

A Combination of Selective Pressure and Disruptiveness of Recombination Operators to Enhance the Evolutionary Behaviour

Carolina Salto

Fac. de Ingeniería - Universidad Nacional de La Pampa
Calle 110 esq. 9 – General Pico (6360) – La Pampa
Rep. Argentina
saltoc@ing.unlpam.edu.ar

Gabriela F. Minetti

Fac. de Ingeniería - Universidad Nacional de La Pampa
Calle 110 esq. 9 – General Pico (6360) – La Pampa
Rep. Argentina
minettig@ing.unlpam.edu.ar

Abstract — When Parallel Evolutionary Algorithms are used for solving optimization problems, their objective is to find an optimal solution using a limited amount of computation. Given these requirements, a good balance between exploration (or diversification) and exploitation (or intensification) is difficult to find. This balance can be found by tuning the various parameters of evolutionary algorithms: selective pressure, population size, mutation and crossover operators and their probabilities, among others. Such variations of the parameter settings in the different subpopulations generate the so-called heterogeneous Parallel Evolutionary Algorithms. These algorithms represent a promising way for introducing a correct exploration/exploitation balance in order to maintain the population diversity and find good final solutions.

This paper presents heterogeneous parallel evolutionary algorithms that apply different crossover operators and selection methods to each subpopulation. Our objective is to analyze the way in which such heterogeneity affects the search process, by considering the influence of selective pressure and the disruptiveness of recombination operators.

Experimental results show that our heterogeneous approaches outperform the homogeneous ones with regard to both population diversity and present similarities in the comparison of best found solutions.

I. INTRODUCTION

Evolutionary algorithms (EAs) are capable of solving complicated optimization tasks in which an objective function $f: I \rightarrow \mathcal{R}$ shall be optimized. Since the crossover operator and the selection operator (which operates on the principle that the fitter survives) produce serious adverse effect during the evolution, their employment may decrease the degree of population diversity and degrade the search capability of the EAs [41].

Diversity preservation methods based on the partition of the population have been proposed in order to avoid premature convergence [14, 16, 29, 31, 32, 33, 35, 39]. Parallel Evolutionary Algorithms (PEAs) try to introduce diversification more naturally by spatial population structure.

PEAs are becoming an important branch of research since they provide a faster and more efficient way of solving known and new problems. There has been extensive research on this field. Different surveys, such as [13, 5, 1, 22, 27], collect, organize, and present the most representative publications on this area.

Making distinctions between the subpopulations of PEAs by applying EAs with different configurations (genetic operators, parameters, representations, etc), we obtain the so-called heterogeneous PEAs.

This paper presents heterogeneous approaches, which apply different crossover operators and selection methods (to create the mating pool) in the diverse subpopulations, to solve a hard constraint problem: the satisfiability (SAT) problem [15, 19]. In this way, we propose simultaneous combinations of the selective pressure and the disruptiveness of the recombination operators.

In the following section, we describe the SAT problem. In Section III we introduce concepts over selection methods and crossover operators. While in Section IV we present a brief review of PEAs. In Section V, we summarize and extend the results in order to analyze and compare the different selection heterogeneous and homogeneous PEAs proposed in this work. Finally, the conclusions and future works are presented.

II. SAT PROBLEM

In a propositional problem (SAT) a propositional formula is given and a truth assignment for its variables is sought that makes the formula true. Without loss of generality, it can be assumed that the given formula is in *conjunctive normal form* (CNF), i.e. it is a conjunction of clauses where a clause is a disjunction of literals. In the 3-SAT version of this problem it is also assumed that the clauses consist of exactly three literals ($k=3$) and a increase number of variables ($n = 20, 30 \dots 1000$) as a form to increase the complexity of the problem.

