

Solving Discrete Deceptive Problems with EMMRS

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ABSTRACT

This paper presents a new method for solving discrete deceptive problems using a genotype to phenotype mapping where a new replacement and shift operator is applied. The method is evaluated using different deceptive problems. Experimental results show how our method obtains a speed-up of 94% with respect to other approaches.

Categories and Subject Descriptors

I.2.8 [Artificial Intelligence]: Problem Solving, Control Methods, and Search—*Heuristic methods*; G.1.6 [Numerical Analysis]: Optimization—*Global optimization*

General Terms

Algorithms, Measurement.

Keywords

Genetic algorithms, deceptive problems, genotype and phenotype mapping.

1. INTRODUCTION

Different techniques have been proposed to tackle deceptive problems. Among them, some papers presented techniques that work with different encodings and representations. In [1] Chow proposes a new encoding technique, the Evolutionary Mapping Method (EMM), to tackle some deceptive problems. Chow uses multiple chromosomes in a single cell for mating with another cell within a single population. As he claimed, the mapping from genotype-to-phenotype is explicitly evolved and maintained. Although this works improved previous reported results, it fails on solving some deceptive problems and the method does not assure a 100% of optimal solutions for all of the tests solved. We present a new method to solve deceptive problems by modifying EMM, called EMM with Replacement and Shift (EMMRS).

2. EVOLUTIONARY MAPPING WITH REPLACEMENT AND SHIFT

We present a variation of the genetic operator applied to the mapping chromosome in [1] by means of which the number of evaluations needed to find the global optimum is reduced. Figure 1 depicts the genetic operators applied to the mapping

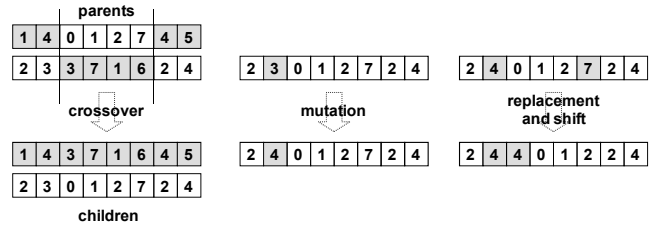


Figure 1: EMMRS. Genetic operators.

chromosome. The crossover operator is a 2-point integer crossover operator. The mutation operator is an integer mutation operator that randomly changes a gene of the mapping chromosome. Finally, we apply a third operator named replacement and shift. This operator randomly picks up two genes at random positions i and j and makes $m[j]=m[i]$, where m is the mapping array. Next, it moves j to follow i , shifting the rest along to accommodate.

By using replacement we reinforce the movement from one schema to another schema in the mapping chromosome.

3. EXPERIMENTAL RESULTS

The experiments were set up to compare our EMMRS algorithm, the dynamic mapping approach (EMM) as in [1] and the traditional GA approach. First, we built two trap-functions using the following equation:

$$f_k(u) = \begin{cases} k-u-d & \text{si } u < k \\ k & \text{si } u = k \end{cases}$$

with $d=1$, $k=4$ and $k=8$, named f_4 and f_8 , respectively. In addition, the 4 and 8 bits of the parameters were concatenated 20 times, extending the chromosomes to 80 and 160 bits. Second, we used two 40 and 60 bits deceptive functions f_U and f_B defined as in [1] (named f_{U40} , f_{U60} , f_{B40} , and f_{B60}). Finally, to test our algorithm in continuous domain, we selected two GA-Hard functions: the Schwefel's and Rastrigin's function [2] [3], where an additional local hill climbing was incorporated (for the Rastrigin's problem the threshold ϵ was lowered from 10^{-12} to 10^{-6}).

For the traditional GA and EMMRS, the crossover rate was set to 0.9 and mutation rate was set to $1/m$, where m is the length of the chromosome. For the EMMRS mapping chromosome, the crossover rate was set to 0.9 and the mutation was set to $0.2/m$. The RS probability was set to $1/m$ after several tests. In the EMM algorithm, the values for the genetic operators were the same as used in [1]. Each of the results is based on data averaged over 100 separate runs. All the experiments used population sizes of 200.

