

# FAST ALGORITHMS OF PLANT COMPUTATION BASED ON SUBSTRUCTURE INSTANCES<sup>1</sup>

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## ABSTRACT

Fast rendering and botanically faithful description of plants are a real challenge in computer graphics. Usually, plant production is computed using the method internode by internode, while there exist a lot of buds in an individual tree, therefore, this approach is quite time-consuming even for a medium-size tree.

In this paper, we present a new algorithm based on substructure instances to quickly compute plants' production, and then, for certain plant architectural models, combine with the geometrical rules to create a substructure library. Finally, we construct 3D virtual plants using 3D organs. Compared with the classical method in computing and constructing plant structures, the algorithm described in this paper is much faster while keeping botanical nature of plant. The algorithm can be generalized to most plant species.

**Keywords:** Plant, Substructure, Fast algorithms

## 1. INTRODUCTION

Natural objects, especially plants, generally exhibit very irregular, highly complex geometry and properties. In nature, there are many kinds of plant species, and each plant species may have different shapes. In a landscape, among plant population, one may find hundreds of trees, billions of grass and flowers. Each tree can contain thousands of leaves, internodes and branches, so it may cost reasonably long time to compute plant production and get realistic images of one complex landscape. Green plants offer an attractive and challenging object for computer graphics. Moreover, the increasing demand of scientific research, education and business for high realistic and real time plants' representation urges to define new methods and tools.

Many scientists have made great efforts in this field. Fractals inspired by Mandelbrot [Mande77] provided a new scientific way to describe

nature. The idea of self-similarity is an obvious character of fractals. Since fractals are suitable to represent the similarity of natural objects, they are widely applied in a number of diverse fields by describing many of the irregular and fragmented patterns around us such as mountains, clouds, plants and so on. The leaf of fern is a famous example of the application of Fractal theory. The geometric notion of fractal self-similarity has become a paradigm in the real world. The concept of an *L-system*, developed in 1968 by Aristid Lindenmayer [Linde68], was initially used in the study of formal languages, but soon came to be recognized by Lindenmayer, Prusinkiewicz and many other scientists [Prusi93, 90, 88] as a mechanism for modelling various plant-like structures. 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 iterated rewriting way. After a given number of iterations, the desired plant's shape can be produced. The idea of repetition is inherent in L-

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systems, and so the geometric objects that result from application of an L-system have fractal properties. Adopting L-systems, Smith [Smith84] presented another modelling technique named graftals, which emphasised the detailed structure of only one individual plant. Both L-systems and Fractal need to integrate plant's genetic rules in order to simulate the plant's growing process from the botanical point of view. In 1970, botanist Halle [Halle70] defined more than 20 kinds of botanical architectural models, which described plant genetic rules, i.e. bud functioning, branching pattern, and death process that produce the particular botanical branching organisation. Based on these models, De Reffye provided automaton theory [Deref88, 90, 97], which is faithful to Botany. Subsequently, scientists in CIRAD [Blaise98] applied Automaton theory to develop AMAP software. Zhao [Zhao 01] improved this method as dual-scale automaton. Both methods can simulate plant-growing process in discrete way. It thus needs a long time to construct even an individual plant structure.

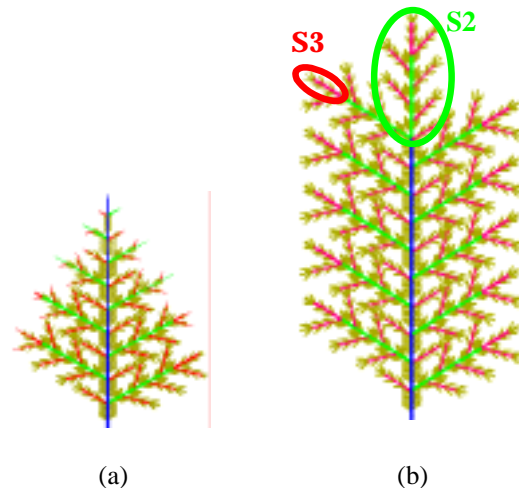
This new method introduced in this paper can meet the following criteria:

- Faithful to nature;
- Highly efficient algorithms to compute plant production, including geometry for visualisation;
- To produce various species of plant.

