

A Structure-Based Coarse-Fine Approach for Diversity Tuning in Cellular GAs

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Abstract—This article empirically assesses a coarse-fine approach for diversity tuning in cellular Genetic Algorithms (cGAs). The coarse tuning is performed through the constant reconfiguration of the grid while the fine tuning is locally achieved through dynamic anisotropic selection which considers individuals' locations in the local neighborhood. Benchmark problems including continuous, real-world and combinatorial problems are evaluated. The experimental results show an improvement in cGAs performance when compared to having a fixed topology configuration or to independently applying dynamic lattice reconfiguration or dynamic anisotropic.

Index Terms—Evolutionary computation, genetic algorithms, parallel algorithms, optimization, adaptive algorithm.

I. INTRODUCTION

Genetic Algorithms (GAs) are stochastic search techniques that have successfully tackled difficult optimization problems presenting characteristics such as multi-modality, epistasis, asymmetry and deceptiveness. Since the early years of GAs' development, parallel approaches also emerged. A general classification of Parallel GAs (PGAs) divides them by the population's grain in coarse and fine PGAs [1]-[4]. Fine grained PGAs are also known as cellular GAs (cGAs) and their main difference is the use of a structured and decentralized population [11]. Normally, cGAs are implemented using a lattice topology placing one individual per grid position. The lattice is connected in a toroidal way with wraparound edges. Other algorithmic parameters need to be configured such as the lattice's shape, the local neighborhood and its corresponding size and shape, among others. Those parameters directly affect the induced selective pressure applied during the search [5]-[7].

Previous studies have focused on using cGAs structure as a way of controlling selective pressure in order to balance population's diversity [8]. Researchers have also proposed dynamically reconfiguring the population topology [9]. However, a form of migration occurs during the relocation of individuals, after grid re-arrangement, inducing a loss of the natural adjacency of individuals. In [10],[14], individuals are eliminated following predefined criteria, inducing disturbances in the landscape to create inner islands and modify population's diversity. Several benchmark problems are assessed and results improve solutions' accuracy but statistical analysis is not provided.

On the other hand, controlling the exploration-exploitation trade-off using cGAs' structure does not need to be an immediate response to changes in phenotypic or genotypic spaces. Instead, a constant internal topology reconfiguration leads to a significant algorithmic performance improvement [15]. Moreover, applying locally a method known as anisotropic selection allows a variable parameter to dynamically adjust selective pressure [17]-[18]. Both approaches take advantage of the structural properties of this evolutionary algorithmic technique. This article assesses algorithmic criteria that use global and local structural properties in order to improve cGAs performance in terms of efficiency and efficacy. Results obtained are statistically analyzed and compared to previously obtained results.

In the following section, a detailed explanation of the effect of controlling selection pressure through internal lattice reconfiguration and the dynamic local selection criterion are presented. In Section III, the new proposed algorithmic approach is introduced. In Section IV, the experimental set-up including benchmark problems is provided. In Section V, results analysis including statistical tests is presented. Finally, Section VI draws conclusions based on results obtained.

II. DIVERSITY TUNING MECHANISM

Using structural properties of cellular GAs to control the exploration-exploitation trade-off has been a topic for research [19]-[20]. It was mentioned in Section I that dynamic lattice reconfiguration and dynamic anisotropic selection separately assessed showed an improvement in cGAs performance in most benchmark problems. Phenotypic diversity, considering the average population's fitness score, and the population's entropy were adaptively assessed as measures to trigger either a change in the topology configuration or to modify the selection probabilities of the neighbors through anisotropic selection [17]. Both measures did not show a significant difference in performance when compared to a constant and periodical application of either mechanism. Therefore the effect of internally modifying the topology configuration resulted in a coarse approach for diversity tuning and it does not need to be applied as a prompt response to changes in phenotypic or genotypic diversity. On the other hand, dynamic anisotropic selection directly affects the probabilities for selection of individuals within neighborhoods, and therefore it finely modifies the induced selective pressure from a local level.

