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Research on Furniture Assembly Sequence Solution Based on Genetic Algorithm

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Abstract. Solving Assembly Sequence problem has occupied a very important position in furniture manufacturing industry. But there were a variety of problems during assembly process, such as the speed of assembly and quality problems. To solve these problems, we need to consider the impact of assembly factors, the relationship between assembly components, and its mathematical model solution. In this paper, by adopting mass customization production mode and utilizing modules and various design and assembly information, a product family model of furniture products that satisfy customers is manufactured. We used genetic algorithm to solve these problems based on the mass customization production model. First, based on the relationship between assembly parts, we drawn assembly diagrams and assembly relation matrix. Then we got the assembly sequence by genetic algorithm (GA), which can help us more quickly find the optimal solution. The example proved that GA algorithm could not only effectively solve the assembly sequence optimal problems, but also improve the furniture industry's production efficiency and reduce production costs. The assembly sequence model proposed in this paper can effectively optimize the design and improve the design efficiency, and can make full use of the components that make up furniture products.

Keywords: assembly sequence, genetic algorithm, mass customization

1 Introduction

Entering the 21st world, with the economic globalization, furniture companies are facing fierce competition. The competition forces companies to continuously improve their management models. Mass customization production models are gradually adopted in the furniture manufacturing industry and gradually integrated into the furniture market [1]. Mass customization furniture, that is, the enterprise treats different consumers as different markets, produces and manufactures furniture according to the individual purchase needs of consumers to meet personalized needs.

Many scientists have carried out in-depth research on mass customization furniture industry [2]. José P. Duarte realized the design and production of mass custom furniture by computer-aided software [3]. Researchers believe that the mass customization production mode can be divided into the following steps, understand different needs of customers, convert customer needs into design tasks, and complete different design tasks according to different needs [4-5]. Afterwards, Yoonseok Shin et al. conducted in-depth research on mass-customized housing [6]. They succeeded in reducing the cost of mass-customized housing, and also effectively expanded customer's choice in the customized production mode [7].

Enterprises gain competitive advantages and economic benefits through mass-customized production [8] models. The use of mass customization theory can systematize product information of products produced by enterprises, and can also improve enterprises' independent innovation capabilities, and enhance market competitiveness [9]. Adopt advanced information technology to improve the traditional furniture manufacturing industry, optimize the allocation of various resources of furniture companies,

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reduce waste of manpower and material resources in the process of producing furniture products, shorten time, achieve leapfrog development, and bring enterprises to maximize economic benefits. In the future, the furniture market will develop in the direction of individualization and modernization in terms of design [10], and mechanization, automation, and collaboration production methods [11].

During the customization and production of large-scale furniture, it is not enough to design and produce spare parts only. Therefore, building a product configuration model based on mass-customized product families are essential in product assembly and design process. Of course, the assembly method and speed are also very important, because it not only determines product quality, but also determines the production speed of products [12]. Only when product quality and product assembly speed meet consumer demand can companies respond quickly to the market to achieve higher efficiency and profits.

Assembly concept is made up of three layers of meaning: (1) The parts of product should be combined; (2) The function of product can be realized; (3) The quality of product is guaranteed. So the assembly emphasizes not only the components combination of products. It is more important to achieve the function of product and achieve the satisfaction of customer to product quality. In order to assemble various parts of product into a molded product, these products must satisfy customer. What we need to do is to understand basic information, like assembly constraints and assembly feasibility [13]. We need to fully understand products to meet customer needs. First, establish the assembly information model of product [14]. And then extract basic assembly information from the parts of product when establishing the assembly information model. Finally, we find out the assembly relationship between parts and components. This paper mainly uses assembly information model in the hierarchical model. The assembly relationship between parts is not obvious and intuitive. In order to find out the assembly relationship between parts more directly, the assembly information model and the relation matrix are obtained by establishing the assembly information model, and then the genetic algorithm is used to solve the optimal assembly sequence. Finally, it is verified by the example of the lockers.

2 Set Up Product Assembly Model

In this paper, the assembly information model of product is established by using Analytic Hierarchy Process (AHP) [15] method. Only when there is a good model of assembly information can we fully reflect the relationship between the parts of assembly. Then we can guarantee to provide the most basic basis in the subsequent development of products. The establishment of the assembly model needs to follow certain constraints, in which the constraint conditions are fixed. At the same time it will not change with the different composition of the assembly to form different structures. The assembly information model includes the basic assembly information of the parts and the relationship between them. The assembly information model is represented by a tree, and the structure of assembly information model is shown in Fig. 1:

