



## Adaptive directed mutation for real-coded genetic algorithms

Ping-Hung Tang<sup>a</sup>, Ming-Hseng Tseng<sup>a,b,\*</sup>

<sup>a</sup> School of Medical Informatics, Chung-Shan Medical University, Taiwan, ROC

<sup>b</sup> Information Technology Office, Chung Shan Medical University Hospital, Taiwan, ROC

### ARTICLE INFO

#### Article history:

Received 20 February 2012

Received in revised form 12 June 2012

Accepted 9 August 2012

Available online 23 August 2012

#### Keywords:

Real-coded genetic algorithm

Function optimization

Adaptive directed mutation

### ABSTRACT

Adaptive directed mutation (ADM) operator, a novel, simple, and efficient real-coded genetic algorithm (RCGA) is proposed and then employed to solve complex function optimization problems. The suggested ADM operator enhances the abilities of GAs in searching global optima as well as in speeding convergence by integrating the local directional search strategy and the adaptive random search strategies. Using 41 benchmark global optimization test functions, the performance of the new algorithm is compared with five conventional mutation operators and then with six genetic algorithms (GAs) reported in literature. Results indicate that the proposed ADM-RCGA is fast, accurate, and reliable, and outperforms all the other GAs considered in the present study.

© 2012 Elsevier B.V. All rights reserved.

### 1. Introduction

Many real-life applications can be modeled as nonlinear optimization problems and, often, their global optimal solution is sought [1]. A typical nonlinear global optimization problem follows the form

$$\begin{array}{l} \text{maximize} \\ \text{minimize} \end{array} f(\mathbf{x} = x_1, x_2, \dots, x_N) \text{ subject to } \mathbf{x} \in \Omega \quad (1)$$

where  $\mathbf{x}$  is a continuous variable vector with search space  $\Omega \subseteq R^N$ , and  $f(\mathbf{x})$  is a continuous real-valued function having  $N$  variables. The domain  $\Omega$  is defined within the upper and lower limits of each dimension. The problem is to find the global optimal solution  $\mathbf{x}^*$  with its corresponding global optimal function value  $f(\mathbf{x}^*)$ . Two major classes of optimization techniques for solving general nonlinear optimization problems can be found in the literature, namely, gradient-based optimizers and evolutionary algorithm optimizers [1,2].

All gradient-based optimizers (also called deterministic optimizers) are point-by-point algorithms and are therefore local optimization techniques in nature. Gradient-based optimization techniques start the search procedure with an initial guess solution. If this guess solution does not come close enough to the global optimal solution, the gradient-based optimization techniques are likely to be trapped in the local optimal solution. In practice, finding such a suitable starting solution is the major difficulty when trying to optimize automatically. Gradient-based optimizers with about 20

variables are usually impractical [2] because as the number of variables increases, so does the number of evaluations. Most of them are designed to solve a particular class of optimization problems with few variables.

In other words, all evolutionary algorithm optimizers work with random sets of potential solutions—they are stochastic searching algorithms and therefore global optimization methods. Evolutionary algorithm optimizers generally scale well to solve higher dimensional optimization problems by comparing with gradient-based optimizers. Evolutionary algorithms consist of three population-based heuristic methodologies: genetic algorithms (GAs), evolutionary programming, and evolutionary strategies. GAs are perhaps the most popular evolutionary algorithms [3].

In traditional GA implementations [4,5], the decision variables were encoded as binary strings, namely, binary coded genetic algorithm (BCGA). The performance of BCGA has been satisfactory on small- and moderate-size problems requiring less precision in the solution, but BCGA entails huge computational time and memory [6] for high-dimensional problems that call for greater precision. To improve these drawbacks when applying BCGA to multidimensional and high-precision numerical problems, the decision variables can be encoded as real numbers, namely, real-coded genetic algorithm (RCGA), which has become increasingly popular [1,7]. The superiority of RCGA to BCGA has been established for continuous optimization problems [8] and medical data mining [9].

