Improved Adaptive and Multi-group Parallel Genetic Algorithm Based on Good-point Set

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Abstract: This paper puts forward an adaptive genetic algorithm to solve the multi-group homogenization in the solution space. The use of good-point set approach improves the initial population, ensuring them a uniform distribution in the solution space. In the evolution, each population implements independent genetic operations (selection, good-point set crossover, and mutation). The introduction of adaptive operator makes crossover and mutation operator self-adaptive. As the algorithm adopts a strategy of retaining the best, a space compression strategy can be designed based on information entropy theory through the information of all sub-populations in the evolution process, which ensures the algorithmic stability and fast convergence to the global optimal solution. Furthermore, in order to explore the feasibility and effectiveness of the improved multi-group parallel algorithm, optimization tests are implemented on some of the typical multi-peak functions, and the results are compared with the analytic solution and optimal solution of basic GA. The outcome suggests that the global searching ability and convergence of the improved algorithm is far better than the basic one.

Index Terms: Good-point Set; Genetic Algorithm; Adaptive Operator; Information Entropy

I. INTRODUCTION

First pioneered by John Holland in his “Adaptation in Natural and Artificial Systems” in the 1970s, Genetic Algorithm (GA) is an optimization solution based on population searching according to C.R. Darwin’s biological evolution theory and G. Mendel’s genetics. Its main idea is to constantly evolve a randomly generated initial population by reproduction, crossover, mutation or other genetic operators, and ultimately achieve the optimal solution[5]. Compared with other optimization methods, GA uses only a single string to describe a problem. And no derivative function or other information is needed as a fitness function is used to optimize computing. The algorithm is particularly suitable to resolve complex and nonlinear problems which other technologies cannot or will be difficult to solve. It is a favored area of artificial intelligence besides expert system and artificial neural network, which has always been a heated topic for research. It has also been widely used in combinatorial optimization, machine learning, adaptive control, intelligent machine system, intelligent manufacturing system, systems engineering, artificial intelligence, artificial life and other areas, becoming one of the key technologies in intelligent computing in the 21st century[2-4].

GA is implemented as follows: ① randomly generating an initial population in the range of possible solutions; ② evaluating the fitness of each individual in the current population through certain selection methods (fitness function); ③ generating a second generation of population from those selected through genetic operators: crossover and/or mutation; ④ re-implementation of the above process until certain conditions are met. The fitness function is similar to the power of natural selection, and the genetic operators: reproduction, crossover and mutation are corresponding to the proliferation, mating and genetic mutation in nature. The selection operator chooses the fitter individuals in the father generation to ensure the optimal search direction; the crossover operator analogs genetic recombination and random exchange of information to ensure the search space; the mutation operator reflects the gene mutation to ensure the global search capability of the algorithm.

Although GA is intuitive and easy to operate, premature convergence may be brought in by some super-individuals. In the simulation of biological evolution, as these super-individuals soon domain the whole population, global optimal solution is unlikely to be found due to the lack of new genes. Another reason is that the selection and crossover operators may lead to early loss of some excellent gene fragments, thus limiting the scope of the search space, so that searches can only be made in the local area to find the local optimization instead of the global one[5]. In particular, for the large-scale and high-precision problems, global optimizations are usually missed. Recently many improvements to GA have been put forward, mostly concentrated in initialization[6], probabilities of selection, crossover and mutation, selection of the fitness function[7,8] ,and process design of the evolution. They are all targeted, but a fundamental solution to the above deficiencies hasn’t been provided.
In response to the above deficiencies and combined with the solving mechanism of GA, we propose an improved multi-group parallel and adaptive Genetic Algorithm based on good-point set (IMPGA-GPS). We use simulation technology to analyze the convergence of the algorithm, and good performance is proved under the strategy of optimal individual reservation, so that it can effectively avoid premature convergence. It is believed to be feasible for large-scale and high-precision optimization, and have broad application prospects in numerical optimization of complex systems.

