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EDITED BY
Yusen He,
The University of Iowa, United States

REVIEWED BY
Tangshao Duan,
Mie University, Japan
Sheng Hu,
Xi'an Polytechnic, China

*CORRESPONDENCE
Qian Fan,
qianfann@outlook.com

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Establishing the energy consumption prediction model of aluminum electrolysis process by genetically optimizing wavelet neural network

Lizhong Yao¹, Qian Fan^{2*}, Lei Zhao¹, Yanyan Li² and
Qingping Mei³

¹College of Physics and Electronic Engineering, Chongqing Normal University, Chongqing, China, ²School of Mechanical Engineering, Sichuan University, Chengdu, China, ³School of Big Data and Information Industry, Chongqing City Management College, Chongqing, China

Nowadays, it is very popular to employ genetic algorithm (GA) and its improved strategies to optimize neural networks (i.e., WNN) to solve the modeling problems of aluminum electrolysis manufacturing system (AEMS). However, the traditional GA only focuses on restraining the infinite growth of the optimal species without reducing the similarity among the remaining excellent individuals when using the exclusion operator. Additionally, when performing arithmetic crossover or Cauchy mutation, a functional operator that conforms to the law of evolution is not constructed to generate proportional coefficients, which seriously restricted the exploitation of the hidden potential in genetic algorithms. To solve the above problems, this paper adopts three new methods to explore the performance enhancement of genetic algorithms (EGA). First, the mean Hamming distance (H-Mean) metric is designed to measure the spatial dispersion of individuals to alleviate selection pressure. Second, arithmetic crossover with transformation of the sigmoid-based function is developed to dynamically adjust the exchange proportion of offspring. Third, an adaptive scale coefficient is introduced into the Gauss-Cauchy mutation, which can regulate the mutation step size in real time and search accuracy for individuals in the population. Finally, the EGA solver is employed to deeply mine the optimal initial parameters of wavelet neural network (EGAWNN). Moreover, the paper provides the algorithm performance test, convergence analysis and significance test. The experimental results reveal that the EGAWNN model outperforms other relevant wavelet-based forecasting models, where the RMSE in test sets based on EGAWNN is 305.72 smaller than other seven algorithms.

Abbreviations: AEMS, Aluminum electrolysis manufacturing system; ANS, Adaptive neighborhood search; BRK-GA, Biased random key genetic algorithm; EC, Enhanced crossover; EGA, Enhanced genetic algorithm; EM, Enhanced mutation; ES, Enhanced selection; GA, Genetic algorithm; IGA, Improved genetic algorithm; MSP, Multi Supper parent; POX, Preserving order-based crossover; RG, Reference group; RMSE, Root mean square error; SD, Standard deviation; SGA, Standard genetic algorithm; SSP, Single supper parent; WNN, Wavelet neural network.

KEYWORDS

aluminium electrolysis, enhanced genetic algorithm, wavelet neural network, energy consumption prediction, intelligent modeling

1 Introduction

The aluminum electrolysis industry consumes enormous energy, and its energy utilization rate is less than 50% (Gui et al., 2018). An effective way to achieve efficiency enhancement and consumption reduction is to determine the optimal operating parameters for maintaining the best condition of the electrolytic cell. However, it is necessary to establish a high-precision and stable prediction model for process energy consumption (Yang et al., 2019). And so far, the methods for predicting the energy consumption of aluminum electrolysis have been roughly divided into two categories (Wu et al., 2019). The first contains physical methods, which tracks the process of aluminum electrolysis based on the exact mathematical mechanism. Because there are many complex physical and chemical reactions inside aluminum electrolysis and unpredictable external interference, it is very difficult to obtain a precise system model through the process mechanism (Slowik and Kwasnicka, 2020). The other category includes data-driven methods, which can acquire the complex corresponding relationships between decision variables and performance indicators (Li et al., 2021a; Li, 2022a). This type of method does not need to know the complex mechanism of a manufacturing system, it performs learning and training only on a series of process data samples (Yao et al., 2019; Li, 2022b). Therefore, such a method is of noticeable value with broad practical applications in modeling algorithms for process manufacturing systems (Yi et al., 2018; Li et al., 2021b).

A wavelet neural network (WNN), as a universal function approximation model that is widely accepted in data-driven methods (Pauline and Zarita, 2019; Khelil et al., 2021), learns the same task with higher accuracy, a simpler structure and faster convergence speed compared with traditional neural networks (Guan et al., 2013). Song et al. (2016) proposed a wavelet-based scheme to generate the individual forecaster. Jha and Senroy (2018) used the wavelet ridge method to analyze the dynamic characteristics of the power system. Sabouri et al. (2017) adopted the orthogonal discrete wavelet transform (ODWT) to research the plasma electrolytic oxidation (PEO) of aluminum at various periods during the electrolysis process. A WNN has the potential to handle the issue of the AEMS modeling.

Nevertheless, the stochastic generation of the initial parameters in a WNN gives rise to the nonconvergence of the whole learning process and even major prediction errors, which hardly satisfy the modeling requirements of high accuracy and stability in an AEMS. There is a consistent trend in current research regarding the integration genetic algorithms into WNNs to adjust their weights and factors (Majeed et al., 2017; Peng and Xiang, 2020; Tian et al., 2020; Khelil et al., 2021). Furthermore, the combination of a GA and a WNN has diversified

applications, such as calculating the greenhouse effects of aircraft cruises (Tian et al., 2020), adjusting the parameters used in a hybrid fuzzy wavelet neural network (Huang et al., 2018), and establishing the thermal error prediction models for machine tools (Li and Zhang, 2019). Compared with the traditional WNN, the model established by a GAWNN can overcome its weakness in obtaining relatively stable initial parameters.

There are two ways to further promote the accuracy of the prediction model. One is to seek breakthroughs from the structure of the WNN, the other is to overcome the premature deficiencies of GA (Tinos et al., 2018) that our studies looked at. Plus, almost all the modified measures revolve around three genetic operators (Song et al., 2019), which are the cores of evolution and determine the performance of the algorithm. Unfortunately, there are still three areas of anxiety that are worthy of our attention and resolution. First, most of the existing studies on the use of crowding selection to eliminate similar individuals are based on the Hamming distance between each individual in the population and the optimal individual (Li and Kou, 2002; Osuna and Sudholt, 2020). Li and Kou (2002) utilized the fitness-sharing method, by which individuals are measured with the Euclidean or Hamming distance (Prugel-Bennett and Tayarani-Najaran, 2012), to maintain population diversity. Although the above methods alleviate overcrowding, they simply curb the uncontrolled growth of certain particular species, and they cannot guarantee sufficient discreteness among advanced individuals. Second, the adaptive crossover principle (Shojaedini et al., 2019; Mishra and Bajpai, 2021; Sun et al., 2021), which can adjust its crossover rate in different fields based on the population fitness of every iteration, has been extensively reported. Although adaptive crossover reduces the adverse effect caused by an improper definition of the rate, its essence is still that of stochastic crossover. Its randomness of intersection inevitably increases the possibility of damaging good genes. Third, the Gauss-Cauchy mixture mutation, a type of the real-coded mutation, has been an investigative hotspot due to its local and global search abilities (Li et al., 2017a; Li et al., 2017b; Wu and Law, 2011). There are some mutation formulas combining the Gauss-Cauchy function that have been recommended in (Li et al., 2017b; Lha et al., 2018). However, the current studies mostly adopt the standard Cauchy function for mixing throughout the mutation process. That results in a relatively single range of variation generated by the mixed formula.

Based on the issues stated in above analyses, the measures utilized by this paper and innovations contained therein are mainly summarized as follows:

- (1) To increase the dispersion of subpopulations and effectively avoid precocity, the presented scheme adopts the mean Hamming distance (H-Mean), which performs secondary selection from the perspective of superior offspring populations, to design the selection operator rather than a single Hamming distance.
- (2) Considering that arithmetic crossover is essentially a linear combination of alleles, the proposed scheme uses it to mitigate the above negative effect. Moreover, by rotating the sigmoid function vertically with $\gamma = 0.5$ as the axis of symmetry, and taking the part of the curve where x is greater than or equal to 0, a new type of α -function that slowly approaches from 0.5 to 0 is designed, to regularly set the cross proportion of parents involved in the evolution. This scheme does not casually destroy the good genes, and ensures that the algorithm can converge to the global optimum.
- (3) In order to improve the accuracy of local search by making the ranges of variation change dynamically with the iteration process, this paper introduces an adaptive scale coefficient γ into the Cauchy function to randomly set the change rate of the fitness of the iterative population. Therefore, the mutation steps can be updated in a timely manner, which will improve the time-variance and convergence rate of the algorithm.

Through the deep integration of the above three strategies, this paper further explores the hidden potential of genetic algorithms. The proposed EGA solver is employed to optimize the weights and factors of a WNN, which helps to establish an energy consumption model for an AEMS. The EGAWNN model overcomes the weaknesses of early convergence and poor search speed in the middle and late stages when the GA is applied to the wavelet network. Finally, the accuracy and improvement of the prediction model are verified through industrial experiments.

The remaining content of this paper is as follows. [Section 2](#) presents the specific implementations of three enhanced strategies. [Section 3](#) provides some standard numerical experiments as well as their results contained tables and figures. [Section 4](#) overviews the design flow and convergence analysis of EGAWNN. An experiment based on a real-world industrial application of aluminum electrolysis is conducted and discussed through certain performance indices in [Section 5](#). [Section 6](#) gives a summary of the paper.

2 Enhanced genetic algorithms

A GA is an adaptive probability optimization technology based on biological genetics and evolution mechanisms. When a GA is used to solve optimization problems, premature convergence and evolutionary obstruction inevitably occur during the solving process. This paper tries to solve the above problems from the following three aspects.

First, taking the dispersion and diversity of the initial population into account, the offspring are selected based on

the H-Mean criterion so that the newly generated individuals can crowd out similar parents. Second, a dynamic nonlinear arithmetic crossover based on the α -function is designed to ensure that the population has sufficient diversity in the early stages without destroying the excellent individuals in the later stages. Finally, an adaptive proportional coefficient is introduced into the Cauchy function to adjust the variation step size, which helps individuals move quickly towards the direction of the global optimum.

