

# A Proposal of Genetic Algorithms with Function Division Schemes

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**Abstract:** We introduce the concept of a bi-population scheme for real-coded GAs consisting of an explorer sub-GA and an exploiter sub-GA. The explorer sub-GA mainly performs global exploration of the search space, and incorporates a restart mechanism to help avoid being trapped at local optima. The exploiter sub-GA performs exploitation of fit local areas of the search space around the neighborhood of the best-so-far solution. Thus the search function of the algorithm is divided. The proposed technique exhibits performance significantly superior to standard GAs on two complex highly multimodal problems.

**Keywords:** Genetic Algorithms, function division, real-coded GAs, explorer and exploiter sub-GAs

## 1 Introduction

As early exploration of the search space gradually gives way to exploitation of a small number of fit regions later on in the search process, conventional GAs tend to face difficulty in solving certain kinds of problem, such as highly multimodal functions, functions with high levels of epistasis, and deceptive functions (Goldberg, 1989; Whitley, 1991). On such problems, typical premature *takeover* of exploitation occurs in conventional GAs, before the early exploration stage has had a chance to set the population in the right direction. Many kinds of modified GA have been proposed to address this and related issues, such as CHC (Eshelman, 1991), mGA (Goldberg et al., 1990), delta coding (Mathias and Whitley, 1995) and fGA (Tsutsui et al., 1993; 1997b). These efforts have mainly been applicable to binary or Gray coded chromosomes.

In recent years, several researchers have concentrated on using real-valued genes. It is reported that, for some problems, real-valued encoding and associated techniques outperform conventional bit string approaches (Davis, 1991; Eshelman and Schaffer, 1993; Wright, 1991; Janikow and Michalewicz, 1991; Radcliffe, 1991). Although real-coded GAs show promise for some problems, they also find it hard to solve highly epistatic multimodal problems. As with any GA, one approach towards dealing with this issue is to concentrate on better ways to balance the degrees of exploration and exploitation at different stages of the search process.

One novel approach to this problem is to use separate populations for exploration and exploitation. Preliminary ideas along these lines were reported in Tsutsui et al (1997a, c), which presented a bi-population GA scheme (bGA). The bGA has two populations; one of these populations, the explorer sub-GA, tries mainly to explore the whole search space and maintain a useful degree of global diversity, while the other population, the exploiter sub-GA, exploits the neighborhood of the best solution obtained so far. Thus the search function of the algorithm is divided into two functions, explorer and exploiter functions. This paper reports on continuing study with this idea and discuss future directions of this study.

The paper is organized as follows. In Section 2, the bGA model is described in detail. Then, in Section 3 empirical results are given. In Section 4, more general form of search function division scheme is presented. Finally, concluding remarks are made in Section 5.

## 2 Models of the Bi-population GA

### 2.1 Components of the bGA

As illustrated in Fig. 1, a bGA consists of three components: (i) an explorer sub-GA, (ii) an exploiter sub-GA and (iii) a monitor. The explorer sub-GA explores the whole search space, and the exploiter sub-GA searches the neighborhood of the best solution obtained so far. If certain pre-specified convergence conditions are satisfied before completion of

search, the explorer sub-GA is *restarted*. In general, the bGA can be in different well defined states, depending on the current activity of the two sub-GAs. The monitor observes the current search process and makes decisions about the following: (a) when to restart the explorer sub-GA, (b) transitions between different bGA states, and (c) adaptive load balancing between the sub-GAs.

## 2.2 Dynamics of the bGA

Although we can consider several kinds of dynamics for bGA (Tsutsui, 97c), in this study we consider the bGA with the state transition diagram shown in Fig. 2. When search starts, only the explorer sub-GA is used. We call this state *E0-STATE*. When the pre-specified restart condition is satisfied, all the individuals of the explorer sub-GA are copied to the exploiter sub-GA and the explorer sub-GA is restarted after randomly re-initializing all the individuals and incrementing the *restart counter* (which is initially set to zero). Thus the best so far solution is maintained in the exploiter sub-GA. The exploiter sub-GA then continues search with the old population members. We call this state *EE-STATE*.

