



INSTITUT NATIONAL DE RECHERCHE EN INFORMATIQUE ET EN AUTOMATIQUE

*Team Digiplante*

*Modeling plants growth and plants  
architecture*

*Rocquencourt*

THEME BIO

*Activity*  
*R* *eport*

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# 2. Overall Objectives

## 2.1. Research fields

**Keywords:** *dynamical systems, optimal control, plant architecture, plant computer simulation and visualizations, plant growth, plant model calibration, source - sink relationships, stochastic processes, structural-functional models, yield optimization.*

The project-team is particularly active in plant architecture modelling and plant growth simulations through the GreenLab model development that concerns several issues:

- Studies on the formalism and the behaviour of the model developed in Inria and Liama, based on instantiations to control the Plant Development.
- Integration of the functioning into the plant structure: bud functioning, biomass production and partitioning both in the deterministic and the stochastic cases.
- Interaction between Organogenesis and Photosynthesis through the biomass supply and the plant demand.
- Interaction plant-environment for physical factors (light, temperature, water)
- Tree structure simplification and scale adaptation.
- Passage from single plant to stand functioning
- Optimization and Control of the dynamical growth to improve yield under constraints.
- Connexion with others research fields: Mechanics, Radiosity, and Genetic.
- Visualization of plants from individual to population, until to landscape level with different approaches of computer graphic techniques.
- Building softwares around the simulation GreenLab model (Scilab and C++).

## 2.2. Objectives

The cultivated areas of Europe, including agricultural land and exploitation forests, have a strong impact on global environmental conditions. Erosion, resource impoverishment due to over-exploitation, and pollution by fertilizers or pesticides are crucial problems that agronomy and forestry hope to solve through harmonious cultivation modes and exploitation strategies. For this purpose, they must take into account production needs on one hand and the environment on the other; that is to say, both quantitative and qualitative criteria. In this context, mathematical models of plant growth describing interactions between the architecture of the plant and its physiological functioning have a key role to play. They allow the exchanges (of water, carbon, minerals etc) between plants and their natural environment to be quantified. GreenLab is just such a functional-structural model, and is the result of a long dialogue between botanists, physiologists and mathematicians. We have developed mathematical tools and their corresponding softwares for a variety of objectives:

- Optimization and control of the cultivation modes: in the case of limited resources, there is an optimal strategy of fertilizing and watering during plant growth. Likewise, controlling plant density or partial forest clearings can be beneficial. In this way, we can improve water resources and land management and reduce pollution by fertilizers.
- Control of plant sanitation and pesticides treatment: by coupling the plant growth model and insect population dynamics, we can control the use of pesticides and thus reduce costs and pollution.
- Selection of crop variety: we are currently working with geneticists, in order to prove that the plant genes directly determine the physiological parameters of the GreenLab model. In this way, we expect to propose better strategies for crop selection.
- Virtual simulation and visualization of plantations: computer graphics techniques allow the results of numerical simulations to be visualized. This is very important in urbanism or landscaping for predicting the long-term evolution of projects. The results of this research seem to show that in the near future, new tools of prediction, optimization and control could be effectively used in agriculture and forest exploitation on a large scale, and would drastically improve the management of the environment.

## 3. Scientific Foundations

### 3.1. Starting Digiplante in INRIA

Derived from the AMAP model developed in the 1990s at CIRAD, GreenLab's new formulation was introduced at LIAMA (Beijing) in 2000, through the GreenLab Associated team with INRIA. Today, the model is studied and improved through the DigiPlant research team that is a joint team of researchers from INRIA, CIRAD and Ecole Centrale Paris, and hosted by INRIA. Some very close partnerships exist with LIAMA, China Agriculture University, Wageningen University, and INRA.

As the GreenLab model is developed and tested in Digiplante, Liama and in Cau, with strong interactions (International exchanges, common publications and Phd), under the guidance of Philippe de Reffye, it is not sensible to isolate Digiplante from its working context, because it shares the scientific foundations and the applications with the other laboratories. Overall objectives

Our approach to develop the mathematical model of plant growth strongly relies on the plant organization described according to Botany. This leads to relevant choices in order to obtain an efficient method of factorization based on plant instantiations. Plant development purely concerns Organogenesis, i.e. the number of organs. Growth depends on photosynthesis that insures organ creation and expansion. We consider here the case without interactions between organogenesis and photosynthesis. On the common assumption of the existence of a global pool of reserves, it is not necessary to consider local conditions and we can distinguish 3 steps to control plant development and growth.

1. Computing the organogenesis. This step can be performed independently on the photosynthesis. It provides the number of organs produced by the buds.
2. Computing photosynthesis. This step needs the Organogenesis results that provide the total plant demand i.e. the sum of sinks. The number and sizes of leaves can be computed and the resulting biomass production can be shared between the different organs according to their sinks to insure their expansion. The yield is thus computed according to the sizes and the weights of the different organs produced.
3. Building the plant architecture for visualization or to study plant interaction with the environment. This last step needs the results of the two previous ones. It needs numerous geometrical operations.

For most applications in Agronomy only the first two steps are necessary, and no geometry is required.

### 3.2. Botanical Instantiations in GreenLab Model

#### 3.2.1. At Metamer Level

**Participant:** X. Zhao (GreenLab associated team, Liama).

In most cases, a dual scale automaton (DSA) is sufficient to describe the full organogenesis. The Automaton controls the bud mutation in different states named physiological ages. The number of physiological ages ((PA.) is small (less than 10). The Plant is organized in Metamers (microstates) and Growth Units (macrostates). Each metamer is a set of organs (internode, leaf, fruits and axillary buds). It is more efficient to create metamers than organs one by one because it gives directly the organ production and speeds up the computing of organogenesis and plant demand. Each growth unit is a set of metamers and the repetition of GUs gives birth to an axis so called "Bearing Axis" (BA).

#### 3.2.2. At Substructure Level

The terminal bud with a given PA produces different kinds of metamers bearing axillary buds of various PA. These buds give birth to axillary branches. Even the PA of the main bud can change by mutation. This phenomenon is represented in the automaton as a transition between macro-states. These processes automatically create substructures. A substructure is characterized by its physiological age PA and its chronological age CA. All the substructures with the same PA and CA are identical if they have been set

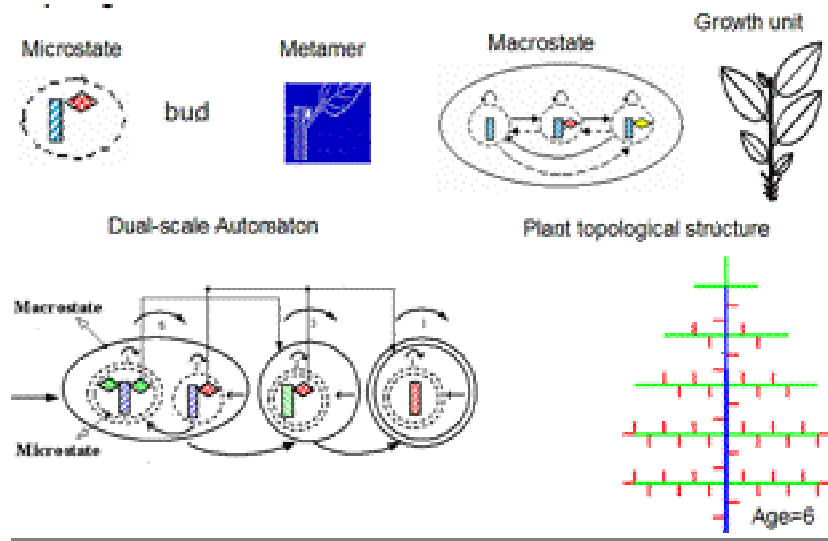


Figure 1. Dual scale Automaton for Plant Organogenesis.

in place at the same moment in the tree architecture. Let us consider the example of a particular 100 year old tree. Its trunk is of PA 1, main branches of PA 2 and live about 15 years, twigs of PA 3, 4, 5 and respectively live about 7, 5, 2 years. Here, the total number of substructures with different PA and CA is about 30. It is small, even if the total number of organs is high. These substructures will be repeated a lot of times in the tree architecture, but they need to be computed only once for each kind of PA and CA. The tree production and construction will be obtained by stacking the substructures in the right way.

### 3.2.3. Factorization of Plant Development

**Participant:** H.P. Yan (GreenLab- Liama associated team to Digiplante).

In the case of parallel simulation, counting the number of organs is a typical bottleneck; the computing time can be tremendous for big trees and forests. To overcome this difficulty, GreenLab model takes advantages of the plant architecture organized thanks to the concept of PA and generated by the DSA.. Similar substructures (of same PA and CA) are found in the main architecture many times.

