



## Study on GA-based matching method of railway vehicle wheels

Jiang Zeng-qiang\*, Chang Xiao-e and Wang Yu-yang

School of Mechanical, Electronic & Control Engineering, Beijing Jiaotong University, Beijing, China

### ABSTRACT

*In the railway vehicle assembly problem, it is asked to choose the optimal combination of the railway vehicle wheels with the multiple constraints of assembly requirements, according to the multi-parameter characteristics of railway vehicle wheels matching, the mathematical model of this problem was built, and the solving method based on genetic algorithm was developed, and the corresponding coding method, crossover operation and mutation operation and so on were designed. The method for matching railway vehicle wheels is established, the efficiency and accuracy of the wheels matching was improved by above method, then the running safety of railway vehicle was improved. Finally the effectiveness of the method was verified by an example.*

**Key words:** Railway Vehicle Wheels, Wheel Matching, Genetic algorithm.

### INTRODUCTION

Wheels assembly is an important part during assembly of the railway vehicle, its assembly quality is directly related to running safety. Matching of vehicle wheels not only needs to comply with relevant provisions, also needs to meet the requirements of various technical parameters and higher accuracy. Now, matching of railway vehicle wheels is basically done by hands or other ways[1][2][3], but these ways need a large workload, the matching quality is not stable, and it is difficult to achieve an ideal result. So, a GA-based matching method is put forward to solve matching problem of the railway vehicle wheels in this paper.

### 1 PROBLEM DESCRIPTION AND MATHEMATICAL MODELING

#### 1.1 Problem description

Matching of railway vehicle wheels is to match axle and wheels according to the parameters of wheel pair. This problem is complex because the wheel and the axle need to meet a series of rigid constraints:

- 1)The diameter difference of the two wheels in the same wheel assembly needs to meet the requirements[4].
- 2)Wheel rim width difference in the same wheel assembly is not more than 5 mm[5].
- 3)Axle and wheel assembly should be carried out matching work according to the requirements of the amount of interference.

#### 1.2 Mathematical modeling

Mathematical model of railway vehicle wheels matching includes an objective function and some constraints. The objective function makes the number of the matched wheel assembly maximal, and constraints is the assembly parts meet some specific requirements.

Assume a P parts and two Q parts are a pair of assembly parts. Now there are P parts( $i = 1, 2, \dots, n$ ) and Q parts ( $j = 1, 2, \dots, s$ ), so the mathematical model for railway vehicle wheel matching is:

$$\text{Objective function: } F(S) = \max \sum_{i=1}^n b_i \quad (1)$$

$$\text{Where } b_i = \begin{cases} 1 & \text{(The } i\text{th assembly group meet the matching requirements)} \\ 0 & \text{(The } i\text{th assembly group don't meet the matching requirements)} \end{cases}$$

Constraints:

$$1) |d_{2j} - d_{2j-1}| < a_1 \quad (2)$$

$$2) |B_{2j} - B_{2j-1}| < a_2 \quad (3)$$

$$3) a_3 < |\phi_i - \phi_j| < a_4 \quad (4)$$

Where  $d_j$  refers to the wheel diameter of the  $j$ th Q part,  $B_j$  refers to the rim width of  $j$ th Q part,  $|\phi_i - \phi_j|$  refers to interference fit between P and Q,  $a_1, a_2, a_3, a_4$  refer to the matching parameters of parts according to the technical specification requirements.

Equation (1) is the objective function expression, it reflects the ultimate goal which makes the number of the matched wheel assembly group maximal.

Equation(2) refers to the constraint of diameter difference in the same group of the two wheels.

Equation(3) refers to the constrain to frim width difference in the same group of the two wheels.

Equation(4) refers to the constraint of the interference fit between axle and the wheel.

## 2 DESIGN AND IMPLEMENTATION OF GENETIC ALGORITHM

From the above mathematical model, the optimal solution needs to be seeked, the optimal solution makes remaining parts least, at the same time, two kinds of matching parts need to meet parameter constraints. For solving this type of discrete variable optimization problems, there are several kinds of methods, such as Genetic Algorithm (GA), Simulated Annealing (SA), Particle Swarm Optimization (PSO), and so on. As implementation processes of these algorithms are relatively simple, they are widely used to solve the optimization of complex system. Compared with GA, SA is not better to control the search space, and computation efficiency is not higher, the PSO is suitable for solving this problem, PSO is simple and convenient, and its solving speed is good, but it is more easy to fall in local optimum. As a global optimization algorithm, GA can achieve good results for many NP problems, so according to the characteristics of the wheels matching problem, a matching method based on GA is put forward[6].

