3D Shape Retrieval considering Assembly Structure

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3D CAD systems are widespread even at the upper stages of product design. Although most 3D CAD models are designed and stored for use in product design, few studies have reported shape retrieval for use in assembly models. In this study, we propose a new 3D shape retrieval method which satisfies the following conditions: 1) a similarity not only between components but also between assembly structures should be evaluated; 2) the similarity measure should not change much even if a minor component or minor subassembly changes in the assembly; 3) the similarity measure should not change between two assemblies consisting of the same components the relative positions of which and orientations only differ; and, 4) the similarity evaluation must be controlled depending on the applications. The features of the component shapes and the assembly structures are extracted from 3D CAD models. A similarity between the two assembly models was found by comparing both the geometric feature of every component and by comparing the contact states, interferences and constraint conditions between the components.

1. Introduction

3D shape retrieval is a technique where a set of 3D shape models that are similar to a query shape model can be automatically retrieved from 3D model databases. The 3D shape retrieval techniques are effective for retrieving components and cases of past design similar to the ones of the current design. Especially, in the field of machine design, the use of 3D CAD systems is now widespread, and many 3D models and a large amount of design information have been stored in the databases held by manufacturers. They are eager to utilize the stored information to design new products. The 3D shape retrieval technique provides a solution for this. The technique enables the designers to obtain the knowledge for the design, understand costs related to manufacturing, and gain technical expertise associated with previous CAD models on design from the viewpoint of a new product model as a query.

In most existing 3D shape retrieval methods, the similarity between the shape in the two components [1,2] has been estimated. However, as is usual in product design, most 3D CAD models are defined as assemblies. In addition, very few studies have reported 3D shape retrieval considering the assembly structures of the CAD models. Andrey et al. [3] proposed a hierarchical shape matching method between 3D molecule structures using zero alpha-shape. Their method compared topologies of two different molecules that were treated as assemblies. Satyandra et al. [4] proposed techniques for retrieving not only single mechanical components but also assemblies. The similarity between assemblies was evaluated by comparing whole volumes of assemblies, component categories, and geometric constraints among components. However, their technique completely ignored geometric similarity among components in the assembly. Suyu et al. [5] developed a contour-based shape representation and a shape matching method where the similarity between a model and the one modeled by stretching and bending

features of the original model could be evaluated. However, their method was limited to only evaluating the similarity of 2D representations of components. None of these studies could realize 3D shape retrieval abilities for 3D assembly structures required in design and engineering fields.

The retrieval method considering the assembly structures in design and engineering fields must satisfy the following four requirements:

1) **Evaluating assembly structure similarity**
   It should evaluate similarity not only between sets of constituent component shapes in two assemblies but also between 3D assembly structures themselves. Evaluating the similarity only between the sets of component shapes in the assemblies ignores the similarity of two 3D assembly structures.

2) **Maximum matching ability**
   The similarity measure should not change much even if a minor component or a minor subassembly changes in the assembly. The similarity evaluation between two assemblies should be done in the "maximum matching" manner, because reusing the past designed parts or subassemblies greatly reduces the manufacturing costs and is often adopted in many design cases.

3) **Insensitivity to the movable components**
   The similarity should not change between two assemblies consisting of identical components the relative positions and orientations of which only differ, because relative positions and orientations of the movable parts in the assembly cannot be uniquely determined and the users of the retrieval system do not know of them in the case of inquiry.

4) **Flexible control of similarity evaluation**
   The similarity can be controlled flexibly according to the targeted models or the applications, because the designers

emphasize the similarity of sizes of the assembly components, on one occasion, but of the geometry and structure of the assembly on another occasion.

Therefore, in this study, we propose a new 3D shape retrieval method considering assembly structure which satisfies the above four requirements. In this method, the similarity not only between two component shapes but also between two assembly structures can be evaluated. The similarity between two components is estimated based on the difference between shape features of two components, while the similarity between two assembly structures is done based on matching the *assembly graph*. A retrieval system prototype is built and part of the system is integrated in a commercial 3D CAD system.

