# A Mutation Operator for Evolution Strategies to Handle Constrained Problems

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## 1. THE BMO APPROACH

In this paper we propose a new efficient mutation operator for evolution strategies (ES) - the biased mutation operator (BMO). This operator is capable of improving the success rate to produce better offspring in constrained landscapes. The idea of our approach is to bias the mutation ellipsoid to lead the mutations into a more beneficial direction. Experimental results show that this bias enhances the solution quality in constrained search problems. The number of additional strategy parameters used in our approach equals to the dimensions of the problem. Compared with the correlated mutation, the BMO needs less memory. In addition, the BMO supersedes the computation of the rotation matrix of the correlated mutation and the asymmetric probability density function of the directed mutation. Therefore, it demands less computational cost and is easier to implement.

## **1.1 Standard Mutation**

Besides crossover, mutation is the source for variations in the evolutionary process. For ES in real-valued search spaces, objective variables are mutated in the following way in the case of uncorrelated mutation with one step size [1]:

$$\vec{x}' := \vec{x} + \vec{z} \tag{1}$$

with the mutation

$$\vec{z} := \sigma(\mathcal{N}_1(0, 1), ..., \mathcal{N}_N(0, 1))$$
 (2)

where  $\mathcal{N}_i(0, 1)$  provides a random number based on a Gaussian distribution with expected value 0 and standard deviation 1. The strategy variable itself is mutated with the

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log-normal rule:

$$\sigma' := \sigma e^{(\tau \mathcal{N}(0,1))} \tag{3}$$

This mechanism is the key to self-adaptation of the step sizes. In the state of the art  $(\mu \ddagger \lambda)$ -ES normally a vector of  $n_{\sigma} = N$  step sizes is used, which results in mutation ellipsoids:

$$\vec{z} := (\sigma_1 \mathcal{N}_1(0, 1), ..., \sigma_N \mathcal{N}_N(0, 1))$$
 (4)

The corresponding strategy parameter vector is mutated with the extended log-normal rule:

$$\vec{\sigma}' := e^{(\tau_0 \mathcal{N}_0(0,1))} \cdot (\sigma_1 e^{(\tau \mathcal{N}_1(0,1))}, ..., \sigma_N e^{(\tau \mathcal{N}_N(0,1))})$$
(5)

The parameters  $\tau_0$  and  $\tau_1$  have to be tuned. Comprising, an individual  $\vec{a}$  consists of the object parameter set, the mutation strength vector and the assigned fitness F(x). So it can be represented as

$$\vec{a} = (x_1, ..., x_N, \sigma_1, ..., \sigma_N, F(x))$$
 (6)

## **1.2 Biased Mutation Operator (BMO)**

Unlike directed mutation [3], the BMO does not change the skewness, but biases the mean of the Gaussian distribution to lead the search into a more beneficial direction. This is reflected in the success rate of producing superior offspring. For the BMO we introduce a *bias coefficient vector*  $\vec{\xi}$ , which indicates the level of bias relative to the standard deviation  $\sigma$ .

$$\vec{\xi} = (\xi_1, ..., \xi_N) \text{ with } -1 \le \xi_i \le 1$$
 (7)

The bias vector  $\vec{b} = (b_1, ..., b_N)$  is then defined for every  $i \in 1, ..., N$  by

$$b_i = \xi_i \cdot \sigma_i \tag{8}$$

Since the absolute value of the bias coefficient  $\xi_i$  is less than or equal to 1, the bias will be bound to the step sizes  $\sigma_i$ . This restriction prevents the search from being biased too far away from the parental individual. The BMO is oriented to the standard mutation:

$$\vec{x}' := \vec{x} + \vec{z}.\tag{9}$$

In detail the mutation for the BMO is defined as

$$\vec{z} := (\sigma_1 \mathcal{N}_1(0, 1) + b_1, ..., \sigma_N \mathcal{N}_N(0, 1) + b_N)$$
(10)

$$= (\sigma_1 \mathcal{N}_1(0, 1) + \xi_1 \sigma_1, ..., \sigma_N \mathcal{N}_N(0, 1) + \xi_N \sigma_N)$$
(11)

$$= (\sigma_1 \mathcal{N}_1(\xi_1, 1), ..., \sigma_N \mathcal{N}_N(\xi_N, 1))$$
(12)

=

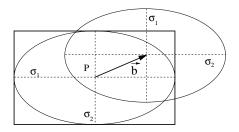


Figure 1: Shift of the center of the mutation ellipsoid within the BMO. The bias vector  $\vec{b}$  is bound to the step sizes  $\vec{\sigma}$ .

