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# Applying Interactive Genetic Algorithms to Disassembly Sequence Planning

Shih-Chen Lee[1] · Hwai-En Tseng[2] · Chien-Cheng Chang[3] · Yu-Ming Huang[2]

**Abstract**

In addition to garbage sorting and resource recycling, green design should be a fundamental method for solving environmental problems, and design for disassembly is an important foundation of green design. This study focuses on providing quantitative assessment methods for designers' reference. This study proposes interactive genetic algorithms to solve the problem of disassembly sequence planning. First, the disassembly factor is measured by the fuzzy scoring procedure method, and then the genetic algorithm is used to select the optimal sequence. With the penalty value provided from the process, a reference is provided for the revised design. Finally, examples are discussed to demonstrate that the proposed approach is a feasible method.

**Keywords** Design for disassembly (DFD) · Block-based genetic algorithms · Interactive genetic algorithms (IGAs) · Penalty matrix

## 1 Introduction

In the general business process, the product design stage determines more than 70% of the product manufacturing cost, and this stage has a high degree of uncertainty. However, for new product development today, a more systematic approach is needed to ensure that the design output meets the needs of customers, production and assembly considerations, product life cycle expectations, and many other concerns [1, 2]. In the past, Boothroyd and Dewhurst [3] studied the assembly constraints, costs, and other factors

that must be considered in product design and proposed the concept of Design for Assembly (DFA). This idea opened up development in this domain and has been recognized by follow-up researchers. Therefore, many studies have also explored related "Design for X" methods, such as Design for Disassembly (DFD) [4], Design for Mass Customization [5], Design for Modularity (DFM) [6, 7], and Design for Environment (DFE) [8]. Discussions in this area can be found in the related literature [9]. Among them, Design for Disassembly (DFD) is also a member of the DFX family. Usually, DFD will be combined with the topic of green design, which is why DFD research is attracting increased attention. This study focuses on the issue of disassembly in the area of DFD.

The purpose of green design is to ensure that a product complies with the requirements of environmental protection so as to reduce the impact on the environment. In addition, environmental protection, cost, quality and other factors must be balanced. An important basic condition of green design is easy disassembly of the product. Moreover, the disassembly sequence planning (DSP) method plays an important role in the framework of DFD. DSP refers to the process of disassembling the product, particularly the sequential order of the disassembly of components. In terms of DSP classification, disassembly can be divided into total disassembly and selective disassembly [10]. Total disassembly

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mainly occurs when the target parts are clearly defined. Therefore, the focus of total disassembly is to find the optimal order (such as the one with the least cost or maximum profit) under various constraints. In contrast, selective disassembly focuses on the search for parts or modules that are worthy of disassembly. At the end of a product's life, the recycling manufacturer can execute the relevant recycling processes according to a predetermined recycling plan. This study focuses on total disassembly.

In the past, some researchers have developed qualitative or quantitative methods to evaluate DFD design. Kroll et al. [11] have proposed an evaluation method for disassembly design; Desai and Mital [12] have further proposed evaluation methods to check whether the disassembly plan is destructive disassembly, total disassembly or selective disassembly; Cappelli et al. [13] discuss the generation of the optimal disassembly sequence to meet the minimum disassembly time and cost; Favi et al. [14] attempted to establish life cycle assessment indicators to further echo the design of the life cycle considerations. Most of these past researchers focused on constructing DFD assessment methods and indicators, and usually designers need to calculate these evaluation indicators manually. However, the practical application of these indicators is a time-consuming task [15]. If an ideal method can be developed in the future, it will enable DFD to further develop in the direction of design automation.

This study attempts to develop interactive genetic algorithms based on the idea of genetic algorithms (GAs) in DFD. In traditional GAs, the encoding of the chromosomes is performed before the processing of the algorithm, after which the chromosomes are decoded and the fit value of each chromosome is calculated, and the mechanism is selected according to the value of the fitness function. A chromosome with a higher fitness value has a greater chance of being selected for the new offspring. After the selection, Crossover and Mutation are performed to generate the next generation of chromosomes. Such process is repeated until the end of the evolution. Because GAs can easily adjust the design according to problems and generate ideas, they are favored by many researchers. In the past, Kongar and Gupta [16] developed the so-called Priority Preservative Crossover (PPX) mechanism, and Giudice and Fargione [17] considered disassembly time, life cycle cost, and environmental impact for the fitness function. Hui et al. [18] studied the mechanism of the Disassembly Feasibility Information Graph (DFIG) to explore GAs; Go et al. [19] took mechanisms similar to those of Kongar and Gupta (2006) to develop genetic algorithms for DSP because GAs are fast and flexible, learning easily. Kheder et al. [20] also adopted the crossover mechanism of PPX and added the idea of maintenance in the exploration of the goal formula. Tseng et al. [21] proposed novel block-based genetic algorithms to escape the regional solution; in that approach, the searching

process is based on the goal formula and the score matrix. During a search, the direction is set toward the formula with better scores, which will greatly reduce the search range and make it easier to find the optimal solution, enhancing the efficiency of the entire algorithm and making GAs applicable to complex cases. It has been found that Block-GAs can effectively promote the efficiency of GAs. Therefore, Block-GAs are used in this study.

To make GAs applicable to the field of design, the developed system must have an interactive mechanism. Interactive Genetic Algorithms (IGAs) comprise one of the branches that later derive a number of genetic algorithms. The main difference between IGAs and traditional GAs lies in the fact that IGAs integrate human thinking. For example, an IGA will add user preferences to the design of fitness functions. In the past, Takagi [22] systematically proposed related methods and the theory of IGAs. Yan et al. [23] replaced the user's scoring method with an evaluation method of Boolean operation. Babbar-Sebens and Minsker [24] proposed the so-called IGMII IGAs, which can improve the evolutionary strategy from expert opinions. Another direction of research is how to make users understand and evaluate the genes in IGAs more accurately [25]. But the application of IGAs in the study of DSP is rarely seen.

One reason for this could be that it is very difficult to quantify the plans or attributes of product design. Therefore, the key to whether the design can initially produce a better concept solution for the next stage is the method of quantifying the product characteristics as much as possible when the product has not yet been clearly formed. To take into consideration the high degree of uncertainty and ambiguity encountered in the initial solution, this study adopts the viewpoint of the Fuzzy set as the basis for fit function design. Based on the above discussion, the study combines fuzzy semantics with Interactive Genetic Algorithms (IGAs) to build the DFD environment.

In this paper, the framework of interactive design is described in Sect. 2, and fuzzification penalty design is discussed in Sect. 3. The operation of Block-GAs is discussed in Sect. 4. Section 5 illustrates examples of design, and finally, Sect. 6 presents our conclusions.

## 2 Construction of Interactive GAs for Disassembly Sequence Planning

In DSP planning, the constraints of the priority order should be met. The engineering properties of the parts also need to be predicted. If the properties of the parts change during disassembly, such changes will cause waste and influence the evaluation of the disassembly sequence, representing the waste of cost by disassembly. Interactive design focuses on the adaptability of the fitness function. The designer can

achieve the desired disassembly result through the calculation results by adjusting the fuzzy scores and priority relation information. The following are the basic ideas underlying this study:

1. *Fuzzy scores* By adjusting fuzzy semantic definitions, the user's ideas and expected results can be brought into the algorithm in a more realistic manner, one in which the user's ideas are added to the calculation of the fitness value.
2. *Adjustment of the priority relations* When the initial priority relation is incorrect, new restrictions need to be added, special requirements need to be defined, or a priority order of special parts may be deleted, then specific

adjustments can be made. Computation will be manipulated to generate solutions that match the designer's idea and produce a correct result.

Based on the above discussion, the framework of disassembly sequence planning in product design proposed in this study is shown in Fig. 1. To meet the needs of the designers, it is necessary to satisfy the considerations of interactive and fuzzy semantics. The major steps are explained as follows:

*Step 1* The user enters the part attributes and the priority relations between parts. According to the user-defined part attributes, establish a penalty value matrix and a relation matrix. The user can also freely set the penalty value
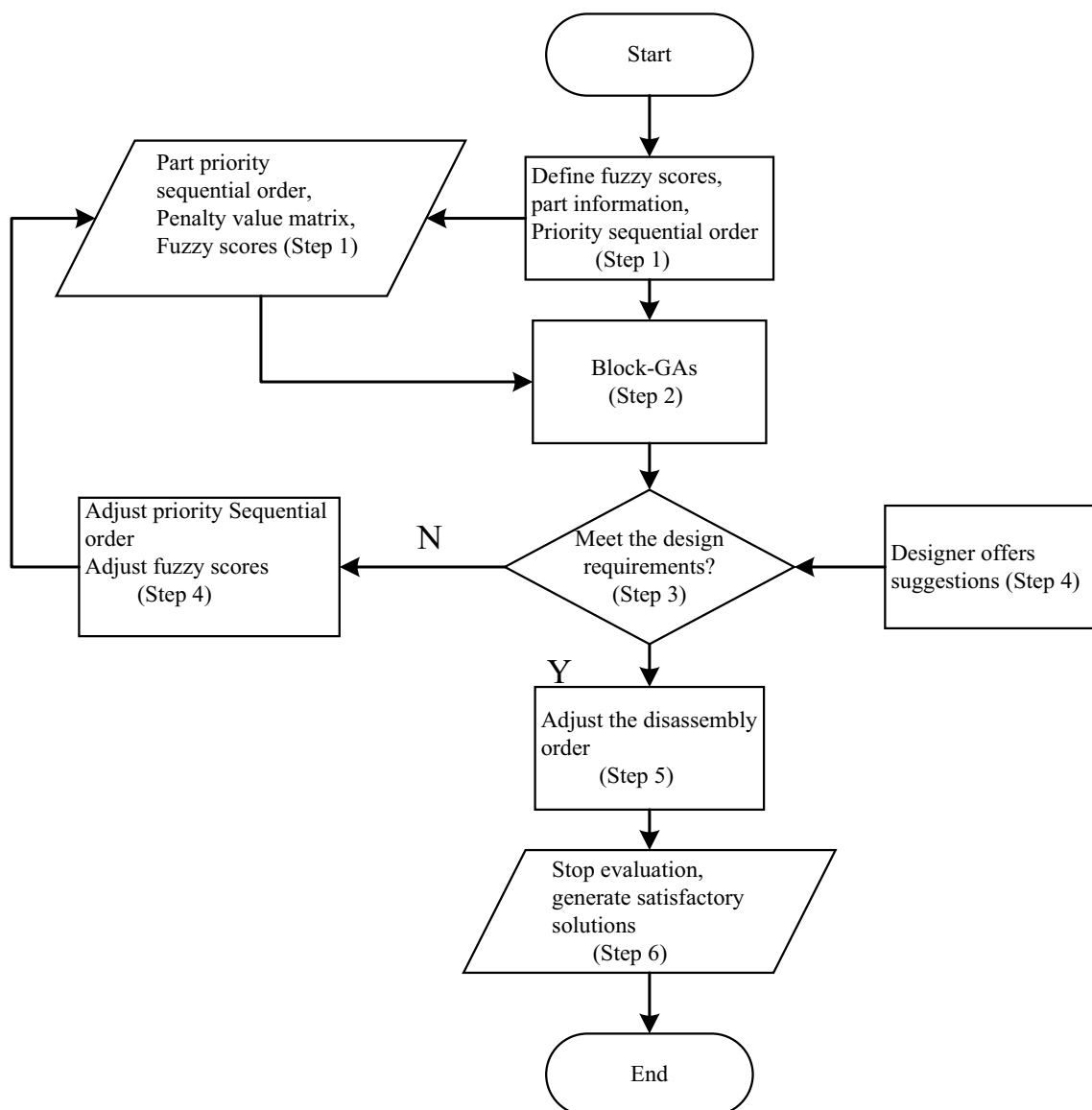


**Fig. 1** Interactive GAs for DSP

matrix to make adjustments. The fuzzy scoring procedure is explained in Sect. 3.

*Step 2* Carry out Block_GAs (Sect. 4).

*Step 3* The user makes decisions based on relevant data such as disassembly time, and the output calculation results and analysis are given to the user for reference. These analyses include the penalty values among parts, the proposed improved parts sequence and part attributes.

*Step 4* Add the designer's idea: The designer judges whether it meets the design requirements. If it meets the requirements, proceed to Step 5. Otherwise, the user can redesign or adjust the priority of parts, the penalty value matrix, control parameters, etc., and repeat Step 4.

*Step 5* Adjust the disassembly sequence order. This is explained in Sect. 5.

*Step 6* Stop the evaluation and generate satisfactory solutions.

## 3 Building a Penalty Matrix by fuzzy Scoring Procedure

In this study, the stapler example in Fig. 2 is used to illustrate how to build a penalty matrix with the fuzzy scoring procedure. The stapler is made up of 18 parts. The priority of the stapler parts is shown in Fig. 3. The labels in the figure are the disassembly priorities, and the circular nodes
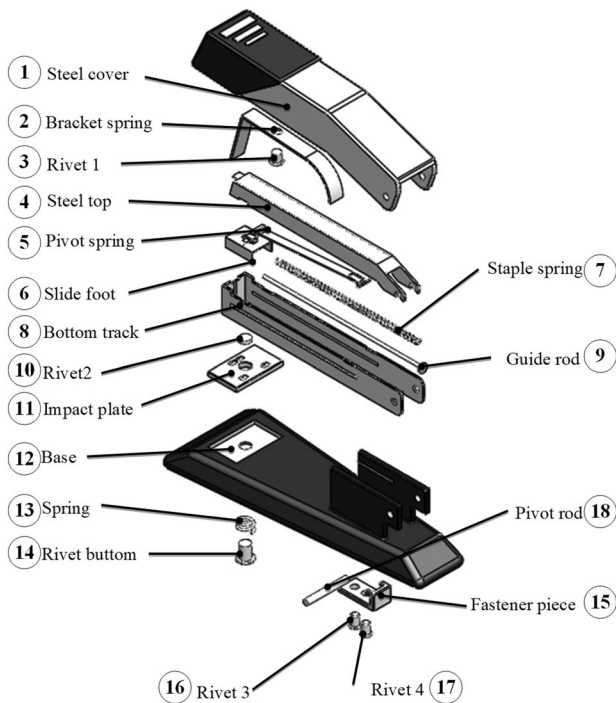


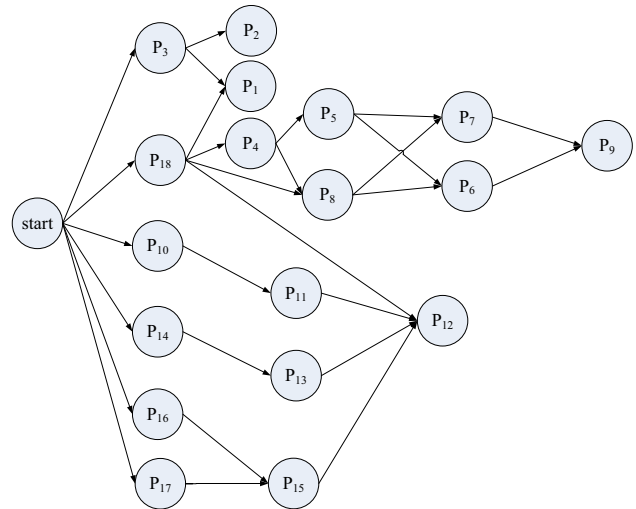**Fig. 3** The sequential priority of the stapler parts



**Fig. 2** The parts of a stapler

are the parts. The direction of disassembly is set to be the six directions in the table. This is based on the professional knowledge of the designer. The disassembly information is divided into part directions, tools, and liaisons. There are 6 different disassembly directions: $+X$, $-X$, $+Y$, $-Y$, $+Z$, and $-Z$. The information of each part is shown in Table 1. In terms of disassembly tools, there are four levels of tools, $T_1$, $T_2$, $T_3$, and $T_4$, according to the degree of difficulty. The details of the parts information are shown in Table 1. The fuzzy items in this study include attribute weights, direction, tools, and liaisons.

### 3.1 The Weighted Semantic Variables

In this study, subjective weights are used, from which users can subjectively give fuzzy semantics directly. Instead of the numerical values of the traditional scores, the weights of the fuzzy parts attributes are adopted here. Generally speaking, the proportions of the distribution weights add up to 1. This study uses fuzzy weights, with the evaluation criteria of fairly important, important, very important, and extremely important. The semantic variables are shown in Fig. 4. According to the user's judgment of the importance of the attributes, the semantic variables are shown in Table 2.

### 3.2 Parts Directions

The direction attribute of a part is expressed in terms of changing the angle, which is mainly divided into changes of less than 45°, changes of about 90°, and changes of about 180°. Three kinds of semantic variables of 0 to 1 are used as the fuzzy numbers. Take the direction of the stapler as an example. Assume $P_3 \rightarrow P_1$ ($\rightarrow$: Part $P_3$ takes priority over Part $P_1$); $P_3$'s direction is $-Y$, and $P_1$'s direction is $+Y$. The

**Table 1** The directions and tool information of the stapler parts

| Parts | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Direction | $+Y$ | $-Y$ | $-Y$ | $+Y$ | $-Y$ | $-X$ | $+X$ | $+Y$ | $+X$ | $-Y$ | $+Y$ | $-Y$ | $-Y$ | $-Y$ | $-Y$ | $-Y$ | $-Y$ | $-Z$ |
| Tool | $T_3$ | $T_1$ | $T_2$ | $T_3$ | $T_4$ | $T_3$ | $T_3$ | $T_3$ | $T_3$ | $T_3$ | $T_1$ | $T_1$ | $T_1$ | $T_2$ | $T_4$ | $T_2$ | $T_2$ | $T_3$ |



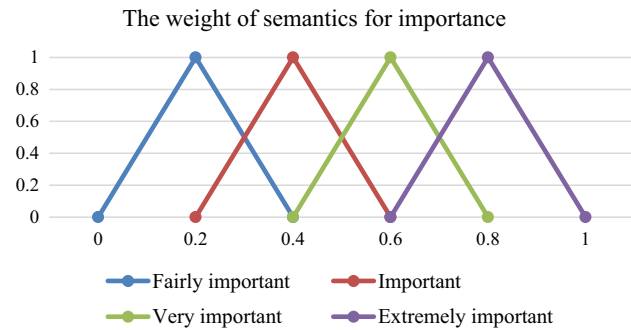**Fig. 4** The weight of semantics for importance

**Table 2** The semantic variables

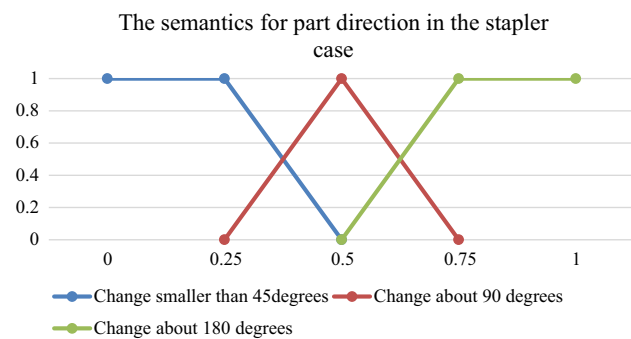| Semantic variable | Fuzzy number |
|---|---|
| Fairly important | (0, 0.2, 0.4) |
| Important | (0.2, 0.4, 0.6) |
| Very important | (0.4, 0.6, 0.8) |
| Extremely important | (0.6, 0.8, 1) |



**Fig. 5** The semantics for part direction in the stapler case

direction changes from $-Y$ to $+Y$, and the change angle is about 180°. Accordingly, the fuzzy numbers of (0.5, 0.75, 0.75) are assigned. The directions of the semantic variables are shown in Fig. 5 and Table 3.