II. (IMPGA-GPS) DESIGN

A. Strategy for Improvement

GA is a simulation of biological evolution, which has been widely used because of its global search capability, strong adaptability and robustness. However, there are still many problems to be improved. Recent efforts to improve the performance of GA mainly focus on the implementation strategy, encoding, and design of the selection, crossover and mutation mechanism. Implementation strategy improvements include hybrid genetic algorithm [12],[14], messy genetic algorithm [13], forking genetic algorithm [14], symbiotic genetic algorithm [15], nonlinear genetic algorithm and parallel genetic algorithm [17]; Encoding improvements include string-coding, real-coding, structured coding and orderly coding; space searching strategies include space adaptive shrinkage [19, 20] and space shrinkage based on statistical theory [21].

On the basis of the above analysis, we apply the good-point set theory of number theory to uniformly design the initial population and the crossover operation, improving the overall performance of genetic algorithm. In the large-scale and high-precision optimizations, we can find the space compression factors according to the entropy strategy. Thus without the loss of optimal solutions, the scope of optimization can be narrowed, which is conducive to achieve more accurate satisfactory solution.

B. Key Point of Algorithm Designed

1) Initialization of population

The search speed of basic GA depends on crossover and mutation operators. Although it has a global search capability, it is dependent on the populations in a certain range. As a result, the initial population has a great influence on the convergence, search efficiency and stability in the algorithm [22]. In the absence of a predictable region of the optimal solution, the initial population must stands for the individuals of the whole space, represents all individual information to the maximum, and fully represents the characteristics of the solution space, thus ensuring the algorithm a fast approach to the optimal solution [23]. The initial population of basic GA is randomly selected (Monte Carlo method), and its coverage space is uncertain, which is prone to the phenomenon of premature convergence. In addition, maintaining the diversity of the population can improve the global convergence of the algorithm. So while ensuring a reasonable distribution of the initial individuals, a reasonable diversity should also be considered. Accordingly, in this paper, we set up initial population in a view of the good-point set.

a) Good-point Set Theory

- Assumptions

(1) Let $G_s$ be an unit cube in an $s$-dimensional Euclidean space, then $x \in G_s$, $x = (x_1, x_2, \cdots, x_s)$, where $0 \leq x_i \leq 1, i = 1, 2, \cdots, s$.

(2) Define a point set (with $n$ points) in the unit cube.

(3) For any point $r = (r_1, r_2, \cdots, r_s)$ in a given $G_s$, we can define a $N_n(r) = N_n(r_1, r_2, \cdots, r_s)$ representing the number of the points satisfying the following inequality in $P_n(k). 0 \leq x_i^n(k) \leq r_i, i = 1, 2, \cdots, s$.

Definition 1 Deviation: Define $\phi(n) = \sup_{r \in G_s} \left\{ \frac{N_n(r)}{n} - |r| \right\}$, where $|r| = r_1, r_2, \cdots, r_s$. So we say the point set $P_n(k)$ has a deviation of $\phi(n)$. If for any $n$, there is $\phi(n) = 0$, we say $P_n(k)$ has a coincident distribution with a deviation of $\phi(n)$.

Definition 2 Good-point Set Suppose $r \in G_s$, and $P_n(k) = \{ \{r_1 * k\}, \{r_2 * k\}, \cdots, \{r_s * k\} \}, k = 1, 2, \cdots, n$ has a deviation of $\phi(n)$. If $\phi(n) = C(r, \varepsilon)n^{-1-\varepsilon}$, where $C(r, \varepsilon)$ is a constant only related to $r, \varepsilon$ (any small positive), $P_n(k)$ is called a good-point set and $r$ a good point.

Definition 3 Good-point set: Let $r_k = \{2\cos \frac{2\pi k}{p}\} (1 \leq k \leq s)$

(1)

If $p$ is the smallest prime satisfying $(p - s)/2 \geq s$, or $r_k = \{e^k\} (1 \leq k \leq s)$, then we say $r$ is a good point. $\{a\}$ Denotes the decimals of $a$.

Theorem 1

If $P_n(k) (1 \leq k \leq n)$ has a deviation of $\phi(n)$ and $f \in B_s (s$-dimensional limited function), then

\[ \left| \int_{G_s} f(x)dx - \frac{1}{n} \sum_{k=1}^{n} f(P_n(k)) \right| \leq V(f)\phi(n) \]

(2)

where $V(f)$ is the total variation of $f$.