The last equation will be mainly used in the BMO mutation. In terms of modifying the mutation strength, the aforementioned log-normal rule is applied. Furthermore, in the BMO the bias coefficients are mutated in the following way:

$$\xi_i' = \xi_i + \gamma \cdot \mathcal{N}(0, 1) \quad i = 1, ..., N.$$
 (13)

The parameter  $\gamma$  is a new parameter introduced for the BMO to determine the mutation strength on the bias. In our experiments the setting  $\gamma = 0.1$  arises to be a recommendable setting. The BMO biases the mean of the mutation and enables the evolution strategies to reproduce offspring outside the standard mutation ellipsoid, i.e.  $\sigma \cdot \mathcal{N}(0,1)$ . To direct the search the BMO uses a relatively simple way in comparison with directed or correlated mutation. However, it has got the same flexibility capable to adapt to disadvantageous search space characteristics. Figure 1 shows a situation in which the BMO is advantageous. The parental individual  $P_1$  has come close to the boundary of the feasible search space. The success rate to produce better offspring is relatively low because many mutations lie beyond the feasible search space or have got a worse fitness. The bias coefficient vector  $\vec{\xi}$  improves the success rate situation. In a word, this approach is as flexible as correlated and directed mutation, but consumes less computational power. Figure 2 shows a comparison of the different mutation ellipsoids of different mutation operators for evolution strategies.

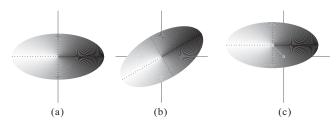


Figure 2: The mutation ellipsoids of the different mutation operators in a two-dimensional search space. From left to the right: (a) scaled standard mutation with N = 2 step sizes, (b) correlated mutation resulting in rotation, (c) biased mutation biasing the search into a certain direction.

#### 2. EXPERIMENTAL RESULTS

For many optimization problems the search space is constrained due to logical or other kinds of conditions. Coello

$\mathbf{p}\mathbf{b}$	$\mathbf{best}$	mean	worst	$\operatorname{std.dev}$
2.40	-4999.7	-4911.5	-4691.6	3.5
g04	-30665.5	-30660.2	-30631.5	0.5
2.40	-5000.0	-5000.0	-5000.0	$1.4 \cdot 10^{-10}$
g04	-30665.5	-30665.5	-30665.5	$3.2 \cdot 10^{-4}$

Table 1: Experimental results of the evolution strategies with standard mutation (upper part) and the BMO (lower part).

[2] provides a comprehensive survey of various constraint handling techniques. For evolutionary algorithms with a self-adaptive step size mechanism like evolution strategies, it is not easy to find an optimum which lies on the boundary of the feasible search space due to premature step size reduction [5]. Individuals with big step sizes have got a smaller probability to produce fit mutations when the optimum is in the vicinity of the infeasible search space than individuals with small step sizes. So, the step sizes reduce selfadaptively before reaching the area of the optimum. This results in premature fitness stagnation before approximating the optimum. The experiments of the upper part of table 1 show this premature fitness stagnation. Given are the results of a (15,300)-ES on problem 2.40 (taken from [5]) running for 1000 generations, and of a (15,100)-ES on problem g04 (taken from [4]) running for 200 generations with uncorrelated standard mutation with n step sizes. The experiments show that the evolution strategies are not able to approximate any of the optima of the constrained problems within the given number of generations. Instead, the ES suffer from fitness stagnation before reaching the optimum. The reason for the fitness stagnation is that the success rate is disadvantageous near the boundary to the infeasible search space and increases for decreasing step sizes. The experimental results of our *biased mutation operator* on the constrained test problems are shown in the lower part of table 1. Due to the BMO approach the ES are capable of approximating the optimum in every run on the two problems 2.40 and g04 within the given number of generations.

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