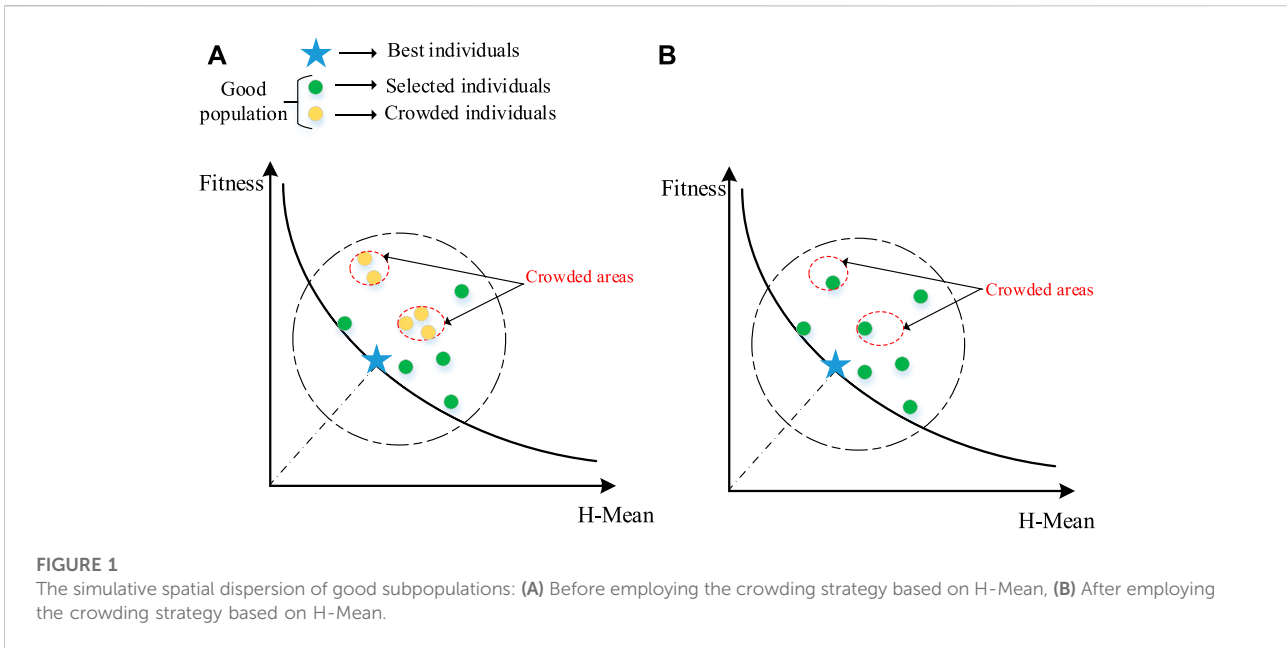
2.1 Crowding strategy based on the H-Mean metric

The proportional selection method in the standard genetic algorithm (SGA) may increase the number of individuals whose fitness values are close to those of others in the later period. The above phenomenon can result in the stagnation of the evolution of the population, or individuals with higher fitness values misleading the evolution direction of the population, which will cause the population to lose diversity and result in premature convergence problems ([Amini and Hu, 2021](#)).

Although the standard crowding method can keep a population diversified and relieve the congestion between the best individual and other excellent populations to some degree, spatial dispersion within an excellent population is difficult to be guaranteed. To address the problem, this study provides a crowding strategy through the ranking of the H-Mean values, for the selection of outstanding individuals with high fitness values and large population differences. This strategy maintains the dispersion of good subpopulations and restrains the endless growth of some superior species.

[Figure 1](#) simulates the spatial dispersion of excellent subpopulations before and after employing the proposed crowding strategy. The two coordinate axes represent the two requirements of high fitness and high H-Mean values. There are good individuals with high fitness values in the large dotted circle above the black curve; the blue star represents the best individual with the highest fitness value in the current evolution; the yellow balls are overcrowded in the small red dotted circle, as seen in [Figure 1A](#). The green balls are made up of two parts: One part contains the individuals with good dispersion in the excellent population; the other part is derived from changes in the remaining individuals by deleting the yellow balls with low H-Mean value, which are plotted in [Figure 1B](#). It is easy to see that a higher H-Mean criterion-based crowding strategy can alleviate the congestion among outstanding individuals and thus increase population diversity.

Definition of the Hamming distance (denoted by (i, j)): Suppose that there are two equal-length strings S_1 and S_2 , where $H(i, j)$ is the minimum number of character substitutions that change one string into the other; i and j represent different individuals in the population.



The basic calculation process is as follows: 1) The population is sorted into superior and inferior population according to the ranking of fitness; 2) In the superior population, the number on each gene site of individuals are kept four significant digits, and then their $H(i, j)$ are calculated; 3) The superior population selects offspring through the elitist strategy and the sorting-elimination rule based on H-Mean (marked as $H_{mean}(i, j)$). The inferior population directly eliminates the individuals in proportion whose fitness values are low; 4) New individuals are randomly generated to replace the eliminated ones. The pseudocode of the specific process is shown in Table 1.

2.2 α -Function-based arithmetic crossover

A crossover operation is the main feature that distinguishes a GA from other evolutionary algorithms, and it is an important method for generating new individuals. The crossover operation of the SGA selects two individuals as objects, and then generates an intersection to exchange gene codes for producing subindividuals (Dang et al., 2016). The widely used adaptive crossover dynamically adjusts its crossing rate in accordance with the fitness values of the population involved in the evolution process. However, the position of a single-point or multipoint crossover is stochastic (Xu et al., 2018). The uncertainty of intersections raises the risk of destroying excellent genes, which may cause the algorithm to swing around the optimal solution at the end of a search, resulting in a state of convergence

stagnation. In addition, it essentially serves the binary encoding genes, which causes part of the genetic information to lose when dealing with unrelated and multi-parameter real encoding. This paper adopts a nonlinear combination crossover to solve the above problem, as shown in Eq. 1.

$$\begin{cases} X_A^{t+1} = \alpha X_B^t + (1 - \alpha) X_A^t \\ X_B^{t+1} = \alpha X_A^t + (1 - \alpha) X_B^t \end{cases} \quad (1)$$

where, X_A^t and X_B^t represent the two selected parents, and X_A^{t+1} and X_B^{t+1} represent the offspring after crossover.

Because α must be in the range of (0, 0.5), we try to design $S(\alpha)$ through a transformation of the sigmoid curve feature; the curve of $S(\alpha)$ is shown in Figure 2.

$$S(\alpha) = \frac{e^{-\alpha}}{1 + e^{-\alpha}} \quad (2)$$

$\alpha = t/\beta$ and $\beta = T/5$, where t is the current number of iterations, and T is the maximum number of iterations. The new crossover strategy is obtained as given in Eq. 3.

$$\begin{cases} X_A^{t+1} = \frac{e^{-\frac{t}{\beta}}}{1 + e^{-\frac{t}{\beta}}} X_B^t + \frac{1}{e^{-\frac{t}{\beta}}} X_A^t \\ X_B^{t+1} = \frac{e^{-\frac{t}{\beta}}}{1 + e^{-\frac{t}{\beta}}} X_A^t + \frac{1}{e^{-\frac{t}{\beta}}} X_B^t \end{cases} \quad (3)$$

Figure 3 indicates the differing principles of adaptive crossover and α -function arithmetic crossover, where we use different colors, i.e., orange, green, pink and blue, to distinguish the genes of different parents. We can see that Figure 3A has a

TABLE 1 Pseudocode of utilizing the H-Mean metric for selection.

Algorithm 1: H-Mean-based crowding algorithm

Input: The initial individual k ($k = 1, 2, \dots, n$) with a fitness value f_k below

InitChrom = [K , F_K]

Output: The selected individual with its fitness value f_k listed below

SelChrom = [K_Sel , F_{K_Sel}]

Steps

1. Initialization

Set the parameters: Number_of_F, Number_of_Scale (1), Number_of_Scale (2)

GoodChrom [], BadChrom []

2. Sort the individuals in InitChrom [] in descending order by fitness value

3. If $f_k > \text{Number_of_F}$ then

i. Individual k enters GoodChrom [], and its number is recorded as n_1

else

i. Individual k enters BadChrom []

end if

4. Calculate the $H(i, j)$ s in GoodChrom [] between individual i and all the remaining individuals

5. Calculate the sum of the $H(i, j)$ s between the i th individual and all the others, namely

$$\sum_{j=1}^{n_1-1} H(i, j), (j = 1, 2, \dots, n_1, j \neq i)$$

6. Calculate the $H_{mean}(i, j)$ of individual i and arrange them in descending order, namely

$$H_{mean}(i, j) = \frac{\sum_{j=1}^{n_1-1} H(i, j)}{n_1-1}$$

7. If $f_k = \text{Max}(f)$ then

i. Individual k enters GoodChrom []; record it as k_best

else

i. Compare the $H_{mean}(i, j)$ s of all individuals except k_best

ii. In GoodChrom [], eliminate the individuals with the smallest $H_{mean}(i, j)$ s according to the ratio of Number_of_Scale (1)