### 3.3 The Disassembly Tool

The disassembly tool attribute is based on the change of tools, with semantics of $T_1$–$T_4$ representing "No change",

**Table 3** The semantic variables for the direction in the stapler case

| Semantic variable | Fuzzy numbers |
|---|---|
| Change smaller than 45° | (0.25, 0.25, 0.5) |
| Change about 90° | (0.25, 0.5, 0.75) |
| Change about 180° | (0.5, 0.75, 0.75) |
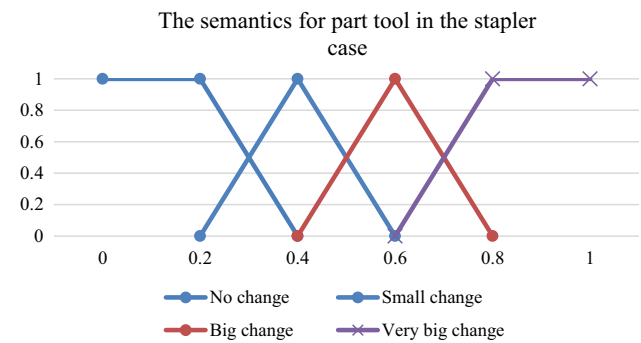


**Fig. 6** The semantics for part tool in the stapler case

**Table 4** The semantic variables for the tool in the stapler case

| Semantic variable | Fuzzy numbers |
|---|---|
| No change | (0.2, 0.2, 0.4) |
| Small change | (0.2, 0.4, 0.6) |
| Big change | (0.4, 0.6, 0.8) |
| Very big change | (0.6, 0.8, 0.8) |

"Small change", "Big change" and "Very big change". The semantic variables use 0–1 for the fuzzy numbers, as shown in the semantic variables map in Fig. 6. The semantic variables are shown in Table 4. For the direction attribute of the stapler, suppose $P_2 \rightarrow P_1$; $P_2$'s tool is $T_1$ and $P_1$'s tool is $T_3$. The tool changes from $T_1$ to $T_3$, the change is big, and the fuzzy numbers (0.4, 0.6, 0.8) are given for the direction attribute of the stapler's case.

### 3.4 Liaison-Type Semantic Variables

The attribute of liaisons is mainly used to describe the degree of relationship between parts. The semantic variables include "With close liaison", "With moderate liaison" and "No liaison". The fuzzy numbers are set between 0 and 1.

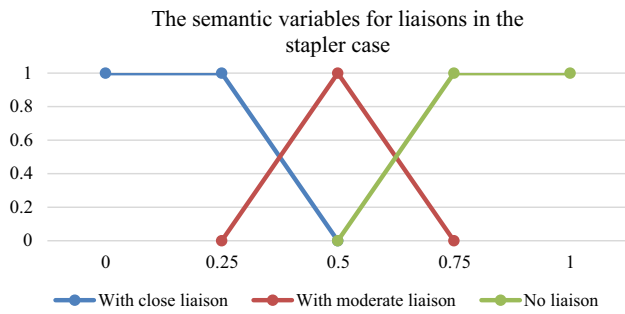The semantic variables for liaisons in the stapler case



**Fig. 7** The semantic variables for liaisons in the stapler case

The semantic variables are shown in Fig. 7. For the stapler case, the semantic variables and their liaisons are shown in Table 5. The liaison graph of the stapler parts is shown in Fig. 8, where N indicates that there is no liaison between two parts, C indicates a liaison between two parts, and I indicates a close liaison between two parts. Designers can examine the relationships between parts from the liaison graph.

## 3.5 Calculate the Penalty Value

At this stage, integral operations are performed based on the fuzzy numbers and fuzzy weights of the fuzzy semantics determined. Assume that the overall order is $P_3 \rightarrow P_{14} \rightarrow P_1 \rightarrow P_2 \rightarrow P_4 \rightarrow P_{18} \rightarrow P_{16} \rightarrow P_{10} \rightarrow P_{11} \rightarrow P_{17} \rightarrow P_{15} \rightarrow P_{13} \rightarrow P_{12} \rightarrow P_5 \rightarrow P_8 \rightarrow P_6 \rightarrow P_7 \rightarrow P_9$. Take the part relation $P_1 \rightarrow P_2$ for example. The change in direction is judged as about 180°, with the corresponding fuzzy numbers (0.5, 0.5, 0.75); the change of tool is a big change, with the fuzzy numbers (0.4, 0.6, 0.8); and the liaison belongs to only some liaison, with fuzzy numbers (0.25, 0.5, 0.75). From the judgment of relative importance, the direction attribute is considered extremely important; the tool attribute, very important; the liaison type, very important. From the user's definition of importance, the corresponding semantic fuzzy numbers are (0.6, 0.8, 1) for extremely important and (0.4, 0.6, 0.8) for very important. The weights are then integrated with the engineering attributes as Formula (1). According to Formula (1),

**Table 5** Definitions of liaisons in stapler case

| Liaison type | Definition | Description | Illustration | Fuzzy numbers |
|---|---|---|---|---|
| No liaison | No contact (N) | No contact between two parts | | (0.5, 0.75, 0.75) |
| With moderate liaison | Contact (C) | Only alignment but no contact between two parts | | (0.25, 0.5, 0.75) |
| With close liaison | Insert (I) | Alignment between two parts | | (0.25, 0.25, 0.5) |

**Fig. 8** The liaison graph in the stapler case
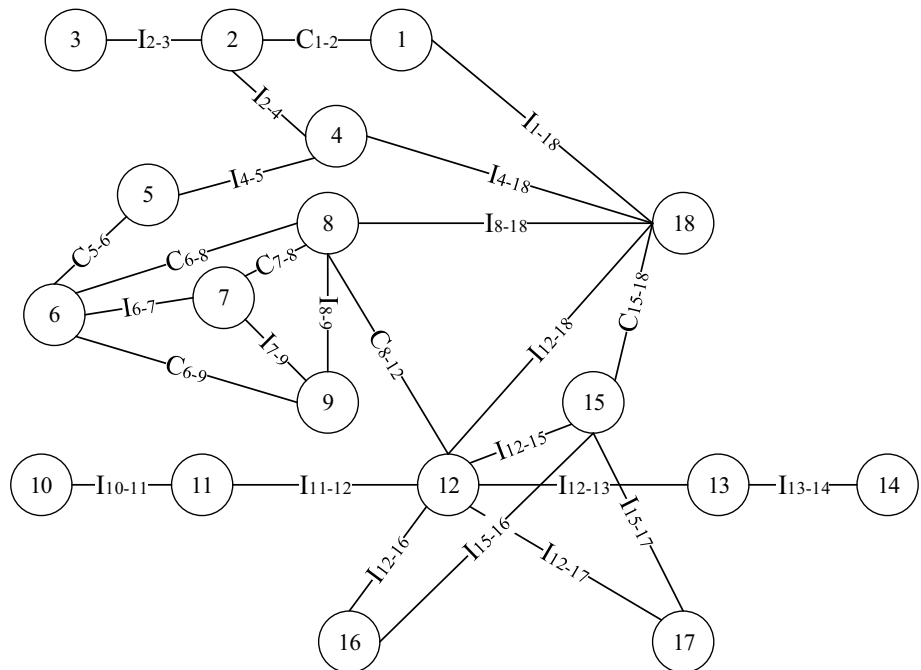
the fuzzy numbers of the $P_1 \rightarrow P_2$ relation can be calculated as $P_{1,3} = (0.61, 1.36, 2.14)$.

$$FuzzyP_{j,seq} = \left( \left( W_{Dl} * D_{j,l} + W_{Tl} * T_{j,l} + W_{Ll} * L_{j,l} \right), \\ \left( W_{Dm} * D_{j,m} + W_{Tm} * T_{j,m} + W_{Lm} * L_{j,m} \right), \\ \left( W_{Dr} * D_{j,r} + W_{Tr} * T_{j,r} + W_{Lr} * L_{j,r} \right) \right) \quad (1)$$

where $Fuzzy\ P_{j,seq}$, the integrated fuzzy number for design attributes; $W$, the weights; $D$, the direction attribute; $T$, the tool attribute; $L$, the liaison attribute; $(l, m, r)$, corresponding fuzzy numbers; $j$, number of current part; $seq$, number in current sequential order.

The main purpose of the defuzzification procedure is to convert the fuzzy numbers into explicit values after the fuzzy operation. In this study, these converted explicit values serve as the penalty values added when the parts are disassembled. As proposed by Bevillacqua and Petroni [26], the center-of-gravity method is used for the defuzzification procedure. The advantage is that a distinct value can be obtained without complicated operations. As shown in Formula (2), the $P_1 \rightarrow P_2$ relation is calculated as $P_{1,3} = 0.61 + 1.36 * 2 + 2.14)/4 = 1.3675$).

$$P_{j,seq} = \frac{l_{j,seq} + 2m_{j,seq} + r_{j,seq}}{4} \quad (2)$$

where $seq$, number in the current sequential order; $P_{j,seq}$, the explicit value between the current part and the next part.

Through the standardization process, the distinct values from defuzzification are transformed into a value of 0–1. The

standardization can be processed from Formulas (3) and (4): $Min(P) = 0.665$, $Max(P) = 0.96$. According to the output of Formula (2), the relation $P_1 \rightarrow P_3$ can be calculated as $P_{1,3} = (1.3675 - 0.665)/0.96 = 0.7318$. Table 6 lists the total penalty values between each two parts.

$$P_{j,seq} = P_{j,seq} - Min(P) \quad (3)$$

$$P_{j,seq} = \frac{P_{j,seq}}{\max(P)} \quad (4)$$

where $P$, the penalty value between each two parts; $Max(P)$, the maximum value in the penalty matrix; $Min(P)$, the minimum value in the penalty matrix.

