

Effect of Topology on Diversity of Spatially-Structured Evolutionary Algorithms

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ABSTRACT

The aim of this work is an investigation on the effects of networks topology to spatially-structured evolutionary algorithms' dynamics. We applied the algorithm on a multi-modal optimization problem and we focused our study on convergence time and diversity of the solutions. Using as algorithms' underlying structure different network models we studied the relationship between algorithm dynamic, i.e. convergence time, first hitting time and number of distinct optima found during the evolution, and networks' characteristics. A comparison with a panmictic evolutionary algorithm is made to study the effects of the introduction of a structure in the mating dynamics, resulting in an enhancement of diversity and containing the convergence time and first hitting time overhead. The results on the proposed multi-modal combinatorial optimization problem using regular graphs and Watts-Strogatz networks show that the underlying network characteristics clearly influences algorithm dynamics and diversity of the solutions found.

Categories and Subject Descriptors

I.2.8 [Genetic algorithms]: Multiple solutions / Niching—
Working principles of evolutionary computing

General Terms

Algorithms, Design, Experimentation

Keywords

Evolutionary Computation, Complex Networks, Spatially-Structured Evolutionary Algorithms

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1. INTRODUCTION

Spatially-Structured Evolutionary Algorithms (ssEAs) are defined as EAs where the mating between individuals is based on a graph (or network). Cellular Evolutionary Algorithms (cEAs) are a class of this kind of algorithms with the characteristic of performing selection and mutation according to an interaction graph, commonly a regular graph such as lattices (1D or 2D). This kind of algorithms, introduced in [16, 13], permits to decentralize the population partitioning it in subpopulations or having partially overlapping neighbourhoods. One of their advantages is the particular suitability for parallel implementation [2, 8]. This decentralization permits to tune the diffusion rapidity of good solutions respect to panmictic algorithms (i.e. standard algorithms where each individual interacts with all the other within the population).

The first studies on cEAs focused on the effects of the shape of the neighbourhood on selection pressure of the algorithms [25], considering the relationship between it and the shape of the topology, commonly a regular lattice. Cellular EAs have been reported as being useful in maintaining diversity with multimodal and epistatic problems [3], in fact exploration/exploitation trade-off can be tuned with the appropriate spatial structure. Theoretical investigations on selection intensity and takeover time has been made on different graph topologies [23, 11] and some on non-regular graphs [26, 9] with particular focus on population update policies. An investigation of selection pressure in scale-free networks is provided in [10, 21] and relations between network characteristics as scaling and assortativity with takeover time is studied in [20]. More recently, some theoretical work about parallel EAs has been presented in [15]. A complete survey on cEAs research could be found in [1].

The purpose of our study is to investigate the relationship between graph structure and diversity maintenance, in particular we test our hypothesis with Small-World models, proposed by Watts and Strogatz [27]. This model has been chosen because of the possibility to tune an important graph feature such as the average path length (APL) changing the value of the rewiring factor r .

This paper proceeds as follows. In Section 2 we introduce the application of spatially-structured EAs to multi-modal optimization, describing in 2.1 the particular algorithm we

used for the experimentations. In Section 3 a brief introduction of complex networks theory is given. Specifically a model that interpolates from a regular lattice to a fully random graph, known as Small-World networks, is presented. Section 4 is devoted to the experimentation of the ssEA on a multimodal optimization problem and, in subsection 4.1 we study the problem on Small-World topologies. Finally, in section 5 our conclusions are drawn and some questions opened by this work are presented.

2. MULTI-MODAL FUNCTIONS OPTIMIZATION WITH SSEAS

Multi-modal functions have multiple optimum solutions, which may be local or global optima. In the case where more than a single global optimum exists, it may be the necessity to find all the optima and not only a single one at the end of the execution of an algorithm. Usually, EAs tends to converge around one optimum, due to the *genetic drift* phenomenon. Two types of diversity maintenance schemes may be adopted in EAs: explicit and implicit. Explicit methods force the population to maintain the diversity, common forms include fitness sharing, niching and crowding [24]. Implicit measures try to avoid forcing methods designing algorithms in the way to separate the whole population into smaller subpopulations, giving them a spatial distribution, e.g. Island Model EAs and cellular EAs.