The basic idea of this method is to recursively decompose one part of the plant (structure) into a set of similar subparts (substructures). A substructure library is therefore built up from top to bottom (i.e. from the end of the trunk to its base, or from the simplest substructures to the most complex) in a substituting way. When we construct the main structure, we only need to retrieve and then paste the corresponding substructures from the substructure library. There is thus no need to repeatedly compute each substructure internode by internode. In Fig. 1, there are 11 instances of the same substructures S2 and 76 instances of S3 in the main structure S1, and 6 instances of S3 in S2. So, the method internode by internode needs about 76 operations, while the new method only requires about 12 operations. In this paper, we will introduce the new method in detail, give some results, and make comparison between the new method and the method internode by internode.

This paper consists of five sections. The first section is a brief review about plant modelling. The second one defines some basic botanical notions, and meanwhile introduces automaton theory briefly. In Section 3 and 4, we describe our novel algorithm

to construct plant structure by substructure decomposition in detail. The conclusions are included in the last section where we will discuss the efficiency of the new method presented in this paper, point out the limitation of this method, and put forward our further work.

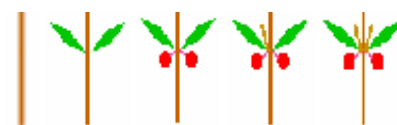


(a) Growing structure 1  
(b) Complete structure 1

## 2. AUTOMATON THEORY AND SUBSTRUCTURES

### 2.1 Some basic botanical notions

According to botanical measurements, a plant bears different growing stages through different meristem actions.






(a) without buds;  
(b) with two leaves and one apical bud;  
(c) with two leaves, two fruits and one apical bud;  
(d) with two leaves, two fruits one apical bud and one axillary bud;  
(e) with two leaves, two fruits one apical bud and two axillary buds

Meristem is basic unit of plant from which new cells are formed and new organs (internodes,

leaves, flowers) are created, as found at the top of a stem or root. These meristem events consist of making new metamers in an apparently irreversible order from the seed to the final plant. A metamer is made of an internode with several buds at its top (without buds in the case of death) (Fig. 2). During each growing interval, the bud sets up one Growth Unit (G.U.). According to their functions, the buds can be classified into three kinds: the apical bud, which adds a new metamer on the top of the internode and thus induces the growing process along the stem; the flowering bud which generates flowers (fruits); the last one is the axillary bud which is able to generate new branches, thus induces the branching process. It is a botanical problem to identify the distribution law of the number of nodes built along the life of a bud and the quantity of each bud ramification. It can be observed that the quantity and quality of a bud's production is varying along its life. That leads to a metamorphosis process.

## 2.2 Automaton theory and substructure

Using Automaton theory, we can simulate the above botanical function. Now, we briefly illustrate the working process of Automaton theory. First, we introduce physiological age to distinguish different metamorphosis stages. Then we use chronological age to represent the real plant growing time, which is expressed in a discrete way in terms of growth cycles (such as years, months, and days) according to plant species and observation. During one growth cycle, the meristem generates one growth unit (G.U. or macrostate) that consists of at least one metamer, also named microstate. All the microstates in a macrostate appear in a particular order. Usually the microstates without axillary buds first appear in series, then the microstates with axillary buds of the maximum physiological age, and then the other microstates appear in series in descending order of the physiological ages of their axillary buds until the macrostate is finished. This phenomenon is called Acrotony. The macrostate of a particular physiological age can be repeated several times, which build up a bearing axis of the current physiological age; then the apical bud will continue its growing process into another kind of macrostate, the physiological age of which is greater than that of its progenitor, and thus another similar growing loop will begin (or die, if without apical bud).

Fig. 3 shows us a plant with 3 physiological ages, which is described in automaton, each kind of square corresponding to one physiological age, i.e.:  stands for physiological age 1,  for physiological age 2,  for physiological age 3. In the macrostate of physiological age 1, there are three kinds of microstates: 3 repetitions of a microstate with 2 leaves and without axillary bud, 2

repetitions with 2 leaves, 2 flowers (fruits) and 1 axillary bud of physiological age 2, 1 repetition with 2 leaves, 2 flowers (fruits) and 2 axillary buds of physiological age 3. 3 repetitions of such a macrostate build up one bearing axis of physiological age 1.

