Computer-aided Geometric Modeling of Plant Cell Shape and Design of its Topological Retrieval Algorithms

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***Abstract*. Using the knowledge of information technology and physical mechanics to simulate the evolution of plant cell shapes is helpful to explore the mechanism of plant tissue and organ formation. However, the traditional numerical modeling based on curves and surfaces is difficult to accurately locate a geometric fragment of cell shape, resulting in the inability to analyze the stress and strain of the fragment freely. In this study, a plant cell shape is firstly decomposed into a body, faces, edges, and vertexes from top to bottom using the n-dimensional generalized mapping theory. Then, the 1-, 2- and 3-dimensional topologies of the cell shape are constructed by combining these topologies from bottom to top using the "half-edge" structure of 0-dimensional topology, and the corresponding retrieval algorithms are designed. Finally, the program is achieved by the C++ programming language and the OpenGL graphics library. The experimental results show that users could not only retrieve the geometric units of cell shape freely, but also highlight the query results in the program through the query interface of this program. The results of this study can provide an automatic topological retrieval of a cell shape for the elastic mechanical modeling of cell shape deformation.**

Keywords: geometric modeling; cell shape; topological retrieval; combinatorial topology

I. Introduction

For more than a century's development, plant biotechnology has experienced three closely-connected and intersecting stages from tissue culture, cellular engineering to genetic engineering. Despite the fact that a large wealth of knowledge on plant growth and genetics has been accumulated, plant scientists presently are still unable to fully predict the genetic regulatory mechanism influencing plant morphogenesis, and continuous efforts are still required in the exploration thereof. As proposed by the German botanist Gottlieb Haberlandt, the cells of a higher plant are totipotent, that is, each individual cell of such a plant contains all its genetic information and is able to develop into a full plant through constant growth and mitosis when the environment is appropriate [1]. The computing technology and mechanics are a useful approach to quantitative analysis to help understand the process of cell deformation. For instance, cell visualization models provide visibility of the evolutionary process of cells and the image simulation technology can be used to validate hypotheses concerning the macro characteristics of plant morphogenesis. Research in this area has been gaining increasing attention from biological researchers [2–6].

II. Related Work

In the field of computer visualization and simulation of cell shape evolution, the Cellular Potts Method (CPM), i.e., a lattice model, has become a highly popular tool for numerical computation [7]. Representing cells as a group of neighboring pixels, CPM is used to track interactive locations through identifying boundary and non-boundary points, and then utilizes the energy function to simulate cell growth, intercellular interaction and how cell shapes are retained. The method has been widely applied in modeling animal cells. For example, Merks et al., employed the CPM method to simulate blood-vessel development in order to help ex vivo reconstruction[8]; Szabó introduced a CPM-based tumor growth model that presented the behaviors of tumor cells like migration and invasion in microscopic environments [9]; Allena et al., simulated individual cells as morphologically variable rigid bodies and fulfilled cell migration on two-dimensional (2D) substrates, with simulation results consistent with those observed in specific experiments [10]. However, plant cells are structurally different from animal cells in a way that the cell walls of the former can retain their geometrical shapes and prevent intercellular sliding between dividing cells. Given a difficulty to fix the geometrical shapes of plant cells and the adjacency relationship between dividing cells, the CPM method faces a challenge in simulating biological phenomena of plant cells like force-induced deformation and division. Focusing on an individual plant cell, this study presents a topological and geometrical approach that allows the construction of a geometrical model for the plant cell that supports topological retrievals.

This study is supported by the National Natural Science Foundation of China (Project No.: 61762048, Project No.: 61562039), and the results of the study constitute a phasic achievement for the above projects.

III. METHOD AND EXPERIMENT

A. Modeling Method

Based on the topological isomorphism between the structural shape of the plant cell wall and an arbitrary convex polyhedron [11], a hollow cuboid has 6 quadrilateral faces, making it convenient to perform force analysis on each face. As such, in this research, the plant cell wall is abstracted into the geometrical structure of a hollow cuboid.

In the geometrical modeling and analysis process, the structural shape of a plant cell is decomposed into n-dimensional topological units. In the 3-dimensional space shown in Fig. 1, the hollow cuboid is decomposed into 6 two-dimensional faces and cycles from left to right, with each cycle being further decomposed into 4 edges in a one-dimensional space and each edge being decomposed into 2 "half-edges" in a zero-dimensional space. Thus, the "half-edge" structure can be combined as a uniform unit into the topological structure of various complex objects.

