Convergence Analysis on Immune Optimization Solving CCP Problems

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Abstract This work concentrates on studying the property of convergence of a sample allocation-based immune optimization approach used in solving linear or nonlinear chance-constrained programming (CCP) with general random variables. First, we make some theoretical studies about existence of optimal reliable solutions and give an approximate relation between the true CCP and the sample average approximation problem, depending on some statistic and analysis theory. Second, a bio-inspired immune optimization approach is developed to assume solving CCP problems. Our theoretical analysis shows that such approach, which is capable of being formulated by a non-homogeneous Markov model, is convergent. Experimentally, performance searching curves reveal that the approach can obtain valuable performances including the optimized quality, noisy suppression and convergence.

Keywords Chance-constrained programming · Immune optimization · Sample average approximation · Convergence

1 Introduction

In practical optimization problems, objective functions and constraints are often inevitably perturbed by uncertainty, and hence a search procedure becomes extremely difficult when searching for their solutions [1]. CCP is a kind of

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stochastic programming with at least a chance or probabilistic one. The key of solving it is to study efficient approximation or transformation approaches to handle chance constraints. In comparison with mathematical approaches for CCP, intelligent optimization is a more useful tool because of simplicity and effectiveness, in which stochastic simulation [2] is often used to deal with uncertainties. Even if a wide range of engineering applications [3], CCP is still studied scarcely by intelligent scholars. The main difficulty is that the noisy environment influences seriously the optimized quality and individual's evaluation, and hence it is almost impossible to obtain the theoretical optimum. Fortunately, several methodological achievements (e.g., see [2, 4]) are reported to solve several kinds of general CCP problems, but their theoretical study, e.g., convergence, is still open. We note that Nakama [5] made a series of meaningful contributions to probing into convergence properties of genetic algorithms (GAs) used for solving expected value optimization problems. Chen and He [6] developed a heuristic sequential allocation procedure to identify the best of individuals in noisy environments. Such procedure as an optimal selection scheme can theoretically find a locally optimal solution asymptotically, but is difficult if applied to CCP problems. Up to now, less theoretical work has been reported about CCP using intelligent optimization.

Immune optimization has become increasingly popular and appeared lots of valuable achievements [7]. To our knowledge, in such branch we take a first step to investigate a bio-inspired immune optimization approach for general CCP problems [8], whereas its theoretical foundations keep open. In the present work, we first study an approximate relation between the CCP problem and the approximation problem; we next develop a general optimization mechanism, i.e., sample allocation-based immune optimization approach (SAIOA), which bases on the above approach. Finally, SAIOA's convergence property is studied by means of Markov theory and the law of large numbers.

2 Problem Description and Existence of Solutions

Consider the following general chance-constrained programming problem (P_α):

$$\begin{aligned} &\underset{x\in D}{Min} f(x) = E[F(x,\xi)] \\ &s.t. \begin{cases} p(x) = \Pr\{G(x,\xi) \le 0\} \ge 1-\alpha, \\ g(x) \le 0, h(x) = 0, \end{cases} \end{aligned}$$

with bounded and closed domain D in R^{p}, decision vector x in D, random vector ξ in Ω with $\Omega \subseteq \mathrm{R}^{\mathrm{q}}$ and significance level α in the interval [0,1), where E[.] and Pr{.} are the operators of expectation and probability respectively; $F(x, \xi)$ and $G(x, \xi)$ denote the general linear or nonlinear stochastic objective and constraint functions, respectively; $g(x)$ and $h(x)$ are the deterministic vector-valued constraint functions with J and K dimensions respectively. We prescribe that the symbol of

$x \leq 0$ stands for $x_i \leq 0$, $i = 1, 2, \ldots, p$, with $x = (x_1, x_2, \ldots, x_p)$. Additionally, once a joint chance constraint appears in practical problems, e.g., $\Pr\{G_i(x, \xi) \leq 0, i = 1, 2, \ldots, K\} \geq 1 - \alpha$, it can be equivalently transformed into the above chance constraint by $G(x, \xi) = \max\{G_i(x, \xi), i = 1, 2, \ldots, K\}$. We say that x is reliable with significance level α or that x is a reliable candidate, if it satisfies the above constraints; otherwise, it is called unreliable. All such reliable candidates constitute the feasible region D_α, where we always assume $D_\alpha \neq \varphi$ in the following theoretical studies. A reliable candidate is called an optimal reliable solution if it possesses the minimal objective value among reliable candidate solutions. All such optimal reliable solutions form a set D_α^*, and the minimum is expressed by z_α^*. Let $\Gamma(x)$, which measures the degree that x is far from the feasible region, be the quantity of constraint violation for x (e.g., see [8]). We next investigate some properties of P_α, based on the following basic assumptions.