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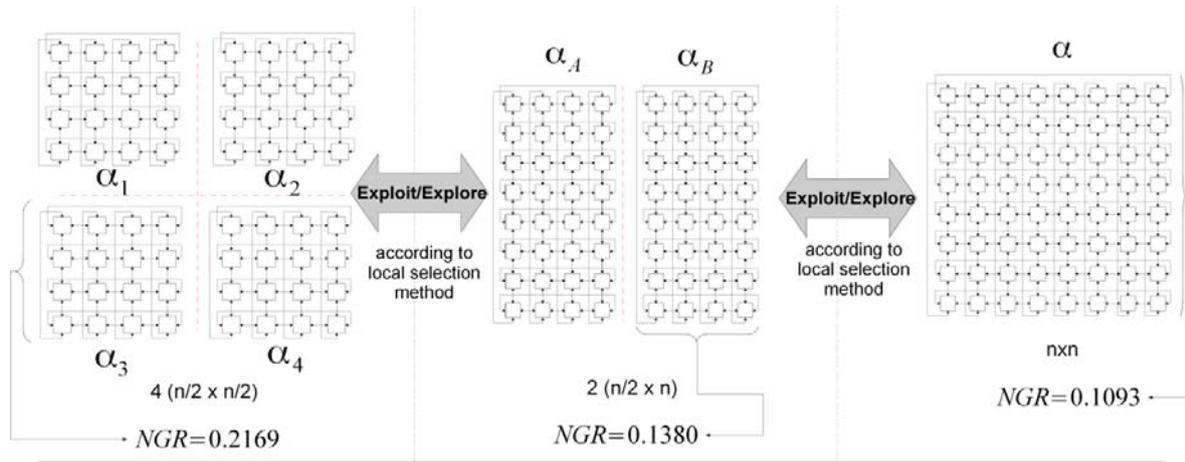


Figure 1. Coarsely, the overall selective pressure is modified by the lattice reconfiguration mechanism according to the local selection method. Finally, at local level, the α parameter for anisotropic selection is changed dynamically either constantly or adaptively

In cGAs, the exploration and exploitation of landscapes is performed concurrently. Thus, exploration is mainly achieved throughout the grid while exploitation is locally promoted within neighborhoods. Dynamic lattice reconfiguration internally creates cellular sub-structures that would imply different levels of selective pressure that as a whole would modify the overall selection pressure. On the other hand, through dynamic anisotropic selection, distinct levels of selective pressure are locally achieved. The combination of both approaches in a coarse-fine diversity tuning mechanism aims to improve cGAs performance in terms of efficiency and efficacy.

A. Coarse Tuning – lattice reconfiguration

Researchers have demonstrated that the exploration-exploitation trade-off can be implicitly controlled in cGAs through the configuration of the population topology and the neighborhood [15]-[16]. A measure known as the neighborhood-grid ratio (NGR) has been defined in order to describe its behavior. The NGR was first introduced in [7]. Its calculation corresponds to measuring the dispersion of p points (each individual position) centered at (x_0, y_0) . A dispersion measure is used because other possible measures, such as the radius of a circle, would give the same value for different population topologies. The dispersion of a point pattern is calculated as follows:

$$D = \sqrt{\frac{(x_i - \bar{x})^2 + (y_i - \bar{y})^2}{p}} \quad [1]$$

where $\bar{x} = \sum_{i=1}^p x_i$ and $\bar{y} = \sum_{i=1}^p y_i$. Hence, the NGR is given by

$$NGR = \frac{D_{\text{neighbourhood}}}{D_{\text{grid}}} \quad [2]$$

In Fig. 1, three population configurations are drawn. Internally, smaller cellular structures imply a higher or lower NGR that as a whole would modify the search making it more exploitative or explorative. A $n \times n$ configuration, where n is the number of individuals per grid side, is the only topology which NGR directly represents its level of selective pressure. A $2(n/2 \times n)$ configuration divides a square grid in two rectangular topologies with $n/2$

individuals on the shorter side. A $4(n/2 \times n/2)$ configuration divides a fully connected square topology in four smaller square toroidal grid configurations with $n/2$ individuals per side. These lattice configurations are used in the experimental set-up.

For topologies in Fig. 1, a compact Von Neumann local neighborhood is used consisting of individuals located at North, East, South and West with a Manhattan distance of one from the central individual. As an example, for a population of 400 individuals, dispersion measure is $D = 0.8944$ with local Von Neumann neighborhood. If individuals are distributed on a 20×20 square topology, corresponding NG ratios, as regards each independent cellular sub-structure, are: $NGR_{n \times n} = 0.1093$, $NGR_{n/2 \times n} = 0.1380$, $NGR_{n/2 \times n/2} = 0.2169$.

Different ratios mean having higher or lower selection pressures. Therefore, decentralized GAs are structurally capable of modifying selective pressure while changing the population's structural configuration. Lower ratios means more exploration is performed while higher ratios imply more exploitation. However, the NGR is a representation of the selective pressure in a fully connected structure or sub-structure. Therefore, it does not reflect the overall induced selective pressure in topologies configurations formed by several cellular sub-structures, like those shown in Fig. 1. In order to analyze the levels of selective pressure that each topology configuration induces, an experimental assessment is carried out to calculate the take-over times following a constant lattice reconfiguration criterion.