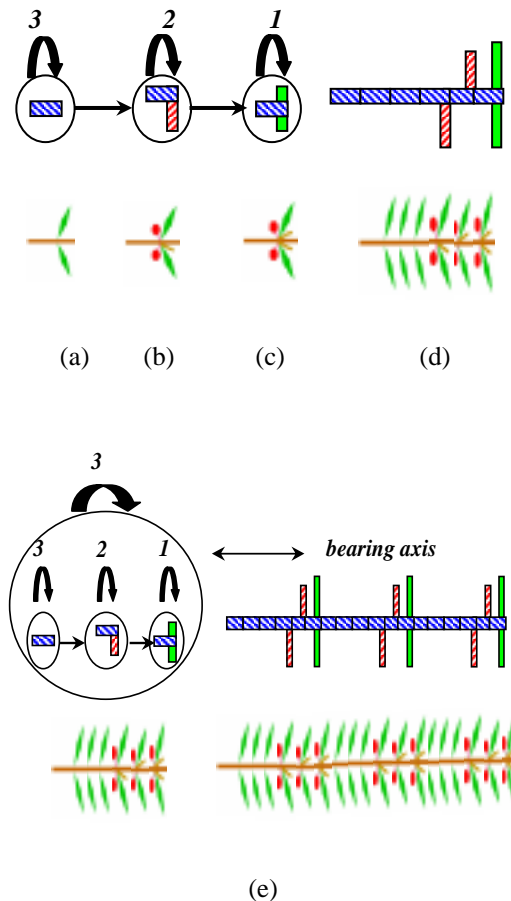


Figure 3: Plant with 3 physiological ages.  
 (a), (b) and (c) metamers;  
 (d) one macrostate;  
 (e) bearing axis

All of such successive bearing axes, which satisfy the metamorphosis rules among all the physiological ages, form the whole plant axis. Each structure is composed of an original bearing axis and a set of branches (lateral substructures), and ended in extension by a terminal substructure. Substructure is an element relative to the whole structure. The smallest substructure can be one growth unit. Let  $k$  be the physiological age of the bearing axis; we call the main structure 'structure  $S_k$ '. We assume that the physiological ages of all the lateral substructures are greater than that of the original bearing axis.

The plant in Fig. 4 has 3 physiological ages, 10 growth cycles aged. A particular botanical

architecture with main structure and substructures is translated into automaton language.

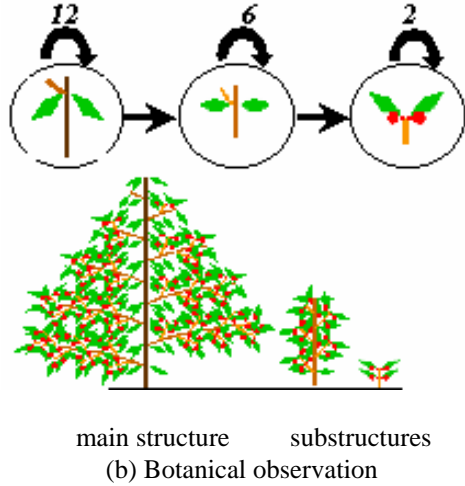
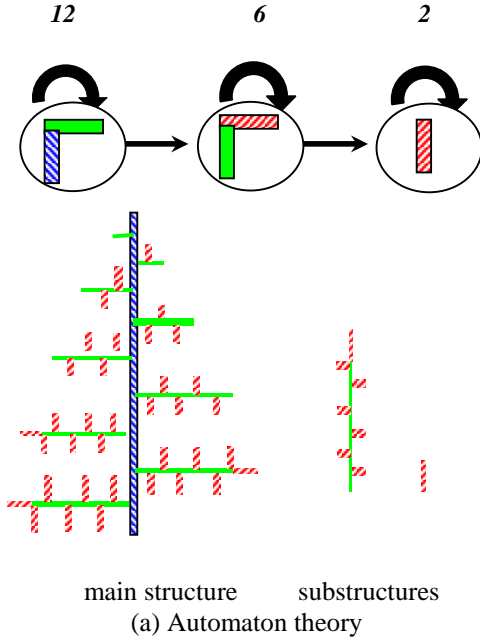