Suppose a tree with  $m$  PA and finite growth for the axes: the repetition of macrostates (i.e. the number of GU) of  $PA=k$  is equal to  $N_k$ . Beyond this limit, the terminal bud can undergo a mutation and change PA (say  $k+1$ ), or die if  $k=m$ . So there are  $m$  kinds of substructures here that are represented by arrays whose fields contain the cumulated number of metamers according to their PA. A structure  $S_k^t$  is defined by its chronological age  $CA=t$  and its physiological age  $PA=k$ . It contains all the cumulated numbers of metamers produced from its birth until GC  $t$ .

$$[S_1^t] = [s_{1,1}, s_{1,2}, \dots, s_{1,m}]^t, [S_2^t] = [0, s_{2,2}, \dots, s_{2,m}]^t, \dots, [S_m^t] = [0, 0, \dots, s_{m,m}]^t.$$

All the items  $s_{i,j}$  with  $j < i$  are null because of the production rules. Structure  $S_1^t$  sums up all the metamers produced at GC  $t$ , for the whole plant. Let  $u_k$  be the number of metamers per GU for a given PA  $k$  and  $n_{i,j}$  be the number of substructures of PA  $j$  branched on the  $i$ th GU of the bearing axis of PA  $k$ . We have to stick the lateral and terminal substructures directly on the bearing axis of PA  $k$ , according to their positions as follows:

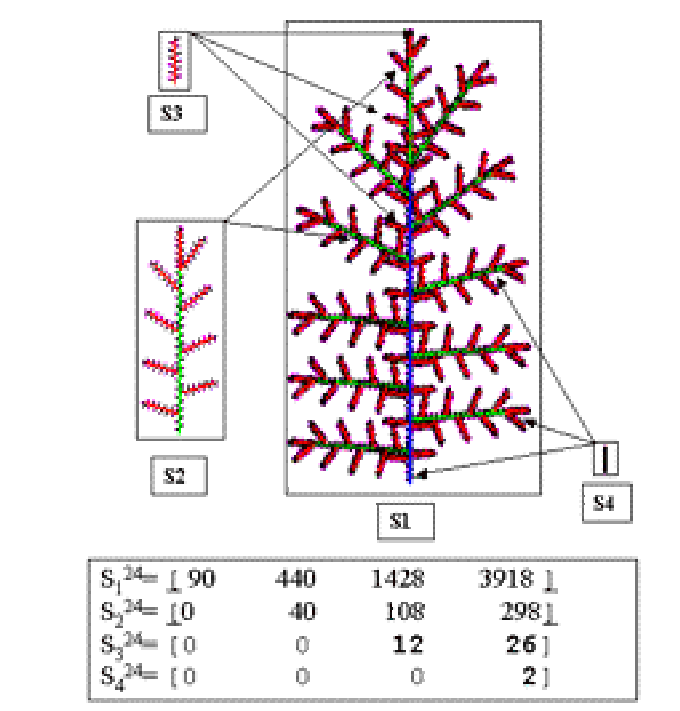


Figure 2. Plant factorization in substructure.

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

If  $t > N_k$ , and along the trunk, an apical terminal substructure of physiological age  $k + 1$  is born thank to the terminal bud mutation, so we have:

$$[S_k^t] = N_k [u_k] + \sum_{i=t-N_k}^{t-1} \sum_{j=k+1}^m (n_{k,j} \cdot [S_j^i]) + [S_{k+1}^{t-N_k}] \quad (t \leq N_k, t < m). \quad (2)$$

This plant construction algorithm is very fast. Obviously, the computation time depends only on  $t * m$  and not on the number of organs produced. The substructures are constructed by a double loop, i.e., bottom up from the youngest CA=1 to the final CA=t and top down from the oldest PA=m to PA=1. A library of substructures is created for each PA and CA and will be used to build substructures of older CA and younger PA. As the number of organs per metamer is botanically known, GreenLab provides a mathematical tool that enables to compute the organ production of a virtual plant very quickly and thus suppresses the drawback of counting the number of organs one by one by simulation. This also leads to an efficient way to compute the plant demand that is no more than the scalar product between the number of organs and their corresponding sinks.

### 3.2.4. Computing the Biomass Production

It is not necessary to build the tree structure to compute biomass production and partitioning at a given chronological age. We only have to compute organ production, plant demand and photosynthesis. All these data can be immediately derived from formula (1) and (2) giving the number of metamers in the plant as we know the number of organs per metamer and their durations.

### 3.2.5. Biomass acquisition

Every leaf produces biomass that will fill the pool of reserves according to an empirical nonlinear function depending on its surface  $A$ , on parameters  $r_1$ ,  $r_2$ , and on water use efficiency at GC  $k$ :  $E(k)$ . We suppose that the size of a leaf depends on its cycle of apparition (because of expansion). Let  $N_k^L$  be the number of leaves produced at GC  $k$ , known from Equation (1), the plant biomass production is:

$$Q_t = \sum_{k=1}^t N_k^L \cdot f(A_k, r_1, r_2, E(k)). \quad (3)$$

The empirical function chosen for the leaf functioning in GreenLab is:

$$f(A_k, r_1, r_2, E) = \frac{E}{r_1/A_k + r_2}. \quad (4)$$

This function can be easily changed according to modellers' choices.

For example the Light can be chosen as the driving force and we will use the Beer Law to compute the light interception by the leaves. Equation (4) is then replaced by:

$$Q_t = \frac{E(t)}{r} \left( 1 - \exp \left( -k \sum_{j=1}^{n(t)} A_j \right) \right) \quad (5)$$

where  $r$  is the resistance related to the transpiration of the leaf area ( $\sum A$ ),  $k$  is the coefficient related to the light interception and  $E(t)$  the light use efficiency at cycle  $t$ .

### 3.2.6. Biomass partitioning

Each organ has a potential biomass attraction value that we name sink or organ demand. This sink  $p_k(i)$  depends on the organ PA  $k$  and on its CA  $i$  (because of expansion). The shape chosen for  $p$  is up to the user,

but it should be able to fit properly any kind of numerical variations of the sinks according to the organ CA, it must be flexible enough to give bell shapes, *c* or *s* shapes, etc.

We define the plant demand at GC *n* as the total biomass attraction of all organs (leaves, internodes, fruits, layers, roots, ...):

$$D_n = \sum_{o=L,I,F} \sum_{i=1}^t N_{t-i+1}^o p_o(i). \quad (6)$$

The  $N_k^o$  are given by Equation (1). It gives instantaneously the biomass  $\Delta q_{i,t}^o$  allocated to an organ of type *o* created at GC  $t - i + l$  and its total cumulated biomass  $q_{i,n}^o$ :

$$\Delta q_{i,t}^o = \frac{p_o(i)}{D_t} Q_{t-1}, \quad q_{i,t}^o = \sum_{j=i}^t \Delta q_{i,j}^o. \quad (7)$$

Eventually, the organ volume depends on its apparent density and its dimensions on allometric rules. All this features can be measured directly from the organ shape.

As functions for organ sinks need to be flexible enough to capture the sink variation. Beta laws were found to be suitable for the purpose.

### 3.3. Towards a formalism for the GreenLab model

One of the first results of the Digiplante team was to give the frame of a mathematical formalism to the model. Such attempt has been undertaken a long time ago by the computer grammars named L-systems. Nevertheless this general formalism until now, doesn't take enough advantage about the botanical knowledge and about the biomass production and partitioning in plants. Starting from the equations of the model, Inria searchers have developed recurrence Grammars particularly suitable for the description of both development and plant growth. It gives birth to compact formulas with a high level of factorization that describes the plant development, growth, and architecture. The deterministic case firstly studied with J.P. Quadrat and M. Goursat is currently extended to the stochastic case, and to the case that manage the retroaction between growth and development, with the Digiplante team: (Kang, Cournede, Mathieu). The generating function of the system gives birth to the distributions of the number of organs and of the biomass variation. This is to be published in 2006.

## 4. Application Domains

### 4.1. Introduction

Once the equations of the plant development and the plant production are settled, it is possible to contemplate different kinds of applications:

### 4.2. Behaviour of GreenLab model

A mathematical model needs several steps to fulfil the common requirement:

1. The equations of the model must be a relevant translation of the reality.
2. The behaviour of the model must be studied.
3. The calibration of the model has to be undertaken on real data, and the model could be modified if necessary.
4. The model is used for various applications using optimization and control.

The GreenLab model has been improved gradually, through the successive Phd subjects. Starting from the GreenLab-Liama Team, the research has been extended to the new Digiplante team born in Inria at the end of 2004.