The expression has to be in conjunctive normal form (also known as a "*product of sums*"), in which each of the l clauses contains exactly three terms:

$$(p_{11} \vee p_{12} \vee p_{13}) \wedge (p_{21} \vee p_{22} \vee p_{23}) \wedge \dots \wedge (p_{l1} \vee p_{l2} \vee p_{l3})$$

In this expression, each p_{ij} is either one of the n free variables occurring in the expression $(\{x_1, x_2, \dots, x_n\})$ or the negation of one of those $(\{\neg x_1, \neg x_2, \dots, \neg x_n\})$. For every i , a clause should contain at most one of $x_i, \neg x_i$. A solution is a valuation $(val(x_1), val(x_2), \dots, val(x_n))$ in which each $val(x_i) \in \{true, false\}$, such that the expression yield *true*.

The corresponding decision problem is one of the most intensive studied NP-complete problems.

III. GENETIC OPERATORS

The crossover operator and selection have been characterized by their contribution to the explorative and exploitative aspects of the search. When the balance between these aspects is disproportionate can produce a lack of diversity on the population [26, 28, 34]. In this section, we present an overview of basic ideas about selection methods and crossover operators.

A. Selection Methods

Selection mechanisms favour reproduction of better individuals imposing a direction on the search process. Rather than creating new individuals, it selects comparatively good individuals from a population for mating. The idea is to generate a competition among individuals with higher fitness because they have a higher probability to be selected for mating. In that manner, selection introduces the influence of the fitness function to the evolutionary process [11, 12, 17, 20, 30], because the fitness of an individual gives a measure of its “goodness”. Moreover, selection is the only operator of a genetic algorithm where the fitness of an individual affects the evolution process. In such a process two important, strongly related, issues exist: selective pressure and population diversity [6].

The selection mechanism has a great responsibility for the diversity of the population [24]. It may maintain or eliminate diversity depending on its current selective pressure, which represents the degree to which the selection mechanism favours the better individuals. If the selective pressure is high then the best individuals are preferred, supplying a large number of copies (which means fewer copies for the rest of the population) and as a result the population diversity is lost. On the other hand, with low selection pressure, the diversity is kept.

In the following we briefly consider four methods that we used in our implementation, a complete description can be found, for example, in [7, 30]. In *linear proportionate selection* the probability of selecting an individual depends linearly on its fitness [25]. *Ranking selection* orders the individuals according to their fitness. The selection probability is, then, a function of the rank [40]. Tournament selection [8] selects the best l out of k individuals. In the *Stochastic Universal Sampling* (SUS) [9], the individuals are mapped to contiguous segments of a line, such that each individual's segment is equal in size to its fitness. Here equally spaced pointers are placed over the line as many as individuals have to be selected.

In [6] have been analysed and compared all important selection mechanisms. From that research arises that the selective pressure increases in the following order: SUS, proportional selection, linear ranking, and tournament selection.

B. Crossover Operators

The crossover operation tries to combine good characteristics from different parents selected in order to yield a new individual. Then this kind of operators is merely explorative. After all, their goal is to create variation. The main idea is the crossover's ability for combining and/or disrupting pieces of information. That is strongly related with the creation and reduction of diversity in the population.

The n -point crossover randomly chooses n crossover points and cuts the two parents of length L into $n + 1$ segments (the same points in both parents). After that, it creates $child_1$ putting together the odd segments from the first parent and the even segments from the second one. $Child_2$ is created by taking the opposite decisions. Usually 1-point or 2-point crossover is used.

A further generalization of n -points crossover is the uniform crossover [36, 38]. For each bit in $child_1$, uniform crossover decides (with some probability p_0) which parent will contribute its value in that position. The second child would receive the bit from the other parent.

IV. PARALLEL EVOLUTIONARY ALGORITHMS

A parallel EA (PEAs) is obtained by the inclusion of parallelism in the operation of EAs. So, PEAs allow: the use of greater populations and the solution of more complex problems with bigger dimensions.

There are three main types of parallel EAs [18]: global single-population [23], fine-grained EAs [29, 37, 32] and coarse-grained EAs [10, 21, 39]. We are interested in the last kind of PEAs.

