Diversity Handling In Evolutionary Landscape

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Abstract

The search ability of an Evolutionary Algorithm (EA) depends on the variation among the individuals in the population [3, 4, 8]. Maintaining an optimal level of diversity in the EA population is imperative to ensure that progress of the EA search is unhindered by premature convergence to suboptimal solutions. Clearer understanding of the concept of population diversity, in the context of evolutionary search and premature convergence in particular, is the key to designing efficient EAs. To this end, this paper first presents a comprehensive analysis of the EA population diversity issues. Next we present an investigation on a counter-niching EA technique [4] that introduces and maintains constructive diversity in the population. The proposed approach uses informed genetic operations to reach promising, but un-explored or under-explored areas of the search space, while discouraging premature local convergence. Simulation runs on a number of standard benchmark test functions with Genetic Algorithm (GA) implementation shows promising results.

1. Introduction

Implementation of EA requires preserving a population while converging to a solution, which maintains a degree of population diversity [7, 8, 9, 12, 13, 14, 15, and 16] to avoid premature convergence to sub-optimal solutions. It is difficult to precisely characterize the possible extent of premature convergence as it may occur in EA due to various reasons. The primary causes are algorithmic features like high selection pressure and very high gene flow among population members. Selection pressure pushes the evolutionary process to focus more and more on the already discovered better performing regions or “peaks” in the search space and as a result population diversity declines, gradually reaching a homogeneous state. On the other hand unrestricted recombination results in high gene flow which spreads genetic material across the population pushing it to a homogeneous state. Variation introduced through mutation is unlikely to be adequate to escape local optimum or optima [17]. While premature convergence [17] may be defined as the phenomenon of convergence to sub-optimal solutions, gene-convergence means loss of diversity in the process of evolution. Though, the convergence to a local or to the global optimum cannot necessarily be concluded from gene convergence, maintaining a certain degree of diversity is widely believed to help avoid entrapment in non-optimal solutions [3, 4].

In this paper we present a comprehensive analysis on population diversity in the context of efficiency of evolutionary search. We then present an investigation on a counter niching-based evolutionary algorithm that aims at combating gene-convergence (and premature convergence in turn) by employing intelligent introduction of constructive diversity [4].

The rest of the paper is organized as follows: Section 2 presents an analysis of diversity issues and the EA search process; Section 3 introduces the problem space for our proposed algorithm. Sections 4, 5 and 6 present the proposed algorithm, simulation details and discussions on the results respectively. Finally, Section 7 presents some concluding remarks.

2. Population diversity and evolutionary search

In the context of EA, diversity may be described as the variation in the genetic material among individuals or candidate solutions in the EA population. This in turn may also mean variation in the fitness value of the individuals in the population. Two major roles played by population diversity in EA are: Firstly, diversity promotes exploration of the solution space to locate a single good solution by delaying convergence; secondly, diversity helps to locate multiple optima when more than one solution is present [8, 15 and 16]. Besides the role of diversity regarding premature convergence in static optimization problems, diversity also seems to be beneficial in non-stationary environments. If the genetic material in the population is too similar, i.e., has converged towards single points
in the search space, all future individuals will be trapped at that single point even though the optimal solution has moved to another location in the fitness landscape. However, if the population is diverse, the mechanism of recombination will continue to generate new candidate solutions making it possible for the EA to discover new optima.

The search ability of a typical evolutionary algorithm depends on the variation among the individuals or candidate solutions in the population. The variation is introduced by the recombination operator to recombine existing solutions, and the mutation operator introducing noise by applying random variation to the individual’s genome. However, as the algorithm progresses, loss of diversity or loss of genetic variation in the population results in low exploration, pushing the algorithm to converge prematurely to a local optimum or non-optimal solution. The following sub-section presents an analysis of the impact of population diversity on premature convergence based on the concepts presented in [13].

