An Enhanced Genetic Algorithm Using Directional-Based Crossover and Normal Mutation for Global Optimization Problems

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Abstract  Global optimization has been employed in many practical modeling processes. Using gradient methods to solve optimization problems may be computationally inefficient and time-consuming, particularly when convexity or differentiability is not guaranteed. On the other hand, nature-inspired techniques offer an effective gradient-free approach for solving complex, non-convex, or non-differentiable problems. Genetic algorithms are one of the most effective and widely used nature-inspired techniques. However, canonical genetic algorithms do not always guarantee convergence to the optimum point owing to the stochastic nature of the genetic operators, and typically require more work to ensure convergence and increase performance. Improving the genetic operators remains an open issue and usually involves a trade-off between the speed of convergence and searchability. In this study, we propose an enhanced genetic algorithm that relies on directional-based crossover and normal mutation operators to increase the speed of convergence while preserving searchability. The proposed algorithm is evaluated using a set of 40 typical benchmark functions in two dimensions. In addition, to examine its performance at higher dimensions, 16 functions from the test set were tested at 10 and 100 dimensions. The evaluation results of the proposed algorithm are compared to the outcomes of three modern optimization algorithms, namely (Whale optimization algorithm, Teacher-Learner based algorithm, and Covariance matrix adaptation evolution strategy). The results revealed that the proposed algorithm outperformed the conventional algorithms at lower dimensions in all test functions and showed a relatively better performance than the other algorithms at higher dimensions.

Keywords  Directional-based crossover, Global Optimization, Genetic Algorithm, Normal Mutation

AMS 2010 subject classifications 90C26, 65K10

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1. Introduction

Modeling and analysis of many practical applications (e.g., finance, health, and engineering) involve an optimization process to search for the best design parameters that optimize the measure of model efficiency (e.g., losses, and gains) [1, 2, 3, 4], many of which are described by the global optimization problem:

\[ \min f(X), \ \text{s.t.} \ X \in \Omega \]

(1)

Where \( X = \{x_1, x_2, ..., x_i\} \in \Omega \) is a design vector, the search space \( \Omega \subset \mathbb{R}^d \) is a hyper-interval defined by the upper and lower bounds of each dimension and \( f : \mathbb{R}^d \rightarrow \mathbb{R} \) is a real-valued objective function. Although gradient-based methods [5, 6] offer a direct and efficient way to optimize (1), they require further advanced computations when convexity or differentiability of \( f(.) \) is not guaranteed [7, 8], in addition to the increasing complexity emerging when the search space gets larger [9, 10].

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1.1. Metaheuristic optimization

Recently, metaheuristic optimization techniques have proven to be efficient in many applications especially with imperfect information about the objective function, in addition to their preferable properties (e.g., gradient-free and easy implementation) [11, 12]. Various types of metaheuristic algorithms have been introduced through the past few decades which can be categorized according to their search strategy in nine groups (physics, social, music, swarm, chemistry, biology, sports, math and hybrid-based) [13, 14, 15]. Metaheuristic algorithms are also classified according to the number of candidate solutions involved in the search process. Some techniques are called “population-based” which, in contrast to “single-point based” techniques, conduct optimization using a set of points/individuals called ”population” sampled from within the search space. A major benefit of having many points distributed over the search space is that most of the features of the objective function are captured and processed during iterations, leading to powerful exploration ability [12].

Genetic Algorithm GA is an important stochastic population-based technique inspired by natural evolution and was first introduced by Holland [16]. GAs have proven to be highly efficient in many practical applications such as resource allocation [17, 18], deep learning and neural networks [19, 20], and control systems [21, 22]. Moreover, GAs are superior to other local search algorithms in effectively searching large spaces effectively [23]. The GA iteratively applies stochastic evolution processes (selection-crossover-mutation), known as genetic operators, to a population of individuals, which are evaluated by a fitness function. The fitter individuals in each population have a higher chance of passing their characteristics to the next population [24], and the iterations end when a stopping condition is met. Unfortunately, because genetic operators are stochastic, the search process would be totally random if they were left to operate without any control, resulting in a slower convergence speed (or perhaps no convergence at all). Therefore, a control scheme should guide genetic operators to create convergence pressure and improve population characteristics. However, if the control scheme is very restrictive, the search process converges quickly before reaching the global optimum, and the algorithm falls into a local optimum. This case is called premature convergence [25, 26].