#### 4.2.1. The deterministic case GL1

**Participant:** H.P. Yan (GreenLab- Liama associated team to Digiplante).

First the deterministic case named GL1 has been studied. The plant development is monitored by the DSA as in Figure 1.

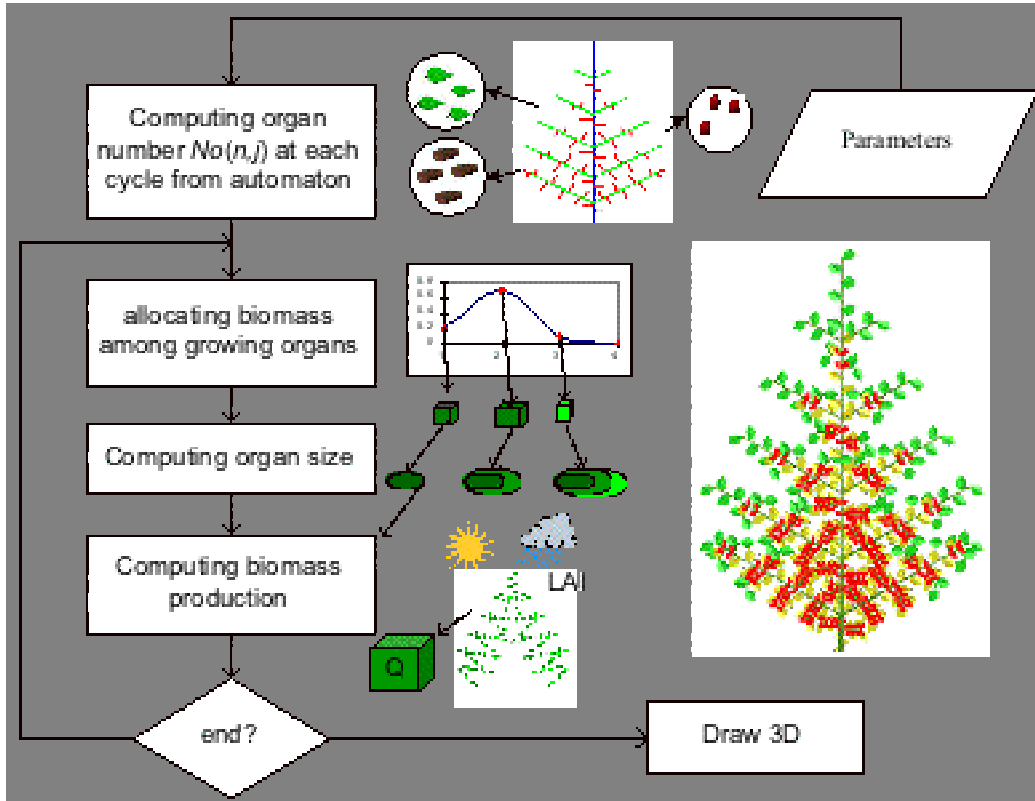


Figure 3. Flowchart for the GreenLab model.

$$\begin{cases} X_{n+1} = F(X_n, U_n) \\ X(0) = X_0 \end{cases} \quad (8)$$

$$\begin{cases} Q_{n+1} = G(Q_n, X_n, V_n) \\ Q(0) = Q_0. \end{cases} \quad (9)$$

At the step  $n$  of growth the number of organs  $X_{n+1}$  to create is computed thank to a function  $F$  deduced from the DSA shape (8). The Biomass production is computed from another equation (for example the Beer Law (5)), that is represented by equation (9). Equation (9) is obtained by replacing the leaf surface by its explicit formulation coming from the source and sink formalism. The recurrence shape of the system is obvious. Sets  $U$  and  $V$  contains respectively the rules of the DSA and the sinks and sources parameters, the system starting from the seed. At this step a simple retroaction occurs between the biomass production and the plant development at the level of the organs geometry.

According to the functioning durations of the different organ types (bud, leaf, internode, fruit, layer, root), and the environmental conditions it is possible to compute the plant growth and to determine the system



stability thank to sinks and sources parameters. It is thus possible to build pure virtual plants, whose organs expansions are exactly controlled during plant growth. Such a plant is described Figure 2. Branches duration is  $t_2=10$  cycles. All organs (leaves, internodes, fruits) have  $t_a=5$  cycles for expansion (with constant sinks  $p_a$ ,  $p_e$ ,  $p_f$ ) and the leaves have 5 cycles of functioning.

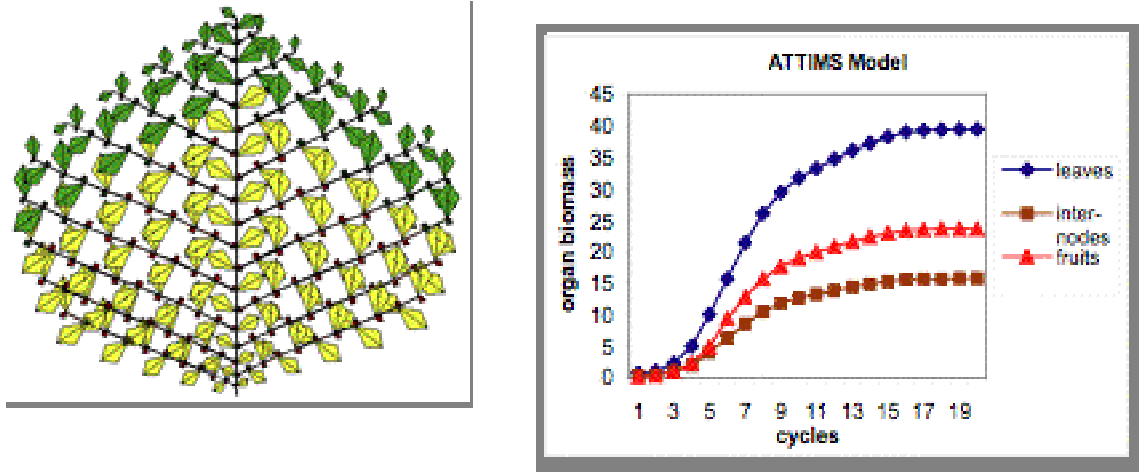


Figure 4. GL1 case: Behaviour of a virtual plant during the growth process.

The generic recurrence equation (8) is available for all the plants built with the GL1 system. Parameters A and B, are a combination of sources and sink parameters coming from equations (3) and (4).

$$Q_n = E \cdot \sum_{i=1}^{t_a} \frac{N_{n-i+1}^a \sum_{j=1}^i \frac{p_j^a Q_{n-(i-j)-1}}{D_{n-(-j)}}}{A + B \sum_{i=1}^i \frac{p_j^a Q_{n-(i-j)-1}}{D_{n-(-j)}}}. \quad (10)$$

The system will stabilize its biomass production  $Q_l$ / cycle according to the solution of equation (9)

$$1 = \sum_{i=1}^{t_a} \frac{E \cdot i(t_2 + 1)}{A \cdot ta(t_2 + 1)(pa + pe + pf) + iBQ_l}. \quad (11)$$

The sizes of organs depend explicitly of the environment E and of the sources and sinks parameters.

#### 4.2.2. The stochastic case GL2

**Participant:** MZ Kang (GreenLab- Liama associated team to Digiplante).

The dual scale automaton can be easily adapted to the stochastic case named GL2 (Liama, Kang MZ Phd). Here we still consider that there are no interaction between the growth and the development schedule of the plant that is now stochastic. In the equation 7 the U set contains also a set of probabilities.

The bud functioning is controlled thank to growth probability  $b_k$ , reliability  $c_k$ , and branching threshold  $a_k$ , that monitor the macrostates creation and also the law of repetitions of the microstates inside macrostates. The means and the variances of both organs and biomass productions have been explicitly computed from the stochastic DSA parameters, using covariance formulations and differential statistic properties. This avoids performing heavy MonteCarlo simulations to get the shapes of the distributions.