2.1 Effect of population diversity on premature convergence

Let \( \vec{X} = (X_1, \ldots, X_N) \in S^N \) be a population of individuals \( Y \) in the solution space \( S^N \), where the population size is \( N \); \( \vec{X}(0) \) be the initial population; \( H \) is a schema, i.e., a hyperplane of the solution space \( S \). \( H \) may be represented by its defining components (defining alleles) and their corresponding values as \( H(a_{i1}, \ldots, a_{ik}) \), where \( 1 \leq K \leq \text{chromosome length} \).

Leung et al. in [13] have proposed the following measures related to population diversity in canonical genetic algorithm.

Degree of population diversity, \( \delta(\vec{X}) \): Defined as the number of distinct components in the vector \( \sum_{i=1}^{N} X_i \); and Degree of population maturity, \( \mu(\vec{X}) \):

\[
\mu(\vec{X}) = I - \delta(\vec{X})
\]

Described as \( \mu(\vec{X}) = I - \delta(\vec{X}) \) or the number of lost alleles.

With probability of mutation, \( p(m) = 0 \) and \( \vec{X}(0) = \vec{X}_0 \), according to Leung [13] the following postulates hold true: For each solution, \( Y \in H(a_{i1}, \ldots, a_{ik}) \mu(\vec{X}_0) : \vec{X}_0 \), there exists a \( n \geq 0 \) such that \( \text{Probability}(Y \in \vec{X}(n) / \vec{X}(0) = \vec{X}_0) > 0 \).

Conversely, for each solution, \( Y \in H(a_{i1}, \ldots, a_{ik}) \mu(\vec{X}_0) : \vec{X}_0 \), and every \( n \geq 0 \) such that \( \text{Probability}(Y \in \vec{X}(n) / \vec{X}(0) = \vec{X}_0) = 0 \).

It is obvious from the above postulates that a canonical genetic algorithm’s search ability is confined to the minimum schema with \( 2^\delta(\vec{X}) \) different individuals. Hence, greater the degree of population diversity, \( \mu(\vec{X}) \), greater is the search ability of the genetic algorithm. Conversely, a small degree of population diversity will mean limited search ability, reducing to zero search ability with \( \mu(\vec{X}) = 0 \).

2.2 Enhanced EAs to combat diversity issues

No mechanism in a standard EA guarantees that the population will remain diverse throughout the run [17]. Although there is a wide coverage of the fitness landscape at initialization due to the random initialization of individuals’ genomes, selection quickly eliminates the least fit solutions, which implies that the population will converge towards similar points or even single points in the search space. Since the standard EA has limitations to maintain population diversity, several models have been proposed by the EA community which either maintain or reintroduce diversity in the EA population [1, 2, 4, 5, 6, 10, 11, 14 and 18]. The key researches can be broadly categorized as follows [15]:

a) Complex population structures to control gene flow, e.g., the diffusion model, the island model, the multinational EA and the religion model.

b) Specialized operators to control and assist the selection procedure, e.g., crowding, deterministic crowding, and sharing are believed to maintain diversity in the population.

c) Reinroduction of genetic material, e.g., random immigrants and mass extinction models are aimed at reintroduction of diversity in the population.

d) Dynamic Parameter Encoding (DPE), which dynamically resizes the available range of each parameter by expanding or reducing the search window.

e) Diversity guided or controlled genetic algorithms that use a diversity measure to assess and control the survival probability of individuals and the process of exploration and exploitation.
Figure 1 summarizes the major methods proposed to directly or indirectly control EA population diversity.

3. Understanding the problem space

Before we present our proposed approach, which aims at achieving constructive diversity, it is important to understand the problem space we are dealing with. For optimization problems the main challenge is often posed by the topology of the fitness landscape, in particular its ruggedness in terms of local optima. The target optimization problems for our approach are primarily multimodal. Genetic diversity of the population is particularly important in case of multimodal fitness landscape. Evolutionary algorithms are required to avoid and escape local optima or basins of attraction to reach the optimum in a multimodal fitness landscape.