At local level, two different selection methods are applied; widely known binary tournament selection and constant anisotropic selection proposed in [17]. These selection methods induce distinctively opposite selective pressures. In order to characterize the selection pressure in cellular GAs, the take-over time concept (also refer to as the proportional growth of the best individual) is used. The take-over time reflects how long it takes for the best individual to spread its solution throughout the entire array when only selection is applied. Longer take-over times represent lower selection pressures and therefore more explorative search; and shorter take-over times correspond to higher selection pressures, equivalent to more exploitative

search. In Fig. 2, proportional growth curves for both selection methods are shown. A hundred experiments for a population of 400 individuals were performed when applying constant anisotropic selection with $\alpha = 0.8$ and binary tournament selection. On a static 20×20 square topology, binary tournament shows higher selective pressure in comparison to constant anisotropic selection with $\alpha = 0.8$ which is more explorative. In the same figure, growth rates corresponding to constant lattice reconfiguration among population topologies drawn in Fig. 1 are shown. Reconfiguring the grid allows internal cellular sub-structures to induce an overall higher or lower selective pressure. In Fig. 2, when locally applying binary tournament selection the overall induced selective pressure becomes lower and therefore more explorative. Constant anisotropic selection with $\alpha = 0.8$ results in higher selective pressure and becomes more exploitative. In fact, binary tournament corresponds to applying uniform anisotropic selection, if $\alpha = 0.25$ all neighbors have the same probability for selection. In the next subsection the fine tuning mechanism based on anisotropic selection is explained.

B. Fine Tuning - dynamic anisotropic selection

Anisotropic selection depends on the direction of an individual's location in a Von Neumann local neighborhood. It consists of individuals at the North, East, South and West positions, at a Manhattan distance of one from the central individual. Anisotropic selection chooses an individual following two probabilistic equations determined by an α parameter: $P_N = P_S = P_0(1 + \alpha)$ and $P_E = P_W = P_0(1 - \alpha)$ respectively. For example, if $\alpha = 0.0$ and $\alpha = 0.25$ uniform probability for all neighbors is applied.

Similar to previous approach, in Fig. 3, take-over times for anisotropic selection, considering $\alpha \in [0.0, 0.9]$, are drawn. These curves are obtained from an average of 100 experiments on a population of 400 individuals and a minimum α step of 0.1. Higher α values promote exploration while lower α values perform a more exploitative search. Moreover, for $\alpha \leq 0.3$ take-over times are very similar. Thus, for these values the expected effect of controlling the selection pressure is null.

The fine tuning mechanism consists in dynamically changing α from 0.0 to 0.9 and thus assigns higher or lower probabilities to individuals located at North/South or East/West positions. In Fig. 1, three internally different topology configurations are presented; a distinct α value is assigned to each cellular structure or sub-structure varying the induced selective pressure according to constant and adaptive criteria.

Combining internal lattice reconfiguration and dynamic anisotropic selection in a coarse-fine mechanism for diversity tuning allows to improve cellular GAs' performance without significantly changing their algorithmic structure and therefore without increasing their computational cost.

C. Coarse-Fine Diversity Tuning

Reconfiguring the population topology as a mechanism for diversity tuning in cellular GAs was assessed in [15]. Four internally different topology configurations were used

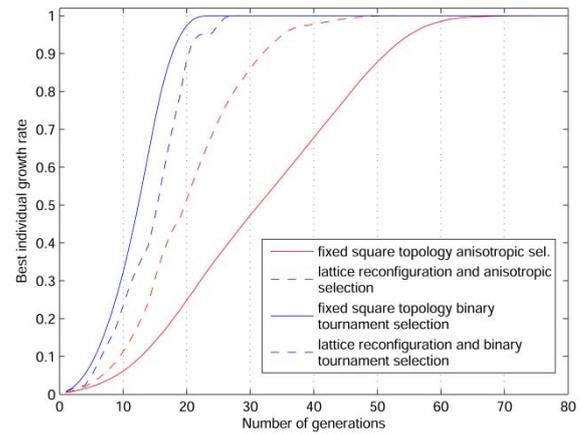


Figure 2. Growth rate for a fixed square topology and constant lattice reconfiguration when applying binary tournament or anisotropic ($\alpha = 0.8$) selection.

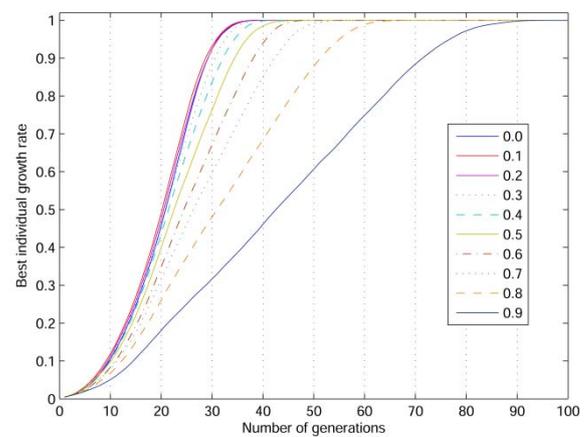


Figure 3. Dynamic anisotropic selection growth rate on a square topology.

including vertical and horizontal alignments for two of them. In this article, three of those configurations are used removing one that divides the population in linear cellular sub-structures and only vertical alignment is used for the topology configuration shown in the middle of Fig. 1. The conclusion of that article suggested that reconfiguring the population topology is a rough approach for diversity tuning and it does not need to be applied as a prompt response to diversity changes in phenotypic or genotypic spaces. In this study, diversity tuning is pursued at two levels, coarsely by constantly applying the lattice reconfiguration mechanism and finely by dynamic anisotropic local selection.

