in terms of time and physical computational resources).

1. Introduction

Almost all interesting processes in nature are highly cross-linked. In many systems, however, we can identify the elements that interact to form compound structures or functions. The interconnected simple elements can form a complex system if they, together, exhibit a high degree of complexity from which emerges a higher order behaviour. Examples of complex systems include ant-hills, ants themselves, human economies, climate, nervous systems, cells and living things, including human beings, the brain, the immune system, the metabolic networks, the economic markets, and the human social networks, as well as modern energy or telecommunication infrastructures, the Internet and World Wide Web. Therefore, a complex system is any system featuring a large number of interacting components, whose aggregate activity is nonlinear and typically exhibits hierarchical self-organization under selective pressures.

More formally, a complex system is any system featuring a large number of interacting components (agents, processes, etc.) whose aggregate activity is nonlinear (not derivable from the summations of the activity of individual components) and typically exhibits hierarchical self-organization under selective pressures [20].

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An interesting problem that appears in such complex systems is the process of coalition formation. The optimization of several models proposed for studying the coalition formation in complex system (politics, economics or sociological systems) are based on simulated annealing [18, 16, 8] or on extremal optimization [4, 6] methods. Both optimization techniques are rather time-consuming and the necessary computational time increases strongly with the system size. The evolutionary techniques could overtake this weakness. It will be shown, in this paper, that the evolutionary methods can simulate very well the true dynamic of such complex systems and they allow analysing the phase transition from the viewpoint of the much-discussed social percolation [24], where the emergence of a giant cluster is observed in many social phenomena.

Physical concepts might prove useful in describing collective social phenomena. Indeed models inspired by statistical physics are now appearing in scientific literature [22]. The process of aggregation among a set of actors seems to be a good candidate for a statistical physics like model [21]. These actors might be countries, which ally into international coalitions, companies that adopt common standards, parties that make alliances, individuals that form different interest groups, and so on. Given a set of actors, there always exists an associated distribution of bilateral propensities towards either cooperation or conflict. The question then arises as to: *How to satisfy such opposing constraints simultaneously?*. In other words, *what kind of alliances, if any, will optimize all actor bilateral trends to respectively conflict or cooperation?*

It turns out that a similar problem does exist in spin glasses (as Ising or Potts models [11, 12, 14]). For these systems, the magnetic exchanges are distributed randomly between the ferro and anti-ferromagnetic couplings. Indeed such an analogy has been used in the past in a few models [21].

The aim of this paper is to provide a new hybrid model in order to investigate the process of coalition formation that can appear in a complex system. Coalition setting among a set of actors is studied using concepts from the theory of spin glasses and from the theory of evolution. Those of evolutionary computation combine the principles of the Potts model. Unlike other solutions proposed until now in order to study the dynamic of such complex system (simulated annealing or Monte Carlo methods), the proposed model is able to deal with large systems and helps us to investigate different phenomena that appear in such systems. The numerical results indicate that the hybrid approach is able to identify the characteristics of the coalition formation process.

The rest of the paper in organised as follows. A short description of the coalition formation problem (and its real implications) is given in Section 2. The Potts model is briefly described in Section 3. Section 4 proposes the

hybrid evolutionary approach for investigating the process of coalition formation. Several numerical experiments are presented and discussed in Section 5. Finally, the last section concludes the paper.

2. Problem formulation

Often-cited examples of complex systems in nature and society include the gene networks, the immune networks that preserve the identity of organisms, the social insect colonies, the neural networks in the brain that produce intelligence and consciousness, the ecological networks, the social networks comprised of transportation, utilities, and telecommunication systems, as well as the economies [20].

The field of complex systems seeks to explain and uncover common laws for the emergent, self-organizing behaviour seen in complex systems across disciplines. Many scientists also believe that the discovery of such general principles will be essential for creating artificial life and artificial intelligence [20]. Complex systems, as their name implies, are typically hard to understand. Traditionally the more mathematically oriented sciences such as physics, chemistry, and mathematical biology have concentrated on simpler model systems that are more tractable via mathematics. The rise of interest in understanding general properties of complex systems has paralleled the rise of the computer, because the computer has made it possible for the first time in history to make models of complex systems in nature that are more accurate.