Theorem 2

If theorem 1 is valid for any $f \in B_s, P_n(k) (1 \leq k \leq n)$ is a point set with a deviation less than $\phi(n)$. This conclusion can be seen as the converse theorem of theorem 1.

Theorem 3

Suppose $f(x)$ satisfies:
The method is as follows: \( f(x_i) \leq L \), \( \frac{\partial f}{\partial x_i} \leq L \), \( 1 \leq i \leq s \);

(2) \( f(x_i) \leq L \), \( 1 \leq i \leq j \leq s \);

(3) \( \frac{\partial^2 f}{\partial x_i \partial x_j} \leq L \), \( 1 \leq i \leq s \).

Then if we use any weighed sum of any given \( n \) points’ function values to approximately calculate the integrals of the function on \( G_s \), we could never expect the error to be smaller than \( O(n^{-1}) \).

Note 1: This theorem is why the above set is called “Good-point Set”

Note 2: Recalling theorem 1, 2 and 3, we can know that using a good-point set for approximate integrals, the order of its error is related to \( n \) only rather than the dimension \( s \), which provides a superior algorithm for higher order approximately calculation.

Note 3: According all above, if we define \( n \) points and use the linear combination of their function values to approximate the corresponding integral, the good-point set can serve as the best solution.

Theorem 4

If \( x_1, x_2, \ldots, x_n \) is a uniform distribution on \( i.i.d. D_i \) and \( \mu_{D_i} = (x_1, x_2, \ldots, x_n) \), the probability of its deviation written as \( D(n, P_n) = O(n^{-1/2} (\log \log n)^{1/2}) \) is 1.

Note 4: Theorem 4 implies that for an unknown distribution, we can randomly select \( n \) points whose deviation is usually \( O(n^{-1/2}) \). If we use good-point set to find the \( n \) points, its deviation is usually \( O(n^{-1+\epsilon}) \). For instance, if \( n = 10, 000 \), the deviation of the former is \( O(10^{-2}) \), while the latter is \( O(10^{-4}) \). Accordingly, the method of good-point set has a much smaller deviation than random selection. That’s the theoretical basis we implement good-point set to improve the crossover and initialization of GA.

b) The Establishment of Initial Population

The establishment of the initial population is essentially an optimal design of how to use limited individuals to scientifically and globally represent the characteristics of the whole solution space. The initial population can neither be randomly generated nor traverse all the conditions, particularly in the multi-variable problems. Only if we set the most representative individuals who best reflect the inherent characteristics of the solution space as the initial population can we better characterize the space.

Uniform design is a scientific and effective method to solve this problem, which has been used to determine the operating parameters of GA.

Therefore, researchers have put forward several methods for structuring uniform design tables. Good lattice point, Latin square and expansion of orthogonal designs have been used in population initializations, which have achieved good results.

But when the number of factors and levels increase, not only the experiment size increases, and the corresponding uniform design tables become very difficult to get, which bring difficulties to the uniform design methods. However, if we use a good-point set strategy whose accuracy has nothing to do with dimension to initialize the population, the mentioned disadvantages can be solved, and better diversity would be generated in the initial population.

Suppose the size of the initial population is \( N \), and the chromosome is \( A_i = \{a_{1i}, a_{2i}, \ldots, a_{ni}\} \). Firstly we define a good-point set containing \( N \) points in a \( s \)-dimensional space \( H \). The method is as follows:

Establish a good-point set containing \( N \) points in a \( s \)-dimensional space \( H \), \( P_k(i) = \{r_1 \times i, r_2 \times i, \ldots, r_s \times i\} \)

With \( i = 1, 2, \ldots, n \), \( r_s = \{2\cos \frac{2\pi k}{p}\}, 1 \leq k \leq s \)

If \( p \) is the smallest prime satisfying \((p - s) / 2 \geq s \) or \( r_k = \{k\} \) (1 \( \leq k \leq s \), then \( r \) is a good point. \( \{a\} \) denotes the decimals of \( a \).