The coarse-grained, or distributed population model, also known as the island model, consists of a number of subpopulations or “demes”. Each one of them being processed by an EA, independently from others. With some migration frequency they exchange individuals between each other over a certain communication topology. The PEAs attempt to overcome the premature convergence by means of the preservation of diversity due to the semi-isolation of the subpopulations.

The island model is a very popular parallel model, because it is very easy to implement on a local network with standard workstations (cluster).

Regarding how similar the EA processes are on different islands, two different types of PEAs can be distinguished:

- Homogeneous EAs: on each island the same parameter settings, objective function, genetic operators and encoding methods are used.
- Heterogeneous EAs: on each island different parameter configurations can be used; in this way different evolutionary behaviour is achieved in each subpopulation. The differences in the evolution result from the variation of the following characteristics: parameter settings, objective function, genetic operators and encoding methods.

The majority of PEAs research deals with the first type. However, the last kind is in progress and some results can be found in [27, 2, 24].

The heterogeneous PEAs, proposed here, show differences in the evolution behavior by varying crossover operators and selection methods for mating in the diverse subpopulations. With that heterogeneity, simultaneous combinations of the selective pressure and the disruptiveness of the recombination operators are generated.

The migration mechanism allows the interchange of individuals among the subpopulations. This allows the cooperation by means of exploitation of promising areas, found by other islands, and reintroduction of genetic material, which was lost in the population. This cooperation is more advantageous for heterogeneous PEAs since the islands with more selective pressure distribute their best individuals to the rest and benefit by the incorporation of genetic material, which was lost due to the influence of high selection pressure.

V. IMPLEMENTATION AND EXPERIMENTAL RESULTS

A. Implementation

All experiments were conducted on our homogeneous cluster of Intel based machines. Each of the machines utilizes the Slackware distribution of the Linux operating system (version 9.1). In each experiment, eight islands were created. Regarding selection methods (see Table 1), in the first two cases heterogeneous PEAs were employed, which use different selection methods for the parent selection in each subalgorithm. While in the last cases, homogeneous PEAs were implemented. All these PEAs were carried out under the three following situations:

1. All islands used the One Point Crossover (OP).
2. All islands used the Uniform Crossover (UX).
3. Some islands used One Point Crossover and others Uniform Crossover (OP+UX).

In the last situation, the seven obtained PEAs are heterogeneous because different crossover operators were considered.

For naming PEAs the following rule is applied:

<Name Case> + <Crossover Method>

for example: if HomP and OP are used, the name is HomP+OP. These combinations summarize 21 algorithms.

These algorithms were run under MALLBA software [3, 4], which was created by research group from Malaga, La Laguna and Barcelona Universities.

Five instances for the 3-SAT were considered (see Table 2). Each PEA was run 50 times. The following PEAs genetic operators and parameters were kept constant throughout all of the testing: big-creep mutation, crossover probability = 0.65, mutation probability = 0.01, population island size $\mu = 30$ (all initial populations were randomly generated), total generations = 10000.

The replacement strategy to create the population for the next generation was $\mu + \lambda$, with $\lambda=30$, while individuals were chosen by proportional selection.

Five migrants are selected by tournament selection with $k=3$, and the target island selects individuals using tournament selection with $k=5$ and each one is replaced if the incoming one is better. The migration frequency is given each 25 generations. The sub-algorithms are disposed in an unidirectional ring with asynchronous communications (the checking of solutions from other populations is performed all generations).

