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Generation of Optimized Robotic Assembly Sequence using Ant Colony Optimization

Surajit Sharma, Bibhuti Bhusan Biswal, Parameshwar Dash, and Bibhuti Bhusan Choudhury

***Abstract*— A robotic assembly sequence is considered to be optimal when it minimizes assembly cost and satisfies the process constraints. The assembly cost relates to assembly operations, assembly motions and assembly direction changes. The present work utilizes an ant colony optimization (ACO) method for generation of optimized robotic assembly sequences. The method reflects the assembly cost to an energy function associated with the assembly sequence. The energy function is iteratively minimized by ACO to generate the desired optimized assembly sequence. A case study is presented to show the effectiveness of the proposed method.**

I. Introduction

Assembly sequence directly influences the productivity of the process, product quality, and the cost of production. The robotic assembly process is faster, efficient and precise than any conventional process. The cost of assembly on an average is 10-30% of the manufacturing cost of a commercial product. The ratio between cost and performance of assembly has gradually increased with respect to the other phases of the manufacturing process and in recent years, this fact has caused a growing interest by researchers. An important aspect of this developing process is represented by the need to automatically generate the assembly plan by identifying the optimum sequence of operations with respect to its cost and correctness. Products with large number of parts have several alternative feasible sequences. A variety of optimization tools are available for application to the problem, but their suitability and/or effectiveness are also under scanner. Traditional computational methods often produce combinatorial explosions of alternatives, with unacceptable computational times. Study of various optimization methods reveals that ant colony optimization (ACO) technique can be advantageously used to solve such problems.

II. Related Work

Some of the major work in the area address the issues on generating correct sequences while some other focus at generating the sequences by alternative but simpler methods. De Fazio and Whitney [1] developed a simplified method for generation of assembly sequences using a series of query-and-answer. De Mello and Sanderson [2] developed a state transition graph which simplifies the average number of operations from the previous one. Cho and Cho [3] developed a method using directional part contact level graphs which contains the information on directional connections for each pair of mating parts. Cho, Shin and Cho [4] described the part motion instability, which is necessary for stability of parts during the process of assembly. Hong and Cho [5] used the neural network method for generation and optimized robotic assembly sequences. But most of the time this method fails to determine the global optima. Hong and Cho [6] tried increased number of assembly constraints for the same method and obtained superior results. But it still has the problem of getting trapped in local optimum point. Hong and Cho [7] used the simulated annealing for moving towards global optima point. Wang, Liu, and Zhong [8] proposed ant algorithm by using the disassembly operations of the parts in assembly sequence planning. The process is silent about the directional changes during the assembly and the cost factor is mostly required to any assembly industries. These methods have the advantage of fast execution time, but they fail to generate the global optimal solution when the number of parts is large. The present modified method is more preferable in robotic assembly sequence generation which considers the assembly constraints and the assembly costs and indicates the interrelationship between the mating parts in every possible direction of assembly.

III. Work Description

A correct sequence for assembly can be generated from the disassembly sequence [1, 2, 9]. A disassembly sequence is represented as an ordered list of disassembly operations (DOs) and the nodes are DO = (n, d), where, n is the number

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Surajit Sharma is a M.Tech. Research Scholar at National Institute of Technology, Rourkela, Orissa, India 769008 (e-mail: surajitnit@gmail.com).

Bibhuti Bhusan Biswal is a Professor at the National Institute of Technology, Rourkela, Orissa, India 769008 (Phone: +91661-2462181, Fax: +91661-2474840, e-mail: bbbiswal@nitrkl.ac.in; bibhuti.biswal@gmail.com).

Parameswar Dash is an Assistant Professor at Institute of Advance Computer and Research, Rayagada, Orissa, India 765005 (e-mail: parameswar_dash@yahoo.com).

Bibhuti Bhusan Choudhury is a Ph.D. Research Scholar at National Institute of Technology, Rourkela, Orissa, India 769008 (email: bbcnit@gmail.com).