In *EE-STATE* two sub-GAs are run concurrently. During this concurrent running process, whenever the restart condition is satisfied, the explorer sub-GA restarts and the restart counter  $r$  is incremented by one. On the other hand, for situations where the best solution of the explorer sub-GA is better than the best solution of the exploiter sub-GA, the current exploiter sub-GA becomes useless and the state transition from *EE-STATE* to *E0-STATE* occurs.

These state transitions continue until the termination condition is satisfied. In the present work, restart of the explorer sub-GA is done only if the current best fitness value is improved by more than the pre-specified value  $\Delta f$  (say) during the last  $K_r$  (say) generations.

As two sub-GAs run concurrently in the *EE-STATE*, questions naturally arise about computational time-sharing, whether or not we assume a serial implementation. Intuitively, at the initial stage of the search more time should be given to the explorer sub-GA, and towards the final stages of search, more time should be allowed to the exploiter sub-GA.

We can use the restart counter  $r$  as a parameter to help implement these intuitions as a model of adaptive load balancing between the two sub-GAs. When  $r$  is small (there have not been many restarts) we give more time to the explorer sub-GA; when  $r$  is larger (the explorer has been restarted several times, and so it is perhaps a good idea to start concentrating on exploitation) we give more time to the exploiter sub-GA. Let  $g(r)$  be the fraction of time given

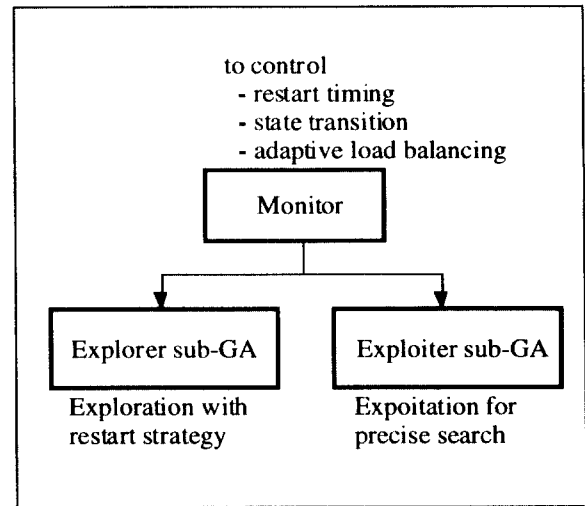


Fig. 1 Block diagram of a bi-population GA

to the explorer sub-GA, and so  $1-g(r)$  is given to the exploiter sub-GA. We use the following function for calculating  $g(r)$ .

$$g(r) = \begin{cases} K_r & \text{if } r < r_1, \\ K_r - \frac{2K_r - 1}{r_2 - r_1} \times (r - r_1) & \text{if } r_1 \leq r \leq r_2, \\ 1 - K_r & \text{otherwise,} \end{cases} \quad (1)$$

where  $0.5 < K_r < 1.0$  and  $1 < r_1 < r_2$ . When  $r$  is less than or equal to  $r_1$ , the bGA searches mainly in the exploration mode. When  $r$  exceeds  $r_2$ , the algorithm searches mainly in exploitation mode. When  $r$  is between  $r_1$  and  $r_2$ , time is shared by both the sub-GAs depending on the value of  $r$ .

## 2.3 Relation to Existing Work

Restart strategies have been discussed elsewhere (Eshelman, 1991; Mathias and Whitley, 1995). The delta coding method used by Mathias and Whitley (1995) is an iterative genetic search strategy that sustains search by periodically re-initializing the population. It also remaps the search hyperspace with each iteration and it is reported that it shows good performance especially when used with Gray coding. The CHC method by Eshelman (1991) is a safe search strategy where restart of the search process is done if it gets stuck at local optima by re-initializing the population with individuals generated by mutating the best solution obtained so far (also keeping the best one). In another study, Tsutsui et al. (1993, 1997b) reported a search space division and restart mechanism so as to avoid getting stuck in local traps.