1.2. Genetic Algorithm.

The searching process of metaheuristic optimization algorithms comprises, in general, two main tools (local and global) search tools. The local search tool is responsible for exploiting neighboring area of the solution candidates for better solutions, whereas the global search tool explores the search space for new promising areas. The evolution process of GA applies local and global search through three steps (selection, crossover and mutation). Researchers sometimes utilize an extra step called a replacement operator, which is periodically applied to renew stagnant population and help the search process avoid getting trapped in a local optimum [27, 28].

Formally, let $P(t)$ be the population at iteration $t$. To create the next population $P(t + 1)$, GA applies the following steps:

1. Selection is the process of choosing individuals from the current population $P(t)$ to form parents that participate in the crossover. In the canonical GA, for the population of $N$ individuals, a selection operator will form $N$ pairs of parents that will produce $n$ children of the next population. However, there may be variations in the numbers of parents, children, or both.
2. 2) Crossover is the second genetic operator in which paired parents recombine their characteristics to form new children. Note that in canonical GA, not all mating must be reproduced by crossover; there is a probability $0 \leq P_x \leq 1$ for a crossover to occur.
3. 3) Mutation is the third operator, which is very important because, if new individuals are generated by crossover only, many features that have not been represented in the initial population might never appear, and there is a high chance that the algorithm loses diversity. Therefore, mutation performs spontaneous changes in individuals after crossover to add more genetic diversity to the algorithm by enforcing mutated individuals to be in new areas of the search space. In addition, there is a probability of $0 \leq P_m \leq 1$ for an individual to undergo a mutation.
4. Although this is not one of the canonical GA operators, many researchers have used this step because the diversity introduced by crossover and mutation operators may not be sufficient to enhance the global
search ability, especially in the case of multi-extrema functions. Hence, the replacement operator is applied periodically to enrich the genetic diversity by preserving the best $k$ individuals and randomly regenerating the remaining $N - k$ [28].

Finally, a new population $P(t + 1)$ with better characteristics is formed. This process continues until a certain stopping condition is satisfied.

1.3. A brief review of existing methods

Several studies have proposed modifications to genetic operators to improve solution quality, accelerate convergence speed, or both. For instance, the authors in [29] proposed grouping selection GS to improve the selection process because traditional selection methods are computationally insufficient [30, 31]. However, after several iterations, the proposed algorithm suffers from a loss of genetic diversity. Other works have introduced a uniform crossover UX, a directed crossover DX operator, and arithmetic, average, and bound crossover [32, 33]. However, these operators are computationally expensive and have a slower convergence speed. Similarly, several studies adopted improved mutation operators. For example, the authors in [34, 35, 36] proposed non-uniform, polynomial, group, and random transfer-vector-based mutation operators. Another perspective of research suggested to combine multiple crossover operators to strengthen local search ability, see for instance [37]. Although these efforts have increased the performance of the algorithm, they are either problem-specific and cannot be generalized or computationally expensive [27].

Based on the survey, improving genetic operators entails a trade-off between the search capability, computational cost, and convergence speed.

1.4. Contributions.

In this paper, we propose an enhanced genetic algorithm EGA based on directional-based crossover and normal mutation to address global optimization problems that can compete with current techniques in low and high dimensions, with lower computation complexity and relatively faster convergence time.

1.5. Organization.

The rest of this paper is organized as follows: Section 2 explains the procedure of the proposed enhanced algorithm, with a detailed explanation of each step. Section 3 provides the experimental results and comparative performance profile analysis of the proposed algorithm tested on 40 standard optimization benchmark functions in two dimensions, 16 of the 40 tested in 10 and 100 dimensions and compared with three selected population-based optimization techniques (Whale optimization algorithm WOA [38], Teaching-Learning based algorithm TLBO [39], and Covariance Matrix Adaptation evolution strategy CMA-ES [40]). Section 4 presents the conclusions of this study.