A cellular EA (cEA) structures the population by the means of “local” small neighbourhoods, maintaining a population whose individuals are spatially distributed in cells. A cellular Genetic Algorithm (cGA) is a genetic algorithm whose selection, recombination and mutation are performed within the neighbourhood of each individual and finally with a replacement strategy which decides whether the individual is replaced by the offspring. The population may be updated in two ways: with a synchronous strategy, where all the population is replaced at the same time, and an asynchronous way where each individual is replaced before passing to the next one.

This kind of EA tries to preserve the diversity by restricting the mating (and the consequent exchange of genetic material) on “physical” distance between individuals. Commonly cGAs are defined on a 1D lattice or square lattice (see [1]) but, as stated before, cGAs based on other graphs topologies can be defined, influencing the diffusion of solutions in base of the characteristics of the underlying graph (network). In this work we define Spatially-Structured EAs (ssEAs) as generic EAs where individuals’ interactions are bound to an undirected graph (interaction graph).

2.1 Case Study

We implemented an elitist ssEA where each individual is associated to a node of the graph. The individual’s neighbourhood is defined with the nodes connected to it with an edge. Hence the size of the neighbourhood, and so the mating pool, is the same of the node degree where the individual is located. In this case, the node degree is defined as the number of edges incident to a specific node. Our proposed algorithm is shown in Algorithm 1.

The selection mechanism is random within the neighbourhood of individual i , thus each individual connected with i has the same uniform probability to be selected. The selected individual is mutated with the following method: each

bit of the genotype of length N of the selected individual is flipped with probability $1/N$. Then a “replace if better” strategy is applied: if the fitness of the mutated solution is higher or equal than the one of individual i then this latter is replaced by the new one (line 8–9 of algorithm 1). Thus, the probability of a given node i to be replaced is the following:

$$P_i^{\text{rep}} = \frac{n}{k_i} \left(1 - \frac{1}{N}\right)^N + \xi(f_i) \quad (1)$$

with n the number of individuals with a fitness higher or equal in the neighborhood, k_i the degree of node i (defined as the number of edges connecting the node) and f_i the fitness value of individual i . The first part of Eq. 1 is the probability to select an individual in the neighbourhood with higher fitness without mutating any bits of its genotype, the second part $\xi(\cdot)$ defines the probability, which is strictly related to the fitness value of i , to mutate the selected individual into an individual with higher fitness. The selection strategy might be defined as ‘elitist’, because optimal solutions are never replaced with non-optimal ones, but an optimal solution may be substituted by another optimal solution with a different genotype.

The population updating is performed synchronously.

We also considered a panmictic version of this algorithm, where each individual interacts with all the other within the population, in this case the interaction graph is a complete graph.

Algorithm 1 A simple ssEA with Random Selection Mutation

```

1:  $P^0 \leftarrow \text{InitializePopulation}()$ 
2: for each individual  $i$  in  $P^0$  do
3:    $fit_i \leftarrow \text{evaluate}(i^0)$ 
4: end for
5:  $t \leftarrow 0$ 
6: while not termination criteria do
7:   for each individual  $i$  in  $P^t$  do
8:      $sel \leftarrow \text{select}(\text{neighborhood}(i^t))$ 
9:      $sel \leftarrow \text{mutate}(sel)$ 
10:     $fit_{sel} \leftarrow \text{evaluate}(sel)$ 
11:    if ( $fit_{sel} \geq fit_i$ ) then
12:       $i^{t+1} \leftarrow sel$ 
13:    end if
14:  end for
15:   $t \leftarrow t + 1$ 
16: end while

