



INSTITUT NATIONAL DE RECHERCHE EN INFORMATIQUE ET EN AUTOMATIQUE

Project-Team digiplante

Modelling plant growth and architecture

Saclay - Île-de-France

Theme : Observation, Modeling, and Control for Life Sciences

Activity
R *eport*

2010

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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 1st, 2008.

1. Team

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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

- PhD defense of Vincent Le Chevalier, Centrale, May 2010.
- PhD defense of Sébastien Lemaire, AgroParisTech, May 2010.
- HDR defense of Marc Jaeger, University Blaise Pascal (Clermont-Ferrand), December 2010.

3. Scientific Foundations

3.1. Digiplante at INRIA

Derived from the AMAP model developed in the 1990s at CIRAD [75], 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 [17] 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 [13].
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 [73] to describe GreenLab organogenesis. However, it was shown to be equivalent to a growth grammar [15], 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 [38], 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 [47]. 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, Digi plante 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.

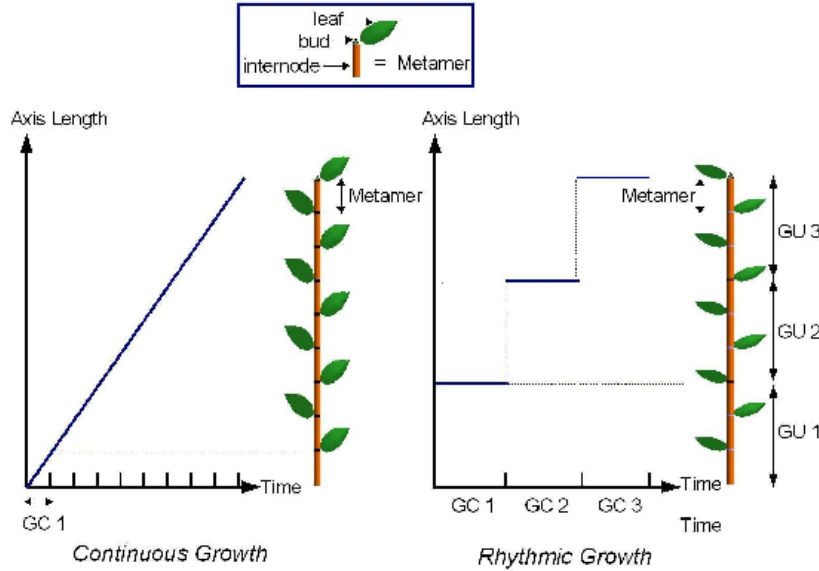


Figure 1. Growth Cycle (GC), Growth Unit (GU) and Metamer in GreenLab. The axis length is given as a function of time for continuous and rhythmic growths

Since metamers may bear axillary buds, plant architecture develops into a hierarchical branching system. [38] 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 [38], 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 [15],[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 [54] [62] $\langle \mathcal{G}, \mathcal{B}, P_r \rangle$ 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 τ and μ characterize meristem differentiation.

A fundamental result [64] 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. [17], [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).

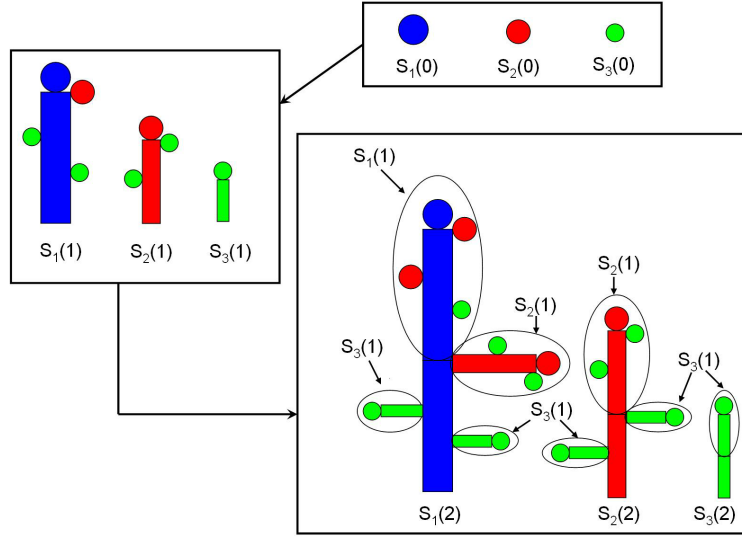


Figure 2. Substructures of physiological ages 1, 2, 3 at chronological ages 0, 1, 2 and their organization: $S_1(0)$, $S_2(0)$, $S_3(0)$ are buds of physiological age 1, 2, 3 respectively. In this example, a growth unit of physiological age 1 is composed of 2 metamers of type m_{13} and 1 metamer of 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).