Figure 4: Automaton plot and botanical observation of a plant of 3 physiological ages, 10 growth cycles aged

Now, consider a plant that is parameterised with  $m$  physiological ages, and grows during  $t$  chronological ages; thus the main structure originated from physiological age 1, called  $S_1^t$ , is composed of a bearing axis  $BA_1^t$  and a set of substructures  $S_p^i$  generated along the bearing axis. The substructure  $S_p^i$  is started from physiological age  $p$  ( $1 \leq p \leq m$ ) and generated at chronological

age  $i$  ( $1 \leq i \leq t-1$ ). In mathematical way, a structure is an array with  $m$  fields  $s_{p,q}$  representing the number of internodes of physiological age  $q$  borne by a structure of physiological age  $p$ , ( $p, q=1, 2, \dots, m$ ). The fields with index less than  $p$  are null (i.e. a borne axis cannot be physiologically younger than its bearer). Let  $n_{p,q}$  be the number of axillary buds in a G.U. of physiological age  $p$ , which can generate branches of physiological age  $q$ ;  $u_k$  is the number of microstates contained in a macrostate of physiological age  $k$ . For a given  $m$ , there might be  $\frac{(m+1)(m+2)}{2} = \sum_{i=1}^{m+1} i$  possible microstates.

### 3. DESCRIPTION OF THE PLANT PRODUCTION ALGORITHM

#### 3.1 Plants with infinite growth

If the number of macrostate repetitions along the bearing axis  $N_p$  approaches infinite, i.e.  $N_p \rightarrow \infty$  ( $p=1, 2, \dots, m$ ), we can use the following formula to compute plant production.

For the structure of physiological age  $m$ , the initial state  $[S_m^1]$  is:

$$[S_m^1] = [u_m] = [0 \quad 0 \quad \dots \quad 0 \quad u_m] \quad (1)$$

And the intermediate states can be expressed as:

$$[S_m^t] - [S_m^{t-1}] = [u_m] = [0 \quad \dots \quad 0 \quad u_m] \quad (t > 1) \quad (2)$$

From Eq.1 and Eq.2, we can obtain the production of every substructure of physiological age  $m$ .

For the substructures of physiological age  $k$  ( $k=1, 2, \dots, m-1$ ), the production of all the substructures can be computed using Eq.3 and Eq.4:

$$[S_k^1] = [u_k] = [0 \quad 0 \quad \dots \quad 0 \quad u_k] \quad (3)$$

and

$$[S_k^t] - [S_k^{t-1}] = [u_k] + \sum_{j=k+1}^m n_{k,j} [S_j^{t-1}] \quad (t > 1) \quad (4)$$

Considering a system with 3 physiological ages, we have:

$$\begin{bmatrix} [S_3^t] \\ [S_2^t] \\ [S_1^t] \end{bmatrix} = \begin{bmatrix} 0 & 0 & u_3 \\ 0 & u_2 & 0 \\ u_1 & 0 & 0 \end{bmatrix} + \begin{bmatrix} 1 & 0 & 0 \\ n_{2,3} & 1 & 0 \\ n_{1,3} & n_{1,2} & 1 \end{bmatrix} \begin{bmatrix} [S_3^{t-1}] \\ [S_2^{t-1}] \\ [S_1^{t-1}] \end{bmatrix} \quad (5)$$

This is a recurrent system.

