INRIA

Team Digiplante

Stochastic, functional and interactive models for plant growth and architecture

Futurs

THEME BIO

Activity Report

2007

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1. Team

Head of project-team Digiplante and associate team Greenlab in China
    Philippe de Reffye [DR Cirad, HdR]

Administrative Assistant
    Martine Verneuille [Rocquencourt for GreenLab]
    Delphine Goyer [Futurs]

Staff member
    Pau-Henry Cournède [CR, ECP]
    Marc Jaeger [en détachement du Cirad]

Associate Research Scientists - CIRAD
    Daniel Barthelemy [DR Cirad, Habilite, 10%]
    Hervé Rey [10%]
    Jean-François Barczi [10%]

Associate Research Scientists - GreenLab
    Baogang Hu [LIAMA - China]
    Zhang Xiaopeng [LIAMA - China]
    Mengzhen Kang [LIAMA - China]
    Zhang Bao Gui [CAU - China]
    Guo Yan [CAU - China]
    Zhan Zhigang [CAU - China]
    Dong Qiao Xue [CAU - China]

Ph. D. student
    Cédric Lois [Ecole Centrale Paris]
    Benoit Pallas [Ecole Centrale Paris]
    Vincent Le Chevalier [Ecole Centrale Paris]
    Véronique Letort [Ecole Centrale Paris]
    Qi Rui [LIAMA and ECP (Sandwich Phd)]

Post-doctoral fellow
    Ma Yun Tao [CAU and LIAMA - China]
    Amélie Mathieu [Ecole Centrale Paris]

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.

2.3. Highlights

The year 2007 should appear as a key year for DigiPlante.

- Dissemination of GreenLab approach reaches its highest level up to now; with 14 accepted articles in international journals in 2007, several invited talks, and an increasing reviewing activity .

- Thanks to industrial partners in France, associate team GreenLab and Chinese partners of CAU and CAF, partners in Netherlands, the model calibration and applications raise new results on real plant crops. Such applications concern plants which are more and more complex on structural aspects (first tentatives on trees), and on functional aspects (bi-annual cycle crops).

- The new research axis on landscape functional modeling, launched in 2006, shows its first results and publications.

- Promising preliminary results are gained on the next plant generator GL4, combining both stochastic aspects and functioning retro-action on organogenesis.

- Changes in administration and logistics. Early Spring, DigiPlante did move from Rocquencourt to Futurs, hosted by Ecole Centrale of Paris. Procedure to label DigiPlante as a project is launched.

3. Scientific Foundations

3.1. Starting Digiplante at INRIA

Derived from the AMAP model developed in the 1990s at CIRAD [48], 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 developped 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[17] 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 [47]. 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).
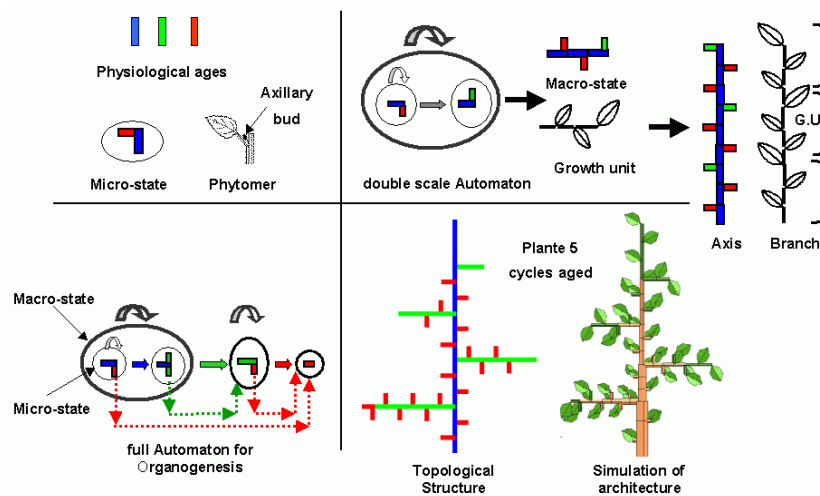
Figure 1. Dual scale Automaton for Plant Organogenesis.

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). See Figure 1 illustrating the automaton principles.

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 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.
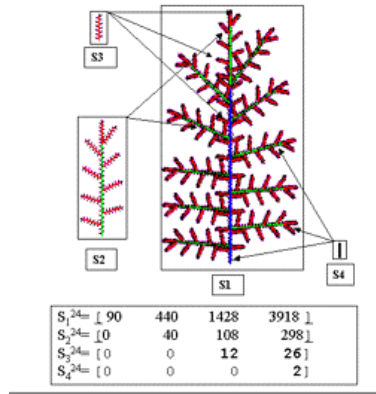
Figure 2. Plant factorization in substructure.

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.

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

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 ith 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:

$$\left[S_k^t\right] = t \cdot [u_k] + \sum_{i=1}^{t-1} \sum_{j=k+1}^{m} \left(n_{k,j} \cdot \left[S_j^i\right]\right) \qquad (t \le N_k)). \tag{1}$$

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:

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

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 [44]. 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 $r1$, $r2$, 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:

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

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

$$f\left(A_k, r_1, r_2, E\right) = \frac{E}{r_1/A_k + r_2}.$$ (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:

$$Q_t = \frac{E_t}{r} \frac{S_p}{k} \left(1 - \exp\left(-k \frac{\sum_{j=1}^{n(t)} A_j}{S_p}\right)\right)$$ (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, E_t the light use efficiency at cycle t and S_p a surface related to the crown projection.

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 exapansion). 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, ...):

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

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 $q_{i,n}^o$:

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

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 [16] started to be extended to the stochastic case (Kang [6]), and then to the case that manage the retroaction between growth and development, with the Digiplante team: (Kang, Cournede, Mathieu [9], [10], [11]). The complete approach (stochastic with retroaction) is under study. The generating function of the system gives birth to the distributions of the number of organs and of the biomass variation.

