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Retrieve CAD Model Based on Face Matching Sequence

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Abstract

A new model retrieval method based on face matching sequence is proposed in this paper. Attribute adjacent graph is used to describe two faces' geometry similarity and topological relationship in CAD model. According to the difference of edge numbers, similarities between two models' faces are computed and face similarity matrix is constructed. Ant colony algorithm (ACA) is applied to obtain an optimal sequence of matching faces between two models. Accumulate similarity values of optimal matching faces to calculate two models' similarity. Experimental results show that this method can evaluate two CAD models' shape difference effectively.

Keywords*: face matching sequence; attribute adjacent graph; CAD model; ant colony algorithm*

1. Introduction

3D model retrieval technology has been widely applied in many areas today. Many researchers are focusing on it. Li extracts modeling information to construct feature dependency graphs and uses design reusability to retrieve CAD models. 3D CAD models are evaluated according to general shape similarity [1]. Quan describes a local shape descriptor which uses geodesic iso-contour's length as a representative for surface features and proposes a part-in-whole matching algorithm [2]. Pu gives a feedback-based interface for retrieving CAD models in which users sketch a model's 2D shape to draw its 3D views. 3D views are applied to compute two models' similarity [3]. Chen presents an algorithm to retrieve CAD models in which oriented bound boxes and normal distribution are used. Shape distribution is adopted to describe a model's global information [4]. Huang employs a feature recognition and filtration method to retrieve 3D models. A model's blend features are used to construct feature dependency graphs. At the same time, a sub-graph isomorphism algorithm is utilized to retrieve CAD models [5]. Zhu extracts spectral distribution information of two models, and their divergences are used to retrieve models, in which a spectral algorithm is adopted [6]. Wang studies the effect of dense sampling strategy and PHOW sampling strategy on CAD model retrieval. At the same time, he also investigates influences of codebook size and distance metric on retrieval performance [7]. Liu gives a new retrieval method by comparing similarities between two 3D models' 2D sketches [8]. Huang uses manufacture semantics to retrieve 3D CAD models. An optimal matching algorithm is employed to seek a match with maximum total weights, which is used to evaluate two CAD models' similarity [9]. Sun presents a model retrieval method based on features, feature topology structures, and feature generation operations. Maximum common sub-graphs are applied to compute the similarity between two CAD models [10].

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Marefat uses features and their spatial relationships to construct a signature, with which an indexing scheme is developed to store and retrieve CAD parts [11]. Leila studies classification methods to compute 3D shape similarity and applies a classification database to design decisions [12]. Wang retrieves CAD models in a sketch-based query interface, in which an image similarity assessment algorithm is adopted to calculate similarities between user sketches and 3D models' views [13]. Wei uses accessibility cone distribution to retrieve 3D CAD models in which random sample points and their normal directions on faces are applied [14]. Jing utilizes L1 distance to compute similarities between visual words' occurrence histograms, on which two CAD models' similarity is evaluated [15].

In this paper, attribute adjacent graph is applied to represent relationship among faces in CAD model. Based on the divergence of edge numbers, the similarity between two faces is computed. Ant colony algorithm is used to find an optimal sequence of matching faces between two models. The similarity of two CAD models is evaluated by accumulating similarities of matching faces.

2. Match Source Model Face with Target Model Face

In order to calculate two faces' similarity easily, their edge numbers are extracted. Attribute adjacent graph can describe two faces' topological and geometrical relationships. Its edge information and node information can reflect models' features accurately.

Attribute adjacent graph is defined as G=(V, E). Here, V=(v_1, v_2, …, v_n) denotes a set of nodes and E=(e_1,e_2, .., e_m) is a set of edges. Node pair (v_i, v_j) can uniquely identify an edge e_k whose nodes are respectively v_i and v_j. Node v_i represents faces f_i and node v_j denotes faces f_j in CAD model. Edge e_k describes adjacent relationship between face f_i and face f_j. Then, attribute adjacent graph is constructed.