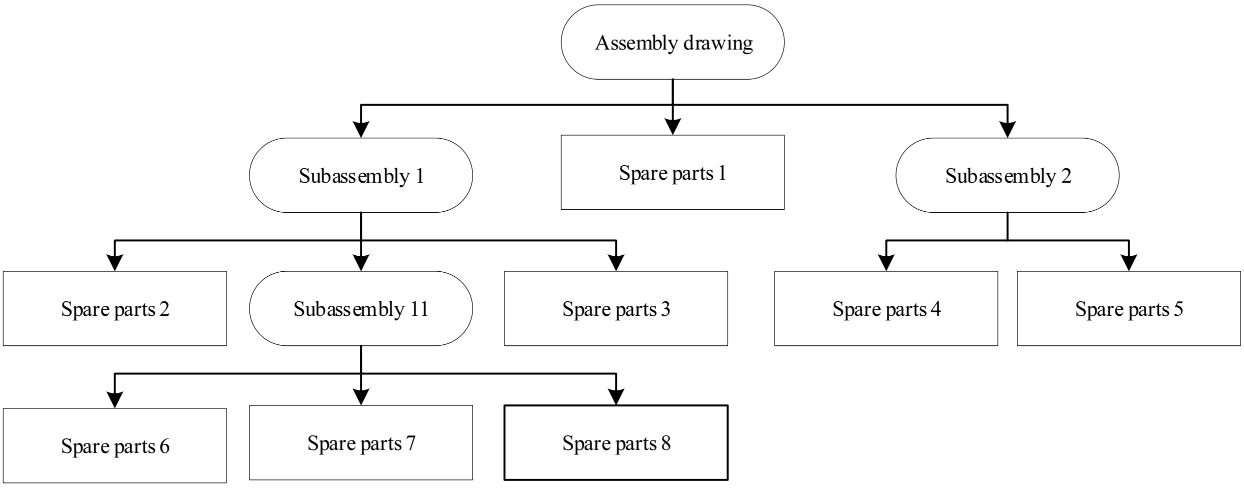

Fig. 1. Assembly information model of product

The diagram above shows the assembly information model of the product, and we can see that the graph is shown in tree form. The diagram includes assembly, sub assembly and parts. The root node in the assembly tree represents the assembly of the product. The nodes which locate between the root and leaf nodes of the tree are called the intermediate nodes [16]. The intermediate nodes of tree represent the subassemblies of the assembly of the ligand or parts. The leaf nodes of the tree represent the final parts. The connection between nodes indicates the relationship between upper and lower nodes. Based on the analysis above, we know that the assembly information model has many advantages, but it also has drawbacks. It is not able to express the assembly relationship between assembly, ligand and parts, so it is necessary to establish the product assembly relationship graph.

2.1 Assembly Diagram

In this paper, assembly relationship diagram is used to represent the assembly relationship between parts, which is very simple and easy to understand. Schematic diagram of the main frame structure is given below the locker entity, as shown in Fig. 2 (left). A expresses the top board cabinet. B represents the bottom of the cabinet. C is the left board cabinet, and D indicates the right board cabinet. E represents the upper plate of the cabinet. F is the lower board cabinet. G stands for the cabinet backplane, and H represents the color door cabinet.

According to the diagram of the main frame structure of lockers, we can get each part name and assembly relations between the parts and draw the assembly diagram, as shown in Fig. 2 (right). From this diagram we can know intuitively that each node in the graph represents the components of the assembly, and the connecting lines between the nodes represent the assembly relations between the parts.

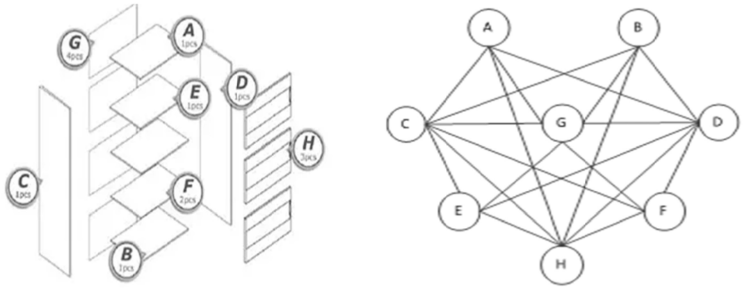

Fig. 2. Schematic diagram of the main frame structure of the lockers (left) and locker diagram (right)

2.2 Assembly Relation Matrix

Products can be drawn according to the assembly relation matrix above assembly diagram, because the locker consists of 8 parts. According to the assembly relationship between parts, there are no assembly relations or the same node, its value is set to 0, else the assembly relationship value is 1. So we can get an 8 order assembly relation matrix, as shown in Fig. 3:

$$R_{8\times 8}=\begin{bmatrix} 0 & 0 & 1 & 1 & 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 1 & 0 & 0 & 1 & 1 \\ 1 & 1 & 0 & 0 & 1 & 1 & 1 & 1 \\ 1 & 1 & 0 & 0 & 1 & 1 & 1 & 1 \\ 0 & 0 & 1 & 1 & 0 & 0 & 1 & 1 \\ 0 & 0 & 1 & 1 & 0 & 0 & 1 & 1 \\ 1 & 1 & 1 & 1 & 1 & 1 & 0 & 0 \\ 0 & 1 & 1 & 1 & 1 & 1 & 0 & 0 \end{bmatrix}$$

Fig. 3. Cabinet assembly incidence matrix

The assembly relation matrix can express the assembly information of product better. The establishment of assembly relation graph and the assembly relation matrix provide favorable conditions for solving the genetic algorithm which is used in the assembly sequence.