## 4 Block-Based Genetic Algorithms

In this study, the Penalty Function is used as the design of the fitness function. The less the attribute changes, the lower the penalty value. The value of the fitness function is used to judge the pros and cons of the disassembly sequence. Considering the interactive characteristic, the formula needs to make the calculation of the fitness value feature the advantages of editing, adjustment and expansion. Its calculation method is shown in Formula (5). This study aims to reduce the number of disassembly directions and tool changes in the disassembly activities, since unnecessary directions and tool changes would cause an inefficient disassembly

**Table 6** The penalty value matrix

|    | 1    | 2    | 3    | 4    | 5    | 6    | 7    | 8    | 9    | 10   | 11   | 12   | 13   | 14   | 15   | 16   | 17   | 18   |
|----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| 1  | 0.00 | 0.73 | 0.44 | 0.31 | 0.75 | 0.48 | 0.48 | 0.31 | 0.48 | 0.63 | 0.56 | 0.88 | 0.88 | 0.75 | 0.75 | 0.75 | 0.75 | 0.17 |
| 2  | 0.73 | 0.00 | 0.13 | 0.56 | 0.69 | 0.73 | 0.73 | 0.88 | 0.73 | 0.56 | 0.63 | 0.31 | 0.31 | 0.44 | 0.69 | 0.44 | 0.44 | 0.73 |
| 3  | 0.44 | 0.13 | 0.00 | 0.75 | 0.56 | 0.61 | 0.61 | 0.75 | 0.61 | 0.44 | 0.75 | 0.44 | 0.44 | 0.31 | 0.56 | 0.31 | 0.31 | 0.61 |
| 4  | 0.31 | 0.56 | 0.75 | 0.00 | 0.44 | 0.48 | 0.48 | 0.31 | 0.48 | 0.63 | 0.56 | 0.88 | 0.88 | 0.75 | 0.75 | 0.75 | 0.75 | 0.17 |
| 5  | 0.75 | 0.69 | 0.56 | 0.44 | 0.00 | 0.46 | 0.61 | 0.75 | 0.61 | 0.44 | 1.00 | 0.69 | 0.69 | 0.56 | 0.31 | 0.56 | 0.56 | 0.61 |
| 6  | 0.48 | 0.73 | 0.61 | 0.48 | 0.46 | 0.00 | 0.63 | 0.17 | 0.48 | 0.48 | 0.73 | 0.73 | 0.73 | 0.61 | 0.61 | 0.61 | 0.61 | 0.48 |
| 7  | 0.48 | 0.73 | 0.61 | 0.48 | 0.61 | 0.63 | 0.00 | 0.34 | 0.00 | 0.48 | 0.73 | 0.73 | 0.73 | 0.61 | 0.61 | 0.61 | 0.61 | 0.48 |
| 8  | 0.31 | 0.88 | 0.75 | 0.31 | 0.75 | 0.17 | 0.34 | 0.00 | 0.17 | 0.63 | 0.56 | 0.73 | 0.88 | 0.75 | 0.75 | 0.75 | 0.75 | 0.17 |
| 9  | 0.48 | 0.73 | 0.61 | 0.48 | 0.61 | 0.48 | 0.00 | 0.17 | 0.00 | 0.48 | 0.73 | 0.73 | 0.73 | 0.61 | 0.61 | 0.61 | 0.61 | 0.48 |
| 10 | 0.63 | 0.56 | 0.44 | 0.63 | 0.44 | 0.48 | 0.48 | 0.63 | 0.48 | 0.00 | 0.56 | 0.56 | 0.56 | 0.44 | 0.44 | 0.44 | 0.44 | 0.48 |
| 11 | 0.56 | 0.63 | 0.75 | 0.56 | 1.00 | 0.73 | 0.73 | 0.56 | 0.73 | 0.56 | 0.00 | 0.31 | 0.63 | 0.75 | 1.00 | 0.75 | 0.75 | 0.73 |
| 12 | 0.88 | 0.31 | 0.44 | 0.88 | 0.69 | 0.73 | 0.73 | 0.73 | 0.73 | 0.56 | 0.31 | 0.00 | 0.00 | 0.44 | 0.69 | 0.44 | 0.44 | 0.42 |
| 13 | 0.88 | 0.31 | 0.44 | 0.88 | 0.69 | 0.73 | 0.73 | 0.88 | 0.73 | 0.56 | 0.63 | 0.00 | 0.00 | 0.13 | 0.69 | 0.44 | 0.44 | 0.73 |
| 14 | 0.75 | 0.44 | 0.31 | 0.75 | 0.56 | 0.61 | 0.61 | 0.75 | 0.61 | 0.44 | 0.75 | 0.44 | 0.13 | 0.00 | 0.56 | 0.31 | 0.31 | 0.61 |
| 15 | 0.75 | 0.69 | 0.56 | 0.75 | 0.31 | 0.61 | 0.61 | 0.75 | 0.61 | 0.44 | 1.00 | 0.69 | 0.69 | 0.56 | 0.00 | 0.25 | 0.25 | 0.46 |
| 16 | 0.75 | 0.44 | 0.31 | 0.75 | 0.56 | 0.61 | 0.61 | 0.75 | 0.61 | 0.44 | 0.75 | 0.44 | 0.44 | 0.31 | 0.25 | 0.00 | 0.31 | 0.61 |
| 17 | 0.75 | 0.44 | 0.31 | 0.75 | 0.56 | 0.61 | 0.61 | 0.75 | 0.61 | 0.44 | 0.75 | 0.44 | 0.44 | 0.31 | 0.25 | 0.31 | 0.00 | 0.61 |
| 18 | 0.17 | 0.73 | 0.61 | 0.17 | 0.61 | 0.48 | 0.48 | 0.17 | 0.48 | 0.48 | 0.73 | 0.42 | 0.73 | 0.61 | 0.46 | 0.61 | 0.61 | 0.00 |

process. This view is similar to the research of Li et al. [27]. In this study, the direction and tool change are integrated in the objective formula so as to find a disassembly sequence with lower numbers of changes in direction and tools on the same product. Consequently, a disassembly sequence with fewer changes is relatively more efficient than one with more changes in the disassembly procedure. According to studies related to Methods of Time Measurement (MTM), this goal can reduce the disassembly time [11, 28]. From the search for a disassembly sequence with fewer changes, a more efficient disassembly sequence can be obtained, as shown in Eq. (5).

$$MS = \sum_{seq=0}^{n-2} P_{j,seq}, \quad \forall j, j = 0, \ldots, n-1 \tag{5}$$

where $MS$, the fitness value; $j$, number of the current part; $seq$, number in the current sequential order; $P_{j,seq}$, the

explicit value between the current part and the next part; $n$, total number of parts.

Figure 9 shows the procedure of Block-based genetic algorithms, which is characterized by introducing the penalty value matrix in the crossover method (Step 4) and the mutation method (Step 5). This offers the direction for searching, thereby improving the quality of the algorithm's solution.

The steps for the Block-based genetic algorithms are described below:

*Step 1* Process non-binary chromosome encoding: generate the feasible initial parent chromosomes with numbers of parameters according to the user-defined part attributes and the part priority matrix.
*Step 2* Calculate the fitness value of each chromosome as a basis for the chromosome evaluation.

**Fig. 9** The block-based GAs
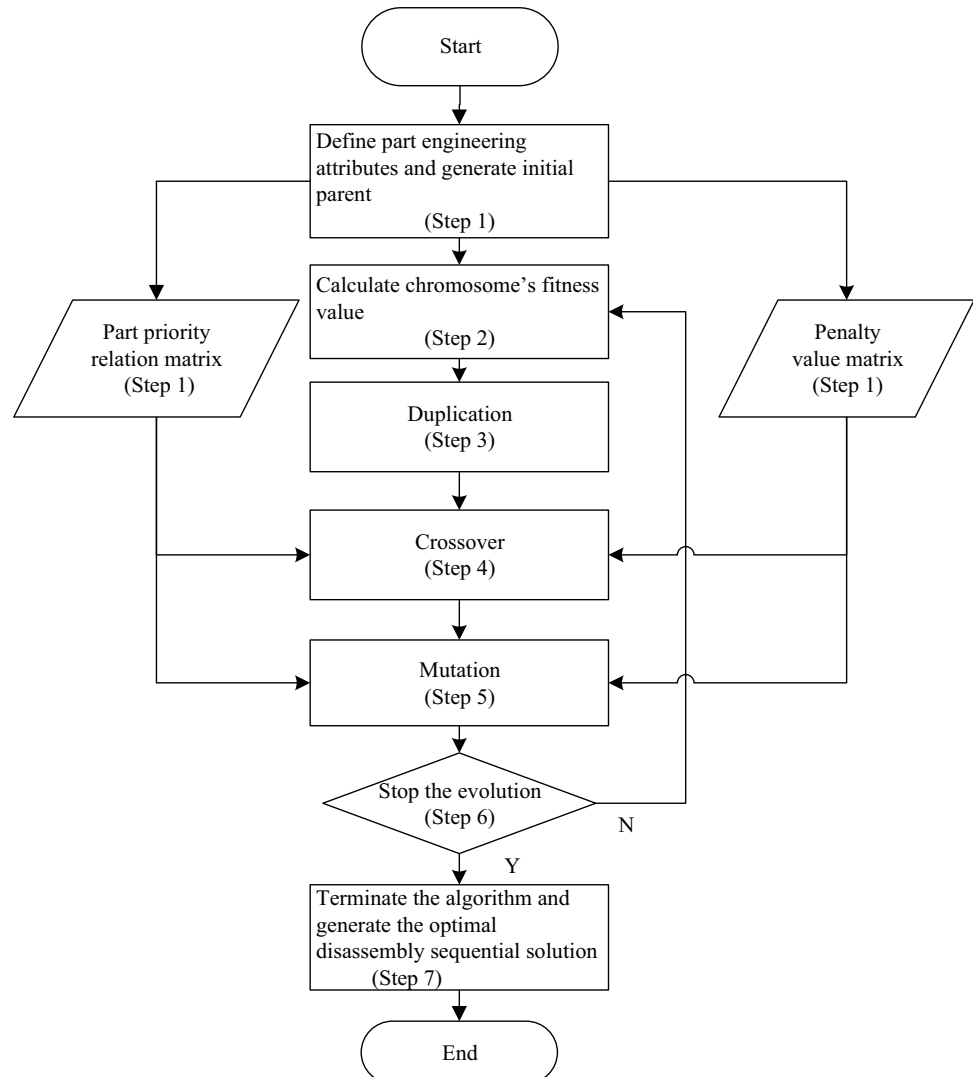
*Step 3* According to the fitness value, duplicate the chromosomes equal to the parent number by the roulette method for the next generation.