TABLE 1: SELECTION METHODS FOR EACH EXPERIMENT

Case	Selection Method
Het1	2 islands with proportional selection, 2 with binary tournament, 2 with SUS and 2 with random selection.
Het2	2 islands with proportional selection, 2 with binary tournament, 2 with SUS, 1 island with random selection and other with linear ranking selection.
HomP	Proportional selection (P)
HomRI	Linear ranking selection (RI). $\eta_{max}=1.5$
HomR	Random selection (R)
HomS	SUS
HomT	Binary tournament (T)

TABLE 2: 3-SAT INSTANCES

Instance	#Variables	#Clauses
3	30	129
5	40	172
6	40	172
7	50	215
10	100	430

B. Variables de Performance

The following relevant performance variables were chosen:

$ebest = (\text{Abs}(\text{opt_val} - \text{best value}) / \text{opt_val})100$

It is the percentile error of the best-found individual when compared with the known, or estimated, optimum value opt_val . It gives us a measure of how far we are from that opt_val .

$epop = (\text{Abs}(\text{opt_val} - \text{pop mean fitness}) / \text{opt_val})100$

It is the percentile error of the final population mean fitness when compared with opt_val . It tells us how far the mean fitness is from that opt_val .

SR = (Success Rate). It is the percentile of the number of times that the optimum was found.

$Bias$ = (measure for final population diversity). The *population diversity* was introduced by Bäck and Hoffmeister [3], in terms of the bias measure defined by Grefenstette [13] as follows;

$$b(P(t)) = \frac{1}{l \cdot \mu} \sum_{j=1}^l \max \left(\sum_{i=1}^{\mu} (1 - a_{i,j}^t), \sum_{i=1}^{\mu} a_{i,j}^t \right)$$

where l is the chromosome length and $a_{i,j}^t$ denotes the allele value. The bias b ($0.5 \leq b \leq 1.0$) indicates the average percentage of the most outstanding value in each position of the individuals. Smaller values of b indicate higher genotypic diversity and vice versa. The bias b can be used to formulate an adequate termination criterion.

C. Comparison and experimental results

In Tables 3 and 4, mean values for $ebest$, SR , $epop$ and $bias$ were established. Those values average the results from all instances.

As regard $ebest$ values, independently of selection methods employed, better results are obtained if UX is applied; meanwhile the OP+UX option plays an intermediate role between OP and UX roles. OP+UX combination achieves more times the optimum (the highest SR values in Table 3) but its $ebest$ value is lower than the obtained for UX. This indicates that the rest of the best-found solutions for OP+UX have less quality than the ones of UX.

Analysing $epop$ values (Table 4), independently of selection methods employed, a similar situation to the one observed with $ebest$ values is presented; meaning that the phenotypic diversity is decreased by considering UX. But at

TABLE 3: SUMMARY OF $EBEST$ AND SR VALUES

	$ebest$			SR		
	UX	OP	OP+UX	UX	OP	OP+UX
Het1	0.41	0.51	0.44	23.60	20.80	22.80
Het2	0.42	0.47	0.41	42.40	43.60	43.20
HomP	2.21	2.29	2.24	1.20	0.40	1.60
HomRI	0.59	0.67	0.60	47.60	46.80	47.60
HomR	2.44	2.54	2.46	0.00	0.40	0.80
HomS	2.10	2.24	2.13	0.40	0.80	2.00
HomT	0.36	0.41	0.36	46.80	46.00	47.60

TABLE 4: SUMMARY OF *EPOP* AND *BIAS* VALUES

	<i>epop</i>			<i>bias</i>		
	UX	OP	OP+UX	UX	OP	OP+UX
Het1	7.04	8.28	8.22	0.92	0.91	0.91
Het2	7.27	7.44	7.35	0.91	0.92	0.92
HomP	10.22	10.30	10.33	0.89	0.90	0.90
HomRI	3.55	3.81	3.66	0.94	0.94	0.94
HomR	11.00	10.98	10.95	0.89	0.90	0.90
HomS	10.21	10.13	10.13	0.88	0.89	0.89
HomT	1.60	1.68	1.66	0.97	0.97	0.97

the same time, their *bias* values are generally lower than the ones obtained for the remainder options. This can indicate that UX operator generates a slight bigger disruption than the others, increasing in this way the genetic diversity. In other words, UX has a biggest amount of quite similar solutions near the optimum (lower *epop* values), but with different genetic conformations (lower *bias* values). This gives a wide set of diverse and good quality solutions.

