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*Project-Team Digiplante*

*Mathematical models for plant growth and  
architecture*

*Saclay - Île-de-France*

Theme : Observation, Modeling, and Control for Life Sciences

*Activity*  
*R* *eport*

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*Digiplante is a common project with Ecole Centrale Paris and CIRAD. The GreenLab team at LIAMA is an “associate team” with which very strong links exist. The team became an EPI on July 1<sup>st</sup>, 2008.*

## 1. Team

### Research Scientist

Philippe de Reffye [ Team Leader, Cirad, HdR ]  
Yves Dumont [ Cirad, HdR ]  
Marc Jaeger [ Cirad ]

### Faculty Member

Paul-Henry Cournède [ Deputy Head, MCF, Centrale Paris, HdR ]  
Véronique Letort [ MCF, Centrale Paris ]  
Amélie Mathieu [ MCF, Agro Paris Tech (Chercheur associé) ]

### PhD Student

Qi Rui [ Centrale Paris, LIAMA ]  
Benoit Pallas [ Centrale Paris ]  
Sébastien Lemaire [ AgroParisTech ]  
XiuJuan Wang [ Centrale Paris, CAU ]  
Cédric Loi [ Centrale Paris ]  
Qiongli Wu [ Centrale Paris ]  
Zhongping Li [ Centrale Paris ]  
Fenni Kang [ Centrale Paris ]  
Feng Lu [ Univ. Montpellier II ]

### Post-Doctoral Fellow

Trevezas Samis  
Bertheloot Jessica

### Administrative Assistant

Christine Guiard

### Other

Thomas Guyard [ Engineer ]  
Benoit Bayol [ Engineer ]

## 2. Overall Objectives

### 2.1. Research fields

Digiplante’s main focus is the mathematical modelling of plant architectural growth by developing the GreenLab model. Several issues are concerned:

- Formalism of the organogenesis model based on stochastic grammars
- Integration of the functioning into plant structure: bud functioning, biomass production and partitioning in both deterministic and stochastic cases
- Interactions between Organogenesis and Photosynthesis
- Plant-environment interactions (light, temperature, water)
- Tree structure simplification and multi-scale representation
- Transition from the individual plant to plant populations
- Optimization and Control of the dynamical growth to improve yield under constraints
- Connexion with others research fields: mechanics, radiosity, genetics
- Visualization of plants from individual to population and landscape level with different computer graphic techniques
- Developing software for the simulation of the 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 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 software 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 thinnings can bring benefits. 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

- Marc Jaeger co-chaired the PMA09 conference.
- 1 PhD (B. Pallas) and 2 HDR (PH Cournède, Y Dumont) were defended.

# 3. Scientific Foundations

## 3.1. DigiPlante at INRIA

Derived from the AMAP model developed in the 1990s at CIRAD [79], GreenLab's new formulation was introduced at LIAMA (Beijing) in 2000, through the GreenLab Associate Team with INRIA. Today, the model is studied and improved owing to the DigiPlant research team that is a joint team of researchers from INRIA, CIRAD and Ecole Centrale Paris. Some very close partnerships exist with LIAMA, China Agriculture University, Wageningen University, INRA, SupAgroMontpellier and AgroParisTech. The development of the GreenLab model is shared between all these partners, with strong interactions (International exchanges, common publications and joint PhD).

Our approach to develop the mathematical model of plant growth strongly relies on the plant organization described by botanists. This leads to relevant choices [18] in order to obtain an efficient method of factorization based on plant instantiations [2]. Plant development concerns organogenesis, i.e. the appearance of organs. Growth depends on photosynthesis that insures organ expansion. 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 organogenesis. It provides the number of organs produced by the buds. It may be determined by plant functioning and the level of trophic competition [20].
2. Computing biomass production and allocation. Leaf surface area is used to determine photosynthesis and the neat biomass production is shared between the different organs (whose numbers are known by the organogenesis step) 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 plant architecture for visualization or to study interactions with the environment. This last step involves geometry applied to the results of the two previous steps.

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

## 3.2. The Equations of Plant Growth and Development

GreenLab combines both organogenesis and functional growth in a mathematical dynamic system. A dual-scal automaton was initially used [77] to describe GreenLab organogenesis. However, it was shown to be equivalent to a growth grammar [16], and this formalism is used from now on to describe the GreenLab organogenesis model. In this section we recall the basic botanical hypotheses used to construct the model of organogenesis, how it defines a growth cycle that is used to synchronize the computation of both organogenesis and functional growth. The construction of the growth grammar is also recalled, with its fundamental property: its factorization, taking advantage of all instantiations in plant architecture. Based on this growth grammar, the functional equations of biomass acquisition and distribution can be derived.

### 3.2.1. Plant Development and Growth Cycle

As explained in [52], organogenesis results from the functioning of undifferentiated cells constituting the apical meristem and located at the tip of axes. When in active phase, this meristem forms buds that will develop into new growth units composed of one or several metamers (also called phytomers). A metamer is a botanical entity chosen as the elementary scale to model plant architectural development in this study. It is composed of an internode bearing organs: axillary buds, leaves, flowers. Depending on species, metamers are set in place rhythmically or continuously.

In the rhythmic case, see Figure 1, the plant grows by successive shoots of several metamers produced by buds. The appearance of these shoots defines the architectural *Growth Cycle*. A *Growth Unit* is the set of metamers built by a bud during a growth cycle. These metamers can be of different kinds and ordered according to botanical rules, like acrotony. For example, most temperate trees grow rhythmically, new shoots appearing at spring. For such plants, and if we do not consider polycyclism and neof ormation, the architectural growth cycle corresponds to one year.

Plant growth is said continuous when meristems keep on functioning and generate metamers one by one, see Figure 1. The number of metamers on a given axis (that is to say generated by the same meristem) is generally proportional to the sum of daily temperatures received by the plant, see [58]. The growth cycle is defined as the thermal time unit necessary for a meristem to build a new metamer, it can be quite short, corresponding to a couple of days. The growth unit is thus simply composed of one metamer. The growth of tropical trees, bushes or agronomic plants is often continuous.

So far, Digiplante does not consider time scales that are smaller than the architectural growth cycle and we study the development of new growth units as a discrete process. The *Chronological Age (CA)* of a plant (or of an organ) is defined as the number of growth cycles it has existed for.

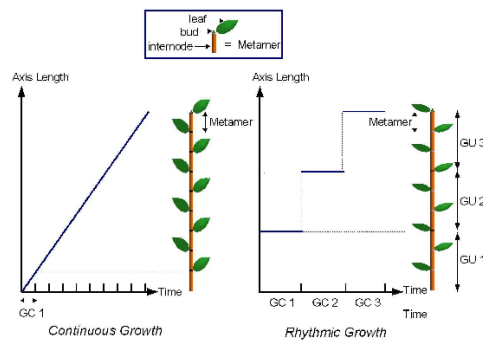


Figure 1. Growth Cycle (GC), Growth Unit (GU) and Metamer in GreenLab. The axis length is given as a function of time for continuous and rhythmic growths



Since metamers may bear axillary buds, plant architecture develops into a hierarchical branching system. [52] underlined that architectural units can be grouped into categories characterized by a particular combination of morphological parameters. Thus, the concept of *Physiological Age* (PA) was introduced to represent the different types of growth units and axes. For instance, on coffee trees, there are two types: orthotropic trunk and plagiotropic branches. The main trunk's physiological age is equal to 1 and the oldest physiological age denoted by  $P$  corresponds to the ultimate state of differentiation for an axis, it is usually short, without branches. We need less than 5 physiological ages to describe the axis typology of most trees. The apical meristem or bud of an axis is thus characterized by the physiological age of the growth unit that it may produce and a metamer is characterized by its physiological age  $i$  (which is the physiological age of the growth unit that it belongs to) and that of the buds that it bears  $j$ . Except in some very rare cases, we always have:  $i \geq j$ . Moreover, along an axis, the morphological features of the growth unit may evolve with the age of the apical meristem. This process is described as the meristem sequence of differentiation by [52], and corresponds to a transition to a superior physiological age of the meristem.