Anisotropic selection makes use of individuals' locations within neighbourhoods to assign probabilities for selecting the second parent as explained in previous subsection. This selection method is based on the structural configuration of cGAs' local neighbourhood. Dynamic modification of the parameter allows a wider span for adjusting the induced selective pressure as the growth rate curves drawn in Fig. 3 show. It is expected that finely and independently tuning the parameter for each cellular sub-structure contribute in a better balance of the exploration-exploitation trade-off and therefore in an improvement of cGAs' performance. In the next section, the algorithmic details are presented.

III. ALGORITHMIC APPROACH

In Fig. 4 the proposed algorithmic approach is presented.

```

1: procedure CGA
2: n×n, α=0.5; //initial configuration
3: (x)←random(); //initial population
4: (f)←evaluation(x); //evaluation
5: while k←1 generations do
6: if k mod c=0 then //constant latt.
  reconf.
7:   if lattConf=n×n then //current
  lattice configuration
8:     lattConf=2(n/2)×n
9:   else if lattConf=2(n/2)×n then
10:     lattConf=4(n/2)×(n/2);
11:   else
12:     lattConf=n×n
13:   end if;
14: else
15: end if;
16: for i←1, popSize do //reproduction
17:   f'←selection(fn, fe, fs, fw)
18:   x'←selection(xn, xe, xs, xw);
19:   (x1, x2)←recombination(x0, x');
20:   (x'1, x'2)←mutation(x1, x2)
21:   f'←evaluation(x0, x'1, x'2);
22:   (x0, f0)←(f', x'); //replace if-better
23: end for;
24: x←xtemp, f←ftemp; //synch.update
25: if  $\bar{f} \leq \text{threshold}$  then
26:   Break;
27: else
28:   [CDA|PDA(f)|GDA(x)]; //fine tuning
29: end if;
30: end while;
31: end procedure;

```

Figure 4. Coarse-fine diversity tuning cellular GA

Evolution starts on a static square grid $n \times n$ and anisotropic selection is configured with $\alpha = 0.5$ (line 2). The population evolves using topology configurations drawn in Fig. 1; the coarse diversity tuning mechanism through lattice reconfiguration occurs constantly every certain number of generations (lines 6-15). The main reproductive cycle follows a synchronous updating policy after the central individual is mated with an individual selected from its neighbors (lines 16-24). Single point crossover is used with probability $P_c = 1.0$ and offspring are mutated with probability $P_m = 0.02$. The current individual is replaced only if offspring achieve higher fitness scores.

Once the whole population has evolved the population's average fitness score is compared to a threshold that secures a high accurate problem's solution. If the threshold has not been fulfilled, the fine tuning mechanism is executed either constantly or adaptively (lines 25-30). Thus, either constant (CDA), phenotypic (PDA) or genotypic (GDA), dynamic anisotropic selection are applied.

Constant anisotropic selection (CDA) is detailed in Fig. 5.

Every certain number of generations, α is increased by $\alpha = 0.1$, once it has reached the highest value $\alpha = 0.9$, it is re-initialized to $\alpha = 0.1$. Constant anisotropic selection is evaluated similar to constant lattice reconfiguration criterion. Both methods are computationally less expensive in comparison to adaptive mechanisms that evaluate phenotypic or genotypic diversity to trigger dynamic changes either at lattice or local anisotropic selection levels. In this article, the population topology is constantly reconfigured in combination with constant and dynamic anisotropic local selection.

```

1: procedure CDA
2: if k mod c=0 then //c is a constant
3:   if α=0.9 then
4:     α=0.1 //reinitialize α
5:   else
6:     α=α+0.1; // increment α
7:   end if;
8: else
9:   end if;
10: end procedure;

```

Figure 5. Constant anisotropic selection

To tune dynamically the α parameter in anisotropic selection for each independent cellular structure ($\alpha_A, \alpha_B | \alpha_1, \dots, \alpha_4$) showed in Fig. 1 diversity measures are calculated separately for each cellular structure formed once the lattice has been reconfigured.