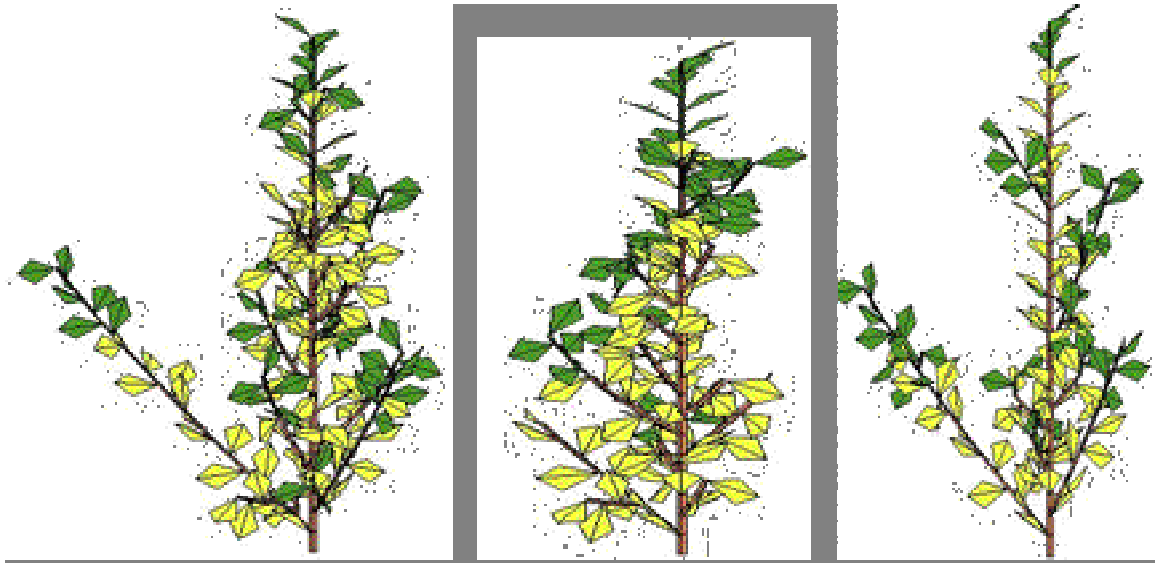


Figure 5. Stochastic plants simulated by GL2 Case.

Even substructure method is used here to shorten the simulation duration. For each chronological age and physiological age a set of limited repetitions is built, and then the accuracy of the simulation depends only of the number of repetitions. The time duration to build a stochastic tree is the same than for the deterministic case, once the substructure collection has been built for the first tree simulation.

The convergence toward Normal laws of the automaton production makes often the use of the computed means and variances sufficient to predict the organs and the biomass distributions.

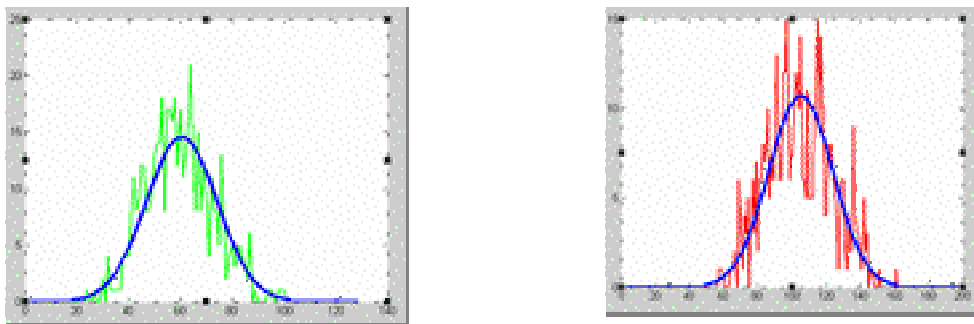


Figure 6. Comparison between theoretical distributions and montecarlo simulations (250 trials) for stochastic trees generated by model GL2.

#### 4.2.3. The interactions between plant development and plant growth: GL3 Case

**Participant:** A. Mathieu.

Thank to the results obtained by the associated team in Liama for levels one and two of GreenLab model, the DigiPlante team was ready to contemplate the integration of the feedbacks between the Growth and the

Development at a third level named GL3. This was the main subject of Amelie Mathieu's Phd from ECP. Locations of the feedback rely in a plant mainly on the buds functioning behaviour. Under different external conditions a same bud can produce more or less metamers and set in place various numbers of axillary branches. As a result of this variation the same tree can be 15 cm or 15 m at 15<sup>th</sup> years old according to shadow or sunny conditions. The matter of such a plasticity was supposed coming from the ratio Q/D of the biomass supply Q coming from the photosynthesis and the plant demand D, that is the scalar product between the organs and their sinks. The main Botanical improvement from GL3 is considering the bud as an organ with a sink, mean while in GL1 and GL2 the demand relies only on the plant organs (leaves, internodes, ...).

The more Q/D is big the more the Growth Unit born from the bud will be developed. A simple linear relationship is assumed between the functioning thresholds and Q/D.

First only the deterministic case is considered and three main thresholds are identified:

- The threshold to start an axillary bud at GC  $n$  is :  $[a_2 + a_2 Q_{n-1}/D_n] > 1$ .
- The span time for the functioning of the bud born at GC  $n$  is :  $t = [t_2 + t_2 Q_{n-1}/D_n]$ .
- The number of microstates of kind  $j$  in a GU of PA  $i$  formed at GU  $n$  is:  
 $Nu_{ij} = \int [u_{ij}^1 + u_{ij}^2 Q_{n-1}/D_n]$ .

This introduces a full retroaction between Development and Growth equations. Equations (8) and (9) becomes:

$$\begin{cases} X_{n+1} = F(X_n, Q_n, U_n, V_n) \\ X(0) = X_0 \end{cases} \quad (12)$$

$$\begin{cases} Q_{n+1} = G(Q_n, X_n, V_n) \\ Q(0) = Q_0. \end{cases} \quad (13)$$

The behaviour of the system made of equation (12) and (13) was successfully studied by Amelie Mathieu. The main results are to determine the conditions of the growth stabilisation according to the parameters, to retrieve the plant plasticity at every stages of growth, to control the conditions of the phenomena apparition into the plant architecture and to generate a periodical functioning that is often observed during growth of trees.

In the simple case of a monocaulis plant, the retroaction between growth and development relies on a variable number of metamers/GU. Under explicit numerical conditions the system will stabilize or not its growth.

In the complex case the effect of the retroaction between plant production and plant development will generate cyclic phenomena at several levels. Biomass production, fruiting and branching alternation, number of internodes/GU etc ... Very simple rules linking thresholds for development with a linear function Q/D depending, are sufficient to retrieve classical phenomena observed in growth of plants.

### Modeling the retroaction between Photosynthesis and Organogenesis during a Growth Cycle

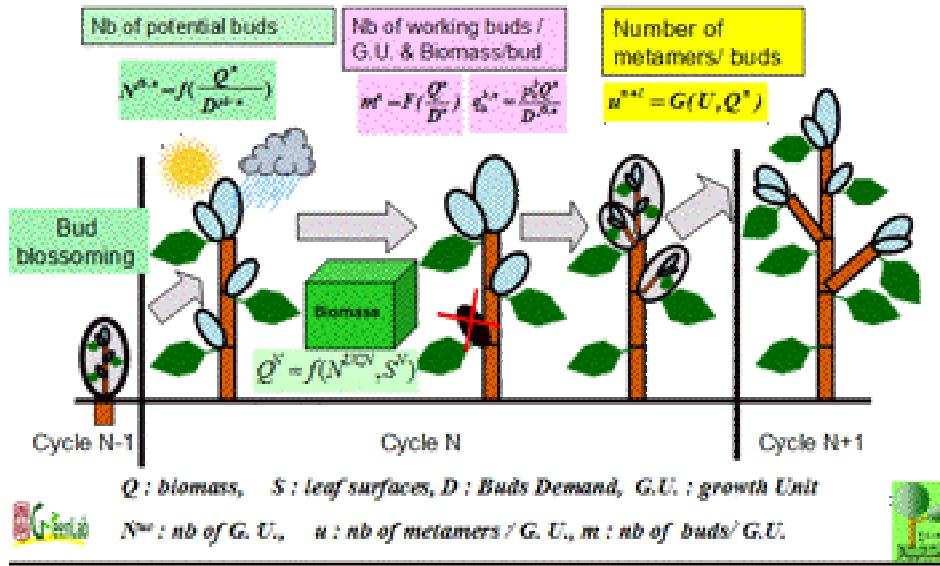


Figure 7. Schedule for the functioning during a growth cycle, for the buds.