end if

8. In BadChrom [], eliminate individuals with the smallest f_k values according to the ratio of Number_of_Scale (2)

9. Randomly generate new individuals to replace the eliminated individuals

10. Put all individuals from GoodChrom [] and BadChrom [], as well as the newly generated individuals, into SelChrom []

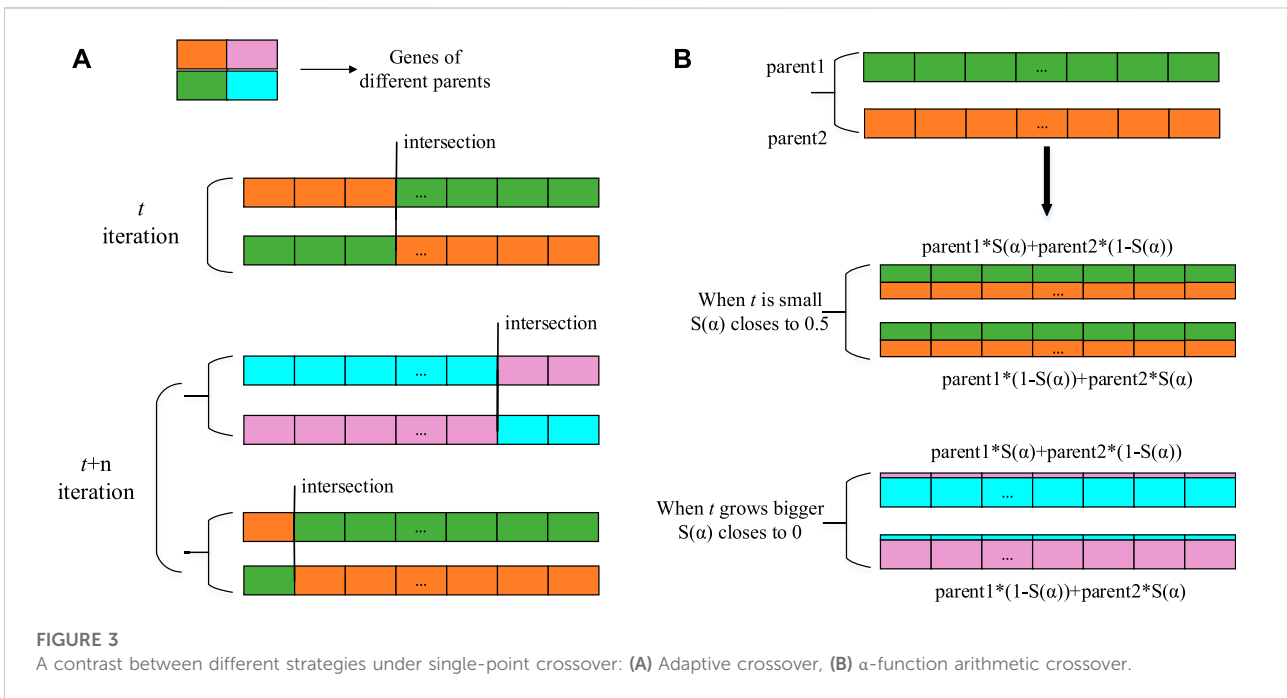
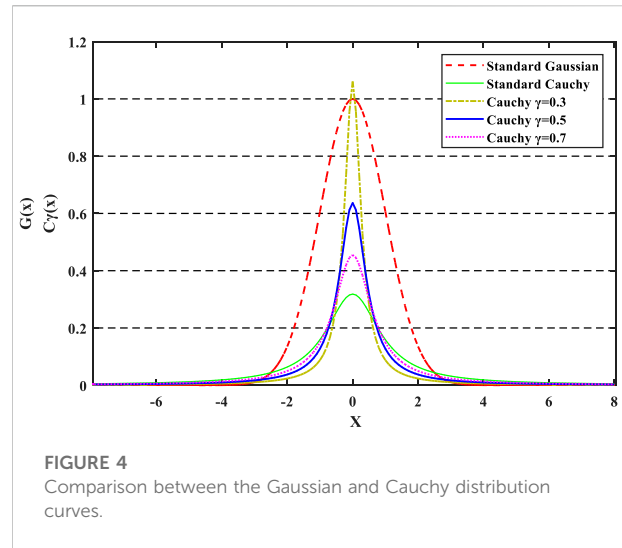
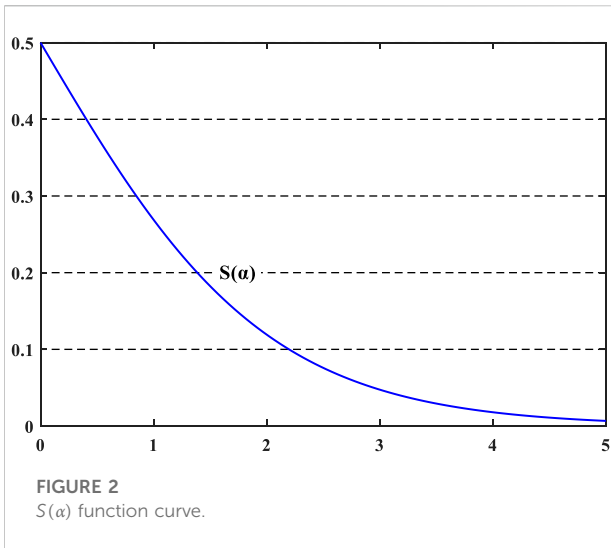
End the H-Mean-GA procedure

different number of parents involved in each crossover from that in Figure 3B, which realizes the requirement of self-control because its crossover rate changes each iteration according to the population fitness. However, the intersection is stochastic, thus making the gens unordered. α -function arithmetic crossover is applicable to floating operations, and its working principle is shown in Figure 3B. Its essence is only a linear combination of the alleles of parental individuals, so no crossover points are required. It is worth mentioning that this paper improves the proportionality coefficient α in arithmetic crossover into a $S(\alpha)$ function related to t (the number of iterations). From Figure 2 and Eq. 3, at the beginning of the iterative process, t is small, resulting in $S(\alpha)$ converging to 0.5, and each offspring inherits half the genes from each parent, such as the orange and green genes in Figure 3B. Therefore, obtaining more diverse offspring from the above crossover increases the possibility of obtaining high-performing individuals. As the number of iterations

increases, t becomes larger, which causes $S(\alpha)$ to be approximately 0, and the paternal genes remain largely unchanged, such as the pink and blue genes in Figure 3B. Small exchanges of parent alleles can increase the local optimization power of the algorithm. In this way, not only can the diversity of the population be maintained but the population also moves towards the direction of global convergence during later iterations without destroying the optimal individuals.

2.3 Gaussian and adaptive Cauchy mutation (Gauss- γ .Cauchy)

The mutation operator replaces the original gene with a new one to improve the local search ability of the GA (Das and Pratihar, 2021), as well as that of an auxiliary method for



generating new individuals to increase population diversity. The real coding number in this paper is up to 108 bits, so it cannot achieve the expected effect if only single-point variation is used. If multipoint variation is employed, the randomness of the mutation value will produce a large uncorrelated disturbance, consequently damaging the original good genes. To solve the above problems, this paper introduces an adaptive proportional coefficient γ to design a hybrid mutation equation on the basis of the Gauss-Cauchy mutation. The designed equation produces related perturbations to change the original genes and overcome

uncertainty. The range of the disturbance produced by the Cauchy function is instantly adjusted by changing the γ , thereby generating a new mutation step that makes the hybrid equation time-varying.

The Gaussian distribution function is given as $G(x) = \frac{1}{\sqrt{2\pi}} \exp(-\frac{x^2}{2})$, $x \in (-\infty, \infty)$, and the Cauchy function is $C_\gamma(x) = \frac{\gamma}{\pi} \cdot \frac{1}{\gamma^2 + x^2}$, $x \in (-\infty, \infty)$, where γ is the scale coefficient. Their density distribution curves are shown in Figure 4.

Figure 4 shows that the standard Gaussian function has a larger peak value at its origin and a shorter distribution on both

sides than the other function. Gaussian mutation can produce disturbances close to the origin, and hence, it has a strong local development ability. Conversely, the Cauchy function has a smaller peak value at its origin and a longer distribution on both sides. Notably, the γ affects the features of the curvilinear distribution. Cauchy mutation can generate a disturbance with a wider range near the current mutated individual, making it easier to leap out of local optima. Combing the distribution features of the two functions, the hybrid mutation equation is introduced as follows (Wu and Law, 2011; Li et al., 2017a):

$$\begin{cases} \eta'_{ij}(t) = \eta_{ij} \exp(\tau C(\gamma) + \tau_1 C_j(\gamma)), & j = 1, 2, \dots, n \\ x'_{ij}(t) = x_{ij}(t) + \eta'_{ij}(t) \cdot G_j(0, 1) \end{cases} \quad (4)$$

$$\tau = (\sqrt{2\sqrt{n}})^{-1}, \tau_1 = (\sqrt{2n})^{-1} \quad (5)$$

where x'_{ij} and η'_{ij} are the target and decision variables of the j th individual; τ and τ_1 are used to define the step size of the whole population and single individual respectively. $C(\gamma)$ represents the Cauchy random numbers of the whole population generated at this time, and it is updated only once per iteration. $C_j(\gamma)$ denotes the Cauchy random number of the single individual. Everyone participating in the current mutation generates one random number and needs to be updated once. $G_j(0, 1)$ indicates a random number from the standard Gaussian distribution. As with $C_j(\gamma)$, each mutation requires a new Gaussian random number.

Since the γ of the Cauchy function affects the curve peak and the distribution features on both sides, the value can be regulated to randomly change the disturbance range. The selection of γ is based on the distance between offspring. First, this paper introduces the range rate of offspring, as given in Eq. 6:

$$P_{dis}(t) = \frac{\max(objv(t)) - \min(objv(t))}{\max(objv(t-1)) - \min(objv(t-1))} \quad (6)$$

where t is the current iteration number and $objv(t)$ is the fitness value of the t th generation. Let $d(t) = P_{dis}(t)/P_{dis}(t-1)$. If $d(t)$ stays stationary on both sides of one or moves slowly to its right during three successive generations, we should reset the mutation size by changing γ .

It can be seen from Figure 4, $\gamma = 0.3$, $\gamma = 0.5$, $\gamma = 0.7$, and $\gamma = 1.0$ are the critical points with large differences, so the proposed scheme sets two intervals. A brief explanation of the mutation process is plotted in Figure 5. Figure 5A uses orange genes to represent the range limit of the mutation at $\gamma = 1$. To visually show the change rule, the interval is artificially set to (0.010 and 0.100). Figure 5B uses green gene to represent the mutation range limit at $\gamma \in [0.7, 1]$. At this time, $d(t)$ fluctuates greatly, so we implement a global search and still assume the interval to be (0.010 and 0.100). The γ in this interval can produce a larger disturbance, so the updated mutation step size can force the process to leap out of the local optimum and ensure the global convergence of EGA. Figure 5B uses a blue gene to show the

mutation range limit at $\gamma \in [0.3, 0.5]$. Currently, $d(t)$ is stable at approximately one for three successive generations, indicating that the evolution has reached the late stage. Therefore, we implement a local search and still assume the interval to be (0.005 and 0.050). In this interval, the distribution is short on both sides of the function curve, and the disturbance is small, which results in diminishing mutation step size.

The specific adjustment process is as below:

When $d(t-i) \sim 1$, $t > 3$, ($i = 0, 1, 2$), let $\gamma \in [0.3, 0.5]$; if not, $\gamma \in [0.7, 1]$, and then put the updated γ into Eq. 6.

3 Numerical experiments and results

The above three methods in Section 2 are implemented in MATLAB R2020a with an Intel Core i5 2.00 GHz CPU. To highlight the performance differences of various methods, we adopt the Enhanced selection (ES), Enhanced crossover (EC), Enhanced mutation (EM) methods and Enhanced genetic algorithm (EGA) combining the above three strategies to compare with the Reference group (RG). Meanwhile, for evaluating the superiority and timeliness of the new algorithm, this paper also performs the following four comparison experiments, which were new strategies proposed by researchers on genetic algorithms in the past 2 years. The above four methods are as follows. 1) Priority based genetic algorithms (PGA) (Mishra and Bajpai, 2021) contained single supper parent algorithm (SSP); 2) PGA contained multi supper parents algorithm (MSP); 3) Biased random key genetic algorithm (BRK-GA) (Cicek and Ozturk, 2021): ELITE and NONELITE selection; BRK crossover; 4) Improved genetic algorithm (IGA) (Zhang et al., 2020): precedence preserving order-based crossover (POX) and adaptive neighborhood search mutation (ANS). All the genetic operators used in the above evolution processes of the functions are shown in Table 2. Bold operators in Table 2 emphasize the innovative part of the corresponding methods.