A CAD model is shown in Figure 1, including faces f_1, f_2, f_3, f_4, f_5, f_6, f_7, f_8, f_9. Face f_1 is adjacent to face f_2, f_4, f_5, f_6. Face f_2 is adjoined with f_1, f_3, f_5, f_7. Face f_3 is adjacent to f_2, f_4, f_5, f_9. Face f_4 is adjoined with f_1, f_3, f_5, f_8. Face f_5 is adjacent to f_1, f_2, f_3, f_4. Face f_6 is adjoined with f_1, f_7, f_8. Face f_7 is adjacent to f_2, f_6, f_8, f_9. Face f_8 is adjoined with f_4, f_6, f_7, f_9. Face f_9 is adjacent to f_3, f_7, f_8.

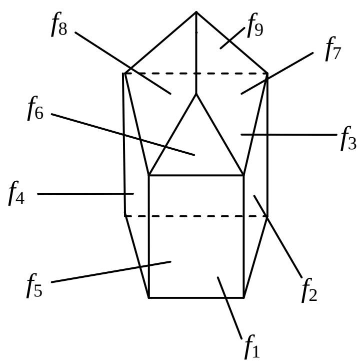


Figure 1. CAD Model

Its attribute adjacent graph is shown in Figure 2. Every node corresponds to a face in CAD model. If face f_i is adjacent to face f_j in CAD model, there is a corresponding edge between v_i and v_j in G.

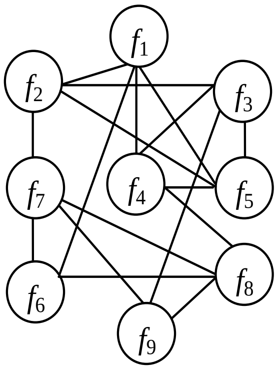


Figure 2. Attribute Adjacent Graph of CAD Model

Faces f_1, f_2, f_3, f_4, f_5, f_7 and f_8 all have four edges. Faces f_6 and f_9 have three edges. $N_e(f_i)$ is edge number of face f_i in model M_s. $N_e(f_j')$ is edge number of face f_j' in model M_t. According to the difference of edge numbers, face similarity is calculated. The similarity $S_f(f_i, f'_j)$ between source face f_i and target face f'_j is shown in formula (1).

$$S_f(f_i, f_j') = 1 - \frac{|N_e(f_i) - N_e(f_j')|}{\max(N_e(f_i), N_e(f_j'))} \tag{1}$$

The value of $S_f(f_i, f'_j)$ is larger, if there is less discrepancy between source face f_i and target face f'_j.

In ant colony algorithm, a heuristic strategy is used to solve combination optimization problems. For example, NP hard problems are always viewed as unsolved ones. If they are regarded as optimization problems, ant colony algorithm can be used to find their optimal solutions with heuristic search strategies. It is widely applied to many areas including graph coloring problems, communication network routing issues, load balancing problems and vehicle scheduling issues.

This algorithm finds optimal paths by simulating the behavior of ant starching food. It simulates the ability that ant colony search foods along the shortest paths. Two ants utilize pheromone to communicate with each other in nature. According to pheromones, ants can find the shortest routes between food sources and their nests. When ants walk towards food sources, pheromone is deposited on roads. If pheromone on a road is more, the probability that other ants walk along this route is bigger. If a lot of ants walk along a path, there is more deposited pheromone on it. Ants on other routes become aware of this road’s pheromone in high density and assemble on it. The result is that more and more ants walk toward food source along a path with highest density pheromone.

There is a mechanism based on positive feedback in ant colony algorithm which guides the whole evolution process toward an optimal solution. It finds a global solution in 1% of known optimal ones. At the same time, multiple ant colonies are good at providing solutions for many larger problems. Ant colony algorithm can search the problem space independently, which improves its reliability and global solution capability.

There is a strong robustness for ant colony algorithm. This is because that it does not depend on initial path. Few parameters are used and it is easy to construct a model. The search process is automatically adjusted and the efficiency of this algorithm is improved.