Each of the substructures  $[S_3^i], [S_2^i], [S_1^i]$  ( $i=1,2,\dots,t$ ) has 3 fields:

$$[S_1^t] = [s_{1,1} \quad s_{1,2} \quad s_{1,3}] \quad (6)$$

$$[S_2^t] = [s_{2,1} \quad s_{2,2} \quad s_{2,3}] \quad (7)$$

$$[S_3^t] = [s_{3,1} \quad s_{3,2} \quad s_{3,3}] \quad (8)$$

And we can define a 3\*3 matrix  $[\Sigma]$ , which contains all the information about the designated plant structure at chronological age  $t$ :

$$[\Sigma]_t = \begin{bmatrix} s_{3,1} & s_{3,2} & s_{3,3} \\ s_{2,1} & s_{2,2} & s_{2,3} \\ s_{1,1} & s_{1,2} & s_{1,3} \end{bmatrix}_t = \begin{bmatrix} 0 & 0 & s_{3,3} \\ 0 & s_{2,2} & s_{2,3} \\ s_{1,1} & s_{1,2} & s_{1,3} \end{bmatrix}_t \quad (9)$$

( $s_{i,j} = 0$  if  $i > j$ )

The recurrent formula can be written as the Matrix system:

$$\begin{bmatrix} 0 & 0 & s_{3,3} \\ 0 & s_{2,2} & s_{2,3} \\ s_{1,1} & s_{1,2} & s_{1,3} \end{bmatrix}_t = \begin{bmatrix} 0 & 0 & u_3 \\ 0 & u_2 & 0 \\ u_1 & 0 & 0 \end{bmatrix} + \begin{bmatrix} 1 & 0 & 0 \\ n_{2,3} & 1 & 0 \\ n_{1,3} & n_{1,2} & 1 \end{bmatrix} \cdot \begin{bmatrix} 0 & 0 & s_{3,3} \\ 0 & s_{2,2} & s_{2,3} \\ s_{1,1} & s_{1,2} & s_{1,3} \end{bmatrix}_{t-1} \quad (t>1) \quad (10)$$

and

$$\begin{bmatrix} 0 & 0 & s_{3,3} \\ 0 & s_{2,2} & s_{2,3} \\ s_{1,1} & s_{1,2} & s_{1,3} \end{bmatrix}_1 = \begin{bmatrix} 0 & 0 & u_3 \\ 0 & u_2 & 0 \\ u_1 & 0 & 0 \end{bmatrix} \quad (t=1) \quad (11)$$

We can define the following Matrix:

$$[\Sigma]_t = \begin{bmatrix} 0 & 0 & s_{3,3} \\ 0 & s_{2,2} & s_{2,3} \\ s_{1,1} & s_{1,2} & s_{1,3} \end{bmatrix}_t \quad (12)$$

$$[U] = \begin{bmatrix} 0 & 0 & u_3 \\ 0 & u_2 & 0 \\ u_1 & 0 & 0 \end{bmatrix} \quad (13)$$

$$[N] = \begin{bmatrix} 1 & 0 & 0 \\ n_{2,3} & 1 & 0 \\ n_{1,3} & n_{1,2} & 1 \end{bmatrix} \quad (14)$$

The above particular system can be generalized to the plant with  $m$  physiological ages only by increasing the size of the matrices, so the production of the plant can be written in a simple recurrent formula:

$$[\Sigma]_t = [U] \quad (t=1) \quad (15)$$

and

$$[\Sigma]_t = [U] + [N][\Sigma]_{t-1} \quad (t>1) \quad (16)$$

After  $t-1$  iterations, Eq.15 and Eq.16 can be rewritten as Eq.17 and Eq.18:

$$[\Sigma]_t = t \cdot [U] \quad (t > 1, [N] = I \text{ or } t = 1) \quad (17)$$

and

$$[\Sigma]_t = [U] + [N]([U] + [N]([U] + \dots [N][\Sigma]_1)) \quad (t > 1, [N] \neq I) \quad (18)$$

Here,  $[\Sigma]_k$  ( $k=1,2,\dots,t$ ) is an  $m$ -by- $m$  matrix, and includes all the substructure instances contained in the main structure of physiological age 1 and  $k$  cycles aged. When  $[N]=I$ , there is only the trunk, no branches in the main structure.

