Fast Construction of Plant Architectural Models Based on Substructure Decomposition

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Abstract Plant structure, representing the physical link among different organs, includes many similar substructures. In this paper, a new method is presented to construct plant architectural models of most plant species. The plant structure is decomposed into a stem, a set of lateral substructures and a terminal substructure, which is called substructure decomposition; then based on substructure decomposition, the plant structures are expressed in an iterative way; and further the derivative formula is employed to compute the number of organs in plant structures to get the geometrical sizes of 3D plant organs by borrowing Hydraulic Model. Using 3D organs, a substructure library is built. Based on the substructures stored in substructure library, one can construct 3D plant structure according to certain topological and geometrical rules. The experiments with different plant species are included in this paper to demonstrate the validity of the new method for constructing plant structures. The experimental results show that the approach follows botanical knowledge with high efficiency in constructing plant structures of most plant species. In addition, this method enables users to check the detail information of plant structure.

Keywords plant structure, substructure decomposition, fast construction, architectural model

1 Introduction

Among the applications of computer graphics, plant is one of the most complex natural objects for modeling and visualization. The main difficulties in plant modeling and visualization arise from the requirement of modeling generality, visualizing rapidity, implementing simplicity and visual reality.

Up to now, many methods have been proposed for plant modeling and visualization^[1-5]. The famous plant models include $\text{Fractal}^{[6]}$, L-System^[7], and Automaton^[8]. Fractal Theory^[9-11], originally presented by Mandelbrot in 1982, aims at generating plant-like models by adopting self-similarity among natural phenomena such as mountains, clouds, plants and so on. Soon after, Fractal models found an application in creating a wide variety of the shapes found in nature. The leaf of ferm

is a famous example of the application of fractals. However, it is very difficult to establish the function to represent the self-similarities existing in different phenomena. Meanwhile, the objects created by using Fractal models look unnatural. Lsystem^[7] was introduced by Aristid Lindenmayer, and then developed by Prusinkiewicz and many other scientists [12-14]. L-system is a string rewriting system. The initial state is a seed expressed as a string of characters, and then a set of rules are adopted to substitute characters or strings in an iterative way. After a given number of iterations, the string which represents plant shape can be produced. For the visual plant, the string, an invisible module, needs to be converted into a visible one. Since 3D structures are represented in 1D string symbols, it is difficult to know what a string creates in L-System. In addition, it is not so easy to find a language to create a string in certain order. Note

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that both L-system and Fractal are recursive approaches, and they need to integrate plant genetic rules in order to simulate plant-growing process from botanical point of view. Automaton Theory^[8] proposed by Philippe de Reffye is an influential botanically inspired model for procedure plant generation. As described in Automaton theory, different organs are formed from meristems, i.e., the undifferentiated plant tissue from which new cells are formed and new organs (internodes, leaves, flowers) are created, as found at the top of stem or root, and thus plant undergoes different intermediate states from an initial leafy state to a final flowering state. The transition laws from a state to another are deduced from the empirical data of real plants. By specifying a small number of parameters, a wide variety of different plant species^[15] can be modeled. Based on Automaton theory^[8] the traditional way to construct plant structure is internode by internode^[16-19]</sup>. Fig.1 illustrates the constructing process of plant structure by using the method of internode by internode. From Fig.1, we can see that the number of operation steps required by the method of internode by internode for plant structure construction is equal to the number of internodes or organs embodied in the corresponding plant. However, as we know, plant may be easily characterized by hundreds of thousands of leaves. internodes or fruits, and thousands of branches, branchlets, and stems oriented in complex directions. It is very time consuming to build even a medium-sized plant structure with the method of internode by internode. Note that there exist identical subparts (defined as substructures in this paper) such as branches in an individual plant, so it is unnecessary to repeatedly compute or construct each similar subpart internode by internode, and it seems reasonable to decompose plant structure into a stack of different subparts, which is named as plant substructure decomposition in this paper, and each subpart only needs to be called once during the constructing process. Obviously, it will take less time to regard plant as a stem and a set of subparts than to regard plant as a set of internodes in building plant structure.



Fig.1. The traditional method of plant structure construction — internode by internode.