The motivation behind this work is to enhance the algorithm’s local and global search abilities while maintaining computation efforts at an acceptable level. To achieve this, the proposed algorithm mainly utilizes the updated directional-based crossover UDX and the updated normal mutation UNM. These operators are improved versions of those introduced in [27], which showed promising performance; however, the search process slows as the dimensions increase. The adopted GS method forces all individuals to participate in the crossover, so that all features captured in the initial population are processed during iterations. The updated operators allow for the most recent fittest individuals attained so far to guide the search process. Finally, a replacement step is periodically applied to preserve the best individuals and reinitialize the remaining individuals to prevent population from stagnating. The introduced mutation and replacement steps are implemented to increase genetic diversity and enhance global search ability while maintaining the speed of convergence achieved so far. Algorithm 1 presents the steps of the proposed EGA, followed by a detailed description of each step.
Algorithm 1 EGA steps

Require: \((N, d, f(X))\)  \(\triangleright\) input parameters
step 1: \(P(0) \leftarrow \text{initial population } N, d\)
while stopping criteria = false do
  step 2: \((p_a(t), p_b(t)) \leftarrow \text{group selection } P(t)\)
  step 3: \(P(t) \leftarrow \text{UDX}(p_a(t), p_b(t))\)
  step 4: \(P(t) \leftarrow \text{UNM}(P(t))\)
  step 5: \(p_r(t) \leftarrow \text{replacement}\)
  \(P(t + 1) \leftarrow \text{new population}\)
end while
return \(X^*, f^*\)  \(\triangleright\) \(X^*\) is the fittest individual in the final population

- **step 1. Initial Population:** Uniform sampling is the most common method for constructing the initial population, and this step can be improved using space-filling sampling techniques such as Latin hypercube sampling [41], quasi-random sequence [42], or stratified sampling [43]. However, these techniques add computational burden or may be infeasible at higher dimensions. Thus, the initial population in this study is generated uniformly from within the hyper-interval \([x^1, x^u]^n\), where \(x^1\) and \(x^u\) are the lower and upper bounds of the decision variable \(x_i\), respectively.

- **step 2. Selection operator:** The core concept of the proposed algorithm is to guide the search process by fitter individuals in each population. Therefore, sorting and defining fitter and worse individuals are reasonable.

The adopted GS takes a population \(P(t) = \{X_1, X_2, \ldots, X_N\}\), and sorts it in ascending order according to the fitness values so that the first individual in the sorted population is the fittest. That is,

\[
\hat{P}(t) = \{X^1, X^2, \ldots, X^N\}
\]  \(2\)

Where \(f(X^1) \leq f(X^2) \leq \ldots \leq f(X^N)\). Then, \(\hat{P}(t)\) is divided into two groups \(p_a(t)\) and \(p_b(t)\), each of size \(\frac{N}{2}\), i.e.

\[
p_a(t) = \{X^1, \ldots, X^{N/2}\}, \quad p_b(t) = \{X^{N/2+1}, \ldots, X^N\}
\]  \(3\)

so that set \(p_a(t)\) has fitter individuals than set \(p_b(t)\). Pairing is performed between an individual from \(p_b(t)\) and one from \(p_a(t)\) to produce an offspring individual. Note that (3) enforces all individuals in the crossover process, that is, the crossover probability \(Pr_c = 1\). Moreover, the selection scheme is directly based on the fitness value without the need to calculate it repeatedly. This simplicity makes it preferable in terms of computational expense.

