An adaptive genetic algorithm with diversity-guided mutation and its global convergence property

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Abstract: An adaptive genetic algorithm with diversity-guided mutation, which combines adaptive probabilities of crossover and mutation, was proposed. By means of homogeneous finite Markov chains, it is proved that adaptive genetic algorithm with diversity-guided mutation converges to the global optimum if it maintains the best solutions, and the convergence of adaptive genetic algorithms with adaptive probabilities of crossover and mutation was studied. The performances of the above algorithms in optimizing several unimodal and multimodal functions were compared. The results show that for multimodal functions the average convergence generation of the adaptive genetic algorithm with diversity-guided mutation is about 900 less than that of adaptive genetic algorithm with adaptive probabilities and genetic algorithm with diversity-guided mutation, and the adaptive genetic algorithm with diversity-guided mutation does not lead to premature convergence. It is also shown that the better balance between overcoming premature convergence and quickening convergence speed can be gotten.

Key words: diversity-guided mutation; adaptive genetic algorithm; Markov chain; global convergence

1 INTRODUCTION

It is known that the performance of the genetic algorithms (GAs) is dependent upon the operator probabilities used. Adaptability of operator probabilities is an attempt to make the genetic algorithm a more effective optimizer. By adopting adaptive operator probabilities some benefits, such as increasing the quality of the obtained solutions and allowing the GAs to find a solution of given quality more quickly, can be attained. Therefore, by employing some methods, some researchers attempted to automatically adjust the operator probabilities according to the quality of solutions~3. It is also known that the premature convergence is a major problem in GAs and adaptive genetic algorithms may lead to premature convergence~4. In order to overcome the premature convergence, the term “diversity” is employed. Diversity is closely related to the performance of GAs, especially when attempts are made to avoid premature convergence and escape local optima. A few researchers~5~8] used diversity measure to control the search direction of evolutionary algorithms.

By means of mixing adaptive crossover and mutation of Srinivas~2] with diversity-guided mutation and modifying adaptive crossover strategies, an adaptive genetic algorithm with diversity-guided mutation (AGADM) was developed. It is proved that AGADM and genetic algorithms with diversity-guided mutation (GADM) will converge to the global optimum when maintaining the best solution by homogeneous finite Markov chains, but adaptive genetic algorithms with adaptive probabilities of crossover and mutation (AGA) do not always do so. The performances of AGA, GADM and AGADM were compared.

2 PRELIMINARY

Genetic algorithms are used to tackle static optimization problem. There are N individuals (candidate solutions) within the population, which can be expressed as binary strings of fixed length \(g_i = g_1g_2...g_l\), \(g_i = 0,1, j = 1,2, ..., l, i = 1,2, ..., N\) and the correspond fitness values are \(f_i < \infty, i = 1,2, ..., N\).

Definition 1 Let \(Z_t\) be a sequence of random variables which represent the best fitness within a population represented by state \(i\) at step \(t\), and \(f^*\) be the global optimum of the problem. If

\[
\lim_{t \to \infty} p(Z_t = f^*) = 1 \tag{1}
\]

then a genetic algorithm converges to the global optimum solution.

In the implement of GAs, if the best fitness values in the population are not improved in \(N_{gen}\) generations, the algorithm will go to the end, which is often the convergence critical. The convergence speed is the generation (terminal-generation) that GA runs before the convergence criterion
holds. In this paper, let $N_{nx} = 300$ in 15-dimension function optimal problems and $N_{nx} = 50$ in 2-dimension function optimal problems.

**Definition 2** A square matrix $A = (a_{i,j})_{n \times n}$ is said to be:

1) nonnegative matrix ($A \succeq 0$), if $a_{i,j} \geq 0$, $i, j \in \{1, \ldots, n\}$;
2) positive matrix ($A > 0$), if $a_{i,j} > 0$, $i, j \in \{1, \ldots, n\}$.

A nonnegative matrix $A$ is said to be:

1) primitive matrix, if there exists $k > 0$ such that $A^k > 0$;
2) stochastic matrix, if $\sum_j a_{i,j} = 1$, $i \in \{1, \ldots, n\}$.

A stochastic matrix $A$ is said to be column allowable, if it has at least one positive element in each column.