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of parts and $d \in \{x, y, z, \bar{x}, \bar{y}, \bar{z}\}$ represents the assembly directions. By observing the value of disassembly operations, the first node to be disassembled is selected. Starting from the first node, ants search the feasible disassembly sequences by travelling all the nodes. Sequences which satisfy precedence constraints, connectivity constraints and energy equations are the solutions to the problem. In the beginning, the tours constructed by the ants are the initial feasible sequences for the problem. The problem is reduced to a great extent by applying the conditions of stability. Thereafter the stable and optimized one is selected corresponding to the assembly constarints. The modified ant algorithm, presented here, generates the optimal assembly sequence corresponding to the energy matrix of the order of 5n × 5n. The search space reduces to the order of 5 × 5 matrices in every next visit of the ants. The precedence constraints between liaisons and the corresponding energy matrix to connect two liaisons were adopted to process the ant algorithm. A pheromone 'τ_{ij}' is used as the shared memory of all ants that corresponds to the energy matrix and is updated during process. This gives the minimum energy path which has to be followed during disassembly.

The objective of the present work is to generate stable and optimal robotic assembly sequence with minimum assembly cost while satisfying the assembly constraints. The present research uses ACO technique considering of the instability of assembly motions and/or directions.

IV. Methodology

A. Product Modeling

A product is considered to be suitable for robotic assembly only when (i) all the individual components are rigid, (ii) assembly operation can be performed in mutually perpendicular directions in space excepting Z direction, and (iii)each part can be assembled by simple insertion or screwing. A product with n parts is represented as:

A = (P, L) (1)

where, A is a product having parts P = $\{p_\alpha \mid \alpha=1, 2\ldots n\}$, and interconnected by liaisons L = $\{l_{\alpha\beta} \mid \alpha, \beta = 1, 2\ldots r.\ \alpha \neq \beta\}$. Here n represents the number of parts of the product and r is the relationship between the connected parts and $(n-1) \leq r \leq n(n-1)/2$. The liaison $l_{\alpha\beta}$ represents the connective relationship between a pair of parts p_α and p_β, and

$l_{\alpha\beta}$ = liaison $(p_\alpha, C_{\alpha\beta}, f_{\alpha\beta}, p_\beta)$ (2)

where, $C_{\alpha\beta}$ is the contact-type connection matrix and $f_{\alpha\beta}$ is fit-type connection matrix and are represented by

$$C_{\alpha\beta} = \begin{pmatrix} Cx & Cy & Cz \\ C\bar{x} & C\bar{y} & C\bar{z} \end{pmatrix} \text{and } f_{\alpha\beta} = \begin{pmatrix} fx & fy & fz \\ f\bar{x} & f\bar{y} & f\bar{z} \end{pmatrix}$$

The assembly directions for robotic assembly are taken to be d, where, $d \in \{x, y, \bar{x}, \bar{y}, \bar{z}\}$. The representation of the elements of contact-type and fit-type are:

$$C_d = \begin{cases} 0: \textit{no contact in the d direction between } p_\alpha \ \&\ p_\beta \\ rc: \textit{real contact in the d direction between } p_\alpha \ \&\ p_\beta \\ vc: \textit{virtual contact in the d direction between } p_\alpha \ \&\ p_\beta \end{cases}$$

and

$$f_d = \begin{cases} 0: \textit{no fit in the d direction between } p_\alpha \ \&\ p_\beta \\ sw: \textit{screwing in the d direction between } p_\alpha \ \&\ p_\beta \\ rf: \textit{round peg in hole fit in the d direction between} \\ \quad p_\alpha \ \&\ p_\beta \\ mp: \textit{multiple round peg in hole fit in the d direction} \\ \quad \textit{between } p_\alpha \textit{ and } p_\beta \end{cases}$$