In the following sections of the paper, the calculation of the shape feature from a 3D CAD model, the generation of the assembly graph and their matching characteristics will be described first. An dissimilarity evaluation between two component shapes and assembly structures based on the assembly graphs will be described next. Finally, the characteristics of the similarity evaluation results are investigated in some experiments and the effectiveness of the retrieval method is discussed.

2. Overview of the 3D shape retrieval

Fig. 1 shows an overview of the proposed 3D shape retrieval system for assembly. The retrieval process consists of two phases, the registration phase and the retrieval phase.

In the registration phase, the shape feature of each component in the assembly is calculated from the 3D CAD model of the component. The system extracts an assembly structure from the 3D CAD model of the assembly and integrates the structure with the shape features of the components to construct an assembly graph G_m. This assembly graph is stored in the database.

While in the retrieval phase, the system generates an assembly graph G_q from the CAD model of a query assembly in the same manner of the registration phase. Then, the dissimilarity between the two assembly graphs is evaluated by matching using the bipartite graph. In the matching, the node that has the closest shape feature to a node in one graph is automatically found from another graph. The user can control some of the weights used in the dissimilarity evaluation.

3. Generation of the assembly graph

In generating an assembly graph, a set of triangle facets and the surface area and volume of every component are extracted from a 3D CAD model. A set of 3D points on the facets of the component are uniformly sampled. On the other hand, the information of contact states, interference states, and geometric constraint conditions between two components are examined using the 3D CAD application programming interface. The contact state indicates that two components are in contact. The interference state indicates that the solids of two components are spatially overlapped. The geometric constraints indicate that a kind of 3D geometric constraint between form features have been defined in the assembly model.

As shown in Fig. 2, an undirected graph entitled, "assembly graph", is generated to evaluate the similarity between two assemblies. In the graph, each component corresponds to a node of the graph. The arc of the graph is generated if there is a contact or interference between the two components or if there is at least one geometric constraint between the two components (i.e. coincident, concentric etc.). Consequently, the assembly graph G is defined in Eq. (1).

$$G = \langle N, E \rangle \qquad (1)$$

where N is a set of graph nodes corresponding to a component in the assembly, and E is a set of graph arcs.

The following attributes of the nodes and the arcs are also attached to graph G. $Area_i$ and V_i are the surface area and volume of component i, and AD_i is the *angle distance* of component i
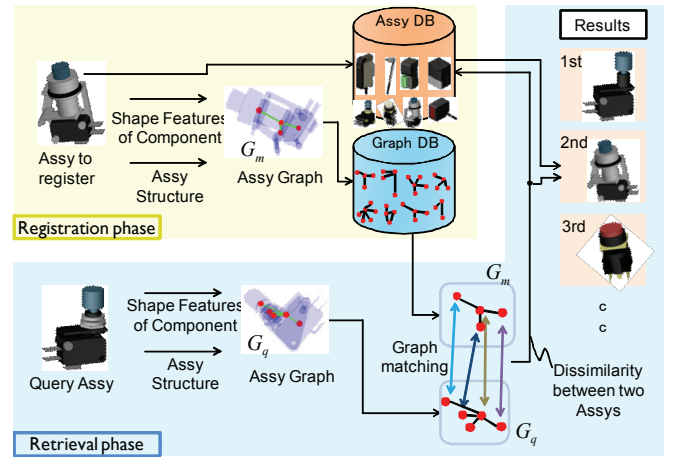

Fig. 1 An overview of the
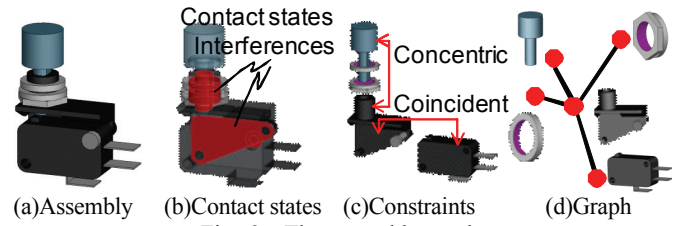3D shape retrieval system considering assembly.

