Confidence interval based crossover using a L_1 norm localization estimator for real-coded genetic algorithms

César Hervás-Martínez, Nicolás García-Pedrajas, and Domingo Ortiz-Boyer

Department of Computing and Numerical Analysis
University of Córdoba, Spain
({chervas, npedrajas, ma1orbod}@uco.es)

Summary. In this work we propose a new multiparent crossover operator for real-coded genetic algorithms based on the extraction of the statistical features (localization and dispersion of genes) of the best individuals of the population. For the construction of the proposed crossover we determine a confidence interval using an estimator of the localization parameter of the gene's distribution of the best individuals of the population using an L_1 norm. This crossover will be called *Confidence Interval based Crossover using L_1 norm* (CIXL1). We construct bilateral confidence intervals for each gene from the statistical distribution of each localization parameter; then we define a crossover operator using as parents the localization parameters and the lower and upper limits of the confidence interval. A theoretical study shows the statistical features of the offspring obtained using this crossover provided that we are in an evolutionary stage with high selective pressure.

The comparison of the proposed operator with BLX-α, UNDX-1, Extended Fuzzy and Seed crossovers for the optimization of different test functions shows the efficiency of the operator both in the optimal value achieved and in the convergence rate.

Key words: Real-coded genetic algorithms; Multi-parent crossover; Confidence intervals; L_1 norm.

1 Introduction

Real-coded genetic algorithms (RCGAs) are used as an approach for solving numeric optimization problems in continuous domains (Wright (1991), Eshelman and Schaffer (1993), Herrera et al. (1998)). These algorithms are specially interesting for the optimization of multimodal and/or epistatic functions with many variables. One of the most important aspects of these algorithms is the design of the crossover operator. This operator generates new individuals

from two members of the population (arity 2 crossovers, Eshelman and Schaffer (1993), Herrera et al. (1994)) or more than two members (arity $n > 2$ or multiparent crossovers, Kita et al. (1999), Eiben (1999)).

Our work is focussed in the design of a new arity n crossover which extracts the most relevant statistical features of localization and dispersion of the fittest individuals of the population. As a working hypothesis we consider that the distribution of the genes of the fittest individual are continuous during all the evolutionary process in order to estimate the localization and dispersion parameters (Ortiz et al. (2001a), Ortiz et al. (2001b)).

Under this assumption, and due to the fact that we do not know the specific distribution of the genes of the best individuals, we will use a localization estimator based on L_1 norm. This estimator is the sample median of the genes of the best n individuals on each generation, it follows a distribution that does not depend on the distribution of the genes and that is a binomial with parameters n and $1/2$.

From this localization estimator and its associated distribution we construct bilateral confidence intervals for each gene, and form three parents for the crossover operation. The first one is made up by the lower bounds of the confidence intervals, the second one is made by the upper bounds of the confidence intervals, and the third one is made up by the localization estimator itself, that is, the sample median of the genes.

This article is organized as follows: Section 2 presents the crossover operator based on L_1 norm; Section 3 shows the results of the comparison of this operator with other multiparent crossover operators in the optimization of different functions; finally, Section 4 states the conclusions of our work.

2 Multiparent crossover using L_1 norm

We will consider the i-th gene without loss of generality. Let β be the set of N individuals that form the population and let $\beta^* \subset \beta$ be the subset of the best n individuals, and q the number of genes of each chromosome. Let us assume that the genes, β_i, of the chromosomes of the individuals in β^* are independent random variables with a continuous distribution $H(\beta_i)$, and a localization parameter of the form μ_{β_i}, then we have a model $\beta_i = \mu_{\beta_i} + e_i$, for $i = 1, \ldots, q$, being e_i a random variable.