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 $v_{pq}(t - n + 1)$.

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.

[15] 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 [14]. 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 \mathcal{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 GreeLab model and its various versions ([17], [14], [4], [16], [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 [61], TOMSIM [45], GRAAL [43]...). 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

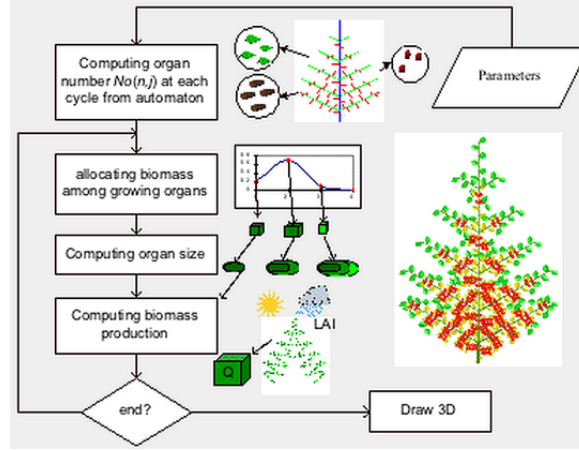


Figure 3. Flowchart of the GreenLab model.

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.

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 β and γ 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: μ 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 [52] 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 [52].

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 [57] 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 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).

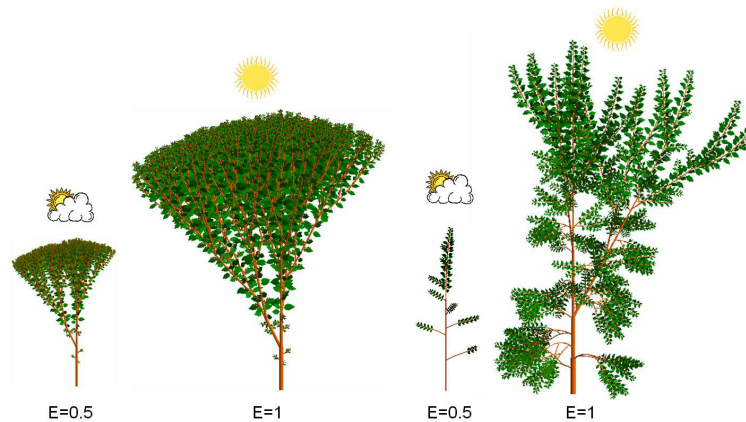


Figure 4. Effects of climatic variations on the GL1 and GL3 organogenesis models: on the left side (GL1), topology is fixed, organs are simply smaller to adjust to the environment; on the right side (GL3), topology is variable and the plant adapts its development to the environmental conditions.

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. 5). 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.

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].

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 6. 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.

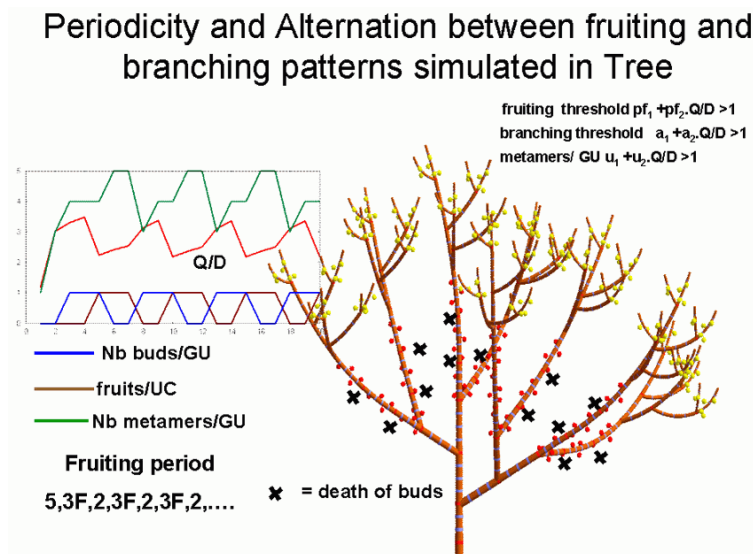


Figure 5. Rhythmic growth for fruiting and branching in alternation depending of the retroaction between plant production and plant development.