Each element of f_d can also be represented as polygon fit (*pf*), a tight fit (*tf*), a caulking (ca), a riveting (ri), a virtual fit (*vf*) or no fit (0). The connection matrix in equation (2) is represented in the following format.

$$l_{\alpha\beta} = liaison\left(p_\alpha, \begin{pmatrix} 0 & rc & rc \\ rc & rc & 0 \end{pmatrix}, \begin{pmatrix} 0 & 0 & rf \\ 0 & 0 & 0 \end{pmatrix}, p_\beta\right)$$

1) Case Study: A grinder assembly as shown in Fig 1(a) is considered for generating the assembly sequence and validating the proposed method. Fig 1(b) shows the directions for assembly or disassembly and Fig 1(c) represents the liaison diagram of the components.

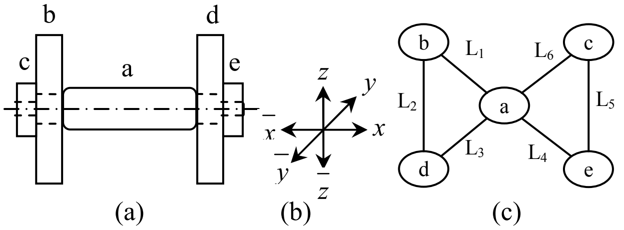


Fig-1(*a*): A simple example of a product (Grinder assembly); (*b*): Directions for assembly or disassembly; (*c*): Liaison graph model of grinder. [a-shaft; b-blade; c-nut; d-blade, and e-nut]

The liaisons of the components are represented as:

$$l_{ab} = liaison\left(a, \begin{pmatrix} o & rc & rc \\ rc & rc & rc \end{pmatrix}, \begin{pmatrix} o & o & o \\ rf & o & o \end{pmatrix}, b\right)$$

$$l_{ac} = liaison\left(a, \begin{pmatrix} o & o & o \\ vc & o & o \end{pmatrix}, \begin{pmatrix} o & o & o \\ sw & o & o \end{pmatrix}, c\right)$$

$$l_{ad} = liaison\left(a, \begin{pmatrix} rc & rc & rc \\ o & rc & rc \end{pmatrix}, \begin{pmatrix} rf & o & o \\ o & o & o \end{pmatrix}, d\right)$$

$$l_{ae} = liaison\left(a, \begin{pmatrix} vc & o & o \\ o & o & o \end{pmatrix}, \begin{pmatrix} sw & o & o \\ o & o & o \end{pmatrix}, e \right)$$

$$l_{bc} = liaison\left(b, \begin{pmatrix} o & o & o \\ rc & o & o \end{pmatrix}, \begin{pmatrix} o & o & o \\ o & o & o \end{pmatrix}, c \right)$$

$$l_{de} = liaison\left(d, \begin{pmatrix} rc & o & o \\ o & o & o \end{pmatrix}, \begin{pmatrix} o & o & o \\ o & o & o \end{pmatrix}, e \right)$$

B. Assembly Constraints

A precedence constraint of a liaison $l_{\alpha\beta}$ is represented by a set of parts, n_p, that must be connected before two parts p_α and p_β are connected. The precedence constraint $PC(l_{\alpha\beta})$ of a liaison $l_{\alpha\beta}$ and the precedence constraint $PC(p_f)$ of the part p_f are expressed by

$$PC(l_{\alpha\beta}) = \{p_\gamma \mid \gamma = \gamma_1, \gamma_2, ..., \gamma_{n_P}\}\ , \qquad \text{and } PC(p_f) = \bigcup_{l=l_1}^{l_q} P(l_{\alpha\beta})$$

where, $P(l_{\alpha\beta})$ is a precedence constraint of a liaison $l_{\alpha\beta}$. The precedence constraints of the liaisons are: $PC(l_{ab})=\{\ \Phi\ \}$, $PC(l_{ac})=\{\ b\ \}$, $PC(l_{ad})=\{\ \Phi\ \}$, $PC(l_{ae})=\{\ d\ \}$, $PC(l_{bc})=\{\ \Phi\ \}$, $PC(l_{de})=\{\ \Phi\ \}$. Hence, the precedence constraints of the parts are: $PC(P_a)=\{\ b,\ d\}$, $PC(P_b)=\{\ \Phi\ \}$, $PC(P_c)=\{b\}$, $PC(P_d)=\{\ \Phi\ \}$, $PC(P_e)=\{\ d\ \}$.

