A Real-Coded Genetic Algorithm using Distance Dependent Alternation Model for Complex Function Optimization

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Abstract

The multi-parental Unimodal Normal Distribution Crossover (UNDX-*m*) that was proposed by Ono et al. and extended by Kita et al for real-coded Genetic Algorithms (GA). shows an excellent performance in optimization problems of highly epistatic fitness functions in continuous search spaces. The UNDX-*m* is a crossover operator that preserves the statistics such as the mean vector and the covariance matrix of the population well. While the crossover operator preserves the statistics of the population, an alternation model used with the crossover is needed to evolve the population through the alternations of the individuals in the population to progress a search. We proposed a distance dependent alternation (DDA) model, which is based on alternations of the elite child with the nearest parent in the family, to progress a search maintaining a diversity of a population. In this paper we show a real-coded GA using the UNDX-*m* combined with DDA model robustly solves 30-dimensional Fletcher-Powell function which is highly multi-modal and has similarity to real-world problems, and has never been solved by every other Evolutionary Algorithms.

1 INTRODUCTION

In solving optimization problems in continuous search spaces by Evolutionary Computation, it is important how to adapt to the fitness landscape of the problem to be solved during search stage for improving performance [Schwefel 95a] [Bäck 96]. Evolution strategies, which utilize adaptive mutation ranges, use recombination operators for global adaptation. Extensions of evolution strategies to multi-parent recombination are also proposed, however these extensions don’t show clear improvement in performance [Schwefel 95b] [Eiben 97].

In applying genetic algorithms to optimization problems, we have to appropriately design coding/crossover and generation alternation scheme. It is important to preserve characteristics of good solutions with appropriate coding/crossovers, and to maintain diversity of populations through generation alternation [Goldberg 89]. Real-coded GAs, which use real number vector representation, show higher performance than those based on binary or Gray code representations when GAs are applied to problems in continuous search spaces [Herrera 98] [Salomon 96]. There are many recombination operators proposed for continuous genes, for example Fuzzy recombination [Voigt 95]. The Unimodal Normal Distribution Crossover (UNDX), proposed by Ono et al., shows good performance as crossover operator for the real-coded GAs, by putting proper inheritance into practice on generating offspring [Ono 97] [Kita98]. Kita et al. has extended the UNDX to multi-parental one (UNDX-m) to improve search performance on optimization problems with poorly scaled coordinate systems [Kita 99].

As for the generation alternation models, Satoh et al. proposed a generation alternation model called the minimal generation gap (MGG) model which is more effective than conventional ones in avoiding premature convergence and evolutionary stagnation [Satoh 96] [Satoh 97].

One dimensional UNDX with the MGG alternation model has shown good performance on several benchmark problems. The UNDX treats mainly two parents at one set of crossover operations, and MGG model alternates two individuals. The elite individual in the family survives for pushing search further, and the one more individual selected by roulette wheel technique survives for maintaining diversity of the population. From a viewpoint, the MGG model is matched with the UNDX-1, because both of them treat two individuals.

If we grasp more than three parents at multi-parental extension of the UNDX as only samples for forming distribution of the offspring, we should be able to treat the two parents randomly sampled from the group of parents as candidates of alternation in the MGG model. However, the aforesaid extension of the UNDX to improve search performance sometimes causes the early convergence with the MGG model. The extension on the UNDX changes the distribution of offspring that are created through the crossover operation. That change ought to be an essential adaptation to the fitness landscape where the population resides. While the distribution of the offspring by the extended UNDX is more suitable to yield superior offspring, it has less diversity and tends to converge at the center of parents group. Hence the MGG is not enough to maintain the diversity of population, and another view-point is required to sufficiently maintain the diversity with the extended UNDX.

We proposed a distance dependent alternation (DDA) model that utilizes distance information between individuals in the population as extension of the MGG model [Takahashi 99a]. The MGG model only uses fitness value for alternation, but the DDA model also uses distance information among the parents and the offspring that is relevant to generation alternation. The basic concept of the DDA model is that the elite among the offspring, will alter the nearest parent individual in multi- parental genetic algorithm.

We have applied this scheme combined UNDX-*m*, to a protein folding problem that has very complicated landscape [Takahashi 99b].

In this paper, we apply the real-coded GA using UNDX-*m* with DDA model to complicated benchmark functions, which are high dimensional Rosenbrock function and Fletcher and Powell function, to confirm the superior performance.

In the next and third section, we review the UNDX as crossover operation, the MGG model as a generation alternation model, and the DDA model as advanced alternation scheme. We show the effectiveness of the DDA model with numerical experiments in the fourth section, and discuss the proposed methods in the fifth section.

2 A REAL-CODED CROSSOVER

Ono et al. proposed the unimodal normal distribution crossover (UNDX), which shows an excellent performance in optimization problems of highly epistatic fitness functions in continuous search spaces [Ono 97]. Further, Kita et al. extended it multi-parental one (UNDX-*m*) [Kita 99]. Here we use the UNDX-*m* as a real-coded crossover operation to solve function optimization problems.