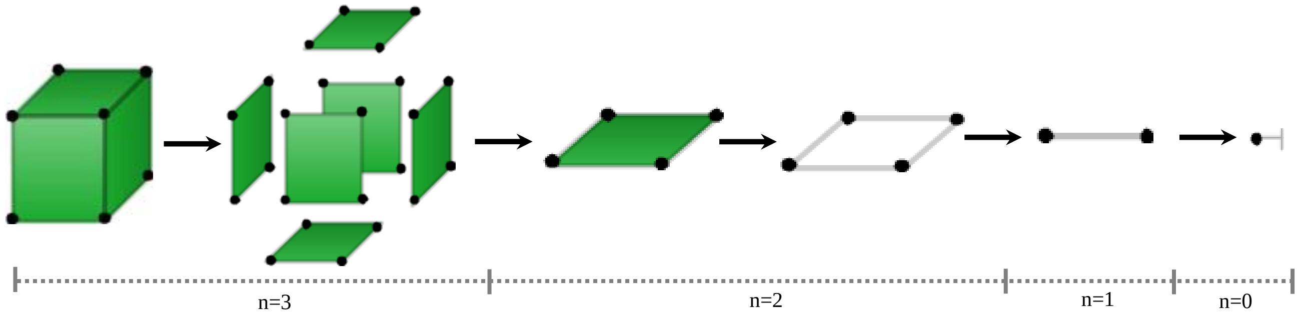

Fig. 1. Decomposition of a cell's geometric shape

In this study, the three-dimensional generalized maps (3-Gmaps) are introduced to restrict these uniform "half-edge" units. This theory is a boundary representation method proposed by Lienhardt based on combinatorial maps [12][13]. 3-Gmaps is a group of operators to define a set S : G =(S , α_0 , α_1 , α_2 , α_3), where the set is comprised of the smallest topological units - "half-edges". As shown in Fig. 2, two "half-edges" are labeled as {1, 2}. If in the zero-dimensional space, $<\alpha_i>(1)=1$ and $<\alpha_i>(2)=2$, then we can say that 1 and 2 are fixed points. If in the one-dimensional space, $<\alpha_j \circ \alpha_i>$ (1)=2, $<\alpha_j \circ \alpha_i>(2)=1$, where $0 \le i \le i+2 \le j \le 3$, then the involution relationship between 1 and 2 can be established by stitching them into an edge.

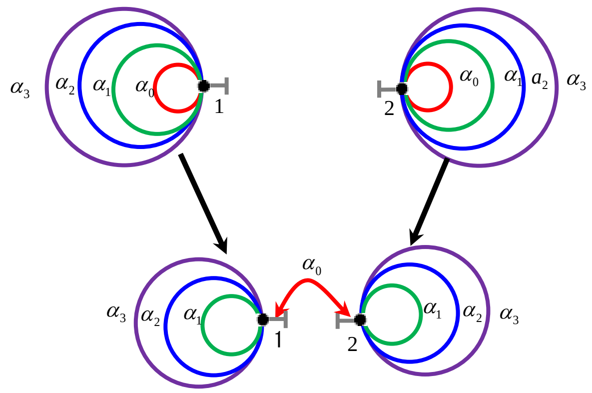

Fig. 2. Topological generation of an edge in one-dimensional space

The steps pertaining to computer geometric modeling of plant cell shapes are as follows: first, the "half-edge" units that are required should be saved, the number of which is 48 in this study; then, the four operators, α_0, α_1 , α_2 and α_3, are defined to restrict the 48 "half-edges" in order for them to be combined into 8 vertexes, 12 edges and 6 faces of the geometric shape of a plant cell, with each vertex being formed by 6 "half-edge" structures. The topological retrieval algorithms are based on the "half-edge" units with a given starting location, and iterate relevant connected components of the 3-Gmpas structure using the $<\alpha_j \circ \alpha_i>$ cyclic combinatorial operators.

B. Data structure and algorithms design

For data description of the geometric shape of a plant cell, as shown in Fig. 3, data structures for topological units, including the vertex, edge, and face, are established respectively. Specifically, the data structures of vertexes include 8 components, with the first three components being the coordinates of a vertex in the Euclidean space. To facilitate the subsequent introduction of computational fluid dynamics (CFD), it is advisable that the three components are expressed in the cylindrical coordinate system. The fourth component is a vertex pointing to the edge topology. Components 5 through 8, denoted by *alpha 0* – *alpha 3*, are fixed points or involution operators. They are used to combinatorially generate the topology of spaces in different dimensions; the data structure of an edge topology includes pointers pointing to the face topology and to the vertex topology. The data structure of a face topology is comprised of only pointers pointing to the edge topology.

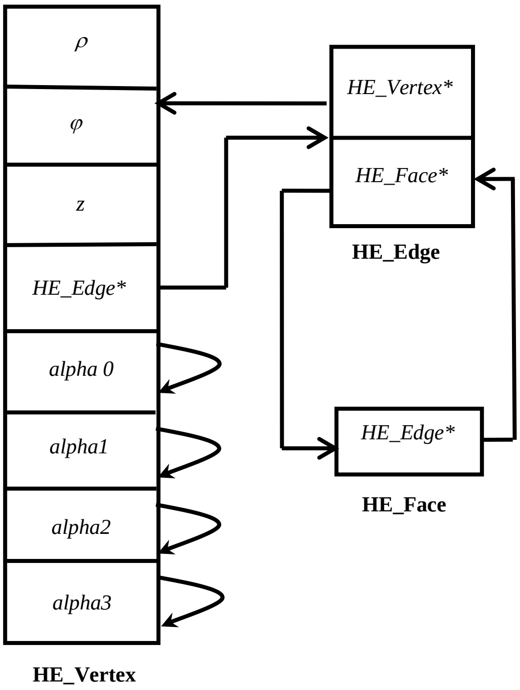

Fig. 3. Logic structure of data description

For the process to create the topology of the plant cell shape, see Fig. 4.