(H1) $F(x, \xi)$ is continuous in x and measurable in ξ; there exists an integrable function $\gamma: \Omega \to R^+$ satisfying $|F(x, \xi)| \leq \gamma(\xi)$ for all $x \in D$;

(H2) $G(x, \xi)$, $g(x)$ and $h(x)$ are continuous in x, and $G(x, \xi)$ is measurable in ξ;

(H3) $p(x^*) > 1 - \alpha$ for each $x^* \in D_\alpha^*$.

The above assumptions guarantee that P_α has the following property:

Theorem 1 *If (H1) and (H2) hold, P_α has at least an optimal reliable solution.*

Proof According to (H1), we claim that $f(x)$ is continuous in x. To this end, suppose that x_n converges to $\bar{x}$ when $n \to \infty$ with any $x_n, \bar{x} \in D$. It follows from (H_1) and Lebesgue dominated convergence theorem that

$$\lim_{n\to\infty} f(x_n) = \int_\Omega \lim_{n\to\infty} F(x_n, \xi)\, dP(\xi) = f(\bar{x}). \tag{1}$$

This implies that $f(x)$ is continuous. Subsequently, introduce an indicator function

$$I_{(-\infty,0)}(z) = \begin{cases} 1, & \text{if } z \leq 0, \\ 0, & \text{otherwise}. \end{cases} \tag{2}$$

Write $\Psi(x, \xi) = I_{(-\infty,0)}(G(x, \xi))$. Since $I_{(-\infty,0)}(.)$ is upper semicontinuous, by means of (H_1) we acquire

$$\Psi(\bar{x}, \xi) \geq \overline{\lim_{G(x,\xi)\to G(\bar{x},\xi)}} I_{(-\infty,0)}(G(x, \xi)) = \overline{\lim_{x\to\bar{x}}} \Psi(x, \xi); \tag{3}$$

namely, $\Psi(x, \xi)$ is upper semicontinuous in x. Hence, Fatou's lemma and Eq. (3) hint that $E[\Psi(x, \xi)]$ is upper semicontinuous. Again,

$$E[\Psi(x, \xi)] = \int_\Omega \Psi(x, \xi) dP(\xi) = \int_{G(x,\xi)\leq 0} dP(\xi) = p(x), \tag{4}$$

this way, p(x) is upper semicontinuous. Hence, as related to (H_2), we obtain that D_α is a nonempty compact set. Thus, $f(x)$ can achieve the minimum on D.

3 Sample Average Approximation and Theoretical Analysis

Let $m(x)$ be the sample size of ξ at the point x, and $\xi_1, \xi_2, \ldots, \xi_{m(x)}$ be $m(x)$ replications of ξ. $p_{m(x)}(x)$ stands for the approximate estimates of $p(x)$ with

$$p_{m(x)}(x) = m(x)^{-1} \sum_{i=1}^{m(x)} I_{(-\infty,0)}(G(x, \xi_i)). \tag{5}$$

So, the sample average approximation problem $(P_\alpha{}^{\mathrm{m}})$ can be formulated:

$$\begin{aligned} &\underset{x \in D}{Min}\ f_{m(x)}(x) = \mu_{m(x)}(F) \\ &s.t., p_{m(x)}(x) \geq 1 - \alpha, g(x) \leq 0, h(x) = 0, \end{aligned}$$