Although the use of a restart strategy is a feature of the

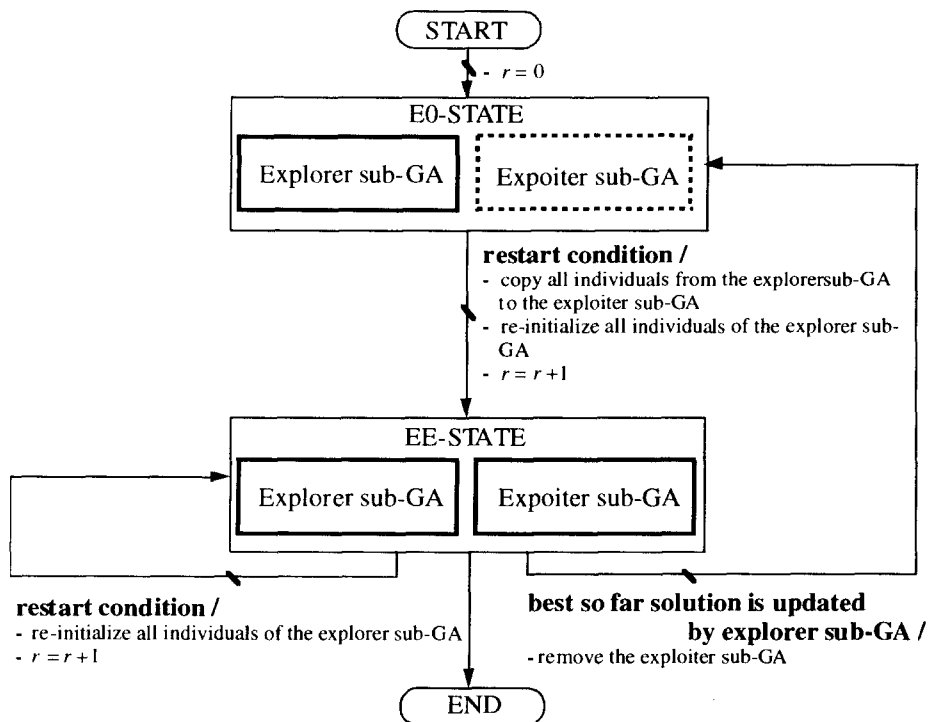


Fig. 2 State transition diagram of Type I bGA

bGA, its main purpose is to maintain a suitable balance between exploration and exploitation during the search process by means of two populations. Multiple population models have been described before (Tanese 1989; Whitley et al. 1990; Gorges-Schleuter, 1991), and are often the choice of underlying GA implementation in application oriented papers, however the populations are not assigned different roles. In contrast, the most closely related previous work appears to be that on *memetic* algorithms (Moscato and Norman, 1992; Radcliffe and Surry, 1994) and other hybridizations of a GA with local search. In these approaches, GA exploration is balanced by exploitation of every chromosome via local search, essentially incorporating local search into the evaluation function. In a memetic algorithm, exploration and exploitation remain tightly interlocked and concurrent, with overall load balancing between these two stages of search and still subject to the vagaries of standard GA dynamics. The bGA can be seen as a (rather radical) variation on such an idea, in which only very few chromosomes are subject to local search, and in which the local search is actually performed by a GA. In addition, a monitoring mechanism makes careful decisions about concentration of effort between the two stages.

### 3 Empirical Study

#### 3.1 Basic Evolutionary Model

The bGA is of course not restricted to a particular underlying evolutionary model, but we will briefly describe here the model used in this study. Evolution in both the explorer and the exploiter sub-GAs is similar to that of CHC (Eshelman, 1991) and  $(\mu+\lambda)$ -ES (Schwefel, 1981). Let the population size be  $N$ , and let the population at time  $t$  be represented by  $P(t)$ . The population  $P(t+1)$  is produced as follows: A set of  $N/2$  pairs of chromosomes is copied from  $P(t)$  to  $I(t)$  (intermediate population at time  $t$ ). Genetic operators are applied to the individuals in  $I(t)$ , generating  $N$  offspring which are placed in  $I'(t)$ . Rank-based selection is then used to select  $N$  individuals from the  $2N$  in  $P(t)$  and  $I'(t)$  to form  $P(t+1)$ . Elitism is employed to make sure that the best solution so far is always included in  $P(t+1)$ .