(a)Assembly (b)Contact states (c)Constraints (d)Graph
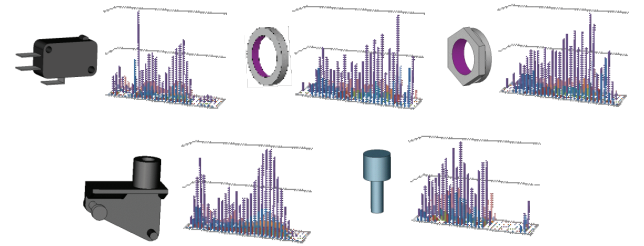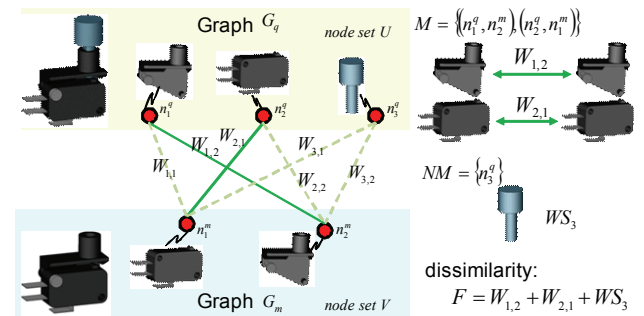Fig. 2 The assembly graph.

Fig. 3 Examples of Angle Distance.

Fig. 4 Bipartite graph matching.

Table 1 Type of constraints.

γ	type p_γ^α	γ	type p_γ^α
1	coincident	12	width
2	concentric	13	lock to scketch
3	perpendicular	14	rack pinion
4	parallel	15	max mates
5	tangent	16	path
6	distance	17	lock
7	angle	18	screw
8	unknown	19	linearcoupler
9	symmetric	20	universaljoint
10	cam follower	21	coordinate
11	gear	22	interference (or contact)

which is a kind of shape feature of the component. $p_\gamma^\alpha \in \{true,\ false\}$ $(\gamma = 1,2,\ldots,22)$ is a boolean flag indicating whether each of the contact, interference and constraint conditions exist between the components corresponding to an arc $e^\alpha \in E$ of the

graph. The meaning of the flag is summarized in Table 1.

The angle distance is a kind of statistical shape feature proposed by Ohbuchi [6] for shape retrieval of components. As shown in Fig. 3, the angle distance is a two dimensional histogram where a normalized distribution of distances between two randomly selected points from the sampled points on the component surfaces corresponds to one direction, and one of the inner products between the two surface unit normal vectors at these points continues in the opposite direction. The constructed assembly graph is finally stored in the assembly database.

4. Dissimilarity evaluation

4.1 Matching between two assembly graphs

As shown in **Fig. 4**, in the retrieval phase, we first perform the maximum bipartite graph matching between a node set N_q in an assembly graph $G_q = \langle N_q, E_q \rangle$ and a node set N_m in $G_m = \langle N_m, E_m \rangle$ which corresponds to query model q and model m in the database. The graph matching finds a set of node pairs between N_q and N_m.

This matching problem can be treated as a modified version of the *stable marriage problem* between two node sets with a different number of nodes that can be solved by the Gale-Shapley algorithm [7].

In the algorithm, an ordered preference list of each node n_i^q in node set N_q is arranged in the ascending order of the "*component pair dissimilarity*" $W_{i,j}$ between the node n_i^q and the node n_j^m in the node set N_m. The components dissimilarity $W_{i,j}$ is described in Section 4.3.

When the number of nodes in the two graphs is different, a complete form of matching cannot be performed. In this case, not only the engaged node pair set M but also the bachelor node set NM are generated after matching.