```

3. COMPLEX TOPOLOGIES AND SSEAS

As the structure of the interactions (e.g. neighbourhood shape) between individuals has showed to play a key role on the spreading of solutions and selection pressure [11, 26], in this work we study the effects of different complex topologies on ssEAs solutions. To investigate the relationship between network topology and dynamical processes that can run on top of them in the last decade a new scientific paradigm has been proposed. This new way of thinking about networks is defined as Complex Networks [5] (CN) Theory. Part of the aim of this new branch of science is the creation of networks growth models able to reproduce real networks structure and provide the tools to analyse them. Another aspect of CN theory is the study of the effects of the structure of

such networks over dynamical processes. Of special interest and strictly related with ssEAs, is the study of spreading processes as epidemics or rumors on complex topologies [18].

In this section we introduce some network models proposed in CN literature as a substrate for ssEAs and some topological features that are strictly related to the ability of a network to spread information. The diffusion of information on a network is a complex process and is influenced by network structure itself. Many topological characteristics are involved in such process but two of them showed to play an important role. They are namely: the average path length and the clustering coefficient [27].

The average path length (APL) represents the mean distance between nodes in a graph, expressed as the number of links in the shortest path between two nodes i and j . It has been shown that many real world networks although composed by a huge number of nodes and connections are characterized by a small APL. This feature has profound implications on the spreading of information and diseases as small distances sensibly reduce the number of steps needed to cover the whole network.

The clustering coefficient (CC) represents a measure of the transitivity of a graph and specifically is evaluated as the probability that two nodes that share a neighbor have also a link connecting them. This definition can be seen also as the probability of finding triangles in the network. Such structures have a profound impact on dynamical processes because it creates clusters of highly connected nodes that are loosely connected with the rest of the network.

To get a first insight on the effects of topology on algorithms' dynamics we start our analysis comparing standard regular topologies such as 1D lattices and complex topologies as random graphs. The simplest example of random network is represented by the so-called Erdős and Rényi (ER) random graphs [7]. ER graphs are characterized by random connections between nodes leading to a poissonian degree distribution. ER networks also present opposite features with respect to regular graphs. In fact such kind of networks are characterized by a low APL and a vanishing CC for large graphs. To create an ER graph it is possible to follow the original algorithm presented in [7]:

1. To create a graph with N nodes start with a set of N disconnected nodes.
2. For each couple of nodes (i, j) connect them with probability p . The resulting graph will be composed by N nodes and $K = N(N - 1)p/2$ links.

Once the two extreme cases of regular graphs and random networks have been analysed, to complete our study we use as a substrate a class of networks that can interpolate, via a tunable parameter r , from a fully regular lattice, characterized by both a high CC and APL to a completely random network with small distances between nodes and a vanishing CC. These networks are defined as Small-World networks [27]. To range between the two extreme cases of networks, the following algorithm, proposed by Watts and Strogatz is used [27]:

1. The process starts with a 1D lattice with N nodes (see Figure 1)
2. For each link (i, j) , with probability r one end of the link is rewired to another node selected randomly avoiding loops and duplications.

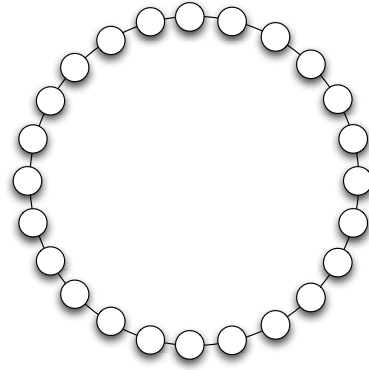


Figure 1: 1-D Lattice with two neighbours for each node

With $r = 0$ no rewiring is performed and the 1D lattice is preserved as it is characterized by $CC = 0.5$ and $APL = N/4$. With $r = 1$ all the links are rewired and a fully random topology is achieved with $CC \rightarrow 0$ for large N and $APL \sim \log(N)$ [5].