3 Assembly Sequence Generation

In this paper, the solution of assembly sequence is a complex optimal problem. In fact, this problem is also a NP (Non-deterministic Polynomial) problem [17]. In other words, it is a nondeterministic problem with polynomial complexity. Genetic algorithm [18] is effective for this problem. Cause genetic algorithm has strong robustness and global searching ability. This paper uses genetic algorithm to optimize the assembly sequence.

First analyze the flowchart of basic genetic algorithm, as shown in Fig. 4. In this diagram, the initial population is the coding of the assembly sequence, and the assembly sequence is assembled by the parts of the assembly. Of course, these components also need to be encoded. Then the initial population of assembly sequence is produced, and the fitness function is calculated. According to the difference of fitness function, the individual can be retained or eliminated, and then a new assembly sequence can be generated through the selection, crossover and mutation genetic factors. Repeat this operation until the individuals who adapt to environment changes are selected and decoded to obtain the optimal solution finally. Then obtain optimal solution, as shown in Fig. 4.

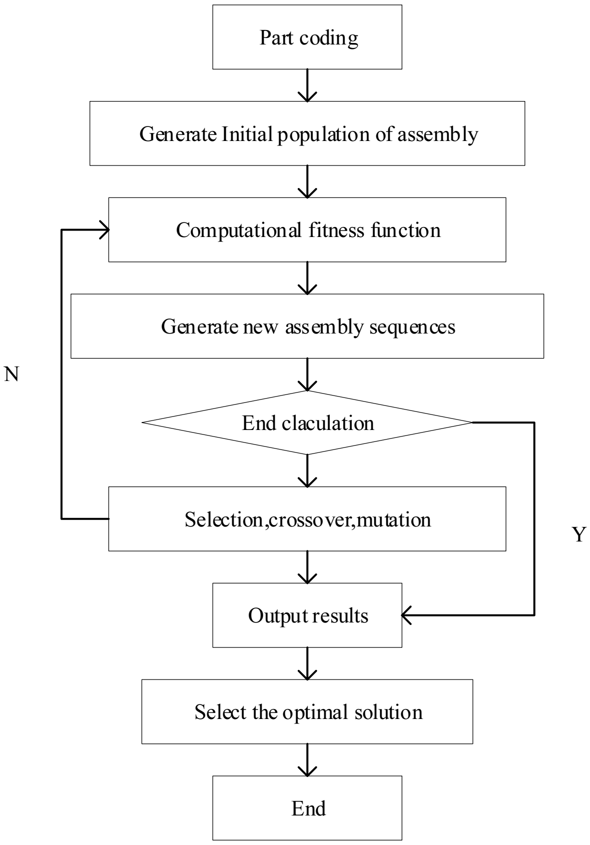

Fig. 4. Flow chart of assembly sequence generation based on genetic algorithm

3.1 Fitness Function

In this paper, genetic algorithm is used to solve the assembly sequence based on simplified assembly relation graph and assembly incidence matrix. The fitness function is mainly based on the time factor. Because the assembly time plays an important role in assembly of the parts, the fitness function of genetic algorithm mainly depends on assembly time. We divided assembly time into basic part assembly time and time required to change assembly tools

(1) Basic parts assembly time (IT), as shown in Eq.(1).

$$IT(i,S_j)=\sum_{i=1}^{i} it(i,S_j) \tag{1}$$

The $it(i, S_j)$ represents the basic assembly time of the *i*th part which is in the assembly sequence S_j, and the basic assembly time of each part is fixed. $IT(i,S_j)$ represents the total assembly time of each part.

(2) Assembly tool change time (TT), as shown in Eq.(2).

$$TT(i,S_j)=\sum_{i=2}^{i} tt(i,S_j) \tag{2}$$

The $tt(i,S_j)$ represents the time of the transformation of the *i*th part in the assembly sequence, and the $it(i,S_j)$ represents the total time used for the assembly of each part. In this paper, the time of the assembly tool is consistent, and it is set to 3s. Therefore, So we can get the formula of $T(i,S_j)$, such as Eq.(3).

$$T(i,S_j)=\sum_{i=2}^{i} tt(i,S_j)+\sum_{i=1}^{i} it(i,S_j) \tag{3}$$

The assembly sequence is *S*, and the fitness function is given below, as shown in Eq.(4).

$$F(s)=C-T(i,S_j) \tag{4}$$

$T(i, S_j)$ represents the total time required for assembly of *i*th of the assembly sequence S_j. *C* represents constants, and author needs to give it a value and a requirement: $C \geq T(i,S_j)$. The purpose of this step is to ensure greater fitness and more excellent assembly sequence.