### Plasticity of tree growth and tree architecture depending of environmental conditions

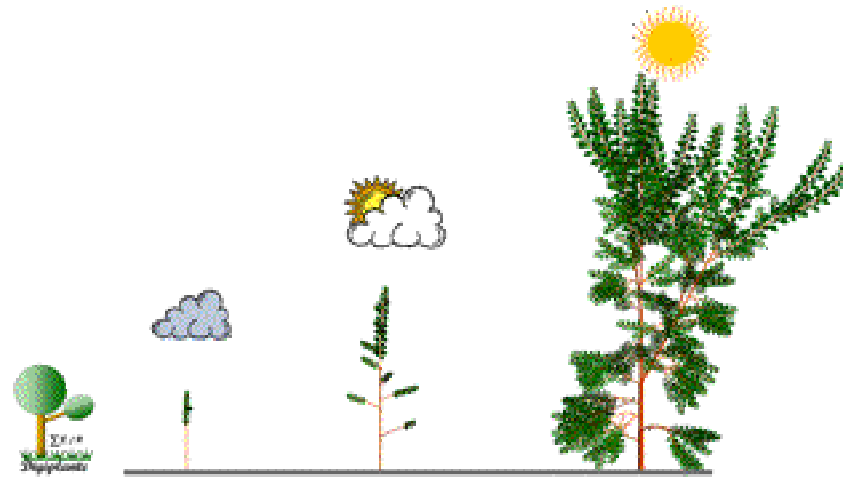


Figure 8. Plasticity of the GreenLab model, to simulate different plant architectures upon various climate conditions.

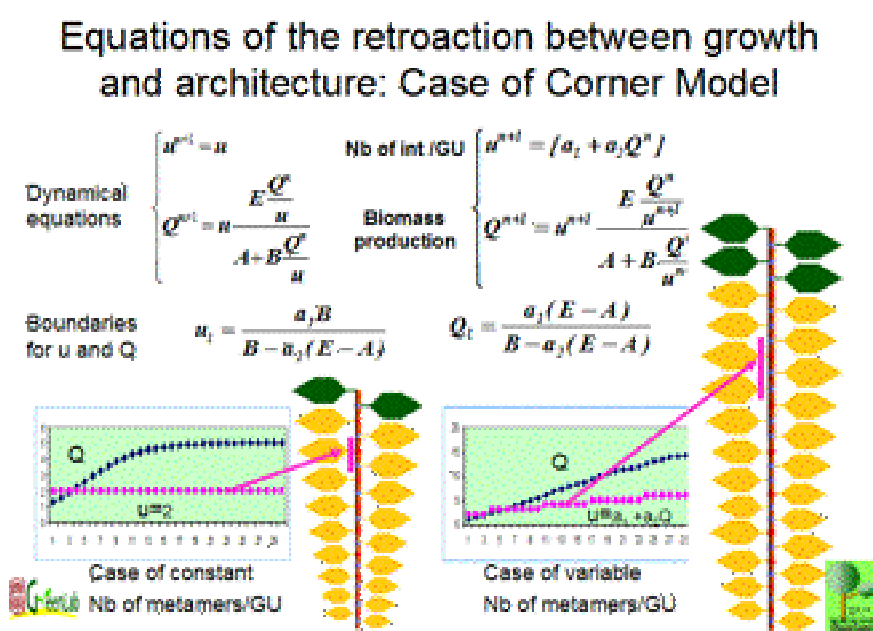


Figure 9. Example of retroaction between the size of the growth unit in number of metamers and the biomass production in the case of a monoculm plant (Corner model).

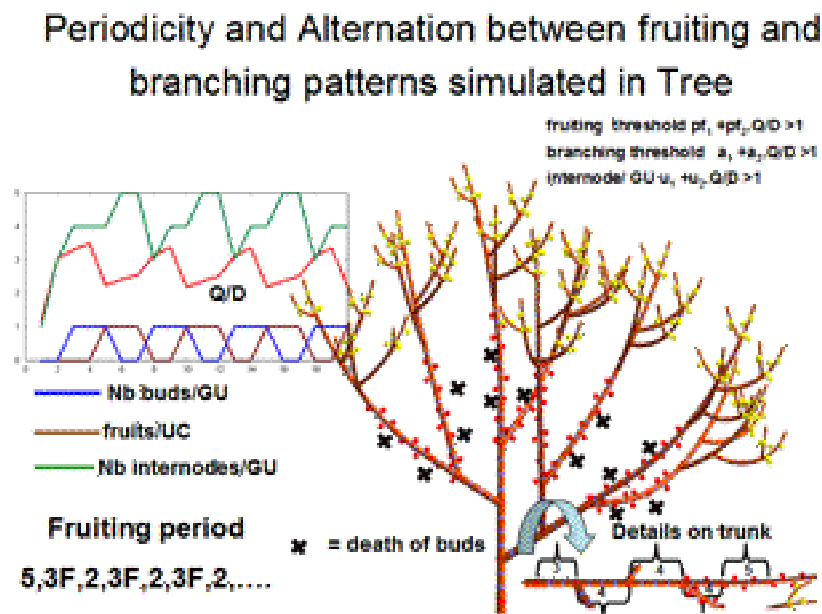


Figure 10. Rhythmic growth for fruiting and branching in alternation depending of the retroaction between plant production and plant development.

### 4.3. Calibration of GreenLab model on real cultivated plants

The plant architecture is a target for the mathematical model, and it is the visual result of the growth process. The hidden parameters of source and sink functions must be optimised in order to fit the best the weights and the sizes of all the organs produced by the plant development at each stage of growth. Theoretically speaking, this inverse method should be able to assess also the effect of the environment (climate and density), the leaf biomass production and the biomass partitioning in each organ from the plant architecture during the growth. The fitting can be done upon the following conditions:

The plant development must be entirely known. This includes the organ numbers, their functioning and expansion durations, their weights and sizes. Moreover allometric parameters that control the organ shape have to be assessed. It is not necessary to have the complete recording of each organ weight and size in a plant. Sparse data from the samples can be sufficient. But to be efficient, the number of measured data must be bigger enough than the number of hidden parameters.

The growth cycle must be defined according to the thermal time. This needs to follow the plant development on several stages of growth to set up the phyllochron. The average value of the environment efficiency  $E_n$  must be known at each G.C.. If no information is available about climate (that is often the case), the value is supposed to be a constant. Slight variations of  $E_n$  usually have no important effect compared to a constant climate, because they are smoothed by the successive organ expansions.

Generalized Least Square Method was used for parameter optimisation of the model. The application of this method to GreenLab was described by Zhan et al. [22] and Guo et al. [16]. Advantages of this method are that it provides rapid convergence and the standard error linked to the parameter values thus indicating the accuracy of the solution. Fitting process means to compare the observed organ weights and sizes, to the model prediction values, so it is not simply curve-fitting. Each class of organs (leaves, internodes, fruits) is a different output of the model corresponding to a set of hidden parameters. In a given class for a given plant age, the variation of the organ age controls its behaviour during the growth.

Fitting can be done on a single architecture (single fitting), or on several stages of growth to follow the trajectory of the dynamical process (multi-fitting). This second case is more accurate. In both cases all the data are fit in the same time by the same parameters set. If Data on root system are available they can be taken into account.

#### 4.3.1. CAU experiments

**Participants:** YT Ma (CAU), MZ Kang.

The Chinese Agriculture University (CAU) has a tight collaboration with DigiPlante and its associate team in Liama, for developing, testing and using GreenLab model. Calibration experiments have been undertaken successfully in CAU on several plants (Wheat, Cotton, Maize, Tomato, ...) and other are in progress ( Rice, Soybean, Pine tree, ...). Here, as a good example we present the Maize case (see Guo et al. 2006 for details). The measurements have been carried out on several stages of growth (8,12,16,21,27,30 G.C.), so multi-fitting is possible. But the plants have to be sacrificed for the measurements at each stage. This introduces noises in the data, linked to different local environments. Nevertheless we can accept this drawback if the plantation is homogeneous. The fitting is done on maize that has a finite development with 21 metamers for the Chinese cultivar. The architecture begins with metamers that have short internodes and is ended by the tassel. The cob location is on the 15<sup>th</sup> internode. The growth still continues and the expansion of organs acts until GC 33. It is obvious that the cob gets a big sink. The parameter  $E$  here is chosen to be the average potential transpiration ETO during the GC. So the resistance  $r$  to water transpiration is linked to the water use efficiency. The problem was to compute the functioning of this plant from the multiple growth stages and to solve the biomass production and the biomass partitioning at each GC.