Dynamic anisotropic selection based on phenotypic diversity (PDA) is presented in Fig. 6, the difference in phenotypic entropy (H_p) among consecutive generations is evaluated as follows:

$$H_p = - \sum_{j=1}^N f_j \log(f_j) \quad [3]$$

where f_j is the proportion of individuals in one generation having fitness j in exponential logarithm base [20]. Thus, the difference between $\Delta H_p, \Delta H_{p_{t-1}}$ and $\Delta H_{p_{t-2}}$ would determine if phenotypic diversity in current generation has or has not significantly changed with respect to previous generations; where $\Delta H_{p_t} = \Delta H_{p_t} - \Delta H_{p_{t-1}}$.

In order to determine genotypic diversity (H_G), the Hamming distance among chromosomes is used as a measure. In Fig. 6, details for GDA procedure are also presented. In line 2, the difference between current $\bar{H}_{G_t} = \bar{H}_{G_t} - \bar{H}_{G_{t-1}}$ and previous ($\Delta \bar{H}_{G_{t-1}}, \Delta \bar{H}_{G_{t-2}}$) generations is calculated, in order to assess genotypic diversity changes. In a similar way to phenotypic diversity, if $(\bar{H}_{G_t} - \bar{H}_{G_{t-1}})$ difference is less than $(\bar{H}_{G_{t-1}} - \bar{H}_{G_{t-2}})$, diversity is being lost and exploration should be encouraged increasing α . On contrast, exploitation should be promoted by decreasing α . If neither of those conditions is satisfied, the α parameter for anisotropic selection remains the same.

```

1: procedure PDA, GDA(f, x)
2:   if ΔHt < (2ΔHt-1) - (ΔHt-2) then
3:     if α = 0.9 then
4:       else
5:         α = α + 0.1; //exploration
6:       end if;
6:     else if ΔHt > (2ΔHt-1) - (ΔHt-2) then
7:       if α = 0.0
8:         else
9:           α = α - 0.1; //exploitation
10:        end if;
11:       else
12:        end if;
13: end procedure;
    
```

Figure 6. Phenotypic or genotypic based anisotropic selection.

IV. EXPERIMENTAL SET-UP

In Table I, benchmark problems are summarized. Three continuous problems: Rastrigin, Griewank and Langerman functions presenting characteristics such as multi-modality, epistasis and non-regularity are tackled [19],[21],[25]. Binary chromosomes encoding has been used with specific minimum step per variable. The aim is to evaluate difficult characteristics of theoretical continuous problems that are commonly found in real-world problems [13].

Three real-world problems: Frequency Modulation Sound (FMS) problem, GPS attitude determination problem [12],[23]-[24] and System of Linear Equations (SLE) are also tackled.[22]. Three combinatorial problems are also tackled: Massively Multi-modal Deceptive Problem (MMDP), Minimum Tardy Task Problem (MTTP) and P-Peaks problem.

A. Experimental constraints

The following experimental constraints are evaluated:

- A population size of 400 individuals is used for most problems, except for GPS and MTTP problems, where a population size of 64 and 100 individuals is used.
- Local neighborhood configuration is Von Neumann composed by four individuals plus the central one.
- 100 independent runs are carried out per case.
- A limit of 500 generations is defined for most problems, except for the Langerman function, the SLE and the MMDP problems where the limit is 700 generations.

In order to statistically support the results, an initial normality test is performed on each set of experimental results regarding the convergence time. First, normality is determined by the Kolmorov-Smirnov test or the Lilliefors test, both at 5% significance. Lilliefors test is suitable when a fully-specified null distribution is unknown, contrary to the Kolmorov-Smirnov test. After, an Analysis of Variance (ANOVA) is applied to results with normal distribution whereas Kruskal- Wallis is applied in any other case. To represent that 5% statistical significance difference has been found among convergence time results, a symbol (+) is used. On the contrary, a (*) symbol indicates that results are not statistically different, and therefore applying proposed dynamic criteria make no difference in terms of number of generations, when compared to a static cGA. On the other hand, having statistically different results does not mean the proposed approaches improve a static cGA performance;