4. EXPERIMENTATIONS

In this section we introduce a combinatorial optimisation problem created by a composition of TWOMAX functions [14, 12], a bimodal equivalent of ONEMAX, where each substring contributes to the total fitness value according to the number of ones it has. This pseudo-Boolean function, called NMAX, has been created by concatenating L TWOMAX strings of b bit each leading to a 2^L global optima. In this paper we put $L = 10$. The fitness function is defined as follows:

$$f_{\text{NMAX}}(S) = \sum_{i=1}^L f_{\text{TWOMAX}}(s_i) \quad (2)$$

with s_i the i -th substring of length b inside the global problem string. The fitness of TWOMAX problem is:

$$f_{\text{TWOMAX}}(S) = \left| \frac{b}{2} - \sum_{i=1}^b x_i \right|, \quad x \in \{0, 1\}^b \quad (3)$$

Given that a TWOMAX problem has two distinct optima (the 0-string and the 1-string), with the concatenation of L strings we obtain a problem with 2^L distinct optima.

As in the previous section, we used the algorithm described in Section 2.1 with the parameters in Table 1. With the aim of finding a good trade-off between the computational time needed by our experimentations and the large networks sizes able to mostly reproduce the topological features of an infinite network we set the population size $N = 10^4$.

We measure the maximum number of distinct optima found by the algorithm, the generation where the fitness converges (FCT) and the first hitting time (FHT).

In our first experiment we simulate 50 runs of the algorithm described in section 2.1 with three typologies of graphs: random graph, lattice 1-D (see Figure 1) and complete graph (i.e. panmictic EA). In Table 2 we show the average results (we omitted the standard deviations for sake of clarity, all the values were under 2%): the lattice topology

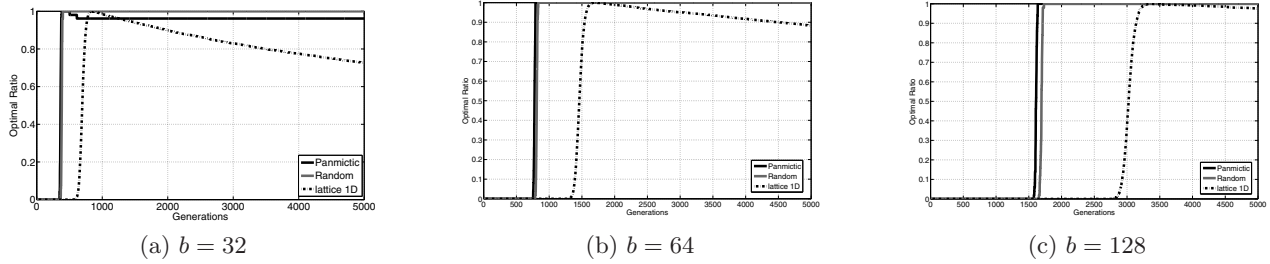


Figure 2: Average ratio of optimal individuals within the population on NMAX problem on 50 runs.

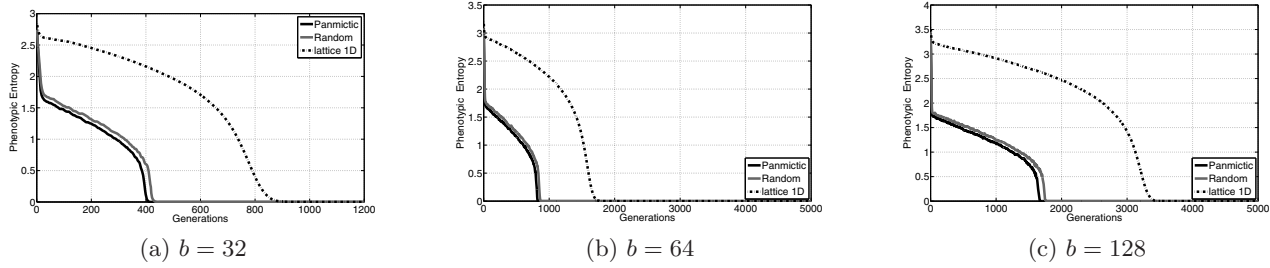


Figure 3: Phenotypic entropy on NMAX problem

Table 1: Parameterization used in the algorithm

Name	Value
Population Size	10000
Mutation Probability	$1/n$
Recombination	none
Max number of generations	5000

leads to a different first hitting time and number of distinct optima from the other two topologies.