AEPs approaches with high selective pressure (HomT and HomRI) show good quality solutions (see *ebest* and *epop* average values). Particularly all individuals from the final population present similar genotypic characteristics, it can be corroborated with the high mean *bias* values. As was to be expected, the remainder homogeneous PEAs obtain varied results in the final population (greater *epop* values and lesser mean *bias* values) without finding individuals so good as HomT and HomRI. The Het1 and Het2 options, proposed to preserve the diversity in the population, obtain good quality solutions (mean *ebest* values close to zero) and a set of very varied individuals (mean *epop* values near to 10% and mean *bias* values close to 0.91). In this way the good results, obtained from tournament and linear ranking selection methods, are combined with a big solution variety in the final population supplied for the other selection methods. This diversity in the final population allows finding alternative solutions near the best-found solutions, and then a static algorithm can be adequate to changes in the problem context.

Considering the study about the influence of both crossover operators and selection methods, the following observation can be made: the resultant heterogeneous PEAs have generally an intermediate behaviour between the homogeneous algorithms with low selective pressure plus OP application and the homogeneous ones with high selective pressure plus UX. Other point can be observed: the selection methods exercise greater influence on the PEA behaviour than the distinct disruptiveness degrees supplied for the different crossover kinds.

Fig. 1, 2 and 3 show *ebest*, *epop* and *bias* values, respectively, for each PEAs considering only instance 6, because it is the most representative instance.

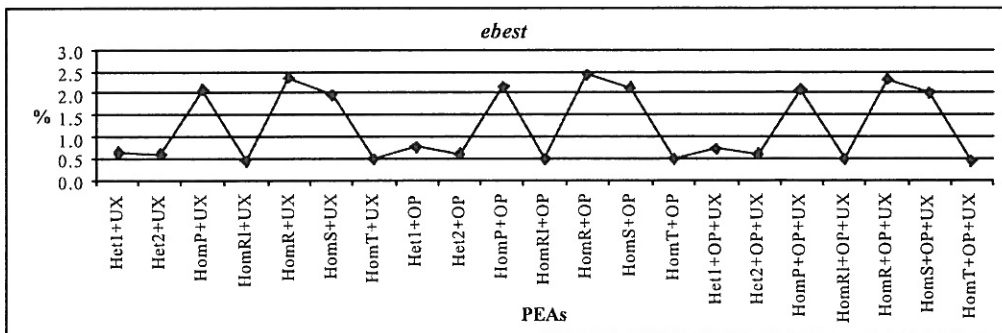
Analysing *ebest* values from Fig 1, independently of the crossover method implemented, the following observation arises: HomR, HomP and HomS (algorithms that use selection methods with low selective pressure) produce a decrease in the solution quality. Meanwhile the error remains under 1% for the rest of the algorithms.

Again only having into account the selection methods, from Fig. 2 the following reflection can be done: PEAs with selection methods having high selective pressure obtain low population errors; while the rest of the options is grouped under an error next to 10.5%. Population errors next to 0% mean that the individuals belonging to the final population have biggest phenotypic similarities. Although, Het1 and Het2 heterogeneous PEAs obtain similar percentile population errors to the ones achieved for the homogeneous PEAs with low selective pressure (Fig. 2), the first obtain good final solution qualities (see Fig. 1).

The selective pressure is reflected on the *bias* value (Fig. 3): a lesser *bias* value means a lower selective pressure. Regarding both this figure and the selective pressure, the following increasing order of PEAs can be obtained: HomS, HomRo, HomP, Het1, Het2, HomRI and finally HomT. In this way, the heterogeneous algorithms (Het1 and Het2) combine advantageous characteristics of algorithms with different selective pressure degrees. That means, these algorithms associate the population variety, supplied for the algorithms orientated to the exploration (low selective pressure), with the concentration of the search to the best individuals given for the algorithms orientated to the exploitation (high selective pressure). So the Het1 and Het2 heterogeneous algorithms achieve a best equilibrium between exploration and exploitation.