If we assume that the genes of the n fittest individuals form a random sample $(\beta_{i_1}, \beta_{i_2}, \ldots, \beta_{i_n})$ of the distribution of the fittest individuals of the population β_i^b, then it can be written:

$$\beta_{ij}^b = \mu_{b_i} + e_{ij}, \quad j = 1, 2, \ldots, n. \tag{1}$$

Using this model we analyze an estimator of the localization parameter μ_{b_i} for the i-th gene based in the minimization of the dispersion function induced

by the L_1 norm, $D_1(\mu_{b_i}) = \sum_{j=1}^{n} |\beta_{ij} - \mu_{b_i}|$. The estimator is the sample median $\hat{\mu}_{b_i} = M_{b_i}$, of the distribution of the β_i^b(Hettmansperger and McKean (1998)). The sample median estimator is a better localization estimator than the sample mean when the form of the H distribution is not known. The confidence interval for a sample of size n, with a confident coefficient of $1-\alpha$, is constructed using the Neyman method, due to the fact that the binomial distribution associated with the median does not depend on the H distribution. With this method we have:

$$P(\beta_{i(k_1)} > M_{b_i}) = \sum_{j=0}^{k_1-1} \binom{n}{j} \left(\frac{1}{2}\right)^n = \alpha/2, \tag{2}$$

and

$$P(M_{b_i} > \beta_{i(k_2)}) = \sum_{j=k_2}^{n} \binom{n}{j} \left(\frac{1}{2}\right)^n = \alpha/2. \tag{3}$$

From these equations we have a confidence interval of the form, being $k_1 = k+1$ and $k_2 = n-k$:

$$I_{1_\alpha}(\mu_{b_i}) = \left[\beta_{i(k+1)}, \beta_{i(n-k)}\right], \tag{4}$$

where $\beta_{i(k+1)}$ and $\beta_{i(n-k)}$ are the gene values at position $k+1$ and $n-k$ once the sample of genes has been sorted. The value of k is determined from the underlying binomial distribution. As we have stated, the proposed interval does not depend on the distribution of the genes. This feature is very important as the distribution of the genes of the best individuals will probably change along the evolution.

As the binomial distribution is discrete, it is possible that we cannot obtain discrete values of $\beta_{i(k+1)}$ and $\beta_{i(n-k)}$ that verify $P(\beta_{i(k+1)} \leq \mu_{b_i} \leq \beta_{i(n-k)}) = 1-\alpha$. This effect is specially important if the number of best individuals considered is small.

In such cases a nonlinear interpolation method is used(Hettmansperger and McKean (1998)) for obtaining the values of the lower bound, using $\beta_{i(k)}$ and $\beta_{i(k+1)}$, and upper bound, using $\beta_{i(n-k)}$ and $\beta_{i(n-k+1)}$, of the confidence interval.

The interpolation method is the following. Let $(1-\alpha) = \gamma$ be the desired confidence interval, and the two possible intervals taken from the binomial tables be $(\beta_{i(k)}, \beta_{i(n-k+1)})$, with a confidence coefficient of γ_k, and $(\beta_{i(k+1)}, \beta_{i(n-k)})$ with a confidence coefficient of γ_{k+1}, where $\gamma_{k+1} \leq \gamma \leq \gamma_k$. Then, the interpolated bounds of the interval are:

$$\hat{\mu}_{b_{iL}} = (1-\lambda)\beta_{i(k)} + \lambda\beta_{i(k+1)}, \tag{5}$$

and

$$\hat{\mu}_{b_{iU}} = (1-\lambda)\beta_{i(n-k+1)} + \lambda\beta_{i(n-k)}, \tag{6}$$

where $\lambda = \frac{(n-k)\gamma_i}{k+(n-2k)\gamma_i}$, and $\gamma_i = \frac{\gamma_k - \gamma}{\gamma_k - \gamma_{k+1}}$.

2.1 Crossover operation

Once we have constructed the described confidence interval, we build three virtual individuals that will act as parents in the crossover. The first one is formed by all the lower bounds of the confidence interval of each gene of the chromosome, it is called CIL; the second one is formed by all the upper bounds of the confidence interval of each gene of the chromosome, it is called CIU; and the third one is formed by all the medians of the values of each gene of the chromosome, it is called CIM. These individuals divide the domain $[a_i, b_i]$ of the i-th gene into three intervals: $I_i^L \equiv [a_i, CIL_i)$, $I_i^M \equiv [CIL_i, CIU_i]$, and $I_i^U \equiv (CIU_i, b_i]$.