### 3.2.2. Alphabet, Growth Grammar and Structural Factorization

This section summarizes results presented in [16],[2],[9]. In GreenLab, the alphabet  $\mathcal{G}$  is given by the set of metamers  $\mathcal{M}$  and buds  $\mathcal{B}$ . A metamer is defined with four indices and is denoted by  $m_{pq}^t(n)$ :

- its chronological age:  $n$ ,
- its physiological age:  $p$ ,
- the physiological age of its axillary buds:  $q$ , ( $q \geq p$ ),
- the chronological age of the plant:  $t$ .

A bud is defined by three indices and is denoted by  $b_p^t(n)$ :

- its physiological age:  $p$ ,
- the number of growth cycles  $k$  for which bud's physiological age has been  $p$  - in the sequel, we will call it *ontogenic age* of a bud,
- the chronological age of the plant:  $t$ .

If  $T$  is the maximum growth time, the organogenesis alphabet is given by:  $\mathcal{G} = \mathcal{M} \cup \mathcal{B}$ , with

$$\begin{cases} \mathcal{M} = \{m_{pq}^t(n) / 1 \leq p \leq P, p \leq q \leq P, 1 \leq t \leq T, 1 \leq n \leq t\} , \\ \mathcal{B} = \{b_p^t(n) / 1 \leq p \leq P, 0 \leq t \leq T, 0 \leq n \leq t\} . \end{cases} \quad (1)$$

We do not consider symbols for organs since the constitution of a metamer is supposed fixed by botanical rules (an internode and a given number of leaves and fruits). If, for example, flowering is particularly studied, symbols denoting flowers could be introduced in the alphabet.

**Definition 1 (Set of words over an alphabet)** The set of words over an alphabet  $\mathcal{A}$  is defined as the monoid generated for the concatenation operator ".", seen as an internal, non-commutative operation, by  $\mathcal{A} \cup \{\mathbf{1}\}$ , where  $\mathbf{1}$  is the neutral element for the concatenation operator (which corresponds to the empty word). It is denoted  $\mathcal{A}^*$ .

$\mathcal{G}^*$  will thus represent all the possible topological structures composed with buds and metamers. For example,  $m_{12}^t(1)b_2^t(0)b_1^t(1) \in \mathcal{G}^*$  represents at growth cycle  $t$  a structure composed of an internode of physiological age 1, bearing a lateral bud of physiological age 2 and an apical bud of physiological age 1. We will see that of course the structures of interest, that is to say botanically relevant, form a small subset of  $\mathcal{G}^*$  (corresponding to a language over  $\mathcal{G}$ ). It is important to consider concatenation as non-commutative when studying plant topology.

As recalled in section 3.1, GreenLab organogenesis can be seen as the combination of two phenomena, branching and meristem differentiation. It can be easily modelled with the grammar formalism and we propose to define it as a FOL-system as follows:

**Definition 2 (GreenLab Organogenesis)** GreenLab organogenesis is defined as a FOL-system [64] [70]  $\langle \mathcal{G}, \mathcal{B}, P_r \rangle$  with the following production rules  $P_r$ :

For all  $(t, n, p) \in [0; T] \times [0; \min(\tau(p), t)] \times [1; P]$ :

$$b_p^t(n) \begin{cases} \xrightarrow{n < \tau(p)} \left( \prod_{q=p}^P (m_{pq}^{t+1}(1))^{u_{pq}(t+1)} (b_q^{t+1}(0))^{v_{pq}(t+1)} \right) b_p^{t+1}(n+1) \\ \xrightarrow{n = \tau(p)} \left( \prod_{q=p}^P (m_{pq}^{t+1}(1))^{u_{pq}(t+1)} (b_q^{t+1}(0))^{v_{pq}(t+1)} \right) b_{\mu(p)}^{t+1}(0) \end{cases}$$

and for all  $(t, n, p, q) \in [1; T] \times [1; t] \times [1; P] \times [p; P]$ :

$$m_{pq}^t(n) \longrightarrow m_{pq}^{t+1}(n+1)$$

with:

- $u_{pq}(t)$ : number of phytomers  $m_{pq}$  in a growth unit of PA  $p$ , appearing at growth cycle  $t$
- $v_{pq}(t)$ : number of active axillary buds of PA  $q$  in a growth unit of PA  $p$ , appearing at growth cycle  $t$
- $\tau(p)$ : number of GC after which a bud of PA  $p$  changes to PA  $\mu(p)$ . Vectors  $\tau$  and  $\mu$  characterize meristem differentiation.

A fundamental result [72] was surprisingly never used in the context of models of plant development: it is the ability to factorize the L-system productions. It showed particularly adapted to the concept of physiological age, cf. [18], [2]. We are thus able to factorize plant structure into smaller parts that may repeat themselves a large number of times.

**Definition 3 (Substructure)** At growth cycle  $t \geq 0$ , a substructure of physiological age  $p$ ,  $1 \leq p \leq P$  and chronological age  $n$ ,  $0 \leq n \leq t$  is a word in  $\mathcal{G}^*$  defined as the complete plant structure that is generated after  $n$  cycles by a bud of physiological age  $p$ . It is also characterized by the ontogenic age  $k$  of the bud generating it. It is denoted by  $S_p^t(n, k)$  (corresponding to the structure generated by  $b_p^{t-n}(k)$  after  $n$  growth cycles).

We show how the structural factorization allows the inductive computation of all the substructures, providing an efficient algorithm to simulate plant organogenesis. We deduce the following important result.

**Theorem 1 (Dynamic Equation of Plant Development)** For all  $t \geq 1$ ,  $n \in [1, t]$ ,  $p \in [1, P]$ ,  $q \in [p, P]$ ,  $k \in [0, \min(\tau(p), t)]$ , we have:

$$\begin{aligned} \text{If } 0 \leq k < \tau(p): S_p^t(n, k) &= \left[ \prod_{p \leq q \leq P} (m_{pq}^t(n))^{u_{pq}(t+1-n)} (S_q^t(n-1, 0))^{v_{pq}(t+1-n)} \right] S_p^t(n-1, k+1) \\ \text{else: } S_p^t(n, \tau(p)) &= \left[ \prod_{p \leq q \leq P} (m_{pq}^t(n))^{u_{pq}(t+1-n)} (S_q^t(n-1, 0))^{v_{pq}(t+1-n)} \right] S_{\mu(p)}^t(n-1, 0) \end{aligned} \quad (2)$$

This decomposition is illustrated on  $S_1(2)$  in Figure 2. If we suppose that all the elements of the alphabet (set of metamers  $m_{pq}^t(n)$ , set of buds  $b_p^t(n)$ ) as well as the sequences  $(u_{pq}(t))_t$  and  $(v_{pq}(t))_t$  are known, Theorem 1 shows us how to build the topological structure of the plant at any growth cycle  $t$  recursively, as follows:

- Substructures of chronological age 0 are buds:  $S_p^t(0, k) = b_p^t(k)$ , • and if all the substructures of chronological age  $n-1$  are built, we deduce the substructures of chronological age  $n$  from Equation 2 as functions of  $m_{pq}^t(n)$ ,  $u_{pq}(t-n+1)$  and  $v_{pq}(t-n+1)$ .

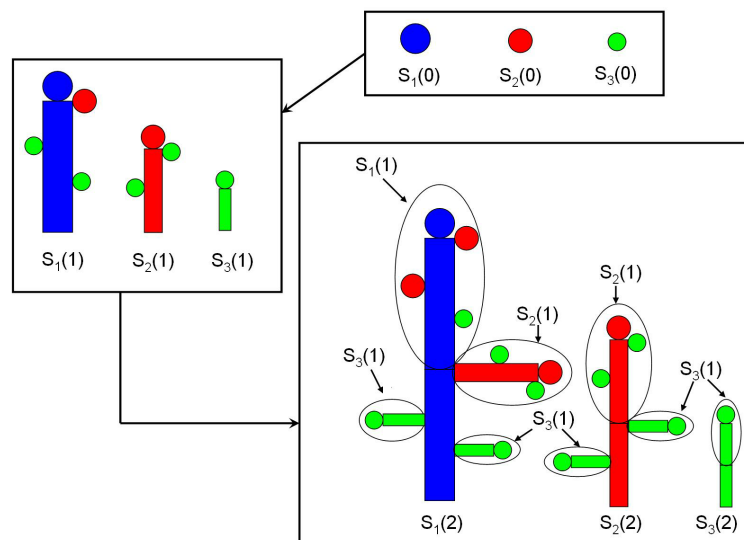


Figure 2. Substructures of physiological ages 1, 2, 3 at chronological ages 0, 1, 2 and their organization:  $S_1(0)$ ,  $S_2(0)$ ,  $S_3(0)$  are buds of physiological age 1, 2, 3 respectively. In this example, a growth unit of physiological age 1 is composed of 2 metamers of type  $m_{13}$  and 1 metamer of type  $m_{12}$ ; a growth unit of physiological age 2 is composed of 2 metamers of type  $m_{23}$ ; a growth unit of physiological age 3 is composed of 1 metamer of type  $m_{33}$  (without axillary bud).