In Figure 2 is shown the evolution of the ratio of optimal individuals (i.e. the value of 1 means that all the individuals have an optimal fitness) within the population. It is evident how the random graph ssEA and the panmictic algorithm behave similarly, differently the monodimensional lattice ssEA shows a slower dynamic (as depicted in Table 2). Because of the replacing strategy we can see that when the algorithm found more than an optima (like for lattice ssEA), during the generations this number tends to decrease. In fact, as described in line 11 of Algorithm 1, each time an optimal individual select another optimal solution in its neighbourhood there is a certain probability (see first part of Eq. 1) to be replaced, with a decrease of overall diversity.

As we studied the convergence speed to the global optimum we measured the genotypic entropy [22] of the population P as follows:

$$H_g(P) = - \sum_{i=1}^M g_i^d \log(g_i^d) \quad (4)$$

where g_i^d is the fraction of solutions with a given distance (in this case Hamming distance) from the origin (the 0-bit string). This metric, derived from statistical thermodynam-

ics, permits to measure the quantity of different solutions (states) inside a population.

Similarly, the phenotypic diversity is defined as:

$$H_p(P) = - \sum_{i=1}^M g_i^p \log(g_i^p) \quad (5)$$

where g_i^p is the fraction of solutions with a given fitness value.

As we can see in figure 4 and 3 in NMAX problem genotypic and phenotypic entropy highlight the multimodality of the problem, in fact when the population becomes homogenous the phenotypic entropy goes to zero (all the individuals have the same fitness) but the genotypic entropy is greater than zero when there are optima with different genotype.

4.1 Small-World topologies

We presented in Section 3 the Watts-Strogatz network model with its critical *rewiring* parameter which, as described in [27], permits the tuning of the average path length and clustering coefficient. In this section we want to investigate the dynamics of the proposed algorithm with the changing of rewiring factor r on the Watts-Strogatz model which consists of a regular network with 4 neighbours and a fraction r of ‘shortcut’ links¹.

We considered 24 different values for r from $2 \cdot 10^{-5}$ to 1, numerical results on NMAX problem with $b \in \{32, 64, 128\}$ are shown in Table 3. We can see that as the r grows the algorithm tend to perform similarly to a random network ssEA as expected (see Section 3). In Figure 6, FHT and FCT of all the problems are shown. The distance between the FHT and the FCT is the width of the “S” shape shown in Figure 2. In Figure 7 is shown the number of distinct optima over 50 simulations on Small-World networks for each

¹All the networks used in this work are available online at <http://www.matteodefelice.name/research/resources/>.

Table 2: Comparison of panmictic EA and ssEA on NMAX problem with different substring sizes (b)

Algorithm	$L = 10, b = 32$			$L = 10, b = 64$			$L = 10, b = 128$		
	FHT	FCT	n. opt.	FHT	FCT	n. opt.	FHT	FCT	n. opt.
Panmictic	362	410	1.04	776	823	1	1610	1659	1
Random	380	433	1.02	810	863	1	1692	1746	1
Lattice 1D	594	911	137	1332	1769	71.63	2846	3452	54.96

