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# Assembly Sequence Planning of Quayside Container Crane Based on Improved Immune Algorithm

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**Abstract:** Quayside container crane is one kind of large scale heavy product. Good assembly plan will minimize the cost of manufacturer and to ensure the safety of assembly operation in container terminal. In this study, we have extensively investigated a novel approach to automatically generate the assembly sequences for industrial field which is especially applied to other large-scale structures. The approach is proposed to find the optimum assembly sequence which will integrate the genetic operators into the immune algorithm. The approach will take advantages of the immune memory for local optimum search and improve the global search ability of immune algorithm by the genetic operators. An example of one type of container quay crane illustrates the use of the physically based approach to generate assembly sequence which shows the efficiency and the operability to guide the assembly work.

**Key words:** Immune algorithm, genetic operator, quay crane, assembly sequence planning

## INTRODUCTION

In the process of the production and maintenance of quay crane, disassembly and assembly are important parts of the entire operating procedures. As the core content of the quay crane assembly process planning, Assembly Sequence Planning (ASP) is an important factor of the decision to the complexity of the assembly process and reliability its advantages and disadvantages directly related to the ease of assembly, assembly quality and cost of the quay crane. The problem of ASP can be considered as combinatorial optimization problem and is highly constrained (Marian et al., 2006) it is difficult to automatically generate feasible assembly sequences because of Combinatorial Explosion (CE) (Wolter, 1989, 1991) when the number of parts in the assembly increased which is shown to be NP-complete (Wilson and Watkins, 1990) in both two-dimensional and tri-dimensional cases (Kavraki et al., 1993; Wilson et al., 1995).

Currently, ASP study methods are mainly two types_F(1) Feasible assembly sequence based on the constraints is generated and using constraint reasoning , demolition method , based on experience and knowledge of the methods to prefer; (2) Adopting the evolution of modern optimization methods to generate feasible assembly sequence, such as genetic algorithms , ant colony algorithm, etc., As ASP problem is essentially an NP combinatorial optimization problem, for complex product with large number of parts, Assembly sequence combinatorial explosion problem will appear, therefore, first class of methods for solving is difficult. In recent years, assembly sequence optimization based on Artificial Intelligence is becoming a research focus; intelligent heuristic algorithm has been widely used in the ASP problem solving. Tseng et al. (2010) based on the Assembly Priority Matrix (APG) and the demolition of the priority matrix (DPG) adopted a double genetic algorithm for assembly sequence planning, the outer layer is for assembly sequence planning and the inner layer is used to generate the initial disassembly sequence planning programs (Sinanoglu and Borklu, 2005) established the assembly sequence planning system based on binary vector notation and adopting neural network method to optimize the assembly sequence analysis (Shan et al., 2009) put forward a new assembly sequence planning method combining with genetic simulated annealing algorithm and the characteristics of the ant colony algorithm which improve search efficiency and the quality of reconciliation; Considering assembly parts between intrinsic and extrinsic precedence constraint relationship, (Marian et al., 2006) used a genetic algorithm to optimize the assembly sequence based on assembly sequence model, assembly process model and assembly precedence relationship model.

Recent years, intelligent optimization methods are used for solving practical problems, such as GA

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Tseng *et al.* (2010), PSO, IA (Cao and Xiao, 2007). Based on the advantage of strong global search capability and convergence rate of the immune algorithm, combining with the characteristics of the assembly sequence planning, the improved immune algorithm which applies to the quay crane assembly sequence optimum is proposed in paper. Making use of assembly relationship between the use of parts which includes Geometric constraints, assembly tools , constraints and rule-bound to establish a multi-objective oriented assembly sequence planning evaluation criteria, Selection operator based on the antibody fitness and concentration of antibodies is given. And using antibody concentration to adjust the regulatory sequences promote and inhibit; The remainder randomly selected method without replacement based on the antibody expectations reproduction rate has been improved which improve the preferential selection operator capacity; Elitist strategy is adopted, through the memory cells to store the optimized individuals in the population evolutionary to ensure the convergence of the algorithm. The assembly instance application results verify the effectiveness of the proposed algorithm.

