INSTITUT NATIONAL DE RECHERCHE EN INFORMATIQUE ET EN AUTOMATIQUE

Project-Team Digiplante

Stochastic, functional and interactive models for plant growth and architecture

Saclay - Île-de-France

THEME BIO

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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^{st}, 2008.

1. Team

Research Scientist

Philippe de Reffye [Team Leader, DR Cirad, HdR]
Marc Jaeger [en détachement du Cirad]

Faculty Member

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

PhD Student

Vincent Le Chevalier [Centrale Paris]
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]
Marlène Puech [Centrale Paris]
Zhongping Li [Centrale Paris]
Feng Lu [Univ. Montpellier II]

Administrative Assistant

Isabelle Biercewicz

Other

Thomas Guyard [Engineer]
Benoit Bayol [Engineer]

2. Overall Objectives

2.1. Research fields

Keywords: *computer graphics*, *dynamic systems*, *functional landscape*, *functional simulation*, *optimal control*, *parameter estimation*, *plant architecture*, *plant development*, *plant growth*, *pmodel identification*, *source - sink relationships*, *stochastic processes*, *structural-functional models*, *yield optimization*.

The project-team is particularly active in plant architecture modelling and plant growth simulations by devloping the GreenLab model. Several issues are concerned:

- Studies on the formalism and the behaviour of the model developed at Inria and Liama, based on instantiations to control the Plant Development.
- Integration of the functioning into the plant structure: bud functioning, biomass production and partitioning both in the deterministic and the stochastic cases.
- Interaction between Organogenesis and Photosynthesis through the biomass supply and the plant demand.
- Interaction plant-environment for physical factors (light, temperature, water)
- Tree structure simplification and scale adaptation.
- Passage from single plant to stand functioning

- Optimization and Control of the dynamical growth to improve yield under constraints.
- Connexion with others research fields: Mechanics, Radiosity, and Genetics.
- Visualization of plants from individual to population and landscape level with different computer graphic techniques.
- Building softwares around the simulation of GreenLab model (Scilab and C++).

2.2. Objectives

The cultivated areas of Europe, including agricultural land and exploitation forests, have a strong impact on global environmental conditions. Erosion, resource impoverishment due to over-exploitation, and pollution by fertilizers or pesticides are crucial problems that agronomy and forestry hope to solve through harmonious cultivation modes and exploitation strategies. For this purpose, they must take into account production needs on one hand and the environment on the other; that is to say, both quantitative and qualitative criteria. In this context, mathematical models of plant growth describing interactions between the architecture of the plant and its physiological functioning have a key role to play. They allow the exchanges (of water, carbon, minerals etc) between plants and their natural environment to be quantified. GreenLab is just such a functional-structural model, and is the result of a long dialogue between botanists, physiologists and mathematicians. We have developed mathematical tools and their corresponding 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 clearings can be beneficial. In this way, we can improve water resources and land management and reduce pollution by fertilizers.
- Control of plant sanitation and pesticides treatment: by coupling the plant growth model and insect population dynamics, we can control the use of pesticides and thus reduce costs and pollution.
- Selection of crop variety: we are currently working with geneticists, in order to prove that the plant genes directly determine the physiological parameters of the GreenLab model. In this way, we expect to propose better strategies for crop selection.
- Virtual simulation and visualization of plantations: computer graphics techniques allow the results of numerical simulations to be visualized. This is very important in urbanism or landscaping for predicting the long-term evolution of projects. The results of this research seem to show that in the near future, new tools of prediction, optimization and control could be effectively used in agriculture and forest exploitation on a large scale, and would drastically improve the management of the environment.

2.3. Highlights

The year 2008 is a key year for DigiPlante, since it marks its officiel start as an EPI at INRIA Saclay, 4 years after its creation as a team.

- 13 publications in international journals and 2 book chapters were published, in addition to some good ranking conferences.
- 2 PhD were defended, V. Letort and J.-F. Barczi.
- the team size increased significantly, with 10 PhD students, the recruitment of two MCF, V. Letort at Centrale and A. Mathieu as an “associate researcher” in the partner institution AgroParisTech, and a pair of engineers to help stabilize software development in the team.
- The organization of PMA09 was launched with M. Jaeger as the general chair.