where $\mu_{m(x)}(F)$ denotes the average of $m(x)$ objective observations at the point x. Meanwhile, after all candidates in D are attached sample sizes, $x \in D$ is said to be empirically feasible, if x satisfies the above constraints. Notice that if all these candidates are attached the same sample size, P_α^{m} is a conventional sample approximation problem of P_α. In the literature, Pagnoncelli et al. [9] investigated the approximate relation between the expected value optimization problem with a bounded variable constraint and the sample average approximation problem. We extend their result to the case where the relation between P_α and P_α^{m} is developed. Since we expect that the minimum of P_α^{m} is sufficiently close to that of P_α in the case where $m(x)$ is sufficiently large for each $x \in D$, in the following theoretical analysis we assume that all $m(x)$, $x \in D$, equal the same large integer M. So, P_α^{m} is expressed by P_α^{M}. Let D_α^{M} represent the set of all feasible candidates for P_α^{M} and $\hat{D}_\alpha^M$ the set of optimal solutions for such problem. Write $z_\alpha^M = \min\{f_M(x), x \in D_\alpha^M\}$. We cite the classical concept of epi-convergence, namely, let $g_{\mathrm{n}}(.)$ and $g(.)$ be real-valued functions from D to R with $n \geq 1$; we say that $\{g_{\mathrm{n}}(.)\}$ epi-converges to $g(.)$, if (1) $g(\bar{x}) \leq \underline{\lim}_{n\to\infty} g_n(x_n)$ whenever $x_n \to \bar{x}$ with $x_n, \bar{x} \in D$, and (2) $\lim_{n\to\infty} g_n(y_n) = g(\bar{x})$ for at least one sequence $y_n \to \bar{x}$.

Theorem 2 *If the above three assumptions hold, then* $z_\alpha^M \to z_\alpha^*$, *w.p.l, as* $M \to \infty$.

Proof By means of the above theorem, one can see that D_α^* is nonempty. Further, as associated to (H_3), we take $x^* \in D_\alpha^*$, and hence the (strong) law of large numbers yields that $p_{\mathrm{M}}(x^*) \to p(x^*)$, *w.p.l*, as $\mathrm{M} \to \infty$. Thus, we have that $p_{\mathrm{M}}(x^*) \geq 1 - \alpha$ when M is large enough, because $p(x^*) > 1 - \alpha$. This hints that $x^* \in D_\alpha^{\mathrm{M}}$, and accordingly $z_\alpha^{\mathrm{M}} \leq f_{\mathrm{M}}(x^*)$. So, it follows again from the (strong) law of large numbers that

$$\overline{\lim_{n\to\infty}} z_{\alpha}^{M} \leq \overline{\lim_{n\to\infty}} f_{M}(x^{*}) = z_{\alpha}^{*}, w.p.l. \tag{6}$$

In addition, as related to the property of continuity of $\Psi(\mathrm{x}, \xi)$ in x, $\mathrm{p_M}(x)$ is upper semicontinuous in x. This, along with the assumptions of $g(x)$ and $h(x)$, implies that D_{α}^{M} is a compact set. Thus, it follows from continuity of $f_{\mathrm{M}}(x)$ in x and the compactness of D_{α}^{M} that P_{α} has at least an optimal solution when M is sufficiently large. Take $x_{\mathrm{M}} \in \hat{D}_{\alpha}^{M}$. Since D is compact, we may suppose that $x_{\mathrm{M}} \to \bar{x}$, $\bar{x} \in D$, as $\mathrm{M} \to \infty$, in order to be simplicity of notation. Again, since $1 - p_{\mathrm{M}}(.)$ is lower semicontinuous, we gain that it epi-converges to $1 - p(.)$, *w.p.l.* This hints

$$1 - p(\bar{x}) \leq \underline{\lim_{n\to\infty}} (1 - p_{M}(x_{M})), \tag{7}$$

and hence

$$p(\bar{x}) \geq \overline{\lim_{M\to\infty}} p_{M}(x_{M}) \geq 1 - \alpha. \tag{8}$$

Thus, Eq. (8) and (H_2) result in $\bar{x} \in \mathrm{D}_{\alpha}$. This illustrates that $f(\bar{x}) \geq \mathrm{z}_{\alpha}^{*}$. Again, since $f_{\mathrm{M}}(.)$ is continuous, it follows from (H_1) that $f_{\mathrm{M}}(.)$ epi-converges to $f(.)$, *w.p.l*, as $\mathrm{M} \to \infty$. Accordingly, we obtain

$$z_{\alpha}^{*} \leq f(\bar{x}) \leq \underline{\lim_{n\to\infty}} f_{M}(x_{M}) = \underline{\lim_{n\to\infty}} z_{\alpha}^{M}, w.p.l. \tag{9}$$

Summarily, Eqs. (6) and (9) ensure that the conclusion is true.