2.1 UNDX

The UNDX proposed by Ono et al. generates children obeying a normal distribution around the parents as shown in Fig.1. The normal distribution is centered at the midpoint of parents 1 and 2, and having a standard deviation proportional to the distance between one of the parents and the midpoint in the direction of the line connecting the parents.

Further, the standard deviations in the perpendicular directions are taken proportional to the distance of the third parent and the lines connecting the parent 1 and 2..

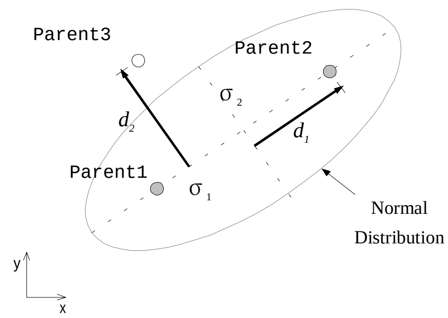

Figure 1 Unimodal Normal Distribution Crossover (UNDX)

2.2 UNDX-*m*

We use the multi-parental version of the UNDX called UNDX-*m* which was extended by Kita et al. This extension is aimed to improve search performance on optimization problems that have poorly scaled coordinate system or have highly compliated fitness landscape. In the UNDX-*m*, *m*+2 parents are selected from the population and the first *m*+1 parents are used to span the *m*-dimensional supspace where the children are mainly distributed obeying a normal distribution. The last parent is used to give perturbation to the children in remaining subspace. UNDX-1 is equivalent to the original UNDX. Please refer to Appendix A added the end of this paper for a detailed definition .

The UNDX-*m* is a crossover operator that preserves the statistics such as the mean vector and the covariance matrix of the population well. Therefore, an alternation model should fill the role to progress a search through the alternations of the individuals in the population

3 ALTERNATION MODELS

Minimal Generation Gap (MGG) Model [Satoh 96] proposed by Satoh et al. as previous alternation model only uses objective values for alternation. We propose utilizing distance information to enhance performance of the alternation model particularly within real-coded GAs.

3.1 PREVIOUS MODEL : MGG

The Minimal Generation Gap (MGG) Model proposed by Satoh et al. is an effective one of generation alternation models [Satoh 96][Satoh 97].

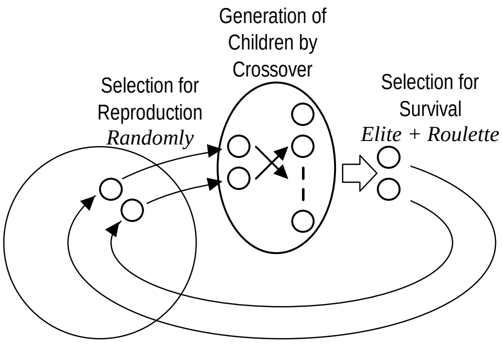

Fig. 2 Minimal Generation Gap (MGG) model

In the MGG model, a generation alternation is done through applying a crossover operation *n* times to a pair of parents randomly chosen from the population. From the parents and their children, we select the best individual and a random one using the roulette wheel technique. With them the original parents are replaced. In this model, original parents are two individuals, and replacing individuals are also two. Then we leave the elite individual for progress in solving a problem, and leave a random individual for maintaining diversity of population. It should also be noted that this model only uses fitness values of each individual. It makes the computational load of the operation light.

3.2 PROPOSED MODEL : DDA

In this section, we propose a Distance Dependent Alternation (DDA) model as an extension of the MGG model. It is designed so as to make the model robust and applicable to the case of more than two parents, utilizing distance information among individuals for selecting a single parent which will be altered to maintain diversity of population.

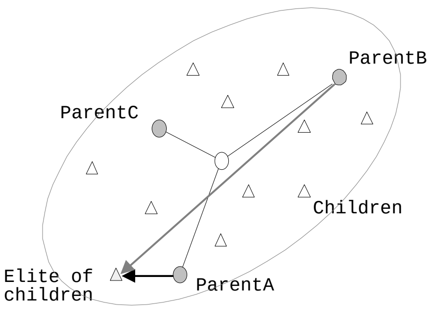

Fig.3 Distance Dependent Alternation (DDA) Model

First, like the MGG, *m*+2 parents are randomly selected from the population. Second, with the UNDX-*m*, the selected parents generate several children. Then, as shown in Fig.3, the DDA selects the elite from the children and finds the parent nearest to it. If the elite child is superior to the parent, the parent is replaced with the child. Otherwise, the procedure finds another parent randomly. If the parent is inferior to the elite child, it is replaced with that.

In the above, the first alternation is aimed to maintain the diversity of the population, and the second alternation is aimed to converge the population. Further, aiming to accelerate the convergence of the population for the exploitation, choose second parent farthest from the elite child. Here we call the former alternation DDA-rf because of random far alternation, and the latter alternation DDA-df because of deterministic far alternation.

4 EXPERIMENTS AND RESULTS

In order to confirm the effectiveness of the proposed real-coded GA combined with the DDA models, we compare with the original MGG model using a few benchmark problems. In the following experiments, we used the UNDX-*m* as a crossover operation in the genetic algorithm scheme. We didn't use any mutation operators here.