Here, ant colony algorithm is adopted to solve the problem of CAD model retrieval. It is applied to find models’ optimal matching faces. The similarity between face f_i and face f'_j is regarded as an information unit. Face similarity values are used to construct similarity matrix A. When ants walk, pheromones accumulate on target faces. If pheromone on target face f'_j is more, the probability that face f'_j is matched with face f_i is larger. Transition probability $P_{ij}(k)$ is used to find optimal matching face pair (f_i, f'_j) and it is computed as shown in formula (2).

$$p_{ij}(k) = \begin{cases} \dfrac{\tau_{ij}^{\alpha}(k)\eta_{ij}^{\beta}}{\sum \tau_{ij}^{\alpha}(k)\eta_{ij}^{\beta}}, & \text{ant } k \text{ selects face } f_j' \\ 0, & \text{ant } k \text{ does not select face } f_j' \end{cases} \tag{2}$$

Here, $\tau_{ij}(k)$ is pheromone total of ant k on target face f'_j and η_{ij} represents heuristic factor whose value is $S_f(f_i, f'_j)$. α is the influence of pheromone accumulation on transition probability. β denotes the influence of the similarity between face f_i and face f'_j on $P_{ij}(k)$. Optimal matching face pairs are stored in tabu[k] for ant k. According to tabu[k], global pheromone on target face is updated. After all target faces are selected, global pheromone is updated according to formula (3).

$$\tau_{ij}(k) = \tau_{ij}(k)(1-\rho) + \sum_{k=1}^{m} \Delta\tau_{ij}^{k} \tag{3}$$

Here, ρ is the pheromone's volatilization coefficient. The pheromone increment $\Delta\tau_{ij}^k$ is computed as shown in formula (4).

$$\Delta\tau_{ij}^{k} = \begin{cases} Q, & \text{ant } k \text{ selects face } f_j' \\ 0, & \text{ant } k \text{ does not select face } f_j' \end{cases} \tag{4}$$

Here, Q represents the pheromone increment on target face.

A method to find an optimal sequence of matching faces based on ant colony algorithm is given and it is shown as follows:

1.Extract edge numbers $N_e(f_1)$, $N_e(f_2)$, ..., $N_e(f_n)$ for faces f_1, f_2,..., f_n in M_s from G. Extract edge numbers $N_e(f_1')$, $N_e(f_2')$, ..., $N_e(f_m')$ for faces f_1', f_2', ..., f_m' in M_t from G.

2.According to formula (1), the similarity between source face f_i and target face f_1' is calculated. Similarity matrix A is constructed based on face similarity values.

3.For(k=1; k<=m; k++)

(1)Set taboo table tabu[k]=Φ. Initialize array Allowed[i][j]=1 (i=1, 2, …, n, j=1, 2, …, m).

(2)Ant k is randomly distributed in matrix A and transition probability $P_{ij}(k)$ is calculated according to formula (2).

do{

①Visit matrix A to find face matching pair (f_i, f'_j) according to $P_{ij}(k)$.

②All elements of the *i*th row in array Allowed are set to 0.

③All elements of the *j*th column in array Allowed are set to 0.

④Compute pheromone increment $\Delta\tau_{ij}^k$ according to formula (4).

⑤Put face pair (f_i, f'_j) into tabu[k].

} Until all target faces are selected.

(3)Update global pheromone according to formula (3).

(4)Record optimal face matching sequence in tabu[k].

4.Output a global optimal face matching sequence.

3. Calculate Two Models' Similarity Based on ACA

Model M_s is surrounded by faces f_1, f_2, …, f_n. Model M_t is surrounded by faces f_1', f_2', ..., f_m'. Model M_s has n faces and model M_t has m faces. When ant colony algorithm is applied, an optimal face matching sequence f_1<–>f'_1, f_2<–>f'_2, …, f_n<–>f'_m is obtained. If every source face is matched with target face in high degree, the model similarity is big. Otherwise, the model similarity is small.