3.2 Genetic Operators

Genetic operators contain selection operator, crossover operator and mutation operator, Genetic operators occupy an important position in genetic algorithm, because they relate to whether the global optimal genetic algorithm can successfully find a solution or not. By these operations, a new population can be generated from the original population. Then the new population continues to produce the next generation of the population. Repeating this process until the optimal solution is produced eventually.

3.2.1 Selection Genetic Operator

Selection operator is based on fitness function of the population. At the same time, selection operator can choose the fittest survival from different groups. In other words, it can keep individuals which adapt well to the existing environment to generate the next generation, and eliminate individuals that are not suitable for the existing environment [19]. In this paper, we adopt the method of fitness value directly mapping to calculate selection probability of the individual [20], as shown in Eq.(5).

$$p_k=\frac{F(k)}{\sum_{i=1}^{n} F(i)} \tag{5}$$

F(kI is the fitness function value of individual k, and *F*(*i*) is the fitness function value of individual *I*, And *k* indicates the existence of an individual. p_k is the probability of selected *k*.

The probability of individual selection is given, and the probability of accumulation is calculated. So what does the cumulative probability mean? The probability of accumulation is the probability that each individual is selected. Then we can determine whether the selected individual can continue to be inherited to the next generation or not. Therefore, the formula for calculating the probability of individual accumulation is given, as shown in Eq.(6).

$$q_k=\frac{p_k}{\sum_{k=1}^{n} p_k} \tag{6}$$

According to the above two formulas, we can calculate the probability of chosen individual and decide whether the selected individual will be inherited to next generation. This is the accumulation probability. The new population is then selected, crossed and variant to get the next generation of the population. It is necessary to determine the fitness value. The above operation is repeated until the fitness value of population is stable in a certain range.

3.2.2 Crossover Genetic Operator

Cross genetic operator is the core operator of genetic algorithm, also known as recombination. Crossover Genetic Operator is designed to replace the original structure of two original chromosomes, and then we generate new individuals. Crossover operator can generate a new generation of individuals by exchanging the partial structure. In this way, we can inherit good genes from parent. Therefore the offspring can inherit the excellent characteristics of parents [22]. This kind of operation has brought great influence on the searching ability of genetic algorithm, which can greatly improve the searching ability of genetic algorithm. The new generations of individuals who have been cross operated are not all good; there are also a few bad individuals. However, after a number of repeated crossover operations, these individuals will reduce the fitness value. In this way, they will eliminate slowly, and then we get excellent offspring. In this paper, the assembly sequence of parts is in a certain order, so this paper uses sequential crossover operator(OX).

The sequential crossover operator is an ordered structure, which can maintain the parts order of existing assembly sequence [22]. For example, there are parent chromosomes P1 and P2, and then they are crossed to produce the offspring chromosomes.

P1: (1 2 3 | 4 5 6 | 7 8 9)
P2: (9 8 7 | 6 5 4 | 3 2 1)

The position between two "|" indicates the part to be crossed.

(1) The requirements of this cross operation: keep the order in P1, select part of P2. To meet the operating requirements, we should put the P2 in the cross section in front of the P1. According to cross operation principle, we remove the overlapping parts of P1 and P2, and then get a new generation of chromosome S1.

(2) We reverse operation by this method. This operation requires: keep the order in P2, select part of P1. In accordance with the operating requirements, we should place the cross section in the P2 at the top of the P1 and delete the overlapping part of the P2 from the P1, and then get a new generation of chromosome S2. The resulting new chromosome is as follows:

S1: (6 5 4 1 2 3 7 8 9)
S2: (4 5 6 9 8 7 3 2 1)

It can be seen from the above operation, different operating requirements will produce different new generation of individuals.

3.2.3 Mutation Genetic Operator

There are several kinds of mutation operators in this paper [23]: transformation mutation, insertion mutation, mutation in place, etc. To solve assembly sequence of product parts problem, we adopt the method of in place mutation. For example, we suppose an individual R1, and randomly select three genes. These genes are placed in the original position which is in the opposite order, and then a new individual R2 is produced. As shown below, the selected genes are stored in the position which is between two "|".

R1: (1 2 3 | 4 5 6 | 7 8 9)
R2: (1 2 3 | 6 5 4 | 7 8 9)

3.3 Genetic Algorithm Parameter Settings

In the genetic algorithm, the initial population is randomly generated by the computer. In addition, the following parameters need to be set up.

(1) Population size

The group size is expressed by M_p. The population size should be set neither too high，nor too small. If it is too high, it will affect calculation speed of genetic algorithm. On the contrary, it will greatly reduce the scope of genetic algorithm search and cause premature phenomenon [24]. The size of the value is too large or too small; both will have an impact on the performance of genetic algorithms. The global search ability of genetic algorithm is destroyed. Based on the in-depth study of the genetic algorithm, we know that the general value range is 20~100.

(2) Crossover probability

P_c represents crossover probability. Just like the population size, the value is neither too big nor too small. If it is too large, although the number of individuals will improve the production of the next generation and speed, it is easy to cause the broken ring to it. If the probability is too small, it will slow down the number of new generation and reduce the number of individuals. Its value range is generally 0.41~0.99.