4.2 Dissimilarity between two assembly graphs

Referring both to the engaged node pair set M and the bachelor node set NM, the *assembly dissimilarity* F between two assembly graphs is evaluated in Eq. (2).

$$F = \sum_{(n_i^q, n_j^m) \in M} volf_{i,j} W_{i,j} + FS \qquad (2)$$

where $\left(n_i^q, n_j^m\right)$ is an engaged node pair included in M. $volf_{i,j} = \left(volf_i^q + volf_j^m\right)/2$ is the *average volume ratio* of the volume ratios of the two components n_i^q and n_j^m. The volume ratio $volf_i^q$ $volf_j^m$ of components i and j is defined in Eq. (3).

$$volf_i^q = V_i / \sum_{n_i \in N_q} V_i, \quad volf_j^m = V_j / \sum_{n_j \in N_m} V_j \qquad (3)$$

$W_{i,j}$ in Eq.(2) is a "*component dissimilarity*" between n_i^q and n_j^m which is calculated from Eq. (4) in Section 4.3. FS is an "*unmatched penalty*" evaluated from the bachelor nodes in NM.

In order to let the significance of the component be proportional to an occupied volume of a component in the assembly, the component dissimilarity is multiplied by the average volume ratio $volf_{i,j}$ in Eq. (2).

In the case that the number of components in the two assemblies is different as shown in Fig. 4, a bachelor node always exists. When evaluating the degree of matching of two node sets N_q and N_m, not only the matched portions indicated by the engaged nodes but the unmatched ones by the bachelor nodes must be evaluated simultaneously. If the matched portions are the same but the unmatched portions are larger, the dissimilarity between the two graphs has to be increased.

Because the *component dissimilarity* $W_{i,j}$ only reflects the matched node pairs, we must add the *unmatched penalty FS* to the dissimilarity F, which reflects the degree of unmatched portions corresponding to the components of bachelor nodes.

The unmatched penalty FS is defined as a weighted sum of a *bachelor component penalty* WS_i of the bachelor node in two assemblies as shown in Eq. (4).

$$FS = \sum_{n_i^q \in NM} volf_i^q WS_i + \sum_{n_j^m \in NM} volf_j^m WS_j \qquad (4)$$

4.3 Component pair dissimilarity

The component pair dissimilarity $W_{i,j}$ between an engaged node pair (n_i^q, n_j^m) is calculated by Eq. (5), where the node n_i^q corresponds to a component i in query assembly q, and n_j^m a component j in an assembly m stored in the database.

$$W_{i,j} = c_{SD} W_{i,j}^{SD} + c_{VD} W_{i,j}^{VD} + c_{AD} W_{i,j}^{AD} + c_{Adj} W_{i,j}^{Adj} \qquad (5)$$

where $W_{i,j}^{SD}$ is a dissimilarity between surface areas of components i and j, $W_{i,j}^{VD}$ a dissimilarity between volumes, $W_{i,j}^{AD}$ a dissimilarity between two angle distances, and $W_{i,j}^{Adj}$ a dissimilarity between the connected node groups each of which is a set of connected nodes to the engaged node n_i^q or n_j^m. c_{SD}, c_{VD}, c_{AD}, and c_{Adj} are the weights for blending these four dissimilarities. The calculation of the above four dissimilarities are described in Section 4.5.

4.4 Bachelor Component Penalty

A bachelor component penalty WS_i for the bachelor component i is evaluated so as to be proportional to the ratios of the surface area, volume, and angle distance of component i with their sum of all nodes in the assembly. This is defined in Eq. (6).

$$WS_i = \frac{c_{SD} Area_i}{\sum_{n_i \in N} Area_i} + \frac{c_{VD} V_i}{\sum_{n_i \in N} V_i} + c_{AD} W_{i,avg}^{AD} \qquad (6)$$

Where, c_{SD}, c_{VD}, c_{AD}, and c_{Adj} are the weights. The $W_{i,avg}^{AD}$ is a dissimilarity of angle distances between the angle distance of component i and the average of the angle distances of all constituent components in the assembly. The calculation of this is described in Section 4.6.