- **step 3. Crossover operator:** In this study, we propose a UDX operator that continuously updates the position of the fittest individual. Note that all paired individuals outputting from (3) have one individual from the fitter set \(p_a(t)\) and the other from the set \(p_b(t)\). Let \((X_a(t), X_b(t))\) be paired parents and \(X^1(t), X^2(t)\) be the fittest two individuals at iteration \(t\); then, \(\vec{v} = X_a(t) - X_b(t)\) is supposed to point at the descent direction. Thus, UDX produces two offspring individuals from each pair as follows:

\[
\begin{align*}
\hat{X}_{i}(t + 1) & = X_a(t) + r_1 \ast \vec{v} + \underbrace{r_2 \ast \vec{v}^i}_{\text{re-correction}}, \\
\hat{X}_{i+1}(t + 1) & = X_b(t) + r_1 \ast \vec{v} + \underbrace{r_2 \ast \vec{v}^i}_{\text{re-correction}}
\end{align*}
\]  \(4a\) \(4b\)

where \(\vec{v}^i = X^{1:\text{recent}}(t) - X_a(t)\) and \(\vec{v}^s = X^{2:\text{recent}}(t) - X_b(t)\) are re-correction directions and \(r_1, r_2 \sim U(0, 1)\). The first parts in (4a) and (4b) guide the search toward the region of the better individual \(X_a(t)\), and the second part has a re-correction effect on the two fittest individuals \(X^{1:\text{recent}}(t)\) and \(X^{2:\text{recent}}(t)\).

The name (recent) refers to the most recent fittest individual attained so far if any paired parents succeeded in creating an individual better than the fittest two in the current population. This step continuously updates the direction of the re-correction effect during the process, thereby accelerating the convergence speed. The reason for using the two fittest individuals in the re-correction part is to add diversity to the local search operator.

The crossover operation produces $N$ individuals, which are compared with the original $N$ parents and the best $N$ of both constitutes offspring population. Using this scheme, there is a high chance of generating a direction that points toward the fittest individual or a similar direction, which increases the probability of creating better individuals and improves searchability and convergence speed. Fig. 1 illustrates a population of size 10 undergoing a crossover operation in the search space of the Michalewicz function. It shows 20 possible directions (two for each pair of parents), which will, in turn, spot the locations of the children. Increasing $N$ increases the direction possibilities, thereby enriching the search diversity.

- **step 4. Mutation operator:** This operator is applied directly after crossover. Note that although UDX maintains a balance between convergence speed and diversity, there is no guarantee that this balance can last during all iterations. Additionally, a completely random mutation operator decreases the convergence speed of the algorithm. Therefore, the UNM operator was proposed to control the mutation process. Let $X^m = (x^m_1, x^m_2, ..., x^m_d)$ be the individual to be mutated at population $t$, and $X^{1:\text{recent}}$ be the most recent fittest individual in the current population $P(t)$ as before. A mutated individual $\hat{X}$ is generated using (5a). Mutated individuals have a high chance of being in the vicinity of the original individual and will not decrease the speed of convergence.

$$\hat{x}_i \sim N(\mu_i, \sigma_i), \ i = 1, 2, ..., d$$

$$\mu_i = x^m_i$$

$$\sigma = \frac{|x^{1:\text{recent}}_i - x^{N/2+1}_i|}{6}$$

According to the adaptive nature of equation (5c), in the beginning, there is a large difference between the fittest individual and all others in the current population. Consequently, $\sigma$ is large, and the mutated individuals are spread over the search space, enhancing global search-ability. However, after several iterations, this difference decreases, and $\sigma$ decreases as well. Thus, the mutated individuals spread closer to the fittest element, enhancing the local search-ability.

- **step 5. Replacement:** According to the mutation operator presented in subsequent populations, all individuals will continue to follow the fittest one in the population. All other individuals become closer as the standard deviation of UNM becomes smaller, eventually causing the search process to stagnate. This requires additional action to help the algorithm to escape from this situation. Therefore, a replacement operation
Table 1. Parameters settings of the EGA

<table>
<thead>
<tr>
<th>$Pr_x$</th>
<th>$Pr_m$</th>
<th>$N$</th>
<th>$t_r$</th>
<th>$k$</th>
</tr>
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<td>1</td>
<td>0.5</td>
<td>60</td>
<td>100</td>
<td>200</td>
</tr>
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</table>