(3) Mutation probability

P_m indicates mutation probability. If the value is larger, it will produce more of a new generation of individuals, but there may be broken chromosomes. On the other hand, if the value is too small, it will produce premature convergence. Because the ability to inhibit the premature decline, so the general value range is 0.01~0.1.

(4) Evolutionary termination iterations

T_m represents evolution termination iterations. According to the actual situation of this paper, the value range of iterations is 200~1000.

4 Example Verification and Analysis

In this paper, the assembly model and solving process of mass customization furniture products were established. Then, an example was given to analyze the case of domestic furniture. First of all, we analyzed and decomposed according to the needs of customers. At the same time, according to the degree of customer preference, the system cluster analysis was used to segment the customer base. According to the needs of customers in the market for furniture products, it was divided into the following six characteristics: aesthetic, environmental protection, price, space, durability and safety. Therefore, we would quantify the requirements of these indicators, and complete the division of user groups finally.

Through the market research, we understood that the different needs of customers could reflect the different preferences of customers. First of all, according to the six elements of customer demand, we took the comparison to quantify these attributes and determined the function values of the six attribute indexes. After each attribute of furniture products were divided into 5 same grades, “excellent”, “good”, “general”, “inferior” and “bad”. Their ranges were 0.9~0.69, 0.7~0.49, 0.5~0.29, 0.3~0.09, 0.1~0.01. Then we could make different combinations according to the different levels of each attribute and got products from different combinations of attributes. According to the survey results of the market, the customers’ personalized needed are summarized, calculated and quantified. At last we created customer demand attributes for lockers and assigned values to them, the results were shown in Table 1.

Table 1. Customer demand attributes for lockers

Customer number	Artistic	Environmental protection	Price	Place	Durable	Security
1	0.49	0.88	0.07	0.56	0.65	0.34
2	0.27	0.5	0.36	0.87	0.56	0.74
3	0.06	0.78	0.49	0.5	0.18	0.57
4	0.5	0.67	0.89	0.24	0.72	0.81
5	0.27	0.87	0.3	0.9	0.46	0.34
6	0.34	0.65	0.3	0.5	0.3	0.9
7	0.42	0.78	0.89	0.48	0.24	0.43
8	0.34	0.81	0.1	0.65	0.35	0.56

Table 1 used the maximum method to standardize the users’ data to get the matrix, as shown in Fig. 5.

$$X = \begin{bmatrix} 0.5568 & 1 & 0.0795 & 0.6364 & 0.7386 & 0.3864 \\ 0.3103 & 0.5747 & 0.4138 & 1 & 0.6437 & 0.8506 \\ 0.0769 & 1 & 0.6282 & 0.6410 & 0.2308 & 0.7308 \\ 0.5618 & 0.7528 & 1 & 0.2696 & 0.8090 & 0.9101 \\ 0.3 & 0.9667 & 0.3333 & 1 & 0.5111 & 0.3778 \\ 0.3778 & 0.7222 & 0.3333 & 0.5111 & 0.3333 & 1 \\ 0.4710 & 0.8764 & 1 & 0.5393 & 0.2697 & 0.4831 \\ 0.4198 & 1 & 0.1235 & 0.8025 & 0.4321 & 0.6914 \end{bmatrix}$$

Fig. 5. Normalized matrix

After cluster analysis of Table 2, we could get the difference between the two users. The Euclidean Distance method was used to obtain the distance matrix. As shown in Fig. 6.

$$R_{8\times 8} = \begin{bmatrix} 0 & & & & & & & \\ 1.9288 & 0 & & & & & & \\ 1.8854 & 1.7648 & 0 & & & & & \\ 2.1336 & 1.9710 & 2.2328 & 0 & & & & \\ 1.1436 & 1.0882 & 1.5436 & 2.7030 & 0 & & & \\ 1.8548 & 1.2442 & 1.3752 & 1.6884 & 1.6112 & 0 & & \\ 1.7926 & 2.0327 & 1.2778 & 1.4504 & 1.7354 & 1.5228 & 0 & \\ 0.9586 & 1.3936 & 1.2498 & 0.2187 & 0.9530 & 1.2281 & 1.6851 & 0 \end{bmatrix}$$

Fig. 6. Distance matrix

Finally, according to the analysis of the above table and matrix, we got the user clustering diagram, as shown in Fig. 7.