The *Confidence Interval based Crossover operator using L_1 norm* (CIXL1) obtains an offspring β^s, from an individual of the population, $\beta^k = (\beta_1^k, \ldots, \beta_p^k)$, and the three individuals defined above. We consider the fitness of the four individuals, function $f(\cdot)$, and the position of the genes of β^k within the three intervals defined above. The three possible cases are:

Case 1: $\beta_i^f \in I_i^L$. If $f(\beta^f) > f(CIL)$ then $\beta_i^s = r(\beta_i^f - CIL_i) + \beta_i^f$ else $\beta_i^s = r(CIL_i - \beta_i^f) + CIL_i$.

Case 2: $\beta_i^f \in I_i^M$. If $f(\beta^f) > f(CIM)$ then $\beta_i^s = r(\beta_i^f - CIM_i) + \beta_i^f$ else $\beta_i^s = r(CIM_i - \beta_i^f) + CIM_i$.

Case 3: $\beta_i^f \in I_i^R$. If $f(\beta^f) > f(CIU)$ then $\beta_i^s = r(\beta_i^f - CIU_i) + \beta_i^f$ else $\beta_i^s = r(CIU_i - \beta_i^f) + CIU_i$.

where r is a random number belonging to [0, 1].

One of the most important aspects of the effect of the proposed crossover on the population is the change that it produces in the localization and dispersion parameters of the probability density function of the population. We are going to analyze the changes produced by the crossover depending on the subinterval of the gene.

First, let us assume that the gene β_i^k involved in the crossover is within the confidence interval $\beta_i^k \in I_i^M$. We consider that in the j-th generation β_i^k is a random variable with $E(\beta_i^k) = \mu_i$ and $V(\beta_i^k) = \sigma_i^2$, and the i-th gene of the fittest individuals follow a distribution $\beta_i^b \in H$ with $E(\beta_i^b) = \mu_{b_i}$ and $V(\beta_i^b) = \sigma_{b_i}^2$. We also consider that the two distributions are independent. The median and the variance of the sample median of the fittest individuals

are: $E(M_{b_i}) = \mu_{b_i}$, and $V(M_{b_i}) = \frac{1}{4nf^2(0)}$, where f is the density function of the random variable e_i. As the underlying distribution function H is unknown we must estimate the standard deviation of the sample median. We propose an asymptotic estimator of the standard deviation based on the length, L, of the confidence interval(Hettmansperger and McKean (1998)), that is:

$$\frac{1}{2n^{1/2}f(0)} = \frac{L}{2}z_{\alpha/2}, \tag{7}$$

where $L = \hat{\mu}_{b_{iU}} - \hat{\mu}_{b_{iL}}$, if we take into account case 2. We have two possibilities: $f(\beta^k) \geq f(CIM)$ with a probability p, and $f(\beta^k) < f(CIM)$ with a probability $1-p$. In the first case $\beta_i^s = (1+r)\beta_i^k - rCIM_i$, so the mean and variance of the distribution of β_i^s are:

$$E(\beta_i^s) = (1+r)E(\beta_i^k) - rE(CIM_i) = (1+r)\mu_i - r\mu_{b_i}, \tag{8}$$

and

$$V(\beta_i^s) = (1+r)^2\sigma_i^2 + r^2\frac{L^2}{4z_{\alpha/2}^2}. \tag{9}$$

In the first stages of the evolution $\sigma^2 >> \sigma_b^2$ and $\mu \neq \mu_b$ as the set of the fittest individuals is a subset of the whole population. Along the evolution, the selection pressure will produce that $\mu \to \mu_b$ and $\sigma^2 \to \sigma_b^2$, yielding:

$$E(\beta_i^s) = (1+r)\mu - r\mu_b = \mu_b, \tag{10}$$

and

$$V(\beta_i^s) = (1+r)^2\sigma_b^2 + r^2\frac{L^2}{4z_{\alpha(2)}^2}. \tag{11}$$

In the second case, if we work the same way we obtain similar results:

$$E(\beta_i^s) = (1+r)\mu_b - r\mu_b = \mu_b, \tag{12}$$

and

$$V(\beta_i^s) = (1+r)^2\frac{L^2}{4z_{\alpha/2}^2} + r^2\sigma_b^2. \tag{13}$$

The distribution of the generated offspring will be a mixture of distributions. This mixture will follow a distribution of parameters:

$$E(\beta_i^s) = p\mu_{b_i} + (1-p)\mu_{b_i} = \mu_{b_i}, \tag{14}$$

and

$$V(\beta_i^s) = p^2(1+r)^2\sigma_b^2 + p^2r^2\frac{L^2}{4z_{\alpha/2}^2} + (1-p)^2(1+r)^2\frac{L^2}{4z_{\alpha/2}^2} + (1-p)^2r^2\sigma_b^2. \tag{15}$$

So, we can conclude that, if $\beta_i^k \in I_i^M$ and along the evolution the values of p and r are appropriate, then the distribution of the offspring will have the same mean than the mean of the fittest individuals, and a variance less than the variance of the fittest individuals. The variance of the offspring will also depend on the distribution of the best individuals of the population, and the performance of the crossover will strongly depend on such distribution.

3 Experimental setup

Taking into account the theorem of *no free lunch*, we have used a set of well characterized functions instead of a large a number of functions in order to test the goodness of the proposed crossover. We have used the four functions extracted from the test set proposed in Eiben and Bäck (1997) that are shown in the following table:

Function	**Expression**	**Range**
Hypersphere	$f_1(\mathbf{x}) = \sum_{i=1}^{q} x_i^2$	$x_i \in [-5.12, 5.12]$
Rastrigin	$f_2(\mathbf{x}) = \sum_{i=1}^{q}(x_i^2 - 10\cos(2\pi x_i) + 10)$	$x_i \in [-5.12, 5.12]$
Schwefel	$f_3(\mathbf{x}) = \sum_{i=1}^{q}\left(\sum_{j=1}^{i} x_j\right)^2$	$x_i \in [-65.536, 65.536]$
Ackley	$f_4(\mathbf{x}) = 20 + e - 20e^{\left(-0.2\sqrt{1/q\sum_{i=1}^{q} x_i^2}\right)}$ $-e^{\left(1/q\sum_{i=1}^{q}\cos(2\pi x_i)\right)}$	$x_i \in [-30, 30]$

For all the functions the minimum is in $\mathbf{x}_m = (0, 0, \ldots, 0)$ and $f(\mathbf{x}_m) = 0$. The dimensionality is a factor that has effects on the complexity of the functions (Friedman (1994)). In order to establish the same degree of difficulty, we have chosen a dimensionality of $q = 30$ for all the functions.

Hypersphere is a simple, continuous, strongly convex, unimodal and separable function. Rastrigin is a continuous, scalable, multi-modal and separable function, its contour is made up by a large number of local minima whose

value increase with the distance to the global minimum. Schwefel is a continuous, unimodal and nonseparable function. Its main difficulty is that its gradient is not oriented along its axis due to the epistaxis of its variables. So, a search using the gradient is very slow. Ackley is a continuous, multimodal, and nonseparable function, where the exponential term covers its surface with a lot of local minima. This function has a moderated complexity because, although a search algorithm using the steepest descent method will probably be trapped in a local optimum, a search strategy analyzing a wider area could find better solutions. Ackley function provides a test case where it is needed for the search strategy to establish an adequate balance between exploration and exploitation.

We have compared CIXL1 with two of the most interesting current crossover of arity two: the BLX-α (Eshelman and Schaffer (1993)) crossover with $\alpha = 0.5$ and Extended Fuzzy (Herrera and Lozano (2000)) with $S2$ strategy; and with two multiparent crossovers: UNDX (Ono and Kobayashi (1997)) with three parents and Seed (Tsutsui and Ghosh (1998)) with a number of parents that is defined by the parameter m. The values of m used are: $m = 16$ for Hypersphere, $m = 8$ for Rastrigin, $m = 2$ for Schwefel, and $m = 6$ for Ackley. These values are the best obtained by the authors of this crossover (Tsutsui and Ghosh (1998)).