In this paper, based on plant substructure decomposition, we propose a new method for fast construction of plant structures with high fidelity to the botanical nature. We decompose plant structure into a stem and a set of substructures from its top to bottom in an iterative way. By substructure decomposition, we can obtain the number of organs in plant structure at different growing stages, which will be used in Hydraulic Model^[17] to compute the geometrical sizes of these organs. Finally, according to the geometrical information of these organs and the relative positions among the substructures, we build 3D plant structure. Some results are given by using the new method, which demonstrate that our method, to a great degree, keeps to botanical knowledge and has high efficiency in plant modeling and plant structure construction.

The rest of this paper is organized as follows. Section 2 briefly illustrates some definitions involved in this paper. Section 3 describes how to represent plant structure and substructures, and compute the number of organs in them by using the new method based on substructure decomposition. Section 4 shows how to build plant structure based on the substructure instances obtained from the process of substructure decomposition. Some results and the comparison between the new method and the traditional method of internode by internode are given in Section 5. The final conclusions are presented in Section 6.

2 Related Definitions

In order to understand well the new method, first we give the related definitions as follows^[17-20].

2.1 Metamer and Growth Unit

According to measurement and observation, plant can live through some very different metamorphosis stages. During each stage, the meristem appears by a Growth Unit which consists of one or several metamers. A metamer is made of an internode with several buds at its top (without buds in the case of death). According to their functions, the buds can be classified into: apical bud, which can add a new metamer on the top of the internode with the growth in the direction of the stem; flowering or leafy bud, which can generate flowers (fruits) or leaves; lateral bud, which is able to generate new branches, thus starts the branching process. Generally, every leafy bud occurs with a lateral bud and/or apical bud during plant growth.

2.2 Physiological Age (PhA) and Chronological Age (ChA)

In our method, we use Physiological Age (PhA) to describe different metamorphosis stages, and Chronological Age (ChA) to represent real plant growing time, which is discrete in Growth Cycles (such as years, months, and days) to monitor automaton production.

2.3 Microstate and Macrostate

Corresponding to Metamer and Growth Unit, we define microstate and macrostate in terms of PhAs. A microstate is a metamer, and we regard its PhA, say p, as that of the internode contained in it. The PhA of the lateral bud, say q, is assumed to be greater than that of its parent internode in the same microstate, i.e., q > p. One or several microstates of PhA p appearing in one growth cycle form one macrostate of PhA p. In Fig.2, the upper pictures are microstates and macrostates, and the lower ones are the corresponding metamers and Growth Units. We assume that all the microstates in one macrostate appear in a particular order. Usually the microstates without lateral buds first appear in series, and then the other microstates in series and in the descending order from the ones with lateral buds of the maximum PhA to the ones with lateral buds of the minimum PhA, i.e., PhA 1, if they exist. Therefore, for a given plant with mPhAs, there will be $\frac{(m+1)(m+2)}{2} = \sum_{i=1}^{m+1} i$ possible microstates.



Fig.2. Microstate, macrostate, metamer and GU. (a) Microstate, metamer. (b) Macrostate, GU.

2.4 Structure and Substructure

Different plant organs constitute plant structure according to certain topological and geometrical information of the plant. Substructure is a part of the corresponding structure. Substructure and structure are a pair of relative terms. According to PhAs

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of microstate or macrostate, different substructures can be identified from the main plant structure. The smallest substructure can be one macrostate. During plant growing process, the macrostate of a certain PhA, say p, may be repeated for given times (the number of macro-states) until the apical bud germinates another macrostate of a different PhA. say v (v > p), which will start another similar growing loop and generate another substructure called terminal substructure, or until the apical bud dies. And that builds up the bearing axis of PhA p. The whole or part of the bearing axis corresponds to the stem in real plant. Meanwhile, the lateral buds along the bearing axis will grow into a set of substructures of different PhAs, say q (q > p), which are called lateral substructures, or branches in real plant. We can use Automaton^[8] to monitor the forming process of plant structure. Fig.3 shows the Automaton representation of a plant with 3 PhAs.



Fig.3. The automaton representation of a simple plant with 3 PhAs.