The population size was 100 in first test problem we used. The population size was 1500, 3000, 6000 and 12000 in second test problem. The number of applying crossovers, *n*, was 100 in both test problems we used. We performed ten trials on each parameter set in both function problems that were the 30-dimensional Rosenbrock function, and the 30-dimensional Fletcher and Powell function.

4.1 ROSENBROCK FUNCTION

The Rosenbrock function is given by

$$f_1(\vec{x}) = \sum_{i=2}^{n}\left[100(x_1 - x_i^2)^2 + (x_i - 1)^2\right],$$
$$-2.048 \le x_i \le 2.048,\ n = 30$$

This unimodal function has a parabolic valley along the curve $x_1 = x_i^2$ (i=2,...,n) with the minimum at the point (1,...,1).

To analyze behavior of evolution using UNDX-m with MGG or DDA alternation model, we define VD-Ratio as follows:

$$VD_{Ratio} = \frac{V}{D}$$

where

$$\begin{cases} D = \left|v - v_o\right| \\ V = \dfrac{1}{N}\sum_{j=1}^{N}\left\|x_j - x_w\right\| \end{cases}$$

v is best value in a population, v_o is the optimum value of the function. x_j is vector of each individual, and x_w is vector of the weight center of the population. And N is population size. We expect this ratio indicate a performance maintaining the diversity of the population while searching phase.

Fig.4.1(a) shows evolution of the best function value, Fig.4.1(b) shows variance of spatial distribution of the searching population, and Fig.4.1(c) shows VD-Ratio