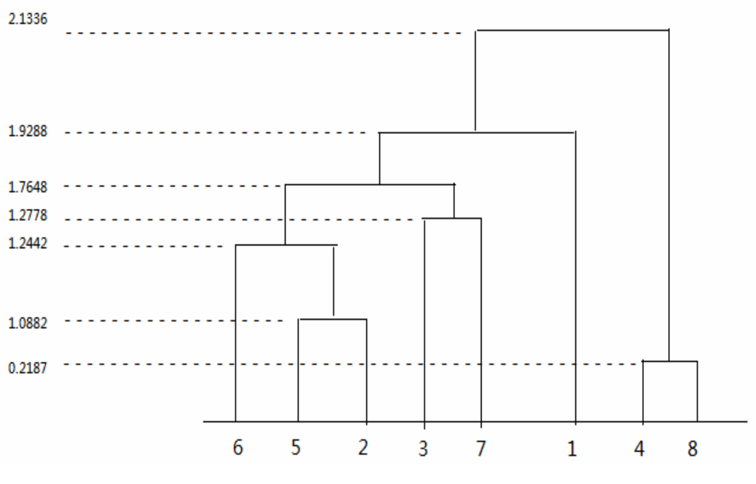

Fig. 7. User clustering

According to the cluster Fig. 7, the lockers can be divided into the following three types of user groups: The first type is {4, 8}, {1, 3, 7} is the second class, the third category is {2, 5, 6}. In the first category of users, price and environmental protection are the main factors influencing the user group. Environmental protection is a prominent feature of user groups in the second type of users. In the third type of users, space and security affect the user group mainly. Therefore, according to the above three clustering results, we should pay attention to the attributes of customer preference, finish the analysis of the customer's personalized needs for lockers and product configuration design and development. This product using the method of system clustering can achieve customer satisfaction, and the validity of the product family configuration design is also improved.

In addition to the above four properties is what we need to focus attention on product configuration design process. The other two attributes also affect the customer demand for products. So they can set up a separate collection. After completing the design and assembly of the main frame of the lockers, we modularized and operated a large collection that is composed of the price and beauty.

After classifying the users, we needed to build the product family model according to the needs of customers. It includes the function model, structure model and function structure configuration model based on product family modeling. Through these models, we could understand the basic part information of the assembly, and lay the foundation for the establishment of the assembly information model. According to the established assembly information model, as shown in Fig. 1, we found the corresponding product parts assembly diagram and assembly relationship matrix, as shown in Fig. 2 and Fig. 3. Based on the assembly information model, assembly relationship diagram and assembly relation matrix, the genetic algorithm was used to solve the assembly sequence.

In the process of solving the assembly sequence, the assembly of the product needs some assembly tools. It was no exception to the lockers in this article. In addition to the assembly of the 8 components, it contains assembly tools. The following is the list of materials used in the assembly tool cabinet, as shown in Table 2.

Table 2. Assembly tools needed BOM lockers

Number	Name of parts	Assembly transformation time(s)	Amount
a	self tapping screws	3	20
b	screws	3	8
c	magnet	3	3
d	door pivot	3	6
e	back button	3	4

Before the assembly sequence was calculated by genetic algorithm, the assembly parts should be coded. In this paper, we used symbol coding. The assembly contains a total of eight assembly parts, so eight numbers (from one to eight) are used to represent different assembly parts. Number one represents cabinet top floor board A. Number two is the bottom plate of the represents cabinet B and Number three is on the left side of the board C. Number four represents of the right board D cabinet. Number five represents the upper cabinet E. Number six is on behalf of the cabinet under the board F and Number seven is on behalf of the cabinet backplane G. Number eight represents cabinet color door plate H. Based on the above analysis, the initial population was obtained. The initial population must satisfy the constraints of assembly and the sequence must be feasible. The population size was M_p=20 and encoding parts were given below the lockers as shown in Table 3.

Table 3. Parts encoding locker

Part Name	Top plate A	Floor B	Left plate C	Right plate D	Upper plate E	Lower plate F	Back plate G	Door plate H
Symbol coding	1	2	3	4	5	6	7	8
Assembly time	8s	8s	5s	7s	9s	10s	4s	15s

Genetic algorithm for assembly sequence optimization process was as follows:

(1) The initial population was generated as follows:

7	1	5	6	2	3	4	8
7	3	1	5	6	2	4	8
7	4	3	1	5	6	2	8
7	1	4	5	6	2	3	8
3	1	5	6	2	7	4	8
3	7	1	5	6	2	4	8
3	7	4	1	5	6	2	8
3	1	7	4	5	6	2	8
4	1	5	6	2	7	3	8
4	7	1	5	6	2	3	8
4	1	7	3	5	6	2	8
4	7	3	1	5	6	2	8
1	7	3	5	6	2	4	8

1	3	5	6	2	4	7	8
1	4	7	5	6	2	3	8
1	7	4	5	6	2	3	8
2	3	7	1	5	6	4	8
2	7	1	5	6	3	4	8
2	4	6	5	1	3	7	8
2	4	7	6	5	1	3	8

(2) We calculated the fitness of the initial population and chose the calculation through the roulette method; the next generation of population was as follows:

7	1	5	6	2	3	4	8
7	3	1	5	6	2	4	8
7	4	3	1	5	6	2	8
7	1	4	5	6	2	3	8
3	1	5	6	2	7	4	8
3	7	1	5	6	2	4	8
3	7	4	1	5	6	2	8
3	1	7	4	5	6	2	8
4	1	5	6	2	7	3	8
4	7	1	5	6	2	3	8
4	1	7	3	5	6	2	8
4	7	3	1	5	6	2	8
7	1	5	6	2	3	4	8
7	3	1	5	6	2	4	8
7	4	3	1	5	6	2	8
7	1	4	5	6	2	3	8
7	1	5	6	2	3	4	8
3	1	5	6	2	7	4	8
3	7	1	5	6	2	4	8
3	7	4	1	5	6	2	8

