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# **Skeleton Approximation of B-Rep Models Using Centroid Graph**

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## Abstract

Skeleton is a shape representation of a B-Rep model with lower dimension. The associate information requirements of the skeleton differ from application to application. For example, object recognition requires only skeleton in order to perform similarity comparison. On the other hand, to reduce the errors in reconstruction process, surface reconstruction requires skeleton with detailed geometry such as distances from the surfaces to the skeleton. Even though skeleton extraction has been studied vastly, most of the previous methods are either sensitive to noise, time consuming, or restricted to specific 3D models. A practical approach for approximating skeletons from general 3D models using Centroid Graph is discussed in this paper. The skeleton approximation process begins with the decomposition of the 3D part model into subvolumes or cells. The loci of Centroids are then computed for all cells in order to complete the skeleton approximation.

Keywords: Shape Representation, Skeleton, Medial Axis Transform

### **1. Introduction**

Skeleton, also called Medial Axis Transform, has been used in biology for a long time. Medial Axis Transform represents 3D shapes with a series of curves or points, like the skeleton of a human body. This concept has been widely used in pattern recognition, shape analysis, and mesh generation.



Figure 1: Medial Axis Transform by Voxelization

Medial Axis Transform can be used to perform geometric reasoning on complex part model because it has lower dimension compared to the model itself. However, finding Medial Axis Transform is very computationally intensive and the result may not be used to perform reasoning since the Medial Axis Transform can be  $R^2$  surfaces embedded in  $R^3$  space. Furthermore,

the redundant information may be misleading and is difficult to process. Figure 1 shows an example of Medial Axis Transform of a simple 3D part.

A novel approach, namely Centroid Graph, is introduced in this paper to approximate the topological and geometrical information of the part models. The approximation of skeleton is easier to compute and can be useful. Instead of searching points with equal distance to the surrounding surfaces to form Medial Axis Transform, the centroids of the part on different locations are obtained to form a Centroid Graph.

Various methods have been studied to compute the shape representations of 3D parts. These methods can be classified into categories as described in the work done by Iyer, N. et al. [1]: (a) Invariant/Descriptor based -Invariants or descriptors of the 3D shape such as volume, and surface area are used as signatures; (b) Statistic/Probability based – A shape function constructed by random sampling of points is used to describe the part. [2] Shape histograms are used to approximate and search for the 3D model [3]; (c) Group Technology based – Two step Group Technology (GT) method is developed by Iyer, S. and Nagi, R., [4] (d) Graph based - Subgraph isomorphism for matching B-Rep graph are employed. [5] Eigenvalues of a model signature graph (MSG) constructed from the B-Rep graph are used as signatures. [6] (e) Feature recognition based - Cells and spatial relationships are computed from part decomposition. [7] (f) 3D Object Recognition based - Aspect graphs are used for 3D shape searching. [8] Geometric Hashing is used in the work done by Lamdam, Y., and Wolfson, H.J. [9]

#### 2. Background

We begin the skeleton approximation process with the decomposition of the 3D part model into sub-volumes or cells by using two types of graphs.

#### 2.1 Face-Edge Graph

We normally use Face-Edge Graph to represent the connectivity of faces and edges of a geometry model. Graph represents faces and edges by vertices or points

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and lines by sequence. Figure 2 shows the geometry model connectivity by Face-Edge Graph.



Figure 2: A Block and corresponding Face-Edge Graph

#### 2.2 Cellular Adjacency Graph

Cellular Adjacency Graph represents cells connection. Each cell is represented by point or vertex as shown in Figure 3. The faces that connect 2 cells together or face interactions are defined by lines. (The interactions are shown as edges.)



Figure 3: Cellular Adjacency Graph

#### 2.3 Cell Decomposition Technique

The decomposition technique is proposed and discussed in detail in the work done by Eiamsa-ard et al [10]. Figure 4 shows the examples of cell decomposition.



Figure 4: Examples of part decomposition

After the decomposition process has been done, the cells are used to find the skeleton of each cell by using centroid graph.

#### 3. Centriod Graph Representation

Similar to Medial Axis Transform, Centroid Graph is also composed of a series of points which are centroids of cross sections of the part at difference locations. A cross section is the intersection of a planar surface with the object. A planar surface can be defined by a position and normal direction. At particular position, there are infinite directions; therefore, there are infinite cross sections that yield infinite Centroid Graphs for an object. Figure 5 illustrates this situation by showing 3 different Centroid graphs along different directions for a simple block.