(1) If \( a_k \times i \) is a single-digit binary, define \( a_k = \{r_k \times i\} \) (If the decimals of \( a < 0.5 \), \( \{a\} = 0 \), otherwise \( \{a\} = 1 \)).

(2) If \( a_k \times i \) is a multi-digit binary, define the range of \( a_k \times i \) as \( \beta_k \times a_k \leq \beta_k \).

Let \( a_k = a_k + \{r_k \times i\} \times \beta_k \), and then transfer \( a_k \) to a binary according to the binary coding rules.

(3) If \( a_k \times i \) is a real code, define its range as \( \beta_k \times a_k \leq \beta_k \), and simply let \( a_k = a_k + \{r_k \times i\} \times \beta_k \).

Other codes can be optimally structured alike.

2) Good-point Set Crossover

Implement the good-point set crossover of the selected individuals under an adaptive crossover probability \( p_c \). Let \( A_i = (a_{1i}, a_{2i}, \ldots, a_{ni}) \) and \( A_j = (a'_{1j}, a'_{2j}, \ldots, a'_{nj}) \) be the father-generation individuals selected for crossover, and structure \( A_i \) and \( A_j \). Assume \( H \) is an aggregate of the
positions in which components differ between $A_i$ and $A_j$, so $H = \{t \mid a_i^t \neq a_j^t, 1 \leq t \leq L\}$ . If $t_1, t_2, \ldots, t_s$ denote elements of $H$, and $t_1 < t_2 < \cdots < t_s$, then we can establish a 
good-point set containing $n$ points in the $s$-dimensional 
space:

$$P_e(i) = \{\{r_i \ast j\} \mid r_1, r_2, \ldots, r_s \in \Rp\} \quad \text{, where}$$

$$i = 1, 2, \ldots, n \text{, } r_k = \{2 \cos \frac{2\pi k}{p}\} \quad 1 \leq k \leq s \text{. If } p \text{ is the}$$

smallest prime satisfying $(p-s)/2 \geq s$ , or $r_k = \{e^k\}$

$(1 \leq k \leq s)$ , then $r$ is a good point. $\{a\}$ denotes the 
decimals of $a$.

In the $n$ offspring given birth by the crossover, the 
kth chromosome

$C_k = (e_{1_k}^k, e_{2_k}^k, \ldots, e_{s_k}^k)$

where $e_{m_k}^k = \left\{ \begin{array}{ll}
    a_{m}^k, & m \not\in H \\
    [r_{ij}^t \times k], & m \in H
\end{array} \right.$ 

$1 \leq k \leq n, 1 \leq m \leq L$ ,

$1 \leq j \leq s$ .And if the decimals of $a < 0.5$ , \([a] = 0$, otherwise \([a] = 1$.

In this way, $n$ offspring are generated in this "family". We take the one with the largest fitness as the crossover offspring. The above-mentioned operation is known as the good-point set crossover operation\[^{[28]}\].

3) Adaptive Operator

The selections of crossover probability $p_c$ and mutation probability $p_m$ have direct impact on the convergence of the algorithm\[^{[29]}\]. With a larger $p_c$, a new individual will be generated faster, but the possibility of destruction of the genetic pattern will also be greater; if $p_c$ is too small, the search process will be slow even stagnant. As for the mutation probability $p_m$, if it is too small, new individual structures will not come out; if it is too large, GA then becomes a pure random search algorithm. For different problems, repeated experiments are required to determine crossover probability $p_c$ and mutation probability $p_m$, which is a cumbersome task. Besides, it is difficult to find a best value that applies to every problem. So in the operation of GA, making amendments on the probabilities based on real-time feedback is an effective means to improve the performance of the algorithm.

When the individual fitness tend to be the same or toward the partial optimization, we can increase $p_c$ and $p_m$, and when individual fitness diverse, we can decrease $p_c$ and $p_m$. Better individuals whose fitness are above the average should be given smaller $p_c$ and $p_m$, protecting them to the next generation, while the others be given relatively larger $p_c$ and $p_m$. Besides, to avoid local optimal solutions at an early stage, the crossover probability and mutation probability of best-fitted individual should be increased respectively to $p_{c2}$ and $p_{m2}$ , correspondingly making a increase in the probabilities of the better individuals. Hence they will not stay in stagnation, but help a faster approach to the global optimization.The commonly used adaptive operators are as follows\[^{[30,31]}\].