Over the years, several new and enhanced EAs have been suggested to improve performance [1, 2, 4, 5, 6, 10, 11 and 14]. The objectives of such research are twofold; firstly, to avoid stagnation in local optimum in order to find the global optimum; secondly, to locate multiple good solutions if the application requires so.

In the second case, i.e., to locate multiple good solutions, alternative and different solutions may have to be considered before accepting one final solution as the optimum. An algorithm that can keep track of multiple optima simultaneously should be able to find multiple optima in the same run by spreading out the search. On the other hand, maintaining genetic diversity in the population can be primarily beneficial in the first case; the problem of entrapment in local optima.

Remarks: The issue is - how much genetic diversity in the population is optimum?

Recombination in a fully converged population cannot produce solutions that are different from the parents; leave alone better than the parents. However, a very high diversity actually deteriorates performance of the recombination operator. Offspring generated combining two parents approaching two different peaks is likely to be placed somewhere between the two peaks; hindering the search process from reaching either of the peaks. This makes the recombination operator less efficient for fine-tuning the solutions to converge at the end of the run. Hence, the optimal level of diversity is somewhere between fully converged and highly diverse. Various diversity measures (such as Euclidean distance among candidate solutions, fitness distance and so on) may be used to analyze algorithms to evaluate their diversity maintaining capabilities.

In the following sections we investigate the functioning and performance of our proposed Counter Niching-based Evolutionary Algorithm [4].

4. Counter Niching EA: Landscape information, informed operator and constructive diversity

To attain the objective of introducing constructive diversity in the population, the proposed technique first extracts information about the population landscape before deciding on introduction of diversity through informed mutation. The aim is to identify locally converging regions or donor communities in the landscape whose redundant less fit members (or individuals) could be replaced by more promising members sampled in un-explored or under-explored sections of the decision space. The existence of such communities is purely based on the position and spread of individuals in the decision space at a given point in time. Once such regions are identified, random sampling is done on yet to be explored sections of the landscape. Best representatives found during such sampling, now replace the worst members of the
identified *donor* regions. Best representatives are the ones that are fitness wise the fittest and spatially the farthest. Here, average Euclidean distance from representatives of all already considered regions (stored in a memory array) is the measure for spatial distance. Regular mutation and recombination takes place in the population as a whole. The basic framework is as depicted in Figure 2.

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Fig. 2. The COUNTER-NICHING based EA framework
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The task described above is carried out by the following three procedures:

Procedure COUNTER NICHING EA: This is the main algorithm.

Procedure GRID NICHING: This procedure is called by COUNTER NICHING EA and is used to identify tendency of genotypic convergence.

Procedure INFORMED OP: This procedure is second in order to be called by COUNTER NICHING EA. This procedure is responsible of genetic operations including informed mutation.

Figure 3 presents the procedure COUNTER_NICHING_EA. For details on the procedures GRID NICHING and INFORMED OP, we refer to our previous work on [4].

5. Simulations

5.1 Test functions

The proposed algorithm is tested on a set of commonly used benchmark test functions to validate its efficacy. The standard benchmark test function set used in the simulation runs consists of minimization of seven analytical functions as follows: Ackley’s Path Function $f_{ack}(x)$, Griewank’s Function $f_{gri}(x)$, Rastrigin’s Function $f_{rpg}(x)$, Generalized Rosenbrock’s function $f_{ros}(x)$, Axis parallel Hyper-Ellipsoidal Function or Weighted Sphere Model $f_{elp}(x)$, Schwefel Function 1.2 $f_{sch}-1.2(x)$ and a rotated Rastrigin Function $f_{rrtg}(x)$.