VI. CONCLUSIONS

In this paper, the reaches in the application of different selection methods and crossover operators in homogeneous and heterogeneous parallel evolutionary algorithms were studied. The motivations for that were keeping the population diversity and obtaining quality in the solutions. The heterogeneity is used to combine advantages from each selection methods and crossover operators. Besides it is used to analyse the possible improvement in the balance between exploration and exploitation of the search space. For analysing the effect of this heterogeneity the following aspects are evaluated: the quality of the best-found

Fig. 1: *ebest* values for instance 6.

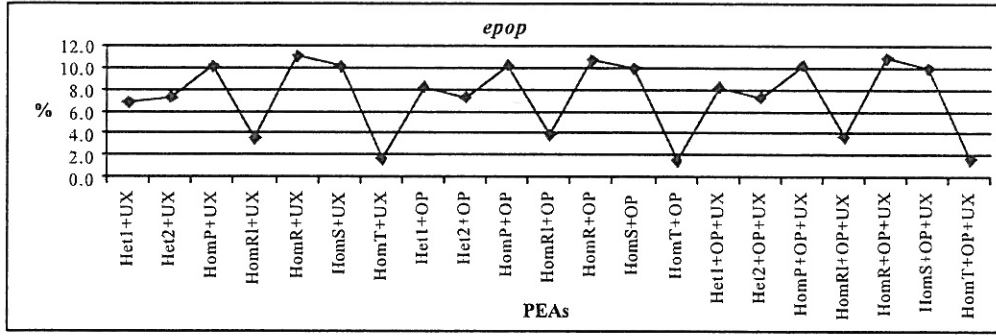


Fig. 2: *epop* values for instance 6.

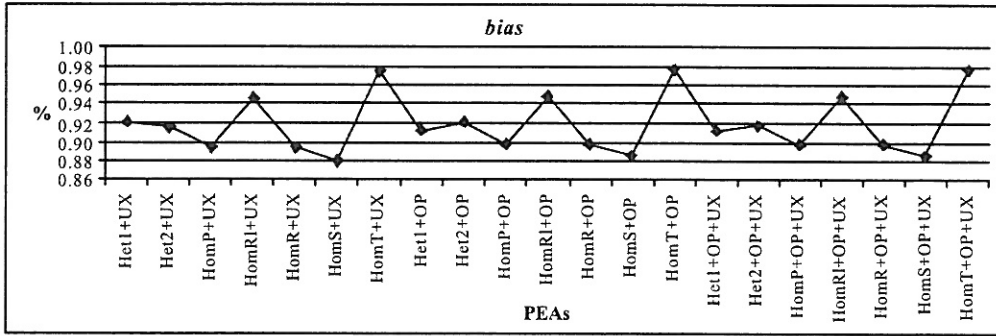


Fig. 3: *bias* values for instance 6.

individual and the final population, the evolution of the population diversity and the number of times that the optimal value was found.

The heterogeneous PEAs, proposed here, show differences in the evolution behavior by varying crossover operators and selection methods for mating in the diverse subpopulations. Five selection methods and two crossover operators were used. The selection methods considered were: proportional, linear ranking, tournament, random and stochastic universal sampling. Meanwhile the crossover operators were: one-point and uniform crossover.

The important point, which is deduced from this job, is the greater equilibrium between population diversity and the good final solutions obtained by the heterogeneous parallel evolutionary algorithms. Therefore, these algorithms can combine the characteristics from the selective methods as many as the ones from crossover operators. In other words, the islands with more selective pressure cooperate distributing their best individuals to the rest and benefit by the incorporation of genetic material, which was lost due to the influence of high selection pressure. Furthermore, the diversity maintenance is helped for those operator crossovers with high disruption degree.

Our experiments show that the combinations of a proper selective pressure and adequate crossover disruptiveness enhance the evolutionary behaviour.