V. Optimization of Assembly Sequence using Aco

A. Energy Function Associated With Assembly Sequence Generation (ASG)

Energy function, E_{seq}, is associated with assembly sequence, and it is represented as:

$$E_{seq} = E_J + E_P + E_C \tag{3}$$

where, E_{seq} , E_J , E_P and E_C are the energy functions associated with ASG, assembly cost, predence constraints and connectivity constraints respectively. The energy associated with precedence constraints is:

$$E_P = C_P \sum_{i=1}^{n} \mu_i \tag{4}$$

where, C_P is a positive constant and μ_i is the precedence index(μ_i=0, if it satisfies the precedence constraints, otherwise 1).

The energy associated with connectivity is:

$$E_C = C_C \sum_{i=1}^{n} \lambda_i \tag{5}$$

In a similar manner connectivity index λ_i is inferred on the basis of liaison relationships. Considering C_J as an energy constant related to assembly sequence cost J, the value of J can be decided as;

$$J = \begin{cases} 1 : if\ it\ violates\ the\ constra\mathrm{int}\, s, or\ is\ unstable \\ \qquad \rho_s C_{as} + \rho_t C_{nt} : otherwise \end{cases}$$

The objective factor, which is linked with heuristic values of ant colony algorithm, and it can be expressed as:

$$E_{seq} = C_J\, J + \sum_{i=1}^{n} (C_P \mu_i + C_C \lambda_i) \tag{6}$$

B. Degree of Motion Instability and the Number of Assembly Direction Changes

The possible assembly directions can be inferred from the liaisons between the interrelated parts. The possible assembly direction will take a general form as $DS_{cdabe}^{k} s\,(k = c, b, a, d, e)$. The ordered lists of possible assembly directions corresponding to the assembly sequence can be expressed by: $DL_i^{cbade}\,(i = 1, 2, ...,m)$. Based upon these expressions, the normalized degree of motion instability, C_{as} and the normalized number of assembly direction changes, C_{nt} are evaluated.

$$C_{as} = \frac{1}{m} \sum_{i=1}^{m} \left\{ \frac{1}{12 \times i} \sum_{j=1}^{i} \left(S\{BA_j\}) _i \right) \right\} \tag{7}$$

where $BA_j\,(j = 1,2,..,5)$ is the in-subassembly formed at the j^{th} assembly step, and $S\{BA_j\}$ means the degree of motion instability of the j^{th} subassembly. A zero degree of motion instability means the parts belonging to the subassembly are completely fixed to each other, whereas twelve degrees means the parts are free to move in any direction. Similarly,

$$C_{nt} = \frac{1}{m} \sum_{i=1}^{m} \left\{ \frac{1}{i} \sum_{j=1}^{i} (NT_j)_i \right\} \tag{8}$$

where, (NT_j) is assigned to 1 if direction change of BA_j occurs for an order list DL_i^{cbade}, otherwise it is 0. If the sequence is unstable for all $(NT_j)_i\,(j = 1,2,3,4,5)$ are assigned to 1. So the number for all C_{as}s and C_{nt}s lie between 0 and 1. The zero means, the sequence completely satisfies the constraints, whereas one means, the relationship is unstable. For a study, a possible sequence $seq = \{c - b - a - d - e\}$ is considered. The assembly directions of mating parts can be inferred from liaisons between the parts. Each set of possible assembly directions are represented as:

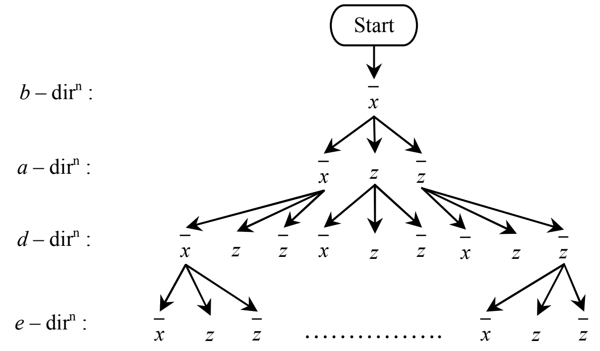
$$DS_{cbade}^{c} = \{\phi\}, DS_{cbade}^{b} = \{\bar{x}\}, DS_{cbade}^{a} = \{\bar{x}, z, \bar{z}\},$$
$$DS_{cbade}^{d} = \{\bar{x}, z, \bar{z}\}, DS_{cbade}^{e} = \{\bar{x}, z, \bar{z}\}$$

The order list of possible assembly directions corresponding to the assembly sequence "*c – b – a – d – e*" for the example product are given by;

$$DL_1^{cbade}=\left\{d_1^c,d_1^b,d_1^a,d_1^d,d_1^e\right\}$$

$$\cdots$$

$$DL_m^{cbade}=\left\{d_m^c,d_m^b,d_m^a,d_m^d,d_m^e\right\}$$


Start
b – dir^n :
a – dir^n :
d – dir^n :
e – dir^n :
$\bar{x}$
$\bar{x}$ z $\bar{z}$
$\bar{x}$ z $\bar{z}$ $\bar{x}$ z $\bar{z}$ $\bar{x}$ z $\bar{z}$
$\bar{x}$ z $\bar{z}$ .... $\bar{x}$ z $\bar{z}$

(a)

$$DL_1^{cbade}=\left\{\bar{x},\bar{x},\bar{x},\bar{x}\right\},DL_2^{cdade}=\left\{\bar{x},\bar{x},\bar{x},z\right\},\cdots\cdot DL_m^{cbade}=\left\{\bar{x},\bar{z},\bar{z},\bar{z}\right\}$$

(b)

Fig-2(*a*): Hierarchical tree structure of possible assembly directions.
(*b*): Ordered list of possible assembly directions

The hierarchical structure of the assembly directions and the ordered list of possible assembly directions are shown in Fig 2(a) and Fig 2(b) respectively. An assembly sequence consists of a number of partial sequences with having energy values. The sum of these values is the objective energy of an individual assembly sequence. The energy matrix for this study is 25× 25, i.e. 5n× 5n matrix. Each cell represents the energy between two elements and the value of E_{Seq} can be determined in the following manner.

Let the partial sequence be (d, ($\bar{x}$)) – (a, ($\bar{x}$)). The precedence constraint for each part is the input to this problem. The precedence constraints for the product is,

PC(a)={b, d}, PC(b)={ Φ }, PC(c)={b}, PC(d)={ Φ }, PC(e)={ d}.

Precedence index μ_i can be calculated from equation (4). Taking the data from previous step, the first position d, ($\bar{x}$), which has a null set, satisfies the precedence constraint. Hence, precedence index for first position is μ_1 = 0 whereas the second position a, ($\bar{x}$) does not obey the precedence constraint. Therefore, μ_2 = 1. After getting these values the energy equation can now be calculated as

$$E_P=C_P\sum_{i=1}^{2}(\mu_1+\mu_2)\text{ , }E_P = 35 \times 1= 35$$

Taking guidelines from the equation (2), the liaison between parts d and a can be extracted as follows:

$$Liaison\ l_{da}=\left(d,\begin{pmatrix}o & rc & rc\\ rc & rc & rc\end{pmatrix},\begin{pmatrix}o & o & o\\ rf & o & o\end{pmatrix},a\right)$$