Here it is obvious from Figure 11, that the GreenLab model works well. We need to compute 12 parameters belonging to the source and sink functions for the calibration, meanwhile the number of data to fit are about 400. The number of organs is few: one kind of leaf, sheath, cob, tassel, and two kinds of internodes (short and long). The accuracy on the parameters that control the sink function is necessarily less for the cob than for the

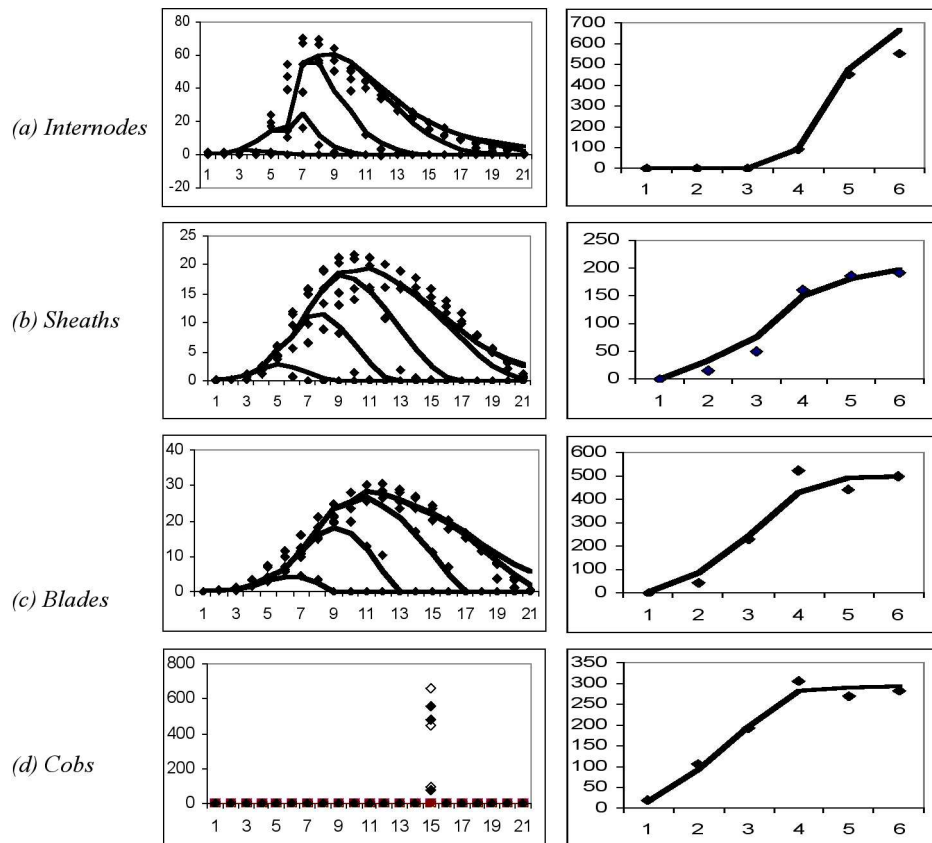


Figure 11. Fitting the maize architecture for biomass along 6 stages of growth. (dots are measurements and line model output PHD of Ma Y.T.. CAU. (Cornerfit Software Zhan Z.)

leaf, because there is only one cob and there are twenty leaves on the Maize plants. Here we are sure that a same set of constant parameters controls the plant growth, because the trajectory of the dynamical process is captured thank to 6 intermediate stages of growth.

*Biomass Production and Biomass Partitioning.* Once the problem of assessing the hidden parameters is done, the problem of biomass production and biomass partitioning is fulfilled. The model gives the amount of biomass fabricated by the plant at each stage of growth and how it is shared into different compartments (figure 12).

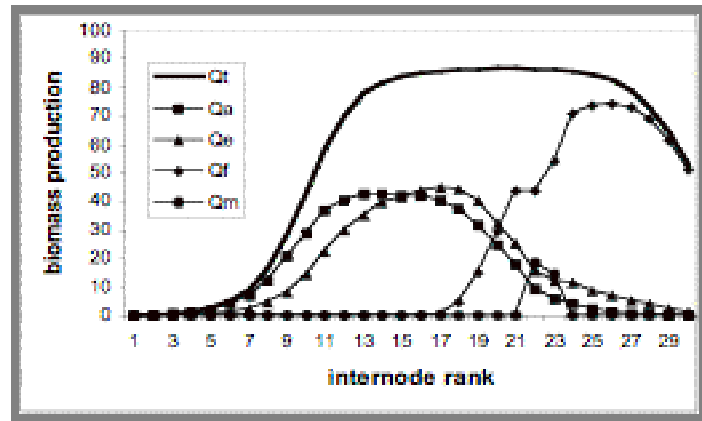


Figure 12. Biomass production and biomass partitioning during maize growth ( $Q_a$  : Blades + Sheaths,  $Q_e$  : internode,  $Q_f$ : Cob,  $Q_m$ : Tassel:  $Q_t$ : Total biomass).

*Simulating 3D.* Simulations of the 3D architectures are shown Figure 13. The 3D organs come from digitalisation and their sizes are related to their weights thank to their allometric rules.

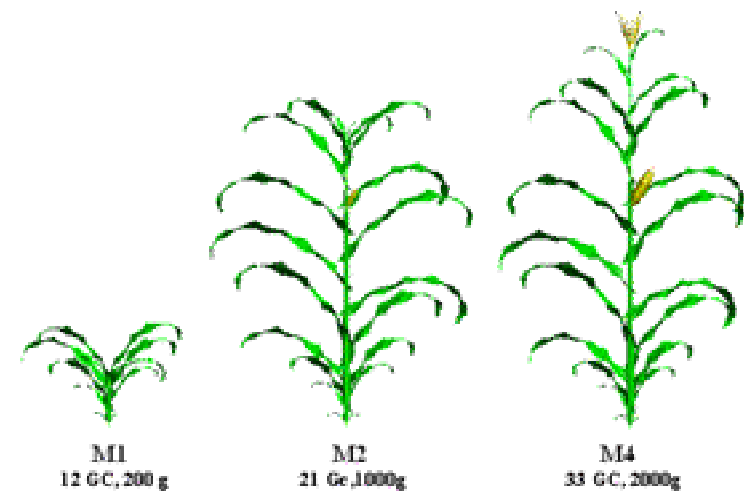


Figure 13. Simulation of 3 growth stages of maize architectures.



The excellent results obtained on Maize in CAU are similar on other plants like Tomato, Rice and Cotton, and they are to be published in 2006. The model seems really to be versatile.

#### 4.3.2. Generalization of the sources and sinks concepts in a plant

**Participant:** V. Letort.

Plants with simple architectures as Maize or Sunflower are not often encountered. In such plants all metamers can be measured for sizes and weights at any growth stages. Usually plants have more or less complex branching patterns that make the recording of the plant structure quite tedious. Therefore it is relevant to simplify the measurements using the substructure formalism that allows transforming a substructure in a meta-organ.

The meta-organ is both source and sink, and its functioning is the result of the sum of the functioning of underlying organs. GreenLab model allows computing the emergent properties at the level of the meta-organ. Several levels of aggregation are possible that needs adapted strategies for plant measurements and Data processing. This generalisation is the subject of V Letort PHD at ECP. It should lead if successfully, to analyse complex trees architectures.

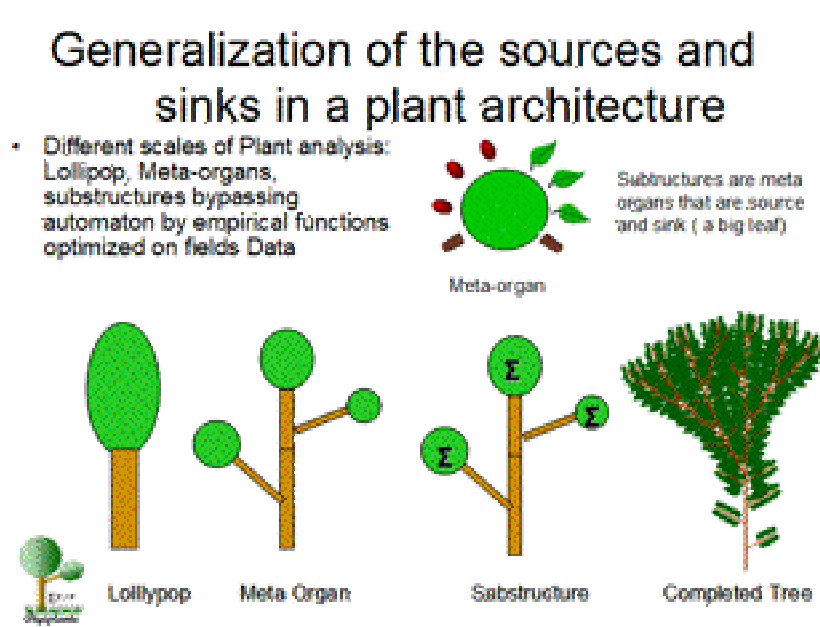


Figure 14. Several scales for the representation of the sources and sinks functioning.

#### 4.3.3. Theoretical issues on plant fitting with the generalized least square method

Applying the GLSQM on the equations of GreenLab model, needs several statistical studies . What about several minima, or what about the sensibility related to the parameters?, or how to compare two plants from their parameters sets? Such study is carried out by PH Cournede and F. Houllier of Inra.