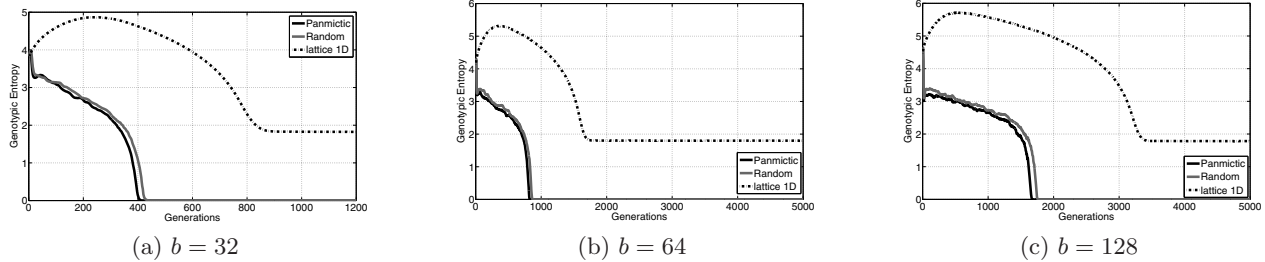


Figure 4: Genotypic entropy on NMAX problem

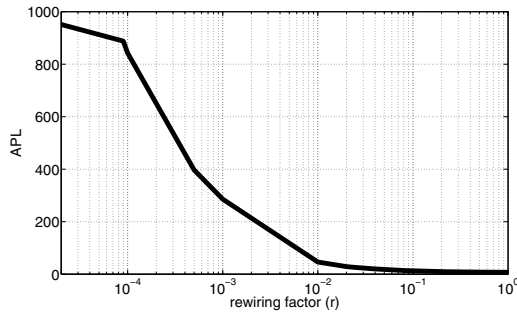


Figure 5: Average Path Length (APL) of Small-World networks considered

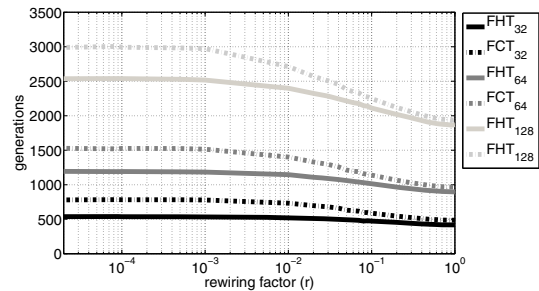


Figure 6: First Hitting Time (FHT) and Fitness Convergence Time (FCT) of Small-World networks considered

value of rewiring factor r . In Figure 8 we show the genotypic entropy of four chosen rewiring factors, is evident how this parameter drastically affects speed of convergence and the diversity of the individuals inside the population. Comparing this figure with the Figure 4 is evident how high values of r lead to an entropy similar to the panmictic and random graph cases.

Observing the Figure 5, where the average path length (see Section 3) of selected networks is shown, we can see a possible relation between this measure (which reflect the efficiency of information ‘spread’ over the graph) and the algorithm entropy and diversity variation.

5. CONCLUSIONS

In this work we presented an investigation of the effects of network topology on the dynamics of a spatially-structured evolutionary algorithm on a multi-modal combinatorial problem. In order to study the effects of the variations of network features, Small-World network models have been chosen due to the possibility of a simple and effective tuning offered by the rewiring factor. The variation of this parameter leads to the exploration of the trade-off of the algorithm between speed of convergence (as shown by the First Hitting Time

measure) and diversity of exploration (measured with the number of different optima found during the evolution). Although the selected problem can be considered simple, it allows us to investigate both the diversity of the solutions found (a very important feature in several application fields) and the speed of convergence. The similarity of behaviour of the panmictic EA and the random graph ssEA was not surprising because of their APL value (three for the random graph and obviously one for the complete graph).

The change of the rewiring factor r leads to a variation of the FHT in the range 15 – 56% (considering all the values of b) with respect to the panmictic version of algorithm (the range for the FCT is instead 17 – 89%), in the same time the diversity of the solutions found (i.e. the number of distinct optima) shows an interesting variety (see Figure 7) with respect to the panmictic which rarely exceeds the single optimum found during the evolution. Moreover, it is evident how the FHT and FCT change slightly from $r = 2 \cdot 10^{-5}$ to $r = 0.1$ while in the same interval the number of optima shows a drastic variation (as also for the APL in Figure 5).