TABLE I. BENCHMARK PROBLEMS

Problem	Fitness function
Rastrigin	$f(x) = 10q + \sum_{i=1}^q (x_i^2 - \cos(2\pi x_i))$ $q = 10, f_T \leq 0.0005$
Griewank	$f(x) = 1 + \sum_{i=1}^q \left(\frac{x_i^2}{4000} - \prod \cos\left(\frac{x_i}{\sqrt{i}}\right) \right)$ $q = 10, f_T \leq 0.0001$
Langerman	$f(x) = -\sum_{i=1}^q c_i e^{-\frac{1}{\pi} \sum_{j=1}^D (x_j - a_{ij}^2)} \cos\left(\pi \sum_{j=1}^D (x_j - a_{ij})^2\right)$ $q = 10, f_T \geq -1.4990$
FMS	$f(t) = a_1 \sin(w_1 t\theta) + a_2 \sin(w_2 t\theta + a_3 \sin(w_3 t\theta));$ $q = 6, f_T \leq 0.04$
SLE	$Ax = b$ $q = 10, f_T \leq 0.04$
GPS attitude	$f(\varphi, \beta, b) = \sum_{i=1}^m \sum_{j=1}^n \cos\left(\frac{2\pi}{\lambda} \left(\frac{DD\phi_{AB}^{ij}}{m(n-1)} - \frac{DD\phi_{AB}^{ij}(\varphi, \beta, b)}{m(n-1)} \right)\right)$ $q = 3, f_T \geq 0.993$
MMDP	$f(q) = \sum_{i=1}^k \text{fitness}_{q_i}$ $q = 25, k - \text{subproblems}, f_T \geq 0.99$
MTTP	$f(x) = \sum_{i=1}^q \text{weight}_{x_i}$ $q = 100, f_T \leq 0.0051$
P-Peaks	$f(x) = \frac{1}{q} \max_{i=1}^P (Q - \text{Hamming}(x, P_i))$ $P = 100, f_T = 1.0$

hence an individual analysis for each problem accompanies the interpretation of the results tables. Results are analyzed in terms of convergence time (efficiency) and search rate (efficacy). Search rate represents the number of experiments that succeeded in solving the problem, out of the total number of experiments which is set to a 100. On each table of results, bold fonts highlight the best performances. Results accuracy is high due to the stop condition which is for all problems highly accurate, see Table 1. The stop condition evaluates the average population fitness score versus a problem specific threshold. The performance of a square topology locally implementing binary tournament or anisotropic selection with $\alpha = 0.0$, and constant anisotropic selection with $\alpha = 0.8$ are included as reference. However, the difference between both methods in terms of the induced selective pressure is significant and reflects directly in the algorithmic efficiency. These scenarios are not included in the statistical analysis in order to avoid results bias.

The hit rate has been statistically evaluated as a Bernoulli trial. A random experiment whose result is either success or failure can be considered a Bernoulli trial [20]. Measuring the standard deviation of successful experiments percentages provides a numerical value that indicates how significantly different are these success search rates. The standard deviation for each experimental sample is calculated as follows:

$$\sigma = \sqrt{r \times \hat{p} (1 - \hat{p})} \quad [4]$$

TABLE II. CONVERGENCE TIME ¹ AND HIT RATE ² RESULTS FOR CONTINUOUS AND THE FMS PROBLEMS THROUGH A FIXED LATTICE SHAPE, LATTICE RECONFIGURATION, DYNAMIC ANISOTROPIC SELECTION AND THE COMBINATION OF BOTH

Fixed lattice shape	Rastrigin	Griewank	Langerman	FMS
Binary tournament				
Square	136.68±9.48 100%, 0.0	272±46.45 89%, 3.12	291.04±103.92 21%, 4.07	210.78±58.76 41%, 4.91
Constant anisotropic				
Square	230.38±15.51 100%, 0.0	438.36±39.04 68%, 4.66	432.61±47.01 21%, 4.07	379.38±58.58 52%, 4.99
Lattice reconfiguration				
Constant	186.89±14.56 %, 0.0	370.11±45.66 89%, 3.12	316.62±66.14 37% , 4.82	305.24± <u>61.08</u> 66%, 4.73
Phenotypic	198.14± <u>14.03</u> 100%, 0.0	392.32±48.94 90%, 3.0	365.42±79.82 19%, 3.92	307.37±58.32 61%, 4.870
Genotypic	199.79± <u>12.54</u> 100%, 0.0	388.31±45.69 91%, 2.86	357.40±70.93 25%, 4.33	329.87±75.44 66%, 4.73
Dynamic anisotropic				
Constant	194.15±13.65 98%, 1.40	398.59±42.02 97%, 1.70	346.31±71.83 22%, 4.14	324.31±51.37 65%, 4.76
Phenotypic	199.98±14.33 100%, 0.0	379.81±47.55 98% , 1.40	359.60±70.98 28%, 4.49	315.38±68.09 51%, 4.99
Genotypic	213.19± <u>19.75</u> 100%, 0.0	422.96±52.15 84%, 3.66	336.00±60.53 28%, 4.49	327.29±66.67 51%, 4.99
Lattice reconfiguration + Dynamic anisotropic				
Constant	183.80± <u>9.84</u> 100%, 0.0	378.32±44.36 97%, 1.7	316.40±78.70 32%, 4.66	278.80± <u>49.58</u> 70%, 4.58
Phenotypic	174.45±11.59 100%, 0.0	360.15± <u>51.42</u> 92%, 2.71	326.00±66.21 34%, 4.70	288.75± <u>59.17</u> 64%, 4.80
Genotypic	261.51±20.84 100%, 0.0	365.29±39.76 94%, 2.37	308.65±75.48 26%, 4.38	284.73± <u>49.28</u> 73% , 4.43
ANOVA / K-W³	+	+	*	+

1 Average number of generations and standard deviations are included. Underlined std. dev. corresponds to non-normal dist.