In Fig.3, we use different patterns to represent the organs of different PhAs. As shown by the Automaton in Fig.3, there are three kinds of microstates in one macrostate of PhA 1: one without axillary bud, one with 1 axillary bud of PhA 2, and another one with 1 axillary bud of PhA 3. Such a macrostate is repeated for 3 growth cycles. After 3 growth cycles, the bearing axis of PhA 1 is built up, and the terminal substructure and meanwhile the lateral substructures germinate or grow. This finally generates the structure of PhA 1. Obviously, Automaton can monitor the forming process of not only the structure but also the substructures. In Fig.3, the patterns on the top, from left to right, are respectively plant axis, which is formed by all the bearing axes of different PhAs growing in the direction of the bearing axis of PhA 1, substructure of PhA 3 at ChA 1, substructure of PhA 2 at ChA 3, and structure of PhA 1 at ChA 6.

2.5 Substructure Decomposition

According to the definitions of structure and substructure, we can easily decompose plant structure into a stem, a set of lateral substructures and a terminal substructure. This is the main idea of substructure decomposition expressed in this paper which is illustrated in Fig.4. In Fig.4, the plant has 4 PhAs, and grows through 9 growth cycles. The biggest structure on the left is the main structure of PhA 1. The right framework is the substructure library of PhAs 2, 3 and 4 after substructure decomposition. The structure in the first row is one substructure of PhA 2 at ChA 4, the ones in the middle are the substructures of PhA 3 at different ChAs, and the ones at the bottom are the substructures of PhA 4 at 1 or 2 ChAs.



Fig.4. Structure and substructure with 3 PhAs.

3 Representation of Plant Structures Based on Substructure Decomposition

Based on the definitions in Section 2, we introduce how to fast represent plant structures based on substructure decomposition. First, we introduce some notations used later. Consider a plant that is parameterized with m PhAs, and grows during t ChAs.

 S_p^i : The structure or substructure of PhA p $(1 \leq p \leq m)$ at ChA i $(1 \leq i \leq t)$.

 $U_p^i :$ The stem of the structure or substructure $S_p^i.$

 $n_{p,q}$: The number of lateral buds in one microstate of PhA p, which can generate branches of PhA q (p < q).

 $n_{p,q}^{I}$: The number of microstates that can generate branches of PhA q in one macrostate of PhA p (p < q); $n_{p,0}^{I}$ denotes the number of microstates without lateral buds that can generate lateral substructures in one macrostate of PhA p.

 u_p : The number of microstates contained in one macrostate of PhA p, and $u_p = n_{p,0}^I + \sum_{q=p+1}^m n_{p,q}^I$.

 N_p : The number of macrostates building the bearing axis of PhA p.

For a plant with m PhAs, its structure or substructure may contain the information of all the mPhAs. Therefore, in mathematical way, a structure or substructure S_p^i can be expressed as a row array with m elements $s_{p,q}^i$ $(p,q=1,2,\ldots,m)$. Here, the q-th element of the array represents the number of microstates of PhA q contained in the substructure S_p^i , and the elements with index q less than p are zero. For the consistency of representation, we express the stem of PhA p, i.e., U_p^i , as a row array with m elements $w_{p,q}^i$ too. The q-th element of the array means the number of microstates of PhA qcontained in the stem of PhA p. As known from the definitions in Subsection 2.4, only the p-th element $w_{p,p}^{i}$ is not equal to zero, and it is the product of the number of macrostates building the stem U_n^i and the number of microstates contained in each macrostate.

Below, we will introduce the new method based on substructure decomposition to represent plant structure and to compute the number of organs on the plant structure.

3.1 Ultimate Substructure S_m^i

According to the definitions given in Subsection 2.4, there is only the stem without branches in the substructure of PhA m, which is called ultimate substructure, so the representation of the substructures S_m^i (i = 1, 2, ..., t) can be expressed as:

$$S_m^i = U_m^i = \begin{cases} [0 \cdots i \cdot u_m \cdots 0]; & i \le N_m \\ [0 \cdots N_m \cdot u_m \cdots 0]; & i > N_m \end{cases}$$
(1)