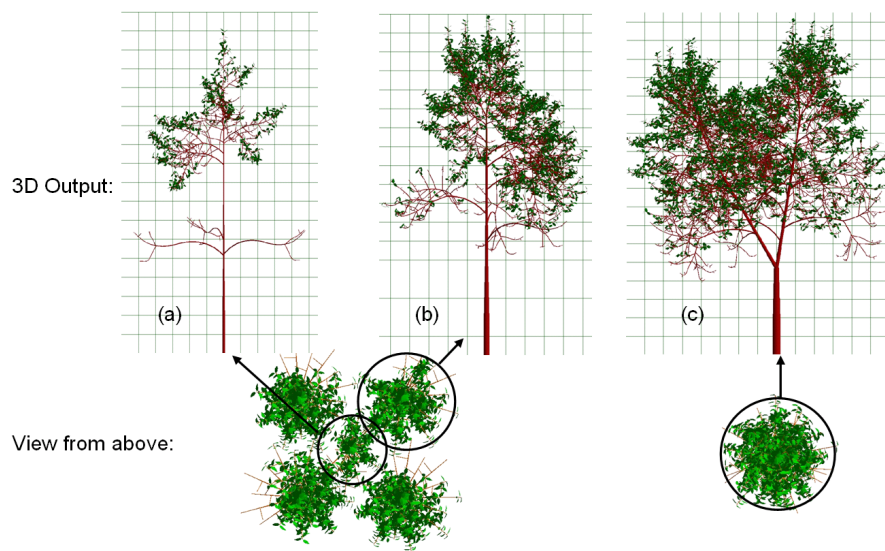


Figure 6. Simulation of tree growth in heterogeneous conditions: view from above and detailed architectures of the individuals. In the upper right corner of the figure, Tree 1 grows in open-field like conditions. In the lower left corner, Tree 3 surrounded by its four neighbours (including Tree 2) severely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

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) [46]. 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 [50], 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. [69] 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 [41], Pine saplings [44], Cucumber [58], Sugar-Beet [51], Cotton [70], Beech[7], Chrysanthemum [49], Grapevine [60]...

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 [51] and are not recalled here. As an illustration, Figure 7 shows the fitting curves.

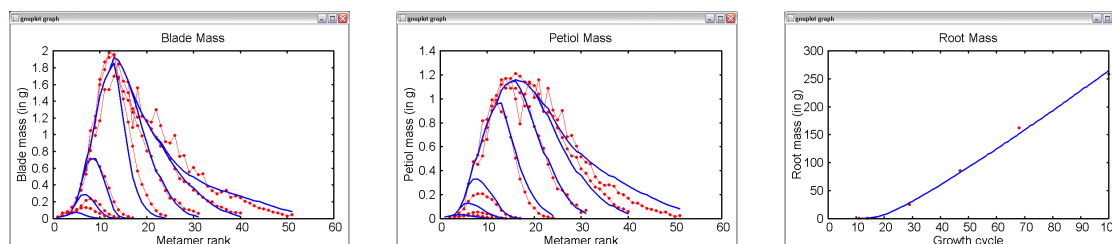


Figure 7. Fitting results: Average plants at organ level: experimental data (in red) and simulated data (lines) (a) Blade dry masses and (b) petiole dry masses according to phytomer ranks, at 7 different growth stages; (c) root dry mass as a function of the growth cycle (with experimental measures at 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 [75], 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 [75], characterized by a high level, device independent 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 operations 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 defined 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 [71]. 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. wWhile 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 developped in the past four years has been published by Wesley in Computer Animation 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 [74] 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 resources (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 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. Digiplante and DGP Suite [DGPModelizer, DGPBuilder, DGPCreator, DGPScene]

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, and 1 Centrale engineer (C. Mouton) new software products based on the simulation module of Digiplante were developed: *DGP Modelizer*, 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.

Finally, DGPScene allows the simulation and management of plant populations. A configuration file (with plant positions, varieties, initial times) is given as input, an analysis of plant competitions is performed and individual-plant growth is then simulated. The scene can then be visualized. Note that the input file can be generated with SIMEO Software developed by F. de Coligny (INRA, UMR AMAP).

All the DGP software is developed in C++ (with libraries Qt, STL, BOOST, OSG, Xerces, Xalan, EXX, ColladaDom) and runs on LINUX, WINDOWS, MAC OS.

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

exxEditor is an XSD based XML editor created by Thomas Guyard. 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/> .