4.5 Dissimilarities between surface areas and volumes

The dissimilarity $W_{i,j}^{SD}$ between surface areas is the absolute difference between the areas of components i and j of the matched node pair which is normalized for the total areas of the query assembly, and is defined in Eq. (7). The dissimilarity $W_{i,j}^{VD}$ between volumes is defined in Eq. (8) in the same manner.

$$W_{i,j}^{SD} = \left| Area_i - Area_j \right| \Big/ \sum_{n_i \in N_q} Area_i \qquad (7)$$

$$W_{i,j}^{VD} = \left| V_i - V_j \right| \Big/ \sum_{n_i \in N_q} V_i \qquad (8)$$

4.6 Dissimilarity between angle distances

The angle distance is a two-dimensional distribution where the first dimension indicates the normalized distribution of distances between sampled points on the component and the second dimension refers to the normalized distribution of inner products between the unit surface normal vectors. An *angle distance* $\mathbf{A}^i$ of component i is defined in Eq. (9).

$$\mathbf{A}^i = \left\{ x_{\alpha,k}^i \middle| x_{\alpha,k}^i \in [0,1], 1 \le \alpha \le I_D, 1 \le k \le I_P \right\} \qquad (9)$$

where $x_{\alpha,k}^i$ is a normalized frequency, I_D a number of intervals showing distance, and I_P that of the inner product value.

When evaluating the dissimilarity $W_{i,j}^{AD}$ between two angle distances $\mathbf{A}^i$ and $\mathbf{A}^j$, taking a simple Euclidian distance between the two-dimensional distributions of $\mathbf{A}^i$ and $\mathbf{A}^j$ causes an irrelevant dissimilarity measure. The reason for this is because the Euclid

distance between the two distributions is often large even if the profiles of the distributions are quite similar to each other but a few intervals have slightly shifted.

Therefore, we adopted elastic matching for evaluating the dissimilarity between two angle distances which was proposed by Obuchi et al.[6] In elastic matching, the dissimilarity between two angles distances $W_{i,j}^{AD}$ are evaluated using dynamic programming. This dynamic programming is done according to the following procedure. First, at different intervals of distance α and β, a simple Euclidian distance between the two inner product distribution $g(\mathbf{X}_\alpha^i, \mathbf{X}_\beta^j)$ is calculated as in Eq. (10).

$$g(\mathbf{X}_\alpha^i, \mathbf{X}_\beta^j) = \sqrt{\sum_{k=1}^{I_p} \left(x_{\alpha,k}^i - x_{\beta,k}^j\right)^2} \qquad (10)$$

Then, the dissimilarity between angle distances $W_{i,j}^{AD}$ can be obtained from solving the following recursive formulae.

$$W_{i,j}^{AD} = g(\mathbf{X}_n^i, \mathbf{X}_n^j) = \min \begin{bmatrix} g(\mathbf{X}_n^i, \mathbf{X}_{n-1}^j) + \Delta g(\mathbf{X}_n^i, \mathbf{X}_n^j) \\ g(\mathbf{X}_n^i, \mathbf{X}_{n-1}^j) + 2\Delta g(\mathbf{X}_n^i, \mathbf{X}_n^j) \\ g(\mathbf{X}_{n-1}^i, \mathbf{X}_n^j) + \Delta g(\mathbf{X}_n^i, \mathbf{X}_n^j) \end{bmatrix} \qquad (11)$$

$$\Delta g(\mathbf{X}_\alpha^i, \mathbf{X}_\beta^j) = |\alpha - \beta| \sqrt{\sum_{k=1}^{I_p} \left(x_{\alpha,k}^i - x_{\beta,k}^j\right)^2} \qquad (12)$$