We used the above nine groups of comparative experiments to optimize the 6 standard single-objective test functions separately, i.e., function1, function2, function3, function4, function5, and function6, as shown in Eqs 7–12. The performance of the nine methods is measured by the objective function value (regarded as the fitness value of the optimal solution). Since the six test functions only have one actual value and one predicted value after each independent run, only the change of fitness is observed while analyzing the global indices and convergence traits. The population size is set to 200, and the maximum number of iterations is set to 500.

Function1. Global minimum $f(x) = 0$; $x(i) = 0$, $i = 1: n$.

$$f_1(x) = \sum_{i=1}^n x_i^2, -5.12 \leq x_i \leq 5.12 \quad (7)$$

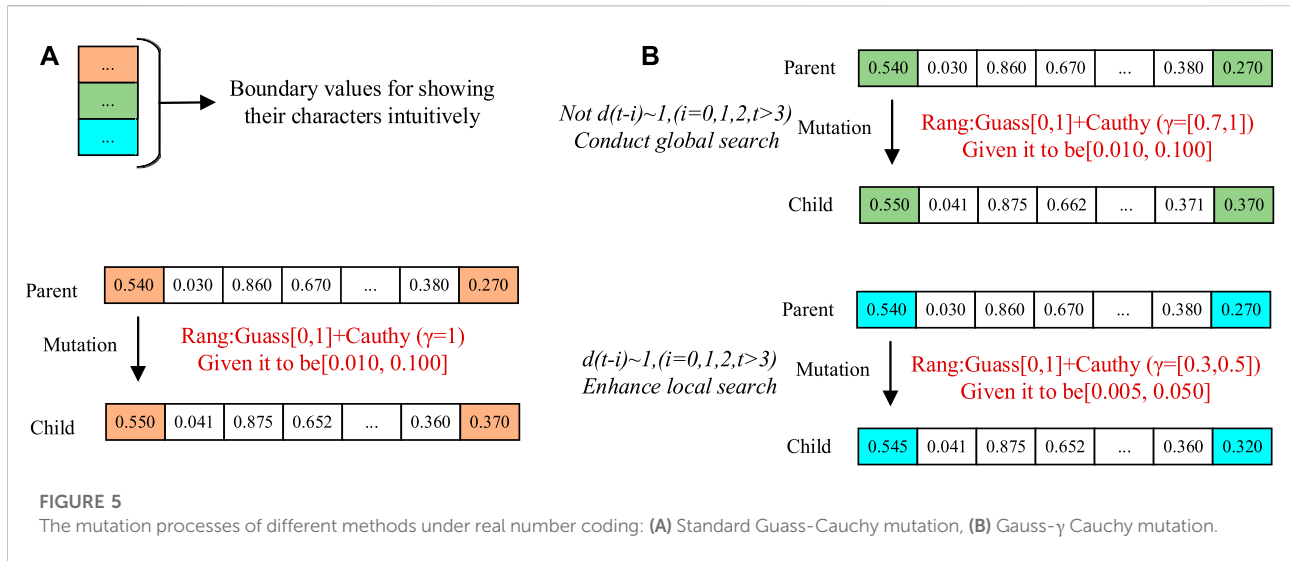


TABLE 2 The genetic operators contained in the nine designed experiments.

No	Methods	Selection operator	Crossover operator	Mutation operator
1	RG	Standard crowding	Single-point adaptive	Standard Gauss-Cauchy
2	ES	H-Mean crowding	Single-point adaptive	Standard Gauss-Cauchy
3	EC	Standard crowding	S(α) arithmetic	Standard Gauss-Cauchy
4	EM	Standard crowding	Single-point adaptive	Gauss-γ .Cauchy
5	EGA	H-Mean crowding	S(α) arithmetic	Gauss-γ .Cauchy
6	SSP	Single Supper parent	Multi-point adaptive	Adaptive mutation
7	MSP	Multi Supper parents	Multi-point adaptive	Adaptive mutation
8	BRK-GA	ELIT/NON-ELITE	BRK	MultiNonUnifMutation
9	IGA	Sus selection	POX	ANS mutation

Function2. Global minimum $f(x) = 0$; $x(i) = 1, i = 1: n$.

$$f_2(x) = \sum_{i=1}^{n-1} 100 \cdot (x_{i+1} - x_i^2)^2 + (1 - x_i)^2, -2.048 \leq x_i \leq 2.048 \quad (8)$$

Function3. Global minimum $f(x) = 0$; $x(i) = 1, i = 1: n$.

$$f_3(x) = 10 \cdot n + \sum_{i=1}^n (x_i^2 - 10 \cdot \cos(2\pi \cdot x_i)), -5, 12 \leq x_i \leq 5.12 \quad (9)$$

Function4. Global minimum $f(x) = 0$; $x(i) = 0, i = 1: n$.

$$f_4(x) = \sum_{i=1}^n \frac{x_i^2}{4000} - \prod_{i=1}^n \cos\left(\frac{x_i}{\sqrt{i}}\right) + 1, -600 \leq x_i \leq 600 \quad (10)$$

Function5. Global minimum $f(x) = 0$; $x(i) = 0, i = 1: n$.

$$f_5(x) = \sum_{i=1}^n |x_i|^{(i+1)}, -1 \leq x_i \leq 1 \quad (11)$$

Function6. Global minimum $f(x) = 0$; $x(i) = 0, i = 1: n$.

$$f_6(x) = -a \cdot e^{-b \sqrt{\sum_{i=1}^n \frac{x_i^2}{n}}} - e^{\frac{\sum_{i=1}^n \cos(c \cdot x_i)}{n}} + a + e^1, -1 \leq x_i \leq 1 \quad (12)$$

In Tables 3, 4, the global indices based on the best, mean, worst, standard deviation (SD), root mean square error (RMSE) and the p -value (from Wilcoxon matched-pairs rank sum test) of the fitness values for 100 runs are tabulated. The bold parts in the Tables 3, 4 indicate the performance index of the proposed method. The significance test is calculated with results of the EGA as the reference group and the single bound value a is set to 0.05. Those values approach perfect modeling results for all enhanced

TABLE 3 Results of global indices for each evolutionary process of design experiments (1).

Test function	Combination forms	Fitness					
		Best	Mean	Worst	SD	RMSE	p-value
Function1	RG	6.38e-09	5.97e-08	4.05e-07	5.64e-08	8.19e-08	5.82e-35
	ES	8.47e-11	1.55e-09	6.88e-09	1.32e-09	2.03e-09	1.95e-08
	EC	7.93e-09	4.67e-08	1.49e-07	2.62e-08	5.35e-08	2.56e-34
	EM	5.34e-10	6.71e-09	3.32e-08	6.13e-09	9.07e-09	1.07e-28
	EGA	3.34e-11	7.70e-10	9.20e-09	1.02e-09	1.27e-09	—
	SSP	5.17e-12	1.40e-07	1.70e-06	2.78e-07	3.09e-07	1.16e-27
	MSP	3.39e-10	5.19e-10	1.05e-09	1.45e-10	5.39e-10	6.11e-02
	BRK-GA	2.63e-05	7.49e-05	1.99e-04	3.18e-05	8.13e-05	2.56e-34
	IGA	1.14e-14	7.95e-08	6.42e-07	1.51e-07	1.70e-07	1.12e-18
Function2	RG	1.17e-10	1.30e-03	4.60e-02	5.20e-03	5.40e-03	1.56e-10
	ES	1.71e-12	3.00e-04	5.60e-03	8.70e-04	9.22e-04	6.25e-02
	EC	0.00	3.28e-04	1.55e-02	1.80e-03	1.80e-03	1.59e-09
	EM	1.89e-12	4.30e-04	9.00e-03	1.30e-04	1.30e-04	6.53e-09
	EGA	0.00	2.00e-04	5.70e-03	7.35e-04	7.64e-04	—
	SSP	1.04e-10	2.30e-03	3.70e-02	5.90e-03	6.30e-03	3.00e-10
	MSP	1.73e-08	1.40e-03	7.40e-03	1.90e-03	3.23e-03	2.78e-19
	BRK-GA	3.48e-09	5.41e-06	5.18e-05	8.57e-06	1.01e-05	1.16e-04
	IGA	—	—	—	—	—	—
Function3	RG	7.64e-10	6.53e-02	5.02e-01	6.93e-02	9.49e-02	2.88e-34
	ES	3.05e-11	1.78e-02	1.18e-01	2.61e-02	3.15e-02	7.10e-24
	EC	5.31e-07	7.71e-05	7.40e-03	7.39e-04	7.39e-04	0.22
	EM	2.60e-09	4.41e-02	3.89e-01	4.92e-02	6.59e-02	4.36e-11
	EGA	1.61e-11	2.04e-10	1.62e-09	2.34e-10	3.10e-10	—
	SSP	1.49e-10	8.72e-03	1.73e-01	1.92e-02	2.10e-02	0.17
	MSP	3.38e-11	5.72e-03	2.86e-02	9.43e-03	1.01e-02	3.70e-10
	BRK-GA	1.36e-05	1.63e-05	1.87e-05	1.09e-06	1.64e-05	0.13
	IGA	1.43e-12	7.84e-09	8.80e-08	1.44e-08	1.63e-08	2.3e-03

measures. Considering the adaptive Neighborhood Search in IGA requires variation points greater than five in hierarchical optimization, while the standard coding length of function2 is 2, so IGA is not used to solve the function2. A comparison of the results based on the performance measures in Tables 3, 4 is also plotted in Figures 6, 7. To obtain the convergence data based on the number of runs, Table 5 details the statistical results that fall into different fitness intervals during the 100 independent runs, in which EGA has been shown in bold. Though for relatively severe standards, 100 runs are not enough, the experienced number of runs is still to attain reasonable level of accuracy, which shows the optimization potential of the method proposed in this paper to improve the optimal solution of objective functions.

Further analysis demonstrates that the three enhanced genetic operators and the EGA balance the distribution and

convergence of the algorithm with the number of iterations. Taking function1 as an example in Table 3, the best values, mean values and worst values for designed experiments 1–5 (from EG to EGA) lie in the ranges of 10^{-09} to 10^{-11} , 10^{-08} to 10^{-10} , and 10^{-07} to 10^{-09} , respectively. Only when using above methods to optimize function4, is the performance of EGA slightly worse than that of the Reference group.

Compared with other strategies proposed in the latest research, the EGA shows certain advantages in different aspects. Specifically, taking function1 as an example, the SD and RMSE of the EGA in Table 3 are smaller than those of SSP, which proves that EGA's stability is higher. Taking function2 and 3 as examples, the performance of the EGA is better than the MSP algorithm in all aspects. In function4,

TABLE 4 Results of global indices for each evolutionary process of design experiments (2).