Table 2. Maximum FEs for each dimension

<table>
<thead>
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<th>$d$</th>
<th>max FEs 1</th>
<th>max FEs 2</th>
<th>max FEs 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>1000</td>
<td>5000</td>
<td>10000</td>
</tr>
<tr>
<td>10</td>
<td>5000</td>
<td>10000</td>
<td>15000</td>
</tr>
<tr>
<td>100</td>
<td>10000</td>
<td>15000</td>
<td>20000</td>
</tr>
</tbody>
</table>

is necessary. Generally, replacement is applied periodically to every $t_r$ population by preserving the best $k$ individuals and randomly regenerating the remaining $N - k$ across the entire search space. According to the results in [44], the performance of the algorithm increases as the change in population size increases. This step mostly simulates the idea of variable population size, but it also directly affects the population diversity.

3. Experimental Results.

3.1. Algorithm Setup.

In the traditional GA, not all individuals participate in the crossover operation, and there is a chance $Pr_x$, typically $(0.5 \sim 0.9)$, for an individual to undergo a crossover operation. However, one major disadvantage of such setting is that some promising individuals not selected from the initial population may not appear at all as the evolution process continues. Therefore, the adopted selection operator is beneficial because all individuals participate in the crossover operation, that is, the crossover probability $Pr_x = 1$, allowing the exploitation of the characteristics of the search space as much as possible. Conversely, not all individuals suffer mutation, and there is a chance $Pr_m$ for each individual to undergo UNM. In our experiments, we set $Pr_m$ to 0.5. The population size is set to 60, 100, and 200 for dimensions 2, 10, and 100, respectively. The number of elitist individuals to be preserved in each iteration is $N/4$, and the replacement operation is performed every $5^{th}$ population by replacing $3N/4$ individuals. Table 1 summarizes the parameter settings of the algorithm.

3.2. Experiment Setup.

To examine the effectiveness of the proposed algorithm, we tested and compared it with three modern optimization techniques (WOA, TLBO, and CMA-ES). These algorithms were tested on a set of 40 standard benchmark functions at $d = 2$ and 16 functions from the set at $d = 10$ and $d = 100$. The initial popualtion must be the same for all algorithms, so the random number population seed is set to (5) in each run. The steps of the experiment are as follows:

1. Run the algorithms on the 40 test functions at $d = 2$ and 16 test functions at $d = 10, d = 100$ (Table 3).
2. Replicate each algorithm 30 times on each function.
3. Terminate the iterations of each algorithm after the maximum number of function evaluations FEs specified in Table 2 is reached.
4. Keep track of the best objective values during iterations.
5. Perform performance profile analysis.

To evaluate our experiment, we used two performance analysis methods: the modified performance profile method (MPPM) [45], which measures how well the algorithms can estimate the global optimum compared to one another for different levels of the FEs budget, and the stochastic performance profile method (PPMS) described in [46], which compares algorithms in terms of sample means and sample variances.
Conversely, in PPMS, the parameter $T$ is used, but the original raw data in 6 is replaced by two stochastic measures, the average $\mu_{p,s}$ and variance $\sigma^2_{p,s}$, of the best function values during a given level of FEs of a given problem $p$ by a given algorithm $s$. These two measures consider the stochastic nature of the algorithms by introducing a comparison based on the general confidence bounds.

### 3.3. Performance Analysis.

Both the MPPM and PPMS methods are extensions of the performance profile method (PPM) in [47]. The original PPM compares different derivative-free optimization algorithms by generating CDFs to display raw data from experiments in terms of the computational cost parameter $t_{p,s}$, which is the number of FEs required for algorithm $s$ on problem $p$ to find a solution $x$ that meets the convergence condition:

$$
\frac{f(x_0) - f(x)}{f(x_0) - f(x_L)} \geq 1 - \epsilon
$$

where $\epsilon > 0$ is a given error (typically $10^{-i}$, $i = 1, 2, 3, \ldots$). $f(x_0)$ is the best function value in the initial population (it must be the same for all compared algorithms), and $f(x_L)$ is the best function value found by any algorithm within a given FEs budget. However, in MPPM, $t_{p,s}$ is replaced by a function value improvement measure scaled to the best function value $f^*$ found by algorithm $s$ on problem $p$; that is:

$$
m_{p,s} = \frac{\hat{f}_{p,s} - f^*}{f_w - f^*}
$$

where $\hat{f}$ is the average function value obtained during a given level of FEs over the 30 replications, $f_w$ is the worst function value found by any algorithm for problem $p$.