(3) After the probability of the function is assigned, the number of assembly parts was obtained. In this paper, we set P_c=0. 65 and concluded that the sequence of multiple crossover operations is:

7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	4	3	8
3	1	5	6	2	7	4	8
3	1	5	6	2	7	4	8
3	7	1	5	6	2	4	8
3	1	5	6	2	7	4	8
4	7	1	5	6	2	3	8
4	7	1	5	6	2	3	8
4	1	5	6	2	7	3	8
4	7	1	5	6	2	3	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	4	3	8
7	1	5	6	2	4	3	8
7	1	5	6	2	3	4	8
3	1	5	6	2	7	4	8
3	7	1	5	6	2	4	8
3	7	1	5	6	2	4	8

(4) At the same time, the variation parameter was given, and the variation parameter was 0.01. Then we obtained the following sequence according to certain assembly constraints.

7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
3	7	1	5	6	2	4	8
7	1	5	6	2	3	4	8
3	7	1	5	6	2	4	8
3	7	1	5	6	2	4	8
7	1	5	6	2	4	3	8
3	7	1	5	6	2	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	4	3	8
7	1	5	6	2	4	3	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
3	7	1	5	6	2	4	8
3	7	1	5	6	2	4	8

5. After the above operation, we got the final population to meet the end conditions:

7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	4	3	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	4	3	8
7	1	5	6	2	4	3	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8
7	1	5	6	2	3	4	8

Finally, the optimal solution was obtained by the steps of gene coding, generation of initial population, genetic operator (selection operator, crossover operator and mutation operator). Here are two of the best sequences:

7	1	5	6	2	3	4	8
7	1	5	6	2	4	3	8

After decoding, the optimal solution of assembly sequence was obtained:

G	A	E	F	B	C	D	H
G	A	E	F	B	D	C	H

According to the convenience of the actual operation, the probability of the first set of sequences was larger. The first sequence was chosen as the optimal solution of the final sequence. It was G-A-E-F-B-C-D-H. According to the above analysis process and steps, the MATLAB software was used to carry out the simulation, and the evolution process was obtained, as shown in Fig. 8.

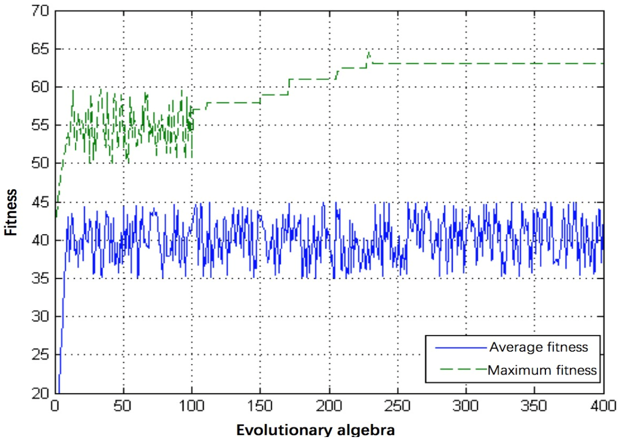

Fig. 8. Evolution chart

It can be seen that the evolution abort iterations is 230. The maximum fitness function was 64, and the sequence was feasible. We assembled the parts according to the optimal solution, and used the five assembly tool parts in Table 1 to connect and fixed the 8 parts of the locker. The main frame structure of the cabinet could be obtained. At last, we should decorate the lockers according to the customer's different needs and assess the value of lockers at the same time. In this way, customers can be satisfied with the product for customer using. In this experiment, the assembly sequence tool can generating the most quality furniture assembly sequence in a shorter time, compared to particle swarm optimization(PSO) algorithm [25]. The process time includes building model and generating optimal solution. Our process time is about 861ms, and the process time of PSO is 877ms.

5 Conclusion

The final purpose of this paper is to solve the assembly sequence of product assembly model. Firstly, the assembly information is modeled, and the assembly sequence problem is transformed into a mathematical model. The mathematical method is used to solve the assembly sequence problem. At the same time, the genetic algorithm is used to solve the assembly sequence of the lockers. And then, we find the optimal generation of the population, it was also called the optimal solution of assembly sequence. Finally, the feasibility and validity of the genetic algorithm are verified by solving the assembly sequence. Through the example, it is proved that the genetic algorithm has the ability to search the optimal solution quickly when solving the practical problem of furniture assembly sequence. By adopting genetic algorithm in mass customization in furniture design, it can help us better understand the characteristics and advantages of product design of domestic and foreign furniture companies, can effectively improve the design efficiency of the designer, and can make full use of the components that make up the furniture product to achieve the purpose of optimal design. The mass customization model adopted in this article is to humanize the design of furniture products, making customer-customized furniture products faster, simpler, and more convenient. It can shorten the development cycle of furniture and meet customers' individual needs, making customers faster and more okay get their satisfied product.