### 3.2 Truncated plants with finite bearing axis and terminal substructures

Now, suppose that the number of macrostate repetitions for a given physiological age  $p$ ,  $N_p$ , is finite, i.e.  $N_p < \infty$  ( $p=1,2,\dots,m$ ) and after  $N_p$  chronological ages, the bud of physiological age  $p$  will metamorphose to physiological age  $n$  ( $n>p$ ). The structures of the maximum physiological age  $m$  bear no branches. So, we have:

$$[S_m^t] = [s_{m,1} \quad \dots \quad s_{m,k} \quad \dots \quad s_{m,m}]_t \quad (19)$$

$$= t \cdot [u_m] = [0 \quad \dots \quad 0 \quad \dots \quad tu_m] \quad (t \leq N_m)$$

and

$$[S_m^t] = N_m \cdot [u_m] = [0 \quad 0 \quad N_m u_m] \quad (t > N_m) \quad (20)$$

If  $t \leq N_{m-1}$ , the structures of physiological age  $m-1$  may bear branches (substructures of

physiological age  $m$ ) and the bearing axis of physiological age  $m-1$ , so we have:

$$[S_{m-1}^t] = t \cdot [u_{m-1}] + n_{m-1,m} \left( \sum_{i=1}^{t-1} [S_m^i] \right) \quad (t \leq N_{m-1}) \quad (21)$$

If  $t > N_{m-1}$ , along the trunk, the last microstate of physiological age  $m-1$  can metamorphose into microstates of physiological age  $m$ , i.e. there are branches, upper part of the trunk (terminal substructures of physiological age  $m$ ) and the bearing axis in the structure of physiological age  $m-1$  at chronological age  $t$ . So we have:

$$[S_{m-1}^t] = N_{m-1} \cdot [u_{m-1}] + n_{m-1,m} \cdot \left( \sum_{i=t-N_{m-1}}^{t-1} [S_m^i] \right) + [S_m^{t-N_{m-1}}] \quad (t > N_{m-1}) \quad (22)$$

Eq.21 and Eq.22 can be rewritten in an extended way:

$$\begin{aligned} & [s_{m-1,1} \quad \cdots \quad s_{m-1,m-1} \quad s_{m-1,m}]_t \\ & = t [0 \quad u_{m-1} \quad 0] \\ & \quad + n_{m-1,m} \sum_{i=1}^{t-1} [s_{m,1} \quad \cdots \quad s_{m,m-1} \quad s_{m,m}]_i \\ & (t \leq N_{m-1}) \end{aligned} \quad (23)$$

and

$$\begin{aligned} & [s_{m-1,1} \quad \cdots \quad s_{m-1,m-1} \quad s_{m-1,m}]_t \\ & = N_{m-1} \cdot [0 \quad \cdots \quad u_{m-1} \quad 0] + \\ & \quad n_{m-1,m} \cdot \sum_{i=t-N_{m-1}}^{t-1} [s_{m,1} \quad \cdots \quad s_{m,m-1} \quad s_{m,m}]_i \\ & \quad + [s_{m,1} \quad \cdots \quad s_{m,m-1} \quad s_{m,m}]_{t-N_{m-1}} \\ & (t > N_{m-1}) \end{aligned} \quad (24)$$

Similarly, we express the production of all the other structures of physiological age  $k$  ( $k=1,2,\dots,m-2$ ) at chronological age  $t$ :

$$[S_k^t] = t \cdot [u_k] + \sum_{i=1}^{t-1} \sum_{j=k+1}^m (n_{k,j} \cdot [S_j^i]) \quad (25)$$

$(t \leq N_k)$

If  $t > N_k$ , along the trunk, an apical terminal substructure of physiological age  $n$  is born, so we have:

$$\begin{aligned} [S_k^t] & = N_k \cdot [u_k] \\ & \quad + \sum_{i=t-N_k}^{t-1} \sum_{j=k+1}^m (n_{k,j} \cdot [S_j^i]) + [S_n^{t-N_k}] \end{aligned} \quad (26)$$