In recent years, there has been a strong upsurge in the study of networks in many disciplines, ranging from computer science and communications to sociology and epidemiology. Some of the areas can profit from the application of complex systems modelling research and development: computational biology (DNA sequencing, micro-array data analysis, genetic regulatory networks, models of genetic regulatory processes), social systems (social networks, decision processes and knowledge structures of multi-agent systems, economic and financial markets modelling, homeland defence and intelligence community), distributed knowledge systems(information retrieval, web technology and digital libraries, knowledge integration), optimization, local search methods, extremal optimization, combinatorial optimization in biology, evolutionary systems (evolutionary algorithms, cellular automata and artificial life).

A network (or graph) is simply a collection of nodes (vertices) and links (edges) between nodes. The links can be directed or undirected, and weighted or un-weighted. Many natural phenomena can be usefully described in network terms.

Recent work [28, 3] have emphasized the importance of "network thinking" in dealing with complex systems in the real world. The purpose of characterizing networks according to degree distribution, clustering coefficient and average path length, is both to better understand networks from a scientific point of view and to develop better technologies for designing and managing networks in desired ways.

Another important application of network analysis is the problem of finding clusters, or community structures, in a given network. This is the problem of finding sub-networks ("communities") that contain dense interconnections, meaning that nodes in a given community are much more likely to be related to nodes in that same community than to nodes in other parts of the network. Finding such communities is related to the problem of graph partitioning in computer science, and to the problem of hierarchical clustering in sociology.

A complex system can be reduced to a full-connected graph this time in order to investigate the clusterization phenomena that appear in these systems. The following clusterization problem is considered: we have a complete graph on n vertices (items), where each edge (u, v) is labelled either $+$ or $-$ depending on whether u and v have been deemed to be "similar" or "different". The notion of similarity of two vertices could be understood as a propensity for cooperation or as a relation of sympathy or agreement between the two nodes. The goal is to produce a partition of the vertices (a clustering) that agrees as much as possible with the edge labels: a clustering that maximises the number of nodes that collaborate within clusters and that minimises, at the same time, the number of nodes that have antipathy relations

3. The Potts model

Understanding human thinking and learning has always been a great challenge for all the scientists and not only. The challenge has taken another dimension as scientists are trying to simulate the learning and thinking processes by using the computers and other devices. The nature inspired and Physics models have been of great help.

Even though very simple, the Ising model and its generalization, the Potts model, have been applied successfully in several computational problems. In its original form, the Ising model describes the evolution of a grid of up and down spins over time. Each spin can change its orientation in time, according to the external temperature and the values of its orthogonal neighbours [1]. The Potts system involves similar dynamics for the spins, but each spin can have more than two (up and down) orientations.

A simple version of a spin glass [19] consists of a d-dimensional hyper-cubic lattice with a spin variable $\sigma_i \in \{-1, 1\}$ placed on each site i, $1 \leq i \leq n$. A

spin is connected to each of its neighbours j via a bond variable $J_{i,j}$ drawn from some distribution $P(J)$ with zero mean and unit variance [21].

The infinite-range p-state Potts glass is usually defined by the Hamiltonian: $H(\sigma) = -p\sum_i \sum_j J_{ij}\delta_{\sigma_i\sigma_j}$, where the $\sigma(i)$ Potts states can take the $0, 1, 2, \ldots, p-1$ values. The sum is extended over all $N(N-1)/2$ pairs and $\delta_{mn} = 1$ if $m = n$ and $\delta_{mn} = 0$ otherwise. The J_{ij} bonds are randomly distributed quenched variables with J_0/N mean, and the variance is presumed to scale as N^{-1}. The system is non-trivially frustrated and computing the thermodynamic parameters is a complex task. The above model has been extensively studied by many authors through different methods [11, 14]. The main idea of these models is to find the "ground states", *i.e.*, the lowest energy configuration S_{min} of the Hamiltonian.

Neda et al. have considered a model resembling the infinite-range Potts glass [21], which can be useful for considering the optimal clusterization problem or for understanding the coalition formation phenomena in sociological systems. A difference to the Potts glass is that now the variance of the J_{ij} bonds scales as N^{-2}. The authors [21] have considered an unrestricted number of Potts states ($p = N$), and limit the study on the ground state ($T = 0$).