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

First the deterministic case named GL1 has been studied. As shown in Figure 1 The plant development is monitored by the DSA .
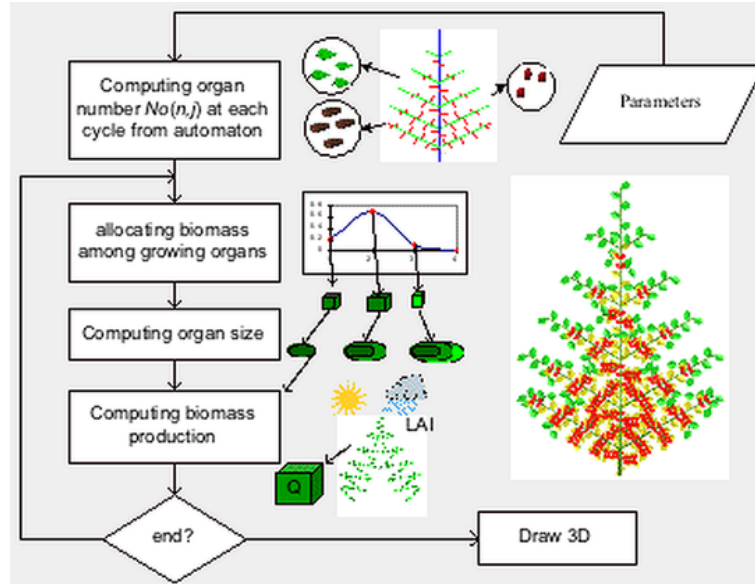
Figure 3. Flowchart for the GreenLab model.

Originally developed by Yan Hong Ping in her PHD of 2003, GL1 is currently use by several laboratories (CAU, Cirad, Inra, U. Wageningen). The softwares Digiplante and GreenScilab are used successfully for the parametric identification of cultivated plants such as Canola, Beetroot, Rice, Wheat, Pine, Tomato, and so on 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).

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

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

The new formulation of GreenLab that uses the light efficiency needs to study the model behaviour. Equation of plant growth integrating Beer-Law that is used is:

$$Q(n) = \frac{E(n).S_p}{r.k}\left(1 - \exp\left(-\frac{k}{e.S_p}\sum_{i=n-t_a+1}^{n} N_a(i)\sum_{j=i}^{n}\frac{p_a(j-i+1).Q(j-1)}{D(j)}\right)\right) \qquad (10)$$

where
E is the light use efficiency

r is a coefficient standing for resistance to transpiration.

S_p is the plant projection surface standing for leaf interception

k is the coefficient of the light interception Beer law

pa stands for the leaf sink, t_a for the leaf functioning duration, e for the specific leaf weight (SLW)

$D(j)$ stands for the plant demand at cycle j

$N_a(n - i + 1$ defines the number of functioning leaves born at cycle i, when the plant total number of cycles is n

$Q(n)$ is the plant biomass production at cycle n

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 illustrated in Figure 2. Branches duration is t2=10 cycles. All organs (leaves, internodes, fruits) have ta=5 cycles for expansion (with constant sinks pa, pe, pf) and the leaves have 5 cycles of functioning.
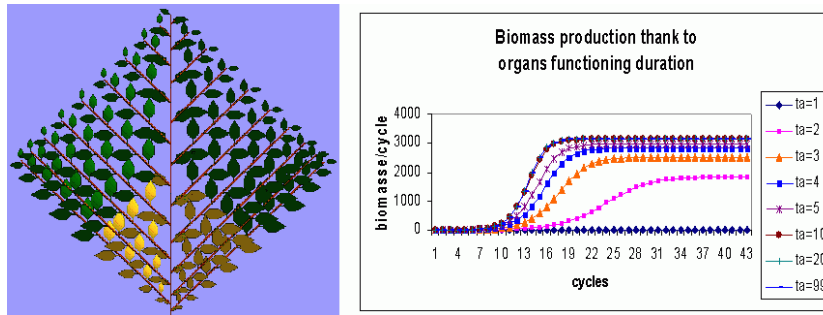
Figure 4. GL1 case: Behaviour of a virtual plant during the growth process.

The system will stabilize its biomass production $Ql/$ cycle according to the solution of equation (9) Vermeer Grange, student of Ecole Polytechnique, has studied the model behaviour during his internship at Beijing in Liama in 2006. When the leaf area index (LAI) is high, a maximum in production per square meter could be reached :(11)

$$Q(n) = \frac{E(n).S_p}{r.k} \tag{11}$$

But according to the time functioning duration of leaves, lower limits can be reached as shown in (Fig 4)

The generic recurrence equation (8) is available for all the plants built with the GL1 system. 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). Originally developed by Kang MengZhen, GL2 begins the phasis of parametric identification on cultivated plant such as cotton plant, wheat. 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.

V. Letort has built up a solver for plant development in Scilab that allows to compute for the buds behaviour, both rhythms and probabilities of death, growth and branching. It allows to analyse complex branching patterns with several physiological ages. The system used both means and variances of the numbers of different types of organs produced by the buds.

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 relie 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 15th years old according to shadow or sunny conditions. The matter of such a plasticity was supposed coming from the ratio Q/D of the
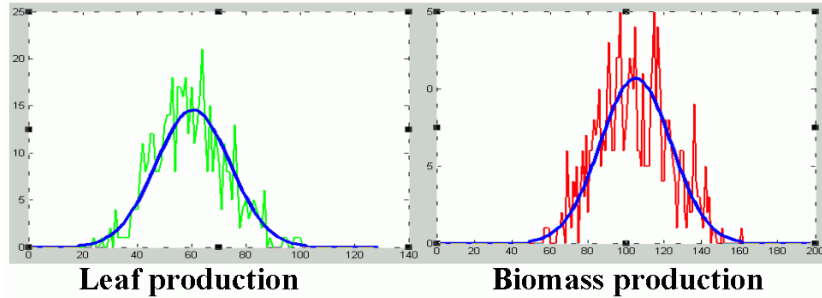
Figure 6. Comparison between theoretical distributions and montecarlo simulations (250 trials) for stochastic trees generated by model GL2.