Table I. Optimization functions

	GA		EMM		EMMRS	
	%	Avg.	%	Avg.	%	Avg.
f_4	100%	1690	100%	916	100%	179
f_8	0%	n/a/	78%	8291	100%	1040
f_{U40}	0%	n/a	100%	1593	100%	105
f_{U60}	0%	n/a	100%	2739	100%	253
f_{B40}	0%	n/a	100%	4578	100%	380
f_{B60}	0%	n/a	64%	9353	100%	550
f_S	83%	3756	74%	1874	82%	2137
f_R	0%	n/a	0%	n/a	100%	3105

Table I shows the percentage of optimal runs and the average of generations needed to reach the global optimum. The averages were calculated for successful runs only. EMMRS successfully found the global optimum in all the discrete deceptive functions. In this case, comparing EMM and EMMRS, the number of

evaluations needed to find the global optimum is reduced by 94% in the best case. Table I shows that EMMRS obtains quite better results than EMM and GA implementations in f_4 , f_8 , f_{U40} , f_{B40} , and f_{B60} functions. Figure 2 depicts the best chromosomes found by all the three algorithms for f_8 , f_{U40} , f_{B40} , f_{B60} , f_S and f_R , using executions close enough to the average values shown in Table I. For the Schwefel's function, 83% of the traditional GA trials found solutions close enough to the optimum, 74% in the case of EMM, and 82% for EMMRS. It should be noted that in this case, EMM obtained the global optimum earlier, as Figure 2e depicts. For the Rastrigin's function, just the EMMRS algorithm found solutions close enough to the optimum (Figure 2f). The traditional GA did not find any optimum even with the lowered threshold, as well as the EMM approach. However, in [1] it is stated that EMM is able to find the global optimum running it for 20000 generations.

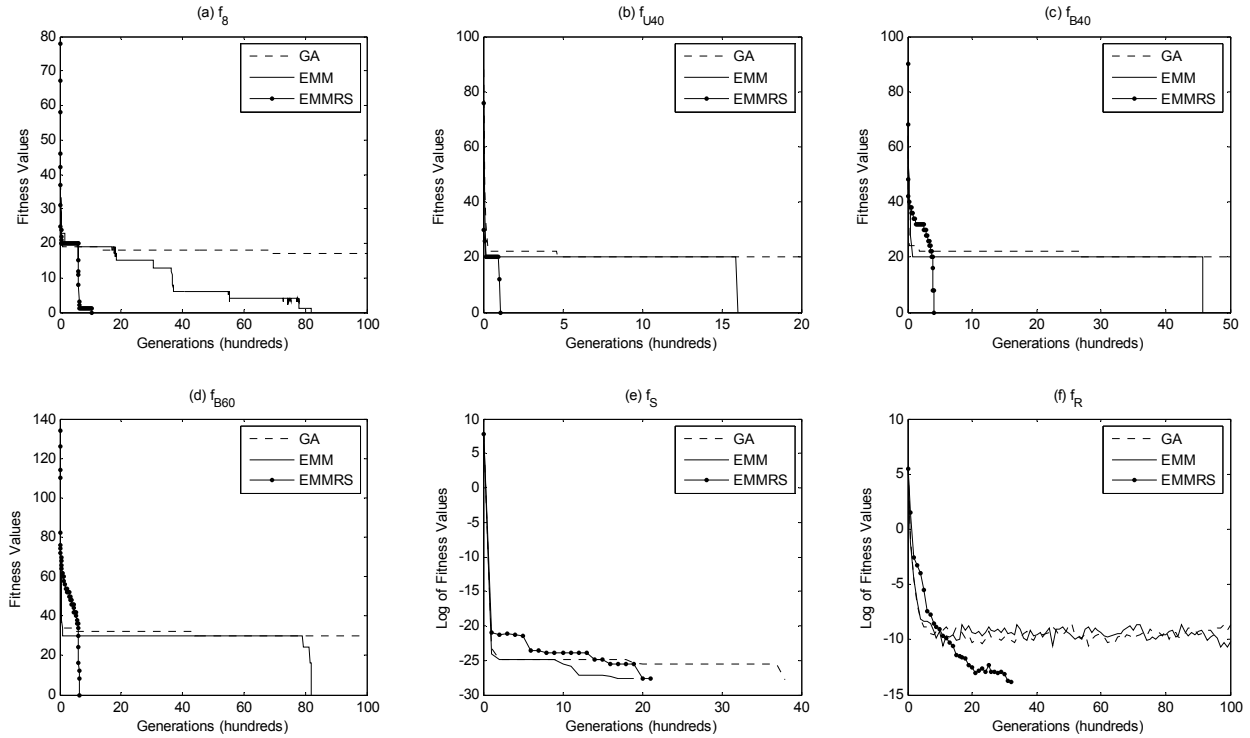


Figure 2. Fitness values of the current best chromosomes for f_8 , f_{U40} , f_{B40} , f_{B60} , f_S , and f_R .

4. ACKNOWLEDGMENTS

This work has been partially supported by INTERLIGARE Institute for Innovation in Intelligence (I4) and Spanish Government Research Grants CICYT TIN2005-5619 and MEC Consolider Ingenio 2010 2007/2011 of the Spanish Council of Science and Technology.

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