*Step 4* Perform the crossover method based on the blocks. The details will be described later.

*Step 5* Perform the block-based mutation method.

*Step 6* Determine whether the evolution should be terminated. In this study, the maximum generation number is set as the termination condition. If the termination condition is satisfied, proceed to Step 7; otherwise, proceed to Step 2.

*Step 7* Stop the algorithm and generate the optimal or close-to-optimal solution to the disassembly sequence order.

Figure 10 illustrates the procedure for the Block-based crossover mechanism, the steps of which are listed below:

*Step 4.1* Select two chromosomes as $Parent_1$: $P_3 \rightarrow P_{14} \rightarrow P_{18} \rightarrow P_{16} \rightarrow P_{17} \rightarrow P_2 \rightarrow P_1 \rightarrow P_4 \rightarrow P_{10} \rightarrow P_{11} \rightarrow P_{13} \rightarrow P_{15} \rightarrow P_5 \rightarrow P_8 \rightarrow P_7 \rightarrow P_6 \rightarrow P_9 \rightarrow P_{12}$ and $Parent_2$: $P_{17} \rightarrow P_{18} \rightarrow P_{16} \rightarrow P_{14} \rightarrow P_3 \rightarrow P_{10} \rightarrow P_{11} \rightarrow P_{15} \rightarrow P_{13} \rightarrow P_{12} \rightarrow P_2 \rightarrow P_1 \rightarrow P_4 \rightarrow P_5 \rightarrow P_8 \rightarrow P_7 \rightarrow P_6 \rightarrow P_9$ for crossover, as shown in Fig. 11a.

*Step 4.2* Randomly generate a block whose size is 0–100% of the total block. The total block size is 18, and assume that the size of the block generated is 88.88%; then the block size is 18*88.88% = 16.

*Step 4.3* Divide the block size of 16 into 3 blocks, as shown in Fig. 11b.

*Step 4.4* Calculate the fitness values for all blocks. This is shown in Table 7.

*Step 4.5* Choose the best block. In this case, the lowest fitness value is 7.8464, indicating that the block $P_3 \rightarrow P_{14} \rightarrow P_{18} \rightarrow P_{16} \rightarrow P_{17} \rightarrow P_2 \rightarrow P_1 \rightarrow P_4 \rightarrow P_{10} \rightarrow P_{11} \rightarrow P_{13} \rightarrow P_{15} \rightarrow P_5 \rightarrow P_8 \rightarrow P_7 \rightarrow P_6$ should be reserved.

*Step 4.6* The chromosome $Parent_2$ is $P_{17} \rightarrow P_{18} \rightarrow P_{16} \rightarrow P_{14} \rightarrow P_3 \rightarrow P_{10} \rightarrow P_{11} \rightarrow P_{15} \rightarrow P_{13} \rightarrow P_{12} \rightarrow P_2 \rightarrow P_1 \rightarrow P_4 \rightarrow P_5 \rightarrow P_8 \rightarrow P_7 \rightarrow P_6 \rightarrow P_9$, and then duplicate $Parent_2$ for $Offspring_1$. The chromosome $Parent_1$ is $P_3 \rightarrow P_{14} \rightarrow P_{18} \rightarrow P_{16} \rightarrow P_{17} \rightarrow P_2 \rightarrow P_1 \rightarrow P_4 \rightarrow P_{10} \rightarrow P_{11} \rightarrow P_{13} \rightarrow P_{15} \rightarrow P_5 \rightarrow P_8 \rightarrow P_7 \rightarrow P_6 \rightarrow P_9 \rightarrow P_{12}$, and duplicate $Parent_1$ for $Offspring_2$.

*Step 4.7* Insert the reserved block in $Parent_1$ to the corresponding positions of $Offspring_1$; $Offspring_1$ is $P_3 \rightarrow P_{14} \rightarrow P_{18} \rightarrow P_{16} \rightarrow P_{17} \rightarrow P_2 \rightarrow P_1 \rightarrow P_4 \rightarrow P_{10} \rightarrow P_{11} \rightarrow P_{13} \rightarrow P_{15} \rightarrow P_5 \rightarrow P_8 \rightarrow P_7 \rightarrow P_6 \rightarrow P_6 \rightarrow P_9$, as shown in Fig. 11c.
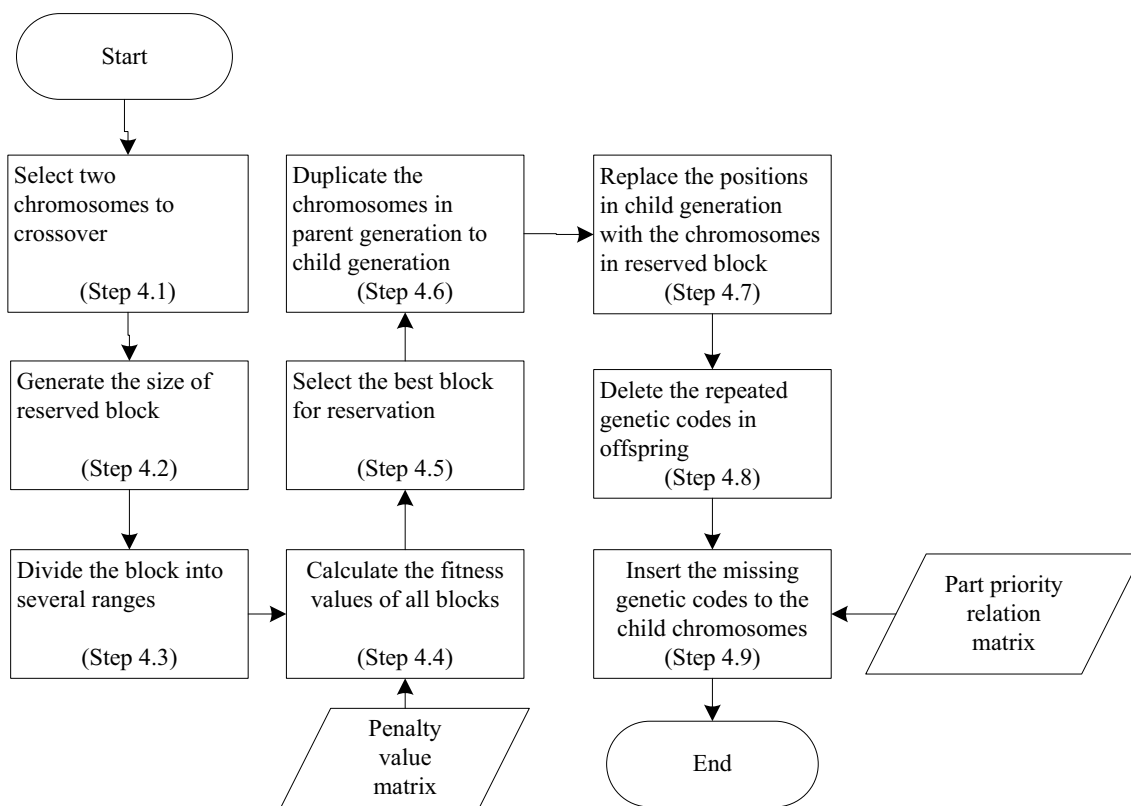


