

**OPEN ACCESS**

## Evolutionary Processes in Complex Networks and Small Worlds

To cite this article: D S Vlachos and K J Parousis-Orthodoxou 2013 *J. Phys.: Conf. Ser.* **410** 012081

View the [article online](#) for updates and enhancements.

### You may also like

- [Complex Networks: from Biology to Information Technology](#)  
A Barrat, S Boccaletti, G Caldarelli et al.
- [From biologically-inspired physics to physics-inspired biology](#)  
Alexei A Kornyshev
- [Exact Space-Times in Einstein's General Relativity](#)  
Kayll Lake



## ECS Membership = Connection

### ECS membership connects you to the electrochemical community:

- Facilitate your research and discovery through ECS meetings which convene scientists from around the world;
- Access professional support through your lifetime career;
- Open up mentorship opportunities across the stages of your career;
- Build relationships that nurture partnership, teamwork—and success!

**Join ECS!**

**Visit [electrochem.org/join](http://electrochem.org/join)**



# Evolutionary Processes in Complex Networks and Small Worlds

**D.S. Vlachos and K.J. Parousis-Orthodoxou**

Department of Computer Science and Technology,  
Faculty of Sciences and Technology,  
University of Peloponnese,  
GR-221 00 Tripolis, Greece

E-mail: [dvlachos@uop.gr](mailto:dvlachos@uop.gr)

## **Abstract.**

In recent years, researchers discovered by empirical studies that the majority of networked systems that occurring in nature and society, exhibit an emerging behavior which is caused by the statistical properties of these systems. Two of the most important factors that characterize those complex systems is the degree distribution of the underlying network and the so called *small world* property. In this work, we examine the application of evolutionary processes on these systems in order to derive useful results for human dynamics modeling. Simulation experiments are used to explain universal properties observed recently in the vote distribution of proportional elections. Moreover, it has been founded that the hierarchical or modular nature of complex networks accelerates the convergent of a hybrid genetic algorithm applied in a rather complex search space.

## **1. Introduction**

Complex systems are those groups or organizations which are made up of a large number of non identical elements connected by diverse interactions. Some representative examples of complex systems include the global climate, economies, ant colonies, immune systems, the Web, the Internet (routers and domains), electronic circuits, computer software, movie actors, coauthorship networks, sexual web, citations, phone calls, metabolic, protein interaction, protein domains, brain function web, linguistic networks, international trade, bank system, encryption trust net, energy landscapes, earthquakes, astrophysical network etc. In such systems the individual parts and the interaction between them often lead to large-scale behaviors which are not easily predicted from a knowledge only of the behavior of the individuals. Such collective effects are called *emergent* behaviors [1]. Examples of such emergent behaviors include short and long-term climate changes, price fluctuations in markets, foraging and building by ants, and the ability of immune systems to distinguish 'self' from 'other' and to protect the former and eradicate the latter.

A straightforward representation of complex systems is by using graph theory. The interacting parts of a complex system are represented by vertices, while the interactions between them with edges. Such networks are called *complex networks* and may be directed (citations) or undirected (sexual web), weighted (international trade), multi-graphed (coauthorship or movie actor network) etc. The size and complexity of the complex networks along with the statistical

behavior of the system that they represent, brought network research close to statistical physics and this new approach has been driven largely by the availability of computers and communication networks. Traditional tools used in graph theory like the adjacency and the incidence matrix, the Laplacian and the set of eigenvalues [2], have been replaced by the characterization of networks by statistical properties.

Of great importance in the field of complex network and modeling of complex systems is their dynamical behavior. The spreading of a virus in human or computer networks is a common example. The range of possible dynamical processes in complex networks is very wide. Watts in [3] studied the impact of clustering on several processes, including games, cooperation, the Prisoner's Dilemma, cellular automata while Lago-Fernadéz in [4] studied synchronization. Wang and Chen in [5] demonstrated that the inhomogeneous scale-free topology plays an important role in determining synchronization in complex networks. Search and random walks in complex networks is another well studied example. But one of the most important, although unexpected, result presented by Pastor-Satorras and Vespignani in [6] and [7] concerning the effect of network topology in the spreading of a disease. They showed that while for random networks a local infection spreads to the whole network only if the spreading rate is higher than a critical value, for scale-free networks any spreading rate leads to the infection of the whole network. This property motivates the work of this paper as it will be explained in the following.

