Search Space Modulation in Genetic Algorithms *

Evolving the Search Space by Sinusoidal Transformations

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ABSTRACT

An experimental form of Modulation (Reinterpretation) of the Search Space is presented. This modulation is developed as a mathematical method that can be implemented directly into existing evolutionary algorithms without writing special operators, changing the program loop etc. The main mathematical principle behind this method is the dynamic sinusoidal envelope of the search space. This method is presented in order to solve some theoretical and practical issues in evolutionary algorithms like numerical bounded variables, dynamic focalized search, dynamic control of diversity, feasible region analysis etc.

Categories and Subject Descriptors: I.2.8 [Computing Methodologies][Artificial Intelligence]: Problem Solving, Control Methods, and Search

General Terms: Algorithms, Theory

Keywords: Search Space Modification-Reinterpretation, Coordinate Transformation, Real coded genetic algorithms.

1. INTRODUCTION

In most classical genetic algorithms the optimization variables are encoded as binary strings; despite that, in [1, 2, 6] it is shown the use of real parameter codification as an effective alternative in the optimization of practical problems. One of the most classical and important works, together with [4, 5] are the works of DeJong [3].

The current techniques for handling this kind of optimization problems by evolutionary techniques requires a specialized set of operators, variable bound control and/or constraint specialized procedures. Here, we present a kind of coordinate transformation that is capable of solving the need for specialized operators and give many other benefits for variable bounded optimization problems. A good 'bioinspired' background work is [8] which establishes the seminal "theory of transformations" that one species evolves into another not by successive minor changes in individual body parts but by large-scale transformations involving the body as a whole. A recent work closely related to this one is exposed in [7] where a mapping of genotype-phenotype is used within a "Meta-Evolution" approach to evolve better mappings of the Search Space.

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2. SEARCH SPACE MODULATION

The mathematical idea is very simple; it consists of an envelope of the search space by a function. Thus:
Given a fitness function: $F_{it}(x_1, x_2, x_3, ..., x_n)$
Then evaluate: $F_{it}(g_1(x_1), g_2(x_2), g_3(x_3), ..., g_n(x_n))$

In this work a special case of the general envelope is presented. Our modulation is achieved by creating sine functions of the optimization variables with some additional parameters in order to fulfill the next desired conditions:
It is desired that the envelope can:

1. handle bounded variables in a simple way
2. be used to control the factor: $\frac{\texttt{speed of covergence}}{\texttt{accuracy of the search}}$
3. move the entire population to a new location, for a good exploration of the search space.
4. expand the space and focus the search for accuracy in a subspace of the problem
5. contract the space, in order to optimize its cover and the efficiency of the search
6. It is needed that conditions 1, 2, 3, 4, 5 can be controlled independently for each individual variable.

A single envelope that fulfills our conditions given some variable x bounded in an interval $[a, b]$ where $a < b$ is:

$$g(x) = \left(\frac{b-a}{2} sin \left(\frac{\alpha}{\sigma} x + \phi \right) + \frac{b+a}{2} \right) \qquad (1)$$

where σ can be interpreted as the accuracy of search, α the speed of convergence, and ϕ a displacement from the original location. This envelope is derived directly from the general equation of a sine wave.

2.1 Examples of Modulation

Given the bounded real variable $x_1 \in [-5, 5]$, using the sinusoidal envelope in Equation 1 we can define a space that is not bounded and is feasible from $[-\infty, \infty]$ as shown in Equation 2:

$$g_1(x_1) = \left(\frac{5-(-5)}{2} sin \left(\frac{\alpha}{\sigma} x_1 + \phi \right) + \frac{5+(-5)}{2} \right) \qquad (2)$$

where $a = -5, b = 5$; note the change in the space by modulating the parameters of $g(x)$ in Figure.1.