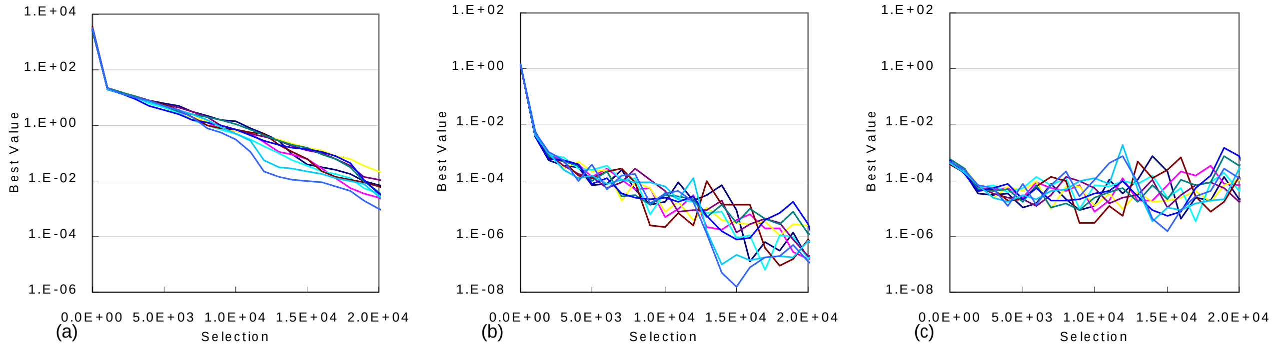

Fig.4.1 UNDX-1 / MGG /

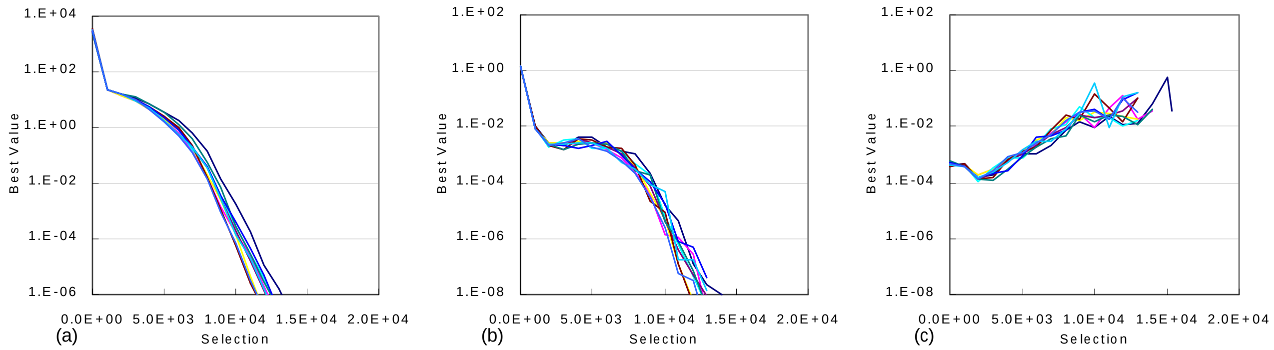

Fig.4.2 UNDX-1 / DDA-rf /

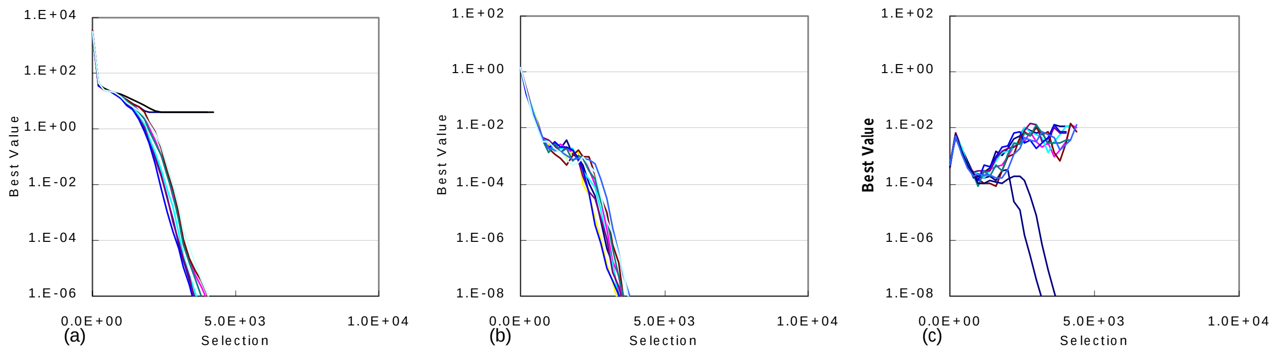

Fig.4.3 UNDX-10 / MGG /

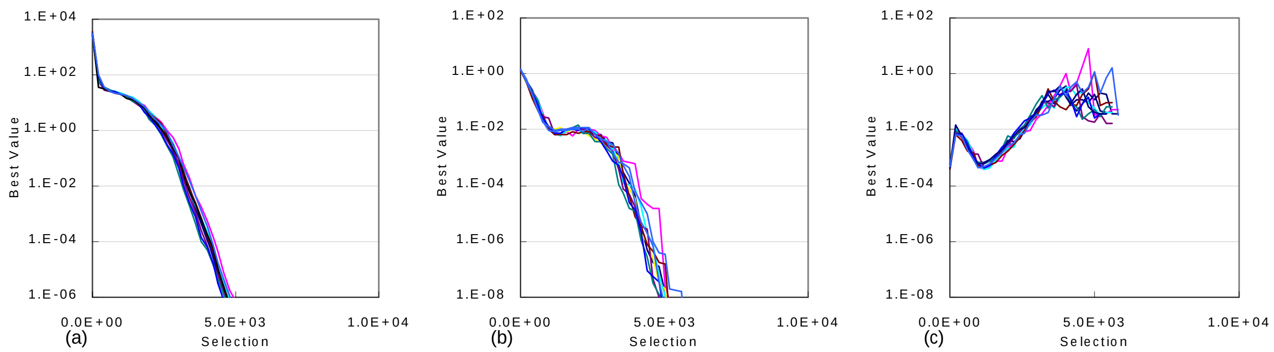

Fig.4.4 UNDX-10 / DDA-rf /

Figure.4 30-dimensional Rosenbrock Function

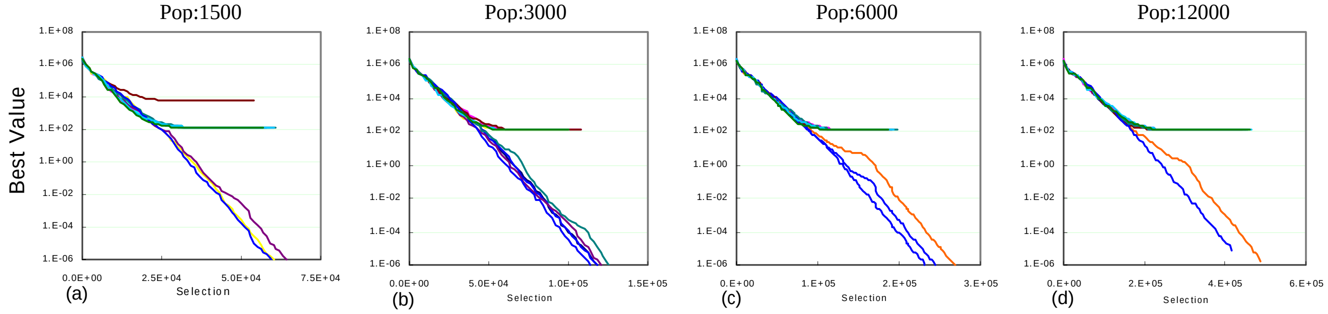

Fig.5.1 UNDX-15 / MGG /

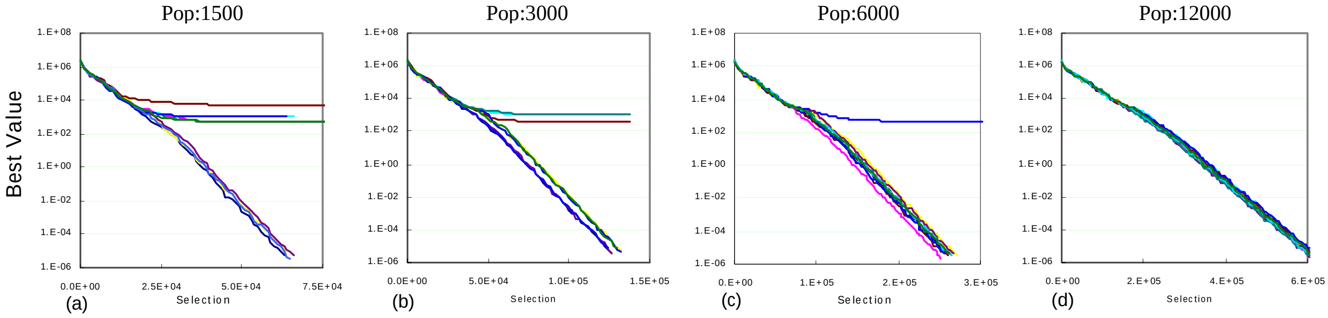

Fig.5.2 UNDX-15 / DDA-rf /

Figure 5. Evolution of the Best Function Value vs Population Size
on 30-dimensional Fletcher and Powell Function

using UNDX-1 with MGG model. Fig.4.2 , Fig.4.3 and Fig.4.4 show behavior using UNDX-1 with DDA-rf, UNDX-10 with MGG, and UNDX-10 with DDA-rf respectively.

4.2 FLETCHER AND POWELL FUNCTION

The Fletcher and Powell function is given by

$$f_2(\vec{x}) = \sum_{i=1}^{n} (A_i - B_i(\vec{x}))^2 \ , \quad \text{for } n = 30$$

where

$$\left.\begin{aligned} A_i &= \sum_{j=1}^{n} (a_{ij} \sin\alpha_j + b_{ij} \cos\alpha_j) \\ B_i(\vec{x}) &= \sum_{j=1}^{n} (a_{ij} \sin x_j + b_{ij} \cos x_j) \end{aligned}\right\} \text{for } i = 1,\ldots,n$$

a_{ij} and b_{ij} are integer random numbers in the range [-100, 100], and α_i are random numbers in the range $[-\pi,\pi]$. The minimum of this problem is a solution of the equivalent system of n nonlinear (transcendental) equations:

$$\sum_{j=1}^{n} (a_{ij} \sin x_j + b_{ij} \cos x_j) = A_i \ , \quad \text{for } i = 1,..,n$$

Obviously the minimum is:

$$x_i^* = \alpha_i, \quad \text{for } i = 1,\ldots,n \ , \quad F(x^*) = 0$$

We used the same set of constant numbers *a*, *b* and α as that are presented at page 265-267 in [Bäck 96].