3.2 Substructure S_p^i

As mentioned in Section 2, we can decompose plant structure into a stem, a set of lateral substructures and a terminal substructure if it exists. This can be represented in mathematical way as follows:

$$S_{p}^{i} = \begin{cases} U_{p}^{i} + \sum_{q=p}^{m} \sum_{k=1}^{i-1} n_{p,q} \cdot n_{p,q}^{I} \cdot S_{q}^{k}, & i \leq N_{p} \\ U_{p}^{i} + \sum_{p=q}^{m} \sum_{k=i-N_{p}}^{i-1} n_{p,q} \cdot n_{p,q}^{I} \cdot S_{q}^{k} + S_{v}^{i-N_{p}}, \\ & i > N_{p} \end{cases}$$

$$(2)$$

In (2), U_p^i represents the stem,

$$U_p^i = \begin{cases} \begin{bmatrix} 0 & \cdots & i \cdot u_p & \cdots & 0 \end{bmatrix}, & i \leq N_p, \\ \begin{bmatrix} 0 & \cdots & N_p \cdot u_p & \cdots & 0 \end{bmatrix}, & i > N_p, \end{cases}$$

 $n_{p,q} \cdot S_q^k$ represents the set of lateral substructures, and $S_v^{i-N_p}$ represents the terminal substructure of PhA v (v > p). If v is equal to zero, $S_v^{i-N_p}$ should be ignored, which means that the last apical bud of PhA p dies, and cannot generate a terminal substructure. When p = 1, (2) is the expression of the main plant structure.

Note that (1) and (2) can not only represent plant substructure or structure at different ChAs S_p^i (i = 1, 2, ..., t) but also compute the number of organs O (O denotes internodes (I), leaves (L), and fruits (F) respectively) contained in S_p^i (i = 1, 2, ..., t) when u_p stands for the number of organs O contained in one macrostate of PhA p.

4 Plant Construction Based on Substructure Instances

Now, based on substructure decomposition, we get different plant substructures of different PhAs at different ChAs, which are then stored in substructure library. Combined with the geometrical sizes of plant organs computed by plant Hydraulic Model^[17] and the relative positions of the substructures in the corresponding structure, we construct 3D plant structure from top to bottom by using the substructure instances stored in substructure library.

Fig.5 shows the construction process. First, from top to bottom, we build the substructures from those of the maximum PhA to those of the minimum PhA. Except for the substructure of the

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oldest PhA, all the other substructures may consist of the substructures of bigger PhAs. The substructures of bigger PhAs will be stored in the substructure library. When we build the substructure of smaller PhA, we only need to retrieve the substructures of bigger PhAs containing it from the substructure library, then according to botanical rules (phyllotaxy, branching angle, ...), rotate and translate them, and finally stick them to certain positions on the stem. In Fig.5, Substructures 3, 2 and 1 mean the substructures of PhAs 3, 2 and 1 respectively. The structure of PhA 1 grows through 10 growth cycles.



Fig.5. Plant visualization based on substructure instances.

Suppose the plant growing direction, i.e., the growing direction of the main bearing axis, is the positive direction of Z axis in 3D world coordinate system. Every organ is built in its 3D local coordinate system, and its physical origin is that of its 3D local coordinate systems. According to the botanical knowledge, the plant organs are located at different positions along the stem according to certain rule, which is called phyllotaxy. The angle between the neighboring organs of the same kind is named as phyllotaxy angle, denoted as θ in our paper, and the angle between each organ and the stem is named as branching angle, denoted as ω . Therefore, we have the following equation to transform each organ from its local coordinate system to the world coordinate system:

$$\begin{bmatrix} X \\ Y \\ Z \end{bmatrix} = T_1 \cdot T_2 \cdot \begin{bmatrix} X_0 \\ Y_0 \\ Z_0 \end{bmatrix} + \begin{bmatrix} 0 \\ 0 \\ P_q^{k,r} \end{bmatrix}$$
(3)

Here, $[X \ Y \ Z]^{\mathrm{T}}$ and $[X_0 \ Y_0 \ Z_0]^{\mathrm{T}}$ are the final and initial coordinates of the inserted organs or lateral substructures; T_1 and T_2 are transformation matri-

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ces:

$$T_1 = \begin{bmatrix} \cos \omega & -\sin \omega & 0\\ \sin \omega & \cos \omega & 0\\ 0 & 0 & 1 \end{bmatrix},$$

and

$$T_2 = \begin{bmatrix} 1 & 0 & 0 \\ 0 & \cos\theta & \sin\theta \\ 0 & -\sin\theta & \cos\theta \end{bmatrix}$$