Substructures and metamers will be repeated a lot of times in the tree architecture, but they need to be computed only once for each kind.

If we only consider topology, we do not need to characterize the metamers by their chronological ages nor by the plant age.  $m_{pq}^t(n)$  can thus be simply be denoted by  $m_{pq}$ . But if we consider the functional growth of a plant, metamers of different chronological ages have different masses and sizes, as well as metamers of the same chronological age, but at different plant ages.

[16] introduced how the dynamic development equation can be extended to build plant geometry with geometric operators replacing the concatenation operator. We will not detail this point here since our objective is to study plant functional growth which only relies on topology and not geometry in GreenLab.

Plant topology can simply be seen as a function of:

- the sequences  $(u_{pq}(t))_t$  and  $(v_{pq}(t))_t$  for all  $(p, q)$  such that  $1 \leq p \leq q \leq P$  (they will be called *development sequences*),
- the vectors  $(\tau(p))_{1 \leq p \leq P}$ ,  $(\mu(p))_{1 \leq p \leq P}$  in case of meristem differentiation.

The GreenLab organogenesis model has been derived in 3 forms:

- GL1 corresponds to the deterministic organogenesis model, without influence of the plant functioning. Mathematically, it corresponds to  $u_{pq}$  and  $v_{pq}$  constant, see [15]. In such case,  $S_p^t(n)$  are (topologically) independent of  $t$ , and the construction does not have to be done at each growth cycle but only once.
- GL2 corresponds to a stochastic model of organogenesis,  $u_{pq}$  and  $v_{pq}$  are stochastic variables. As a consequence, substructures of the same chronological and physiological ages can be very different:  $S_p^t(n)$  is a stochastic variable with values in  $S^*$ . More details are given in section [5] and in [9].
- GL3 corresponds to a deterministic model with total retroaction between organogenesis and photosynthesis.  $u_{pq}(t)$  and  $v_{pq}(t)$  are functions of the biomass produced by the plant at growth cycle  $t - 1$  and  $t$  respectively, see [12].

$U^t$  will denote the vector  $(u_{pq}(t))_{1 \leq p \leq q \leq P}$  and  $(U^t)_t$  the associated sequence of vectors. Likewise,  $V^t$  will denote the vector  $(v_{pq}(t))_{1 \leq p \leq q \leq P}$  and  $(V^t)_t$  the associated vector of sequences.

### 3.2.3. Functional Growth

Literature is already abundant on the functional concepts underlying the GreenLab model and its various versions ([18], [15], [4], [17], [3]). The fundamental principles common to all these versions are actually very general and are shared (to some extent) with various other models (for example LIGNUM [69], TOMSIM [56], GRAAL [54]...). The central equation of GreenLab describes the growth of an individual plant potentially in a population (field crops, forest stands...). Competition with other individuals for light, water, nutrients can thus be taken into account and affects the computation of biomass production, see [3] regarding competition for light or [6] for competition for water.

GreenLab aims at describing the source-sink dynamics during plant growth. Sources correspond initially to the seed and then to biomass production and reserve remobilization. Sinks are demands for biomass of all living organs. So far, all sinks have access to all sources since we consider a common pool of biomass. However, this hypothesis is not fundamental and could be relaxed. Since structural development is described in GreenLab at the level of organs, the computation of demands is coupled with organogenesis. For this reason, a consistent time unit for architectural growth and photosynthetic production is defined in order to handle a constant structure. It allows the derivation of the discrete dynamic system of growth, see Figure 3

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 derived recursively by applying structural morphisms [2] to the dynamic equation of plant development (2) giving the number of metamers in the plant as we know the number of organs per metamer and their life spans. The functional growth is then described by the two following steps, biomass acquisition (production) and distribution among living organs.

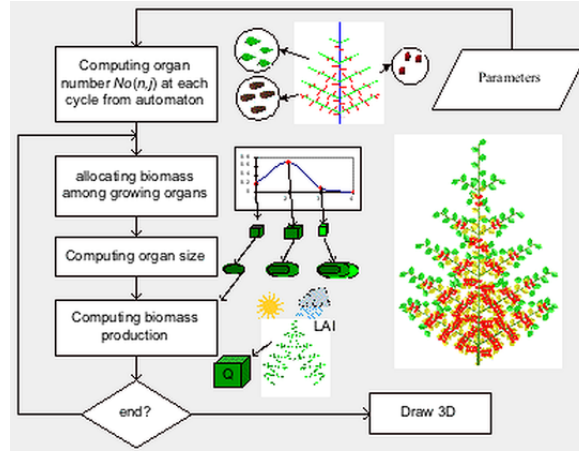


Figure 3. Flowchart of the GreenLab model.

#### Biomass acquisition :

Different strategies were used and are currently used in GreenLab according to plants to compute  $Q^t$ , the biomass production at growth cycle  $t$ . There are mostly 3 sources to provide biomass for allocation: seed, resource acquisition by photosynthesis and reserve remobilization (from roots, layers or senescent organs). We will not speak about the seed, which usually gives  $u^0$  and may be considered as emptying on several growth cycles, that is to say also contributing to  $u^1, u^2 \dots$

Classically, the biomass production at growth cycle  $t$   $Q^t$  is taken as a parametric function of  $\mathcal{A}^t$ , the total photosynthetic leaf area, and of the environmental conditions. To keep it simple, we sum up all the environmental effects in  $E^t$ , which may be chosen as a function of the Photosynthetically Active Radiation (PAR), hydric stress (Fraction of Transpirable Soil Water), temperature (for biologic efficiency)... Only simple functions have been tested so far in GreenLab. A possible production function inspired by classical crop models and Beer-Lambert's law ([4] and [3] for details) can be written:

$$Q^t = E^t \beta (1 - \exp(-\gamma \mathcal{A}^t)) \quad (3)$$

where  $\beta$  and  $\gamma$  are empirical parameters.

It is helpful to rewrite this equation by changing the parametric structure:

$$Q^t = E^t \mu S_p \left( 1 - \exp\left(-k \frac{\mathcal{A}^t}{S_p}\right) \right) \quad (4)$$

with the parameters having now a more relevant physical meaning:  $\mu$  is an energetic conversion efficiency,  $k$  is the extinction coefficient of the Beer-Lambert law and  $S_p$  is related to a characteristic surface for resource acquisition.

In her PhD, V. Letort [63] proposed that, after some time, a proportion of organ biomass is given back to the common pool and reallocated to new organs in expansion.

#### Biomass partitioning :

We recall that  $m_p^t(n)$  denotes at growth cycle  $t$  a metamer of physiological age  $p$  and chronological age  $n$ . It contains organs of type  $o$  (where  $o = b, p, i, f$ , for blades, petioles, internodes, flowers or fruits respectively) whose masses are denoted by  $q_{o,p}^t(n)$  at growth cycle  $t$ . Let  $T_{o,p}$  denote the maximal life span of organs of type  $o$  and physiological age  $p$ . The allocation equation is thus given for all  $t \geq 0$  by:

$$\begin{cases} q_{o,p}^{t+1}(n+1) = q_{o,p}^t(n) + \frac{p_{o,p}^t(n)}{D^t} Q^t & \text{if } 0 \leq n \leq \min(T_{o,p} - 1, t) \\ q_{o,p}^t(n) = 0 & \text{if } n = 0 \text{ or } n \geq \min(T_{o,p}, t + 1) \end{cases} \quad (5)$$

where:

- $p_{o,p}^t(n)$  is the sink of an organ of type  $o$  in  $m_p^t(n)$
- $D^t$  is the total demand of the plant at growth cycle  $t$  (that is to say the sum of all sinks)

$$D^t = \sum_{o,p} \sum_{n=0}^{T_{o,p}} N_{o,p}^t(n) p_{o,p}^t(n) \quad (6)$$

where  $N_{o,p}^t(n)$  is the number of organs of type  $o$ , physiological age  $p$ , chronological age  $n$  at time  $t$ .