#### 4.4. Optimal control for plants

**Participant:** L. Wu (GreenLab associated team).

The ultimate goal of mathematical models is to optimize different situations under various constraints. A good example for plants models is the water supply in stress conditions. How to provide the optimal quantity

of water at each growth cycle in order to optimize the yield? The amount of water in the soil depends of the water supply and of the plant transpiration that drive the plant photosynthesis. The Phd of Wu Lin from GrennLab associated team working in Idopt Inria project, as solved this problem, using the optimal control method. The soil water balance model chosen was the FSTW, acting with the theoretical plant transpiration given by the GreenLab model.

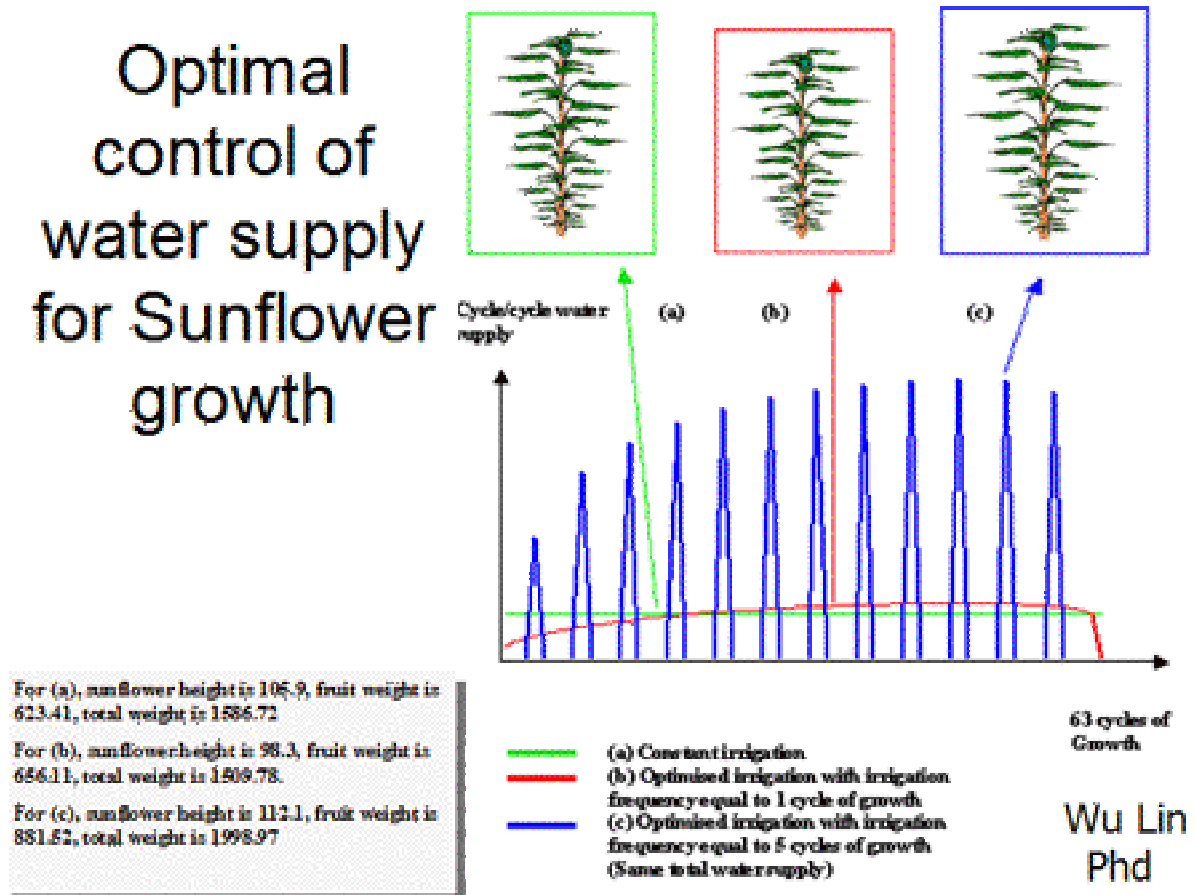


Figure 15. Optimization of water supply for the Sunflower during the growth.

Results show that both the shape of the distribution of the water supply per growth cycle and the period of the supply are important. Compare to the control uniform distribution it was found by computation that a 5 days period for irrigation under an optimized water distribution improve the yield of more than 30 %. This result is a first step towards virtual agronomical experiments. The same kind of applications could be undertaken on fertilizers, or to prevent excessive pollution from the use of insecticides or herbicides.

#### 4.5. From single plant functioning to field functioning

**Participant:** P.H. Cournède.

The results on single plant growth modelling have to be extended at the field level, in order to attempt to simulate the crop production. This needs integrating the competition for light and for soil resources among

the plants. This is undertaken at a mathematical level using the Beer-law, and at computer graphic level using radiosity. The field production is computed from the LAI and the canopy transpiration. Back to the single plant production this allows to monitor the plant development using the Q/D ratio.

Digiplante team works with Cyril Soler (Inria) for interfacing PlantRad software and GreenLab softwares. Results are to be published in 2006.

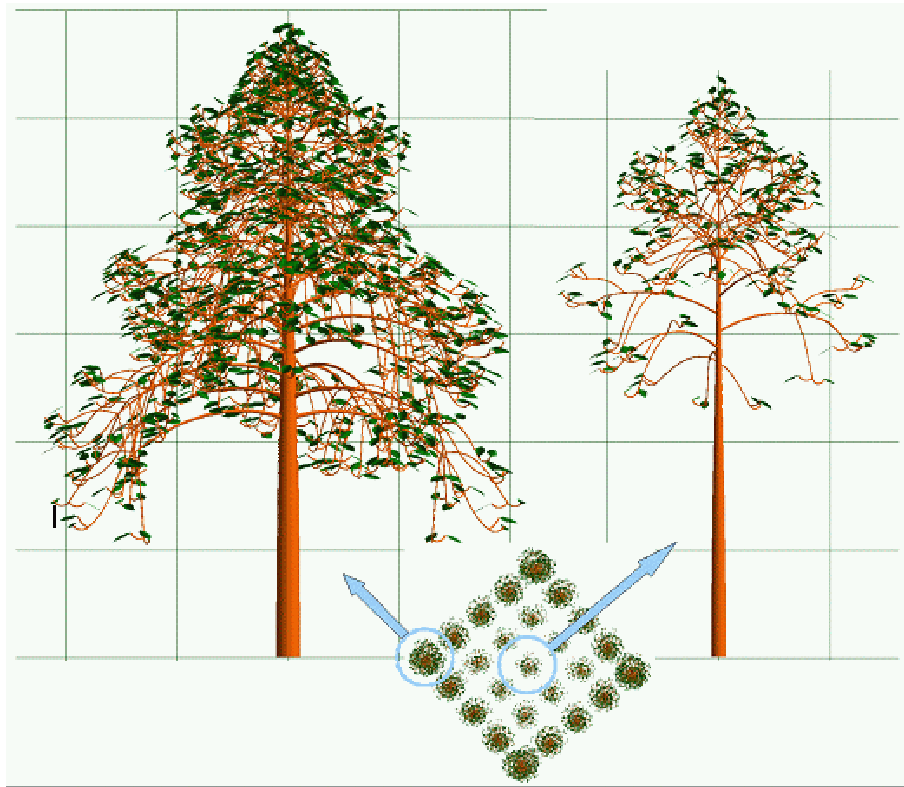


Figure 16. Functioning of a forest stand. Growth and Development of a single tree according to the spatial position.

## 5. Software

### 5.1. Software

Digiplante and GreenLab associated team are carrying out development of codes in several places that run the model for different purposes. This is done for specific or generic applications: the simulations build the plant architecture, through the development, the biomass production and the biomass partitioning. In China (CAU) Ma Yun Tao develops a software for Maize growth and Dong Qiao Xue, another for Tomato growth. Zhan Zhigang, in an other hand has built up a source and sink solver for monocaulus plant (Maize, Sunflower).

Generic and versatile codes are developed also:

- In Cirad JF Barczi (Digiplante) develops “AMAP” software that is specialized in Botany. Until now it is used as a geometrical model. But it begins to integrate the growth process. The aim is to simulate with accuracy the plant development with new features as the balance between the bud neoformation and the bud preformation controlled by the biomass reserve.

- In Liama Kang Mengzhen develops “GreenScilab software” in cooperation with Inria (Metalau, Digiplante, Scilab team). The code is open source in SCILAB (Inria), devoted to teaching and research. It integrates stochastic features (see figure 5) and a source and sink solver. The code is used in Wageningen University to model wheat and chrysanthemum growth.
- In ECP, Paul Henry Cournède develops “Digiplante software” in C++. The aim is to develop a generic source and sink solver for all kind of plants architectures and to integrate the spatial competition to simulate plant production at the field level. Tools for optimization and control linked to Agricultural issues (water, fertilizer, density, will be integrated little by little. Digiplante focus particularly on the retroaction between plant growth and plant development.