4.7 Dissimilarity between connected node groups

$W_{i,j}^{Adj}$ is defined as a dissimilarity between component groups connected to the engaged node pair $(n_i^q, n_j^m) \in M$ and calculated in Eq. (13) as shown in Fig. 5. $W_{i,j}^{Adj}$ displays a dissimilarity between not only component pairs but also connected component groups, and reflects the similarity between component layouts or structures near the engaged node pair in two assemblies. This satisfies the first requirements for the retrieval described in Section 1.

$$W_{i,j}^{Adj} = \sum_{(n_k^q, n_l^m) \in M \wedge adj(n_i^q, n_k^q) \wedge adj(n_j^m, n_l^m)} \left\{ vol f_{k,l} \left(W_{k,l}' + W_{k,l}^{arc} \right) \right\} \qquad (13)$$

where $adj(n_i^q, n_k^q)$ is true if the nodes n_i^q and n_k^q are adjacent in an assembly graph. $W_{k,l}'$ is an *adjacent dissimilarity* between two connected component groups each of which is adjacent to the node n_k^q or n_l^m as defined in Eq. (14),

$$W_{k,l}' = c_{SD}^{Adj} W_{k,l}^{SD} + c_{VD}^{Adj} W_{k,l}^{VD} + c_{AD}^{Adj} W_{k,l}^{AD} \qquad (14)$$

where $W_{k,l}^{arc}$ is an *arc dissimilarity* obtained from the contact, interference or constraint condition of the arcs e_α^q and e_β^m between (n_i^q, n_k^q) and (n_j^m, n_l^m) in each assembly graph. The *arc dissimilarity* $W_{k,l}^{arc}$ is defined in Eq. (15).

$$W_{k,l}^{arc} = \sum_{\gamma=1}^{26} \left(p_\gamma^\alpha \oplus p_\gamma^\beta \right) \Big/ \Gamma \qquad (15)$$

where p_γ^α and p_γ^β respectively display the boolean variable, which indicates that the γ-th constraint condition exists as shown in Table 1. $\oplus$ means an exclusive OR.

5. Experimental results
5.1 Assembly structure similarity evaluation

Assembly dissimilarities F were evaluated for a set of eleven 3D assembly models of the pneumatic cylinders[8]. The results are shown in Fig. 6 and Fig. 7 at different settings of the weights for the dissimilarity calculation. In case of Fig. 6, the weights for calculating the dissimilarity were set to: $c_{SD} = 0.4$, $c_{VD} = 0.4$, $c_{AD} = 0.1$, and $c_{Adj} = 0.1$. On the other hand, the weights were set to $c_{SD} = 0.0$, $c_{VD} = 0.0$, $c_{AD} = 0.8$, and $c_{Adj} = 0.2$ in the case of Fig. 7. These weight settings were intended to clarify whether our proposed retrieval method satisfies the first and fourth requirements as listed in
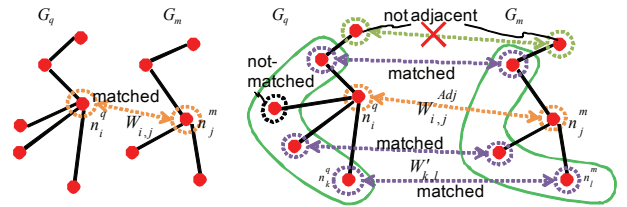

Fig. 5 Dissimilarity between connected node groups

Fig. 6 Result of "mass-driven" similarity evaluation

Fig. 7 Result of "geometry-driven" similarity evaluation

Section 1.

Geometry and geometric constraint information were obtained from 3D assembly models of a commercial CAD system (SolidWorks 2008) using its application-programming-interface functions.

In the retrieval result of Fig. 6, the assembly dissimilarity between the query model Q and the retrieved model M_1 is zero when only one component position is different from Q. In this case, the component sets of Q and M_1 are identical. On the other hand, the dissimilarities among Q and M_2, M_3, M_4, and M_5 are much smaller than the ones among Q and M_8, M_9 and M_{10}. This is because M_2, M_3, M_4, and M_5 belong to the same product series as Q, while M_8, M_9 and M_{10} do not. In Fig. 6, the dissimilarity between Q and M_8 is smaller than among Q, M_6, and M_7 even considering that M_8 does not belong to the same

product series of Q. This is because the similarities between volumes and surface areas of the components played a greater role in the evaluation than those of angle distances and assembly structures at the weight setting.