Due to the good results obtained, further research will be oriented to deeper study of the heterogeneity by the modification of other algorithmic parameters.

VII. ACKNOWLEDGEMENT

We acknowledge the cooperation of the project groups for providing new ideas and constructive criticisms. Also to the

Universidad Nacional de La Pampa from which we receive continuous support.

VIII. REFERENCES

- [1] P. Adamidis, "Review of parallel genetic algorithm bibliography", Technical Report, Version 1, Aristotle University of Thessaloniki, 1994.
- [2] P. Adamidis and V. Petridis, "Co-operating populations with different evolution behavior", in *Proceedings of the Second IEEE Conference on Evolutionary Computation*, pp. 188-191, 1996.
- [3] E. Alba Torres et. al., "MALLBA: a library of skeletons for combinatorial optimisation", in *Proceedings of Eighth International Euro-Par Conference*, pp. 927-932, 2002.
- [4] E. Alba Torres and C. Cotta, "Optimizaci3n en entornos geogr3ficamente distribuidos". Proyecto MALLBA. 2002.
- [5] E. Alba Torres and M. Tomassini, "Parallel and evolutionary algorithms", in *IEEE Transactions of Evolutionary Computation*, vol. 6, No 5, pp 443-463. 2002
- [6] T. Bäck, "Selective pressure in evolutionary algorithms: a characterization of selection mechanisms", in *Proceedings of the First IEEE Conference on Evolutionary Computation*. pp. 57-62. 1994.
- [7] T. Bäck, *Evolutionary Algorithms in Theory and Practice*, Oxford University Press. 1996.
- [8] J.E. Baker, "Adaptive selection methods for genetic algorithms", in *Proceedings of the First International Conference on Genetic Algorithms and their Applications*, pp. 101-111, 1985.