Conversely, in PPMS, the parameter $t_{p,s}$ is used, but the original raw data in 6 is replaced by two stochastic measures, the average $\mu_{p,s}$ and variance $\sigma^2_{p,s}$, of the best function values during a given level of FEs of a given problem $p$ by a given algorithm $s$. These two measures consider the stochastic nature of the algorithms by introducing a comparison based on the general confidence bounds.

### 3.3.1. Modified Performance Profile Method

Each curve in the plots is non-decreasing and indicates the performance of each algorithm. The vertical axis $\rho_s(T)$ represents the percentage of all problems for which algorithm $s$ has a performance ratio within a factor $T$. That is, for $T = 1$, $\rho_s(1)$ is the probability that an algorithm will first find the best solution on average. The final value of any curve depends on how well a particular algorithm performs on average.

Table 3. Test functions and dimensions

<table>
<thead>
<tr>
<th>no.</th>
<th>function name</th>
<th>dimension tested</th>
<th>no.</th>
<th>function name</th>
<th>dimension tested</th>
</tr>
</thead>
<tbody>
<tr>
<td>$f_1(x)$</td>
<td>Modified Ackley’s Function</td>
<td>2,10,100</td>
<td>$f_{21}(x)$</td>
<td>Holder Table Function</td>
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<tr>
<td>$f_2(x)$</td>
<td>Ackley’s Function</td>
<td>2,10,100</td>
<td>$f_{22}(x)$</td>
<td>Levy function</td>
<td>2,10,100</td>
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<tr>
<td>$f_3(x)$</td>
<td>Adjiman Function</td>
<td>2</td>
<td>$f_{23}(x)$</td>
<td>Levy N.13 Function</td>
<td>2</td>
</tr>
<tr>
<td>$f_4(x)$</td>
<td>Alpine N.1 Function</td>
<td>2,10,100</td>
<td>$f_{24}(x)$</td>
<td>Matyas Function</td>
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<tr>
<td>$f_5(x)$</td>
<td>Alpine N.2 Function</td>
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<td>Michalewicz Function</td>
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<td>$f_{26}(x)$</td>
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<td>$f_{27}(x)$</td>
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<td>$f_{28}(x)$</td>
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estimates the best solution among other algorithms. In other words, if the value of a curve is less than one at the last value of $T$, it indicates that on some problems, the corresponding algorithm became stuck in some local minima, and its best solutions were dominated by the best solutions found by other algorithms at multiples of $T$ on the horizontal axis. Fig. 2 shows the performance profile of the algorithms at dimension $d = 2$ with three maximum FEs levels. When the maximum FEs was 1000, as shown in Fig. 2.(a), the EGA and CMA outperformed all other
Figure 3. Performance Profile on Average of Best Objective Function Values for $d=10$ with (a) max Fe 5000. (b) max Fe 10000. (c) max Fe 15000.

algorithms over the entire $T$ range. When $T = 1$, EGA and CMA found the best solutions in approximately 50% of the total test functions, whereas at $T = 50$, EGA found the best solution in over 80% of the total test functions and was approximately 4% better than CMA. At higher levels of maximum FEs, fig.2.(b) and 2.(c), WOA showed the worst performance among the algorithms, whereas EGA, CMA, and TLBO showed competitive performances against each other at almost all values of $T$. 
In Fig. 3, the performances of all algorithms for dimension $d = 10$ are relatively close to each other when the maximum FEs was 5000. However, the probability $\rho_s(1)$ of finding the best solution in the first place is twice that of WOA and TLBO, and EGA outperformed the other algorithms for $T > 15$. This situation is not the same when the level of FEs was 10000 and 15000. Fig. 3 shows that the probability of finding the best solution in the first place
of the EGA degrades as the maximum FEs increases. However, the EGA succeeded in finding the best solution at approximately 70% and 60% when FEs were 10000 and 15000, respectively.