The crossover probability can be expressed as:

$$p_c = \left\{ \begin{array}{ll}
    k_1(f_{max} - f)/(f_{max} - f_{arg}), & f \geq f_{arg} \\
    k_2, & f < f_{arg}
\end{array} \right. \quad (3)$$

The mutation probability can be expressed as:

$$p_m = \left\{ \begin{array}{ll}
    k_4, & f \geq f_{arg} \\
    k_3 \exp[-k_3(f - f_{arg})], & f < f_{arg}
\end{array} \right. \quad (5)$$

And $k_1, k_2, k_3, k_4$ : Integers no larger than 1.0

$f_{max}$ : The largest fitness value in the population

$\bar{f}$ : The average fitness value of each generation

$f$ : The fitness value of the mutating individuals

Adaptive approach can provide the best $p_c$ and $p_m$. So the adaptive GA guarantees the convergence of the algorithm as well as a diversity of the population.

4) The Determination of Space Compression Factor

Multi-population algorithm firstly generates $M$ initial populations whose search spaces are the same and genetic operations are implemented independently on each population according to the constraints of designed variable sizes. As there is a certain randomness of genetic evolution, the evolitional results of the $M$ groups are varied, but they can reflect the information which will help determine the best solution. With the processing of evolution, the design will be gradually approaching the optimal solution, that is, the optimal solution will gradually clear from the initial uncertainty in the design space, and search space will also be gradually reduced and finally close to zero (or a given accuracy), making the design tend to fixed-point to achieve optimization.
Set the initial search space as $D_0[\alpha_0, \beta_0]$, and the space compression factor of each population is $R_j, j = 1, 2, \cdots, M$, where $M$ is the number of population. After all $M$ populations go through $K$ generations of evolution respectively, the search space will change to:

$$D_j(K + 1) = R_jD_j(K)$$ (7)

Go on with the genetic iteration in the compressed space until convergence. To define the space compression factor, we construct the following information entropy optimization model:

$$\begin{align*}
\min & = \sum_{j=1}^{M} p_j F(x) \\
\min H &= -\sum_{j=1}^{M} p_j \ln p_j & (8) \\
\text{s.t} & \sum_{j=1}^{M} p_j = 1, 0 \leq p_j \leq 1 
\end{align*}$$

$p_j, j = 1, 2, \cdots, M$ is the probability the optimal solution falls in population $j$, $F(x)$ is the objective function. When the optimal solution falls in population $j$, $
\sum_{j=1}^{M} p_j F^*(x^*) = F^*(x^*)$. The information entropy $H$ constantly optimizes the uncertainty of the optimal solution during the evolution. At the beginning, the solution is totally unknown, so $p_j = 1/M, (j = 1, 2, \cdots, M)$, the entropy get maximum value. With the processing of optimization, the uncertainty of optimal solution is reducing, and $p_j$ and $H$ will change accordingly. When the optimal solution is approached, the uncertainty reduces to zero, that is, $\min H = 0$.

Formula (8) is a multi-objective optimization problem. We introduce this model because the explicit solution of $p_j$ can be easily approached in it, thus the space compression factor can be found.

$$R_j = 1 - p_j$$ (9)

Obviously, the best population has the largest space compression. To solve $p_j$, we use the weighted coefficient method of the multi-objective optimization to rewrite Formula (8) to a single-objective optimization problem.

$$\begin{align*}
\min & = -(1-\lambda)\sum_{j=1}^{M} p_j F(x) - \lambda\sum_{j=1}^{M} p_j \ln p_j \\
\text{s.t} & \sum_{j=1}^{M} p_j = 1, 0 \leq p_j \leq 1 
\end{align*}$$

Where $\lambda$ and $1-\lambda$ are the weighted coefficient. So the Lagrangian merit function of formula 17 is

$$L(x, \lambda, \mu) = -(1-\lambda)\sum_{j=1}^{M} p_j F(x) - \lambda\sum_{j=1}^{M} p_j \ln p_j + \mu\sum_{j=1}^{M} p_j - 1$$

$$\lambda \in (0, 1)$$ (11)

$\mu$ is the Lagrangian multiplier, the objective value of the best individual in $j$ populations. We can then simply get:

$$p_j = \exp[\eta F_j(x)]/\sum_{j=1}^{M} \exp[\eta F_j(x)]$$ (12)

Where $\eta = (\lambda - 1)/\lambda$.