## ASSEMBLY SEQUENCE PLANNING MODEL

**Assumptions:** To reduce the complexity of ASP solving problems, the following prerequisites are put forward: (1) Detachable can be loaded, taking the reverse order of the disassembly sequence as the assembly sequence; (2) Only two components operate the implementation in each assembly process; (3) Various parts are rigid body; (4) Parts assembly direction is parallel to the axes and the assembly movement always along the line direction; (5) Assembly sequence is monotonous which is that assembly relationships between the parts are created once and the relative position to other assemblies unchanged in the subsequent assembly process.

**Assembly feasibility analysis:** Geometric feasible assembly sequence refers to parts do not interfere with other parts when it assembles along the coordinate axis and between the parts of the assembly in place does not produce interference phenomena. Introducing interference matrix to describe geometric constraints of assembly, each matrix element represents the interference of parts and other parts when it moves in one direction to infinity. According to the model assumptions, assembly sequence planning method is generated in the reverse order of the disassembly sequence due to that the demolition process and the assembly process are reciprocal. Part is to be assembled from a direction parallel with the axis, using integrated interference matrix to describe parts'

interference in $\pm X, \pm Y, \pm Z$ direction of the six other parts in order to avoid the creation of six independent interference matrix to produce redundant information, the expression of demolition interference matrix $I_D$ is as follows:

$$I_D = \begin{bmatrix} I_{11x}I_{11y}I_{11z} & I_{12x}I_{12y}I_{12z} & \cdots & I_{1nx}I_{1ny}I_{1nz} \\ I_{21x}I_{21y}I_{21z} & I_{22x}I_{22y}I_{22z} & \cdots & I_{2nx}I_{2ny}I_{2nz} \\ \cdots & \cdots & & \cdots \\ I_{n1x}I_{n1y}I_{n1z} & I_{n2x}I_{n2y}I_{n2z} & \cdots & I_{nnx}I_{nny}I_{nnz} \end{bmatrix} \quad (1)$$

where, matrix elements $I_{ijx}$ represents the parts's $P_i$ interference with part $P_j$ along the +X direction demolition process, If there is interference, definite $I_{ijx} = 1$, otherwise $I_{ijx} = 0$. Obviously, the process is as same as the part's $P_i$ interference with part $P_j$ along the -X direction demolition, thus explicit interference matrix $I_D$ can also implicitly introduce that the interferometer relationship of the parts in the direction of -X,-Y and-Z.

The feasible assembly direction of part $P_j$ depends on the m-th the remaining unassembled parts, this feasible assembling direction of the parts $P_j$ to be assembled can be represented by the equation:

$$\psi_d = \bigcup_{i=1}^{m} I_{ijd} \quad (2)$$

The above equation represents interference with unassembled parts of $P_i$ along the d direction, If the $P_j$ and all unassembled parts do not interfere, that is d = 0, The $P_j$ can be assembled along the direction d(+X, C+y, C+Z, C-X, C-Y, C-Z), d direction can be assembled direction; On the contrary it can't be assembled.

**Assembly sequence planning criterion:** In the practical application, different objectives and production conditions vary the corresponding assembly sequence evaluation criteria. This study from three aspects to evaluate the assembly sequence: (1) Assembly feasibility, that is disassembly (Based on reversible assumptions in assembly and disassembly), geometric interference in the demolition process does not produce which is the first condition that the assembly sequence should satisfy;(2) The number of the assembling direction redirection;(3) The changing number of assembly tools.

In order to obtain the overall evaluation value, comprehensive evaluation function of assembly sequence can be defined for the evaluation weighted superposition:

$$f(s) = \min \left\{ C_c n_c(s) + C_d n_d(s) + C_t n_t(s) \right\} \quad (3)$$

where, $C_c$, $C_d$, $C_t$ are, respectively to consider the assembly feasibility, assembly direction changes and the mounting tool changes the weight coefficient of the objective function and $C_c + C_d + C_t = 1$ the objective function and decision variables are:

- The objective function of assembly direction feasibility:

$$n_c = \sum_{i=2}^{N} c_i$$

N is the total number of parts. The decision variables are:

$$c_i = \begin{cases} 1 & \text{if part i and part i-1 do not interfere} \\ 0 & \text{if part i and part i-1 interfere} \end{cases}$$