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Algorithm 1: Procedure COUNTER NICHING EA
1: begin
2: t = 0
3: Initialize population $F(t)$
4: Evaluate population $F(t)$
5: while not termination condition do
6:     begin
7:         $t = t + 1$
8:         (* Perform pseudo-niching of the population*)
9:         Call Procedure GRID_NICHING
10:        (* Perform informed genetic operations *)
11:     end
12:     Create new population using an elitist selection mechanism
13: end
14: Evaluate $F(t)$
15: end
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5.2 Algorithms considered for comparison

The algorithms used in the comparison are as follows: (a) the “standard EA” (SEA), (b) the self organized criticality EA (SOCEA), (c) the cellular EA (CEA), and (d) the diversity guided EA (DGEA). The SEA uses Gaussian mutation with zero mean and variance $\sigma^2 = 1 + \sqrt{t+1}$. The SOCEA is a standard EA with non-fixed and non-decreasing variance $\sigma^2 = \text{POW}(\alpha)$, where $\text{POW}(\alpha)$ is the power-law distribution. The CEA uses a 20x20 grid with wrapped edges. The grid size corresponds to the 400 individuals used in the other algorithms. The CEA uses Gaussian mutation with variance $\sigma^2 = \text{POW}(10)$. Finally, the DGEA uses the Gaussian mutation operator with variance $\sigma^2 = \text{POW}(1)$. The reader is referred to [15] for additional information on the methods.

5.3 Experiment set-up

Simulations were carried out to apply the proposed COUNTER NICHING based EA with real-valued encoding with parameters $N$ (population size) = 300,
\( p_m \) (mutation probability) = 0.01 and \( p_r \) (recombination probability) = 0.9. In case of the algorithms used for comparison as mentioned in Section 4.2, namely, (i) SEA (Standard EA), (ii) SOCEA (Self-organized criticality EA), (iii) CEA (The Cellular EA), and (iv) DGEA (Diversity guided EA), experiments were performed using real-valued encoding, a population size of 400 individuals, binary tournament selection. Probability of mutating an entire genome was \( p_m = 0.75 \) and probability for crossover was \( p_r = 0.9. \) All the test functions were considered in 20, 50 and 100 dimensions. Reported results were averaged over 30 independent runs, maximum number of generations in each run being only 500, as against 1000 generations in used [15] for the same set of test cases for the 20 dimensional scenarios. The comparison algorithms use 50 times the dimensionality of the test problems as the terminating generation number in general, while the COUNTER NICHING EA uses 500, 1000 and 2000 generations for the 20, 50 and 100 dimensional problem variants respectively.

6. Results and discussions

This section presents the empirical results obtained by the COUNTER NICHING EA algorithm when tackling the seven test problems mentioned in Section 5.1 with dimensions 20, 50 and 100.

6.1 General performance of COUNTER NICHING EA

Table 1 presents the error values, \( (f(x) - f(x)^*) \) where, \( f(x)^* \) is the optimum. Each column corresponds to a test function. The error values have been presented for the three dimensions of the problems considered, namely 20, 50 and 100. As each test problem was simulated over 30 independent runs, we have recorded results from each run and sorted the results in ascending order. Table 1 presents results from the representative runs: 1\(^{st}\) (Best), 7\(^{th}\), 15\(^{th}\) (Median), 22\(^{nd}\) and 30\(^{th}\) (Worst), Mean and Standard Deviation (Std). The main performance measures used are the following:

“A” Performance: Best of the fitness values averaged as mean performance. (Represented as ‘Best’ in Table 1).

“B” Performance: Best of the fitness values averaged as mean performance. (Represented as ‘Best’ in Table 1).

As can be observed COUNTER NICHING EA has demonstrated descent performance in majority of the test cases. However, as can be seen from the highlighted segment (highlighted in bold) of Table 1, the proposed algorithm was not very efficient in handling the higher dimensional cases (50 and 100 dimensional cases in this example) for the rotated Rastrigin Function \( f_{rrtg} \). Keeping in mind the concept of No Free Lunch Theorem, this is acceptable as no single algorithm can be expected to perform favorably for all possible test cases. The chosen benchmark test functions represent a wide variety of test cases.