**Lemma 1** Let $C, M$, and $S$ be stochastic matrices, where $M$ is positive and $S$ is column allowable, then the product $CMS$ is positive.

**Theorem 1** Let $C, M, M', S$ be stochastic matrices. If $M$ is positive, $S$ is column allowable and $M'$ diagonally positive, then the product $P = CMM'S$ is positive.

**Proof** Let $M = (m_{i,j})_{n \times n}$, $M_a = (p_{i,j})_{n \times n}$ and $M_b = M'M_a = (u_{i,j})_{n \times n}$. Since $M$ is positive, we have

$$u_{i,j} = \sum_{k=1}^n m_{i,k} p_{k,j} \geq m_{i,j} p_{i,j} > 0.$$

So, $M_b$ is positive.

Note that the product of stochastic matrices is also a stochastic matrix. According to lemma 1, $P = CMM'S$ is positive. Hence, the proof is completed.

3 MODIFIED ADAPTIVE GENETIC ALGORITHM (AGADM)

The modified genetic algorithm with diversity-guided mutation and adaptive crossover, mutation probabilities (algorithm 1) can be described as follows:

choose an initial population;
calculate the fitness of each individual;
perform selection;
repeat {
perform crossover with adaptive probability;
perform diversity-guided mutation;
perform mutation with adaptive probability;
calculate the fitness of each individual;
perform selection;}
until some stopping criterion applies.

Algorithm 1 is hereafter referred to adaptive genetic algorithm with diversity-guided mutation (AGADM). In algorithm 1, the operation of "perform diversity-guided mutation" (algorithm 2) is described as follows:

calculate diversity of the population;
if diversity measure $d < \lambda_1$,
perform mutation with probability $k_1$;
else if diversity measure $d < \lambda_2$,
perform mutation with probability $k_2$;
else
perform mutation with probability $k_3$;
end.

In algorithm 2, $0 < \lambda_1 < \lambda_2 < 1$, $0 < k_2 < k_3 < 1$, and $k_3 > 0$ is almost equal to 0.

In algorithm 1, adaptive crossover and mutation probabilities of individuals (denoted as $i$ and $j$) within the population are represented by $p_c(i, j)$ and $p_m(i)$, respectively, which are determined by individual fitness evaluations within the current population. The famous calculating method for $p_c(i, j)$ and $p_m(i)$ proposed by Srinivas is as follows:

$$p_c(i, j) = \begin{cases} k_1 \frac{f_{\text{max}} - f'}{f_{\text{avg}} - f_{\text{avg}}}, & f' > f_{\text{avg}} \\ k_2, & f' < f_{\text{avg}} \end{cases}$$

$$p_m(i) = \begin{cases} k_3 \frac{f_{\text{max}} - f}{f_{\text{avg}} - f_{\text{avg}}}, & f > f_{\text{avg}} \\ k_4, & f < f_{\text{avg}} \end{cases}$$

where $0 < k_1 < k_2 < k_3 < 1$, $f_{\text{avg}}$ and $f_{\text{max}}$ are respectively the average fitness value and the maximum fitness value of the population, and $f'$ is the larger one of fitness values of the individuals $i$ and $j$ to be crossed. $f$ is the fitness value of the individual $i$ to be mutated.

ZONG et al improved Srinivas's adaptive genetic algorithm by means of modifying formulae (2) and (3). Their adaptive genetic algorithms can increase the converge speed, but there are at least two disadvantages:

1) Crossover probability of the best individuals is very small (close to zero), so the building-blocks of the best/better individuals do not spread out.
2) Their adaptive genetic algorithms often lead to premature convergence.

In order to propagate the building-blocks of the best/better individuals, $f'$ in formula (2) is replaced with

$$p_c'(i, j) = \begin{cases} k_1 \frac{f' - f_{\text{min}}}{f_{\text{avg}} - f_{\text{min}}}, & f' > f_{\text{avg}} \\ k_2, & f' < f_{\text{avg}} \end{cases}$$

where $f_{\text{min}}$ is the minimum fitness value of the population, and $f'$ is the smaller one of fitness values of the individuals $i$ and $j$ to be crossed.

The role of formula (4) is to increase the chance of crossover when the individuals are better. If both individuals to be crossed are better, after the building-blocks of them are exchanged, much better children of them may be produced. If one of the individuals to be crossed is good, and