5.5. PYGMALION

A platform for Plant Growth Model Analysis and Identification. B Bayol, PH Cournède, C Mouton develop this software dedicated to the statistical and mathematical analysis of plant growth models and their parametric estimation, in C++. Several models are implemented in this platform: different version of the GreenLab model (discrete and continuous), PILOTE, SUNFLO, SUNLAB, CORNFLO, STICS and others ...

5.6. GLOUPS

Digiplante at Amap-Cirad develops the Gloops software both in Matlab and Java that integrates interesting new features : stochastic growth and development including pre and neoformation, polycyclism, herbaceous growth with basipetaly and acropetaly, remobilization etc... The inverse methods are available for new complex plants that are arriving for the sources and sinks studies.

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 [48]. 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].

Plants as Combinatorial Structures and Development of a Symbolic Method :

A new generalization of these results was also developed, in collaboration with Jean Françon (Univ. Strasbourg), based on the symbolic method of Flajolet [63]. A symbolic method is proposed in [55] to compute the distribution associated to the number of occurrences of a specific pattern in a random text generated by a stochastic OL-system. To that purpose, a semiring structure is set for combinatorial classes composed of weighted words. This algebraic structure relies on new union and concatenation operators which, under some assumptions, are admissible constructions. Decomposing the combinatorial classes of interest by using these binary operators enables the direct translation of specifications into a set of functional equations relating generating functions thanks to transformation rules [33].

A specific application of this method is the parametric identification of stochastic model of plant development [24]: counting the number of phytomers in trees or observing their ages is not always easy. So the classical methods of parameterization of the stochastic processes of organogenesis based on the observation of the distributions of the number of organs is not always appropriate. The new method allows considering distributions of patterns easier to observe, like the number of apical buds (branch tips) or Y structures (forks).

Tree Crown Analysis :

The method of 'tree crown analysis' developed in UMR Amap by Philippe de Reffye also allows to compute the parameters of the stochastic model of tree development, using the means and the variances of the number of phytomers of the observed branches at the rank K from the top of the stem. The system has been upgraded for variable probabilities and applied to Eucalyptus (cooperation with CAF institute China) and coffee tree (cooperation with IRD). This system has successfully provided the main parameters of the tree development from the analysis of architectural data. It is possible to simulate the tree development in order to obtain random structure or to define an average tree for the branching and death patterns, *cf.* fig:stochPdR. The parameters of the tree development are essential to assess the plant demand made of the sum of all the sink organs. An article has been submitted on the results obtain in China (CAF) on the Eucalyptus tree development. A genetic study of the variability of the Coffee tree development among different species (Arabica, robusta, racemosa) is carrying on in the PHD of Akafou (IRD).

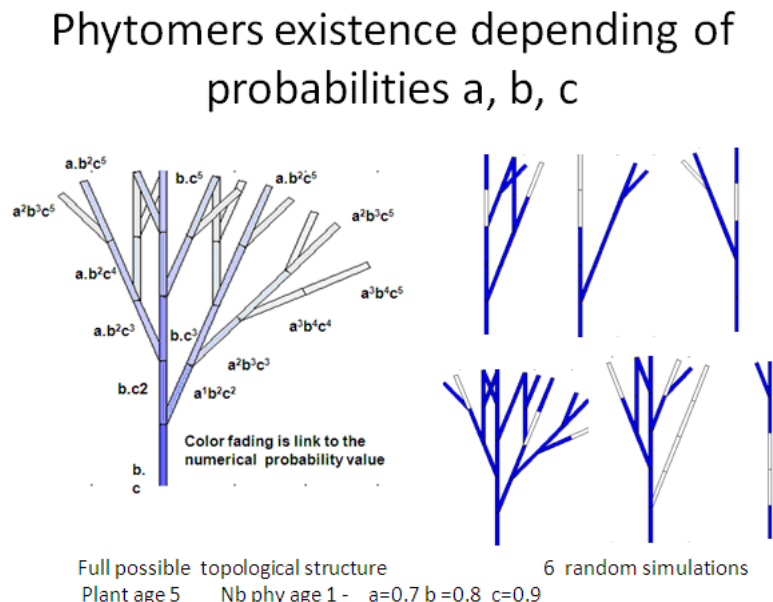


Figure 8. Existence of phytomers according to probabilities of the organogenesis model