### 2.1 Encoding method and initial solution

When GA is used to solve the problem, it must be necessary to build a link between individual genes string structure and the practical problem, There presentation of practical problem can be represented as a one-dimensional array of individual representation. Encoding method has a great impact on the function and design of genetic operators which includes crossover operator and mutation operator. In view of this, this paper adopts the sequence encoding (integer permutation encoding) on the basis of comparing various coding methods [7], which regards the parts' order number as a gene of chromosomes.

The numbers of P parts and Q parts are determined in this problem, and one P part and two Q parts constitute an assembly group. For the convenience of coding and operation, the following rules are set up: Only Q parts are encoded, the  $i$ th P part and the two Q parts whose number is  $2i$ th and  $2i-1$ th genes codes in the genome are a assembly group. So the P parts are only used in calculating fitness value when the constraints are meeted, thus the complex multi-layer encoding problem becomes a single encoding problem.

For example: there are 4 P parts, they are  $p_1, p_2, p_3, p_4$ , and 8 Q parts, they are  $q_7, q_6, q_4, q_2, q_5, q_1, q_8, q_3$ .

For Q part Numbers for: (7, 6, 4, 2, 5, 1, 8, 3).

According to the above code, assembly groups after decoding are shown in Fig.1:

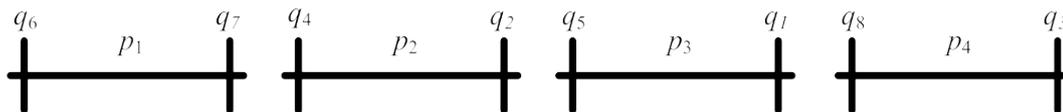


Fig. 1. Sample of assembly

After complete chromosome coding, it is necessary to generate an initial population, so we need to decide the number of the initialize population. From the general experience, the number depends on the part quantity. The value is between 30 ~ 100.

2.2 Fitness function

The purpose of fitness function is to calculate individual fitness value. Individual fitness value determines whether to choose the individual by comparing individual fitness value. It can measure individual quality, and it is the only basis for selection in the evolution process. Fitness function for this problem is:

$$F(S_m) = \sum_{i=1}^n b_i \tag{5}$$

The individual's fitness function is to say the more the assembly groups that satisfy the constraints in matching scheme, the bigger the fitness value, and the better the matching scheme[8].

2.3 Choice of genetic operators

1) Select operator

In order to improve the average fitness of population and get the best individuals whose fitness is the greatest in a population, so optimal preservation strategy is used firstly. Two individuals with better genetic fitness are directly into the next generation. Because this method is difficult to eliminate local optimal individual, and it makes the algorithm's global search ability is not strong. Therefore, this paper uses the roulette method as a complement in the end.

- (1) Calculate sum of the individual fitness in the group:  $F = \sum_{i=1}^N f(s_m)$ , in which  $f(s_m)$  expresses the fitness of an individual;
- (2) Calculate choice probability of the individuals in the group:  $P(s_m) = f(s_m)/F$ ;
- (3) Calculate selection probability of the individuals in the group:  $q_m = \sum_{j=1}^{m-1} P(x_j)$ ,  $q_0=0$ ;
- (4) Generate a random number  $r \in [0,1]$ , If  $r \in [q_{m-1}, q_m]$ , choose the individual  $S_m$ ,  $m \in (1,2 \dots \dots N)$ .

2)Crossover operator

Crossover operation is a main way to generate new individual, it can determine genetic algorithm global search ability. According to the sequence encoding, if crossover operator adopts single point crossover method, illegal chromosome will be generated. There is no guarantee that the genetic code appears only once in the encoded string. So the circular cross[9] (partial mapping hybrid) is used. Circular cross will restructure the current parent individual reference to another parent individual.

For example: there are parent individual 1 (7,6,4,2,5,1,8,3) and theparentindividual2 (4,5,2,1,8,7,3,6), Fig.1 shows the process how to generate the child individual 1 . Number in a circle represents steps.

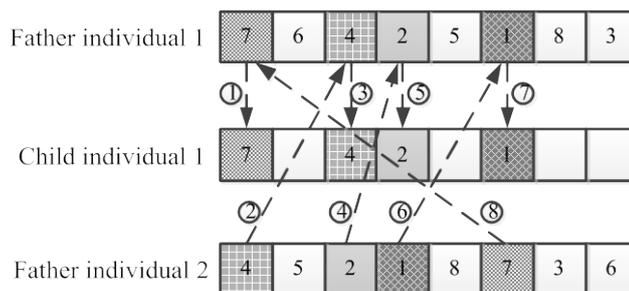


Fig. 2.Crossover operator

There will be a circulation when it goes to step 8, at this time, the operation should be stop, the child individual gap code in the genetic is the genetic code of father individual 2 in the corresponding position. So we get child individual 1 gene (7, 5, 4, 2, 8, 1, 3, 6). Similarly we get the child individual 2 gene (4, 6, 2, 1, 5, 7, 8, 3).