Therefore, this non-trivial optimization problem can be mathematically formulated resembling a zero-temperature Potts glass type model. To prove this, a cost-function, K, (a kind of energy of the system) has been defined. This function has been increased by $S_iS_j|Z_{ij}|$ whenever two conflicting actors (i and j) are in the same coalition or two actors which have a tendency towards collaboration are in different coalition. The cost-function is zero, when no propensity is in conflict with the formed coalitions. The number of possible coalitions is unrestricted (the maximal possible number is N), and the coalition in which actor i is denoted by $\sigma(i)$ [21]. The cost function then writes as

$$K = -\sum_{i<j} \delta_{\sigma(i)\sigma(j)} Z_{ij} S_i S_j + \frac{1}{2}\sum_{i<j}(Z_{ij}S_iS_j + |Z_{ij}S_iS_j|) \tag{1}$$

The order parameter considered by Neda et al. in [21] has been the relative size r of the largest cluster:

$$r = \left\langle \overline{max_i \left\{ \frac{C_x(i)}{N} \right\}} \right\rangle_x , \tag{2}$$

where $C_x(i)$ stands for the number of elements in state i for an x realization of the system [21].

4. The evolutionary-based coalition model

Evolutionary algorithms (EAs) have been successfully applied in various domains: mathematics, engineering, chemistry, physics, medicine, etc. The great advantage consists of their ability to obtain more solutions in a single run due to their capacity to deal with a population of solutions.

These algorithms have been introduced in 1965 by John Holland [15]. Many surveys in EAs and their applications can be found [7, 9, 13]. The EAs use a population of feasible solutions. The population is randomly generated initially over the search space, which is the definition domain. These solutions (called also chromosome, individuals) are improved by applying genetic operators (like selection, mutation, crossover, etc.). Each individual from the population is evaluated based on its fitness function. The best individuals are selected at each generation by using this quality function. Many selection mechanisms have been implemented [2, 13]. The chosen individuals are modified by applying the crossover and/or mutation operator. Various forms of these operators can be found [10, 23, 25, 26]. New solutions are obtained in this way. Some of these new solutions can be better than the existing ones. There are many modalities to accept the new solutions (also called offspring) in population. Some algorithms accept the new solution only if this solution is better than his parent (or parents).

4.1. **Motivation.** Evolutionary Computation (EC) methods allow a quickly and non-restrictive optimization, which is so useful in order to model the complex systems. Why? Because the nature solved many problems, so any algorithm showing the same behaviour might be good. EC can also handle non-linear, high dimensional problems without requiring differentiability or explicit knowledge of the problem structure. In addition, the evolutionary algorithms (EAs) are very robust to time-varying behaviour, even though they may exhibit low speed of convergence.

All these strengths of the EAs allow investigating the process of coalition formation in complex systems: the appearance of social percolation and the emergence of a giant cluster that is observed in many social phenomena.

For implementing a realistic dynamics for coalition formation one should also take into account that coalitions are not formed instantaneously and simultaneously. Once an agent is assigned to a coalition, it can (and probably will) change its propensities towards other agents. Agents will adjust their propensities according to the already formed coalitions and this feedback presumably reduces the frustration in the system.

4.2. **Representation.** A hybrid model that uses the GAs in order to evolve the realizations $\sigma(i)$ of a network configuration who's energy reaches a minimal

value is proposed. Actually, each GA individual is a fixed-length string of genes. The length of a chromosome is equal to the number of nodes from the network. Thus, a GA chromosome represents a possible clusterization of the network nodes in order to form an optimal coalition. Because the maximal number of coalitions (or clusters) is equal to the number of network's nodes, each gene is associated to the index of such a cluster. Therefore, each gene is an integer number from $\{1, 2, \ldots, N\}$ set (where N represents the number of nodes from the network). Or, in terms of the Potts model, each gene g_i from a GA chromosome is associated to a Potts state $\sigma(i)$.