Test function	Combination forms	Fitness					
		Best	Mean	Worst	SD	RMSE	<i>p</i> -value
Function4	RG	4.30e-06	5.34e-02	2.91e-01	6.27e-02	8.21e-02	0.10
	ES	5.18e-07	4.82e-02	2.65e-01	5.70e-02	7.44e-02	0.50
	EC	6.66e-08	4.63e-02	3.07e-01	5.54e-02	7.20e-02	0.18
	EM	1.91e-06	5.21e-02	6.00e-01	8.03e-02	9.54e-02	0.06
	EGA	2.64e-05	4.44e-02	2.60e-01	4.92e-02	6.60e-02	—
	SSP	1.81e-06	1.72e-02	8.83e-02	1.81e-02	2.49e-02	4.19e-05
	MSP	3.80e-07	8.90e-03	6.38e-02	1.03e-02	1.36e-02	3.03e-11
	BRK-GA	3.12e-04	1.10e-03	2.60e-03	4.01e-04	1.20e-03	1.97e-05
	IGA	4.85e-13	1.39e-08	1.53e-07	2.68e-08	3.01e-08	2.56e-34
Function5	RG	6.81e-13	3.80e-10	2.80e-09	5.82e-10	6.93e-10	7.14e-30
	ES	4.68e-14	8.59e-11	2.55e-09	2.94e-10	3.05e-10	1.23e-10
	EC	1.84e-14	3.61e-11	4.22e-10	6.97e-11	7.82e-11	9.67e-31
	EM	2.18e-14	4.62e-11	1.13e-09	1.47e-10	1.54e-10	3.73e-05
	EGA	1.25e-14	9.20e-12	4.32e-10	4.42e-11	4.49e-11	—
	SSP	3.37e-13	7.58e-13	9.08e-13	1.34e-13	7.70e-13	6.80e-03
	MSP	1.31e-13	6.93e-13	9.07e-13	1.66e-13	7.12e-13	2.30e-03
	BRK-GA	6.59e-15	9.83e-10	7.01e-09	1.45e-09	1.74e-09	2.71e-29
	IGA	3.17e-13	3.45e-09	3.02e-08	5.48e-09	6.46e-09	6.32e-31
Function6	RG	6.42e-09	5.31e-01	2.31e+01	7.77e-01	9.30e-01	5.87e-36
	ES	1.73e-10	5.90e-01	2.01e+01	7.03e-01	9.21e-02	4.79e-34
	EC	1.44e-06	3.28e-06	7.32e-06	1.10e-06	3.45e-06	2.56e-34
	EM	1.36e-09	3.90e-01	2.01e+01	6.57e-01	7.61e-01	1.47e-34
	EGA	6.73e-12	1.83e-10	9.22e-10	1.91e-10	2.64e-10	—
	SSP	1.51e-05	1.76e-05	1.90e-05	8.20e-07	1.77e-05	2.56e-31
	MSP	1.36e-05	1.63e-05	1.87e-05	1.09e-06	1.64e-05	3.16e-34
	BRK-GA	1.06e-03	3.04e-03	7.10e-03	8.73e-04	3.17e-03	5.27e-31
	IGA	1.18e-06	7.96e-05	4.65e-04	7.70e-05	1.10e-04	3.56e-34

for example, the best value in 100 runs is smaller than BRK-GA as shown in Figure 7. Compared with IGA, although the performance enhancement of EGA in function4 is average, the optimization effect of function5 and six are better as shown in Figure 7.

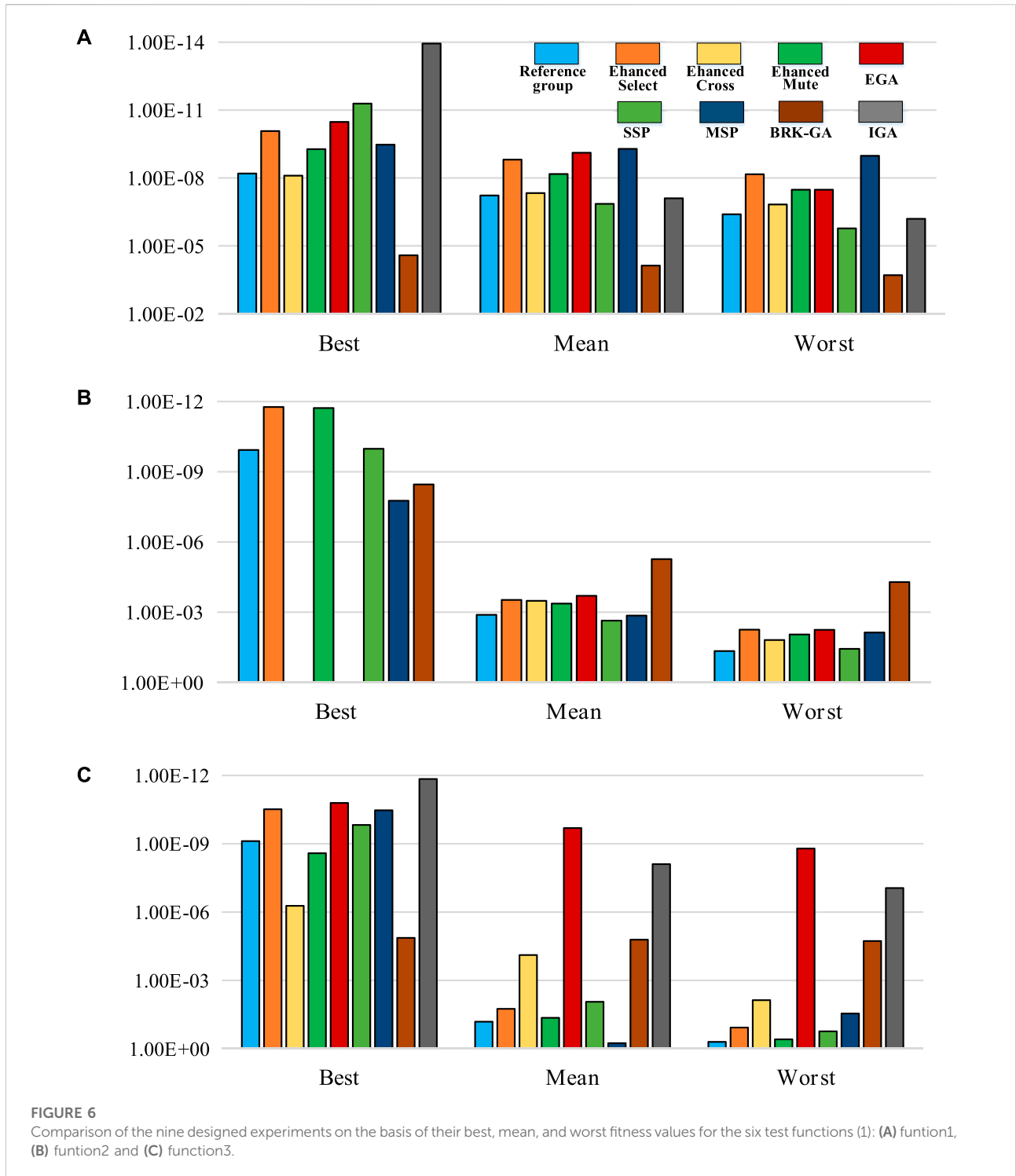
As long as *p*-value is less than α (0.05), the two results can be considered to be significantly different. According to the simulation results of rank sum test, except for the Enhanced crossover, SSP and BRK-GA in function3, which are greater than α , all the other results are far less than α . It can be said that the EGA proposed in this paper shows superiority over the latest algorithms.

These results show the effectiveness and superiority of the proposed EGA scheme in terms of accuracy and convergence.

4 Design and analysis of enhancement of genetic algorithms wavelet neural network

4.1 Wavelet neural network

The WNN (Tinos et al., 2018) has always been deemed a wavelet-based functional linkage network or an extension of radial basis function (RBF) network containing its unique virtue, i.e., potent self-adaptability, and brief network structure. From the perspective of its structural form, the transfer neuron of a single hidden layer in the WNN is the Morlet wavelet windowing function, where the built-in function includes scaling and shifting arguments. Each neuron connects to its adjacent neuron *via* connection weights (Peng and Xiang, 2020). The basic topology of the WNN is shown in Figure 8.



In Figure 8, X_1, X_2, \dots, X_k are the input signals of the WNN, and Y_1, Y_2, \dots, Y_m denote the output signals of the WNN. ω_{ij} and ω_{jk} are the connection weights from the input layers to the hidden layers and from the hidden layers to the output layer, respectively.

In this paper, the Morlet function is employed as φ (wavelet basis function), and it is given as follows:

$$\psi_{a,b}(x) = \cos(1.75x) \exp(-x^2/2) \tag{13}$$

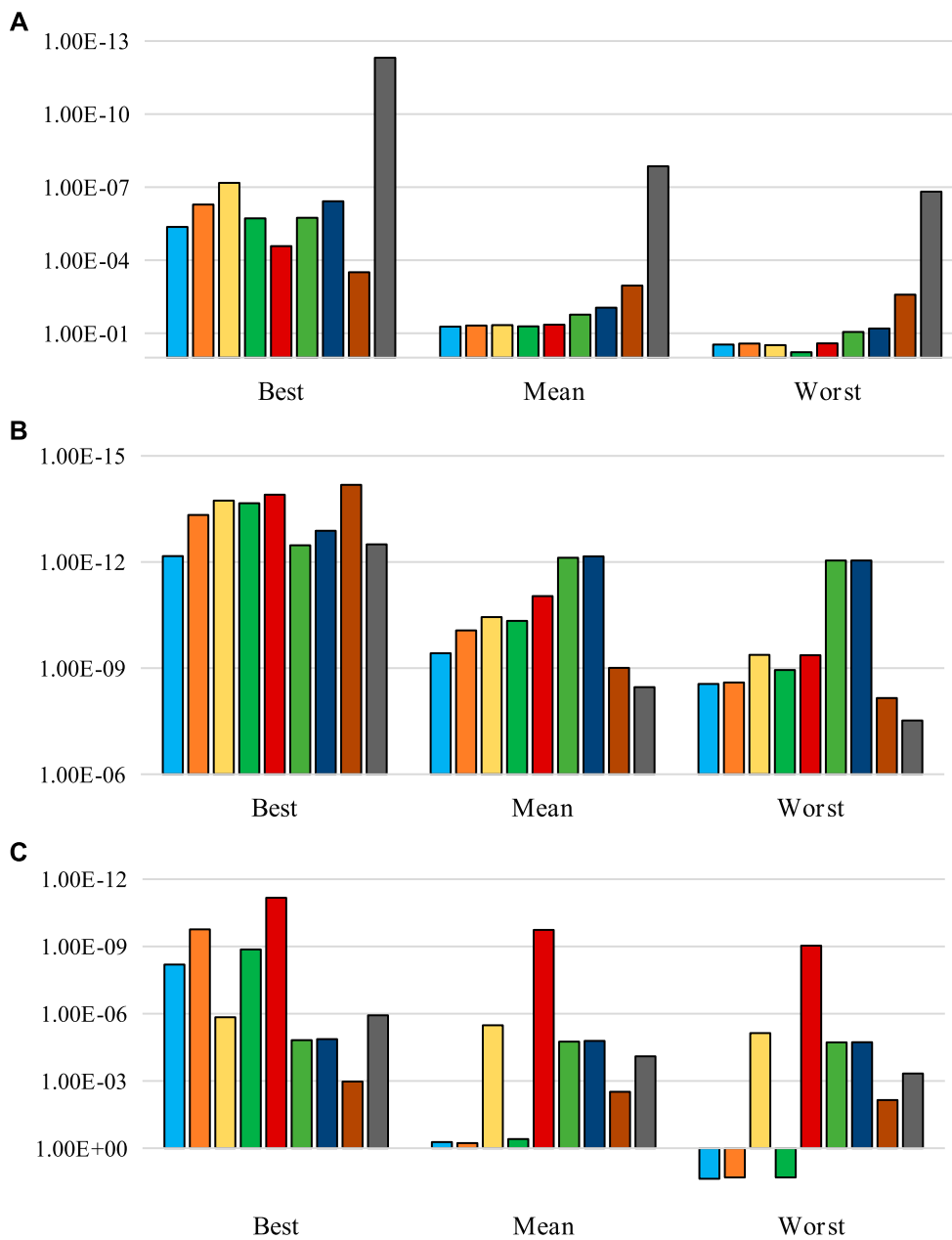


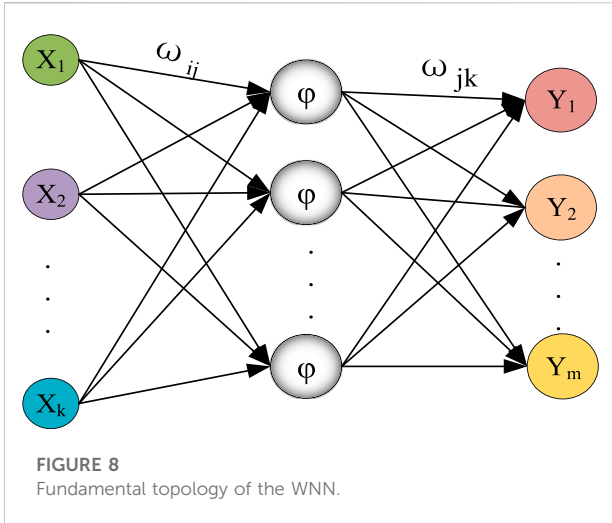
FIGURE 7 Comparison of the nine designed experiments on the basis of their best, mean, and worst fitness values for the six test functions (2): (A) funtion4, (B) funtion5 and (C) function6.

4.2 The design flow of enhancement of genetic algorithms wavelet neural network

Considering that the EGA has a strong global search ability and high search precision, optimizing the initial weights, as well as the scaling and shift factors of the WNN, with the EGA is expected to make improve the prediction performance of the network model. The enhanced algorithmic flow is shown in Figure 9.

The specific implementation steps are as follows:

- (1) The topology of the WNN (as described by Figure 8), where the wavelet basis function is the Morlet function, is used by the EGA algorithm to find $\omega_{ij}, \omega_{jk}, a_j, b_j$.
- (2) Population initialization: determining the population size and the maximum number of iterations. Individuals are coded with real numbers, and each individual is composed of weights ω_{ij} and ω_{jk} , a scaling factor a_j , and



- (4) Genetic operations: i. Selection: The H-mean crowding strategy is carried out according to the pseudocode in Table 1 ii. Crossover: New individuals are generated by performing nonuniform arithmetical crossover on the selected parents, as shown in Eq. 3. iii. Mutation: The Gauss-r. Cauchy function is performed on the participating individuals, as shown in Eqs 4, 5.
- (5) The loop is stopped, the current optimal solution is obtained, and the decoded weights ω_{ij} and ω_{jk} , scaling factor a_j and shift factor b_j are used as the initial input parameters of the WNN.
- (6) The WNN is used for training; it is judged whether the network training process is finished according to the preset error and number of iterations. Finally, ω_{ij_best} , ω_{jk_best} , a_{j_best} , and b_{j_best} are obtained by the above steps, and then the parameters are applied to the WNN model.
- (7) The trained model is used to test the samples, and the resulting performance indicators are analyzed.

4.3 The convergence analysis of enhancement of genetic algorithms wavelet neural network

The essence of EGAWNN is to optimize the initial parameters of the WNN through the EGA solver so that they are independent of the operation process. We only need to prove the convergence of the EGA and WNN. Regarding the convergence of the WNN, references (Jafarmadar, 2020), (Li et al., 1997; Liu et al., 2021) have given relevant proofs, so there is no need to repeat these steps. The convergence analysis of the EGA is given below.

Reference (Wang et al., 1996) deduced sufficient conditions for the convergence of the GA. The intensity function f of this

paper is Eqs 14, 15, the problem space N is the code of the solution, and each point has a corresponding solution.

The class S existing in N satisfies the following derivation:

$$\exists r \in V, (\forall i \in N, i \in S \Rightarrow f(i) \geq r) \cap (f(i) \geq r \Rightarrow i \in S); \text{ then, } S \text{ is a superior class. According to theorem one in (Wang et al., 1996), class } S \text{ is a conformance class.}$$

Because the crowding strategy in this paper divides a population into GoodChrom and BadChrom, the following derivation conforms to the above properties:

$$\exists r \in \text{BadChrom}_V, (\forall i \in S, \text{GoodChrom} \in S \Rightarrow f(i) \geq r) \cap (f(i) \geq r \Rightarrow i \in S)$$

In summary, the EGA proposed by this article contains a conformance class S .

For each class $S^r \in N$, the following theorem two from (Liu et al., 2021) holds:

$$\text{If } f(S^r, N) \geq f(S, N), \quad \exists S^r \cap N \subseteq S \quad \text{or} \\ f(S \cap S^r, N) > f(S^r, N), \quad \text{class } S \text{ has stability.} \\ f(\text{Pop}, N), \text{Pop} \in N \text{ is the average fitness of Pop.}$$

Because the elitist strategy is used in the selection process of this article, $f_{t+1}(\text{best}) \geq f_t(\text{best}), \text{best} \in S$ must hold, so $\exists \text{best} \in S^r, S^r \in S \Rightarrow S^r \cap N \subseteq S, \text{st. } f(S^r, N) \geq f(S, N)$.

The above derivation proves that regardless of the number of iterations, S^r does not replace S in the next generation; instead, they grow together, which ensures that the conformance class is not replaced by other classes.

If the conformance class is stable, the GA can converge to the optimal solution (Wang et al., 1996). Additionally, Pan (Pan, 1998) proved that adopting the elitist model can enhance the stability of the algorithm, and this model makes the SGA easily converge to the global optimum with a probability of one in the end. All of the above factors certify that the EGA is convergent.

5 An industrial experiment regarding aluminum electrolysis

5.1 Experimental objects and model parameters

A new-type aluminum cell, combined with a perforated anode and a heteromorphic cathode, is used to test the reliability of the EGAWNN solver, as shown in Figure 10, where W represents the DC energy consumption per ton of aluminum, the perforated anode has multiple holes built into it to allow air bubbles to escape and the heteromorphic cathode can reduce molten aluminum fluctuations by optimizing cathode structure.

Modern aluminum electrolysis devices are complex process equipment with multiphase and multifield

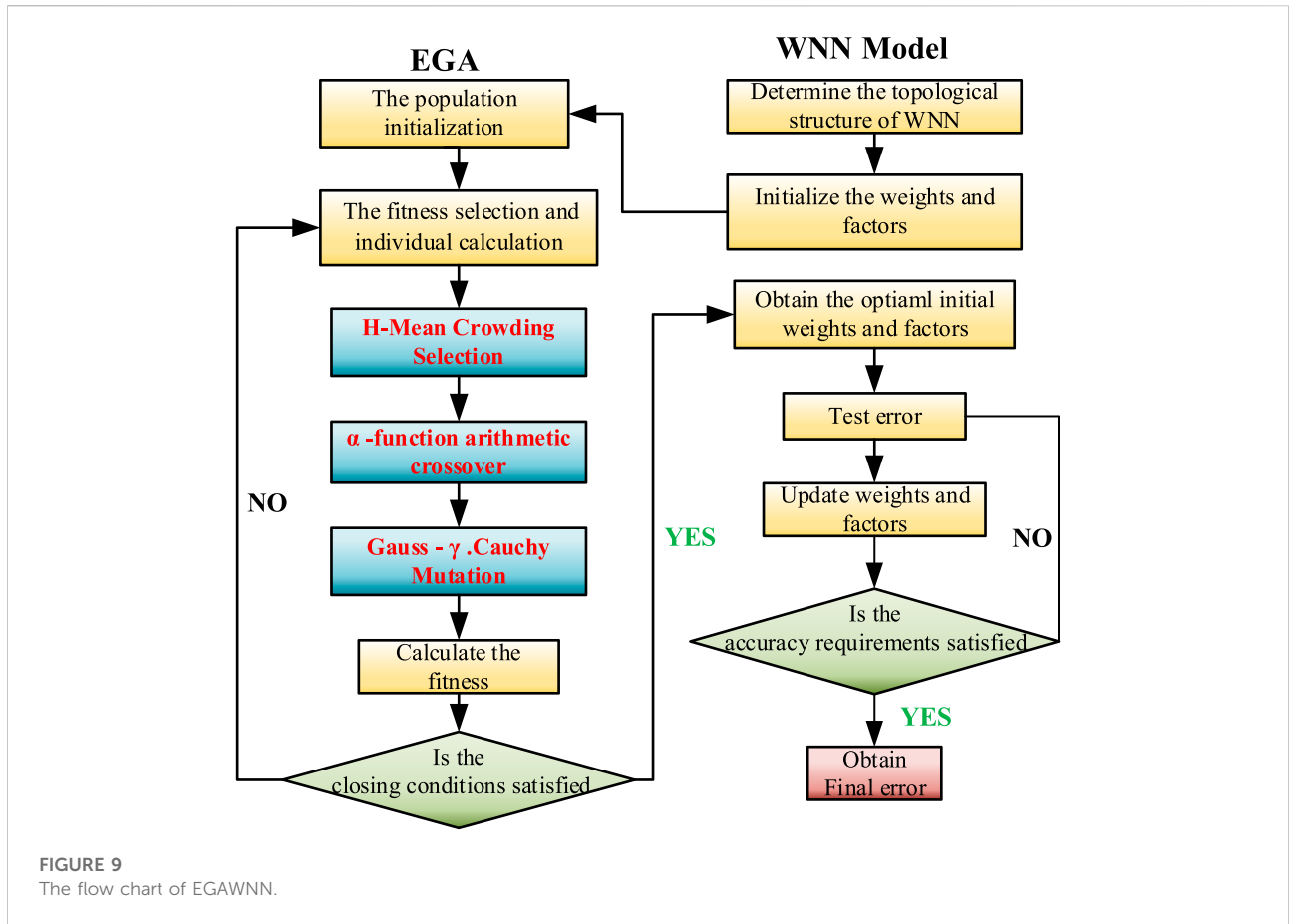


FIGURE 9 The flow chart of EGAWNN.

interactions (Gui et al., 2018). There are diversified physical and chemical changes inside these devices, as well as frequent exchanges of raw materials, energy and labor information with the external environment. When modeling the energy consumption of aluminum electrolysis using the traditional WNN, the structure is unstable due to the stochastic determination of the initial parameters, which may lead to a large forecasting error. The proposed EGAWNN solver can mine the best initial weights and factors and thereby increase the accuracy and authenticity of the prediction results.