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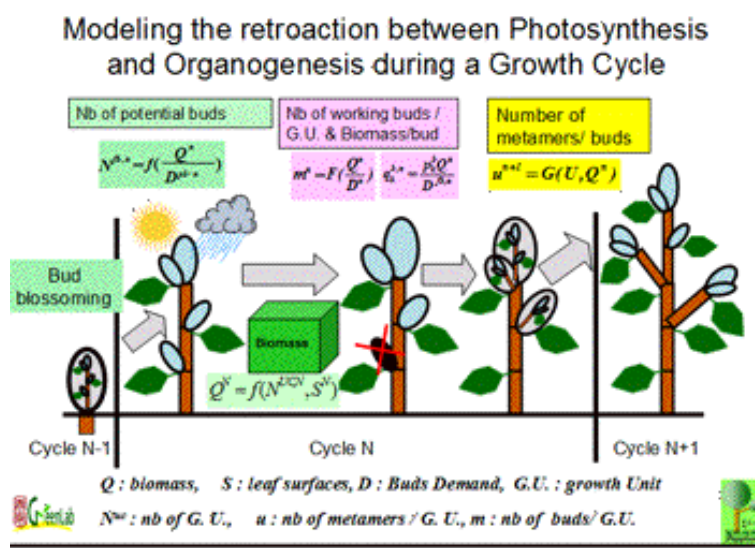
Figure 7. Schedule for the functioning during a growth cycle, for the buds.

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: $Nu_{ij} = \int \left[u_{ij}^1 + u_{ij}^2 Q_{n-1}/D_n \right]$.

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

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

$$\begin{cases} Q_{n+1} = G\left(Q_n, X_n, V_n\right) \\ Q(0) = Q_0. \end{cases} \tag{13}$$
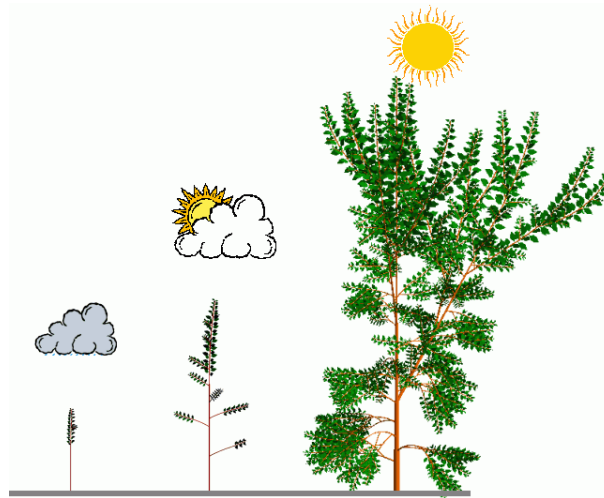
Figure 8. Plasticity of the GreenLab model, to simulate different plant architectures upon various climate conditions.

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 monocaulus 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.

One of the major issues of the retroactions between plant growth and plant development concern the rhythms in the branching patterns and the fruit abortions. GL3 also begins parametric identifications on plant such as tomatoes, cucumbers and sweet-peppers. Experimentations are working out in Netherland and China. Thresholds based on the ratio supply/demands (Q/D) has to be identified in order to predict the positions of the different types of organs.

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).
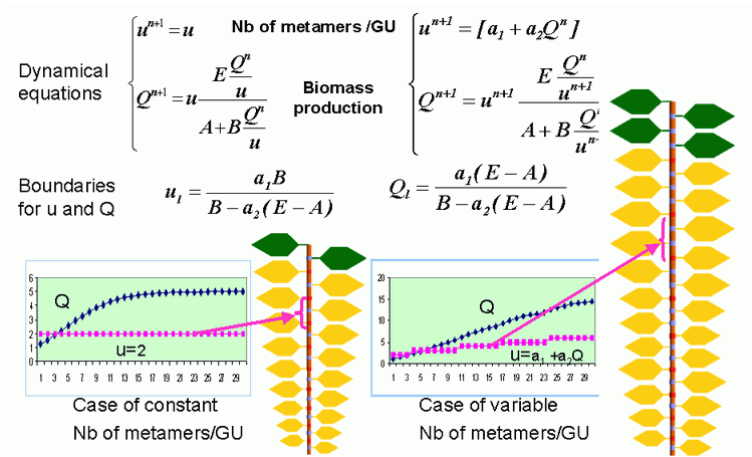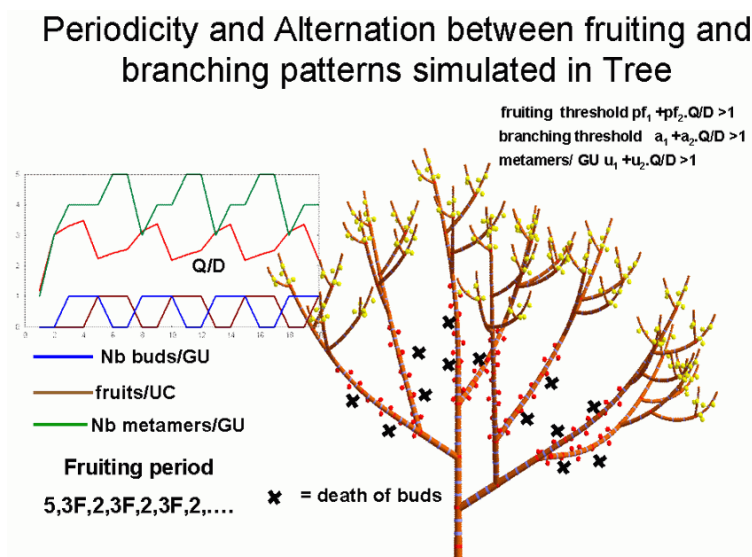

Figure 10. Rythmic growth for fruiting and branching in alternation depending of the retroaction between plant production and plant development.

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. [45] and Guo et al. [3]. 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 [3]). 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 15th 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
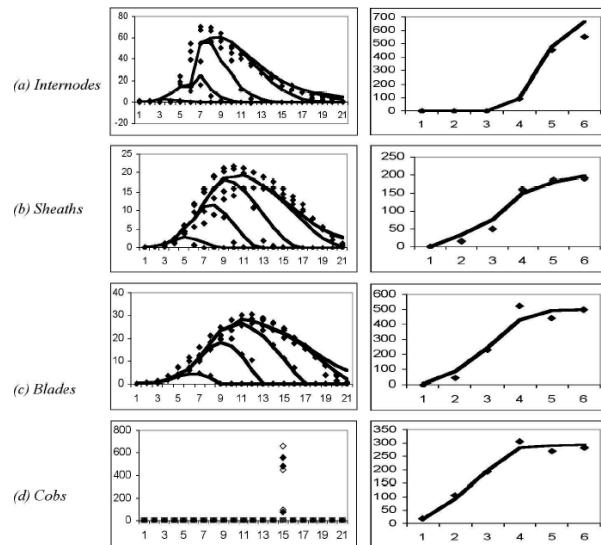
Figure 11. Fitting the maize architecture for biomass along 6 stages of growth. (dots are measurements and line model output PHD of Ma Y.T.. CAU. (Cornerfit Software Zhan Z.)