The performance of GAs relies on efficient search operators to guide the system toward global optima. One problem afflicting GAs is premature convergence. To mitigate or even avoid trapping into the local optima, the mutation operator provides a mechanism to explore new solutions and maintains the diversity of the population

\* Corresponding author at: School of Medical Informatics, Chung-Shan Medical University, Taiwan, ROC.

E-mail address: [mht@csmu.edu.tw](mailto:mht@csmu.edu.tw) (M.-H. Tseng).

in GAs search, but it does so at the cost of slowing down the learning process. In GAs literature, relatively less effort has been put into designing a new mutation operator for RCGAs [1]. The step size and search direction are major factors that determine the performance of mutation operator [10]. The present study seeks to propose a novel, simple, and efficient RCGA based on the adaptive directed mutation (ADM) operator, and whose performance is demonstrated on a set of complex function optimization problems.

The remainder of this paper is organized as follows: Section 2 gives a brief review of the mutation operator in RCGAs. Section 3 provides a detailed description of the proposed methodology. The set of benchmark problems, the compared algorithms, and the experimental results are reported in Section 4. Finally, Section 5 presents a number of conclusions from the present study.

## 2. Review of literature on mutation operator

In general, a typical RCGA involves three main operators—selection, crossover, and mutation—to evolve the fitness of a population of guesses over a sequence of generations toward convergence at the global optimum. The method can be viewed as an evolutionary process. The mutation operation is used to change the offspring genes. Mutation is a key operator to increase the diversity of the population, hence enabling GAs to explore promising areas of the search space [10]. For common mutation operations, the random mutation (RM), uniform mutation, non-uniform mutation (NUM), polynomial mutation (PLM), and Gaussian mutation can be found [1,11].

Research effort has recently been spent to improve GAs performance by using different mutation techniques. Following the concept of induced mutation in biological systems, Bhandari et al. [12] first used directed mutation technique to improve BCGAs. Based on gradient or extrapolation, the directed mutation deterministically introduces a new point in the population guided by the information acquired in the previous generations. Zhou and Li [13] proposed a directed variation technique for mutation operator to adjust some individuals by using the feedback information from the current population. Berry and Vamplew [14] suggested a co-evolutionary technique where each component of a solution vector is added one extra bit to determine the direction of mutation by using the feedback information from the current population. Temby et al. [15] introduced a directed mutation based on momentum, where each component of an individual is attached a standard Gaussian mutation and the current momentum to mutate that component. Korejo et al. [10] proposed a directed mutation operator to improve the directed variation technique [13], in which the statistics information regarding the fitness and distribution of individuals over intervals of each dimension is calculated according to the current population and is used to guide the mutation of an individual toward the neighboring interval that has the best statistics result in each dimension.

Srinivas and Patnaik [16] described an adaptive BCGA for multimodal function optimization. In this adaptive GA, the probabilities of crossover and mutation are varied depending on the fitness values of the solutions. High-fitness solutions are protected while solutions with sub-average fitness are totally disrupted. According to the information of population evolutions in the impact of changes on fitness level, Chen and Liao [17] suggested an adaptive mutation operator to appropriate adjustment searching policies in RCGAs by using the simulation of gradient or counter-gradient direction. Tseng and Liao [18] proposed two adaptive strategies to improve the evolutionary efficiency of GAs. One strategy is to change crossover operators, which can randomly substitute the current crossover operator for another crossover operator at any time. The other strategy is to implement an adaptive adjustment

of the crossover and mutation rates to increase the level of genetic diversity and guide the system toward global optimum if the system sinks into the local optimum. A state-of-the-art method for adaptive mutation is Covariance Matrix Adaptation Evolution Strategy (CMA-ES) [19]. CMA-ES outperforms many other parametric optimization algorithms, as witnessed in the 2005 CEC algorithm contest, and is recommended by experts [20].

Ling and Leung [7] suggested the wavelet mutation, which is based on wavelet theorem. Deep and Thakur [1] designed the power mutation (PM) operator for RCGAs based on power distribution. By applying the underlying biological and mathematical idea to the generic framework of RCGAs, Vafae and Nelson [21] proposed an adaptive mutation method based on the frequency of the best chromosomes' genes.