- $Q^t$  is the biomass available for allocation.

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

**Remark 1** This general formulation concerns primary growth of the above ground organs. For the complete model, we need to consider the root system demand, and for trees, the ring demands (for the secondary growth). A detailed presentation of the different types of modelling strategies can be found in the PhD thesis of V. Letort [63].

The shape chosen for the sink variation function  $p$  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 chronological age. Beta laws were found to be suitable for the purpose.

### 3.2.4. Interactions between Plant Architectural Development and Functional Growth

During her PhD, A.Mathieu [66] modelled a retroaction of plant functioning on plant topology controlled by the state of trophic competition (GL3 model). Such model illustrates in a very simple way how plant plasticity is expressed under environmental constraints.

The vectors  $U^t$  and  $V^t$  that give the rules of the organogenesis model (that is to say that control the bud behavior) are chosen as functions of the ratio of available biomass to demand. Integer part of linear functions are usually chosen. In Figure 3.2.4, we see the difference between the GL1 model (with constant sequences  $(U^t)_t, (V^t)_t$ ) and the GL3 model, (with sequences  $(U^t)_t, (V^t)_t$  functions of  $u^t$ ).

$U^t$  is a function of  $\frac{Q^{t-1}}{D^{t-1}}$  and  $V^t$  a function of  $\frac{Q^t}{D^t}$  (they are usually chosen as linear functions). The behaviour of the system was studied by A. Mathieu during her PhD. The conditions of the growth stabilisation were determined according to the parameters. Moreover, an interesting emerging property was obtained: under some conditions, rhythmic phenomena may be generated by the system (Biomass production, fruiting and branching alternation, number of internodes per growth unit ..., see Fig. 3.2.4). Such phenomena are often observed during plant growth but were poorly modelled so far.

As detailed in the section giving the new research results of the team, some important results concerning the calibration of the thresholds of fructification have been obtained on cucumber plants (in collaboration with the Chinese Agricultural University and Wageningen).

The objective is now to give a parobabilistic framework to this model of interaction.

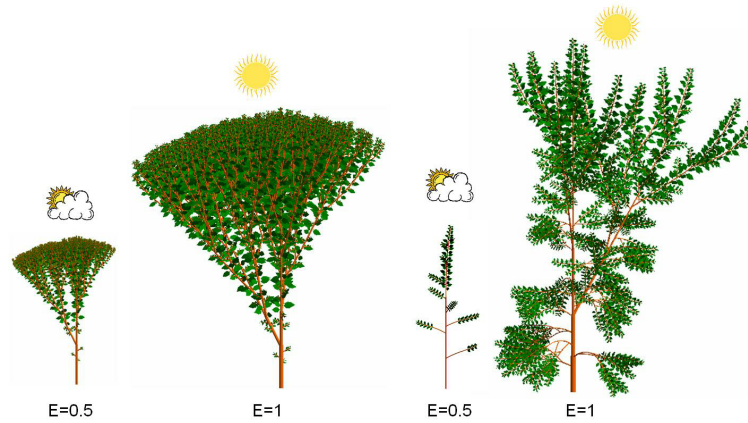


Figure 4. Effects of climatic variations on the GL1 and GL3 organogenesis models: on the left side (GL1), topology is fixed, organs are simply smaller to adjust to the environment; on the right side (GL3), topology is variable and the plant adapts its development to the environmental conditions.

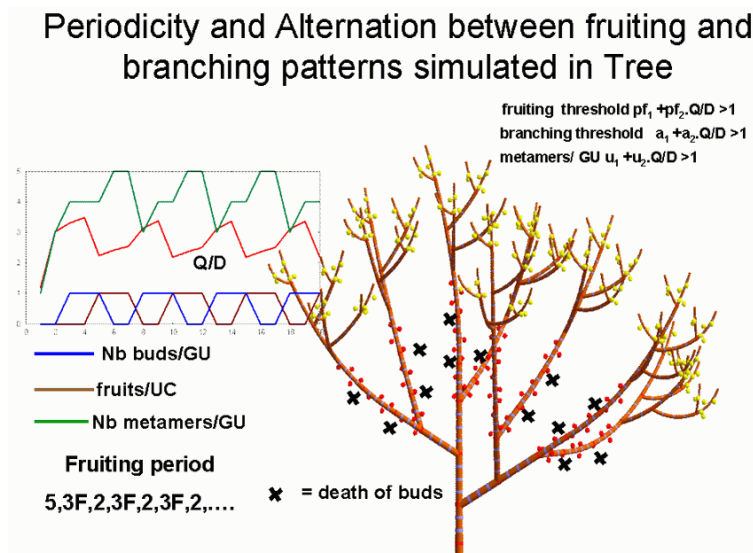


Figure 5. Rhythmic growth for fruiting and branching in alternation depending of the retroaction between plant production and plant development.

### 3.2.5. Extension of GreenLab to Field and Stand Levels

The results on single plant growth modelling are extended at the field and stand level, in order to simulate crop and forest production. It needs to integrate the competition for light and for soil resources among plants.

*A model of competition for light :*

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, [3].

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 [12].

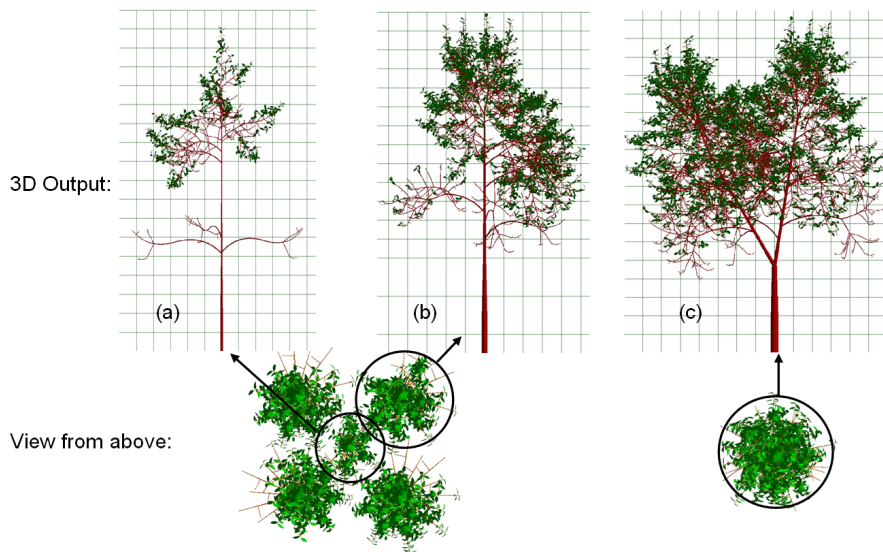


Figure 6. Simulation of tree growth in heterogeneous conditions: view from above and detailed architectures of the individuals. In the upper right corner of the figure, Tree 1 grows in open-field like conditions. In the lower left corner, Tree 3 surrounded by its four neighbours (including Tree 2) severely suffers from competition

The model was applied to mono-specific field crops and forest stands.

The application of the model to trees illustrates the expression of plant plasticity in response to competition for light, cf. Figure 3.2.5. 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.

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) [57]. 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.

*Functional landscapes :*



Models of landscape functioning aims at simulating, crop plantations and small landscape with a “reactive” environment. The goal is to simulate water exchanges (rain, runoff on terrain and absorption, diffusion in soil, plant water uptake and evapotranspiration) and competition in interaction with the GreenLab growth model. The difficulty of the approach lies in the multiphysics and multiscale models to implement. After some preliminary works carried out at LIAMA, it is now the PhD subject of V. Le Chevalier, under the supervision of Marc Jaeger.

Two successive prototypes were developed. The first prototype, voxel based, was a simple simulator synchronizing all events at a daily schedule (water rain, run-off, diffusion, plant growth). Models were basic, and run-off simulated as a diffusion process on the land surface [61], using a discrete volume spatial grid. This model was implemented in C++ under QT environment and tested on BULL Novascale HPC (16 cores). The second prototype, is still based on a spatial discrete grid, but limited to the layer. It involves an appropriate water run-off model, and the plant model is a simple version of the GreenLab crop model and involves more advanced visualisation tools.