- Goals function of the change in assembly direction:

$$n_d = \sum_{i=2}^{N} d_i$$

N is the total number of parts. The decision variables are:

$$t_i = \begin{cases} 0.2 & \text{if not the same assembly tools} \\ 0 & \text{if the same assembly tools} \end{cases}$$

- Goals function of the change in assembly tool:

$$n_t = \sum_{i=2}^{N} t_i$$

N is the total number of parts. The decision variables are:

$$t_i = \begin{cases} 0.2 & \text{if not the same assembly tools} \\ 0 & \text{if the same assembly tools} \end{cases}$$

**Improved immune algorithm:** When adopting the immune algorithm to solving ASP problem it is going to solve the problem with the data input, for instance: the objective function, the constraint conditions, etc,. as the antigen; Antibody corresponds to the solution of the problem, the candidate assembly sequence; The affinity between the antibody and antigen as the rating of solutions, higher affinity, the more close to the optimal solution; Corresponding to the affinity between the antibody and the antibody to solve the similarity. Meanwhile, based on the concentration of anti-body and the affinity between the antibody and antigen-antibody to promote and suppress the antibody.

**Antibody concentration definition:** The definition: In the particular and the scale of M antibody group, assuming that each antibody can be expressed as a one-dimensional vector that has N elements. Given antibody $v = \{v_1, v_2, v_n\}$ V and antibody x in antibody group Euclidean distance $w = \{w_1, w_2, w_{nn}\}$ is denoted by d (v, w), the fitness is $f_v$ and $f_w$, supposing x is a reasonably small number of normal ($\varepsilon > 0$ QUOTE $\varepsilon > 0$ ), if the:

$$Q_s(v,w) = d(v,w) + \alpha |f_v - f_w| \le \varepsilon \tag{4}$$

So, antibody v is similar to antibody w, with the number of similar antibody, antibody w is referred to the concentration of the antibody of w, recorded as $C_w$, $C_w > 1$. Where, $Q_s$ (v, w) is the quality similar indicator that reflects antibody v and antibody w; $\alpha$ reflects the Euclidean distance of d (v, w) fitness difference $|f_v - f_w|$ factors the relative importance of a parameter in $Q_s(v,w)$ and $\alpha > 0\varepsilon$ is called the antibodies similarity threshold. In this definition, Euclidean distance d (v,w) reflects the two antibodies in the structural similarity while fitness difference is used to reflect the similarity of two antibodies in quality. The antibody concentration $C_w$ simultaneously meets with antibody w similar structure and quality similar to the number of the antibody.

In this study, Euclidean distance between antibody v and antibody w is defined as:

$$d(v,w) = \sqrt{\frac{1}{n} \sum_{i=1}^{n} (v_i - w_i)^2} \tag{5}$$

Take Eq. 5 into equation 4 which is the solving formula the antibodies similarity of this article:

$$Q_s(v,w) = \sqrt{\frac{1}{n} \sum_{i=1}^{n} (v_i - w_i)^2} + \alpha |f_v - f_w| \le \varepsilon \tag{6}$$

**Selection operation:** For the scale of M and the specific antibody population, firstly define the adaptation of antibody v:

$$f_v = \frac{100.0}{C_v + 1} \tag{7}$$

The expected rate of reproduction $e_v$ of antibody v is defined as:

$$e_v = \frac{f_v}{(C_v)^\beta} \tag{8}$$

The selection probability of antibody v is:

$$P_{sv} = \frac{e_v}{\sum\limits_{i=1}^{m} e_i} \qquad (9)$$

where, $C_v$ is the concentration of antibody v; $\beta$ is the parameters important that reflects adaptation and concentration of the antibody in a desired reproduction rate of the relative. The selection operator of the Immune Genetic algorithm simulates the antibodies reproductive strategy of natural immune system it introduces the adjustment mechanism of antibody concentration and the high concentration of antibody is inhibited effectively which maintains a better understanding of the diversity of the population. From the Eq. 8, the individual selection probability of immune algorithm is proportional to the fitness of the antibody and its concentration is inversely proportional. Therefore it is not only to ensure the convergence rate of the algorithm but also to maintain the diversity of antibodies.