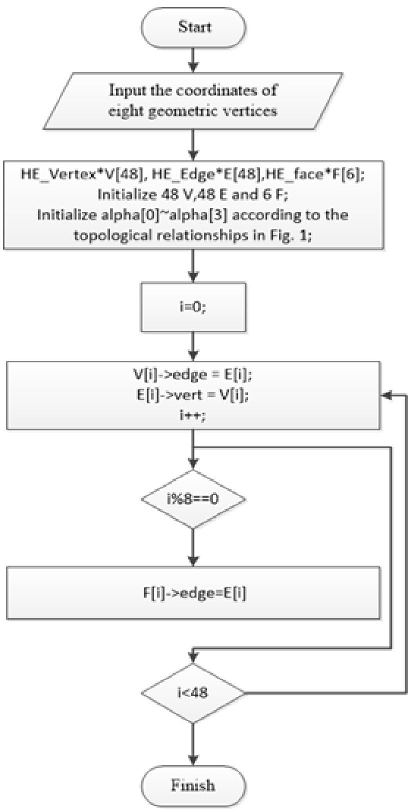

Fig. 4. Process of creating topological relationships

IV. Results and Discussion

Three functions, namely ***findVextex****(Vector<float> cont, int nv)*, ***findEdge****(Vector<float> cont, int ne)*, ***findFace****(Vector<float> cont, int nf)*, are defined using the C++ programming Language, where the variable *cont* is used to save the data of Vertex Shader of VBO in the OpenGL, and variables of *nv*, *ne* and *nf* are index values that should be put in when inquiring a vertex, an edge or a face. The vertex query process based on the given geometric modeling is presented by Algorithm 1.

Algorithm 1. Retrieve a vertex

Input: Vector<float> *cont*, **int** *nv*;
Output: *cont*;
1. Initialize: *i*=0;
2. *nv*=*nv** 6 – 1;
3. **while** *i* **less than** 48
4. if **V**[*nv*] **is equal to V**[*i*]
5. **Replace** the color value of the vertex with red color in *cont*;
6. *i*=*i*+1;

Specifically, step 2 of Algorithm 1 transforms the *nv*-th vertex entered by the user into the "half-edge" label in the cell data structure. An edge query process is presented by Algorithm 2.

Algorithm 2. Retrieve an edge

Input: Vector<float> *cont,* **int** *ne*;
Output: *cont*;
1. Initialize: *i*=0;
2. *ne*=*ne**4 –1;
3. **while** *i* **less than** 48
4. if **E**[*ne*]->vertex->*alpha 0*->edge **is equal to E**[*i*]
5. **Replace** the color value of the edge with
6. red color in *cont*;
7. *i*=*i*+1;

The face query process is presented by Algorithm 3:

Algorithm 3. Retrieve a face

Input: Vector<float> *cont*, **int** *nf*;
Output: *cont*;
Initialize: *i*=0;
nf=*nf**6 –1;
while *i* **less than** 48
  if **F**[*nf*]->edge->vertex->*alpha 0*->*alpha 1*->face **is equal to E**[*i*]
    Replace the color value of the face with red color in *cont*;
  i=*i*+1;

In regular scenarios, the time complexity of the 3 query algorithms stated above can be retained to O(n). The query results will be highlighted via the OpenG L3.3 graphics library, as shown in Fig. 5. Presented from left to right are the original cell structure, the vertex query result for the 2-nd vertex, the edge query result for the 2-nd edge and the face query result for the 2-nd face, respectively.

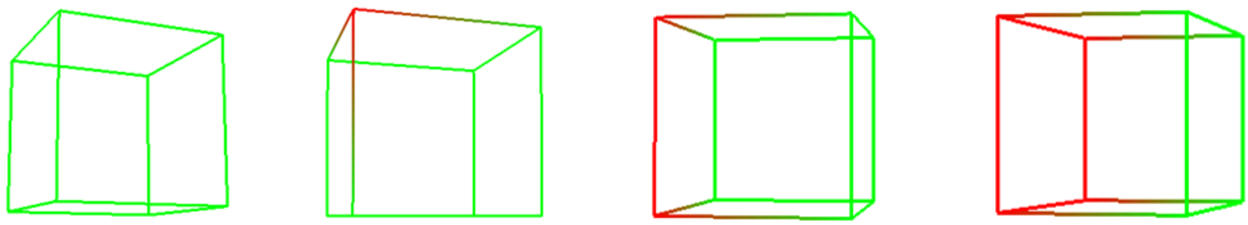

Fig. 5. Rendering results

V. Conclusion

1) Topology-based geometrical shape modeling of plant cells allows users to freely inquiry arbitrary units of a geometric model.

2) The n-dimensional generalized maps enable the description of the topology of plant cell shapes in a uniform way, providing convenience for subsequent model maintenance.

3) Using a hollow cuboid to simulate the shape of plant cells facilitates the introduction of force analysis given its regular quadrilateral structure.

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