At this stage, visualisation of functional landscape simulations aims at visualizing 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. The originality of the developed tools lies in the fact that all these maps are dynamic (daily change), and thus not compatible with classical approaches (all in memory). Vegetation representation is rough, limited to a simple color definition merged with the relief texture. A “pseudo realistic” landscape visualisation can be performed representing the cumulated biomass by spheres, converting somehow the crop production to a “tree crow”. The corresponding tool (SURFVIEW) is written in C++ with GLUT and OpenGL libraries.

The system was tested on synthetic cases, with real climate conditions and published in JCST journal [6]. Both prototypes show strong conceptual limitations especially on two crucial points: model synchronism and data integrity. Time synchronism is a strong critical aspect in our case since we have to face calendar asynchronism processes (rain, run off) with thermal time cycles (plant development). However plant functioning must be simulated at short periods of calendar time in order to uptake the appropriate water supply. Concerning data now, and more precisely water resources, the various models (run off, absorption, plant growth interact spatially on the same data with high risk of collision). Since end 2006, concepts to develop the design of landscape functional simulators are extensively studied leading slowly to discrete event simulation formalisms.

### 3.3. Parameter Identification of the GreenLab Model from Experimental Data

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 estimated in order to fit the weights and 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), biomass production and biomass partitioning to each organ during the growth from the architectural data. However, the identifiability issue has not been studied yet. Only a lot of numerical tests on a wide variety of real plants have helped us define a proper experimental framework for identification, see for example [4].

The Generalized Least Square Method was used for parameter estimation of the model. The application of this method to GreenLab was described by Zhan et al. [73] and Guo et al. [4]. 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 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 one is more accurate, since it helps retrieving the dynamics of sink variation more easily. In both cases all the data are adjusted at the same time by the same parameter set.

This methodology for parametric identification was implemented in *Digiplant* software, and used on several plants: Maize [10], Arabidopsis [53], Pine saplings [55], Cucumber [67], Sugar-Beet [62], Cotton [74], Beech[7], Chrysanthemum [60], Grapevine [68]...

We give beneath an example on the sugar beet. It corresponds to an industrial partnership with the French institute for Sugar Beet Research (ITB). Concerning the experimental data from which the model parameters are estimated, biomass measurements were carried out at seven different stages. At each date, seven individuals plants were selected and the dry mass of every individual organ (blades, petioles and root storage) was measured. The average of the seven plants was constructed. The numerical values of the parameters as well as their variances are given in [62] and are not recalled here. As an illustration, Figure 7 shows the fitting curves.

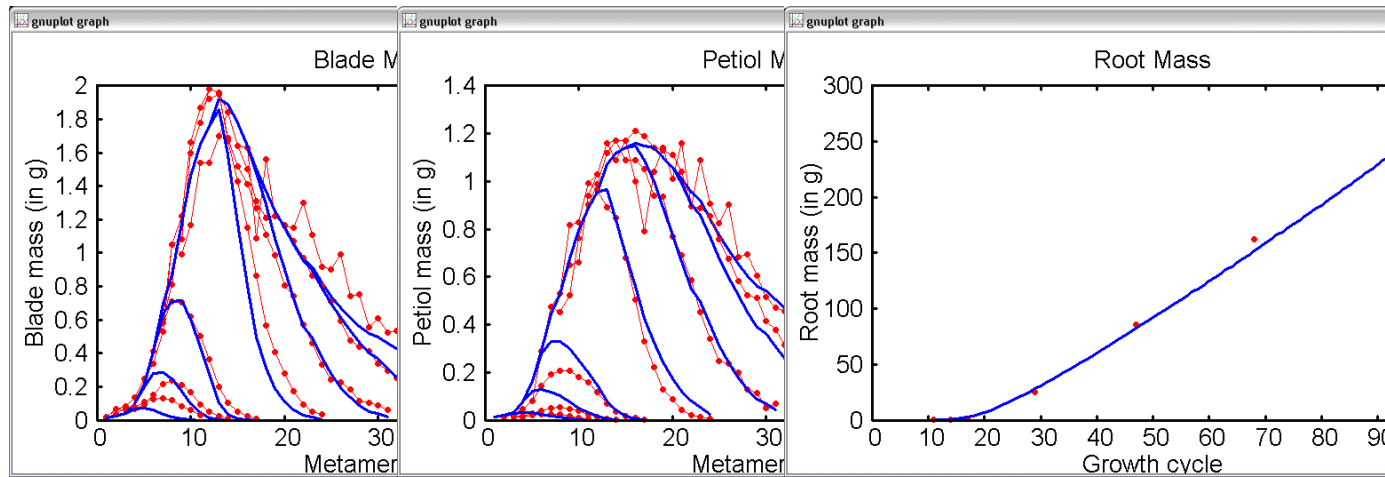


Figure 7. Fitting results: Average plants at organ level: experimental data (in red) and simulated data (lines) (a) Blade dry masses and (b) petiole dry masses according to phytomer ranks, at 7 different growth stages; (c) root dry mass as a function of the growth cycle (with experimental measures at the same 7 stages)

If the goodness of fit is excellent, the statistical analysis of the estimation results is not properly done yet. The variances of the estimates are given under the assumption that the error model chosen is the good one. But the hypothesis of a diagonal noise covariance matrix which is used in the generalized least square method, is quite gross. It corresponds to using only the deterministic part of the dynamical model, which is really restrictive since in dynamic models, errors propagate. Current studies aim at improving estimation by modelling the dynamics of the covariance matrix of the model noise.

### 3.4. Computer Graphics

The computer graphics in DigiPlante inherits from the long tradition of AMAP works [79], and is mostly conducted since 2004 in close partnership with the GreenLab team at LIAMA (Dr. ZHANG XiaoPeng and his students).

#### 3.4.1. Simple plant LOD models and real time plant rendering

*Principles and main research axis hold in the frame of the project :*

Plant simulated visualization in DigiPlante project is still based on the AMAP principles [79], characterized by a high level, device independant simulation output, called the line-tree. Geometrical output is a final process in the simulation stage, that can be processed or not. The Linetree structure describes a plant by a list of organs, referred by basic identification information (organ type, age) and organ positioning in space 3D origin relative to seed position, and 3D orientation. Orientations (main direction, normal and secondary) are scaled, story thus internode diameter/length and other organ sizes. These geometrical informations are stored in a 3 by 4

matrix, similar to a classical OpenGL Matrix Model Viewer. This data structure shows several interests and drawbacks:

- The Line tree structure does not store an exhaustive geometry, but just the list of each plant component with its orientation
- The structure is flat, no hierarchy or topology information is given. However, extension were developed, using a separated structure storing the component father-son relations. From these, pruning operation are available as well as branch per branch output or other hierarchical tree based data exploring schemes.
- The structure cannot be displayed directly; each component must be given an exhaustive geometrical description, build from instance from CAD-CAM tools. On the other side, the tree skeleton is obvious to be extracted and displayed; each component can be simply represented by a simple line linking its origin to the end point of its main direction (which is scaled). This approach allows thus a wide range of representations, open to many graphical systems. It can be compared to a classical Display List, in which primitive objects are to be defined according to the viewing system for each kind of organ (usually a simple cylinder for branch, and specific shapes for the other organs). Organ representation must be normalized; i.e. each organ must be defined using the same main axis and normal axis and normalized in size: unit volume or length for branch/fruits, unit area for leaves.
- Graphical rendering aspects, including illumination properties, textures are thus independent for the line tree, since define at the organ geometry description level.
- The structure allows Level of Details approaches and simplifications. According to component sizes (length / diameter ) selection can be done in order to extract components of interest (trunk and main axis). Coupled to statistical selection of leaves/flower, fruits, lower graphical model can be generated, without losing the global shape of the simulated plant. On branches, successive components can be concatenated, replacing list of internodes by a straight branch piece.
- The Line tree structure has shown a large interest for easy visualisation of complex trees on a wide range of systems, but is poorly adapted to advanced LOD models (such as hybrid polygonal/billboards models) and fast huge scene representation.

Scenes such as crops, forest, up to landscape visualisation was, up to now, mainly developed on a plant basis (not on a landscape use basis, as it is more and more the case in commercial products); and also without advanced dynamics, especially without plant/environment dynamics.

In the frame of the digiplante project, computer graphics development axis aims at developing new methods and approaches aiming to visualize large vegetation scenes in acceptable time (close to real time), in respect to plant structure and functioning. Priority is thus given to approaches keeping biological consistency (for instance leaf area) to approaches keeping aesthetic aspects. Research axis do concern single plant LOD model definition, and new landscape simulation/visualisation approaches.