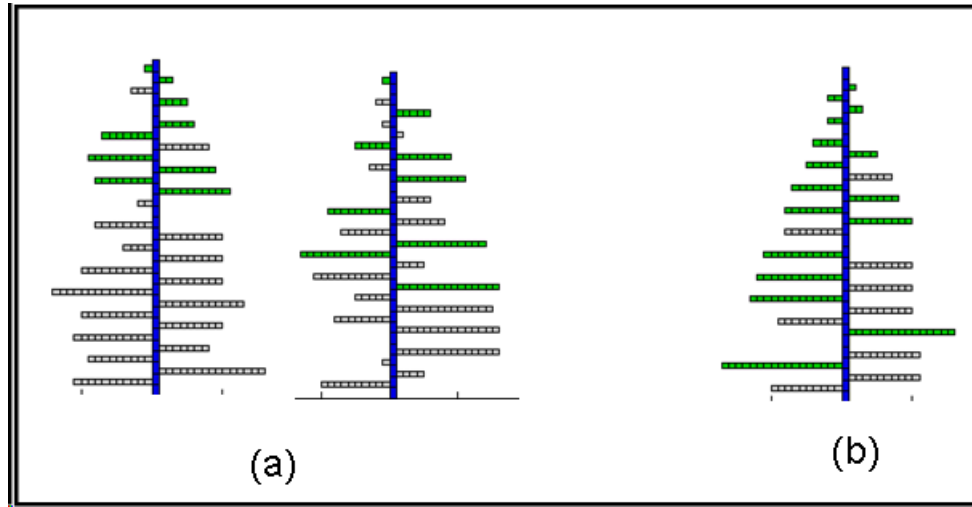


Figure 9. (a) random simulations of tree development ; (b) average structure. (green branches are still alive, grey branches are dead).

6.1.2. Methods for parameter estimation

A new type of target for trees :

Computing the sources and sinks parameters needs to adapt the Data measured from Tree to the stochastic case. The notions of physiological age and common pool of biomass allow to arrange the data in a very efficient way, quite disconnected from the topological structure. Considering the alive branches of a given physiological age, all the phytomers situated at the rank K from the top of the branch are identical. This is a consequence of the common pool of biomass. So an average branch can be constructed from data for each physiological age. The plant development gives the number of phytomers corresponding to a given rank. As it is its simplify a lot the way to fit the plant architecture as it was used in GreenLab. More over the method can be extended to the stochastic case. But the age of the phytomer of the rank K is no more K , but follows a binomial negative distribution K, b where b is the growth probability of the meristem. Then fitting the sources and sinks parameters follows the same way than in the deterministic case.

Estimation of GreenLab parameters in the frame of Hidden Models :

Instead of considering the state variables as the vector of organ masses varying with time, the observed organ masses are organized into ordered sequences, in which the ordering is taken with respect to the growth cycle of organ appearance. Such sequences lead to an equivalent description of the dynamic system in the framework of hidden (latent variable) models (*cf.* [40]): model equations can be interpreted as a bidimensional stochastic process, which describes the evolution of system variables. More precisely, let $\tilde{Y} := \{Y_n\}_{n \in \mathbb{N}^*}$ be the sequence of observed organ biomasses, ordered as described above with n the growth cycle of appearance. Each Y_n is generally a multidimensional vector, that can be divided into subvectors $Y_{o,n}$, each one corresponding to a different type of organ. Let also $\tilde{Q} := \{Q_n\}_{n \in \mathbb{N}}$ be the sequence of successively produced biomasses Q_n , at each growth cycle n , where Q_0 corresponds to the seed mass. Q_n is considered to be distributed to the different organs at cycle $n + 1$. The following assumptions describe generally the representation of the model in this framework, and the dependence relations among system variables: Therefore, simulation based methods are in progress in order to implement proper stochastic versions of the EM algorithm and stochastic gradient methods for state and parameter estimation. In this direction, the class of sequential Monte-Carlo (or particle filter) algorithms, which can be used for maximum likelihood estimation

(see [42]), seems particularly adapted to our case. When the complete likelihood function belongs to the exponential family, the EM algorithm is usually well suited and a set of sufficient statistics simplifies the maximization step. In our case, the model parameterization makes the maximization step more complicated, and thus stochastic gradient as well as stochastic EM algorithms will be developed and compared.

Bayesian Estimation of GreenLab parameters for stochastic models of plant growth :

When organogenesis is stochastic, we propose a new mathematical descriptions of FSPM (and GreenLab in particular) with stochastic organogenesis in the frame of Jump Markov Systems. We can then and to apply bayesian estimation methods adapted to this frame, namely Rao-Blackwell Particle Filtering and Convolution Particle Filter to estimate the functional parameters of the model.