6.2 Comparative performance of COUNTER NICHING EA

Simulation results obtained with COUNTER NICHING EA in comparison to SEA, SOCEA, CEA, and DGEA (see Section 5.2 for descriptions of these algorithms) are presented in Table 2. Results reported in this case, for COUNTER NICHING EA were averaged over 50 independent runs. These simulation results ascertain COUNTER NICHING EA’s superior performance as regards to solution precision in all the test cases particularly for lower dimensional instances. This may be attributed to COUNTER NICHING EA’s ability to strike a better balance between exploration and exploitation. However, the proposed algorithm’s performance deteriorates with increasing dimensions. Also, the algorithm could not handle the high dimensional versions of the high epistatis rotated Rastrigin function to any satisfactory level. For the reported results as shown in Table 2, the 100 dimensional scenarios of the test problems used 5000 generations for each of the compared algorithms, namely, SEA, SOCEA, CEA and DGEA. On the other hand, COUNTER NICHING EA used only 2000 generations to reach the reported results.

6.3 An analysis of population diversity for COUNTER NICHING EA

In the next phase of our experiments, we have investigated COUNTER NICHING EA’s performance in terms of maintaining constructive diversity. There are various measures of diversity available. The “distance-to-average-point” measure used in [15] is relatively robust with respect to population size, dimensionality of problem and the search range of each
Table 1. Error Values Achieved on the Test Functions with Simulation Runs for COUNTER NICHING EA. Dimensions of Each Function Considered are 20, 50 and 100.

|      | f_ack | f_gri | f_rtg | f_ros | f_elp | f_sch | f_nrg |
|------|-------|-------|-------|-------|-------|-------|-------|
| 1st  | 1.00 E-61 | 4.3E-62 | 1.11 E-61 | 1.01 E-60 | 2.01 E-50 | 2.01E-50 | 3.89 E-6 |
| 7th  | 1.11 E-61 | 4.41 E-62 | 1.13 E-61 | 1.01 E-60 | 2.01 E-50 | 2.01E-50 | 3.89 E-6 |
| 15th | 1.11 E-61 | 4.96 E-62 | 1.21 E-61 | 1.11 E-60 | 2.89 E-50 | 2.71E-50 | 3.9E-6 |
| 22d a| 1.95 E-61 | 5.61 E-62 | 2.02 E-61 | 1.92 E-60 | 2.91 E-50 | 2.91E-50 | 3.93 E-6 |
| 30th | 3.11 E-61 | 8.71 E-62 | 3.30 E-61 | 2.01 E-60 | 2.91 E-50 | 2.91E-50 | 3.99 E-6 |
| Mean | 1.12 E-61 | 5.02 E-62 | 1.21 E-61 | 1.12 E-60 | 2.92 E-50 | 2.72E-50 | 3.9E-6 |
| Std. | 8.33 E-62 | 1.64 E-62 | 8.6E-62 | 4.71 E-61 | 4.62 E-61 | 4.22E-51 | 3.88 E-8 |
| 1st  | 0.56 E-29 | 1.00 E-30 | 1.00 E-30 | 1.21 E-29 | 1.01 E-30 | 2.21E-20 | 9.01 |
| 7th  | 0.71 E-29 | 1.01 E-30 | 1.01 E-30 | 1.41 E-29 | 1.01 E-30 | 2.40E-20 | 9.01 |
| 15th | 0.71 E-29 | 1.01 E-30 | 1.10 E-30 | 1.90 E-29 | 1.10 E-30 | 2.90E-20 | 9.11 |
| 22d a| 0.91 E-29 | 1.91 E-30 | 1.81 E-30 | 1.92 E-29 | 1.51 E-30 | 2.91E-20 | 9.22 |
| 30th | 0.99 E-29 | 1.99 E-30 | 1.99 E-30 | 1.98 E-29 | 1.92 E-30 | 2.91E-20 | 9.24 |
| Mean | 0.73 E-30 | 1.11 E-30 | 1.11 E-30 | 1.91 E-29 | 1.11 E-30 | 2.90E-20 | 9.12 |
| Std. | 1.55 E30 | 4.76 E31 | 4.41 E31 | 3.16 E30 | 3.66 E31 | 3.16E-21 | 0.09 |
| 1st  | 1.00 E-9 | 1.20 E-9 | 1.90 E-9 | 2.09 E-8 | 2.09 E-8 | 2.09E-5 | 10.5 |
| 7th  | 1.01 E-9 | 1.51 E-9 | 1.92 E-9 | 2.91 E-8 | 2.92 E-8 | 2.59E-5 | 10.6 |
| 15th | 1.12 E-9 | 1.72 E-9 | 1.99 E-9 | 2.99 E-8 | 2.99 E-8 | 3.29E-5 | 11.0 |
| 22d a| 1.36 E-9 | 1.86 E-9 | 2.21 E-9 | 3.21 E-8 | 3.21 E-8 | 3.79E-5 | 11.6 |