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.

Figure 12. Biomass production and biomass partitioning during maize growth (Qa : Blades + Sheaths, Qe : internode, Qf: Cob, Qm: Tassel: Qt: Total biomass).

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).

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.

The excellent results obtained on Maize in CAU are similar on other plants like Tomato, Rice and Cotton. 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.
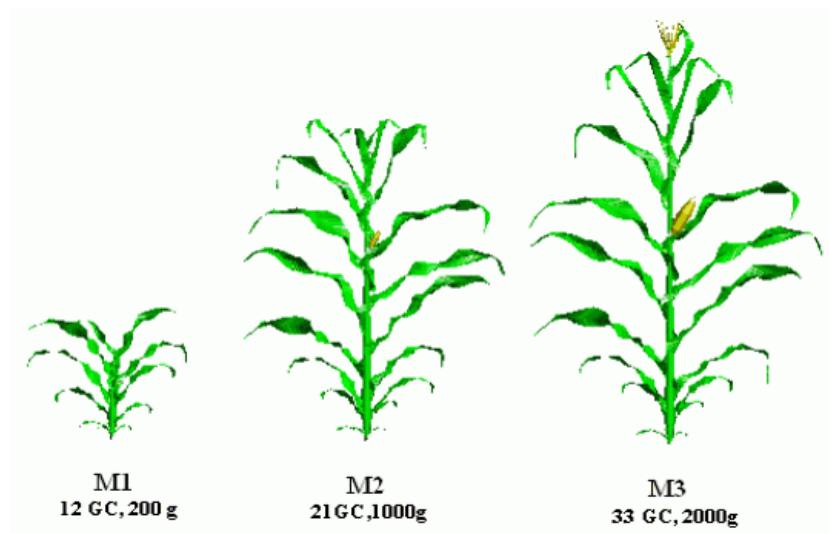
Figure 13. Simulation of 3 growth stages of maize architectures.

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 as shown in Figure 14. This generalisation is the subject of V Letort PHD at ECP. It should lead if successfully, to analyse complex trees architectures.
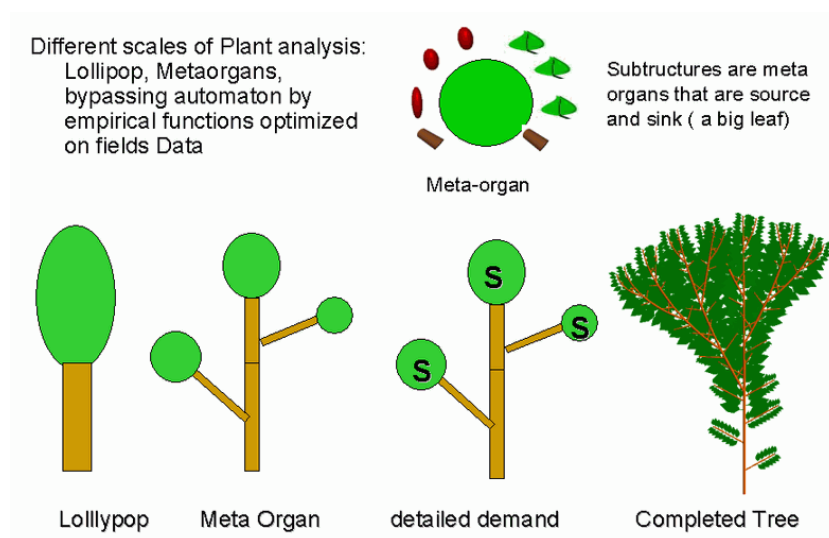
Figure 14. Several scales for the representation of the sources and sinks functioning.

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 [13].
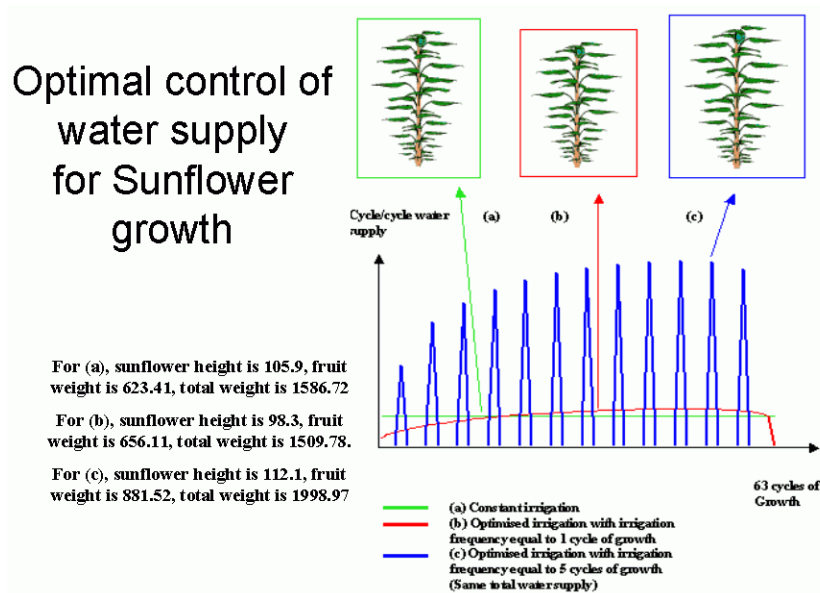
Figure 15. Optimization of water supply for the Sunflower during the growth.