#### *Single Plant LOD Models. :*

Concerning single plant representation. In cooperation with LIAMA, we developed a set of algorithms dedicated to generate continuous LOD geometrical model from a Line tree and its associated hierarchical topology. The principles of the approach are the following:

- The tree structure (trunk and branch) is converted to a Frenet Diagram. This diagram can be compressed, merging consecutive elements together, under control (error controlled). A branch part of the diagram is then described by an equation. At the rendering stage, according to the viewing parameter, the appropriate Diagram is retrieved, and the discretisation of branch in polygons is performed, also according to viewing parameters. If branch diameter gets lower than a pixel, transparent lines are used for rendering.
- For foliage, the proposed approach is to merge leaves two by two until reaching a simple quad for the whole plant crown [75]. Various methods were explored to obtain an efficient merging process. The main idea is to collapse leaf candidates within specific clusters, faithful to botanical

hierarchical structures. Hierarchical Leaf Union keeps more leaf surface area, keeping functional consistency of the DigiPlant model. In the various collapsing models, principles of the LOD schemes are unchanged, while preprocessing stages are revisited, making the approach operative for huge trees and heavy forest scenes .

- in order to avoid multiple exchanges between GPU and CPU, scenes are rendered according to tree species and individuals (to optimise instantiations). The full foliage lod models are stored in a simple table, compressed and send to the GPU. wWile rendering, CPU computes the adequate LOD model, sending then the corresponding indexes of the table to the GPU. GPU draws then all items lying in the table between these indexes.

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.

An extensive summary paper covering many aspects developed in the past four years has been published by Wesley in Computer Anination and Virtual Words journal CAVW08

### 3.4.2. 3D Reconstruction of tree crowns

This topic started two years ago at LIAMA, in the frame of the GreenLab project, with the objective to generate plant geometry from laser range point data. The work of PhD Zhu Cao is dedicated to the foliage crown. The proposed approach uses alpha shape (extension of voronoi diagrams). Originality of the approach lies in the automate definition of the alpha parameter (that controls the "smoothness" of the crown shape) , using a topological criteria: we want the surface to be a manifold. This approach, presented at Edutainment 08 [78] shows also a high interest on simulated plants, generating thus simplified shapes of crowns. 3D reconstruction from laser range point becomes a hot topic in forestry sciences. Both LIAMA GreenLab team and Digiplante were sollicitated to participate to an ANR Bioenergy project "EMERGE", planning to evaluation wood ressource for energy (project is accepted and started begining 2009)

## 4. Application Domains

### 4.1. Application Domains

The main application domains of the Digiplante team are: Agriculture, Forestry, Ecology, Computer Graphics. In the context of an increasing importance of the biomass ressources (both for alimentary or non-alimentary purposes), it is crucial to both predict and control crop yields or forest productions, both from a quantitative and qualitative points of view. Such goals can be achieved by proper simulations and optimization of the dynamic system modelling plant growth in interaction with the environment. We are mainly confronted to two types of optimization problems, direct optimization for the design of ideotypes and optimal control to design optimal cultivation modes (management of water, nitrogen, pesticide supplies).

Regarding ecology applications, they are mostly based on the techniques developed in functional landscape simulation and visualization. In our scope of research, the strategy is to study the impacts of several climatic scenari on landscape evolution: what is the consequence of an increase of 1 degree in temperature, what is the consequence of two conecutive years of drought...Some classical aspects in plant ecology (like seed dispersion and plant generations) should still be implemented to widen the scope of potential applications.

Finally, computer graphics and plant or forest visualization can be of great help for town and landscape planning, architectural projects, ecosystem management, but also video games or different types of simulators. A company born from AMAP (Bionatics) is specialized in this type of applications. The results of the Digiplante team on functional growth and functional landscapes is a key to improve plant realism and broaden the perspectives of applications.

## 5. Software

### 5.1. The plant toolbox Greenscilab

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. 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 (M.Z. Kang). It is co-developed by the DigiPlante team (Qi Rui, Letort). 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 University 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. DigiPlante and DGP Suite

P.H. Cournède has developed the DigiPlante software since 2002, with the help of P. Labatut, A. Mathieu, V. Letort. It is dedicated to the simulation of the GreenLab model and its parametric identification on real experimental data. Compared to GSL, which is mainly devoted to teaching activities, DigiPlante is used in the partner institutions for research: CAU, INRA Montpellier, INRA Grignon, ITB, Univ. of Wageningen, China Academy of Forestry, CIRAD, IRD.

With the work of the two INRIA engineers, B. Bayol and T. Guyard, new software products based on the simulation module of DigiPlante were developed: *DGP Simulator*, with a new editor insuring a better compatibility between the different software versions (*cf. exxEditor*), and a new visualization module *DGP Builder*. Moreover, a simplified user-friendly version was also developed *DGP Creator* allowing simulations of predefined plants, at different ages and in different environmental conditions.

### 5.3. Surfview

M. Jaeger has developed a tool for the visualization of functional landscape simulations. Several prototypes of functional landscape simulators exist (at LIAMA and in the DigiPlante team) and rely on this tool for the scientific visualization of the simulation results.

### 5.4. exxEditor

XSD based XML editor For our research projects we have to parametrize complex simulations. We use a tree data structure to store these input parameters. The simulator include a widget to modify these parameters and then launch a simulation. During the research process the simulator is modified and the structure of the input parameters may change. Thomas Guyard (INRIA IA) developed a solution a very generic solutions, which allows to include these changes without a lot of modifications in our software. We store the input data in an XML file. We developed an XML editor named *exxEditor*, using an XMLSchema to generate a tree based GUI. This software is developed using Qt4 and Xerces c++. The idea is simple : First we read the XMLSchema file then we generate a Qt4 tree (using the model view Framework in Qt). So we have a very easy to use tool to edit XML files, that can be modify just by modifying the XMLSchema file. Due to a good software design we can include this editor in every Qt based program. The program *exxEditor* and the generic libraries used to construct it are free software. You can download the source code in license CECILL-C at <https://gforge.inria.fr/projects/dgp-public/> .

## 6. New Results

### 6.1. Modelling and Applied Mathematics

#### 6.1.1. Stochastic Dynamic Equations of Growth

The stochastic version of GreenLab (GL2) was developed by M.Z. Kang [5]. A stochastic formal language adapted to the botanical concepts underlying the GreenLab organogenesis model was introduced in [59]. 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.

From 2008, these preliminary results were extensively revisited by a new PhD student, C. Loi. A new probabilistic framework for stochastic L-systems was introduced, and linked to multitype branching processes. The results were applied to the Greenlab organogenesis model in order to characterize the probability distributions and moments of the numbers of organs in plant structure. Plant organogenesis can be seen as the combination of two subprocesses driving the bud population dynamics, branching and differentiation. The generating function of the whole process is shown to be the composition of the generating function associated to the two subprocesses. The modelling of stochastic branching is classical but, to model differentiation, we introduced a new framework based on multivariate phase-type random vectors. By differentiating the generating function of the whole process, we were able to write the recursive relationships for the expectation and the variance of the number of metamers in the plant. These results were published [9].

A new generalization of these results was also developed, in collaboration with Jean Françon (Univ. Strasbourg), based on the symbolic method of Flajolet [71]. Generating functions of any kind of substructures (or patterns) can be derived for any stochastic OL-Systems [36].

#### 6.1.2. Parameter identification of trees

The theoretical advances concerning the GL3 model (model of interaction between growth and development) [13] and the development of new tools allowed confronting the model to new plant species, with more complex architectures than the previous versions. Based on the PhD of V. Letort, there is an important work on the validation of the GreenLab model for trees. Important results were published in [7] and new works are carried on in China on pine trees (in collaboration with the Chinese Academy of Forestry), in Guyana on *Cecropia* (in collaboration with P. Heuret, INRA-AMAP) and in Africa on *Accacia* (in collaboration with UMR BIOEMCO). The last results were published in PMA09 conference [32], [20].

#### 6.1.3. Sensitivity and Uncertainty Analysis

In order to make the model more robust and suitable for applications, it is necessary to master its uncertainty. For this purpose, mathematical studies on model structure and parameterization are carried out. It concerns Qiongli Wu's PhD and the post-doctoral work of Samis Trevezas.