6.1.3. Combining process based models and GreenLab model

Process Based Models (PBM) in agronomy work at the level of the m^2 . They assess the production of a population of plants without consideration about the plant density and the individual plant. The inputs are the Leaf Area Index (LAI), the daily environmental parameters (radiation, temperature, irrigation), the harvest index (proportion of the biomass going to the yield) and the outputs is the cumulated biomass produced by the photosynthesis and the the yield. We have chosen to use Pilote, that is the PBM developed by CEMAGREF. As GreenLab model works like a PBM at the plant level for biomass production, using a individual and optimized LAI. It is interesting to compare the performance of GreenLab model and Pilote on the same Data coming from field. This is the subject of the PhD of Feng Lu at Cirad.

At the field level there are two sources of variation that are mixed up if only the yield/ m^2 and the LAI is considered. First one is the variable delay of germination. So the development of the plants follows a distribution according to the time. This makes a mixture of plant growths. Second one is that the competition for space is not homogeneous. So there is a distribution of the plant weights.

By inverse method we can match the LAIs and the Biomass productions produced by both models by optimizing the law of delay of the germination, see Figure 10. In another hand using "differential statistics" we can assess the variance of the parameter S_p that optimized the LAI/plant in order to fit the variability of weights between plants. Results were successful and GreenLab model can simulate a field of Maize that integrates the plant growth and development variability and provide the same prediction that Pilote. Thus GreenLab model could be an interesting extension of PBMs to go further in the study of the components of the yield.

6.1.4. Sensitivity 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 with PH Cournède.

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 [67]. 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 based on an efficient use of model evaluation to compute variance decomposition. Moreover, an estimation of the error of computation (as a function of the number of samples or model evaluations) was computed. The results are submitted to J of Rel. Eng. and Sys. Safety for publication.

Moreover, the method was tested on a wide variety of functional-structural plant models, in order to set in place a specific methodology adapted to this type of models [35]: GreenLab model of maize and sugar beet growth, GL3 model of tree growth (characterized by strong interactions between functioning and architectural development) and finally the NEMA model of Nitrogen and Carbon budget in plant growth, a complex ecophysiological model involving more than 80 parameters.

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

Germination heterogeneity:

**P.BM. Drive a mixture of growing plants of different ages.
 FSPM drive the single plant growth. Fitting both models
 needs to use the delay distribution of germination**

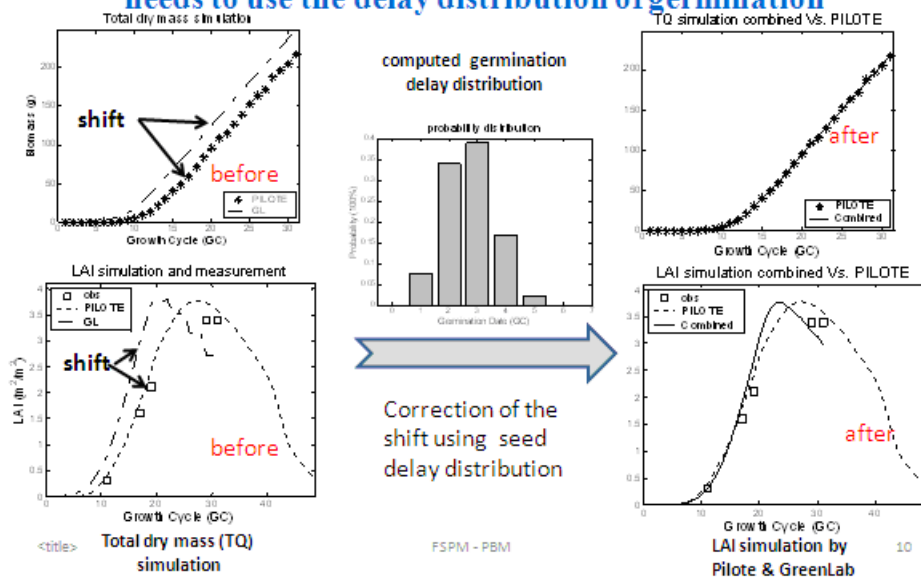


Figure 10. Germination heterogeneity

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 was developed. 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 [53].

The coupling of this continuous model with the Pilote model of soil water budget ([56]) was achieved in collaboration with Jean-Claude Mailhol (Cemagref, UMR G-EAU, Montpellier), and likewise a numerical scheme was derived. This work is submitted for publication.