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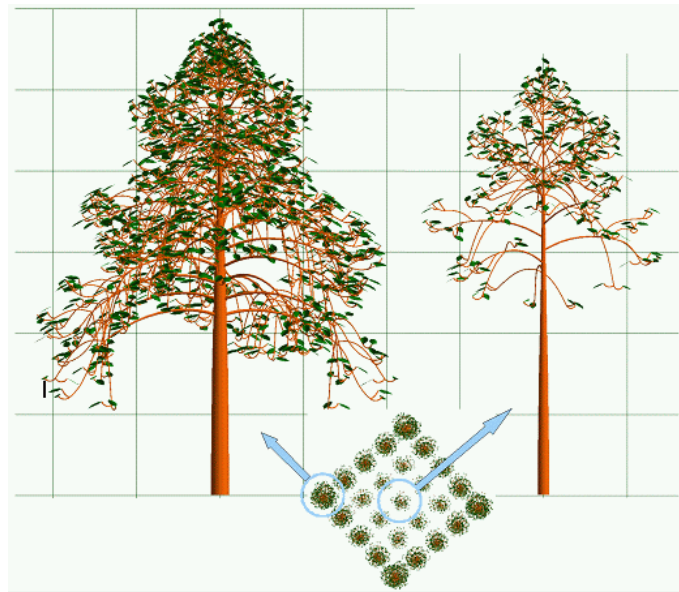
Figure 16. Functioning of a forest stand. Growth and Development of a single tree according to the spatial position.

5. Software

5.1. The plant toolbox Greenscilab

Participants: M.Z. Kang [GreenLab associated team], R. Qi, V. Letort.

The first prototype of the plant toolbox built in Scilab and named GreenScilab that runs the GreenLab model has been completed and is available on the Liama web site since July 2006. The tool was presented at 2005 Scialb Workshop in China [42], at MESM06 [7] conference, and at 2007 Scilab workshop [40]. It is intended to teaching activities and to spread the model in the research communities on plant modelling. Main developer is at the project GreenLab-Liama (Kang MZ). It is co-developed by the Digiplant team (Qi Rui, Letort ECP). GreenScilab should increase each year as well for the possibilities (calibration and optimization on plants) as for the documentation support for teaching and training. It has been for a common course between INA-PG, Master of Orsay Univeristy and Ecole Centrale Paris.A GreenSciLab page is now also on line on SciLab site. See: http://liama.ia.ac.cn/wiki/projects:greenscilab:home
And, on SciLab site: http://www.scilab.org/?page=greenlab.html

5.2. Software for Data Analysis

At ECP an internship Bryan Brancotte developed software for data management and data processing, dedicated to the experimental data necesseray to estimate GreenLab parameters. Data are organized and output files are generated in the proper form to be processed by the DigiPlante Software. This should improve consequently the efficiency of the data processing and speed up the studies on real plants.

6. New Results

6.1. Modelling and Applied mathematics

6.1.1. *Optimization and Control*

Participants: R. Qi, B.-G. Hu [GreenLab associated team], P.-H. Cournède, P. de Reffye.

The PhD of Qi Rui (LIAMA - ECP) aims at solving problems of optimization and control for applications in agriculture, based on the dynamical system of plant growth GreenLab. It first concerns variety selection, by optimizing the model parameters driving source-sink relationships in the plant in order to get the best yield, according to various criteria. It also concerns the determination of optimal cultivation modes, like water and fertilizer supplies, density, pruning strategies ...

Some test cases have been solved:
- sink optimization for fruit yield (cotton, sunflower, maïze, tomato), root yield (sugar beet), wood yield (trees)
- pruning strategies to optimize quantity / quality criteria (tea plant)
The complexity of the problems involved generally implies using heuristic methods (evolutionary algorithms, particle swarm optimization). Moreover, multi-objective optimization with determination of Pareto fronts is also implemented to tackle more realistic issues (as for tea plants, where both quality and quantity of leaves have to be considered.) Part of these advances where presented at 2007 Scilab workshop [40].

6.1.2. *A new Model of Competition*

Participants: P.-H. Cournède, P. de Reffye.

The empirical production equation of GREENLAB is extrapolated to stands by computing the exposed photosynthetic foliage area of each plant. The computation is based on the combination of Poisson models of leaf distribution for all the neighbouring plants whose crown projection surfaces overlap. This proposal has been published in AoB Journal [19] and available in PMA06 IEEE proceedings [32]. To study the effects of density on architectural development, we link the proposed competition model to the model of interaction between functional growth and structural development introduced by Mathieu [11] (2006). The model was applied to mono-specific field crops and forest stands. For high density crops at full cover, the model is shown to be equivalent to the classical equation of field crop production (Howell and Musick, 1984) [41]. However, our method is more accurate at the early stages of growth (before cover) or in the case of intermediate densities. It may potentially account for local effects, such as uneven spacing, variation in the time of plant emergence or variation in seed biomass.
The application of the model to trees illustrates the expression of plant plasticity in response to competition for light. Density strongly impacts tree architectural development through interactions with the source-sink balances during growth. The effects of density on tree height and radial growth that are commonly observed in real stands appear as emerging properties of the model.

6.1.3. *Multiscale formalism for the analysis of plants*

Participants: V. Letort, P.-H. Cournède, P. de Reffye.

During her Phd, V. Letort has worked on the analysis of plants with complex architecture. Three levels of simplifications of the model were defined and theoretical equivalences between the levels were studied, see Figure 14. The objective was to keep the same description at organ level for the trunk and the same compartment biomass on branches. As soon as the production equation uses the total blade surface as variable, it is possible to write a simplified model with equivalent sinks for primary growth. As regard secondary growth, a new model was developed by P.-H. Cournède and Ph. de Reffye in two steps: (i) the total amount of biomass allocated to ring compartment depends on the vigour of the plant (state variable Q/D, as introduced by A. Mathieu [43] and [11]) and (ii) layer repartition is calculating according to the number of active leaves above each metamer and thus is strongly dependent on the branch topology. So no simple equivalence could be found for layer repartition in the meta-organs from this current version of the complete model (but an independent simplified model was written).

6.1.4. *Stochastic Dynamical Equations of Growth*

Participants: C. Loi, M.-Z. Kang [GreenLab associated team], P.-H. Cournède, P. de Reffye.

The stochastic version of GreenLab (GL2) was developed by Kang in 2004 [5] A stochastic formal language adapted to the botanical concepts underlying the GreenLab organogenesis model was recently introduced. It is based on stochastic L-systems (parallel rewriting grammars) and on multi-type branching processes: stochastic processes control bud productions and at each growth cycle, each new growth unit is the result of a random variable. This formalism allows determining inductively the generating functions of the resulting plant structures and of the numbers of organs, which fully characterizes the plant development resulting from the elementary stochastic processes of bud productions.