Figure 5: Centroid Graph Along 3 Different Directions

#### 5. Centroid Graph Computation

The skeleton computation of a cell starts at the cross sectional base of cell direction according to cell decomposition technique.

Let  $C_k$  and  $L_i$  be the current cell and the current layer.  $\overline{G}_{r(i)}$  is the real centroid of the cross section surface at layer i<sup>th</sup>. Unit vector  $\hat{n}_{r(i)}$  is the real normal vector of layer i<sup>th</sup>. The value h is the desired height for each layer.

The 3D cross section algorithm always starts with the prediction step. Point  $\overline{C}_{g(i+1)}$  is a guessed point for the next layer i+1<sup>th</sup> given by:

$$\vec{C}_{g(i+1)} = \vec{G}_{r(i)} + h \cdot \hat{n}_{r(i)}$$
(1)



Figure 6: Slicing based on 3D layer

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Use  $\vec{C}_{g(i+1)}$  as the seed point, and a slice is generated shown with a dashed line in Figure 30. The centroid of this slice  $(\vec{G}_{g(i+1)})$  is then calculated. If  $(\vec{C}_{g(i+1)} - \vec{G}_{r(i)})$  and  $(\vec{G}_{g(i+1)} - \vec{G}_{r(i)})$  are the same, that means the prediction point  $\vec{C}_{g(i+1)}$  matches with the real point  $\vec{G}_{g(i+1)}$ . Therefore, in this case,  $\hat{n}_{r(i+1)}$  equals  $\hat{n}_{r(i)}$  as well.

In general, however,  $\vec{C}_{g(i+1)}$  and  $\vec{G}_{g(i+1)}$  are not the same point.  $\vec{G}_{g(i+1)}$  is used as the fixed seed point while the normal vector of the slicing plane is being honed by incrementally shifting the direction from  $(\vec{C}_{g(i+1)} - \vec{G}_{r(i)})$  to  $(\vec{G}_{g(i+1)} - \vec{G}_{r(i)})$  as far as possible. (Both heights  $h_{1(j)}$  and  $h_{2(j)}$  have to maintain to be positive.) Obviously, the value of h\* is now bigger than h at the step. Given the h value is always very small, the correction of the height can be simplified as shown in Figure 7.



Figure 7: Shifting the layer down to the desired height

In order to get the desired height h, the layer is shifted down by y\*-y along the vector  $\vec{C}_{g(i+1)} - \vec{G}_{r(i)}$ . (where y is given in equation 16.)

$$y = \left[\frac{h}{h^*}\right] y^* \tag{2}$$

The normal vector of the final honing slice  $\hat{n}_{g(j+1)}$  is used as the predicted normal vector  $\hat{n}_{r(j+1)}$  for the next layer i+2. Centroid of layer i+1 denoted as  $\vec{G}_{r(i+1)}$  is calculated after the layer is shifted down to be used for the prediction step for layer i+2. (Figure 8)

These procedures need to be repeated until the whole cell has been sliced. Then the series of points can be generated from  $\overline{G}_{r(i)}$  of every layer. All points are connected to perform a skeleton like. Let S be the Skeleton of a cell.

$$\mathbf{S} = \vec{G}_{r(1)} \bigcup \vec{G}_{r(2)} \bigcup \vec{G}_{r(3)} \bigcup \dots \bigcup \vec{G}_{r(i)}$$
(3)

Centroid Graph or the loci of centroids is shown in Figure 9.



Figure 8: Layer i+1<sup>th</sup> after adjusting the height



Figure 9: Skeleton of 3D model

#### 6. Experimental Result

Skeleton approximation by Centroid Graph of a Three-D model is the combination of the Centroid Graphs of all cells in that model. A couple of examples are shown in Figure 10.





(a)

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Figure 10: Three-D Models and Centroid Graphs

Our process of skeleton approximation can be separated to 3 steps as following.

- Cell Decomposition Process
- Centroid Graph Computation Process
- Cell combination Process

These 3 steps are illustrated in Figure 11.







Figure 11: Three steps of skeleton approximation

## 7. Conclusion

The skeleton approximation proposed in the paper is relatively easy to compute. The result can be used to

perform object recognition, especially to classify symmetrical and Non-symmetrical model.

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