In order to avoid the " Degradation " of traditional roulette method, that is the loss of choice for the individuals with higher fitness, resulting in a dramatic shock results which is difficult to converge to the optimal solution, the paper improves basic selection operator with the method of selecting operator based on the arrangement of the roulette without replacement, Literatures (Kaya, 2011; Cui, 2008) show that the selection operator can effectively improve the convergence of the algorithm. The specific implementation steps are as follows:

- To calculate the expected survival number $N_v$ of each individual parent groups in the progeny groups:

$$N_v = N \cdot f_v / \sum\limits_{v=1}^{m} f_v \qquad (10)$$

- Take the integer part of $[N_v]$ in $V_n$ which is the corresponding the number of the survival of the individuals in the progeny populations:

$$\sum\limits_{v=1}^{m} [N_v]$$

number of individuals in the offspring population can be determined

- As:

$$f_v - [N_v] \cdot \sum\limits_{v=1}^{m} f_v / m$$

a new fitness of each individual, using the basic roulette Select method to randomly determine the number of individuals of the:

$$N - \sum\limits_{k=1}^{m} [N_k]$$

progeny population that has not been determined

- Store all new individuals and returns. In summary, the operator combines selection method based on the probability with the determined selection method in order to ensure fitness reserved than some individuals of average fitness to the next generation, whose select error is smaller

**Immune genetic algorithm:** To combine the characteristics of immune algorithm in assembly sequence planning application, specific implementation steps are shown in Fig. 1:
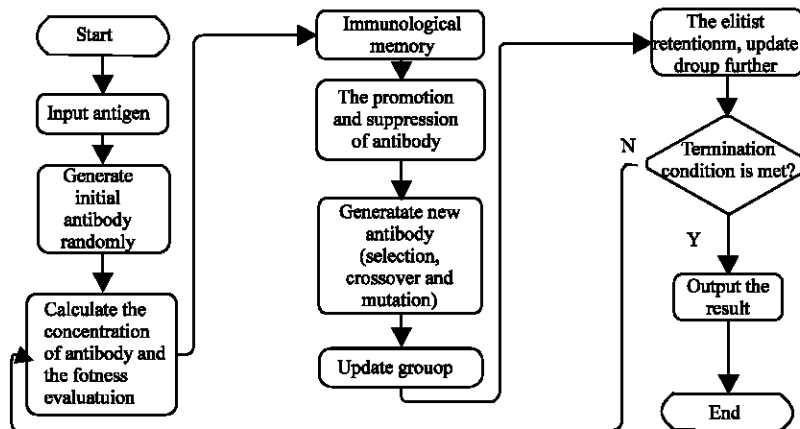


Fig. 1: Immune genetic algorithm

- **Step 1 Determine the coded form:** This study model represents an antibody assembly sequence, each antibody consists of four parts: Parts of the assembly sequence, the direction of assembly operations, required for assembly tools and assembly precedence constraint. That is the antibody coding which adopts the 4 stages string, for assembly problems with N parts, the first part is a part string $g_{i1} \in \{1, 2..,N\}$, the second part is the direction of the string $g_{i2} \in \{d_1,d_2..,d_N\}$, the third part is the tool string $g_{i2} \in \{t_1,t_2..,t_N\}$, the fourth part is priority string $g_{i4} \in \{c_1,c_2..,c_N\}$

- **Step 2 population initialization:** To input interference matrix, assembly tools and assembly direction parameters as antigen to initialize the parameter values of algorithm. For primary immune response, that is the first encounter of this kind of problem which randomly generates initial antibody; For secondary response, immune memory library gets part of the initial antibody by the memory function of the immune mechanism

- **Step 3 Determine whether an individual is feasible:** Decoding chromosomes as the normal sequence, to judge assembly reference member and whether satisfy the precedence constraint relations or not, the feasible individuals will be reserved while infeasible individual is of variation