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References

[1] C. Xiaolei, S. Yanjun, S. Jun, Research on the development background and present status of furniture mass customization, Forest Engineering (5)(2014).

[2] Q. Guoning, G. Xinjian, Y. Qinghai, Y. Junhe, Research on the principle and key technology of mass customization, Computer Integrated Manufacturing Systems 9(2003) 57-64.

[3] Y. Wang, J.P. Duarte, Automatic generation and fabrication of designs, Automation in Construction 11(3)(2002)291-302.

[4] Z. Jiayan, Study on inventory control of furniture company s in mass customization, [thesis] Taipei: East China University of Science and Technology, 2015.

[5] X. Xianqing, W. Yana, F. Lu, W. Zhizhi, W. Yuwei, Study on quick response mechanism and key technology of the mass customization furniture, Production and Application 43(1)(2016) 47-52.

[6] Y. Shin, S.-H. An, H.-H. Cho, G.-H. Kim, K.-I. Kang, Application of information technology for mass customization in the housing construction industry in Korea, Automation In Construction 17(7)(2008) 831-838.

[7] X. Can, The research on furniture product family of residential small units, [thesis] Hunan: Central South University of Forestry and Technology, 2013.

[8] H.-E. Tseng, C.-C. Chang, S.-H. Chang, Applying case-based reasoning for product configuration in mass customization environments, Expert Systems With Applications 29(4)(2005) 913-925.

[9] T. Lihra, U. Buehlmann, R. Beauregard, Mass customization of wood furniture as a competitive strategy, International Journal of Mass Customization 2(3/4)(2008) 200-215.

[10] E. Liu, S.-W. Hsiao, S.-W. Hsiao, A decision support system for product family design, Information Sciences 281(2014) 113-127.

[11] X. Xianqing, W. Zhihu, Development and application technology of the mass customization furniture, Journal of Nanjing Forestry University (Natural Sciences Edition) 37(4)(2013) 160-166.

[12] L. Xi, C. Hu, Z. Shuai, Study on parallel assembly sequence planning method based on assembly ligand, Mechanical Engineer (2)(2015) 99-102.

[13] Z. Yue, W. Zhihui, Establishment and extraction of solid wood furniture assembly model, Furniture 35(2)(2014) 12-18.

[14] W. Xiaoyi, W. Huifen, Z. Youliang, W. Quanxian, Reconfigurable assembly model for assembly planning, Computer Intergrated Manufacturing Systems 17(1)(2011) 53-61.

[15] T.L. Saaty, How to make a decision: The analytic hierarchy process, European Journal of Operational Research 48(1)(1990) 9-26.

[16] Y.J. Tseng, F.Y. Yu, F.Y. Huang, A green assembly sequence planning model with a closed-loop assembly and disassembly sequence planning using a particle swarm optimization method, The International Journal of Advanced Manufacturing Technology 57(9-12)(2011) 1183-1197.

[17] B.H. Hasan, M.S. Mustafa, Comparative study of mutation operators on the behavior of genetic algorithms applied to non-deterministic polynomial (np) problems, in: Proc. International Conference on Intelligent Systems, Modelling And Simulation, 2011.

[18]K.B. ing, H. eifa, Z. Yanru, S. Yonghou, An efficient approach of assembly sequence planning based on genetic algorithms, Modern Manufacturing Engineering 12(2005) 69-71.

[19] D. Limin, The research of assembly sequence planning based on genetic algorithm, [thesis], Hebei: Hebei University of Technology, 2004.

[20] C. Yingyue, W. Haojie, Research on disassembly sequence optimization based on improved genetic algorithm, Journal of Xiamen University of Technology 5(2014) 72-77.

[21] W. Liang, P. Zhang, X. Chen, M. Cai, D. Yang, Genetic algorithm (ga)-based inclinometer layout optimization, Sensors 15(4)(2015) 9136-9155.

[22] C. Lu, J.-F. Fei, An approach to minimizing surplus parts in selective assembly with genetic algorithm, in: Proc. Institution of Mechanical Engineers 229(3)(2015) 508-520.

[23] A. García-Nájera, C.A. Brizuela, I.M. Martínez-Pérez, An efficient genetic algorithm for setup time minimization in PCB assembly, The International Journal of Advanced Manufacturing Technology 77(5-8)(2015) 973-989.

[24] L. Wang, K.-H. Hou, W.-Z. Liao, Z.-M. Jie, C. Chen, Y.-F. Zhang, Research on random mixed-model two-sided assembly line balancing using genetic algorithm, in: Proc. 21st International Conference on Industrial Engineering and Engineering Management, 2014.

[25] W. Pan, Y. Wang, X. Chen, Domain knowledge based non-linear assembly sequence planning for furniture products, Journal of Manufacturing Systems 49(2018) 226-244.