4 Algorithm Statement and Illustrations

We develop a general immune optimization framework for CCP problems, which bases on our previous work [8]. As associated to P_{α} and ${P_{\alpha}}^{\mathrm{m}}$, a real-encoded antibody is viewed as a candidate in ${P_{\alpha}}^{\mathrm{m}}$; the antigen is regarded as P_{α}. Our task is to find the best antibody (i.e., optimal reliable solution) through running SAIOA on ${P_{\alpha}}^{\mathrm{m}}$. Note that we recall that all candidates in P_{α}^{m} have their respective sample sizes under a given sample allocation rule. Let M_{n}, which increases with iteration number n, denote the sample size of a given antibody population X with size N, namely the total of sample sizes attached by elements in X is equal to M_{n}. Further, for $x \in X$, $aff(x)$, $\delta(x)$ and $\Gamma_{\mathrm{m}(x)}(x)$ represent in order the antibody affinity, suppression radius and constraint violation (i.e., the estimates of $\Gamma(x)$). They can be used to seek diverse antibodies in X based on a niche-like method. To this point, we firstly rank decreasingly all antibodies in X according to their affinities; secondly, those elements, whose affinities are between $aff(x)$ and $aff(x) + \delta(x)$, are said to be suppressed by x. This way, survival antibody x can obtain the number of

antibodies suppressed by it. This number is called the suppression size of x. Based on these preliminaries, we describe SAIOA below.

Step 1. Set $n \leftarrow 1$. Generate initial population A_n of N random antibodies, and set $m(x) = m_0$ for all $x \in A_n$; calculate $f_{m(x)}(x)$ and $\Gamma_{m(x)}(x)$ with all $x \in A_n$.
Step 2. Allocate population sample size M_n to all elements in A_n according to the rule that better antibodies can obtain larger sample sizes.
Step 3. Calculate $f_{m(x)}(x)$, $\delta(x)$ and $\Gamma_{m(x)}(x)$ with all $x \in A_n$.
Step 4. A reproduction scheme is enforced on A_n; namely, those survival antibodies are only admitted to proliferate their clones in terms of their suppression sizes, and hence a clonal population B_n is formed with size N.
Step 5. All clones, with time-varying mutation rates conversely proportional to their respective affinities, are mutated through a mutation rule with ergodicity; such mutated clones with the same sample size m_n constitute a temporary population C_n; subsequently, their empirical averages and constraint violations are calculated.
Step 6. Combine A_n with C_n, and select N better antibodies to form A_{n+1}.
Step 7. If a stopping criterion is satisfied, the procedure is terminated; otherwise, set $n \leftarrow n + 1$, and return Step 2.

5 Convergence Study

SAIOA can be considered as an evolution chain: $A_n \rightarrow B_n \rightarrow C_n \rightarrow A_{n+1}$. Through the algorithm description, A_{n+1} only depends on the state of A_n, while the mutation rate depends on n. So, $\{A_n\}_{n \geq 1}$ is a nonhomogeneous Markov chain. Assume that the decision domain D as in Sect. 3 is a finite set. Let S represent the antibody space; S^N stands for a state space composed of antibody populations with sizes N; $X \in S^N$ is called a state. $\Pr\{x \rightarrow y\}$ presents the probability which x is mutated into y with $x, y \in S$. As associated to SAIOA's formulation, we acquire the following properties.

Lemma 5.1 *If the above assumptions* (H_1)–(H_3) *holds, and both* M_n *and* m_n *are sufficiently large as* $n \rightarrow \infty$, *then there exists* $N_1 > 0$ *such that when* $n > N_1$, $\Pr\{A_{n+1} \cap D_\alpha^* = \phi | A_n \cap D_\alpha^* = \phi\} = 0$.

Proof We know that $D_\alpha^* \neq \varphi$ by Theorem 1. Assume that $A_n \cap D_\alpha^* \neq \varphi$. Through Step 3 as in SAIOA, the best antibody in A_n can obtain the largest sample size decided by M_n. Again, since M_n increases with n, it follows from the law of large numbers and (H_3) that there exists a sufficiently large positive integer N_1, such that when $n > N_1$, $p_{m(x^*)}(x^*) \geq 1 - \alpha$ for each $x^* \in A_n \cap D_\alpha^*$. Accordingly, x^* is empirically feasible. We claim that when n is sufficiently large, $aff(x^*) \geq aff(x)$ for any $x \in A_n$. Otherwise, if there exists $x_0 \in A_n$ but $x_0 \notin D_\alpha^*$ such that