The next step of this study concerns the implementation of optimal control techniques to optimize irrigation strategy. Previous studies have been achieved in the GreenLab context, based on a variational formulations. However the non-convexity of the problem forced the use of heuristic methods (genetic algorithms) to solve a simplified version of the problem (parametric function of water supply). The method implemented is the iterative dynamic programming, which both allows to handle the non-convexity and, more efficiently than what was done previously, the time-delay system.

6.1.6. Coupling Carbon and Nitrogen Metabolisms in Plant Growth Models

The post-doc of Jessica Bertheloot helped develop a model integrating fully both Carbon and Nitrogen metabolisms [39], in collaboration with Bruno Andrieu (INRA, UMR EGC). Different sub-modules are defined: organogenesis, senescence, photosynthesis, Carbon distribution, Nitrogen acquisition, Nitrogen fluxes, with strong interactions between these modules. The parameterization of the model is difficult. The first evaluations of the model was conducted for wheat. Global sensitivity analysis was conducted [34] in order to deduce the most important parameters. Experimental results were then used to estimate these parameters.

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. 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 adapted the model to rapeseed. A statistical analysis of data collected in 2008 and 2009 in Grignon was conducted. Different versions of the model were compared. 2 articles were submitted.

6.2. Computer Graphics (partially in collaboration with LIAMA and Tongji University)

Since 2009, activities hold in cooperation with LIAMA in Computer Graphics areas move its gravity center from LoD model developments to 3D reconstructions from laser scans. do increase as well as studies involving GPU and Web visualization. At Cirad, specific new trends are also explored, involving high level structural and functional data.

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

Level of Detail single plant models, is considered as a closed research topic at this stage. However, engineering valorisation is still operative. French and Chinese plant growth simulator 3D output (line trees) were normalized and can be visualized with the same tools. The graphical tool "LIGDRAW" dedicated to single tree visualization and graphical material property definitions, designed by M. Jaeger includes new animation output facilities, and plug-ins implementing several LoD approaches. allowing conversions of line-trees to LOD models (branches only so far). The tool is used at ECP and LIAMA, and at Cirad was used to define several animations presented at "Arbre, regard croisés" exhibition (September 2010, Jardin du Luxembourg, Paris).

6.2.2. 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 urban vegetalized scenes [59] and forest scenes. Significant progress were gained on point cloud segmentation, using combinations of three different criteria: distance, local normals, local curvatures on practical complex data set of forest. In this term, INRA Lerfob provided numerous complex acquisition of forests. Specific developments were hold on fast automated tree trunk detection. The scan set is divided into a lower part the detection is performed on, and an upper one, mainly containing branches and crown points. After trunk detections, the lower trunk parts are used to refine the terrain surface. trunk direction are then used to assign crowns points at the various trunks. The approach seems efficient and fast, tested on several heterogeneous forest scans coming from France (in the frame of the ANR EMERGE project) and China (publication at VRCAI) [32]. The proposed algorithms may thus show interest in the forestry community, and quantitative aspects are now to be studied such as automated trunk diameters and volume estimations.

6.2.3. Exploring new ways of single plant visualization (with AMAP)

In the late 2009 months we show that internal simulation structures allowing stop and go actions, representing the simulated plant with a flat metamer graph and its functional properties (leaf volume, metamer volume, pith volume) can be used to generate the plant geometry. First tries were hold on this point, defining metamer lengths and diameters from production. With simple angle rules, and allometry rules, we have shown that we could easily generate 3D outputs from this very compact internal data structure. In 2010, significant new results were gained using this approach. We first demonstrated that a simple topological metamer graph avoiding substructure redundancies reduces drastically the topology encoding complexity. This encoding was shown being efficient on GreenLab dual scale automaton and also on other structural models such as L-systems. Second we show that this approach can be used to generate past geometrical reconstruction. We demonstrated that the tree graph is thus an interesting new approach to reconstruct a wide range of plant geometries from a single simulation [30] (MCCSIS in Freiburg - Germany in July 2010).

After exploring the potential of rule based Web visualizations [66] [65], this new tree graph structure applications for graphics becomes an interesting basis for further research developments related to plant plasticity as underlined in M. Jaeger recent Habilitation à diriger des recherches [18].