The probability distribution of a random structure $S_p(k)$ can be described by its generating function $\mathcal{S}_p(k)$. It is defined as:

$$\mathcal{S}_p(k) = \sum_{w \in \mathcal{A}^*} P\left(S_p(k) = w\right) w \ . \tag{14}$$

where $P\left(S_p(k) = w\right)$ is the probability that the random structure $S_p(k)$ is equal to w.
We will denote:

$$\mathcal{S}(k) = \begin{pmatrix} \mathcal{S}_1(k) \\ \vdots \\ \mathcal{S}_P(k) \end{pmatrix} \ .$$

The generating functions of plant structures are multivariate polynomials in the letters of the alphabet. They are non-commutative for the multiplicative (concatenation) operator if we are interested in the plant topology and commutative if we simply consider the numbers of metamers and buds. Words are monomials. We consider differently $M = (m_1, ..., m_P)$ (the set of metamers of all possible physiological ages, which are terminal symbols) and $S = (s_1, ..., s_P)$ (the set of buds of all possible physiological ages, which are non-terminal symbols).
$\mathcal{S}_p(k)$ can thus be written:

$$\mathcal{S}_p(k)(M, S) = \sum_{w \in \mathcal{A}^*} P\left(S_p(k) = w\right) w(M, S) \ .$$

We can deduce $\mathcal{S}_p(k)$ from $\mathcal{S}_p(k-1)$ by exploring all the possible growth units that the buds of $S_p(k-1)$ may develop into. It corresponds to compose $\mathcal{S}_p(k-1)$ with the generating functions of order 1.

$$\mathcal{S}_p(k)(M,S) = \sum_{w \in \mathcal{A}^*} P\left(S_p(k-1) = w\right) w(M, \mathcal{S}(1)(M,S)) \ .$$

This holds for all p, and we can write in a compact way:

$$\mathcal{S}(k)(M,S) = \mathcal{S}(k-1)(M, \mathcal{S}(1)(M,S))$$

From classical properties of multi-type branching processes , we also have:

$$\mathcal{S}(k)(M,S) = \mathcal{S}(1)\left(M, \mathcal{S}(k-1)(M,S)\right) \tag{15}$$

The moments of the stochastic distributions of the numbers of organs are also explicitly deduced. Principles of this formalism is described in Simulation Journal [2], and the latest developments in Mathematics and Computers in Simulation [22] (to appear).

6.1.5. *Parameter identification on plants with complex architecture*

Participants: V. Letort, A. Mathieu, P. de Reffye, P.-H. Cournède, B. Pallas [ITB].

The theoretical advances in modelling and the development of new tools allowed confronting the model to new plant species, with more complex architectures than the previous

The Phd of A. Mathieu has brought significant advances allowing realistic and efficient simulations of tree growth. However, due to the topological complexity of their architecture and to their high number of organs, the identification of the parameter values required defining new types of target data. During the phd of V. Letort, three levels of simplification were defined for both topological description and organ or compartment mass measurements. The target format and the adequate fitting procedure were implemented in the DigiPlante software. The associated experimental protocols were applied to pine tree (Pinus tabulaeformis, Chinese Academy of Forestry), beech tree (INRA Nancy, LerFob) and wheat with tillers (Wageningen University, The Netherlands).

Pine tree was calibrated with a complete average topology defined from the measurement. The assumption of constant sink ratios for organs of each physiological age (branching order) was tested and validated on the data, except for organs of physiological age 1, the sink of which seem to vary during the tree growth. The fitting results were compared in the case of a complete average target and a simplified target. These results were presented to PMA06 [35]

The beech tree potential topology was chosen according to the botanical knowledge on its architecture. Then the topological and functional parameters were fitted on data from biomass compartments on the branches and individual organs on the trunk. For the beech tree, the ring biomass repartition was found to be less dependent on the structure than for the pine tree (in proportion).

Measurements on wheat with tillers included organ numbers at several growth stages with repetitions. Thus it was possible to fit the stochastic version of the model (developed by M. Kang, LIAMA) using the theoretical mean and variance. Then functional parameters were fitted using the mean organ numbers at each growth cycle instead of a particular topology. Results are now published in journal AoB [24]. In 2008, this work will be continued using new data on cotton tree.

6.1.6. *Parametric Identification : functional parameters*

Participants: P.-H. Cournède, P. de Reffye.

A generalization of the estimation procedure initially developed by Zhang (2003) [45] has been implemented in the DigiPlante software (PH Cournède). Branching plants with interactions between growth and development can be analyzed. Moreover, several plants with different topological structures or different ages can be fitted by the same set of functional source and sink parameters.

Besides, some theoretical work is done to improve the statistical method of parameter estimation, especially to determine the covariance matrix of the noise entailed by model errors, measurement errors and control errors. No publlications so far.

6.1.7. *Parametric Identification : Stochastic Model of Development*

Participants: V. Letort, A. Mathieu, P.-H. Cournède, P. de Reffye, C. Loi.

Studies on the calibration of the stochastic development of plants have begun in 2006. A procedure based on the plant production analysis at the compartment level to fit the number of organs and the biomass production, both in means and variances, has been worked out. The analysis uses different growth stages with several repetitions of the same plant. For each compartment means and variances are provided and the information is sufficient to compute the state probabilities of bud functioning and the parameters of sink and source relatioship using generalized least square method.

It is not necessary to study the detailed topological structure of each plant, which is tedious, but only the distribution of the cumulative production for both organs and biomass for each kind of compartment. Studies on the expression of the generating function have been carried out with the collaboration of Kang, Cournède and Quadrat (Metalau project). Two publications have been submitted. Development of software for GL2 level is in progress. A prototype exists in GreenScilab developed by Kang and Letort) and the first plant to be analysed for its stochastic behaviour is the wheat (for tillering). Data are coming from the Wageningen University.

6.1.8. *Interaction between plant growth and architectural development*

Participants: A. Mathieu, P.-H. Cournède, P. de Reffye, C. Loi.