## 6. New Results

### 6.1. Apply mathematics

New results In 2005 the Digiplante and the GreenLab associated teams have got results in several fields.

#### 6.1.1. Studies on plant structure factorization

The substructure method was extended to GL3 that concerns retroaction between plant development and plant growth. Study on writing in a general way the generating functions of the plant productions is undertaken by J.P. Quadrat (Metalau project), P.H Cournède ECP and Kang Mengzhen (postdoc Inria). The stochastic case is submitted to a journal. Papers will be submitted this year.

#### 6.1.2. On the use of Neural networks

In Liama Professor Hu invests on possible applications of neural networks to complete the heuristic tools developed for Greenlab. A Phd student is currently working on the subject. The idea is to replace heuristic tools where classical optimization methods do not work properly.

#### 6.1.3. Computer Graphics issues

Marc Jaeger (Liama) works on functional landscapes visualisation. The aim is both a fast 3D representation and a computation of the functioning of the plants on a large scale according to the GreenLab model. The driving force chosen is the water supply and a simple model allows the water circulation into the terrain. Evolution of the vegetation is simulated along the time in a realistic way.



Figure 17. example of rendering plantations:900 trees scene (300 M. polygons) conversion (2') and rendering (2')

### 6.2. GreenLab Calibration on cultivated plants

The Chinese Agriculture University partner of GreenLab and Digiplante teams had carried out successfully the calibration of two cultivated plants : Maize (Phd Ma Yun tao, see 4.2.1) in open fields and Tomato (Phd Dong Qiao Xue) in greenhouses. The Phd Defences will be hold in 2006. Results are quite interesting and reliable.

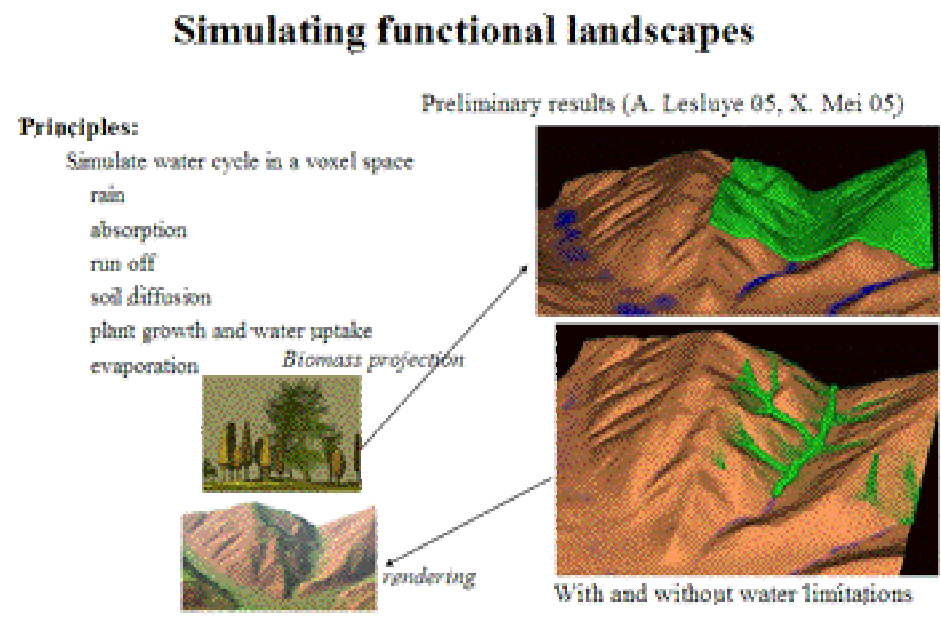


Figure 18. Functioning Landscape: plantations made of simple plants growing with water supply according to GreenLab model.

Experiments on several years prove that a set of constant sink and source parameters (less than 12) control the dynamical process with accuracy. Several stages of growth allow following the trajectory. Hundred of data (organs weights) are fitted correctly showing that the biomass production and the biomass partitioning are well performed during the growth process. Moreover the climate effect is studied.

#### 6.2.1. Case of Tomato

Dong Qiao Xue Phd (CAU) subject is to compare the behaviour of Tomato growth when the plant is either isolated or in high density. In the second case, distances between plants are 25 cm, and competition for light occurs. The biomass production and the biomass partitioning are quite different in both cases although for a given experiment the source and sink parameters remain constant through the growth process. Density effect makes the leaf thinner and the internodes and petiols longer and slows down the plant development. Computing hidden parameters shows that internode sink increases meanwhile fruit sink decreases. In another hand the effects of incident light and of light interception on the plant growth can be also computed from the architectural data by the inverse method.

The effect of incident light was modelled as:

$$E(n) = 1 - \exp(-C \cdot L(n))$$

where  $L(n)$  is the cumulated light energy received by the plant at cycle  $n$  of the growth. For the light interception two models were to be compared. One using the simple Beer law, another using the radiosity model Plantrad provided from Inria (C. Soler). Both models give very close results and more over the light efficiency and the light interception effect were found to be the same. This is the first experiment using GreenLab model that computes at the same time by inverse method the source and sink parameters of the plant functioning and the effect of light on the Tomato growth .

## Multifitting on Tomato with GreenLab model influence of light

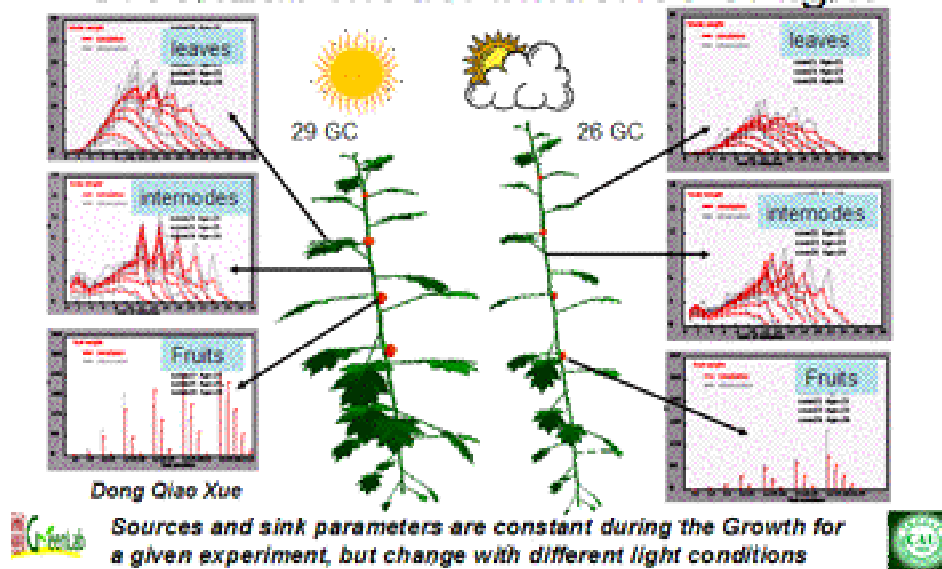


Figure 19. Calibration of GreenLab model on Tomato.

## 7. Contracts and Grants with Industry

### 7.1. Contracts and Grants with Industry

Digiplante research team is in contact with a company that wants to adapt the GreenLab model for crop prediction. This needs a calibration of the model on several cultivated plants for assessing the effect of different driving factors of the growth as climate, fertilizer, water supply, density. The results obtain with the GreenLab on various cultivated plants generic model are quite encouraging and using it in an industrial process looks reasonable. A contract should be signed in 2006.

## 8. Other Grants and Activities

### 8.1. Dissemination

The GreenLab model begins to be uses in several laboratories in China, in Holland and in France. The softwares are currently used for plant calibration in these places.

- In China, Liama and two laboratories of Chinese Agriculture University (CAU) master the model and apply it on Maize, Rice, Cotton, Pine tree. About ten Phd defences have already been hold. A new institute of Forestry (CAF) is joining the team.
- In Holland two laboratories of Wageningen university ( Pf E. Heuvelink and J. Vos, have successfully modelled Chrysanthemum and Wheat growth, in cooperation with Kang Mengzhen a Digiplante postdoc of Inria, coming from Liama.
- In France Digiplante has a good dissemination in Cirad (Amap and Ecotrop) and Inra ( 4 laboratories, involved in genetic, forestry and ecophysiology).
- Teaching on the model will be done in a European course on biological modelling in 2006. A course of 20 hours is planed in ECP for the first scholarship year.

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