3) Mutation operator

The purpose of mutation operation is to improve the local search ability of genetic diversity and maintain group diversity, it can prevent premature phenomenon. Mutation strategy randomly exchange two points position over the same period of chromosome, thus chromosome mutation completes.

For example: as shown in Fig. 3, chromosome gene (7, 6, 4, 2, 5, 1, 8, 3), code 4 and 8 are randomly selected from the genetic, the new individual genes is(7, 6, 8, 2, 5, 1, 4, 3).

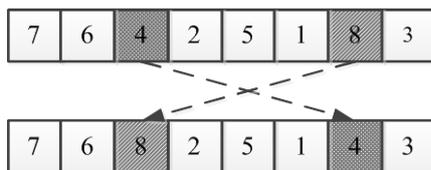


Fig. 3. Mutation operator

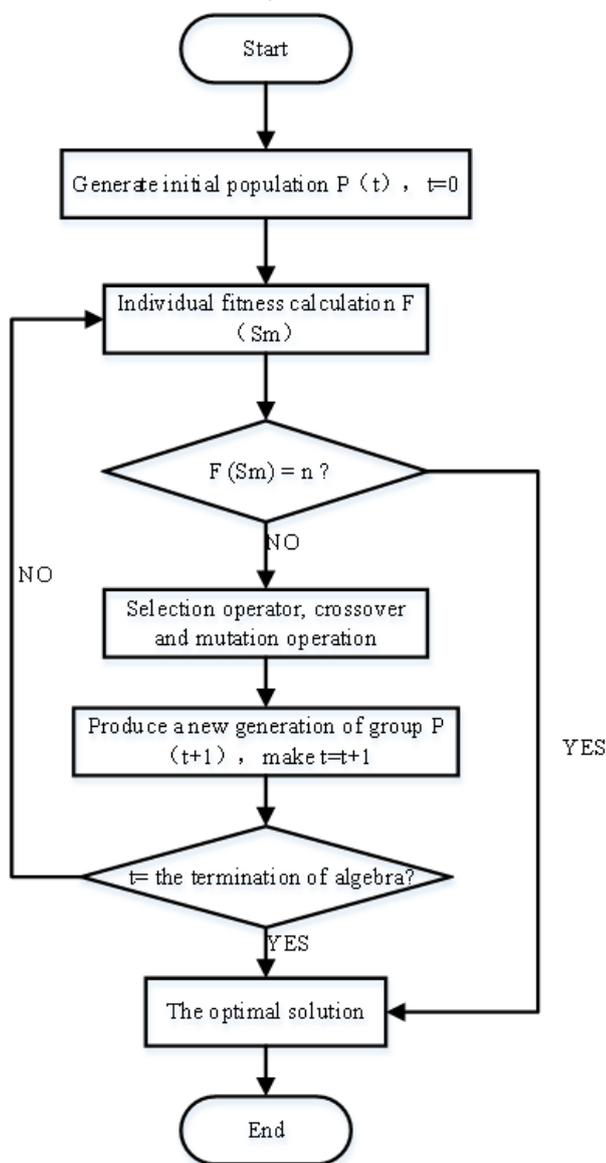


Fig. 4. Algorithm steps

2.4 The implementation steps and termination conditions

As shown in Fig. 4, the algorithm includes generated initial population, fitness value calculation, selection individual, crossover and mutation operation and other steps, and the final termination conditions are set at the end, finally, the optimized results are obtained. The paper uses two termination conditions: 1)  $F(S_m)$  is equal to  $n$ , 2) Number of iterations is equal to stated value of terminate the generation.

3 CALCULATION EXAMPLE

The CRH5 train is as an example to verify the algorithm in this paper. Fig. 5 is the schematic drawing of the wheel assembly. Requirements: the two wheel diameters difference in the same wheel assembly should be less than or equal to 3 mm, the rim width difference should be less than or equal to 5 mm, the amount of interference should be less than or equal to 0.3 mm and greater than or equal to 0.24 mm. Namely  $a_1 = 3$  mm,  $a_2 = 5$  mm,  $a_3 = 0.24$  mm,  $a_4 = 0.3$  mm. Tab. 1 and tab. 2 are the actual size of 15 axles (P) and 30 wheels (Q), genetic algorithm is used to solve this question, the final result is got by Matlab software. The population size  $M = 80$ , crossover probability  $P_c = 0.9$ , the mutation probability  $P_m = 0.2$ , the maximal evolutionary generations  $T = 450$ .