If m is less than n, the number of faces in M_t is less than the number of faces in M_s. Then, M_t is regarded as target model and M_s is viewed as source model. When ant colony algorithm is applied, face matching sequence f_{s1}<–>f'_{t1}, f_{s2}<–>f'_{t2}, …, f_{sm}<–>f'_{tm} is obtained. $S_m(M_s, M_t)$ represents model similarity between M_s and M_t. It is calculated by accumulating face similarities $S_f(f_{si}, f'_{ti})$ between source face f_{si} and target face f'_{ti} (i=1, 2, …, m). $S_m(M_s, M_t)$ is calculated as shown in formula (5).

$$S_m(M_s, M_t) = \frac{1}{m}\sum_{i=1}^{m} S_f(f_{si}, f'_{ti}) \tag{5}$$

If m is larger than or equals to n, the number of faces in M_t is larger than or equals to the number of faces in M_s. Then, M_s is viewed as target model and M_t is regarded as source model. According to the above algorithm, face matching sequence f_{s1}<–>f'_{t1}, f_{s2}<–>f'_{t2}, …, f_{sn}<–>f'_{tn} is obtained. $S_m(M_t, M_s)$ is computed as shown in formula (6).

$$S_m(M_t, M_s) = \frac{1}{n}\sum_{i=1}^{n} S_f(f_{si}, f'_{ti}) \tag{6}$$

4. Experiment

Four CAD models are selected to verify the proposed method's correctness in this paper. Target model is a triangular cone and it is shown in Figure 3. It contains four faces and each face has three edges.

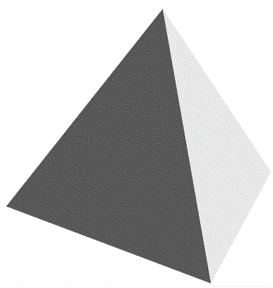
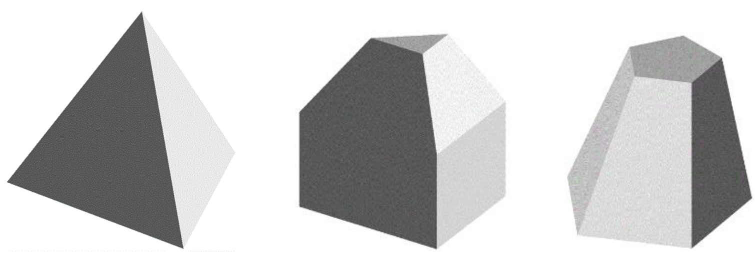


Figure 3. Target Model M_t

Three source models are selected as shown in Figure 4. Source model M_A is a triangular cone. Source model M_B is a combined model including a triangular frustum of pyramid and a triangular prism. Source model M_C is a pentagon frustum of pyramid.



Source model M_A Source model M_B Source model M_C

Figure 4. Source Models

The above method is applied to compute the similarity between source model and target model. They are shown in Table 1.

Table 1. Similarity between Source Model and Target Model

Source model	Face number	Edge number	Vertex number	Model similarity
M_A	4	6	4	1
M_B	8	15	8	0.875
M_C	7	14	10	0.75

Model M_A is a triangular cone which has four faces, six edges and four vertices. Ant colony algorithm is adopted to find an optimal face matching sequence between source model M_A and target model. Formula (6) is used to compute $S_m(M_A, M_t)$ and its similarity value is 1. A triangular frustum of pyramid and a triangular prism compose model M_B. There are eight faces, fifteen edges and eight vertices in model M_B. Ant colony algorithm is applied to find an optimal face matching sequence. Formula (5) is utilized to compute $S_m(M_B, M_t)$ and its result is 0.875. Model M_C is a pentagon frustum of pyramid which has seven faces, fourteen edges and ten vertices. Ant colony algorithm is adopted to find an optimal face matching sequence between source model M_C and target model. Formula (5) is used to compute $S_m(M_C, M_t)$ and its similarity value is 0.75.

Source model M_A is the same with target model M_t in shape. So, its similarity is maximal in 3 source models. There is less difference between source model M_B and target model M_t in shape. So, the similarity value is higher in 3 source models. Source model M_C is large different from target model M_t in shape. So, the similarity is minimal in 3 source models. Experiments indicate that this method can measure shape differences between two models effectively.

5. Conclusions

Model retrieval method is important in CAD design and manufacture field. In this paper, geometric and topological relationship of a model is described by attribute adjacent graph. Face similarity is computed by discrepancy of edge numbers and face similarity matrix is constructed. A method to find an optimal sequence of matching faces based on ant colony algorithm is given. By accumulating similarity values of optimal matching faces, two models' similarity is evaluated. Experimental results show that this method is reliable.

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