2 Success search rates' standards deviations are included next to the percentage.

3 Statistical tests results: statistical difference is proved (+)/ is not proved(*)

where \hat{p} represents the probability of successful experiments and r is the total number of experiments.

V. RESULTS ANALYSIS

Results corresponding to Rastrigin, Griewank and Langerman functions are presented in Table II. For the Rastrigin problem applying constant high selective pressure results in the best convergence time and hit rate is 100% in all cases. Although hard to solve, the Rastrigin problem is regular and separable thus is not as difficult as the other continuous problems. In the case of the Griewank problem, convergence time is reduced in approximately 75 generations by the proposed coarse-fine approach in comparison to anisotropic selection with $\alpha = 0.8$. The hit rate is significantly improved when applying dynamic anisotropic selection and the proposed coarse-fine approach; from 89% and 68% to 98% (dynamic anisotropic) and 97% (coarse-fine approach), corresponding to statistical significance values of 3.12 and 4.66 to 1.40 and 1.70 respectively. For the Langerman function similar efficacy is obtained through binary tournament and anisotropic selection with $\alpha = 0.8$ improving when constant lattice reconfiguration and the proposed coarse-fine approach are applied with reduced statistical significance (from 21% to 37% and 34%). Binary tournament shows the best

convergence time which is similar to the proposed coarse-fine approach efficiency.

In Tables II and III, results obtained for real problems are presented. Algorithmic efficiency is improved when applying anisotropic selection with $\alpha = 0.8$. In general, binary tournament or anisotropic selection with $\alpha = 0.0$ provides the best convergence time but not the best hit rate. For the FMS problem a reduction in approximately 100 generations is achieved by the proposed coarse-fine approach when comparing to anisotropic selection with $\alpha = 0.8$ together with an improvement in efficacy of around 20%, both metrics with statistical difference. For the SLE problem convergence time is improved with respect to anisotropic selection with $\alpha = 0.8$ in around 150 generations by measuring phenotypic diversity. Higher success search rate (45%) is also obtained, although it is not significantly different to applying binary tournament selection (39%). Finally, the GPS problem presents a slight improvement in efficiency, with two algorithmic approaches presenting similar convergence times: dynamic anisotropic selection and the proposed combined approach, both while measuring phenotypic diversity. Hit rate is improved from 57% (binary tournament or anisotropic selection) and 76% (anisotropic selection with $\alpha = 0.0$) to 87% (combined

TABLE III. CONVERGENCE TIME ¹ AND HIT RATE ² RESULTS FOR REAL AND COMBINATORIAL PROBLEMS THROUGH A FIXED LATTICE SHAPE, LATTICE RECONFIGURATION, DYNAMIC ANISOTROPIC SELECTION AND THE COMBINATION OF BOTH

Fixed lattice shape	SLE	GPS	MMDP	MTTP	P-Peaks
Binary tournament					
Square	297.28±72.56 39%,4.87	73.12±28.69 57%,4.95	431.31± <u>38.45</u> 89%,3.12	259.65±44.16 99%,0.99	169.46± <u>19.99</u> 100%,0.00
Constant anisotropic					
Square	594.21±54.32 19%, 3.92	80.73± <u>15.43</u> 76%,4.27	568.98±54.01 97%,1.70	444.45±36.92 31%,4.62	286.19±35.95 99%,0.99
Lattice reconfiguration					
Constant	469.50±114.32 42%,4.93	72.76±16.93 78%,4.14	550.86±55.63 94%,2.37	437.34± <u>65.97</u> 100% ,0.00	256.77± <u>28.67</u> 100%,0.00
Phenotypic	482.66± <u>95.83</u> 33%, 4.70	82.39± <u>20.51</u> 78%,4.14	602.77±52.03 85%,3.57	429.14±46.50 81%,3.92	277.00±46.50 100%,0.00
Genotypic	511.00±118.66 30%, 4.58	86.01±22.22 84%,3.66	599.05±47.81 92%,2.71	432.82±37.70 68%,4.66	268.78± <u>32.56</u> 100%,0.0
Dynamic anisotropic					
Constant	511.73±69.36 38%,4.85	68.93± <u>16.75</u> 76%,4.27	590.08±49.01 92%,2.71	394.42±48.42 95%,2.17	247.47± <u>24.74</u> 100%,0.0
Phenotypic	509.70±93.72 44%, 4.96	65.71± <u>11.38</u> 80%,4.00	605.15±50.66 94%,2.37	400.81±50.42 88%,3.24	257.48± <u>30.39</u> 100%,0.00
Genotypic	530.88±96.49 27%,4.43	74.51± <u>21.58</u> 82%,3.84	651.86± <u>32.036</u> 45%,4.97	440.00±35.62 51%,4.99	282.82± <u>32.97</u> 100%,0.00
Lattice reconfiguration + Dynamic anisotropic					
Constant	460.09± <u>94.86</u> 42%,4.93	66.78± <u>12.72</u> 82%,3.84	538.81±44.33 99% ,0.99	380.62± <u>36.26</u> 97%,1.70	252.47± <u>26.20</u> 100%,0.00
Phenotypic	442.95±93.32 45% , 4.97	65.48± <u>27.37</u> 87% ,3.36	537.77±48.60 98%,1.40	383.88±51.75 94%,2.37	256.00± <u>29.38</u> 100%,0.00
Genotypic	447.11±96.63 43%,4.95	68.68± <u>16.85</u> 77%,4.20	533.53±55.63 97%,1.70	380.92±48.44 95%,2.17	256.52±31.74 100%,0.00
ANOVA / KW³	+	+	+	+	+