Let us prove this approach with the Rastrigin function:

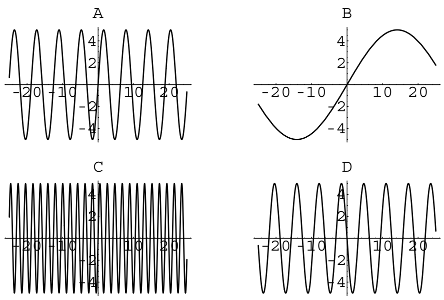

Figure 1: (A) $|\frac{\alpha}{\sigma}| = 1$, (B) expanded $|\frac{\alpha}{\sigma}| < 1$, (C) contracted $|\frac{\alpha}{\sigma}| > 1$, (D) out of phase $\phi \neq 0$

$R(x, y) = 20 + x^2 + y^2 - 10\ (\cos(2\,\pi\,x) + \cos(2\,\pi\,y))$
with $(-5 \leq x \leq 5)$ and $(-5 \leq y \leq 5)$

This function can be modulated with the functions:
$g(x) = 5\ \sin(\frac{x}{20}), g(y) = 5\ \sin(\frac{y}{20})$

As can be seen in Figure 2, in this modulated space should be more "easy" to find the minimum, because *the population is confined* to a reduced region of the space and the operators will only produce individuals in that region.

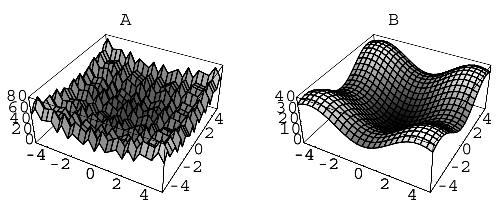

Figure 2: (A) Original, (B) Modulated

3. EXPERIMENTS

We have selected four classical test functions: Ellipsoidal (f_{elp}), Schwefel (f_{sch}), Generalized Rosenbrock (f_{ros}) and Rastrigin (f_{rtg}) for minimization. We are using the Genetic Algorithm Toolbox of $Matlab^{tm}$ 7 Release 14 and for all tests we have used the standard parameters for mutation type/rate, crossover type/rate, fitness scaling etc. The population initial range was $(-20, 20)$ with a population size of 250 individuals.

We are experimenting with different strategies for modifying the modulation parameters. Such strategies are:
(a)Setting parameters interactively by a human operator.
(b)Evolving parameters within the genome.
(c)Controlling parameters with feedback/gradient techniques.
We have selected the option (b) for our tests, then, the genotype was defined as a vector of real variables of length n, and, in the case of the modulation of the search space, the Equation 1. is used as the modulating function with all variables bounded in the interval [a,b](-20,20). Thus, the length of the vector is $n+3$, being the last three variables the parameters (α, σ, ϕ) of the modulation and the genotype vector of the modulated version will be:

$$Genotype = [x_1, x_2, x_3, ..., x_n, \alpha, \sigma, \phi] \qquad (3)$$

Tables 1, 2 and 3 shows the results in the optimization of the benchmark function set. The results shows that the same genetic algorithm with the method of search space modulation performs several orders of magnitude better than the non modulated version.

Table 1: n=10 variables, 30 runs, 200 generations

Function	Non Modulated		Modulated	
cases:	best	worst	best	worst
$f_{elp}(x)$	0.01200	0.350	0.000	0.007
$f_{sch}(x)$	0.44300	5.739	0.000	59.660
$f_{ros}(x)$	7.14000	346.470	0.000	8.222
$f_{rtg}(x)$	2.31500	6.142	0.000	3.984

Table 2: n=50 variables, 30 runs, 200 generations

Function	Non Modulated		Modulated	
cases:	best	worst	best	worst
$f_{elp}(x)$	447.150	890.930	0.000	2.060
$f_{sch}(x)$	1021.000	2111.900	0.205	6093.200
$f_{ros}(x)$	9687.100	50892.000	0.006	47.855
$f_{rtg}(x)$	204.190	294.620	0.002	61.792

Table 3: n=100 variables, 30 runs, 200 generations

Function	Non Modulated		Modulated	
cases:	best	worst	best	worst
$f_{elp}(x)$	10941.0	20347.0	0.003	2.875
$f_{sch}(x)$	6413.6	10304.0	0.003	23861.000
$f_{ros}(x)$	620330.0	1352800.0	0.019	104.930
$f_{rtg}(x)$	1006.7	1419.2	0.003	248.980

4. CONCLUSIONS

We have presented a method to improve the performance of genetic algorithms in optimization tasks. This method could be used directly into an existing genetic algorithm without requiring an specialized set of new operators and control loop modifications.

We have tried to integrate a research area where the apparently opposite thesis of "On Growth and Form" and the thesis that one species evolves into another by successive minor changes in individual body parts can be studied as an integrated evolutionary framework.

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