**Fig. 10** The procedure for the crossover mechanism

**Fig. 11** The conceptual diagram of the crossover mechanism
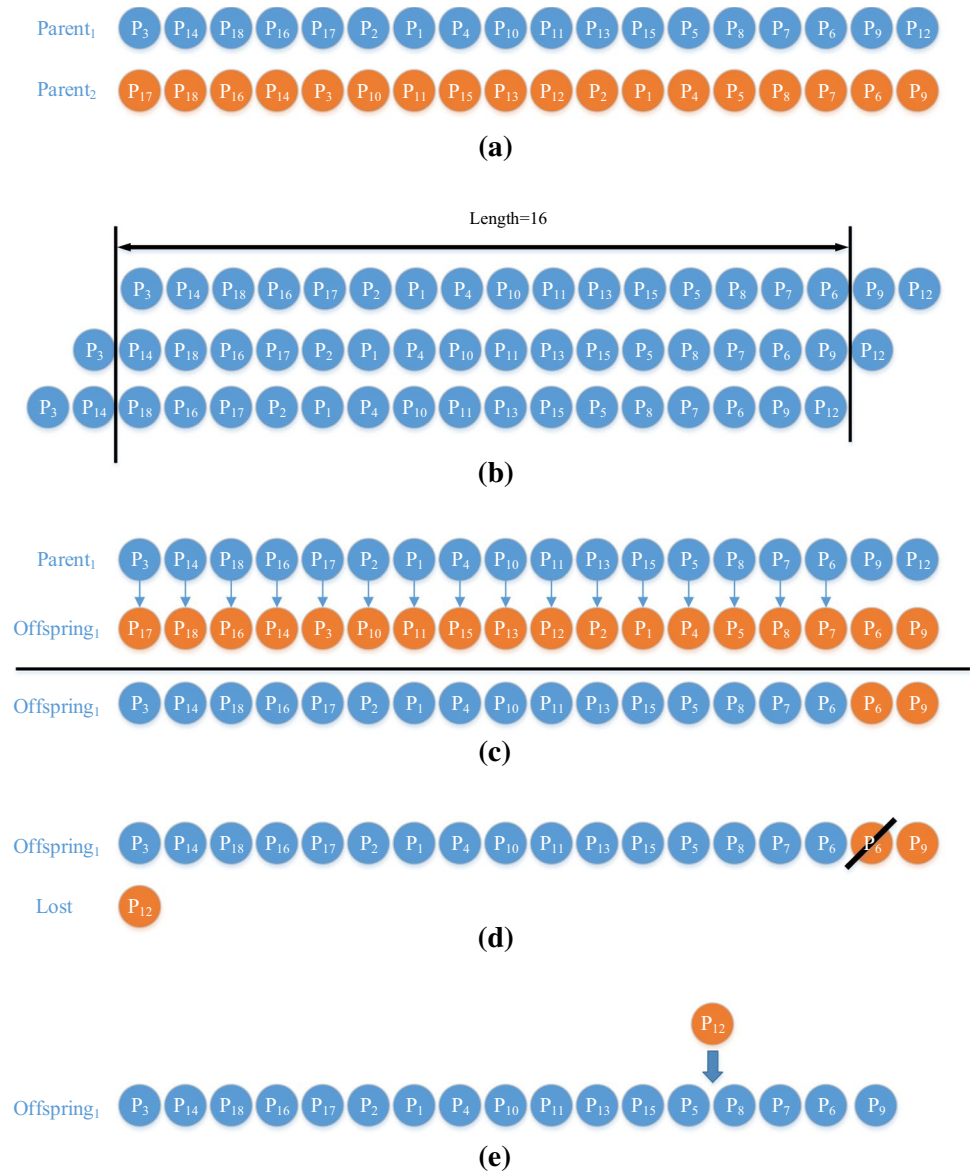


(a)

(b)

(c)

(d)

(e)

**Table 7** Fitness values for blocks in Parent₁

| 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | Fitness value |
|---|---|---|---|---|---|---|---|---|----|----|----|----|----|----|----|----|----|---------------|
| **P₃** | **P₁₄** | **P₁₈** | **P₁₆** | **P₁₇** | **P₂** | **P₁** | **P₄** | **P₁₀** | **P₁₁** | **P₁₃** | **P₁₅** | **P₅** | **P₈** | **P₇** | **P₆** | P₉ | P₁₂ | 7.85 |
| P₃ | **P₁₄** | **P₁₈** | **P₁₆** | **P₁₇** | **P₂** | **P₁** | **P₄** | **P₁₀** | **P₁₁** | **P₁₃** | **P₁₅** | **P₅** | **P₈** | **P₇** | **P₆** | **P₉** | P₁₂ | 8.02 |
| P₃ | P₁₄ | **P₁₈** | **P₁₆** | **P₁₇** | **P₂** | **P₁** | **P₄** | **P₁₀** | **P₁₁** | **P₁₃** | **P₁₅** | **P₅** | **P₈** | **P₇** | **P₆** | **P₉** | **P₁₂** | 8.14 |

Bold indicates block interval

*Step 4.8* Search for the repeated genetic codes in Offspring$_1$, and find that P$_6$ is repeated and P$_{12}$ is missing. Remove the repeated P$_6$; Offspring1 is then P$_3 \rightarrow$ P$_{14} \rightarrow$ P$_{18} \rightarrow$ P$_{16} \rightarrow$ P$_{17} \rightarrow$ P$_2 \rightarrow$ P$_1 \rightarrow$ P$_4 \rightarrow$ P$_{10} \rightarrow$ P$_{11} \rightarrow$ P$_{13} \rightarrow$ P$_{15} \rightarrow$ P$_5 \rightarrow$ P$_8 \rightarrow$ P$_7 \rightarrow$ P$_6 \rightarrow$ P$_9$, as shown in Fig. 11d.

*Step 4.9* Search the range for inserting P$_{12}$ into Offspring$_1$, and find the ranges from P$_{15}$ to P$_9$ and from P$_{13}$ to P$_{18}$. Calculate the penalty values for feasible insertion positions, as shown in Table 8. The lowest value is found in P$_{14}$, and the output Offspring$_1$ is P$_3 \rightarrow$ P$_{14} \rightarrow$ P$_{18} \rightarrow$ P$_{16} \rightarrow$ P$_{17} \rightarrow$ P$_2 \rightarrow$ P$_1 \rightarrow$ P$_4 \rightarrow$ P$_{10} \rightarrow$ P$_{11} \rightarrow$ P$_{13} \rightarrow$ P$_{15} \rightarrow$ P$_5 \rightarrow$ P$_{12} \rightarrow$ P$_8 \rightarrow$ P$_7 \rightarrow$ P$_6 \rightarrow$ P$_9$, as shown in Fig. 11e.

For the block-based mutation mechanism, the detailed procedure is illustrated in Fig. 12 and described below:

*Step 5.1* Process the mutation mechanism in the selected chromosomes.

*Step 5.2* Randomly generate the mutation amount (1 to number of total parts); the amount of mutations equals the number of mutated genes. It is assumed to be 10 in this case.

*Step 5.3* Randomly select a gene for the mutation point and remove it from the chromosome, as shown in Fig. 13a.

*Step 5.4* Insert the mutation point to the most suitable position in the gene (Step 4.8 to Step 4.9), as shown in Fig. 13b.

*Step 5.5* Repeat Step 5.2 to Step 5.4 ten times (the amount of mutations is 10) and complete the mutation mechanism.

To verify the performance of the block-based genetic algorithms, this study compared it with the GA of Kongar and Gupta [16] and the Ant Colony Optimization (ACO) of Dorigo and Gambardella [29]. The solution effect is tested with a stapler example. The results are shown in Table 9. From the convergence graph in Fig. 14, it can be found that the solution quality of the block-based genetic algorithm is better than those of the other two methods. In terms of the execution time, the block-based genetic algorithm is similar to Ant Colony Optimization but better than Kongar and Gupta's GAs.

## 5 Sample Tests

### 5.1 Fine-Tuning Design

The fine-tuning design is herein defined as displacement of the part position. After the order is generated, the user can select the part to be adjusted. If the disassembly order is P$_{18} \rightarrow$ P$_4 \rightarrow$ P$_5 \rightarrow$ P$_{10} \rightarrow$ P$_3 \rightarrow$ P$_2 \rightarrow$ P$_{11} \rightarrow$ P$_1 \rightarrow$ P$_8 \rightarrow$ P$_6 \rightarrow$ P$_7 \rightarrow$ P$_9 \rightarrow$ P$_{16} \rightarrow$ P$_{17} \rightarrow$ P$_{14} \rightarrow$ P$_{15} \rightarrow$ P$_{13} \rightarrow$ P$_{12}$, the penalty value is 5.9152 from the fuzzy score calculation in this disassembly sequence order (Fig. 15a). If we want to move part P$_{15}$, then P$_{15}$ is input as the part to be moved, and all the movable results are confirmed after checking the priority sequential orders (Fig. 3). After calculation of the Block-based GAs, the result is shown in Fig. 15b. It can be found that sequential order No. 1 has the lowest penalty value of 5.7578, so it can be selected. Now P$_{18} \rightarrow$ P$_4 \rightarrow$ P$_5 \rightarrow$ P$_{10} \rightarrow$ P$_3 \rightarrow$ P$_2 \rightarrow$ P$_{11} \rightarrow$ P$_1 \rightarrow$ P$_8 \rightarrow$ P$_6 \rightarrow$ P$_7 \rightarrow$ P$_9 \rightarrow$ P$_{16} \rightarrow$ P$_{17} \rightarrow$ P$_{15} \rightarrow$ P$_{14} \rightarrow$ P$_{13} \rightarrow$ P$_{12}$ is the new