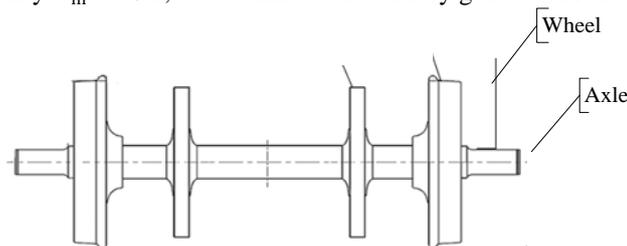


Fig.5. Schematic drawing of the wheel assembly

Tab.1. Axle relative parameter data

Axle No. (P)	Wheel seat diameter (mm)
1	192.261
2	192.246
3	192.248
4	192.257
5	192.254
6	192.257
7	192.247
8	192.259
9	192.26
10	192.242
11	192.261
12	192.244
13	192.245
14	192.241
15	192.243

Tab.2. Wheel related parameter data

Wheel No. (Q)	Wheel diameter (mm)	Rim width (mm)	Wheel hub hole diameter (mm)
1	830.6	130.5	191.993
2	857.5	134	191.967
3	840.4	129.4	191.969
4	815.6	131.6	191.982
5	838.9	134.3	191.978
6	864.9	134.8	191.986
7	838.3	131	191.976
8	850.9	134	191.997
9	839.2	130.1	191.966
10	841.3	131.7	191.999
11	818.5	130.4	191.993
12	867.2	127.8	191.99
13	848.9	131.1	191.975
14	879.5	134.4	191.972
15	831	128.5	191.967
16	834.5	129.3	191.973
17	882.3	134	191.981
18	862	127	191.996
19	826.9	132.5	191.995
20	816.9	134.5	191.977
21	834.4	128.5	191.966

22	816.3	134.1	191.969
23	822.9	131	191.981
24	889.1	128.7	191.966
25	864.1	131.8	191.996
26	862.9	131.5	191.991
27	874.8	134.7	191.974
28	835.7	127.5	191.999
29	820.4	128.8	191.975
30	822.5	128.1	191.98

Fig.6 shows the convergence process of the algorithm, the dashed lines shows the convergence process of fitness values, the solid line shows the relationship between average and evolution generations. We can see the optimal value 12 for the first time when the program runs to about 170 generations, procedure becomes stable, optimal value is 12, so we can determine optimal value is 12 under the constraints, which can matching successfully 12 wheel groups with the given constraints, the matching results are shown in Tab. 3.

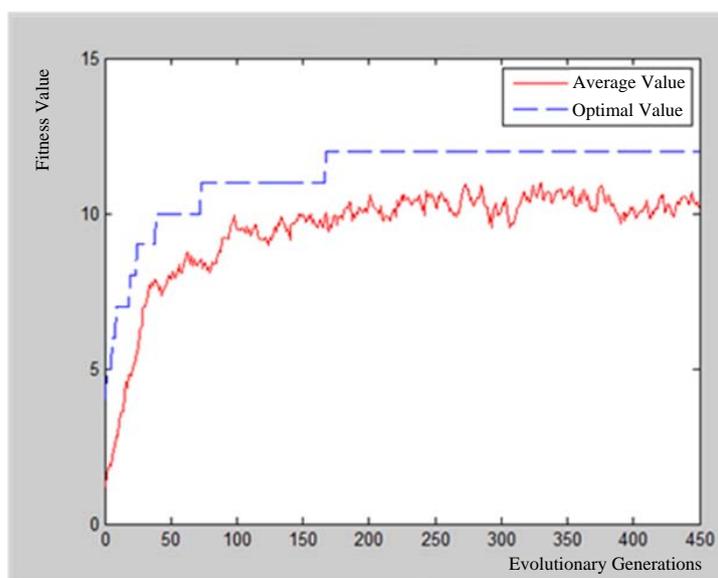


Fig. 6. Process of convergence of the algorithm

Tab.3.Matching results

Assembly group	1	2	3	4	5	6	7	8	9	10	11	12
P (axle)	1	2	3	4	5	6	7	8	9	10	11	12
Q (wheels)	11\22	3\10	23\30	1\15	6\25	7\28	4\20	8\13	18\26	14\17	16\21	5\9

## CONCLUSION

Paper describes the problem of the railway vehicle wheel matching, because of low efficiency of the wheel selection, the mathematical model of this problem was studied, and algorithm based on genetic algorithm was designed. The example proved the method is effective. It is fast to match large quantities vehicle wheels with multiple parameters, the working efficiency of the maintenance workshop and effective utilization of wheels both are improved, the idle and waste of the parts will be avoided, and the efficiency of the bogie workshop operation was improved.

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