#### 3.2 Explorer and Exploiter sub-GA Models

Here, we describe the genetic operators and the control parameters for the explorer and the exploiter sub-GAs.

Several crossover operators have been proposed in the literature (Wright, 1991; Eshelman and Schaffer, 1993; Ono, et al., 1997) for real coded GAs. BLX- $\alpha$  (Eshelman and Schaffer, 1993) as shown in Fig. 3 is one of them and is reported to work well on a wide range of problems. In this study BLX- $\alpha$  is commonly used for both the sub-GAs..

With regard to mutation, several mutation methods such as creep mutation (Davis, 1991) have been proposed. For the explorer sub-GA, a *coarse-grained mutation* method, and for the exploiter sub-GA a *fine-grained mutation* method, seem to be suitable choices. However, to use different mutation methods for different sub-GAs will increase the number of control parameters to be tuned. Instead, we use the following *relative mutation* method. In this method, the distance  $|I|$  (see Fig. 3) between parents is multiplied by  $M$  ( $M > 1.0$ ) with mutation probability. This allows coarse mutation in the explorer sub-GA because the distance between parents will be relatively large, and fine mutation in the exploiter GA where distances between parents will be relatively small.

For efficient exploitation, intuition suggests that the population size of the exploiter sub-GA should be rather less than  $N$ , which is the population size of the explorer sub-GA. We therefore examined the effects of different population sizes for the exploiter sub-GA, namely:  $N$ ,  $N/2$ ,  $N/4$  and  $N/10$ .

The following parameters and experimental conditions were used. The crossover operator was BLX- $\alpha$  with  $\alpha = 0.5$ . Mutation probability was 0.1 and  $M = 3.0$ . The population size of the explorer sub-GA ( $N$ ) is fixed to 100. As regards the restart conditions of the explorer sub-GA,  $K_h$  was 50, and  $\Delta f$  was 0.1. The number of simulations used for each experiment was 10. The values of  $K_r$ ,  $r_1$  and  $r_2$  of Equation (1) were 0.7, 5 and 6, respectively.

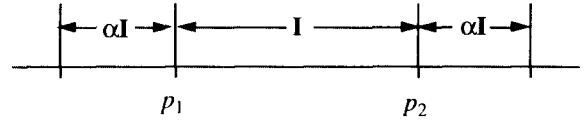
### 3.3 Test Functions

The test functions used are as follows:

**a) FMS (Frequency Modulation Sounds) parameter identification problem:**  $f_{\text{fms}}$  (Tsutsui et al., 1993, 1997b). Here the problem is to specify 6 parameters ( $a_1, w_1, a_2, w_2, a_3, w_3$ ) of the FM sound model represented by

$$y(t) = a_1 \sin(w_1 t \theta) + a_2 \sin(w_2 t \theta) + a_3 \sin(w_3 t \theta), \quad (2)$$

with  $\theta = 2\pi/100$ . The function  $f_{\text{fms}}$  is defined as the summation of square errors between the evolved data and the model data as follows:



BLX- $\alpha$  uniformly picks new individuals with values that lie in  $[I-\alpha I, I+\alpha I]$ , where  $p_1$  and  $p_2$  are two parents

**Fig. 3 BLX- $\alpha$**

$$f_{\text{fms}} = \sum_{t=0}^{100} (y(t) - y_0(t))^2, \quad (3)$$

where the model data are given by the following equation:

$$y_0(t) = 1.0 \times \sin(5.0t\theta) - 1.5 \times \sin(4.8t\theta + 2.0 \times \sin(4.9t\theta)). \quad (4)$$

Each parameter is in the range -6.4 to 6.35. The maximum number of trials was set to 160,000. This function is a highly complex multimodal (Fig. 6) function having strong epistasis, with minimum value  $f_{\text{fms}} = 0$ .