$(t > N_k)$

By extending way, Eq.26 can be expressed as Eq.27:

$$\begin{aligned} & [s_{k,1} \quad \cdots \quad s_{k,k} \quad \cdots \quad s_{k,m}]_t \\ & = t [0 \quad \cdots \quad u_k \quad \cdots \quad 0] \\ & \quad + \sum_{i=1}^{t-1} \sum_{j=k+1}^m n_{k,j} [s_{j,1} \quad \cdots \quad s_{j,k} \quad \cdots \quad s_{j,m}]_i \\ & (t \leq N_k) \end{aligned} \quad (27)$$

and

$$\begin{aligned} & [s_{k,1} \quad \cdots \quad s_{k,k} \quad \cdots \quad s_{k,m}]_t \\ & = N_k [0 \quad \cdots \quad u_k \quad \cdots \quad 0] \\ & \quad + \sum_{i=t-N_k}^{t-1} \sum_{j=k+1}^m n_{k,j} [s_{j,1} \quad \cdots \quad s_{j,k} \quad \cdots \quad s_{j,m}]_i \\ & \quad + [s_{n,1} \quad \cdots \quad s_{n,k} \quad \cdots \quad s_{n,m}]_{t-N_k} \\ & (t > N_k) \end{aligned} \quad (28)$$

### 3.3 Computation of the number of leaves and fruits

The above formulas only show how to calculate the number of internodes in the plant structure. Based on the number of internodes, the number of leaves and fruits for a given physiological age at certain growth cycle can be computed using Eq.29 and Eq.30:

if  $i \leq Tu - fO$

$$Nb - O_p^i = (S_p^i - S_p^{i-1}) \cdot \sum_{k=p}^{m+1} Nu - O_{p,k} / U_p \quad (29)$$

if  $i > Tu - fO$

$$Nb - O_p^i = (S_p^i - S_p^{i-Tu-fO}) \cdot \sum_{k=p}^{m+1} Nu - O_{p,k} / U_p \quad (30)$$

Where, 'O' represents different organs such as fruit (F), leaf (B), internode (I) etc.  $Nu - O_{p,k}$  means the number of leaves or fruits generated by a metamer of physiological age  $p$ , with buds of physiological age  $k$  ( $k=1,2,\dots,m$ ), or without buds ( $k=m+1$ ).  $Tu - fO$  means the functioning time of organs.

## 4. PLANT CONSTRUCTION BASED ON SUBSTRUCTURE INSTANCES

Using the above formulas, we can obtain plant production of different physiological ages at different chronological ages, and then according to the information, we can construct plant structures. In this section, we will introduce how to construct plant architecture based on substructure instances.

According to botanical measurements, we get the shape of 3D organs and the angles between bearing and borne branches. Now we dress 3D plant structures and substructures using existing 3D organs from top to bottom. First, we set up substructure library for every physiological age at every chronological age. The substructure of the



maximum physiological age  $m$  remains unbranched. So, except for the substructure library of the oldest physiological age, all the other substructures of younger physiological ages may be decomposed into one bearing axis and a set of substructures of older physiological ages. We construct a plant starting from the substructures of the oldest physiological age to that of the youngest physiological ages. In other words, we begin to construct the substructures of the oldest physiological age  $S_m^1 \rightarrow S_m^t$ , and set up substructure library of physiological age  $m$ , and then using the existing substructures, we dress the substructures of younger physiological age  $m-1$ :  $S_{m-1}^1 \rightarrow S_{m-1}^t$ . In a similar way, we can get all the substructures that build up the main structure  $S_1^t$ .

Since the corresponding substructures have already been stored in an existing substructure library of older physiological ages, we only need to put them together according to geometrical transformation matrices. The geometrical transformation matrices [Rober76] are obtained according to the phyllotaxy angle for rotation around the bearing axis, the branching angle for rotation around the secondary axis, and the position coordinates along the bearing axis for translation.

## 5. RESULTS AND CONCLUSIONS

In this paper, we present a new algorithm to compute plant production that allows constructing plant topological structures corresponding to different plant architectural models. This algorithm concerns all the plant architectural models and can bear geometric patterns and self-similarity, so the geometric objects that result from application of this algorithm have properties of both fractals and L-systems, and thus we can integrate fractal with L-system in our method.