It first involves a proper parameter sensitivity analysis of the model, in order to assess the importance of each parameter and their potential source of uncertainty [45]. Sobol's method is used. The complexity of the functional structural model and of the number of parameters involved led us to develop new powerful computing techniques.

Regarding uncertainty on parameter estimation, the current estimation process used in the DigiPlante software, does not provide a precise quantification of the parameter uncertainty. The difficulty lies in the estimation of the covariance matrix of the observation error. A new statistical framework is currently developed by S. Trevezas and should hopefully lead to interesting results.

#### **6.1.4. Modeling Inter-Individual Variability**

Modeling heterogeneity in field crops is a key issue for a better characterization of field production. First works were achieved on sugar beet. Several sources of individual variability within plant populations are identified: namely, initial condition (seed biomass, emergence delay), genetic variability (including phyllochron) and environment (including spacing and competition). A mathematical framework is introduced to integrate the different sources of variability in plant growth models. It is based on the classical method of Taylor Series Expansion, which allows the propagation of uncertainty in the dynamic system of growth and the computation of the approximate means and standard deviations of the model outputs. The method was applied to the GreenLab model of plant growth and more specifically to sugar beet [50]. It opens perspectives in order to assess the different sources of variability in plant populations and estimate their parameters from experimental data.

#### **6.1.5. A continuous version of the GreenLab model**

To model plant-environment interactions, the synchronization of the plant growth model with biophysical models has revealed limitations of the discrete formulation of the GreenLab model at the growth cycle step. Therefore, a continuous approach to model functional-structural plant growth was developed by V. Le Chevalier and Z. Li, based on the discrete GreenLab model. The continuous dynamics is driven by a system of differential equations with respect to calendar time, with a continuous mechanism of senescence introducing delay terms. A numerical scheme for solving the system is studied. It was tested on the model of sugar beet growth, to compare different approximation methods including the classical discrete model. With a higher precision, the simulation based on the continuous approach reveals significant differences with the discrete model. Moreover, an approximation of the continuous model is derived with a daily time step, which makes it suitable for agronomy applications [33].

#### **6.1.6. Plant - environment interactions**

So far, experiments for GreenLab calibration were conducted in unstressed conditions. In order to develop optimal control for agriculture, it is important to develop a good model of plant - soil interactions, especially for water and nitrogen.

A new PhD (Z. Li) has started in collaboration with CEMAGREF Montpellier (J.C. mailhol), with the objective of coupling the GreenLab model with a model of soil water budget. The first result is the combination of the GreenLab model of plant production to the PILOTE model [65]. A proper study of the model is in process and experiments on wheat and maize will help estimate the model parameters.

Moreover, the post-doc of Jessica Bertheloot helped develop a model integrating fully both Carbon and Nitrogen metabolisms [25]. The parameterization of the model is difficult and more work is necessary to validate the model.

Another study is to represent 3D landscapes from the outputs of the classical Process Based Models (PBM) used to compute yield of crops in agronomy and from the outputs of Empirical Forestry Models (EFM) used to assess wood quality and quantity in forestry. The data provided by these models are uncomplete, but it is possible to add a relevant botanical knowledge, coming from similar plants previously studied. For instance PBMs provide only dry biomass, LAI, harvest index, and EFMs provides only lengths, diameters and branch numbers on the trunk. Adding GreenLab knowledge about plant functioning and plant architecture allows to reconstruct 3D representations faithful to plants and thus to visualize a field, which is a first step towards "functional landscapes". PBMs and EFMs are numerous so it could be a chance for the GreenLab model to be widely used in Agronomy. This is the PhD subject of Feng Lu cosupervised by DigiPlante and the Chinese University of Agriculture. The PBMs and EFMs used come from Cemagref (Pilote), Inra (Stics), Wageningen (Tomsim), CAF (Simtree).

#### **6.1.7. Functionnal Landscape: coupling and synchronising models**

A new formalism framework allowing model composability was defined in 2009. The new conceptual approach is close to P\_DEVS approach (developped by Ziegler). Our approach allows to build simulation

platforms coupling various models sharing data in a synchronous way. The approach is based on Models components and Caches components to access Data. Data update is performed by a specific Model, the Manager at specific time steps, computed for model internal time requests. Models are responsible for their own evolution, and specify to the manager their time of Data update. The approach is modular, allows hierarchical nesting and parallel implementation.

This approach was implemented and two showcase developed: a specialized water competition example (set of pumps), and a specific GreenLab model plant model. The model was revised, redesigned using a continuous formalism in order to fulfill approach requirements.

These results were submitted and recently accepted at PMA09 conference

This topic is confirmed being a growing concern in the team, involved in the coordination of several regional projects (RTRA-INRIA) dedicated to animate landscape integrative modelling and their platform at regional level, in aim to build a scientific platform with its partners (CIRAD-GREEN, INRA LISAH, etc). In the frame of this network, those partners launch a new event dedicated to Integrative modelling and simulation platform at landscape and ecosystems levels: LANDMOD2010, to be held on february 2010 in Montpellier, with the support of RTRA (Computation plants and Eco-systems Agropolis Foundation-INRIA Call)

### **6.1.8. Floral biology and fertility models**

An important component of the yield that was not taken in account until now in GreenLab model is the production of seeds. Cirad working on tropical trees (Palm tree, Cocoa tree, Coffee tree) has developed previously such model to simulate the seed production from the ovules distribution in the flowers, the distribution of pollen seeds, and the abortion laws of seeds and pods. Few parameters calibrated from the measurements on flowers and fruits control quite well the seeds distribution in the pods. This allows separating the environment effect (weak pollination) from genetic effects (ovule fertility). Such issue occurs also on temperate crops such as rapeseed. A PhD Wang Xiujuan coming from CAU and cosupervised by Digiplante, Inra EGC, and CAU, works to improve the Cirad model in its mathematical shape and applied it successfully to the rapeseed in Grignon. The model is generic and can be used in many crops.

### **6.1.9. Yield optimization and plant architecture**

The harvest index is the ratio between the yield and the total biomass produced by the field. Depending on the type of crop, the yield concerns seeds (corn), root (beetroot), fruits (tomato), wood (tree), and even leaves (salad, tea plants ...) that are source organs! The yield depends on the source and sink balance through plant growth and development. The strategy to follow for yield optimization is complex and must be adapted to plant architecture. Yield also depends on the interaction between plants and their environment. A first study was conducted in Digiplante, in cooperation with EPI Idopt (Le Dimet), to control irrigation. Another important problem is the interactions between plant growth and pest (fungus, insect). The thermal time drives both insect and plant developments and the leaf surface is the spot of their interaction. Insects need to eat leaves and plant need leaf area. Such issue has been previously studied by Cirad. In Digiplante, the Phd of Qi Rui (joint ECP - Liama) studies mathematically the three-antagonists model obtained, and its control.

### **6.1.10. Towards functional sinks**

Formulations of the sources and sinks functions in GreenLab are constantly improved, with a more mechanistic approach. In 2006, the source function based on the hydraulic plant architecture was replaced by the light interception at the canopy level (Beer-Lambert Law) and adapted to individual plant using an optimized projection surface computed by inverse method. It allows the passage from Individual plant to plant population. Symmetrically studies on sink function are carried out between Digiplante, Liama and CAU. Sinks are relative, time duration of organ expansion is complicated to assess directly. Although the empirical sink functions used in Greenlab are very efficient and can be assessed by inverse method they are only descriptive, they depend on the thermal time and have no physiological meaning. A new formalism based on ecophysiological considerations (number and expansion of cells inside an organ) is proposed. Fitting the source and sink balance on crops with this new formulation has given promising results. Advantages are that the sinks can be absolute and it is no more required to assess the expansion time of organs. Once this study is completed in 2010, it could



be possible to swap the sink function in 2010 as we did for the source function. The assumptions underlying the GreenLab model would thus be entirely functional.

## **6.2. Computer Graphics (in collaboration with LIAMA)**

As planned in 2008, activities in Computer Graphics in this term shows significant topic changes. LoD model developments are nearly closed while activities related to 3D reconstructions do increase as well as studies involving GPU and Web visualisation. Specific new trends are also explored, involving high level structural and on functional data. Scientific animation is also developing, a networking project VLS-LRC has gained supports of Agropolis foundation and INRIA, to develop a regional network (from Barcelona to Montpellier) involving key players on Virtual Landscape visualisation and their applications.