The selection of the mutation operator is closely related to the crossover operator and the problem to solve. Using the previous results in Ortiz (2001), Herrera and Lozano (2000), Eshelman (1991), Ono and Kobayashi (1997) and Tsutsui and Ghosh (1998), we have chosen the following mutation operators: for the Hypersphere and Schwefel functions the non-uniform mutation (Michalewicz (1992)), for the Rastrigin and Ackley functions the non-uniform mutation for arity 2 crossovers, and the discrete and continuous modal mutation respectively for multiparent crossovers (Voigt and Anheyer (1994)).

The parameters used for CIXL1 are (Ortiz (2001)) $n = 5$ and $1-\alpha = 0.70$, for all the functions, except for Rastrigin where we used $1 - \alpha = 0.95$.

The genetic algorithm has a fixed size population of 100 individuals randomly initialized, a crossover probability of 0.6, a probability of gene mutation of 0.05, and a tournament selection method with 2 opponents and elistism. Each experiment will be repeated 10 times with different random seeds and the population will evolve for 5000 generations.

3.1 Results

As we can see on Table 1 the best results for Rastrigin, Schwefel and Ackley are obtained using the CIXL1 operator. For Hypersphere the Seed crossover obtained the best results, nevertheless, the performance of CIXL1 is also very good.

Table 2 shows the results of a Tamhane statistical test for the comparison of the results of all the crossovers applied. For three out of four problems the results of CIXL1 are significantly better than the results obtained with the

other operators with a significance level 0f 0.01. The results for Hypersphere cannot be compared as the variance of the experiments is 0. Table 3 shows the result of a Student t test between CIXL1 and the second best crossover for every problem.

Table 1. Results of the five crossover operators on the test functions

	Mean	SD	Best	Worse	Mean	SD	Best	Worse
Crossover	Hipersphere				Rastrigin			
CIXL1	1.22e-16	0.00e+00	1.22e-16	1.22e-16	7.12e-11	1.82e-10	0.00e+00	5.74e-10
BLX-α	2.97e-15	1.51e-15	1.33e-15	5.33e-15	3.43e+01	7.98e+00	2.09e+01	4.77e+01
Ext. Fuzzy	8.26e-11	4.92e-11	2.31e-11	9.10e-11	3.38e+01	6.68e+00	1.79e+01	4.18e+01
UNDX	9.55e-11	2.36e-10	0.00e+00	7.66e-10	2.74e+01	5.74e+00	1.74e+01	3.98e+01
Seed	0.00e+00	0.00e+00	0.00e+00	0.00e+00	2.38e-03	4.32e-04	1.70e-03	3.03e-03
Crossover	Schwefel				Ackley			
CIXL1	1.34e-05	4.02e-22	1.34e-05	1.34e-05	2.78e-08	2.76e-08	9.03e-09	9.41e-08
BLX-α	5.51e-01	2.11e-01	1.64e-01	9.65e-01	1.84e-07	8.12e-08	7.9e-08	3.5e-07
Ext. Fuzzy	2.21e+01	9.15e+00	1.15e+01	3.96e+01	3.14e-05	1.20e-05	1.26e-05	5.14e-05
UNDX	3.77e+00	2.60e+00	1.24e+00	9.74e+00	4.75e-01	6.94e-02	3.8e-01	5.9e-01
Seed	1.89e+01	1.17e+01	4.81e+00	4.63e+01	3.16e-02	4.49e-03	2.60e-02	4.18e-02

Table 2. The table shows the difference, $I - J$, between the mean with CIXL1, I, and the other crossover J, and the significance of this difference using a Tamhane test