- [9] J.E. Baker, "Reducing bias and inefficiency in the selection algorithm", in *Proceedings of the Second International Conference on Genetic Algorithms*, pp. 14-21, 1987.
- [10] T.C. Belding, "The distributed genetic algorithms revisited", in *Proceedings of the Sixth International Conference on Genetic Algorithms*, pp. 114-121, 1995.
- [11] T. Blickle and L. Thiele, "A comparison of selection schemes used in genetic algorithms", Technical Report 11 TIK, Swiss Federal Institute of Technology, December 1995.
- [12] A. Brindle, *Genetic Algorithms for Function Optimization*, Doctoral Dissertation, University of Alberta, Edmonton, 1981.
- [13] E. Cantù-Paz, "A survey of parallel genetic algorithms", Technical Report IlliGAL no. 97003, University of Illinois at Urbana-Champaign, 1997.
- [14] R.J. Collins, *Studies in Artificial Evolution*. Doctoral dissertation, University of California. 1992
- [15] S.A Cook, "The complexity of theorem-proving procedures", in *Proceedings of Third Annual ACM Symposium on the Theory of Computing*, pp. 151-158, 1971.
- [16] Y. Davidor, Y. "A naturally occurring niche & species phenomenon: the model and first results" in *Proceedings of the Fourth International Conference on Genetic Algorithms*, pp. 257-263, 1991.
- [17] S. Esquivel, A. Leiva and R. Gallard, "Selection mechanisms in evolutionary algorithms"- in *Fundamenta Informaticae*, IOS Press, vol 35, No 14, pp 17-33. 1998.
- [18] S.E. Eklund, "A massively parallel GP engine in VLSI", in *Proceedings of 2002 Congress on Evolutionary Computation*, pp. 629-633, 2002.
- [19] M. Garey and D. Johnson, *Computers and Intractability: a Guide to the Theory of NP-completeness*. Freeman. 1979.
- [20] D.E. Goldberg and K. Deb, "A comparison of selection schemes used in genetic algorithms", in *Foundations of Genetic Algorithms*, pp. 69-93. 1991.
- [21] D.E. Goldberg et. All, "Critical deme for serial and parallel genetic algorithms", IlliGAL Report no. 95002, 1995.
- [22] V.S. Gordon and D. Whitley, "Serial and parallel genetic algorithms as function optimizers", in *Proceedings of the Fifth International Conference on Genetic Algorithms*, pp.93, 1993.
- [23] J.J. Grefenstette, "Parallel adaptive algorithms for function optimization". Technical Report no. CS-81-19, Vanderbilt University, Computer Science Department Nash village, TN, 1981.
- [24] F. Herrera, F. and M. Lozano, "Gradual distributed real-coded genetic algorithms", Technical Report no. DECSAI-97-01-03, 1997.
- [25] J. Holland, *Adaptation in Natural and Artificial Systems*, The MIT Press Cambridge, MA, second edition. 1992.
- [26] T-H. Li, C.B. Lucasius and G. Kateman, "Optimization of calibration data with the dynamic genetic algorithm", in *Analytica Chimica, Acta*. 2768, pp. 123-134, 1992.
- [27] S. Lin, W. Punch, and E. Goodman, "Coarse grain parallel genetic algorithms: categorization and new approach", in *Proceedings of the Sixth IEEE Symposium on Parallel and Distributed Processing*, 1994.
- [28] S.W. Mahfoud, "Niching methods for genetica algorithms", IlliGAL Report no. 65001, 1995.
- [29] B. Manderick and P. Spiessens, "Fine-grained parallel genetic algorithms", in *Proceedings of the Third International Conference on Genetic Algorithms*, pp. 428-433, 1989.
- [30] M. Michalewicz, *Genetic Algorithms + Data Structures = Evolution Programs*. Springer Verlag, third, revised an extended edition, 1999.
- [31] H. Mühlenbein, "Parallel genetic algorithms, population genetics and combinatorial optimizations", in *Proceedings of the Third International Conference on Genetic Algorithms*, pp. 416-421, 1989.
- [32] H. Mühlenbein, M. Schomisch and J. Born, "The parallel genetic algorithm as function opitimizer", in *Parallel Computing*, vol 17, pp. 619-633, 1991.
- [33] H. Mühlenbein, "Evolution in time and space- The parallel genetic algorithm", in *Foundations of Genetic Algorithms*, vol. 1, pp. 319-337, 1991.
- [34] J.C. Potts, T.D. Giddens, and S.V. Yadav, "The development and evaluation of an improved genetic algorithm based on migration and artificial selection", in *IEEE transaction on Systems, Man, and Cybernetics*, vol 24, pp. 73-86, 1994.
- [35] J. Sarma and K. De Jong, "An analysis of local selection algorithms in a spatially structured evolutionary algorithms", *Proceedings of the Seventh International Conference on Genetic Algorithms*, pp. 181-186, 1997.
- [36] W. M. Spears and K.A. De Jong, "On the virtues of parameterized uniform crossover", in *Proceedings of the Fourth International Conference on Genetic Algorithms*, pp. 230-236. 1991.
- [37] P. Spiessens and B. Manderick, "A massevely parallel genetic algorithm", in *Proceedings of the Fourth International Conference on Genetic Algorithms*, pp. 279-286, 1991.
- [38] G. Syswerda, "Uniform crossover in genetic algorithms", in *Proceedings of the Third International Conference on Genetic Algorithms*, pp. 2-9, 1989.
- [39] R. Tanese, "Distributed genetic algorithms", in *Proceedings of the Third International Conference on Genetic Algorihtms*, pp. 434-439, 1989.
- [40] D. Whitley, "The GENITOR algorithm and selection pressure: Why rank-based allocation of reproductive trials is best", in *Proceedings of the Third International Conference on Genetic Algorithms*, pp. 116-123, 1989.
- [41] Z.B. Xu and Y. Gao, "The characteristic analysis and prevention of premature convergence of genetic algorithms", in *Science in China*, vol. 26 no. 4, pp. 364-375, 1996.