A. Mathieu got her Phd degree at the ECP in April 2006. The document contains the first studies of the behaviour of the model of interactions between organogenesis and photosynthesis [43]. It gives a good explanation to the major events that occurs in the plant architecture during the Growth process (young stages, apparition of reiterations, fruits, tree aging, etc.) One of the interesting properties of the model is the possible apparition of a rhythmic mode of functioning as a result of the balance between the sources and sinks. Studies of such behaviours on cultivated plants like sweet-pepper or cucumber, will be undertaken in 2007 in collaboration with agronomic centers (Wageningen, CAU). First steps on the calibration of the thresholds that trigger the retroactions have been tried on such plant as young beech trees, coffee tree, rice tillers. Recent papers have been accepetd for publications in journal [30] and conference [38]. The objective is now to give a parobabilistic framework to this model of interaction. A new PhD is starting on the subject (C. Loi).

6.1.9. *Functional Landscape*

Participants: V. le Chevalier, M. Jaeger.

Marc Jaeger join DigiPlante at november 2006, as well as Vincent Le Chevalier (ECP) starting a PhD, working on this new research axis. Landscape functioning aims to simulate crop plantations and small landscape with a "reactive" environment. The goal is to simulation water exchanges (rain, runoff on terrain and absorption, diffusion in soil, plant water uptake and evapotranspiration) in interaction with DigiPlante growth model.
In 2005 and 2006, in the frame of the associate team GreenLab at LIAMA, two successive prototypes were developed by A. Lesluye, M. Jaeger, X. Mei and V. le Chevalier. First prototype, voxel based, was a simple simulator synchronzing all events at a daily schedule (water rain, run-of, diffusion, plant growth). Models were basic, and run-of simulated as a diffusion process on the land surface. This prototype and its underlying models was presented at PMA06, published end 2007 in the IEEE proceedings of the event [36].
The second prototype, is surface based. It involves an appropriate water run-off model, and the plant model is the recent GreenLab crop model and involves more advanced visualisation tools (see Computer Graphics section). The system was tested on synthetic cases (see Figure19), with real climate conditions and published in JCST journal[25].

Both prototypes show strong conceptual limitations. Since end 2006, concepts to develop the design of landscape functional simulators are extensivily studied. A new formalism of resource containers is on work, leading to a new software architecture. Up to now, part of this conceptual work is implemented and tested with prooved hydrological models in colaboration with CEMAGREF (Dr J.C. Maihol in Montpellier). Collaboration with this recognized team should help to asses the conceptual choices, to chose specific implementations and to validate the approach on real data with comparisons to existing models, before beeing extended to spatial heterogeneity.

6.2. Computer Graphics (in collaboration with LIAMA)

6.2.1. *Simple plant LOD models and real time plant rendering*

Participants: X.P. Zhang [associate team GreenLab], Q.Q. Deng [associate team GreenLab], M. Jaeger.

The collaboration with Dr. Xiaopeng Zhang and its team in LIAMA is still runing well with DigiPlante. In the past year progress were gained on LOD foliage geometrical compression [46]. Principles of the LOD schemes remind unchanged, while preprocessing stages were revisited. Especially, Organ Union tests for collapse are now drastically reduced thanks to hierarchical clusters, making the approach operative for huge trees and heavy forest scenes as shown in Figure17.

Figure 17. Real time view (close-up) on forest scene including conifers and broadleaves. From[34].

Specific LOD shemes were also defined for coniferes, replacing graphical primitives (cylinders) by lines, and defining line set replacement patterns by simple lines on far trees. Adaptative billboards is currently in study for further compression and huge scene display.

Dr Zhang Xiaopeng and PhD Student Deng QingQiong came to France in September - October, in the frame of the ANR (MMDA) NATSIM project. They gave talks of the current advances in LIAMA at CIRAD, INRIA Roquencourt (MIRAGE project), and ECP. Their visit to France did cover several aspects:

- finalising common publications (one submission to FSPM conference and 2 conference proceedings are concerned) [34][33]

- technical exchanges, especially LOD algorithms developed under Visual C++ in LIAMA were sucessfully adapted to run under free environments (Visual Express and Linux)

- further work planing and actions schedule

M. Jaeger is planned to stay half a month en 2007 in LIAMA, in Zhang Xiaopeng's team. The objective is to connect LOD's model developped in LIAMA with DigiPlante simulator geometrical output for end 2008.

6.2.2. *Rendering natural scenes with global illumination*
Participants: J. Teng [associate team GreenLab], M. Jaeger.

No major developments were hold on this field in 2007, dedicated mainly to dissemination activities. In LIAMA, PhD Teng Jun (under M. Jaeger co-supervision), has published its new ambient-occlusion approach, linear (literature has only quadratic approaches) in JCST journal [31]. Comparisons were hold with the classical approach, and results were presented at PMA06 (see illustration in Figure 18) and are available in the IEEE proceedings of the event [39].

Figure 18. Ambiant Occlusion Approximation on simulated Apricot Tree.

Teng Jun did successfully succeed his Phd Defense mid summer 2007. He joined Thomson's R-D Lab in Beijing autumn 2007, working on advanced Computer Graphics real time applications.

6.2.3. *Functional Landscape Visualisation*
Participant: M. Jaeger.

Visualisation of functional landscape simulations started in 2007. It aims to visualize combination of maps (among terrain altitudes, water soil content, run off, daily biomass, cumulated biomass, temperature, ...). Classical surface mesh tools were written, as well as histogram, and curve display tools, allowing comparisons during a given period, or spatial heterogeneity comparisons at a given stage as shown in Figure19 . Principals of the developped visualisation functions and illustration examples are part of the communications -Simulation and Visualisation of Functional Landscapes: Effects of the Water Resource Competition between Plants- in journal JCST[25] and in IEEE PMA06 proceedings -A Functional Landscape Prototype to simulate Water Resource competition between Plants-[36].

6.2.4. *Volume imaging*
Participant: M. Jaeger.