## 3. Methodology

### 3.1. The proposed ADM

The objective of the present study is to introduce a new mutation operator, namely, ADM, and to evaluate its performance against other mutation operators existing in literature. The ADM operator was designed to avoid both concentration of each chromosome caused by a crossover operator and an unsystematic search of the system due to RM. The ADM operator will introduce a new solution in the population. The new searching point is guided by the solutions obtained earlier based on the adaptive direction of gradient, hence its name. The direction of gradient is derived from the evolution of fitness value for each individual. The definition of  $\Delta f(t-1)$  and  $\Delta f(t)$  are variations of the fitness value for each chromosome  $\mathbf{x}$  in the three consecutive generations ( $t-2$ ,  $t-1$ , and  $t$ ):

$$\Delta f(t) = f(\mathbf{x}(t)) - f(\mathbf{x}(t-1)) \tag{2}$$

$$\Delta f(t-1) = f(\mathbf{x}(t-1)) - f(\mathbf{x}(t-2)) \tag{3}$$

where  $\mathbf{x} = \{x_1, x_2, \dots, x_k, \dots, x_N\}$  is a chromosome,  $f(\mathbf{x}(t))$  is the fitness value of chromosome  $\mathbf{x}$  at the  $t$  generation. The variations of the  $k$ -dimensional gene for chromosome  $\mathbf{x}$  in the three consecutive generations ( $t-2$ ,  $t-1$ , and  $t$ ) are defined as

$$\Delta x_k(t) = x_k(t) - x_k(t-1) \tag{4}$$

$$\Delta x_k(t-1) = x_k(t-1) - x_k(t-2) \tag{5}$$

Combining (2) with (5), the new solution of  $x_k$  will be iteratively updated as

$$x_k(t+1) = x_k(t) + (\Delta f(t), \Delta f(t-1), \Delta x_k(t), \Delta x_k(t-1), x_k(t), x_k^{UB}, x_k^{LB}) \cdot p_m \tag{6}$$

where  $x_k^{UB}$  and  $x_k^{LB}$  are the upper bound and lower bound of  $x_k$ , respectively.  $p_m$  is the adaptive probability of mutation [16]. It makes the bad chromosomes undergo a more substantial change in the population, and it can be expressed as follows:

$$p_m = \begin{cases} 0.5 \cdot \frac{f_{\max}(t) - f(\mathbf{x}(t))}{f_{\max}(t) - \bar{f}(t)}, & \text{if } f(\mathbf{x}(t)) \geq \bar{f}(t) \\ 0.5, & \text{if } f(\mathbf{x}(t)) < \bar{f}(t) \end{cases} \tag{7}$$

where  $f_{\max}(t)$  is the maximum fitness value of the population,  $\bar{f}(t)$  is the average fitness value of population.

In Eq. (6), the function of  $g(\cdot)$  can be termed as an acceleration function which controls the directed mutation. In the present study, four guided strategies were proposed based on nine different evolution trends for any chromosomes. These are “directional small-scale mutation,” “random small-scale mutation,” “random medium-scale mutation,” and “random large-scale mutation.” The

متن کامل مقاله

دریافت فوری ←

**ISI**Articles

مرجع مقالات تخصصی ایران

- ✓ امکان دانلود نسخه تمام متن مقالات انگلیسی
- ✓ امکان دانلود نسخه ترجمه شده مقالات
- ✓ پذیرش سفارش ترجمه تخصصی
- ✓ امکان جستجو در آرشیو جامعی از صدها موضوع و هزاران مقاله
- ✓ امکان دانلود رایگان ۲ صفحه اول هر مقاله
- ✓ امکان پرداخت اینترنتی با کلیه کارت های عضو شتاب
- ✓ دانلود فوری مقاله پس از پرداخت آنلاین
- ✓ پشتیبانی کامل خرید با بهره مندی از سیستم هوشمند رهگیری سفارشات