$aff(x^*) < aff(x_0)$. We see that x_0 is empirically feasible according to the design rule of antibody affinity. Therefore, $f_{m(x0)}(x_0) < f_{m(x^*)}(x^*)$. Again, as related to the sample allocation rule in step 3, $m(x_0)$ must be sufficiently large when $n > N_1$. This, together with the law of large numbers, implies that $f(x_0) \leq f(x^*)$. This is not true because of $x_0 \notin D_\alpha^*$. All these illustrate that x^* is best in A_n when $n > N_1$. On the other hand, if there exists some element x in C_n such that x is not inferior to x^*, x must be empirically feasible for $P_\alpha{}^m$ when $n > N_1$, and hence x must be an optimal reliable solution of P_α. Summarily, when $n > N_1$, we have that $A_{n+1} \cap D_\alpha^* \neq \varphi$ if $A_n \cap D_\alpha^* \neq \varphi$.

Lemma 1 *If there exists $0 < \delta < 1$, such that $Pr\{x \to y\} \geq \delta$ for any $x, y \in S$, then there exists $0 < \varepsilon < 1$, $0 < \beta < 1$ and $N_2 > 0$, such that $Pr\{A_{n+1} \cap D_\alpha^* \neq \varphi | A_n \cap D_\alpha^* = \varphi\} \geq (1 - \varepsilon^n)^2 \beta$ with $n > N_2$.*

Proof Let $A_n = X$ and $A_{n+1} = Y$, $X, Y \in S^N$, with $X \cap D_\alpha^* = \varphi$ and $Y \subseteq D_\alpha^*$. Based on the formulation of SAIOA, step 3 causes that the empirical values of antibodies in A_n are updated; step 4 selects deterministically some parents to proliferate N clones; step 6 picks up deterministically N better antibodies to constitute the next population from $A_n \cup C_n$ in terms of their empirical values. Thus, the law of large numbers implies that when n is sufficiently large, we can acquire that, (1) $\Pr\{B_n = Z_0 | A_n = X\} > 1 - \varepsilon^n$ for some state $Z_0 \subseteq X$, $Z_0 = (z_1, z_2, \ldots, z_N)$, and (2) $\Pr\{A_{n+1} = Y | C_n = Y\} > 1 - \varepsilon^n$, where ε is a sufficiently small positive number. Again, relying upon the assumption of ergodicity, for any $W = (w_1, w_2, \ldots, w_N) \in S^N$ we obtain $\Pr\{z_i \to w_i\} \geq \delta$, with $1 \leq i \leq N$. Consequently, we derive out that $\Pr\{C_n = W | B_n = Z_0\} \geq \delta^N \equiv \beta$. Hence, it derives from K–C equation that

$$\begin{aligned} &\Pr\{A_{n+1} = Y | A_n = X\} = \textstyle\sum_{Z,W \in S^N} \Pr\{B_n = Z | A_n = X\}. \\ &\Pr\{C_n = W | B_n = Z\} \Pr\{A_{n+1} = Y | C_n = W\} \\ &> (1 - \varepsilon^n)^2 \Pr\{C_n = Y | B_n = Z_0\} \geq (1 - \varepsilon^n)^2 \beta \end{aligned} \tag{10}$$

Thereby, there exists a positive integer $N_2 > 0$ such that when $n > N_2$,

$$\Pr\{A_{n+1} \cap D_\alpha^* \neq \varphi | A_n \cap D_\alpha^* = \varphi\} \geq \Pr\{A_{n+1} = Y | A_n = X\} \geq (1 - \varepsilon^n)^2 \beta. \tag{11}$$

Theorem 3 *If the above three assumptions hold, SAIOA is weakly convergent in probability, i.e.,* $\lim_{n \to \infty} \Pr\{A_n \cap D_\alpha^* \neq \varphi\} = 1$.