Dynamical process in general can be modeled by genetic algorithms. Genetic algorithms are one class of agent based modeling techniques that were designed to capture the essence of evolution and adaptation and yet to be simple enough to be mathematically tractable. In genetic algorithm methods one studies the evolution of simple strings of symbols on a computer, or fragments of computer code, rather than attempting to simulate the behavior of real organisms. An early result from research on genetic algorithms was the mathematical characterization of adaptation as a near-optimal trade off between exploitation of traits that have been already been found to be useful and exploration for new useful traits. Genetic algorithm research has also led to mathematical characterization of the roles of mutation, sexual recombination, diploidy, and other genetic processes and characteristics. In addition, genetic algorithms have a practical use as computational search and learning methods inspired by evolution. In general, in a genetic algorithm, a set of individuals-members constitute a population in which genetic operation like mutation and crossover produce offsprings which populates the next generation through a process of selection. There are many flavors and implementations of genetic algorithms which try to optimize either the effect of genetic operators or the coding of information inside each member of the population. On the other hand, a number of techniques have been developed for the implementation of the selection operation, mainly through a fitness function, capable to handle even large number of constraints. A nice short review of proposed methods with selected references can be found in [8].

One of the most important challenges one has to face, when implementing a genetic algorithm, is the so called exploration-exploitation trade-off. Exploration is needed to ensure every part of the search space is searched thoroughly in order to provide a reliable estimate of the global optimum. Exploitation is important since the refinement of the current solution will often produce a better solution. Population-based heuristics (where genetic algorithms [9] and estimation of distribution algorithms [10] are found) are powerful in the exploration of the search space, and weak in the exploitation of the solutions found.

The purpose of this work is two folded; first, we design and implement a special hybrid genetic algorithm, the population members of which 'live' on the vertices of a complex network. Crossover now is restricted only between members that correspond to adjacent vertices of the network. The small world property of the network assures that finally, information from every member will be available to the whole population, while the degree distribution and the transitivity of the network will enhance the exploration capabilities of the algorithm. On the

other hand, we present a model for the evolution and opinion formation in a human network using a special designed genetic algorithm. This model will be used to explain the recently observed property of the distribution of votes received by candidates in proportional elections which is the same function in different countries and years, when the number of votes is rescaled according to the strength of the party to which each candidate belongs [11].

## 2. Hybrid genetic algorithm on complex networks

- (i) Assign at each vertex of the network a chromosome. This can be done randomly or we can load to the network a pre calculated population.
- (ii) Crossover each vertex with all the adjacent ones. Here we can use the crossover probability used in standard genetic algorithms. In the case that no crossover is selected, the offsprings are copies of the parents.
- (iii) Make a copy of each offspring to both parents.
- (iv) After finishing with crossover, every vertex of the network has the chromosome from the previous population plus a number of offsprings. Using this set of chromosomes, we estimate the distribution of genes in the chromosomes and finally produce a chromosome according to that distribution. This chromosome is the one who enters the next generation.

Since the chromosome who finally survives to the next generation is produced randomly (following of course a given distribution), there is no need for mutation.

## 3. Simulation results

Since the aim of this work is to examine the effect of network topology in the exploration-exploitation dynamics of the genetic algorithm, we use a special designed fitness function with several local minima. The used function is taken from [12] and is given by

$$f(x, y) = \sum_{j,k=1}^5 j \cdot k \cdot \cos((j+1) \cdot x + j) \cdot \cos((k+1) \cdot y + k) \quad (1)$$