In a similar manner, connectivity index λ_i can be evaluated. In this case, λ_1=0, for the C_d matrix and λ_2=0, for constraints. From equation (5), the energy value becomes:

$$E_C=C_C\sum_{i=1}^{n}(\lambda_1+\lambda_2)\text{ , }E_C = 45\text{ X }0= 0$$

The detail procedures for extracting the possible assembly directions, order lists and the number of directions changes are discussed in section-V. On the basis of that, the possible assembly directions for partial sequence become:

$DS_{da}^{a}=\{\Phi\}$, $DS_{da}^{a}=\{x\}$

The instability of the subassembly BA_1 which contains the parts a and d calculated as:

$S\{BA_1\}=1+2=3$.

According to the hierarchy the number of order list (m) is found to be 1 for the partial sequence in question. Putting these values in equation (7), we get

$$C_{as}=\frac{1}{1}\sum_{i=1}^{1}\left\{\frac{1}{12\times1}\sum_{j=1}^{1}(3)\right\}=0.25$$

In the assembly sequence d – a, it is assumed that during the time of handling there is no change of directions as because the changing of directions unnecessarily increase the assembly cost. So for this case NT_1 = 0 and

$$C_{nt}=\frac{1}{1}\sum_{i=1}^{1}\sum_{j=1}^{1}(0)=0$$

The value of C_J is found from the simulation conditions and it is C_J = 45. As the sequence is a valid one, the equation of assembly cost is: $J = \rho_s\, C_{as} + \rho_t\, C_{nt}$

Hence, $J=(0.5\times0.25)+(0.5\times0)=0.125$

The energy related to the assembly cost is:

$E_J = C_J$ X J = 45 X 0.125 = 5.625

Taking the date from above three steps the total energy of a partial sequence (d, ($\bar{x}$)) – (a, ($\bar{x}$)) is:

E_{Seq} = $E_P + E_C + E_J$ = 35 + 0 + 5.625 = 40.625

If both the connectivity indices λ_1 and λ_2 in step 2 are found to be one, then the partial sequence indicates that there is no connection or very poor connection available between two parts. This is not suitable for robotic assembly environment.

Hence, it is not necessary to find the order lists as the partial sequence is unstable.

VI. APPLYING ACO TO ASG

According to Marco Dorigo [10] the basic concept of an ant colony algorithm is to solve combinatorial optimization problems within a reasonable amount of time. Artificial ants iteratively tour through a loop that includes a tour construction biased by the artificial pheromone trails and the heuristic information. The main idea in modified algorithm is that the good tours are the positive feedback given through the pheromone update by the ants. The shorter is the tour the more is the amount of pheromones deposit on the selected path. This means that the path have higher probability of being selected in the subsequent iterations of the algorithm. If the assembly consists of 'n' number of parts, then the disassembly operations (Dos) are having '5n' number of nodes i.e. (n, x), (n, y), (n, z), $(n, \bar{x})$ and $(n, \bar{y})$. The disassembly operation DO is assigned a value '1' if there is interference in that direction, otherwise it is '0'. That means if DO=1, it cannot be disassembled from the product. In the modified ACO algorithms, a pheromone 'τ_{ij}' is used as the shared memory of all ants and simultaneously it considers the energy matrix (5n× 5n) which is to be minimized. The pheromone 'τ_{ij}' is updated during the processing. In this study the pheromone is expressed as 5n × 5n matrix as because one of the (+) ve Z directions is restricted for robotic assembly.