Table 3: First Convergence Time and First Hitting Time of ssEA on Watts-Strogatz Small-World networks

Rewiring factor	$N = 10, b = 32$			$N = 10, b = 64$			$N = 10, b = 128$		
	FHT	FCT	n.opts	FHT	FCT	n.opts	FHT	FCT	n.opts
$r = 2 \cdot 10^{-5}$	536	778	99.09	1193	1527	62.38	2536	2990	38.38
$r = 9 \cdot 10^{-5}$	538	783	98.98	1190	1519	61	2538	3005	37.97
$r = 1 \cdot 10^{-4}$	536	782	98.04	1191	1526	61.21	2538	2993	37.06
$r = 5 \cdot 10^{-4}$	535	782	93.92	1187	1524	56.38	2528	2983	31.44
$r = 0.001$	533	778	88.88	1183	1515	49.08	2516	2972	25.28
$r = 0.01$	521	732	31.2	1145	1401	8.58	2398	2713	1.84
$r = 0.02$	512	686	12.7	1108	1329	2.36	2323	2570	1.14
$r = 0.03$	503	679	9.46	1092	1294	2.1	2284	2506	1.02
$r = 0.04$	498	660	6.26	1073	1259	1.6	2244	2455	1.06
$r = 0.05$	490	631	4.38	1058	1212	1.48	2214	2380	1
$r = 0.1$	472	588	2.22	1012	1139	1.14	2111	2247	1
$r = 0.2$	454	545	1.78	969	1065	1.02	2019	2119	1
$r = 0.5$	426	498	1.16	913	989	1	1901	1980	1
$r = 1.0$	418	486	1.16	895	966	1	1870	1941	1

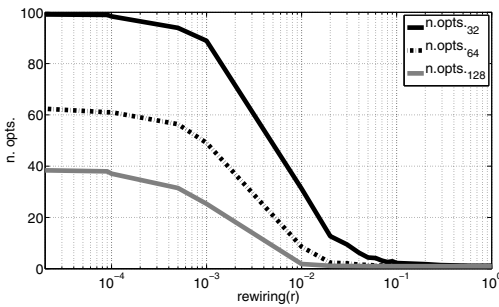


Figure 7: Average of maximum number of optima found using Small-World networks

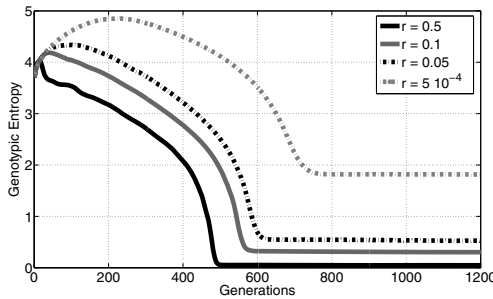


Figure 8: Genotypic Entropy on four Small-Worlds models with NMAX $b = 32$

5.1 Future Work

Although this work shed some light on the relationship between network structure and ssEAs performances many problems in this field still remain open. As the problem of the diffusion and creation of the optima and the spreading of a rumor or an infectious disease are strictly related [17], it is possible to model the evolution of an ssEA as a spreading phenomena on a network (as suggested in [19]) and get some analytical insights on the diversity of the solutions or the convergence time. Another important problem is represented by not only the effects of topology on ssEAs but also how an algorithm can shape network structure to achieve de-

sired performances, i.e. how to design a network in order to tune the exploitation/exploration trade-off of the algorithm. As future steps, the first should be the study of the application of epidemic models (especially compartmental models as SIR models [4, 6]) to ssEAs, after that a comparison with classical ssEAs (like CEAs) might be performed on several benchmark optimization problems.

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