C. The Realization of Multi-group Parallel Genetic Algorithm

1) Implementation steps

Step1. Initialization: Use the good-point set approach to generate $M$ initial populations in initial space $D_0(0)$. The size of each population is $N$, and the generation counter is set $K = 0$.

Step2. For each sub-population, implement independent genetic operations to retain the best, and get the best fitness function of all sub-populations and the best individual as well. Record the results of the individual and their corresponding fitness, and then get into the next step.

Step3. Calculate the probability of the optimal solution falling in each population $p_j$, and get the space compression factor $R_j$. From formula 14 we can calculate the compressed space of all populations $D_j(K+1)$, and correspondingly amend the upper and lower limits.

$$a_j(K + 1) = \max \{X_j(K) - [D_j(K+1)/2], a_j(0)\}$$ (13)

$$b_j(K + 1) = \min \{X_j(K) + [D_j(K+1)/2], b_j(0)\}$$ (14)

Where $X_j(K)$ denotes variable $i$ of the best individual in population $j$ in generation $K$.

Step4. Go on searching in the compressed space $D_j(K+1)$ of all populations: calculating the fitness function, implementing the selection, good-point set crossover and mutation operations, retaining the best and recording the results of the individual and their corresponding fitness.

Step5. Repeat step 3-4 until $D_j(K) \leq \varepsilon$ is satisfied. $\varepsilon$ is a given small decimal. Then, we can compare the best fitness values of all populations, and get the optimal value and individual.

To sum up, we use the space compression accuracy as a criterion to judge the convergence of the algorithm. When the space is compressed to the given accuracy, the result of the evolution is optimal, so that the algorithm convergence can be effectively controlled. However, it should be noted that the
optimal solution here is just the best numerical solution the algorithm can find, which may have a certain degree of error with the theoretic optimal solution due to the given restrictions on calculation accuracy.

2) The Parallel Genetic Algorithm Design

Firstly, search in the initial space for \( m \) times, and \( m \) initial sub-populations are generated, uniformly distributed in the solution space and the size of each is \( n \). Then, genetic operations are implemented independently for several generations in each sub-population in the way designed in this paper. Through information exchanges among sub-populations, the points would be concentrated on the most promising region, thus the search space of each sub-population would become smaller. As there is more than one population and the compression speed of each population differs, the optimal solution will be always included in the search space. In each sub-population we can find one or more local extreme points. Such an algorithm has high speedup ratio and efficiency. The schematic diagram of the algorithm operation is in figure 1.

![Figure 1. The Flow Chart of IMPGA-GPS](image)

III. INSTANCE SIMULATION

Instance 1:

Maximize

\[
 f(x_1, x_2) = -0.5 + \frac{\sin^2 \sqrt{x_1^2 + x_2^2} - 0.5}{[1 + 0.001(x_1^2 + x_2^2)]^2}
\]

s.t \(-100 \leq x_1, x_2 \leq 100\).

The function is multi-peak, whose global minimum is \( f(0,0) = -1 \) at \((0,0)\). We solve the problem through the basic GA and our algorithm respectively, and set the accuracy to four decimals. Set the parameters are as follows:

Basic GA: Pop-size=80; Gen-max=100; Crossover probability \( p_c = 0.6 \); Mutation probability \( p_m = 0.002 \). And the iterative result is as Fig.2
Our algorithm: Initial sub-population=4; Pop-size=80; Gen-max=100; Crossover probability \( p_c = 0.6 \); Mutation probability \( p_m = 0.002 \); , \( \alpha = 0.5 \), \( \epsilon = 0.001 \). And the iterative result is as Fig.3.