The Fletcher and Powell function is periodic one, while the UNDX-*m* is basically one of search around the weight center of population. Therefore it is important where the weight center is. We should define where it is on optimizing periodic functions using the UNDX-*m*. Here we pick up *m*+2 parents from the population. We define a bound for each dimension by minimizing variances of elements of each parent's vector.

At the first, focusing a dimension, we sort *m*+2 parents by the value in the dimension. Then calculate variances for each bound between parents, and select the bound having minimum variance on the dimension. Do it for all dimensions.

Fig.5.1(a) shows evolution of the best function using UNDX-15 + MGG with population size 1500, Fig.5.1(b), (c) and (d) shows evolution with 3000, 6000 and 12000 respectively.

Fig.5.2(a) shows evolution of the best function using UNDX-15 + DDA-rf with population size 1500, Fig.5.2 (b), (c) and (d) shows evolution with 3000, 6000 and 12000 respectively. We tested same conditions using UNDX-1 or DDA-df, but leave out the results here because the evolution behavior show same tendencies. It should be noted that the search using UNDX-1 evolves a few times slower than that using UNDX-15. The result seems to indicate superior performance to adapt the search population to the landscape.

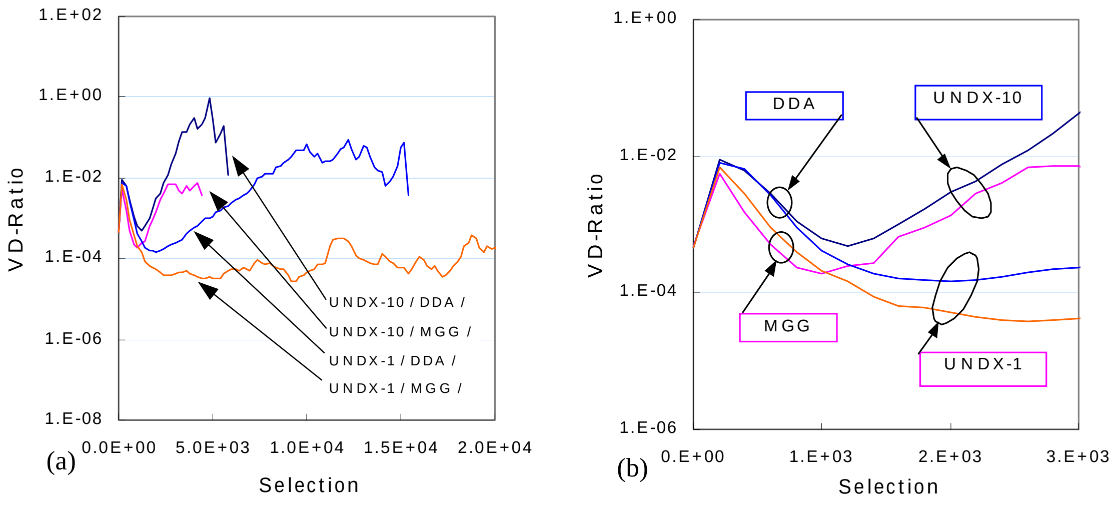

Figure 6 VD-Ratio on 30-dimensional Rosenbrock Function

5 DISCUSSION

For both function problems, the DDA is constantly the more robust one in obtaining the optimum, and accelerates searching by maintaining the diversity of the population in some cases.