- **Step 4 Fitness evaluation:** Firstly, in accordance with the Equation 4 to calculate the concentration of each antibody to suppress the high concentration of antibody in the current population while high fitness and low concentrations of antibody are promoted. In accordance with the Equation 7 to seek antibodies the fitness value, that is the fitness of each assembly sequence, then calculating the sum of population fitness value to determine the evolution of the best individual so far and record the average fitness of antibody. Adaptive value of the objective function is:

$$f(v) = 1/(\omega_1 \cdot n_p + \omega_2 \cdot n_d + \omega_3 \cdot n_t)$$

$\omega i (i = 1, 2, 3)$ is the weight coefficient

- **Step 5 Antibody selection:** According to the results of the evaluation one by one to select the optimal worst individual, then take the alleged antibodies into the memory library. Selection operator based on arrangement roulette without replacement is adopted to select algorithm for antibody, respectively in accordance with the Equation 8 and 9 to calculate the desired reproduction rate of the antibody and its selection probability

- **Step 6 Crossover and mutation operations:** Using the two-point cross randomly selected the crossover

operation of antibody genes bits, the new individual chromosome mutation is implemented the single-point mutation operation of probability $P_m$ and determine whether a mutated individual meets the constraints, if not, continue to perform mutation operation

- **Step 7 Elitist retention operation:** Based on the thinking of the best individual Preservation Act, taking larger individual fitness value in each population not to conduct operation which can left it to the next generation without crossover and mutation operations it used to improve the speed of optimization and then update the current population

- **Step 8 Termination of judgment:** The termination condition is set for the optimal solution for 200 generations to exit the loop, the difference between the mean of fitness function of adjacent two generations is small. If satisfied, then terminate the iteration to end the optimization; otherwise, return to Step 3 to continue operating

## CASE STUDY

**Parts hierarchy:** The horizontal wheel assembly of a certain type of quayside composed of 43 parts is taken as the example to illustrate our physically based approach. We dealt with the same type parts as one part in order to reduce the size of the problem because of the same assembly operation. For instance, part 1 represents the six bolts, part 4 represents four bushings, therefore and the horizontal wheel assembly is simplified as a product with 12 assembly parts.

According to the assumptions it can take the sub-assembly as a part-level node of the sequence concentration for the complex assembly that is constituted by a number of sub-assemblies and parts, the rational division of assembly-level assembly structure can effectively solve the assembly sequence. Assembly structure can use the hierarchical model, assembly, sub-assemblies, parts are expressed as the affiliation between father and son as to an assembly tree structure image. Fig. 2 shows the horizontal wheel assembly tree, the parts that consist of sub-assembly have a preferred assembly constraint relations compared with spare parts.

**Initial conditions:** According to the encoding rules, coding the assembly information of spare parts, sub-assembly, the assembly information of part code, assembly tools and assembly type are listed in Table 1. $I_D$ means a 12×36 interference matrix generated from the constraint relation through the disassembly analysis, that is:
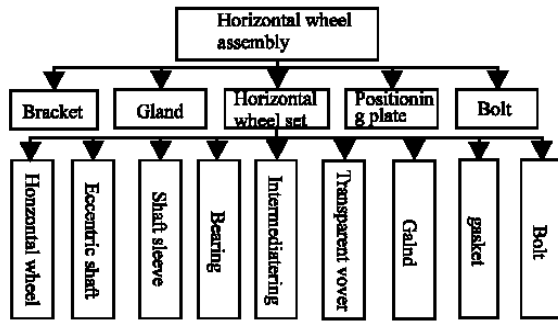
Fig. 2: Structure tree of horizontal wheel assembly