### **6.2.1. Simple plant LOD models and real time plant rendering (with LIAMA)**

Level of Detail single plant models, based on simulator Line Tree output has shown few new developments in the last period. Both DigiPlante and associate team (Dr. Xiaopeng Zhang and his students in LIAMA) do consider that this subject is mature and entering in a valorization process. Focus was thus given on common tool specification and writing, especially on tools generating tree structures. French and Chinese plant growth simulator 3D output (line trees) were normalized. A graphical tool "LIGDRAW" dedicated to single tree visualisation and graphical material property definitions was designed by M. Jaeger. This tool also aims to host wrappers between several representation, allowing conversions of line-trees to LOD models (branches only so far). The tool is already used at ECP and LIAMA. This engineering work (Qt based) is still ongoing.

### **6.2.2. Real time visualisation involving strongly GPU techniques (with LIAMA and BJFU)**

GPU techniques are more and more explored with the help of Yang Gang specialist of BJFU (Image and Graphics lab, Beijing). This year, two main threads were explored: use of GPU for simple shape rendering and Use of GPU for real time shadow computations. On this last subject, the work is a simple extension on past results gained last year on foliage and instantiations. The approach uses the classical depth map; the contribution lies on the computation of the appropriate LOD Model constrained by two views (camera and light) Concerning basic shapes. The idea is to send to the GPU the 3D skeleton of the plant and not the 3D geometry mesh. Up to know, we could defined tools generating 2D 1/2 shapes (ellipsoids and branch pieces) from single skeletons. The results are promising, and will go on (no publication so far)

### **6.2.3. 3D reconstruction from images and laser scans (with LIAMA)**

This topic has shown significant progress at LIAMA. In the collaboration with DigiPlante, the work mainly addresses reconstruction from 3D laser scans. On tree crown shapes, PhD of Zhu Chao made progress on crown shape reconstruction (alpha shapes). The 3D point cloud of the full tree is segmented in different clusters, based on distance to trunk and main branch identification. This preprocess speeds up the 3D crown reconstruction (since not linear) and gives better results, extracting a colony of crowns instead a single one. Nice progress were also gain on point cloud segmentation, using combinations of three different criteria: distance, local normals, local curvatures. Depending on the target of the reconstruction, those criteria are combined differently in order to cluster and then segment objects in the point range scene. Two specific cases were detailed: building and vegetation extractions from large scenes, and foliage/branch classification on single trees. This area led to several publications at PMA09, ICGVR and VRCAI conferences.

### **6.2.4. Exploring new ways of single plant visualisation (with AMAP)**

With the development of new simulators packages, new internal structures and disk output are available. Especially data allowing stop and go actions, representing the simulated plant with a flat metamer graph and its functional properties (leaf volume, metamere volume, pith volume) can be used to generate the plant geometry. First tries were hold on this point, defining metamere lengths and diameters from production. With simple angle rules, and allometry rules, we show that we could easily generate 3D outputs from this very compact internal data structure. This preliminary study is promising.

### 6.2.5. Volume imaging

There is still some work hold in this area, mainly valorizing past experiences. The team and associated team was invited to publish an extended paper on tree structure extractions from voxel shapes, on the basis of the publication to VRCAI conference (an is related journal IJVR) [76]. This collaborative work hold on voxel image tree data hierarchical segmentation should be edited soon as book chapter in Pattern Recognition (Springer Ed).

## 7. Contracts and Grants with Industry

### 7.1. Contracts and Grants with Industry

#### *Running contracts*

- 2007-2009 year of industrial contract with ITB (French Research Institute for Sugar Beet).
- 2007-2009 of the Terra Data project in the context of the “Pôle de compétitivité” Cap Digital.
- 2007-2011: ANR project (07-CIS) 3Worlds project linking INRIA-DigiPlante with ENS, CNRS, IRD (Geodes), IFI Hanoi, Australian National University. Co-ordinator: ENS
- 2008-2010 the Terra Magna project in the context of the “Pôle de compétitivité” Cap Digital.
- 2006-2010: ARCUS Languedoc Rouillon ChongMing Project (involved M. Jaeger)

#### **3d reconstruction, crown analysis:**

- 2008-2012: ANR Bioenergy EMERGE (involved M. Jaeger)

#### **Scientific Animation (All aspects)**

- 2008-2010: PMA09. Many supports: RTRA Agropolis, French Embassy, INRIA, CIRAD, INRA, NSFC, CAU, CAU
- 2009: RTRA-INRIA integrative landscape modeling (Co-ordinator M. Jaeger, involved V. le Chevalier)
- 2009: RTRA-INRIA platforms for landscape modeling (involved M. Jaeger, V. le Chevalier)
- 2009-2010: RTRA-INRIA Regional network to promote virtual reality tools for landscape applications

#### **International exchanges:**

- 2009 Supports from French Embassy and CIRAD international department (stays for senior scientist) 1 each.

## 8. Other Grants and Activities

### 8.1. Visiting Scientists

#### *Main overseas visits :*

- P de Reffye in China (9 weeks): Partners CAU, BJFU, CAF, LIAMA (Beijing)
- M Jaeger in China (2 weeks): Partners CAU, LIAMA (Beijing), Tongji (Shanghai)
- V Letort in China (3 weeks): Partners CAU, CAF, LIAMA (Beijing) - V Le Chevalier in China (3 weeks): Partner LIAMA (Beijing) - PH Cournède in China (1 week): Centrale Pékin, LIAMA.

#### *Visitors Hosted in DigiPlante team (ECP MAS and Cirad Amap locations) :*

- LEI Xiangdong and GUO Hong, Professors at the Chinese Academy of Forestry, 2 weeks in ECP MAS, September. - JIA Jinyuang, 1 month in CIRAD-AMAP, September, Professor at Graphics and image Research Center of Tongji University, in China.
- YANG Gang, 1 month in CIRAD-AMAP, June, Associate-Professor at Liama-Casia in China
- ZHANG Xiaopeng, 1 month in CIRAD-AMAP, September, Associate-Professor at Liama-Casia in China (with LI HongJun, PhD student)

## 9. Dissemination

### 9.1. PhD and HDR

- B. Pallas, "Modélisation dynamique des interactions plante-environnement. Application à l'étude des interactions entre les relations sources-puits et les processus de développement chez la vigne", Ecole Centrale Paris, Sep. 2009
- P.H. Cournède, "Dynamic System of Plant Growth", Univ. Montpellier II, March 2009

### 9.2. Conference and workshop committees, invited conferences

#### *International Events :*

- M. Jaeger is main board and scientific editor of 3rd international Symposium of Plant Growth Modelling, Simulation, Visualisation and Applications (PMA09), held in Beijing November 9-13, 2009, Beijing, China. <http://pma.cirad.fr>
- M. Jaeger is co-organizer of the 2010 international conference on integrative landscape modelling (Land-Mod2010), held in Montpellier February 3-5, 2010, Montpellier, France. <http://www.umr-lisah.fr/rtra-projects/landmod2010.html>

#### *Seminars :*

- M. Jaeger gave several talks in China on plant fast visualisation and functional landscapes at Department of Software Engineering of University of Tongji (Shanghai), and in CASIA-LIAMA (Beijing)
- M. Jaeger gave a talk at 3eme Colloque INTS; Montpellier (19 November 2009)
- P. de Reffye gave several talks in China (Fuzhou Univ., Taiwan)
- P.H. Cournède gave seminars at Beihang University and Centrale Pékin on Plant Growth Modelling

#### *Boards :*

- M. Jaeger is main board of international symposium PMA09 <http://pma.cirad.fr>
- P.de Reffye, P.H. Cournède and M. Jaeger are members of the Scientific Committee of PMA09

### 9.3. Courses and Tutorials - Media

GreenSciLab, the free GreenLab model implementation running under Scilab environment is now available with tutorial pages and study cases on LIAMA web site with a new easy to use interface and simple case demos. A one day tutorial was organized at PMA09 conference.

We detail below the teaching activities directly linked to our research field in plant growth modeling. The other courses concerning more general topics in mathematics and applied mathematics are not detailed.

- A course of 24H between was given at master level at Agro Paris tech by A. Mathieu on "Functional-Structural Plant Modelling" with practice on GreenScilab.
- Several student projects are also given each year at Centrale Paris linked to the research activities of Digiplante.

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