**Table 8** The penalty values for insertion positions in Offspring$_1$

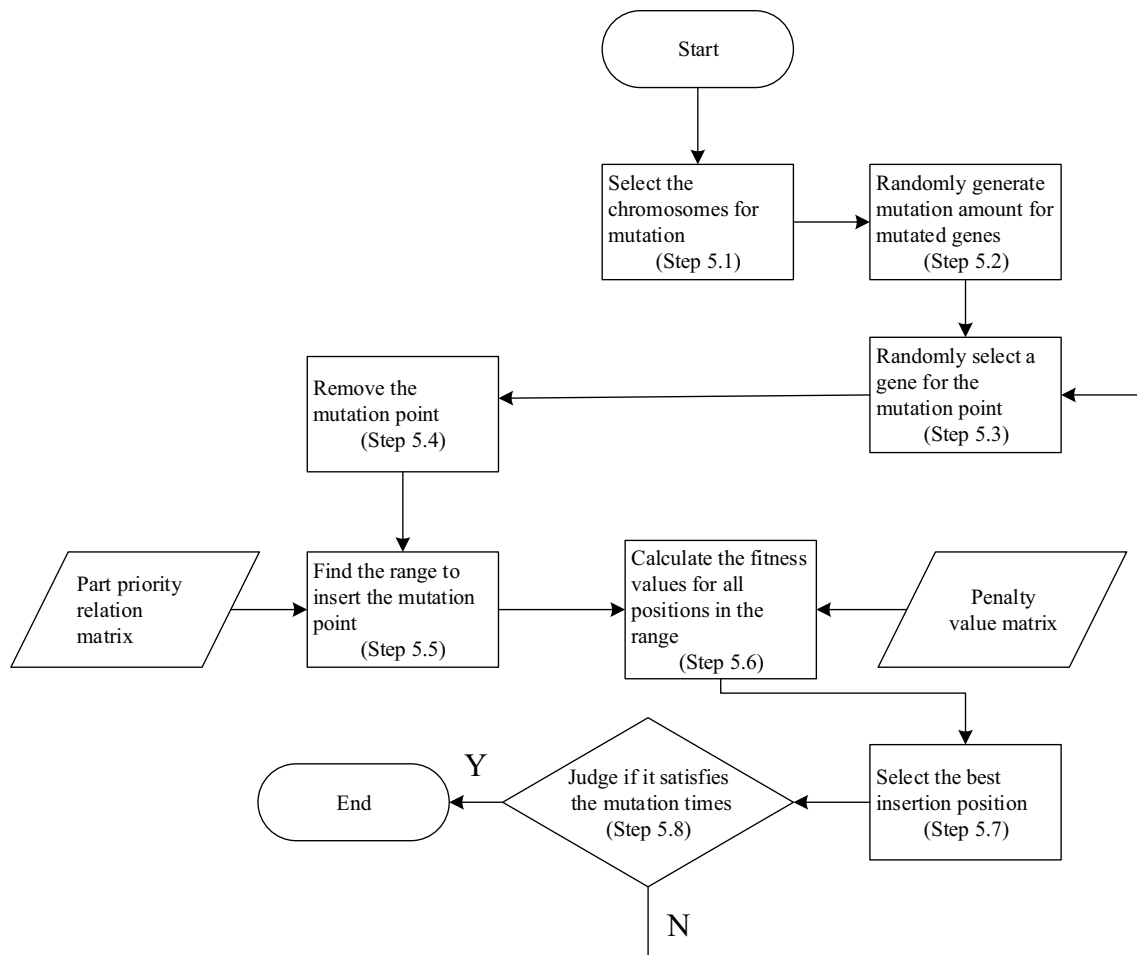| Position number | P$_{13}$ | P$_{14}$ | P$_{15}$ | P$_{16}$ | P$_{17}$ | P$_{18}$ |
|---|---|---|---|---|---|---|
| Penalty value | 9.39 | 9 | 9.45 | 9.17 | 9.31 | 9.06 |

**Fig. 12** The procedure for block-based mutation

sequential order for disassembly, as shown in Fig. 15c. The designer can adjust the position of the disassembly sequence of a single part until it meets the requirements. In analyzing the overall sequential orders, it is suggested that different attributes be changed to reduce the penalty value.

The related disassembly information for all possible results of the new design is summarized in Table 10. If the designers focus on $P_{18} \rightarrow P_4$ (disassemble $P_{18}$ before $P_4$), suggestions can be offered for the adjustment of part attributes. According to Table 10, it can be found that some part relations, those where there exist continuous changes of direction and tool in the part relationship, may cause increases in penalty value. Obviously, reducing such changes can reduce the penalty value, and it can be simulated to improve the
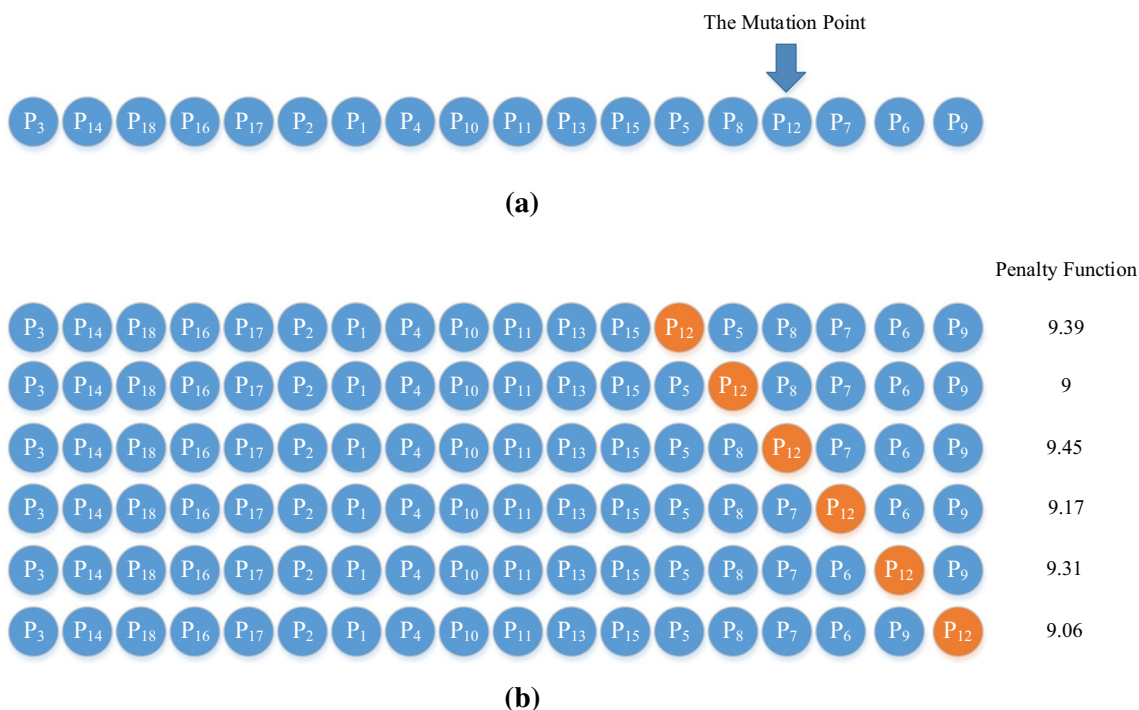
The Mutation Point

$P_3$ $P_{14}$ $P_{18}$ $P_{16}$ $P_{17}$ $P_2$ $P_1$ $P_4$ $P_{10}$ $P_{11}$ $P_{13}$ $P_{15}$ $P_5$ $P_8$ $P_{12}$ $P_7$ $P_6$ $P_9$

**(a)**

Penalty Function

$P_3$ $P_{14}$ $P_{18}$ $P_{16}$ $P_{17}$ $P_2$ $P_1$ $P_4$ $P_{10}$ $P_{11}$ $P_{13}$ $P_{15}$ $P_{12}$ $P_5$ $P_8$ $P_7$ $P_6$ $P_9$       9.39

$P_3$ $P_{14}$ $P_{18}$ $P_{16}$ $P_{17}$ $P_2$ $P_1$ $P_4$ $P_{10}$ $P_{11}$ $P_{13}$ $P_{15}$ $P_5$ $P_{12}$ $P_8$ $P_7$ $P_6$ $P_9$       9

$P_3$ $P_{14}$ $P_{18}$ $P_{16}$ $P_{17}$ $P_2$ $P_1$ $P_4$ $P_{10}$ $P_{11}$ $P_{13}$ $P_{15}$ $P_5$ $P_8$ $P_{12}$ $P_7$ $P_6$ $P_9$       9.45

$P_3$ $P_{14}$ $P_{18}$ $P_{16}$ $P_{17}$ $P_2$ $P_1$ $P_4$ $P_{10}$ $P_{11}$ $P_{13}$ $P_{15}$ $P_5$ $P_8$ $P_7$ $P_{12}$ $P_6$ $P_9$       9.17

$P_3$ $P_{14}$ $P_{18}$ $P_{16}$ $P_{17}$ $P_2$ $P_1$ $P_4$ $P_{10}$ $P_{11}$ $P_{13}$ $P_{15}$ $P_5$ $P_8$ $P_7$ $P_6$ $P_{12}$ $P_9$       9.31

$P_3$ $P_{14}$ $P_{18}$ $P_{16}$ $P_{17}$ $P_2$ $P_1$ $P_4$ $P_{10}$ $P_{11}$ $P_{13}$ $P_{15}$ $P_5$ $P_8$ $P_7$ $P_6$ $P_9$ $P_{12}$       9.06

**(b)**

**Fig. 13** The conceptual diagram of the mutation mechanism

**Table 9** Test results

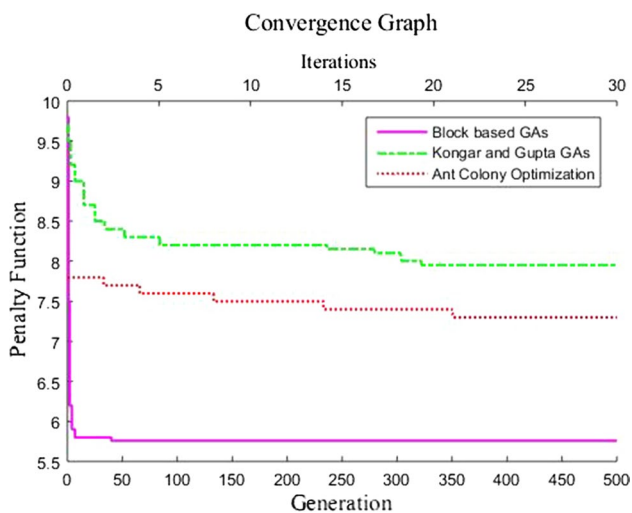| Method | Second/time | Average score | Optimal score |
|---|---|---|---|
| Block-based GAs | 3.1765 | 5.9631 | 5.7578 |
| Kongar and Gupta's GAs | 0.4982 | 8.2631 | 7.9505 |
| Ant colony optimization | 0.3126 | 7.5669 | 7.3125 |

The number of tests is 10



**Fig. 14** The convergence graph

outcome. The simulated results for these part attributes are shown in Table 11 and Table 12. The designer can evaluate whether the changed attributes are feasible and able to reduce the penalty value by adjusting the original attributes of the parts.