 $P_q^{k,r}$ is the position of the r-th $(1 \leq r \leq n_{p,q}^I)$ lateral substructure S_q^k in one macrostate of PhA p along the stem of S_p^i , which depends on the length of the internodes below the inserting point along the stem. We can determine $P_q^{k,r}$ by the following formula:

$$P_q^{k,r} = \sum_{j=i}^{k+2} (u_p \cdot H_{p,j}^I) + \left(\sum_{d=q+1}^m 1 + n_{p,0}^I + r\right) \cdot H_{p,k+1}^I$$
(4)

Here, $H_{p,j}^{I}$ is the length of the internode of PhA p appearing at ChA j on S_{p}^{i} .

5 Results

We have explored how to construct a 3D plant by using the new method presented in the above sections. We apply this new method to some plant models defined by botanist^[15], and obtain some results (see Figs.6, 7 and 8). Figs.6(a), (b) and (c) are the structure and substructures of Leeuwenberg^[15] plant with 7 PhAs. (a) is the main structure of PhA 1 at ChA 7, (b) is the substructure of PhA 3 at ChA 5, and (c) is the substructure of physiological 6 at ChA 2. The main structure and substructures of Rauh model^[15] with 4 PhAs are given in Fig.7. In Fig.7, (a), (b), and (c) are the main structure of PhA 1 at ChA 10, the substructure of PhA 2 at ChA 6, and the substructure of PhA 3 at ChA 3 respectively. The structure and substructures of a 3D Rauh plant^[15] with 3 PhAs are shown in Fig.8.

Table	1.	Efficiency	Comparison
	(C	PU time, se	conds)

(Or o time, seconds)			
Branch	Substructure	Internode by	
order	decomposition	internode	
1	0.1	3.3	
2	0.3	437.2	
5	0.7	4,743.0	

We make comparison between the new method and the traditional method of internode by internode^[16-19]. Table 1 gives the consumed time for different plant simulations with different branch orders by using these two methods. (Here, branch order means branch density and depth. If there is only the stem, the level of branch order is 0; if branches are directly born from the buds on stem and no more branchlets on them, the branch order is 2, and so on. For example, the branch orders of the plants in Figs.6, 7 and 8 are respectively 6, 3, and 2. The figures in Table 1 were obtained on an SGI O2 computer and the CPU time is expressed in seconds. We applied the new method to a 35-year-old pine tree, which only cost 2 minutes instead of 2 hours with the method of internode by internode^[16-19].



Fig.6. Skeletons of structures and substructures for Leeuwenberg model^[15]. (a) Main structure. (b) Substructure S_3^5 . (c) Substructure S_6^2 .



Fig.7. Skeletons of structures and substructures for Rauh model^[15]. (a) Main structure. (b) Substructure S_2^6 . (c) Substructure S_3^3 .



Fig.8. Structures and substructures of a 3D plant. (a) Main structure. (b) Substructure S_2^7 . (c) Substructure S_3^3 .

6 Conclustions

In this paper, we present a new method to construct 3D plants. Compared with L-system, Fractals and other plant modeling techniques [1-5], since the new method is based on Automaton theory^[8], it is more faithful to the botany. In addition, compared with the internode by internode method [16-19], the new method avoids repeatedly computing the same or similar parts in plant structure, and therefore can save a lot of time in computing the number of organs and constructing plant structures. The results in Section 5 show that the new method presented in this paper is highly efficient for plant modeling with high complexity. The more complex the plant structure is, the more efficient the new method is. Moreover, the new method enables us to separately display any substructures of a given PhA at a given ChA, which is very convenient to check the details of each part of 3D plant structure. Finally, the new method can be generalized to most plant species defined by botanists^[15].

To simulate natural phenomena during plant growing process and satisfy the requirement of agronomy in a qualitative and quantitative way, some other techniques such as Hydraulic Model, stochastic model, root system and environmental parameters are introduced into our system by taking the advantage of the high efficiency of the new method presented in this paper. Related work has already been published^[20,21] or will be introduced in the later papers.

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YAN H P et al.: Substructure-Based Plant Construction

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