Table 1: Initial data of horizontal wheel assembly

| Name | Tool | Direction |
|------|------|-----------|
| Bolt 6×M10×25 | T1 | +Z |
| Transparent cover | T3 | +Z |
| Gasket | T3 | +Z |
| Bushing set | T3 | +Z |
| Horizontal wheel | T4 | +Z |
| Gland 1 | T3 | -Z |
| Bolt set 6×M8×20 | T2 | -Z |
| Self-aligning roller bearing 1 | T5 | +Z |
| Outer spacer | T3 | +Z |
| Inner spacer | T3 | +Z |
| Self-aligning roller bearing 2 | T2 | +Z |
| Eccentric shaft | T3 | +Z |

$$I_D = \begin{bmatrix} 000 & 111 & 111 & 000 & 111 & 000 & 000 & 000 & 000 & 000 & 000 & 000 \\ 110 & 000 & 001 & 001 & 001 & 001 & 001 & 000 & 000 & 000 & 000 & 001 \\ 110 & 000 & 000 & 000 & 001 & 000 & 000 & 000 & 000 & 000 & 000 & 000 \\ 000 & 000 & 000 & 000 & 110 & 000 & 000 & 001 & 000 & 001 & 001 & 111 \\ 110 & 000 & 000 & 110 & 000 & 111 & 111 & 110 & 110 & 110 & 110 & 110 \\ 000 & 000 & 000 & 000 & 110 & 000 & 111 & 000 & 000 & 000 & 000 & 110 \\ 000 & 000 & 000 & 000 & 110 & 110 & 000 & 000 & 000 & 000 & 000 & 000 \\ 000 & 000 & 000 & 000 & 111 & 001 & 001 & 000 & 001 & 001 & 001 & 111 \\ 000 & 000 & 000 & 000 & 111 & 001 & 000 & 000 & 000 & 110 & 001 & 110 \\ 000 & 000 & 000 & 000 & 110 & 000 & 000 & 000 & 110 & 000 & 001 & 111 \\ 000 & 000 & 000 & 000 & 111 & 001 & 000 & 000 & 000 & 000 & 000 & 111 \\ 000 & 000 & 000 & 110 & 111 & 110 & 000 & 110 & 110 & 110 & 110 & 000 \end{bmatrix}$$

**Parameter setting:** The parameters of assembly sequence planning model based on the improved immune algorithm are given. The size of antibody population is N = 20, the probability of crossover is $P_c$ = 0.8, the mutation probability is $P_m$ = 0.1, the maximum of calculated algebra is $G_{max}$ = 200.

**Planning results:** As is shown in Fig. 3, the largest fitness function value is stable at 6.67, the function value of average fitness is increased with the iteration number which approaches the maximum fitness value, the thirty-sixth generation algorithm obtains the optimal solution and the average search time is 0.23 seconds. The optimal results of assembly sequence planning that is sought out is 1-2-3-4-7-6-5-8-10-9-11-12, Fig. 4 show the changing curve of population fitness.
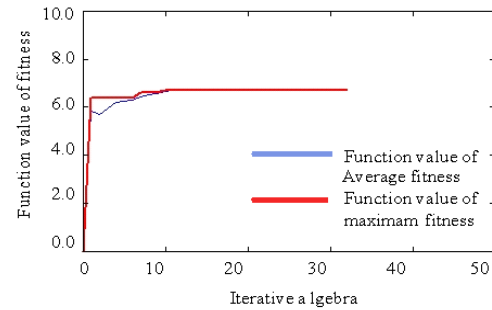


Fig. 3: Convergence curve of population fitness value

Immune algorithm has more powerful global searching ability because of its diversity conservation which effectively overcomes the easy premature convergence of the other algorithm. Algorithm can make rapid response to processed antigen due to the introduction of memory mechanism at the same time which makes the algorithm be able to search the optimal solution in a relatively short period of time.

**CONCLUSIONS**

According to the characteristics of ASP problem, an improved immune algorithm is proposed for the bridge assembly sequence planning. In order to guarantee the convergence rates of solutions, selection operator based on arrangement roulette without replacement is adopted to avoid the degradation phenomenon that prone to the traditional roulette operator. Immune algorithm overcomes the defect in the other optimization algorithms that prone to premature convergence and long search time. It can quickly find optimal assembly sequence that is optimal or near optimal in a certain practical significance in engineering, compared with other algorithms it is emphasized on how to maintain the population diversity and the selection mechanism based on the concentration. Immune algorithm is a new trial of efficient solutions application in assembly sequence planning of Quayside Container Crane, if the automatically sub-assembly, considering the parts and sub-assembly stability can be identified in the algorithm it is no doubt very important for the immune system to solve the problems of assembly sequence planning which is also the focus in the future.

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