Considering the experiences of expert and the impact of the real process on the DC energy consumption of an aluminum electrolyzer, we select the following nine effective decision parameters: the series current (A), molecular ratio (1), aluminum level (cm), electrolyte level (cm), cell temperature ($^{\circ}\text{C}$), aluminum output (kg), daily consumption of fluoride salt (kg), NB times (s), and cell voltage (mV) (Tai-Fu et al., 2014). Based on the computer measurement and control system of Chongqing Tiantai Aluminum Co., Ltd. in Southwest China, the daily reported data of the electrolytic cell are collected, and 773 groups of data samples are obtained, as shown in Table 6.

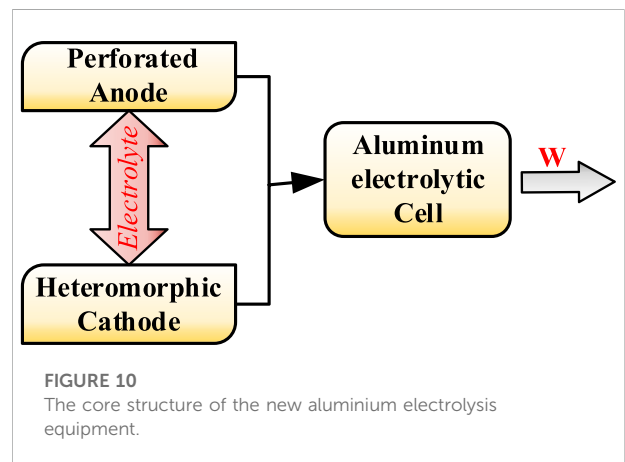


FIGURE 10 The core structure of the new aluminium electrolysis equipment.

5.2 The analysis of the experimental results based on enhancement of genetic algorithms wavelet neural network

The 773 groups of aluminum electrolysis data samples in Table 6 are assigned to the training group ($n = 700$) and test group ($n = 73$). The inputs are the nine selected decision

TABLE 6 Data samples of aluminium electrolytic cell.

Parameters	Samples				
	1	2	3	—	773
Series current (A)	1,679	1,679	1,685	—	1,682
Molecular ratio	2.32	2.43	2.41	—	2.54
Aluminium level (cm)	22.1	18	21	—	23
Electrolyte level (cm)	17	15	16.2	—	17
Cell temperature (°C)	948	951	942	—	947
Aluminium output (kg)	1,240	1,280	1,310	—	1,300
Daily consumption of fluoride salt (kg)	19.8	29	22.4	—	21
NB times (1)	952	947	948	—	961
Cell voltage (mV)	3,712	3,679	3,808	—	3,721
DC power consumption (kW.h/t-Al)	11,842	11,839	11,359	—	11,863

parameters, and the output is the unit DC power consumption. When the number of hidden layers is too small, the error rate of the predicted output may be too large. When the number of hidden layers is 9, the errors are reduced to a small amount. Therefore, the wavelet network structure is 9-9-1. Thus, it can be concluded that the dimensions of the state variable in EGAWNN are $9 \times 9 + 1 \times 12 + 1 \times 12 + 1 \times 12 = 118$. In this algorithm, the selection rate η_s is 0.87; the number of parents for crossover η_c is three; the number of mutation η_m individuals is two; the population size N is 40; the maximum number of iterations (MAXGEN) is 100; the learning rate of the WNN lr_1 is 0.01, and lr_2 is 0.001; the adjustment rate is 1.04; and the wavelet basis function is the Morlet function.

To prove the validity of the presented algorithm, under the same experimental samples and simulation platform, MATLAB R2020a (CPU: RTMi5-1038NG7; RAM: 15.8 GB; CPU: 2.00 GHz), the WNN, GAWNN, particle swarm optimized wavelet neural network (SOWNN), the four new algorithms mentioned in Section 3 optimized the WNN (SSPWNN, MSPWNN, BRK-GAWNN, and IGAWNN) and EGAWNN are separately used to model the energy consumption of the aluminum electrolytic tank, helping obtain contrastive experimental results.

Figure 11 visually shows the fitting effect of the real process energy consumption based on the above-mentioned eight modeling techniques. The performance ranking of process energy modeling effect from excellent to poor is as follows: EGAWNN, IGAWNN/BRK-GAWNN, MSPWNN, SSPWNN, GAWNN, PSOWNN, and WNN, where the fitting effect of IGAWNN and BRK-GAWNN is close. Overall, the prediction performance of EGAWNN is better than other models, which proves that this approach is feasible to further develop the modeling capabilities of the GAWNN.

The EGAWNN uses three enhanced operators, i.e., the H-Mean selection strategy, a new crossover function and an adaptive proportional coefficient γ into the Cauchy mutation, to mine the optimal parameter combination inside the model, which greatly enhances the convergence and the prediction accuracy of the built model. Based on the above analysis and Figure 12, EGAWNN has a lower relative error rate and better predictive performance than the other seven models, especially on some of the data with large fluctuations. The above analysis also shows that EGAWNN has good stability.

Table 7 compares the indicative data of each energy consumption model, for which 6 regression evaluation indicators, significance tests and algorithmic complexity metrics are listed, including the Maximum, Minimum, Mean, error sum of squares (SSE), mean square error (MSE), and RMSE. In addition, we carry out an analysis of algorithmic complexity and perform hypothesis testing based on the Wilcoxon matched-pairs signed-ranks test, where the significance test is calculated with the prediction results of EGAWNN as the reference group, and the single bound value α is set to 0.1, as shown in Table 7. The bold part in the table highlights the performance of the proposed method.

According to the numerical results in Table 7, it can be seen that the absolute error indicators of EGAWNN are obviously lower than those of WNN, GAWNN and PSOWNN, and slightly better than those of SSPWNN, MSPWNN, BRK-GAWNN, and IGAWNN. From the perspective of algorithmic complexity, compared with GAWNN control groups, the time complexity of EGAWNN increases due to secondary sorting in the selection operation of the EGA. However, this small difference does not affect the feasibility of the algorithm. The above results prove that the method proposed in this paper has certain modeling advantages over other methods.

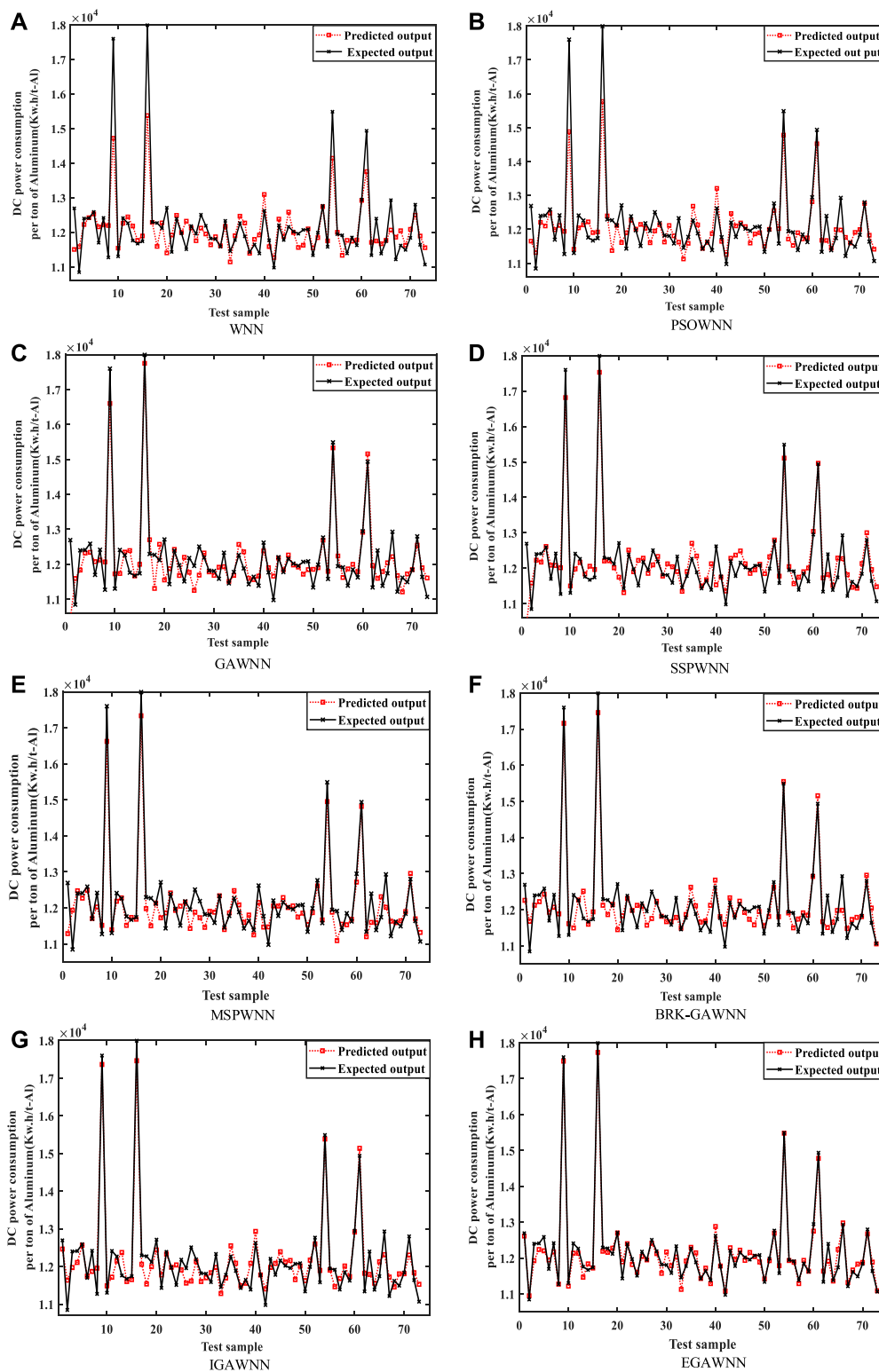


FIGURE 11

The prediction outputs in terms of DC power consumption based on: (A) WNN, (B) PSOWNN, (C) GAWNN, (D) SSPWNN, (E) MSPWNN, (F) BRK-GAWNN, (G) IGAWNN, and (H) EGAWNN.

