1. HYPER-PARAMETERS SETTING

In our architecture we use a 64-bits sequences represent a algorithm, the coding of all algorithms is shown in Table S1.

The decoding rules are described in following section. In addition, we provide source code for decoding (see https://github.com/loujiabin1994/decoder_ep). Uniformly, we give each algorithm a 25-generation iteration cycle, and each generation sets 10 individuals.

Table S1. Binary encoding of all algorithms

algorithm	coding sequence
GA	0100011000 1001011101 0100001101 0001100110 0000000000 0000000000 0000
CIPSO	0100011000 1111101110 1010011101 0000000110 0000000000 0000000000 0000
CIPDE	0100011110 1101111111 0110110000 1101010110 0001011010 1010110010 1011
JADE	0100011100 1111111010 0101111111 0010100110 1000000101 0111101111 0000
mWPS	01000111010 1110011000 0001101111 1100101100 0100011010 0110000100 0001
HHPSO	0100011000 1001011101 1100001101 0111100110 0111011011 0100101000 0010

2. DECODING RULES

The decoder will covert a genome into the related program according to the criterion established at the time of encoding. This section will describe the criterion in detail.

- **Initialization**

In the term of initialization, 10-bits genes are encoded to represent some specific operators, as seen in Table S2. Concretely, there are four candidates in Di, i.e., default, Island Model, MAPS, CEGDA, and four options in Cv, i.e., Bezier, B-spline, RTS, Tangent circle.

Table S2. 11-bits genes for Initialization

Token	Summary	Coding	Order
#CP	the number of Control points	[00, 11]	0
#P	the number of populations	[00, 11]	2
#I	the number of individuals in a population	[000, 111]	5
Di	the methods of dividing populations	[00, 11]	7
Cv	the Curve used to smooth the Control points	[00, 11]	9

- **Sorting and Selection**

As shown in Table S3, So implies sorting operators, which consist of Penalty Function, Non-dominated Sorting, α-level comparison and the Number of unfulfilled constraints; Se, which denotes selection operators, consists of Tournament selection, Truncation selection, Roulette Wheel Selection and Stochastic Universal Sampling; $Rank$ assigns scores as selection criterion to the sorted individuals, these scores could be linear, logarithmic, exponential, etc.

- **exploitation and exploration**

The genes in this section can be depicted in Table S4, where $Twins$ and $Infer$ operate on the offspring after exploitation and exploration, respectively.

- **Ending Criterion**

The Ending Criterion is a crucial option to avoid additional calculation. Generally, we end up a EA with fixed generation or running time, which is encoded in the token End and End_{param}. But there exist some cases denoting that even we keep executing the algorithm, the progress we make will be quite limited. For example, when the prematurity happens, which means that the algorithm is trapped into local minimum, we could stop this population to avoid wasting

Table S3. 13-bits genes for sorting and selection

Token	Summary	Coding	Order
So	the measure method for sorting	[00, 11]	11
So_{param}	the parameters of the measure method	[000, 111]	13
$Elitism$	select top $n\%$ as survival	[00, 11]	16
$Rank$	the ranking system to evaluate the solutions	[00, 11]	18
Se	the selection method used to pick a individual	[00, 11]	20
Se_{param}	the parameters of selection method	[00, 11]	22

Table S4. 12-bits genes for exploitation and exploration

Token	Summary	Coding	Order
$Exploit$	the algorithm chosen as exploitation operator	[000, 111]	24
$Exploit_{param}$	the parameters of $Exploit$	[00, 11]	27
$Twins$	if allow two children (if exist) to next	[0, 1]	29
$Explore$	the algorithm chosen as exploration operator	[000, 111]	30
$Explore_{param}$	the parameters of $Explore$	[00, 11]	33
$Infer$	if reserve the inferior generated by exploration operator	[0, 1]	35

computational resources. The definition of prematurity and related parameters are encoded in $Case1$ and $Case1_{param}$, consisting of default setting (do nothing in this term), evolutionary stagnation, population homogenization and goal achievement. Similarly, in $Case2$, where the population is similar to a solved population in the situation of multi-population, the options are default, reset, killing, and adjustment.

Table S5. 13-bits genes for Ending Criterion

Token	Summary	Coding	Order
End	the method used as ending criterion	[0, 1]	36
End_{param}	the parameters of End	[000, 111]	37
$Case1$	the definition of prematurity	[00, 11]	40
$Case1_{param}$	the parameters of $Case1$	[00, 11]	42
$Case2$	the operation when the population is similar to a solved one	[00, 11]	44
$Case2_{param}$	the parameters of $Case2$	[00, 11]	46
$Case3$	if restart the algorithm when it stops early	[0, 1]	48

- **other operators**

Besides the previously proposed operations, there are other non-standard operators to improving the performance of algorithm and speed up the convergence. As presented in Table S6, the $Cell$, $Injc$, $Anti$, $Fbcl$ and $Decy$ are used to maintain the diversity of the population. And the rest of operators are used mainly for improving the rate of convergence.

Table S6. 15-bits genes for other operators

Token	Summary	Coding	Order
Cell	Using Cellular	[0, 1]	49
Injc	Using Injection method	[00, 11]	50
Rpar	Using Repair algorithm to enforce the feasibility	[00, 11]	52
Mgrt	Using migration operator to keep the info sharing between populations	[00, 11]	54
Anti	Using Antibody to prevent the domination of one genotype	[00, 11]	56
Fbcl	Forbidding the clones in the population	[0, 1]	58
Decy	using the Decay Factor Algorithm	[00, 11]	59
PFIH	using the PFIH to optimize the solution	[000, 111]	61