## 4. Experimental results

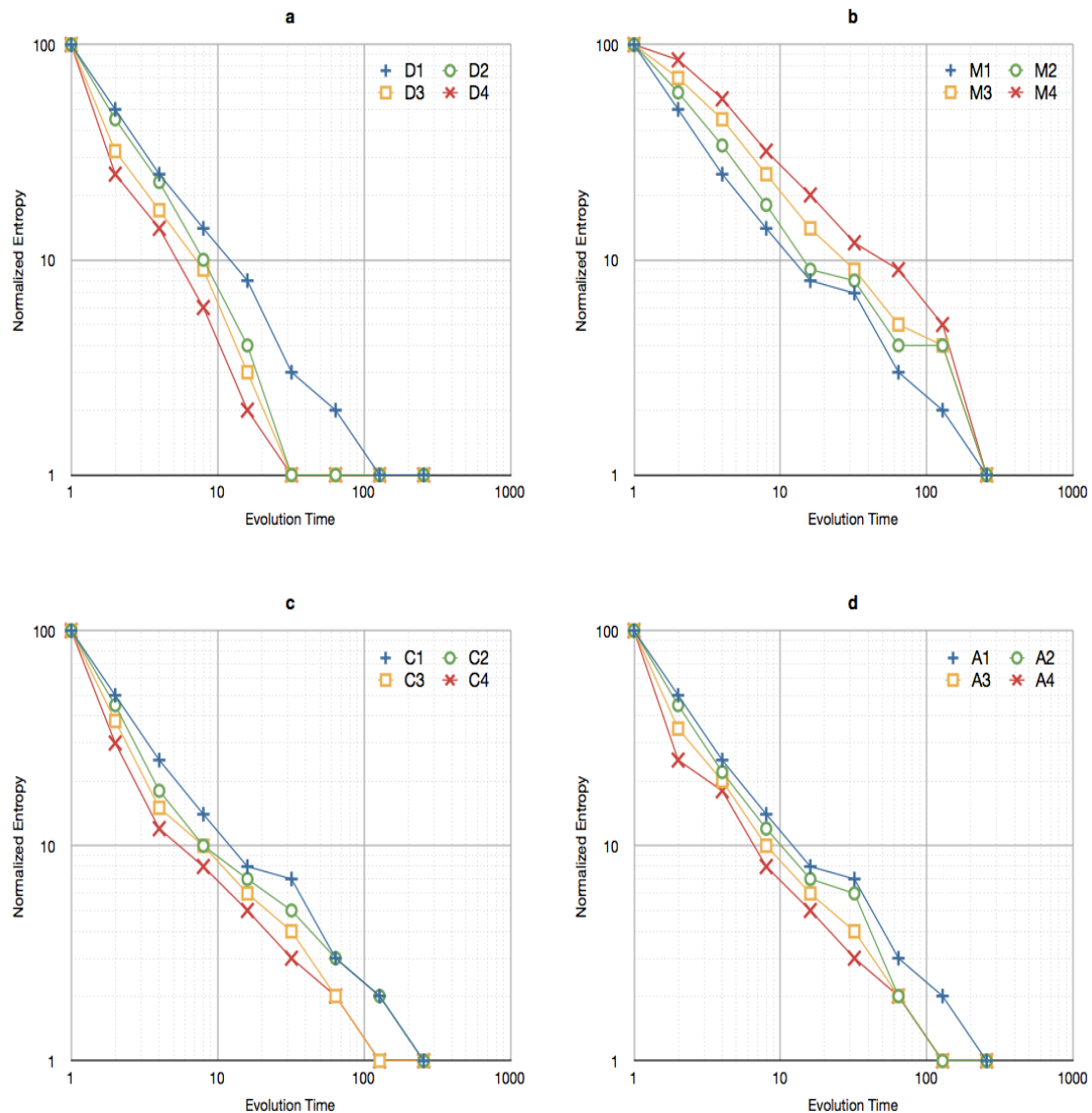
In figure 1 the results of the dynamics of the genetic algorithm are shown. As a first test, we study the entropy of the population as a function of the evolution time. The networks that have been tested vary in degree distribution (scale free networks with different exponent), modularity, clustering and assortativity.

## 5. Conclusion

In this work, the dynamics of a hybrid genetic algorithm has been studied for different topological properties of the population. The population has been modeled with a complex network and the entropy has been measured as a function of the evolution time. The results show that the diversity of the population is decreased with decreasing exponent in the degree distribution, with increasing modularity, clustering and assortativity.

## References

- [1] Mitchell M and Newman M 2002 *Encyclopedia of Evolution*, M. Pagel (ed.) (New York: Oxford University Press)
- [2] Biggs N 1993 *Algebraic Graph Theory* (Cambridge: Cambridge University Press)
- [3] Watts D 1999 *Small Worlds: The dynamics of networks between order and randomness* (Princeton, NJ: Princeton University)
- [4] LF Lago-Fernández R Huerta F C and Siguenza J 2000 *Phys. Rev. Lett.* **84** 2758–2761
- [5] Wang X and Chen G 2001 *preprint cond-mat/0105014* 445–455



**Figure 1.** (a). Evolution of entropy for various exponents of degree distribution (decreasing exponent from D1 to D4). (b) The same for various modularities (increasing modularity from M1 to M4). (c) The same for various clustering coefficients (increasing from C1 to C4). (d) The same for various assortativity coefficients (increasing from A1 to A4).

[6] Pastor-Satorras R and Vespignani A 2001 *Phys. Rev. Lett.* **86** 3200–3203  
 [7] Pastor-Satorras R and Vespignani A 2001 *preprint cond-mat/0102028*  
 [8] Farmani R and Wright J A 2003 *IEEE Trans. Evol. Comput.* **7** 445–455  
 [9] Holland J 1975 *Adaption in natural and artificial systems* (Ann Harbor, MI: The University of Michigan Press)  
 [10] Larranaga P and Lozano J 2001 *Estimation of Distribution Algorithms. A New Tool for Evolutionary Computation* (Norwell, MA: Kluwer Academic Publisher)  
 [11] Fortunato S and Castellano C 2007 *Phys. Rev. Lett.* **99** 138701  
 [12] W Huyer A N Global optimization by multilevel coordinate search Technical report Institut fr Mathematik Universitt Wien