Variable. Hence, we have used this measure of diversity in our investigation. The “distance-to-average-point” measure for N dimensional numerical problems can be described as below [15].

$$diversity(P) = \frac{1}{|P|} \cdot \left(\sum_{i=1}^{N} \sum_{j=1}^{M} |s_{ij} - \bar{x}_j|^2 \right)$$

where, $|P|$ is the length of the diagonal or range in the search space $S \subseteq \mathbb{R}^N$, $P$ is the population, $|P|$ is the population size, $N$ is the dimensionality of the problem, $s_{ij}$ is the $j$'th value of the $i$'th individual, and $\bar{x}_j$ is the $j$'th value of the average point $\bar{x}$. It is assumed that each search variable $s_k$ is in a finite range, $s_{k_{\min}} \leq s_k \leq s_{k_{\max}}$. Table 3 depicts the average diversity for four test problems with COUNTER NICHING EA simulation runs. The values reported in Table 3, averages the value of the diversity measure in equation (1) calculated at each generation where there has been an improvement in average fitness over 500, 1000 and 2000 generations for the 20, 50 and 100 dimensional cases respectively. Final values were averaged over 100 runs. To eliminate the noise in the initial generations of a run, diversity calculation does not start until the generation, since which a relatively steady improvement in fitness has been observed. Table 3 shows that the COUNTER NICHING EA does not necessarily maintain very high average population diversity. However, EA’s requirement is not to maintain very high average population diversity but to maintain an optimal level of population diversity. The high solution accuracy obtained by COUNTER NICHING EA proves that the algorithm is successful in this respect.

### 6.4 Statistical significance of comparative analysis

Finally, a t-test (at 0.05 level of significance; 95% confidence) was applied in order to ascertain if differences in the “A” performance for the best average
Table 2. Average Fitness Comparison for SEA, SOCEA, The
CEA, DGEA, and COUNTER NICHING EA. Dimensions of
Each Function considered are 20, 50 and 100. '-' Appears
Where the Corresponding Data is Not Available.

| Function | SEA | SOCEA | CEA | DGEA | C_EA |
|----------|-----|-------|-----|------|------|
| ack(x) 20D | 2.494 | 0.633 | 0.239 | 3.36E-5 | 1.08E-61 |
| gri(x) 20D | 1.171 | 0.930 | 0.642 | 7.88E-8 | 4.6E-62 |
| rtg(x) 20D | 11.12 | 2.875 | 1.250 | 3.37E-8 | 1.21E-61 |
| xack 20D | 8292.3 | 406.490 | 149.05 | 8.127 | 1.91E-29 |
| xgri 20D | 11.12 | 2.875 | 1.250 | 3.37E-8 | 1.21E-61 |
| xrtg 20D | 106.21 | 86.364 | 58.380 | 6.56E-5 | 2.00E-9 |
| xros 20D | 91251.300 | 30427.63 | 6053.870 | 880.324 | 3.00E-9 |
| xelp 20D | - | - | - | - | - |
| sch1.2 20D | 8292.3 | 406.490 | 149.05 | 8.127 | 1.91E-29 |
| xrrtg 20D | - | - | - | - | - |