On the other hand, in Fig. 7, the weights for the angle distance dissimilarity and connected nodes dissimilarity are larger than those in Fig. 6, and the dissimilarities in volume and surface area can be ignored. The result of Fig. 7 indicated that all assemblies (M_1, M_2, …,M_7) belonging to the same series as Q have dissimilarities smaller than those of the different series M_8, M_9, and M_{10}. In addition, M_{11}, which had quite a different shape from Q, displayed the greatest dissimilarity.

These results suggested that controlling the four dissimilarity weights enables the users to choose "mass-driven retrieval" which is better aware of the similarities between component sizes or "geometry-driven retrieval", and is more aware of the similarities between component shape or between assembly structures. Furthermore, the results suggested that the proposed method could reflect well the first and fourth requirements for the retrieval of assembly models.

5.2 Maximum matching ability

Fig. 8 shows a retrieval result when the unmatched penalty FS was completely ignored in calculating the dissimilarity between two assemblies. The weight settings in Fig. 8 were the same as in Fig. 7.

The number of components in assembly M_2 is less than in Q. On the other hand, a component set of M_2 was a subset of that of Q, the assembly structure of M_2 was identical to the partial assembly structure of Q, and the dissimilarity between M_2 and Q was zero. In addition, the partial components in assemblies M_3, M_4, M_5, M_6, and M_7 were also subsets of those of Q. In this case, all of the dissimilarities were also zero.

The results indicated that the maximum matching ability of the retrieval can be realized when setting the unmatched penalty to zero, and we can easily find the assemblies of past designs, which include the subset of the query assembly by considering the assemblies with zero dissimilarity values. This result reflects the second requirement listed above in Section 1.

5.3 Assembly structure similarity evaluation and insensitivity to the movable components

Fig. 9 shows the dissimilarity evaluation results of three assemblies: M_{12}, M_{13}, and M_{14} for the query model Q in Fig. 9. M_{12}, M_{13}, and M_{14} have the same component set as Q. The assembly M_{12} has the same assembly structure as Q but has a relatively different position of the rod than Q. The assembly M_{13} has different geometric constraints than that of Q. The assembly M_{14} also has different geometric constraints than that of Q.

The dissimilarity between M_{12} and Q was zero, and it indicated the dissimilarity was insensitive to the relative positions and orientations of the assemblies with movable parts. The dissimilarity among M_{13}, M_{14}, and Q was not zero, and it indicated that the dissimilarity was sensitive to the change of the assembly structures even if the components sets are identical in two assemblies.

These results showed the retrieval method satisfied the first and third requirements as mentioned in **Section 1**.

6. Conclusions and future work

A new 3D shape retrieval method considering assembly structure was proposed in this paper. The dissimilarity measurement between two assembly models was estimated based on the assembly graph matching the difference between shape features of two components and the one between two assembly structures evaluated simultaneously. Characteristics of the dissimilarity can be changed by controlling weights of evaluation. The experimental results showed that the proposed method satisfied four requirements: (evaluation of assembly structure similarity, maximum matching ability, insensitivity to the movable components, and flexible control of
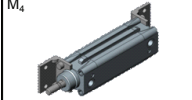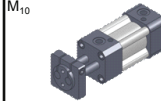

Fig. 8 Result of "geometry-driven" similarity evaluation without FS
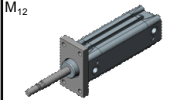
Fig. 9 Result of similarity evaluation between assemblies of different constraint conditions

similarity evaluation) on 3D assembly model retrieval in design and engineering processes.

However, in the current system, the weights of the dissimilarity evaluation have to be determined manually. Automatic and appropriate control of these weights still needs to be realized in the future.

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