In higher dimensions, as shown in Fig. 4, the WOA dominates all other algorithms at the three levels of maximum FEs. The proposed EGA came in second place at the three levels with probability $p_s(1)$ of approximately 30% − 40% and succeeded in estimating the best solution for approximately 70% − 80% of test functions for $T > 10$, competing with TLBO, whereas CMA showed the worst performance among them.

The above discussion implies that the EGA performs well at low and moderate dimensions and has very promising performance at higher dimensions, particularly in applications where the maximum FEs budget is limited to lower values.

![Graphs showing performance profiles for different algorithms](image)

Figure 5. Stochastic Performance Profile for $d=2$. (a) sample means, $\epsilon = 10^{-3}$ (b) confidence bounds, $\epsilon = 10^{-3}$ (c) sample means, $\epsilon = 10^{-5}$ (d) confidence bounds, $\epsilon = 10^{-5}$

### 3.3.2. Stochastic Performance Profile Analysis

For the best function values found by algorithm $s$ on problem $p$ during a given FEs level for a given convergence error of $\epsilon$, CDFs are generated for the sample means $\mu_{p,s}$ and variances $\sigma^2_{p,s}$. In this experiment, the level of the maximum FEs is set to 10000 and the convergence error to $10^{-3}$ and $10^{-5}$. The plot of PPMS for each set of FEs and convergence error consists of two graphs; one is the CDFs for sample means that show the performance curve of each algorithm. The second graph shows the CDFs for the upper confidence bound of the winner algorithm from the first graph against the lower confidence bounds for the other algorithms to show whether there is a significant difference between the algorithms or not.

Fig. 5 shows the profile plot of the sample means and confidence bounds for all algorithms in dimension $d = 2$ for a convergence error $\epsilon = 10^{-3}$ and $10^{-5}$. Clearly, the proposed EGA performs better than the other algorithms, and...
Figure 6. Stochastic Performance Profile for $d=10$. (a) sample means, $\epsilon = 10^{-3}$ (b) confidence bounds, $\epsilon = 10^{-3}$ (c) sample means, $\epsilon = 10^{-5}$ (d) confidence bounds, $\epsilon = 10^{-5}$

the profile plot of the confidence bounds shows that the EGA performance is significantly better than that of the other algorithms. A similar situation is illustrated in Fig.6. For dimension $d = 10$, EGA still performs better than the other algorithms in terms of the average best function values, and its upper confidence bound is better than the lower bounds of the other algorithms.

In Fig.7, the WOA indicates a better performance on the average best function values, which is consistent with the results of the previous section. However, Fig. 7(b) and (d) show that the lower confidence bounds of the EGA are better than the upper bounds of the rest. This result implies that there is no significant difference in the performance between them. Overall, the PPMS analysis results support the conclusion of the previous section; that is, the proposed EGA is much better in lower and moderate dimensions and performs quite well in higher dimensions.

4. Conclusion.

Whereas gradient-based methods show degrading efficiency in solving global optimization problems in cases where convexity or differentiability is not guaranteed, population-based techniques offer an efficient solution in the same situation. Genetic algorithm is a population-based technique inspired by nature and is widely used in global optimization problems owing to its good performance and simple implementation. Because of the stochastic nature of genetic operators, more control should be applied to guide the search process. However, this control
scheme entails a trade-off between the speed of convergence and search diversity. Therefore, to improve the GAs’ performance, we propose an enhanced algorithm that depends on updated-directional-based crossover and updated normal mutation that continuously updates the location of the most recent fittest individual to accelerate the convergence speed without losing search diversity. The proposed algorithm is tested against three selected modern population-based optimization techniques (whale optimization algorithm, Teacher-Learner based optimization and covariance matrix adaptation evolution strategy). The performance profile analysis shows that EGA can outperform other algorithms at low dimensions and has a better performance, on average, at relatively high dimensions. In the future, the proposed EGA could be utilized in practical optimization problems, such as deep learning or control systems, and compared with existing solutions to examine its proficiency.