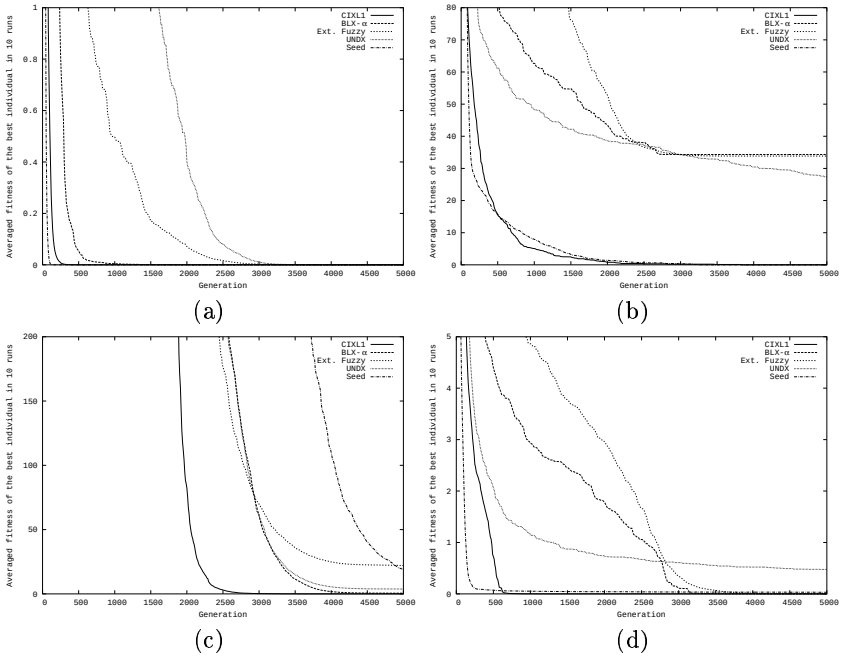
	Sphere		Rastrigin		Schwefel		Ackley	
Crossover	$(I-J)$	Sign.	$(I-J)$	Sign.	$(I-J)$	Sign.	$(I-J)$	Sign.
BLX-α	-2.85e-15	-	-3.43e+01	0.000	-5.51e-01	0.000	-1.56e-07	0.001
Ext. Fuzzy	-8.26e-11	-	-3.38e+01	0.000	-2.21e+01	0.000	-3.14e-05	0.000
UNDX	-9.55e-11	-	-2.74e+01	0.000	-3.77e+00	0.013	-4.75e-01	0.000
Seed	1.22e-16	-	-2.38e-03	0.000	-1.89e+01	0.002	-3.16e-02	0.000

Table 3. student t test between the results of CIXL1 and the second best crossover for each test function

Function	Crossover	Sig. Levene test	Mean difference	Standard Error	Sig. t test
Hypersphere	Seed	-	1.22e-16	-	-
Rastrigin	Seed	0.000	-2.38e-03	1.36e-04	0.000
Schwefel	BLX-α	0.003	-5.51e-01	6.67e-02	0.000
Ackley	BLX-α	0.014	-1.56e-07	2.71e-08	0.000

Figure 1 shows the convergence rate of each function using the different crossovers. For the Hypersphere function the convergence rate of CIXL1 is slightly worse that the convergence rate of Seed. For Rastrigin and Ackley functions, CIXL1 and Seed show similar convergence rates, nevertheless the

Fig. 1. (a) Averaged fitness of the best individual in 10 runs for Hypersphere(b), Rastrigin (c), Schwefel (d), and Ackley



solution obtained by CIXL1 is closer to the global optimum. For Schwefel function, CIXL1 converges faster than all the other crossovers. For this function Seed shows a premature convergence to a local optimum very far from the global solution.

4 Conclusions and future work

In this work we have proposed a new crossover operator that uses the information obtained from the localization and dispersion parameters of the subset of the best individuals of the population, in order to establish a balance between the exploration and exploitation of the search space. This operator generates offsprings in the region where the best individuals of the population are localized, sampling this way a region where is probable to obtain fitter individuals. This region is established by the confidence interval of each gene.

We have compared the performance of CIXL1 with that of commonly used crossover operators, namely, BLX-α, Extended Fuzzy, UNDX, and Seed for the optimization of unimodal, multimodal, and epistatic functions. The comparison shows the robustness of the proposed crossover, that also shows a

fast convergence to values close to the global optimum, without being trapped in local minima.

It is obvious that the number of best individuals and the confidence coefficient have an important influence over the performance of the proposed crossover. Now, we are working in a sensibility analysis that can guide us in the most suitable values of these parameters depending on the kind of problem to solve. A more deep knowledge about the distribution of the genes along the evolution would be also very interesting for improving the results of this new crossover operator.

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