Volume imaging is a past research and development action of M. Jaeger during its stay in LIAMA. In 2007, the modules developed in 2002-2003 (LIAMA project 01-08) were used to generate voxel-based landscapes and single tree output for collaborations with Philippe Decaudin (INRIA-EVASION) and Zhang Xiaopeng (LIAMA). Their respective aims are real-time landscape rendering with texture slices, and 3D plant reconstruction from cloud points.
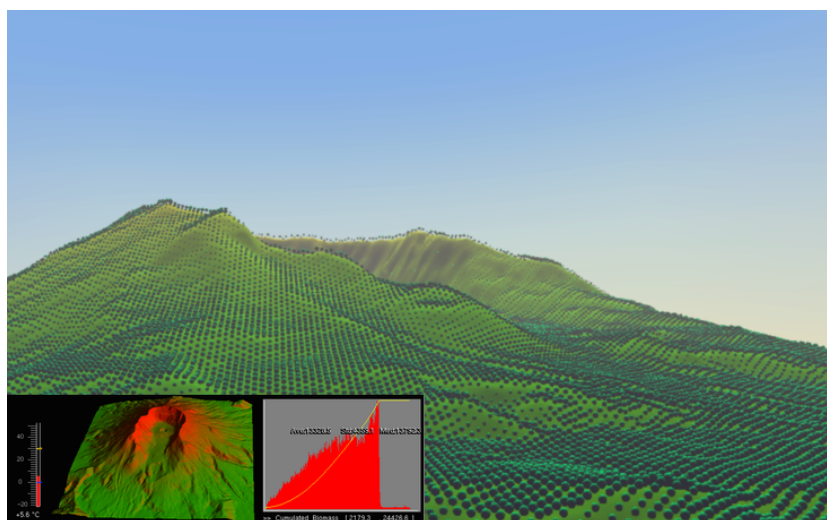
Figure 19. Functional Landscape simulation and visualisation. Biomass values map to colors (red, left) or to sphere radii.

In 2007, a publication to prestigious US PNAS journal [21] was published, in which these modules where applied with chinese partners (2003-2005) to register and reconstruct CT scan exams of the recent Giant Panda fossil discovery.

7. Contracts and Grants with Industry

7.1. Contracts and Grants with Industry

- The contract with ITB has been signed for 3 years with Digiplant. Fundings are 100000 euros/ year. It allows to grant a Phd and a postdoc at fulltime on the job. The society S2B is studying currently new contracts on Potato, Barley and Canola plants.

- Digiplante participates to the project "Tera data " in the context of the "Pôle de compétitivité" Cap Digital. It will grant a new Phd for Digiplante.

- Despite the fact that ANR (05-MMSA-45) Natsim does not involve DigiPlante team itself, M. Jaeger is still representative of LIAMA with Dr Xiaopeng Zhang in the project, until end 2008. On this opportunity, collaboration with IRIT (Co-ordiantor) and INRIA Evasion can still go on and fund exchanges between France and China.

- Digiplante is involved in a the ANR (07-CIS) 3dWorlds project linking INRIA-DigiPlante with ENS, CNRS, IRD (Geodes), IFI Hanoi, Australian National University, just accepted. Co-ordinator: ENS

8. Other Grants and Activities

8.1. Visiting Scientists

- Zhang Baogui, 2 monthes, 1 stay, Professor at CAU in China.

- Zhang Xiaopeng, 6 weeks, 2 stays, Associate-Professor at Liama-Casia in China
- Deng QingQiong, 2 monthes, 2 stays, Doctorate student at Liama-Casia in China
- Cheng Zangling, 1 month, 1 stay, Doctorate student at Liama-Casia in China

9. Dissemination

9.1. Conference and workshop committees, invited conferences

Invited speakers:

- P. de Reffye was an invited speaker to RNSC colloqium ,"Vers une science des systèmes complexes" March 21-23, CNRS, Paris
- P. de Reffye is an invited speaker to "Donnees et Modeles pour les systemes complexes et applications à l'environnement ", November 29-30 INRIA Rhône-Alpes, Grenoble
- M. Jaeger was an invited speaker to CoReach seminar (FP6 EU project on Europe-China Cooperation), June 4-5, Royal Society, London

Participation to international conferences:

- FSPM07 V. Letort, A. Mathieu November 2007, New Zeland

Seminars.

- P. de Reffye was an invited speaker to Models in Agronomy Seminar, May 2007, Xian, China
- Seniors and several students of Digiplante team did participate to GreenLab seminar (7 talks given) on March 11-11, at CIRAD Montpellier
- M. Jaeger and V. le Chevalier did participate to the "Paysage et Peuplement" seminar (2 talks given) on May 30 - June 1, at CIRAD Montpellier
- M. Jaeger did participate to "Root Architecture" seminar (1 talk given) on September 12, at CIRAD Montpellier

Boards:

- Folowing First International Symposium on Plant Growth Modelling and Applications PMA03 [1], organised by GreenLab and CAU, for the second edition PMA06, P.de Reffye, P.H. Cournede and M. Jaeger are members of the Scientific Committee.
- Marc Jaeger is member of Executive Commitee of Edutainment planned in 2008, June 4-5, Nanjing, China

Reviewing (besides boards member):

- P.de Reffye, P.H. Cournede and M. Jaeger did review papers submitted to Annals of Botany.
- P.H. Cournede and M. Jaeger did review papers submitted to JCST.
- M. Jaeger did review papers submitted to JVR, Eurographics 08 and Computer Animation and Virtual Worlds.

9.2. Courses and Tutorials - Media

The GreenLab model is more and more be used in several laboratories in China, in Holland and in France. GreenSciLab, the free GreenLab model implementation running under Scilab environment is now available with tutorial pages and study cases on LIAMA web site. This tool is therefore used by DigiPlante partners.

- In the frame of an ERASMUS project leaded by Wagueningen University: 7 hours course on the GreenLab model (Ph. de Reffye) at University of Orsay (Paris).

- A joint course of 15H between AgroParisTech and Centrale Paris at master level was given by P.H. Cournède and P. de Reffye on "Functional-Structural Plant Modelling" with practice on GreenScilab.

- A lecture (2H) was also given at Orsay University at master level on "Modelling in Plant Sciences" by P.H. Cournède

- Several student projects are also given each year at Centrale Paris linked to the research activities of Digiplante.

Philippe de Reffye was invited to "epistemologic" talks, as an experiment reseracher in multi-disciplinary topics.

- P. de Reffye was invited to the seminar "Biologies face a la modelisation et l'interdisciplinarite", October 8th, ENS, with JC Mounolou

- P. de Reffye was invited on France Culture Broadcast - Emission du jeudi 13 septembre 2007 La modélisation informatique"

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