High dimensional Rosenbrock function has the deep valley, where the populations gather, and therefore diversity of the populations in tracing phase is important to keep speed of moving population. Lack of the diversity causes less robustness and stopping of searching. The MGG shows less robustness with UNDX-10 because of its random alternation. Fig.4.3(a) shows faster evolution than the Fig.4.1(a) without robustness. But Fig.4.4(a) using DDA shows faster than the Fig.4.1.(a) with same robustness as that shows. The UNDX-10 can accelerate search by adapting searching area to the fitness landscape, but needs to maintain the population diversity adequately.

Fig.4.2(b) shows larger variance of population than the Fig.4.1(b). That means DDA model has higher ability of maintaining diversity of searching population. Expanded population can move faster, as the result Fig.4.2(a) shows faster evolution than the Fig.4.1(a). To extract this tendencies, Fig.4.1(c), Fig.4.2(c), Fig.4.3(c) and Fig.4.4 (c) show VD-Ratio. Collecting all Fig.(c), Fig.6 show four VD-Ratio lines of mean lines of ten trials, but eight success trial at UNDX-10 with MGG .

Fig.6(b) shows early stage of search as same Fig.6(a). Fig.6 shows performance related with maintaining diversity of the population, and higher VD-Ratio seems to mean good searching ability. And less VD-Ratio in early searching stage tends to lose robustness for searching.

Increasing of VD-Ratio means that progress of superior fitness is faster than convergence of searching population. At the first 2000 selections, searching population can find easily superior fitness point around the origin. At the next 10000 selections, the searching population converges to adapt to the shape of the valley. The population with DDA can maintain the diversity more than that with MGG. After the first 10000 selections, the searching population with UNDX-10 increases VD-Ratio more than that with UNDX-1. It means that multi-parental UNDX has higher searching ability of finding out next superior point by adapting to the landscape of the problem.

While, Fletcher and Powell function is heavily multi-modal function having 2^{DIM} local minima, and has complicated landscape, therefore is more difficult than the Rosenbrock function.

A larger population size is needed to solve it robustly. Of course, convergence speed of search will be slower as the population size is larger.

Fig.6 shows the convergence speed will be slower in proportion to the population size. Table 1 is collected that number of success trial times within fifty trials. We have already found out twelve optima of this 30-dimensional Fletcher and Powell function (see Appendix B). UNDX-15 with MGG often finds out an optimum S_1, and is easily trapped into a local minimum L_1 which function value is approximately 137. And UNDX-15 with DDA easily finds out an optimum S_3, and is occasionally trapped into another local minimum L_2 which function value is approximately 484.

Table 1 shows that robustness is not improve by increasing population size using with MGG alternation model, but with DDA alternation model. The search with MGG using larger population size tends to be trapped into the L_1, while the search with DDA using larger population size robustly finds out the S_3.

Table 1: Number of success trials within fifty trials on 30-dimensional Fletcher and Powell function

Alt. Model	MGG				DDA			
Pop. Size	1500	3000	6000	12000	1500	3000	6000	12000
S_1	6	8	6	10	1	0	0	0
S_3	5	7	7	1	29	40	43	48
Any Optima	14	18	15	11	30	40	43	48
L_1	29	30	35	39	0	0	0	0
L_2	0	0	0	0	9	5	5	1
Any Local	36	32	35	39	20	10	7	2

It seems to be important what kind of shape of landscape in this function, and how to adapt to this landscape. These two types of alternation scheme cause different type of adaptation, even with same crossover operation.

To comprehend this phenomenon, it is needed to analyze these behavior by theoretical analysis like [Mühlenbein 93] [Mühlenbein 94]. It is an assignment to be solved in the near future.

6 CONCLUSION

We proposed a distance dependent alternation (DDA) model as a generation alternation model on real-coded genetic algorithms to improve its performance by maintaining diversity of populations. Using the DDA with the multi-parental unimodal normal distribution crossover (UNDX-*m*) shows effectiveness of the proposed method, and robustly obtained the optimal solutions of 30-dimensional Fletcher and Powell function.