**b) Griewank function:**  $f_{\text{Griewank}}$  (Torn and Zilmskas, 1989). This function is defined as follows:

$$f_{\text{Griewank}} = \sum_{i=1}^{10} x_i^2 / 4000 - \prod_{i=1}^{10} \cos(x_i / \sqrt{i}) + 1. \quad (5)$$

parameter  $x_i$  is in the range -512 to 511. Maximum number of trials was set to 100,000. This function has its global minimum  $f_{\text{Griewank}} = 0$  at  $x_i = 0, i = 1, \dots, 10$ . This function is also highly multimodal and epistatic.

### 3.4 Results and Analysis

Fig. 4 (a) shows the mean best functional values achieved for the different approaches on  $f_{\text{fms}}$  achieved by the two types of bGA. A single pool GA without restart (non-bGA) is also tested for baseline comparison. Comparing the bGAs and the non-bGA we can see that the bGAs show much better performance. As regard to the population size of the exploiter sub-GA,  $N/2$  seemed to deliver the best results. Smaller population sizes for the exploiter sub-GA seemed very prone to entrapment in local optima, particularly in the  $f_{\text{fms}}$  case. This is probably because  $f_{\text{fms}}$  has many local optima around the global optimal point, rendering local search with a rather small population size rather vulnerable to failure.

Fig. 4 (b) shows the mean best functional values

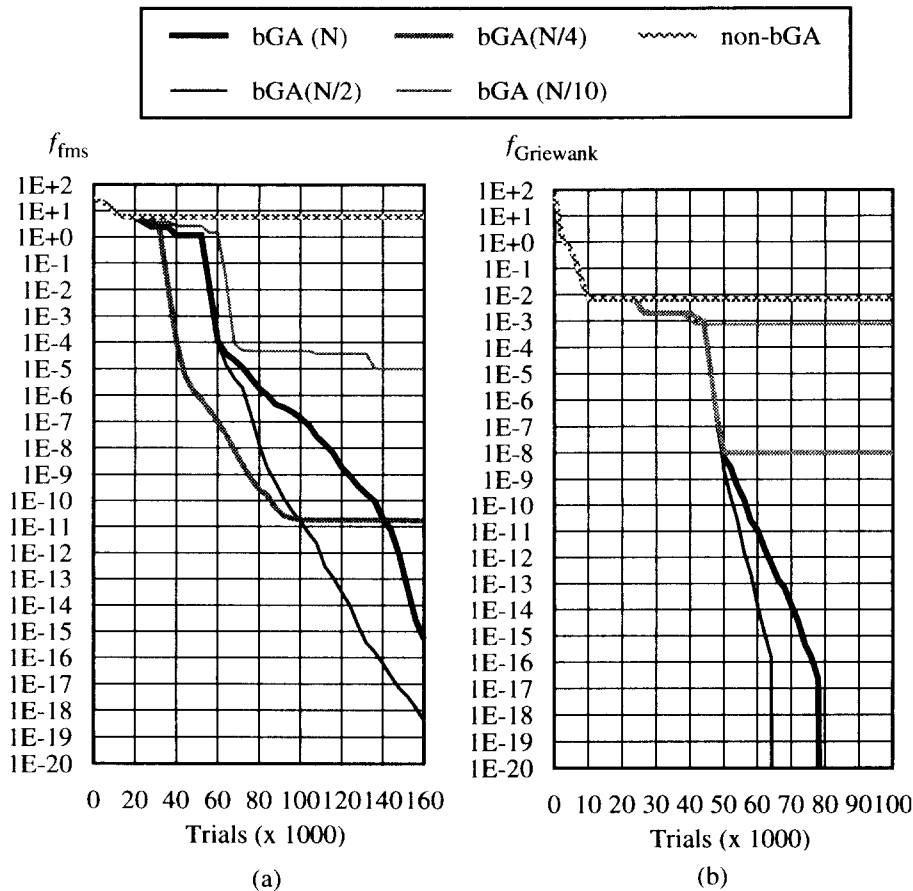


Fig. 4 Mean best functional values

achieved for the different approaches on  $f_{Griewank}$ . For this function also, the non-bGA showed poorer performance. As regards population size of the exploiter sub-GA,  $N/2$  ( $= 50$ ) again showed the best performance. Resizing the population to lesser values is seen to trap the search scheme to local optima again, corroborating the earlier findings.