1. Average number of generations and standard deviations are included. Underlined std.dev. correspond to non-normal dist.
2. Success search rates' standards deviations are included next to the percentage.
3. Statistical tests results: statistical difference is proved (+)/ is not proved (*)

approach) with statistical difference. Hit rate percentages that are close to 50%, which is the mean chance expectation, are more likely to occur by chance, therefore statistical measures show minor numerical differences.

In Table III, results for combinatorial problems are shown. For the MDDP problem an improvement in efficacy of 10% with statistical difference of 2.13 is achieved through the proposed coarse-fine approach when comparing to a static square topology with binary tournament or anisotropic selection with $\alpha = 0.0$. Comparing anisotropic selection with $\alpha = 0.8$ and the best efficacy achieved by the proposed coarse-fine approach the improvement is reduced but still statistically significant with a difference of 0.71. For the same comparative scenario, the average convergence time is also reduced in around 30 generations with statistical proof. The MTTP problem results show that applying a constant high selective pressure through binary tournament provides the best overall performance. However, very low hit rate is achieved by anisotropic selection with $\alpha = 0.8$ and both efficiency and efficacy are improved by the proposed coarse-fine technique for diversity tuning with statistical proof. Similarly, the P-Peaks problem is successfully tackled when applying high selective pressure on a square topology; though among dynamic approaches there is a slight improvement in convergence time with 100% efficacy with respect to implementing anisotropic

selection with $\alpha = 0.8$. Results show a reduction in convergence time when applying high selective pressure through binary tournament or anisotropic selection with $\alpha = 0.0$. However, that strength in selective pressure does not lead to a proper balance in the exploration-exploitation trade-off negatively influencing the algorithmic efficacy of most benchmark problems. Applying the proposed coarse-fine approach shows better performance in terms of efficiency and efficacy when comparing to locally applying anisotropic selection with $\alpha = 0.8$. Although, in a couple of problems (Rastrigin and P-Peaks problems) using a static square topology with high selective pressure induced locally achieves the best performance. Convergence times are improved by dynamically applying the coarse-fine approach through adaptive configuration of the α parameter, which is based on phenotypic or genotypic diversity changes, but this difference is limited when comparing to a constant change. In the next section, conclusions of this study are presented.

VI. CONCLUSIONS

The role of the population's structure at coarse and fine levels as a mean for promoting diversity during the evolutionary process is the main contribution of the proposed algorithmic technique.

Algorithmic efficacy is the performance metric that has been improved through the proposed coarse-fine approach

for diversity tuning. Applying constant high selective pressure using binary tournament or anisotropic selection with $\alpha = 0.0$ results in shorter convergence times but efficacy is significantly affected in most problems. Two exceptions are the Rastrigin and the P-Peaks problems where better overall performances are achieved by a combination of a square topology and high local selection pressure. In most benchmark problems better convergence times are obtained by the proposed coarse-fine approach when comparing to locally apply anisotropic selection with $\alpha = 0.8$ (low selective pressure). Similar or improved hit rates are obtained by the proposed coarse-fine approach in comparison to separately applying lattice reconfiguration or dynamic anisotropic local selection.

Results herein presented are based only on performance metrics at algorithmic level. However, for real-world problems such as the GPS attitude determination problem, hard real-time constraints can also be fulfilled. For example, a cGA algorithmic platform is used in [24] to develop a hardware architecture to solve the problem. Execution times fulfil hard real-time constraints required for this application. Thus, implementing the proposed approach for diversity tuning would improve even further those already obtained execution times.

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