Proof Since $0 < \varepsilon < 1$ and $0 < \beta < 1$, there exists $N_3 > 0$ and $0 < \eta < 1$ such that when $n > N_3$, we have $\eta \geq 1 - (1 - \varepsilon^{N_3})$. Take $N_0 = \max\{N_1, N_2, N_3\}$. When $n > N_0$, Lemmas 1 and 2 indicate that

$$\Pr\{A_{n+1} \cap D_\alpha^* = \varphi\} \leq (1 - \eta) \Pr\{A_n \cap D_\alpha^* = \varphi\}. \tag{12}$$

Further, by induction, it follows from Eq. (12) that

$$\Pr\{A_n \cap D_\alpha^* = \varphi\} \leq (1-\eta)^{n-N_0}. \tag{13}$$

6 Experimental Study

Our experiments are executed on a personal computer with CPU/3.00 GHz and RBM/512 MB. In order to examine SAIOA's performance characteristics, three well-known mutation rules of polynomial mutation, classical Gaussian mutation and nonuniform mutation are designated in order as its mutation operations; correspondingly, three similar optimization approaches are acquired, where we simply call them SAIOA-P, SAIOA-G and SAIOA-U respectively. Take $N = 40$, $m_0 = 20$, and $m_n = 30$. Also, take the maximal iteration number as 200.

Example Feed Mixer Problem [2]

$$Max\, f(x) = E[24.55x_1 + 26.75x_2 + 39.00x_3 + 40.50x_4 + \eta],$$

$$s.t., \begin{cases} \Pr\{x_1\xi_1 + x_2\xi_2 + x_3\xi_3 + x_4\xi_4 \geq 21\} \geq 1-\alpha, \\ 2.3x_1 - 5.6x_2 - 11.1x_3 - 1.3x_4 \geq 5, \\ x_1 + x_2 + x_3 + x_4 = 1, x_1, x_2, x_3, x_4 \geq 0, \\ \eta \sim N(0,2), \xi_1 \sim N(12, 0.53), \xi_2 \sim N(11.9, 0.44), \\ \xi_3 \sim N(41.8, 4.5), \xi_4 \sim N(52.1, 0.79). \end{cases}$$

The difficulty of solving such CCP model consists in the fact that the random factors influence seriously the optimized quality. Such model can be transformed into an analytically equivalent nonlinear optimization one, and thus we can find its

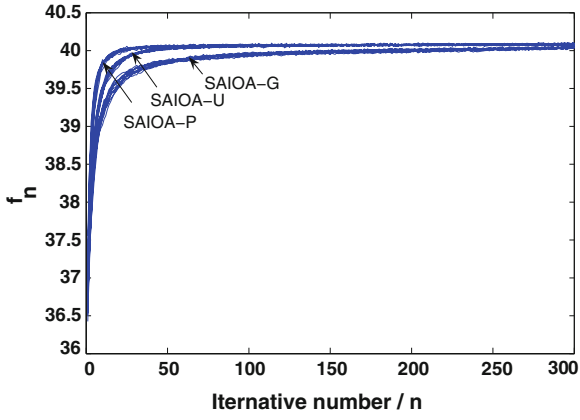

Fig. 1 Comparison of average search curves

theoretical minimum 39.9337 whatever α takes between 0 and 1. Next, the above three algorithms directly run respectively 50 times on the sample average approximation model P_{α}^{m} of the above CCP. They can all obtain reliable solutions during each execution and with any given significance level between 0 and 1. Figure 1 displays the average search curves.

Although the optimized qualities acquired by the approaches are influenced by noises, SAIOA-P and SAIOA-U can find the same optimal reliable solution for any execution and each designated significance level, and appear stable search performances because of extremely small variances caused. Thus, they share abilities of strong exploitation, exploration and noisy suppression. However, SAIOA-G can only find sub-optimal solutions, as Gaussian mutation results in its weak ability of global exploitation. All these demonstrate that SAIOA is a useful optimization framework for chance-constrained programming, and meanwhile Fig. 1 also demonstrates that it is convergent.

7 Conclusions and Further Work

We in this paper give a sufficient condition for existence of solutions of CCP, and also analyze the approximate relation between the true CCP and the sample average approximation problem. We next develop an available and extensible immune optimization approach for CCP problems, while its convergence is proven to be true. Despite of strongly noisy disturbance, experimental results show that SAIOA is convergent with probability 1. It also displays many merits, e.g., simplicity, low computational complexity, and convergence. Comparative experiments illustrate that different mutation rules make SAIOA expose different performance characteristics; SAIOA-A and SAIOA-U perform well over SAIOA-G; relatively, SAIOA-U is a more potential tool for complex CCP problems than SAIOA-P.

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