For instance, for a network with $N = 5$ nodes (actors, elements) two possible chromosomes could be:

a) $C_1 = (1, 2, 3, 4, 5)$ - this chromosome encodes a clusterization where each group contains just an actor: $g_i \neq g_j$ or $\sigma(i) \neq \sigma(j)$, $i = 1, 2, \ldots N$ (see Figure 1(a));
b) $C_2 = (1, 1, 3, 1, 5)$ - this chromosome encodes a coalition with 3 clusters (see Figure 1(b));

FIGURE 1. Two possible configurations of the network in which: (a) each group is only formed by an element (it corresponds to the chromosome C_1); (b) one group contains 3 nodes (n_1, n_2, n_4) and the other two groups contain 2 nodes each (n_3 and n_5, respectively) – it corresponds to the chromosome C_2. A dashed edge between two nodes i and j means that there is no sympathy (no tendency for cooperation) between these nodes and a solid edge means that the nodes i and j tend to collaborate. The value associated to each node represents the index of the cluster where that node is placed.

4.3. **Initialisation.** Regarding the chromosome initialization each gene of a chromosome is initialized with a random value from the {1, 2, ..., N} set; in this case two or more nodes could take part to the same coalition from the start of the search process (like in the previous example from Figure 1(b)).

4.4. **Fitness assignment.** The array of integers encoded into a GA chromosome represents the structure of a coalition. In order to compute the quality of a coalition, the cost function proposed by Neda et al. [21] has been used. The simple case when $S_i = S_j = 1$ and $Z_{ij} = +1$ with a probability q and -1 with a probability $1 - q$ has been considered:

$$f = -\sum_{i,j=1}^{N} Z_{ij} \times \delta_{g_i,g_j}, \text{ where: } Z_{ij} = \pm 1, \text{ and } \delta_{g_i,g_j} = \begin{cases} 1, & \text{if } g_i = g_j \\ 0, & \text{if } g_i \neq g_j \end{cases} \quad (3)$$

A lower value of this function indicates a better quality. Therefore, the GA has to solve a minimization problem.

For instance, the chromosome C_2 (Figue 1(b)) is better than the chromosome C_1 (Figure 1(a)) because:

- $Fitness(C_1) = 0$ (because all Z_{ij} are -1 and all δ_{g_i,g_j} are 0);
- $Fitness(C_2) = -3$.

4.5. **Search operators.** The search operators mainly used within the GA are the crossover and mutation. Note that the action of the genetic operators does not change the structure of the network (the interactions between the actors). The crossover and the mutation change the coalitions only, which are formed in the system.

4.5.1. *Crossover.* By crossover, two selected parents are recombined. For instance, within the cutting-point recombination, two possible coalitions (one from each parent) exchange the elements placed between the cutting-points. A cutting point is considered within the following two parent chromosomes after the third gene. The offspring provided by the recombination operation are:

$$P_1 = (\ 1,\ 2,\ 3,|4,\ 5\ ) \qquad O_1 = (\ 1,\ 2,\ 3,\ 2,\ 4\ )$$
$$P_2 = (\ 3,\ 2,\ 1,|2,\ 4\ ) \qquad O_2 = (\ 3,\ 2,\ 1,\ 4,\ 5\ )$$

In Figure 2 is presented the network-based visualization of this crossover operation.

4.5.2. *Mutation.* By mutation, some information inside a chromosome could be changed. In other words, some of the network actors could change their group affiliation. Therefore, by mutation, a gene change its value into another one (off course, from the same discrete domain $\{1, 2, \ldots, N\}$).

FIGURE 2. Network-based crossover. Remark that the crossover operation does not change the tendency for cooperation of the nodes from the network. The cluster affiliation of some nodes is only modified.

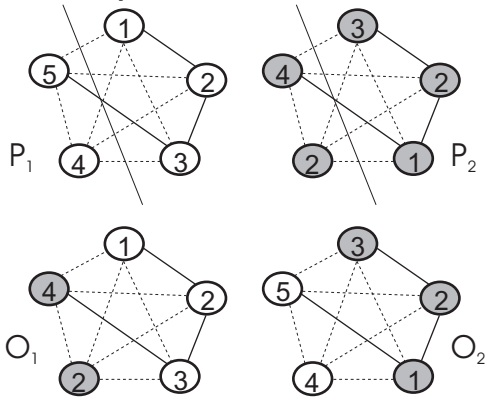
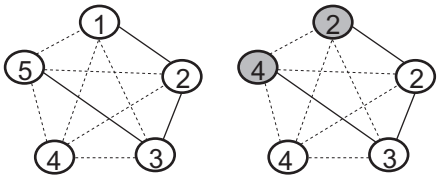


FIGURE 3. Network-based mutation. Note again that the network structure is not changed.