The equation for interference matrix and disassembly operations in (+) ve X, Y, Z directions are given by:

$$DM = \begin{array}{c|cccc|} & e_1 & e_2 & & e_n \\ e_1 & I_{11x}I_{11y}I_{11z} & I_{12x}I_{12y}I_{12z} & \cdots & I_{1nx}I_{11y}I_{11z} \\ e_2 & I_{21x}I_{21y}I_{21z} & I_{22x}I_{22y}I_{22z} & \cdots & I_{2nx}I_{2ny}I_{2nz} \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ e_n & I_{n1x}I_{n1y}I_{n1z} & I_{n2x}I_{n2y}I_{n2z} & \cdots & I_{nnx}I_{nny}I_{nnz} \end{array} \tag{9}$$

$$DO_{i,(+d)} = \bigcup_{j=1}^{n} I_{ijd} \tag{10}$$

$$DO_{i,(-d)} = \bigcup_{j=1}^{n} I_{jid} \tag{11}$$

where, I_{ijd} is equal to 1 if component e_i interferes with the component e_j during the move along d-axis; otherwise I_{ijd} is equal to 0. The initial disassembly matrix and disassembly operation are calculated as:

$$DM = \begin{array}{c|ccccc|ccccc|ccccc|ccccc|ccccc|} & \multicolumn{5}{c}{a} & \multicolumn{5}{c}{b} & \multicolumn{5}{c}{c} & \multicolumn{5}{c}{d} & \multicolumn{5}{c}{e} \\ & x & y & z & \bar{x} & \bar{y} & x & y & z & \bar{x} & \bar{y} & x & y & z & \bar{x} & \bar{y} & x & y & z & \bar{x} & \bar{y} & x & y & z & \bar{x} & \bar{y} \\ a & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 1 & 1 & 1 & 0 & 1 & 1 & 0 & 1 & 1 & 1 & 1 & 0 & 1 & 1 & 1 & 1 & 0 & 1 \\ b & 1 & 1 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ c & 1 & 1 & 1 & 0 & 1 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ d & 0 & 1 & 1 & 1 & 1 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & 0 \\ e & 0 & 1 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{array}$$

$$\begin{bmatrix} DO_{a,x}=1 & DO_{a,y}=1 & DO_{a,z}=1 & DO_{a,\bar{x}}=1 & DO_{a,\bar{y}}=1 \\ DO_{b,x}=1 & DO_{b,y}=1 & DO_{b,z}=1 & DO_{b,\bar{x}}=1 & DO_{b,\bar{y}}=1 \\ DO_{c,x}=1 & DO_{c,y}=1 & DO_{c,z}=1 & DO_{c,\bar{x}}=0 & DO_{c,\bar{y}}=1 \\ DO_{d,x}=1 & DO_{d,y}=1 & DO_{d,z}=1 & DO_{d,\bar{x}}=1 & DO_{d,\bar{y}}=1 \\ DO_{e,x}=0 & DO_{e,y}=1 & DO_{e,z}=1 & DO_{e,\bar{x}}=1 & DO_{e,\bar{y}}=1 \end{bmatrix}$$

where, U is the Boolean operator OR. The result will be equal to 0 if all the elements involved in the operation are 0. This means the element can be disassembled in that direction. If the DO is equal to 1, the element cannot be disassembled. In this study, the initial feasible disassembly operations are (c, $\bar{x}$) and (e, x).

A. Approaching Solutions

Robotic assembly is a case of combinatorial optimization problem. The problem is similar to TSP i.e. to give the shortest path with minimum cost. In ant system, *m* ants simultaneously build a solution of the ASG. Initially ants are put in first feasible DO. At each construction step, ant *k* applies a probabilistic state transition rule, called random proportional rule, to decide which node is to be visited next. The next visit is selected on the basis of the probability rule given by:

$$P_k^{(i,j)} = \begin{cases} \dfrac{[\tau(i,j)]^{\alpha}[\eta(i,j)]^{\beta}}{\sum\limits_{u \in C_k(i)} [\tau(i,j)]^{\alpha}[\eta(i,j)]^{\beta}}, & if\ j \in C_k(i) \\ 0, & otherwise \end{cases} \tag{12}$$

where, $\tau(i,j)$ is the quality of pheromone corresponding to the heuristic matrix $\eta(i,j) = {}^{1}\!/_{E_{Seq}}$ is the problem dependent heuristic information corresponding to the search algorithm. $C_k(i)$ is the candidate list generated by DM after the component of DO *i* has been disassembled. The parameters α and β determine the relative importance of pheromone versus heuristic information. The inverse of the energy value between the two parts is taken as $\eta(i,j)$.