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Appendix A

Algorithm of UNDX-*m*

1. Select $m+1$ parents $\boldsymbol{x}^1,\ldots,\boldsymbol{x}^{m+1}$ randomly from the population.
2. Let the center of mass of the these parents be $\boldsymbol{p}=(1/(m+1))\sum_i \boldsymbol{x}^i$ and let the difference vector of $\boldsymbol{x}^i$ and $\boldsymbol{p}$ be $\boldsymbol{d}^i = \boldsymbol{x}^i - \boldsymbol{p}$.
3. Select another parent $\boldsymbol{x}^{m+2}$ randomly from the population.
4. Let D be the length of component of $\boldsymbol{d}^{m+2} = \boldsymbol{x}^{m+2} - \boldsymbol{p}$ orthogonal to $\boldsymbol{d}^1,\ldots,\boldsymbol{d}^m$.
5. Let $\boldsymbol{e}^1,\ldots,\boldsymbol{e}^{n-m}$ be an orthonormal bases of the sub-space orthogonal to the subspace spanned by $\boldsymbol{d}^1,\ldots,\boldsymbol{d}^m$
6. Generate offspring $\boldsymbol{x}^c$ by the following equation:

$$\boldsymbol{x}^c = \boldsymbol{p} + \sum_{k=1}^{m} w_k \boldsymbol{d}^k + \sum_{k=1}^{n-m} v_k D \boldsymbol{e}^k \qquad (1)$$

where $\boldsymbol{w}_k$ and $\boldsymbol{v}_k$ are random variables that follow normal distributions $N(0,\sigma_\eta^2)$ and $N(0,\sigma_\xi^2)$ respectively, and σ_ξ and σ_η are parameters.

The following values are recommended:

$$\sigma_\xi = \frac{1}{\sqrt{m}}, \quad \sigma_\eta = \frac{0.35}{\sqrt{n-m}} \qquad (2)$$

Appendix B

S_0 = (
0.4359340 , 0.5505950 , 1.2834100 , -0.0734284 , -2.6051900 ,
2.1041000 , 1.8675400 , -3.0127500 , 0.8628350 , 0.0666833 ,
2.3361100 , -0.6581490 , -3.1124300 , -3.0755600 , 0.8418540 ,
-0.6925490 , 3.0628400 , -0.9173990 , 0.2111350 , -1.4526100 ,
2.4824400 , 2.0083400 , 0.9061900 , -0.1087510 , 0.6348730 ,
1.4588100 , 1.2409200 , 2.3031100 , -2.3116000 , -2.1476100
).

S_1 = (
0.5887962 , 0.3939944 , -1.4647246 , -0.1486393 , -2.7690399 ,
2.1595126 , 1.6226731 , 3.1010519 , 0.7203299 , 0.2517679 ,
2.1874032 , -0.7638653 , 3.1338894 , -2.8989833 , 0.9650634 ,
-0.6928817 , 3.0996685 , -0.8031746 , 0.1247986 , -1.2970015 ,
2.3899521 , 2.0167984 , 0.9000619 , -0.0510353 , 0.6856467 ,
1.2384135 , 1.1093453 , 2.5651887 , -2.1219102 , -2.3890335
).

S_2 = (
0.9508094 , -1.0019224 , -0.6054171 , 3.1031666 , -2.9036729 ,
2.6810708 , 0.4671725 , -3.1225633 , 2.2760880 , -1.4185380 ,
2.9648185 , -0.9781928 , -1.2151489 , -1.3739757 , -2.7617006 ,
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0.7050543 , 3.1209988 , 0.3215678 , -0.3326112 , 1.3996025 ,
1.6911580 , 0.4793400 , 1.7431345 , -2.9413090 , -2.2910249
).

S_3 = (
1.3229105 , -0.1220803 , -0.5824470 , 2.3357811 , -2.7470651 ,
-3.0479469 , 1.4447478 , -2.7852180 , 1.7713400 , -0.2360309 ,
2.5305723 , -0.9531785 , -2.3932366 , -1.2796731 , -1.7230129 ,
-1.4204484 , -3.0876287 , -0.8774122 , 0.0097913 , -2.2233063 ,
2.8667060 , 2.6539410 , 0.4497844 , 0.0644262 , 0.3351055 ,
2.2105073 , 1.6245019 , 2.6125752 , 2.9808433 , -1.8957689
).

S_4 = (
1.3800112 , 0.3897986 , -0.5845000 , 2.9600050 , -3.0846836 ,
2.7924390 , 0.2106994 , -3.0983034 , 2.1445059 , -0.2953477 ,
2.9597149 , -0.9003345 , -1.3265849 , -1.5493844 , -2.9450899 ,
-1.3383398 , 2.9987879 , -0.7069842 , 0.9368414 , -0.4624298 ,
0.7007844 , -2.8811925 , 0.0624738 , -0.0498179 , 1.6664774 ,
0.8830288 , 0.2943369 , 1.9554092 , -2.5410975 , -2.9257773
).

S_5 = (
1.3831561 , 0.1900180 , -0.2963182 , -2.7938217 , 2.9171288 ,
2.5357890 , 0.3936099 , -2.7206903 , 1.2499892 , -0.7675018 ,
3.0450492 , -0.5394358 , -1.8001648 , -1.5119587 , -2.4880293 ,
-0.7625356 , 2.9803860 , -0.5062950 , 0.0294834 , -1.4175860 ,
2.0274788 , 2.0745932 , -0.1984758 , 0.2330446 , -0.3957370 ,
1.1380580 , 1.2761314 , 1.7514713 , 2.8569164 , -2.2768589 ,
).