4.6. **The algorithm.** A GA [13] is used in order to evolve the coalition formation. The steady-state evolutionary model [27] is used as an underlying mechanism for the GA implementation. The algorithm starts by creating a random population of individuals. The following steps are repeated until a given number of generations is reached: two parents are selected by using a binary tournament selection procedure. The parents are recombined in order to obtain two offspring by performing a one cutting-point crossover. The offspring are considered for mutation. The best offspring O replaces the worst individual W in the current population if O is better than W.

5. NUMERICAL EXPERIMENTS

In this experiment the dynamic of the coalition formation through the order r parameter (like in [21]) is studied in full connected networks (there is a positive connection - a sympathy - or a negative connection - an antipathy -

between every 2 nodes of the network). In addition to this study, the results are compared to those computed by using Monte Carlo methods for small systems (up to $N \leq 10$). Several numerical results are presented also for larger systems (e.g. $N = 100$ or $N = 150$).

5.1. **Experiment 1.** The GAs are used in order to obtain the optimal coalition formation for small systems in which an exact enumeration is possible. The exact enumeration means that one can computationally map the whole phase-space (all $\sigma(i)$ realizations) for a generated Z_{ij} configuration and determine the minimum energy state. The order parameter considered is the relative size r of the largest cluster.

Moreover, for $N \leq 7$ it was also possible to map all the Z_{ij} configurations as well. The results from [21] up to $N \leq 7$ are thus exact. In the $7 < N \leq 10$ interval, although the minimum energy states are exactly found, due to greatly increased computational time and memory needed, it was possible to generate only a reasonable ensemble averaged for Z_{ij} (5000 configurations) [21]. The results obtained by the evolutionary approach proposed in this paper up to $N \leq 10$ are averaged over the same reasonable ensemble of 5000 network configurations.

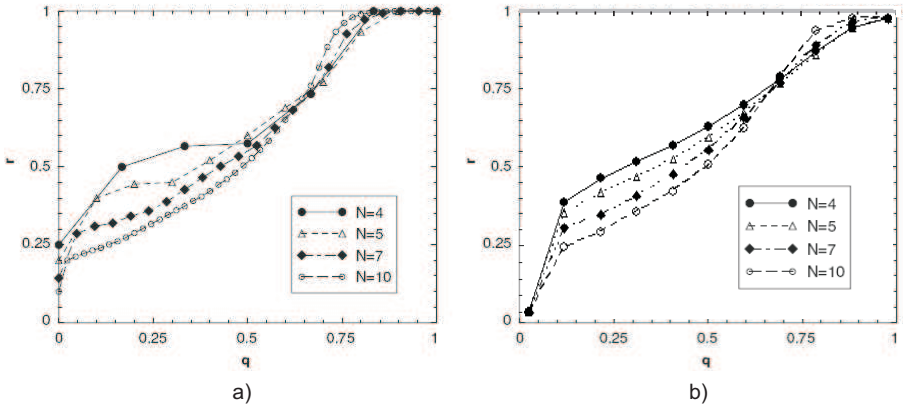
Note that for each structure of the network Z_{ij}, $i, j \in \{1, 2, \ldots, N\}$ a GA is run in order to find the optimal coalition formation. Therefore, the results presented here are the corresponding r values for the best solutions found by the evolutionary algorithm in the last generation. Moreover, in order to obtain a realistic approach, the results are averaged over all 5000 network configurations.

In this experiment, the GA works by 100 chromosomes that are evolved during 100 generations. The crossover and the mutation operators are applied by $p_c = 0.8$ and $p_m = 0.1$, respectively, probabilities.

The comparison exact enumeration is performed of two purposes. First, the trends of the $r(q)$ curves as a function of increasing system size is checked. Secondly, these results offer a good "standard" for the proposed optimisation method, used for larger system sizes (in the next experiment). As the results in Figure 4 show, the $r(q)$ curves have a similar trend as those suggested by Neda et al. in [21], i.e., as the system size increases, the slopes for $r(q)$ are increased around a non-trivial q value.