#### 4 A Ladder Climbing Genetic Algorithm

In Section 2 and 3, a bi-population GA (bGA) based on the concept of search function division scheme is discussed. Here, we can consider more general genetic algorithms with the function division scheme. Fig. 5 shows such an example.

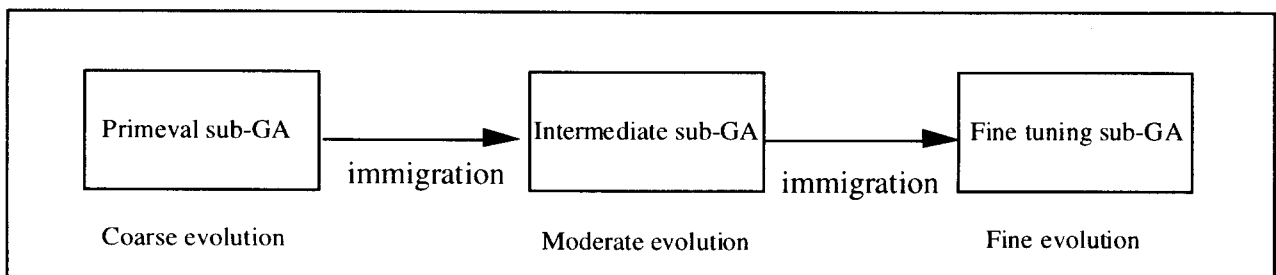


Fig. 5 A Ladder climbing GA

In the figure, the algorithm consists of three sub-GAs, the *primeval* sub-GA, the *intermediate* sub-GA, and the *fine tuning* sub-GA. In the primeval sub-GA, we evolve the population drastically with larger size of population and coarse mutation. On the contrary, in the fine tuning sub-GA, we evolve the population fine with smaller size of population and fine mutation. In the intermediate sub-GA, we evolve the population in a moderate manner. Individuals in the primeval sub-GA, which have good genetic characteristics, may immigrate to fine tuning sub-GA via intermediate sub-GA. By introducing intermediate sub-GA, we may provide a flexible bridge between both side sub-GAs. We call this GA shown in Fig. 5 a *ladder climbing genetic algorithm* since individuals which have good genetic characteristic move from left to right like climbing a ladder. Although we introduce only one intermediate sub-GA in Fig 5, we can introduce more than one intermediate sub-GAs.

## 5 Conclusions

The bGA which consists of an explorer sub-GA and an exploiter sub-GA is introduced. The main tasks for the sub-GAs are different; one mainly does exploration, and avoids being trapped in local optima by means of restart mechanism; and the other does exploitation by concentrating within the neighborhood of the best so far solution. An adaptive load balancing mechanism which allocates time between the explorer and exploiter sub-GAs is performed by a monitor which supervises the search process. The monitor also controls the state transitions during the search process.

The effectiveness of the proposed technique is shown by solving two complex multimodal function optimization problems, although further experimentation is needed to better test the performance of the bGA relative to other GAs, hillclimbing, and a standard GA with restart, for example. The explorer sub-GA with a larger population size and the exploiter sub-GA with a smaller population size showed the best performance.

Many opportunities for further research related to the present topic exist. Strategies to avoid the explorer sub-GA getting trapped by strong attractors multiple times, employing traditional local search techniques for the exploiter sub-GA, are yet to be tried. Evaluating the effectiveness of bGAs on real problems, comparing them with other multi-population based schemes, and extending them for permutation problems also remain to be investigated. Co-evolution of the two sub-GAs will also yield ideas for future research. The effectiveness of the ladder climbing GA, an extension of the bGA is also need to be studied.

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