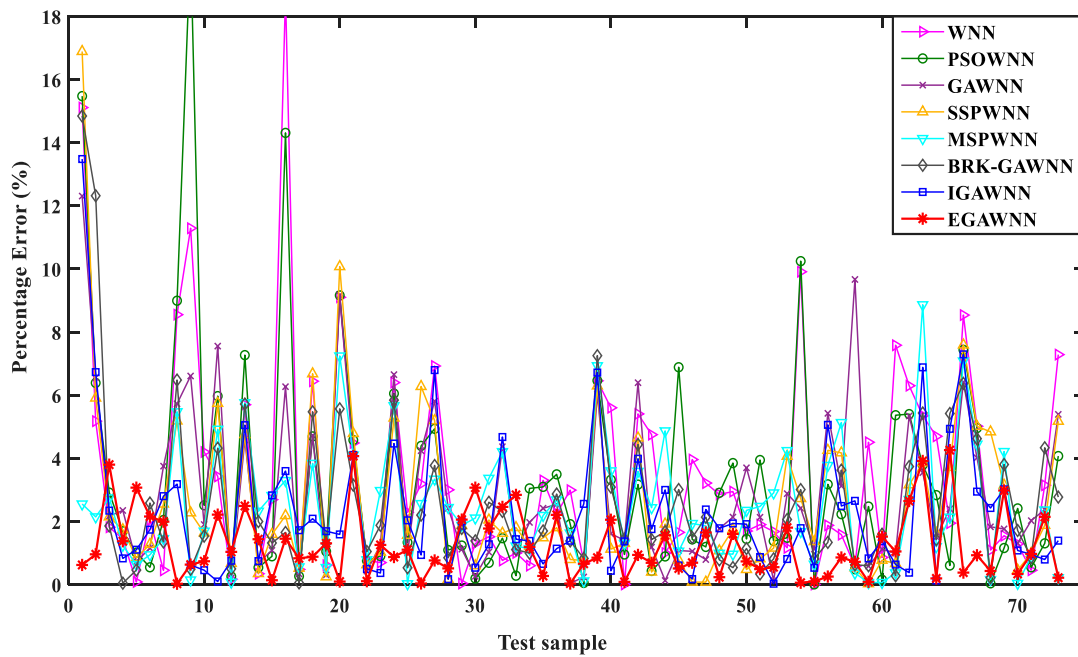


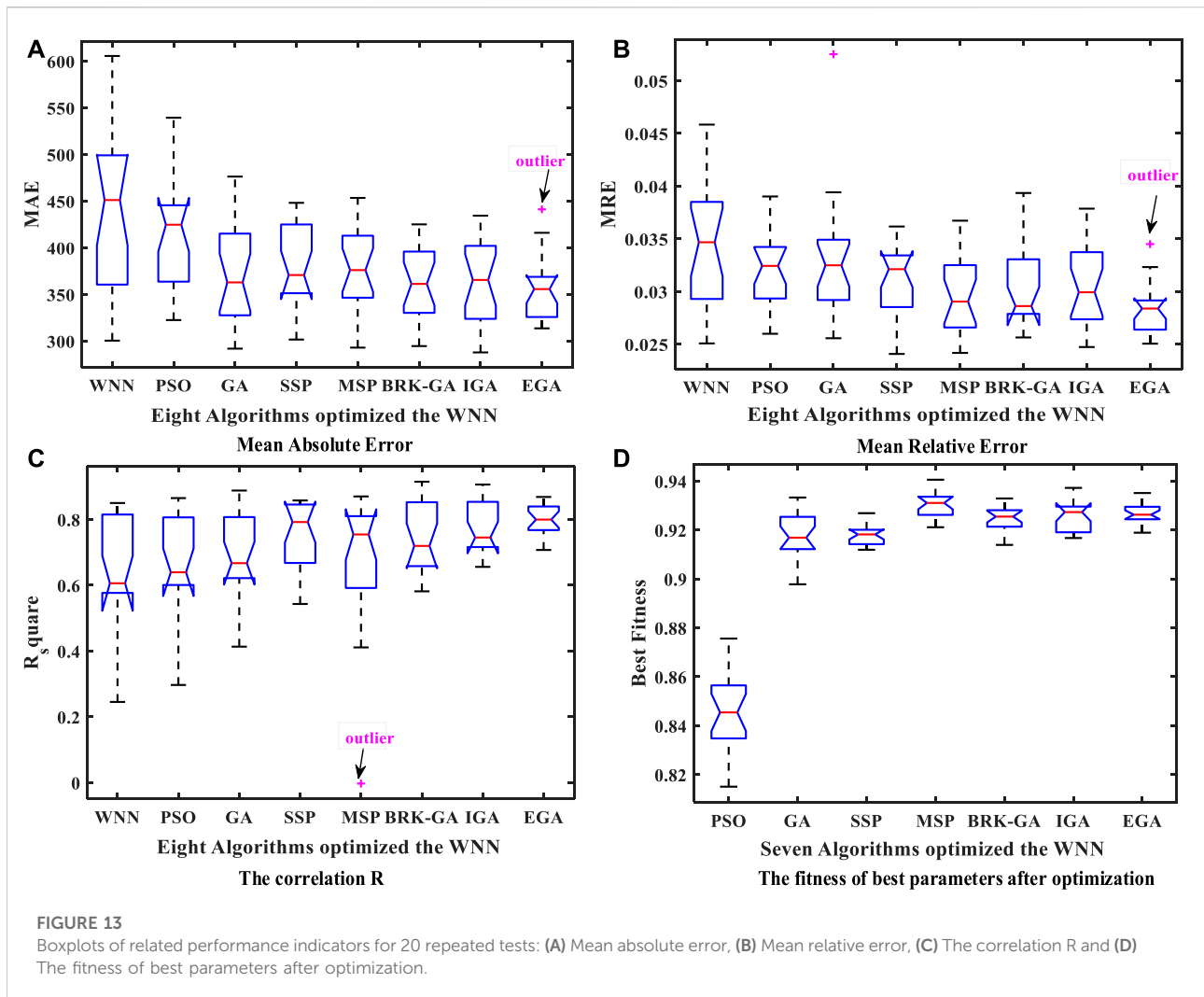
FIGURE 12
A comparison of the relative error percentages yielded by different models.

TABLE 7 Relevant performance indices yielded by different models.

Model	Comparison of absolute error indicators in test sets						Statistical test	Complexity	
	Max	Min	Mean	SSE	MSE	RMSE	<i>p</i> -value	Time	Space
WNN	18.6	2.6e+03	3.5	2.97e+07	4.08e+05	638.72	0.04	O (n ²)	O (n ²)
PSOWNN	20.2	5.9e+03	3.3	3.26e+06	2.38e+05	571.45	0.06	O (n ²)	O (n ²)
GAWNN	12.3	3.7e+02	2.9	1.89e+07	2.59e+05	508.90	0.09	O (n ²)	O (n ²)
EGAWNN	6.3	2.5e+02	1.2	1.62e+05	2.21e+03	305.72	—	O (n ³)	O (n ²)
SSPWNN	16.1	2.7e+02	2.6	1.57e+07	2.15e+05	464.60	0.10	O (n ³)	O (n ²)
MSPWNN	8.7	2.6e+02	2.4	1.07e+07	1.46e+05	382.17	0.13	O (n ³)	O (n ²)
BRKWNN	14.0	4.2e+02	2.6	1.39e+07	1.91e+05	437.55	0.20	O (n ³)	O (n ²)
IGANWNN	11.4	2.7e+02	2.2	1.11e+07	1.52e+05	389.91	0.32	O (n ³)	O (n ²)

To avoid the accidental influence of the original randomized parameters on the model evaluation, this algorithm conducts 20 independent repeated experiments on each model. Then, the relevant performance indicators are calculated based on the experimental results, including the mean absolute error (MAE), the mean relative error (MRE), the correlation (R) (Li W. et al., 2017) and the best population fitness value. Figure 13 shows the favorable stability of the energy consumption model based on EGAWNN in the form of boxplots. Simultaneously,

compared with the SGA, although the SSP, MSP, BRK-GA IGA, and EGA all improves the best fitness value of the population, EGA’s effect is more obvious. These results verify the advantage and validity of the EGA, which can deeply mine the predictive potential of the model by finding the optimal initial parameter combination of the energy consumption model. Meanwhile, the limitation of the proposed method in this paper for industrial production is that the input parameters of the model need to be collected continuously.



6 Conclusion

To obtain a high-precision energy consumption model for an AEMS, this study presents a novel framework based on a WNN and the EGA. In the EGAWNN algorithm, there are three main improvements, as follows:

- (1) The H-Mean metric is developed to maintain the discreteness of the crowding strategy and is effectively applied to prevent premature convergence.
- (2) A new sigmoid-based function $S(\alpha)$ is designed to update the nonuniform arithmetic crossover operation by setting intersections regularly.
- (3) An adaptive proportional coefficient γ is introduced into the Gauss-Cauchy mutation to flexibly adjust the mutation step size.

A series of numerical experiments are performed, and these prove the efficacy of the proposed scheme. The algorithm has good potential to be exploited as an alternate, accurate and robust computing framework for building prediction models in various complex systems. However, it is worth highlighting here that the EGA is restricted to obtaining only the initial weights and factors of the WNN. In the future, we will explore the integration of the EGA into the internal topology structure of the WNN during every training process.

Data availability statement

The original contributions presented in the study are included in the article/supplementary material, further inquiries can be directed to the corresponding author.

Author contributions

Conceptualization, LY and QF; methodology, LY and QF; software, QF and YL; validation, LY; formal analysis, LZ, LY, and QF; data curation, LZ and QM; writing—original draft preparation, LY and QF; writing—review and editing, YL and QM; visualization, LY and QF All authors have read and agreed to the published version of the manuscript.

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