fitness function are statistically significant when compared with the one for the other techniques used for comparison. The $P$-values of the two-tailed $t$-test are given in Table 4. As can be observed, the difference in “A” performance of COUNTER NICHING EA is statistically significant for majority of the techniques across the test functions in their three different dimensional versions.

Table 3. Average Population Diversity Comparison For COUNTER NICHING EA (Fixed Run). An average of 100 Runs Have Been Reported In Each Case.

| Function | 20D | 50D | 100D |
|----------|-----|-----|------|
| ack(x) 50D | 0.001350 | 0.001811 | 0.002001 |
| gri(x) 50D | 0.001290 | 0.001725 | 0.002099 |
| rtg(x) 50D | 0.003000 | 0.003550 | 0.004015 |
| ros(x) 50D | 0.001718 | 0.002025 | 0.002989 |

7. Conclusions

In this paper we investigated the issues related to population diversity in the context of the evolutionary search process. We established the association between population diversity and the search ability of a typical evolutionary algorithm. Then we presented an investigation on an intelligent mutation based EA that tries to achieve optimal diversity in the search landscape. The framework basically incorporates two key processes. *Firstly*, the population’s spatial information is obtained with a pseudo-niching algorithm. *Secondly*, the information is used to identify potential local convergence and community formations. Then diversity is intelligently introduced with informed genetic operations, aiming at two objectives: (a) Promising samples from unexplored regions are introduced replacing redundant less fit members of over-populated communities. (b) While local entrapment is discouraged, representative members are still preserved to encourage exploitation. While the current focus of the research was to introduce and maintain population diversity to avoid local entrapment, this Counter Niching-based algorithm can also be adapted to serve as an inexpensive alternative for niching GA, to identify multiple solutions in multimodal problems as well as to suit the diversity requirements of a dynamic environment.
Table 4. The $P$-values of the t-test with 99 degrees of freedom. Dimensions of Each Function considered are 20, 50 and 100. ‘-‘ appears where the corresponding data is not available.

| Function | C_EA - SEA | C_EA - SOCEA | C_EA - CEAI | C_EA - DGEA |
|----------|------------|--------------|-------------|-------------|
| $f_{ack}$ (x) 20D | 0.1144 | 0.4263 | 0.625 | 0.9954 |
| $f_{gri}$ (x) 20D | 0.2793 | 0.3349 | 0.4231 | 0.9998 |
| $f_{rtg}$ (x) 20D | 0.0099 | 0.0901 | 0.2636 | 0.9999 |
| $f_{ros}$ (x) 20D | 0 | 0 | 0 | 0.0044 |
| $f_{ack}$ (x) 50D | 0.0903 | 0.217 | 0.4198 | 0.9873 |
| $f_{gri}$ (x) 50D | 0.2037 | 0.2843 | 0.3098 | 0.9725 |
| $f_{rtg}$ (x) 50D | 0 | 0 | 0.0002 | 0.9989 |
| $f_{ros}$ (x) 50D | 0 | 0 | 0 | 0 |
| $f_{ack}$ (x) 100D | 0.0891 | 0.1363 | 0.2857 | 0.975 |
| $f_{gri}$ (x) 100D | 0.1337 | 0.2019 | 0.2776 | 0.9546 |
| $f_{rtg}$ (x) 100D | 0 | 0 | 0 | 0 |
| $f_{ros}$ (x) 100D | 0 | 0 | 0 | 0 |

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