After all the ants have constructed their tours, the pheromone trails are updated. The pheromone evaporation is given by $\tau(i,j) \leftarrow (1-\rho)\tau(i,j)$, where $0 \le \rho \le 1$ is the pheromone evaporation rate. After evaporation, all ants deposit pheromone on the arcs they have crossed in their tour. The pheromone evaporation is given by:

$$\tau(i,j) \leftarrow (1-\rho)\tau(i,j) + \sum_{k=1}^{m} \Delta\tau_k(i,j) \qquad (13)$$

where, m is the number of ants that find the best sequences through iterations and $\Delta\tau^k(i,j))$ is the amount of pheromone ant k deposits on the arcs it has visited. It is expressed by the equation:

$$\Delta\tau^k(i,j) = \begin{cases} \dfrac{1}{E_{seq}^k(i,j)}, if\ (i,j) \in sequence\, of\ ant\, k \\ 0, \quad otherwise \end{cases} \qquad (14)$$

where, $E_{seq}^k(i,j)$ is the tour energy of the k^{th} ant belonging to that tour. During the construction of sequences, local pheromone updating encourages exploration of alternative solutions, while global pheromone updating encourages exploitation of the most promising solutions.

B. Simulation Condition

The assembly constraints, C_P, C_C and C_J in equation (10) are assigned random values from 5 to 75 with the increment of +5. These have been chosen in such a way that the objective function converges. It is assumed that the selected factors behave in the same manner in other tours also. The simulation parameters and their values are listed in Table I and Table II.

TABLE I
THE SIMULATION CONDITION FOR ENERGY CONSTANTS

Energy Constants			Cost Constants	
C_J	C_P	C_C	ρ_t	ρ_t
45	35	45	0.5	0.5

TABLE II
THE SIMULATION CONDITION FOR ANTS PARAMETERS

Influencing Parameter of Pheromone Trail		Pheromone Evaporation Rate	Base Part	Assembly Directions
α	β	ρ	a	$x, y, \bar{x}, \bar{y}, \bar{z}$
1	2	0.25		

VII. RESULTS AND CONCLUSIONS

The research work focuses on the constraints and contact relationships of the assembly parts, and defines a method of generating optimal disassembly sequence. Experiments to verify the effectiveness of the method confirm that the generated disassembly sequence is the optimal or near optimal solution which gives out the minimal energy by satisfying the mentioned constraints. The result of the work with the specific example product is obtained in the form of $(e,x)-(c,\bar{x})-(b,\bar{x})-(d,x)-(a,x)$. This essentially represents the sequence of disassembly of the parts and hence, the optimal assembly sequence is given as $(a,\bar{x})-(d,\bar{x})-(b,x)-(c,x)-(e,\bar{x})$. The performance of the method is found to be strongly affected by the energy function and the connective relationships. It is concluded that the modified approach successfully generates robotic assembly sequences with minimum assembly cost. A number of products with varying number of components and contact relationship are tried to test the effectiveness of the method and the results obtained though these studies are quite encouraging. However, due to limitation of space, the study on one product is presented in this paper. The very philosophy of ACO makes it more suitable for its application. The problem as such is not acquiescent to any mathematical modeling. Comparable techniques such as GA can also be an alternative proposition for such type of problem. The results obtained amply suggest that ACO is one of the most suitable techniques for solving problems of this type.

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