Appendix A: Matlab code for the algorithm

```matlab
function [best,best_fit] =Ega(objective_function,max_FEs, Vars_upper, Vars_lower)

%% objective_function.. set to one of the test suit functions
%% max_FEs.. maximum function evaluations, set to values according to table
```
%% Vars_upper, Vars_lower..are the upper and lower limits for each variable respectively
% ---- algorithm settings-------
Prm=.. probability of mutation
NP=.. population size
D=.. problem dimension
tr=.. replacement frequency
n=.. number of elitest individuals
%. set to values in table 1

%-- initial population--
pop = Vars_lower + (Vars_upper-Vars_lower)*rand(NP, D);
fit = objective_function(pop);
FEs=0; gen=1;
    for i = 1 : NP
        FEs = FEs + 1;
        if FEs > Max_FEs; break; end
    end
    [fit, index] = sort(fit, 'ascend');
    pop= pop(index,:);
    elite=pop(1:n,:); elite_fit=fit(1:n);
while FEs < Max_FEs
    pop_a=pop(randperm(NP/2),:);
    pop_b=pop(NP/2 +1:end,:);
    new_pop=[]; new_fit=[];
%-- crossover ---
    for i=1:NP/2
        v = pop_a(i,:) - pop_b(i,:);
        v1 = elite(1,:) - pop_a(i,:);
        v2 = elite(2,:) - pop_b(i,:);
        child1 = pop_a(i,:) + rand(1,D).*v + rand(1,D).*v1;
        child2 = pop_b(i,:) + rand(1,D).*v + rand(1,D).*v2;
        [child1, child2] = bound([child1;child2]);
        child_fit = objective_function([child1;child2]);
        FEs=FEs+2;
        if any(child_fit<elite_fit(1,2))
            [update_fit, id] = sort([elite_fit(1,2) child_fit]);
            dummy = [elite(1:2,:);child1;child2];
            update_elite= dummy(id,:);
            elite(1:2,:) = dummy(1:2,:);
        end
        if FEs > Max_FEs; break; end
    end
    new_pop=[new_pop;child1;child2];
    new_fit=[new_fit child_fit];
end
[new_fit, index] = sort(new_fit);
new_pop=sortrows(new_pop, index);

%-- mutation ---
for i=1:NP
if rand < Prm
    C = abs(elite(1,:)-new_pop(NP/2 +1,:));
    mu = new_pop(i,:);
    new_pop(i,:) = mvnrnd(mu,C);
    new_pop(i,:)=bound(new_pop(i,:));
    new_fit(i)=objective_function(new_pop(i,:));
    FEs=FEs+1;
    if FEs > Max_FEs; break; end
    if new_fit(i)<elite_fit(1)
        elite_fit(1)=new_fit(i);
        elite(1,:)=new_pop(i,:);
    end
end
end

%---replacement----
if mod(gen,tr)==0
    replace_pop= Vars_lower + (Vars_upper-Vars_lower).*rand(NP-n,D);
    replace_fit = objective_function(replace_pop);
    FEs=FEs+ NP -n;
    if FEs > Max_FEs; break; end
    new_pop = [elite;replace_pop];
    new_fit = [elite_fit replace_fit];
else
    [new_fit,index]=sort([elite_fit new_fit]);
    new_pop=sortrows([elite;new_pop],index);
    gen=gen+1;
end
pop = new_pop(1:NP,:);
fit = new_fit(1:NP);
end

[best_fit,imin] = min(fit);
best = pop(imin,:);
end

function x = bound(x,pop)
    xl = repmat(Vars_lower, 1, D);
    xu = repmat(Vars_upper,1,D);
    pos = x < xl;
    x(pos)=(pop(pos)+xl(pos))/2;
    pos = x > xu;
    x(pos)=(pop(pos)+xu(pos))/2;
end

REFERENCES