S_6 = (
1.4278240 , 0.0697957 , 0.0481930 , -2.8241326 , -2.9691482 ,
2.1309627 , 0.4187940 , -3.0200482 , 1.8196768 , -0.6495134 ,
-2.8703809 , -0.6659400 , -1.2643161 , -1.3181813 , -2.9301052 ,
-0.7248207 , -2.9650538 , -0.2057313 , 0.5121340 , -0.1737286 ,
0.9046374 , 3.0892062 , -0.0314932 , -0.3794554 , 0.0296870 ,
1.5818876 , 0.8908292 , 1.4173493 , -2.8470593 , -2.3957300
).

S_7 = (
1.5011133 , -0.1529267 , 0.5415116 , -2.5195812 , 2.2703002 ,
2.4241509 , 0.5582488 , -3.0467478 , 0.8355191 , -0.4668392 ,
2.8231316 , -0.8507113 , -1.6788331 , -0.8841403 , 2.0459210 ,
-0.2852481 , 3.0720069 , -1.2423283 , -0.2819745 , -0.2766858 ,
2.0557351 , 1.6810092 , 0.4168828 , -0.1358508 , 0.2879444 ,
1.7147954 , 0.9994823 , 1.7826002 , -3.0725436 , -1.7046922 ,
).

S_8 = (
1.5691450 , -1.2673987 , -0.0163166 , 2.7328659 , -2.8934387 ,
2.8834479 , 0.6940810 , -3.0454237 , 2.0728056 , -1.0282905 ,
3.0031600 , -1.2289199 , -1.3706436 , -1.0738561 , -3.0144802 ,
-0.6806876 , -3.0745219 , -1.4305973 , 0.5347918 , 0.2794004 ,
0.4498730 , -2.6214904 , 0.1903925 , -0.9387272 , 1.4220082 ,
2.1117874 , 0.6668268 , 2.1466118 , -2.7166905 , -2.2556335
).

S_9 = (
1.6550296 , 0.2562875 , 0.6218612 , -3.0829109 , 2.1083686 ,
2.6342060 , 0.9445864 , -3.0687553 , 0.6669303 , -0.1154873 ,
2.6911697 , -0.7847445 , -2.0528764 , -0.6794014 , 1.9494709 ,
-0.2835823 , 3.1291191 , -1.5371437 , -0.1697194 , -0.2823548 ,
2.4044153 , 1.8996380 , 0.5311002 , -0.2490868 , 0.9624447 ,
1.7997230 , 1.1265972 , 2.0161059 , -2.5345366 , -1.5730101
).

S_{10} = (
1.7172808 , -0.6121376 , 0.3339531 , -2.9318654 , -2.9028194 ,
2.1871001 , 0.6290469 , -3.0417125 , 2.0486119 , -0.5417564 ,
-3.0826771 , -1.2681397 , -1.0372846 , -1.0859631 , 2.8045051 ,
-0.4174407 , -2.6914972 , -0.8059719 , 0.1780457 , 0.2803567 ,
0.7030197 , -2.6298777 , 0.0843651 , -0.7081998 , 0.1052507 ,
2.0133543 , 0.8076030 , 1.8915427 , -2.7671989 , -1.9904227
).

S_{11} = (
1.8524860 , 0.7552170 , 0.0406680 , 2.7451204 , 3.0279022 ,
2.6471339 , 0.3155313 , -2.7492724 , 1.2540469 , -0.2069582 ,
-2.6770898 , -0.3142468 , -2.2159794 , -1.3540833 , -3.0352450 ,
-0.5287075 , 2.8918646 , -0.4534223 , 1.0030371 , -0.2151764 ,
1.3276964 , 2.2739658 , -0.3326342 , -0.0340549 , 1.1709726 ,
1.2607763 , 1.1354878 , 1.8405047 , -2.6937141 , -2.9119825
).

L_1 = (
0.7204213, 0.1115169, -1.8622760, -0.5643940, 3.1242375,
1.8564961, 0.4881529, -2.9345531, 0.8483405, 0.0044127,
2.2498797, -0.7690196, -1.7880371, -2.4260741, 1.6296683,
-0.9809676, 3.0083064, -0.9176372, 0.3199409, -1.2149525,
1.5239780, 1.9580814, 0.4498120, 0.2206419, 0.4936575,
0.5503629, 0.0187881, 2.7036354, -2.9470306, -2.6253119
).

L_2 = (
2.0258580, 0.2074013, -1.1351508, 1.5550806, -2.6939775,
2.9199553, 1.0980645, -3.0049606, 2.1591860, 0.7195571,
1.9839867, -0.9990309, -3.1184491, -1.9444017, -2.4062554,
-0.6311515, 2.7813206, -0.6257584, 0.1089228, -1.4207572,
2.6142578, -2.9424260, 0.8015303, 0.2200731, 1.0673690,
1.3492585, 1.2387309, 2.8709828, -2.1360623, -2.5381020
)