As can be seen from the figures, the 4 population only go through 5 generations before getting to the global extreme point in our algorithm.

**Instance 2:**
\[
f_1(x_1, x_2) = x_1^2 + 2x_2^2 - 0.4 \cos(3\pi x_1) - 0.6 \cos(4\pi x_2) \\
0 < x_1, x_2 < 100
\]

The global minimum point lies in \((0,0)\), and the minimum is \( f_2(0,0) = -1 \), around which there are numerous sub-minimum points. Due to its strong oscillation and as the minimum point is surrounded by sub-minimum points, it’s hard to find the global minimum point through general algorithm.

We solve the problem through the basic GA and our algorithm respectively and set the parameters are as follows:

**Basic GA:** Pop-size=80; Gen-max=100; Crossover probability \( p_c = 0.6 \); Mutation probability \( p_m = 0.001 \). The objective function value is -0.8235, as Fig.4 shows.

**Our algorithm:** Pop-size=80; Gen-max=100; Crossover probability \( p_c = 0.6 \); Mutation probability \( p_m = 0.001 \); Initial sub-population=4; \( \alpha = 0.3, \epsilon = 0.001 \). The objective function value is -1, as Fig.5 shows.

Moreover, for instance 2, we implement five items simulation tests on the convergence of two algorithms, and the results are as Table I.
Table 1. Five tems simulation tests results and comparison

<table>
<thead>
<tr>
<th>No</th>
<th>Optimal Solution</th>
<th>Generation</th>
<th>Average Convergence Time (s)</th>
<th>Optimal Solution</th>
<th>Generation</th>
<th>Average Convergence Time (s)</th>
</tr>
</thead>
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<tr>
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<td>1.3120</td>
<td>-0.9998</td>
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<td>1.2810</td>
<td>-0.9999</td>
<td>4</td>
<td>2.5665</td>
</tr>
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<td>14</td>
<td>1.3280</td>
<td>-1</td>
<td>5</td>
<td>2.6440</td>
</tr>
<tr>
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<td>4</td>
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</tr>
<tr>
<td>Average</td>
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<td>1.3310</td>
<td>-0.9999</td>
<td>4.4</td>
<td>2.28145</td>
</tr>
</tbody>
</table>

From Table 1, we can find our algorithm provides a much better accuracy while a remarkably decreasing convergence generation. And its average convergence time differs little from BGA.

Still for instance 2, we use our algorithm and set the number of initial sub-populations to be 4, 5, 6, 8 respectively, the pop-size to be 100, and \( \alpha = 0.3, \varepsilon = 0.001 \), then we can get results as shown in Table 2.

Table 2. Iterative result of different sub-populations

<table>
<thead>
<tr>
<th>number of sub-populations</th>
<th>Optimal Solution</th>
<th>Generation</th>
<th>Average Convergence Time (s)</th>
</tr>
</thead>
<tbody>
<tr>
<td>4</td>
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<td>2.0330</td>
</tr>
<tr>
<td>5</td>
<td>-0.9999</td>
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<td>2.8370</td>
</tr>
<tr>
<td>6</td>
<td>-1</td>
<td>5</td>
<td>3.1440</td>
</tr>
<tr>
<td>8</td>
<td>-1</td>
<td>6</td>
<td>3.9650</td>
</tr>
<tr>
<td>Average</td>
<td>-0.99993</td>
<td>5</td>
<td>2.99475</td>
</tr>
</tbody>
</table>

From Table 2, we can find the accuracy of the solution improves along with the number of sub-populations, while the generations and average convergence time increase correspondingly. If the computer configuration is relatively high, the algorithm has more advantages.

IV. CONCLUSIONS

There are premature convergence, low accuracy, and other shortcomings in the practical application of Basic GA (BGA), making it difficult to find the optimal solution or satisfactory solution in the complex optimization situation with a lot of variables. However, the improved multi-group parallel and adaptive genetic algorithm we propose has a strong ability to jump out of the local extreme. The stimulation shows that this algorithm can effectively prevent the early convergence, and to a large extent improve the accuracy of solution, which is suitable for large-scale, high-precision optimization problems.

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