Plant age	Substructures	Internode by internode
5 years	0.1 seconds	3.3 seconds
10 years	0.3 seconds	437.2 seconds
15 years	0.7 seconds	4743.0 seconds

Table 1: Efficiency comparison between both methods (Rauh Model, 4 physiological ages)

Using the algorithm, we can save time on computing plant production and thus constructing plant architectural models. By intuition, we can guess the complexity of the new method and the classical method, and explain timesaving without any proof. Let  $t$  be the plant age,  $n$  the average

number of microstates that can build up a macrostate,  $b$  the level of branching order. The new method then requires only about  $O(t.n.b)$  operations, while the method internode by internode could be accomplished with about  $O((t.n)^b)$  operations. It shows that the higher the complexity of the plant (i.e. branching density and depth) is, the more efficient the new method is. The values in Table 1 and the 3D Rauh model (Fig. 6) and Massart plant images (Fig. 7) were obtained on a SGI O2 computer and the CPU Time is expressed in seconds. Since the production doesn't include any stochastic processes, the results of designated plants are exactly the same with both methods.

Moreover, the new method enables us to separately display any substructures of a given physiological age at a given chronological age, so it is very convenient for us to check the detail of the 3D plant structure (Fig.5). It is impossible for us to do without the substructure library.

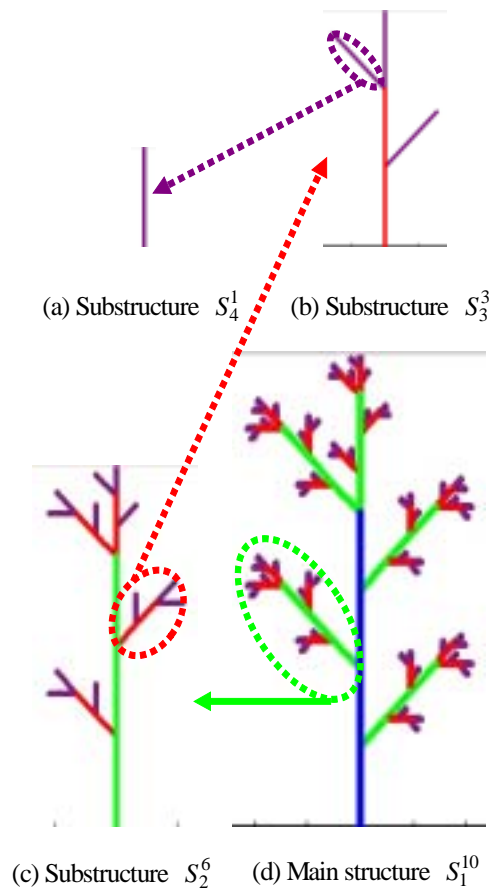


Figure 5: Substructure extraction and visualisation according to their physiological ages (Rauh model with 4 physiological ages)

Of course, there is still a lot of work to do. In order to simulate natural phenomena during plant growing process and satisfy the requirement of agronomy in a qualitative and quantitative way, some other techniques like hydraulic model, stochastic model, root system and environmental parameters will be introduced in the future by taking advantage of the high efficiency of the new method based on substructure instances.



Figure 6: 5-10 years-old Rauh model with 4 physiological ages

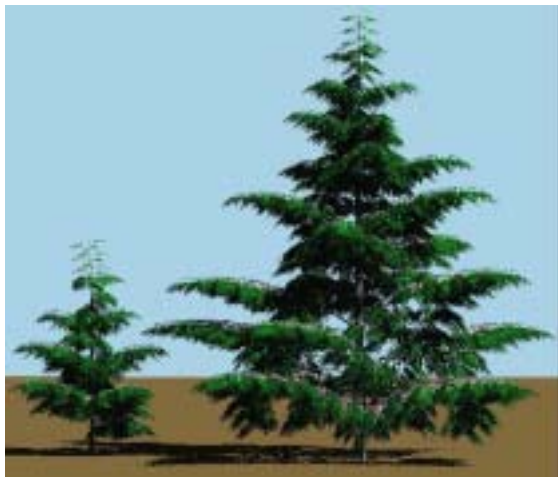


Figure 7: 5-15 years old Massart model

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