The GA results are in perfect agreement with the ones from exact enumerations [21], giving confidence in to use evolutionary optimisation methods. In addition, the complexity of the proposed approach is smaller than the complexity of the traditional methods, which have been applied in order to investigate the coalition formation process. Therefore, the time that is needed in order to identify the optimal clusterization of the "actors" in such system by the

FIGURE 4. Results of the dependence of the order parameter as a function of q for different sizes of the network (N). For comparison purposes on (a) the exact enumeration results are shown and on (b) the GA optimisation results.



evolutionary methods is reduced. Another, and maybe the most important advantage of the proposed hybrid approach is the given by its ability of handle non-linear, high dimensional problems without requiring differentiability or explicit knowledge of the problem structure. This characteristic is very important and it favours a new direction in studying the phenomena that appear in very large complex systems.

5.2. **Experiment 2.** In [21] the authors have considered two Monte Carlo optimisation methods: the classical simulated annealing [17] and the recently proposed extremal optimization method [4, 5]. Both approaches are rather time-consuming and the necessary computational time increases sharply with system size. The computational resources allowed the authors to study only the systems by sizes up to $N \leq 60$.

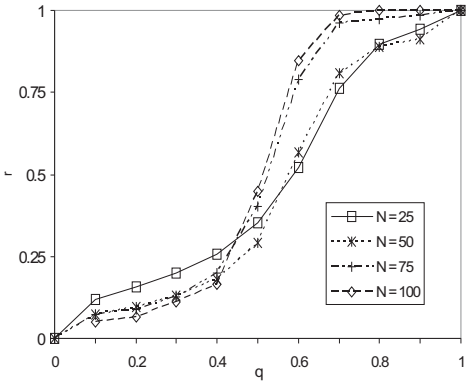
The evolutionary approach proposed in this paper is time-consuming also, but the computational resources allow investigating the coalition formation in systems by larger size. Therefore, the evolution of the order parameter $r(q)$ is analysed in four large systems: $N = 25$, $N = 50$, $N = 75$ and $N = 100$ with a statistic of 100 realisations.

The GA parameters used in these experiments are presented in Table 1. Even if, for the large systems, large populations are evolved during more generations than those used for small systems, the computational time that is needed in order to obtain good solutions is reasonable.

TABLE 1. GA parameters

N	#Generations	Population Size
25	100	100
50	100	200
75	2000	500
100	5000	5000

FIGURE 5. Results of the dependence of the order parameter as a function of q for large systems. The optimal values of the order parameter r are obtained by the evolutionary approach.



The relationship of the order parameter as a function of probability q are presented in Figure 5. From the numerical results presented in Figure 5 several aspects can be remarked:

- when in the system there are more relations of collaboration than the conflict ones ($r \to 1$), usually the nodes tend to form a single cluster in order to satisfy the conflicting interactions.
- when the tendency for collaboration is the same with that of conflict, the order parameter is changing strongly with small variations of q. Therefore, in this case, the process of coalition formation is sensitive to the structure of relations within the network.
- when in the system there are more relations of conflict than the collaboration ones ($r \to 0$), usually the nodes tend to form a large number of clusters. For very small values of q (for very few relations of collaborations), the nodes tend to form the one's own cluster (the number of clusters tends to be equal to the number of elements from the network).

6. Conclusions

A hybrid evolutionary framework has been proposed in this paper in order to study the process of coalition formation that appears in complex systems. Two types of full connected networks have been investigated: small networks (up to 10 nodes) and large networks (from 10 up to 100 nodes), which are closer to the real systems than the smaller ones. The numerical results obtained in both cases indicate the relationship between the number of coalitions and the structure of the network.

Future works will be focused on the study of the coalition formation in full connected networks in which the relations (of collaboration or conflict) between the elements are weighted (instead to have only $+1$ or -1 links between 2 nodes, some fuzzy relations will be defined on $[-1, 1]$ range). The optimal clusterization will be also investigated in networks that are more sophisticated: random networks, small world networks, and scale-free networks.

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