6.2.4. Volume imaging

The team and associated team was invited to publish an extended paper on tree structure extractions form voxel shapes, on the basis of the publication to journal IJVR [72]. This collaborative work on voxel image tree data hierarchical segmentation was recently edited soon as a book chapter in Pattern Recognition [37]. Past volume imaging applications led this year again to a publication. In cooperation with CAU, we developed an application on serial colored wheat root microscopic images. Those images are aligned in order to build

an image volume set. Images are segmented and vessels extracted. Statistical analysis is done on these vessel and 3D Vrm models are built. The techniques applied on several data sets on the root tip to top allows then biologist to study and interpret vessel structure changes and development. A first paper is published in PMA09 [68], an another one more detail was submitted end 2010 to Annals of Botany.

7. Contracts and Grants with Industry

7.1. Contracts

Running contracts

- 2007-2011: ANR project (07-CIS) 3Worlds project linking INRIA-DigiPlante with ENS, CNRS, IRD (Geodes), IFI Hanoi, Australian National University. Co-ordinator: ENS
- 2008-2012: ANR Bioenergy EMERGE (involved M. Jaeger)
- 2006-2010: ARCUS Languedoc Roussillon ChongMing Project (involved M. Jaeger)
- 2009-2010: RTRA-INRIA integrative landscape modeling (Co-ordinator M. Jaeger, involved V. le Chevalier)
- 2009-2010: RTRA-INRIA plateforms for landscape modeling (involved M. Jaeger, V. le Chevalier)
- 2010-2012: CANTIA project (pôle de compétitivité Industrie Agro-Ressources): developing models and methods for decision-aid in agriculture (project leader: S2BVisio)
- 2009-2010: RTRA-INRIA Regional network to promote virtual reality tools for landscape applications
- 2010-2011: Project INRA-INRIA with UMR EGC (Grignon): modeling of rapeseed growth

8. Other Grants and Activities

8.1. International Initiatives

Beside conference attendance, several international visits have been done by DigiPlante researchers for scientific collaboration:

- P. de Reffye in China (2 months, LIAMA, CAU, CAF, Hanzhou) and Canada (2 weeks, Institute of Botany and Uqam University)
- V. Letort in China (1 month, LIAMA, CAU, CAF) and USA (1 week, Univ. of Columbus)
- PH Cournède in China (2 weeks, LIAMA, BUAA, CAF)

8.2. Exterior research visitors

- Pr. Zhang Bao Gui (China Agriculture University) (1 month at Centrale, July 2010, Digiteo Fundings)
- Kang Meng Zhen (LIAMA) (1 month at Centrale, July 2010, Digiteo Fundings)
- Katarina Smolenova (Univ. Goettingen) (1 month at Centrale, October 2010)
- Rodrigue Perleau (UC Louvain) (1 week at Centrale, October 2010)
- Sun Ruoxi, 10 weeks, 1 stay in CIRAD-AMAP (Arcus ChongMing Project), March-May, Master 2 student from Graphics and image Research Center at Tongji University, in China.
- Zhang Xiaopeng, 1 month, 1 stay in CIRAD-AMAP (ANR EMERGE Project), August-September, Professor at Liama-Casia in China
- Li HongJun, 1 month, 1 stay in CIRAD-AMAP (ANR EMERGE Project), August-September, Doctorate student at Liama-Casia in China
- Zhang YiKan, 1 month, 1 stay in CIRAD-AMAP (ANR EMERGE Project), June, Associate Professor at Liama-Casia in China
- Hua Jin, 1 month, 1 stay in CIRAD-AMAP (GreenLab associate team Project), June, Doctorate student at Liama-Casia in China
- Hu Baogang, 1 week, 1 stay in CIRAD-AMAP (for M. Jaeger HdR), December, Professor at Liama-Casia in China
- Benedicte Wenden (UK) (2 weeks at CIRAD-AMAP)
- Elodie Vavitsara (Madagascar) (3 months at CIRAD-AMAP)
- Hery Ranarijaona (Madagascar) (3 months at CIRAD-AMAP)
- Doffou Akafou (Ivory Coast) (3 months at CIRAD-AMAP)

9. Dissemination

9.1. Animation of the scientific community

- M. Jaeger co-chaired the LANDMOD2010 Conference (February 3-5, Montpellier)
- 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>. Proceedings were edited by IEEE in February 2010
- M. Jaeger gave an invited talk at 92th congress of Morphologist association, University of Medicine of Montpellier, March 11-13, 2010

9.2. Teaching

PH Cournède and V Letort teach at Centrale Paris in applied mathematics and bio-mathematics for their services as Professor and Associate Professor.

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