## 5.2 Redesign

According to the results of the research method and the part attribute analysis, the user can adjust the penalty value through the output part information. If the result does not meet the design requirements, the following three-part output information can be observed: (1) $P_{15}$, $P_{16}$ and $P_{17}$ are consistent in direction ($-Y$) and liaison (close liaison) (see Table 1 and Fig. 7). (2) From the disassembly sequence order, it is found that these three parts, $P_{15}$, $P_{16}$, and $P_{17}$, will be disassembled one after another; in other words, they will be removed in order. (3) According to the stapler diagram of Fig. 3 and the priority sequence diagram of Fig. 2, $P_{15}$, $P_{16}$, and $P_{17}$ are located in the same area. Given these proposals and the check for priority in the disassembly sequence order (Fig. 3), these three parts can be combined with $P_{12}$, as shown in Fig. 16, to form a one-piece component, as shown in Fig. 15d. Such a design has the following three advantages: (1) it reduces the complexity in the priority sequence diagram; (2) it reduces the number of changes of part attributes and the waste caused by disassembly as well
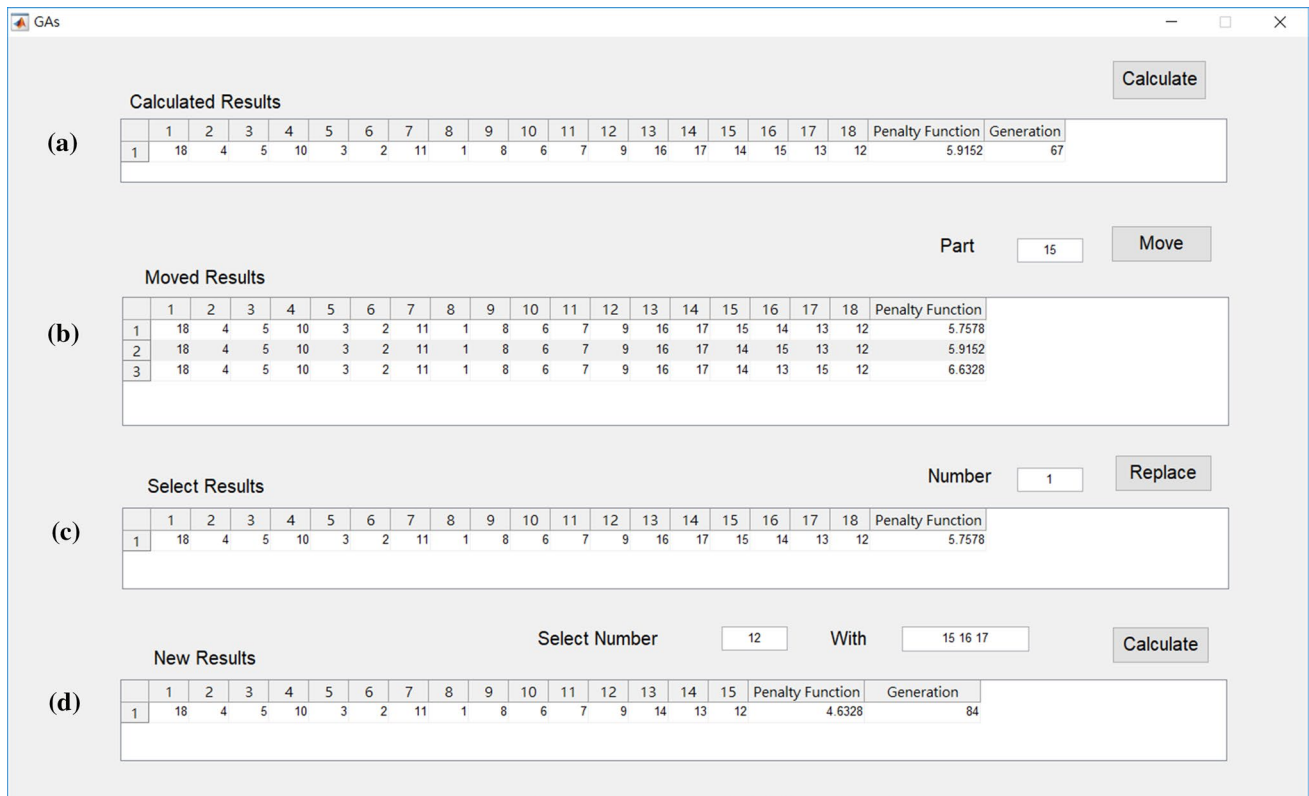
**Fig. 15** Tuning mechanism for the disassembly sequence order

**Table 10** Analysis of the results for all disassembly sequence orders

| 1. Part relation | 2. Direction | 3. Tool | 4. Liaison | Total score |
|---|---|---|---|---|
| $P_{18} \rightarrow P_4$ | 0.17 | 0 | 0 | 0.17 |
| $P_4 \rightarrow P_5$ | 0.31 | 0.13 | 0 | 0.44 |
| $P_5 \rightarrow P_{10}$ | 0 | 0.13 | 0.31 | 0.44 |
| $P_{10} \rightarrow P_3$ | 0 | 0.13 | 0.31 | 0.44 |
| $P_3 \rightarrow P_2$ | 0 | 0.13 | 0 | 0.13 |
| $P_2 \rightarrow P_{11}$ | 0.31 | 0 | 0.31 | 0.63 |
| $P_{11} \rightarrow P_1$ | 0 | 0.25 | 0.31 | 0.56 |
| $P_1 \rightarrow P_8$ | 0 | 0 | 0.31 | 0.31 |
| $P_8 \rightarrow P_6$ | 0.17 | 0 | 0 | 0.17 |
| $P_6 \rightarrow P_7$ | 0.31 | 0 | 0.31 | 0.63 |
| $P_7 \rightarrow P_9$ | 0 | 0 | 0 | 0 |
| $P_9 \rightarrow P_{16}$ | 0.17 | 0.13 | 0.31 | 0.61 |
| $P_{16} \rightarrow P_{17}$ | 0 | 0 | 0.31 | 0.31 |
| $P_{17} \rightarrow P_{15}$ | 0 | 0.25 | 0 | 0.25 |
| $P_{15} \rightarrow P_{14}$ | 0 | 0.25 | 0.31 | 0.56 |
| $P_{14} \rightarrow P_{13}$ | 0 | 0.13 | 0 | 0.13 |
| $P_{13} \rightarrow P_{12}$ | 0 | 0 | 0 | 0 |

The total score equals the sum of columns 2, 3, and 4; they are the same as the penalty value matrix in Table 7

**Table 11** Suggestions for the part direction in disassembly

| Part | Direction | Suggestion | Reduced penalty value |
|---|---|---|---|
| $P_4$ | $+Y$ | $-Y$ | 0.31 |
| $P_6$ | $-X$ | $+X, +Y$ | 0.31 |

**Table 12** Suggestions for the tools in disassembly

| Part | Direction | Suggestion | Reduced penalty value |
|---|---|---|---|
| $P_5$ | $T_4$ | $T_3$ | 0.25 |
| $P_{15}$ | $T_4$ | $T_2$ | 0.5 |

**Fig. 16** The stapler parts before
and after redesign
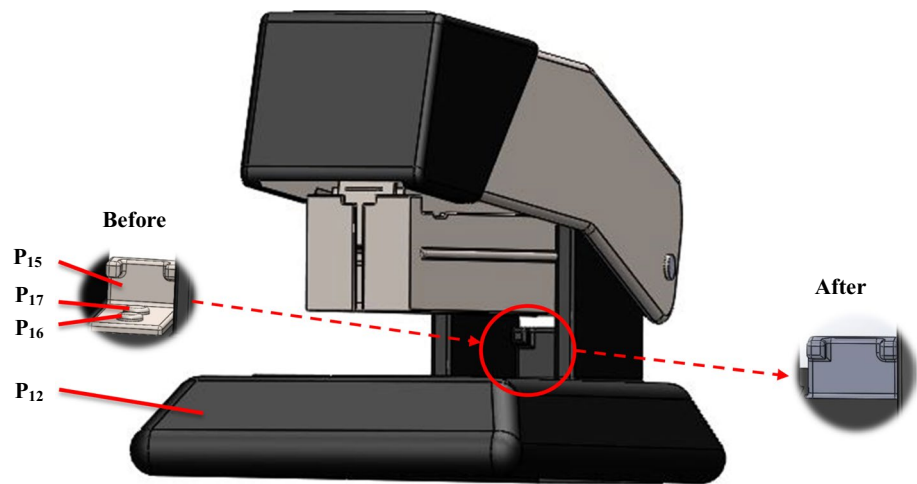


as the penalty value; (3) it reduces the number of parts. The addition of the decrement design concept not only complies with the goal of green design but also mitigates the impact on the environment.

## 6 Conclusions

In this study, an interactive genetic algorithm is proposed and successfully applied to disassembly planning design. The fuzzy penalty scores are first offered for designers' reference, and then Block-based GAs are used to solve the disassembly sequence order. Using the quantitative fuzzy penalty scores, designers can evaluate the quality of the design.

This study makes the following contributions: (1) according to their demands, designers can define fuzzy scores and part information and verify the solution by adjusting the disassembly sequence order; (2) the goal of solution quality and an interactive approach are integrated in the algorithm, enhancing the value of the quantitative evaluation; (3) design for disassembly (DFD) will help to transmit environmental awareness back to the source of product design. Based on green design considerations, if a certain part should be removed, all of the disassembly routes should be assessed to achieve the purpose of resource recycling.

In future research, the implementation of green design still needs further efforts. Other quantitative assessment factors, such as the economic valuation of parts or the recycling of different parts (or subassemblies), as in reuse and remanufacturing, can be taken into consideration in the near future.

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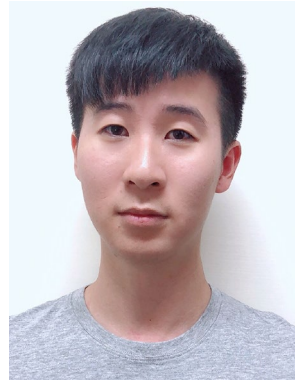
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