3. Scientific Foundations

3.1. Digiplante at INRIA

Derived from the AMAP model developed in the 1990s at CIRAD [81], GreenLab's new formulation was introduced at LIAMA (Beijing) in 2000, through the GreenLab Associated team with INRIA. Today, the model is studied and improved through the DigiPlant research team that is a joint team of researchers from INRIA, CIRAD and Ecole Centrale Paris. 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 Phd).

Our approach to develop the mathematical model of plant growth strongly relies on the plant organization described according to Botany. This leads to relevant choices [21] in order to obtain an efficient method of factorization based on plant instantiations [2]. Plant development purely concerns Organogenesis, i.e. the number of organs. Growth depends on photosynthesis that insures organ creation and expansion. We consider here the case without interactions between organogenesis and photosynthesis. On the common assumption of the existence of a global pool of reserves, it is not necessary to consider local conditions and we can distinguish 3 steps to control plant development and growth.

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

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

3.2. 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 [79] to describe GreenLab organogenesis. However, it was shown to be equivalent to a growth grammar [19], and this formalism is mostly used from now on to describe the GreenLab model of plant development. 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 [53], 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 neoformation, 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 [62]. 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.

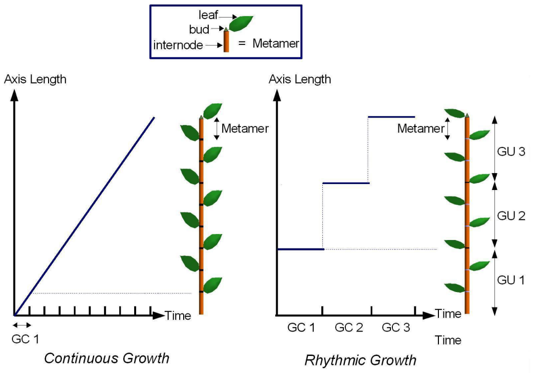


Figure 1. Growth Cycle (GC), Growth Unit (GU) and Metamer in GreenLab. The axis length is given as a function of time for continuous and rhythmic growths

Since metamers may bear axillary buds, plant architecture develops into a hierarchical branching system. Barthélémy and Caraglio 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 not considered in this study, 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 [53], and corresponds to a transition to a superior physiological age of the meristem.

3.2.2. Alphabet, Growth Grammar and Structural Factorization

This section summarize results presented in [19],[2],[6],[12]. 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.

The organogenesis alphabet is given by:

$$\mathcal{G} = \mathcal{M} \cup \mathcal{B} \tag{1}$$

with

$$\mathcal{M} = \{m_{pq}^{t}(n) \ / \ 1 \leq p \leq P, \ \ p \leq q \leq P, \ \ 1 \leq t \leq T, 1 \leq n \leq t\} \ , \tag{2}$$

and

$$\mathcal{B} = \{b_{p}^{t}(n) \ / \ 1 \leq p \leq P, \ \ 0 \leq t \leq T, 0 \leq n \leq t\} \ . \tag{3}$$

T denotes the maximum time of the simulation (possibly $+\infty$).

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 would be introduced in the alphabet without difficulty.

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 the concatenation operator 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 F0L-system as follows:

Definition 2 (GreenLab Organogenesis) GreenLab organogenesis is defined as a F0L-system [67] [73] $\langle \mathcal{G}, \mathcal{B}, P_r \rangle$ with the following production rules P_r:

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

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

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

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

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

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.

In the following, we will denote the F0L-system of GreenLab organogenesis as Γ.

A fundamental result [74] 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.* [21], [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 illustrates the way substructures are organized. The total number of different substructures in a plant of chronological age t is very small even if the total number of organs is high. It is comparable to Pt if there is no differentiation, and to Pt^2 if there is.

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:

If $0 \leq k < \tau(p)$:

$$S_p^t(n,k) = \left[\prod_{p \leq q \leq P} \left(m_{pq}^t(n)\right)^{u_{pq}(t+1-n)} \left(S_q^t(n-1,0)\right)^{v_{pq}(t+1-n)}\right] S_p^t(n-1,k+1) \tag{4}$$

else :

$$S_p^t(n,\tau(p)) = \left[\prod_{p \leq q \leq P} \left(m_{pq}^t(n)\right)^{u_{pq}(t+1-n)} \left(S_q^t(n-1,0)\right)^{v_{pq}(t+1-n)}\right] S_{\mu(p)}^t(n-1,0)$$

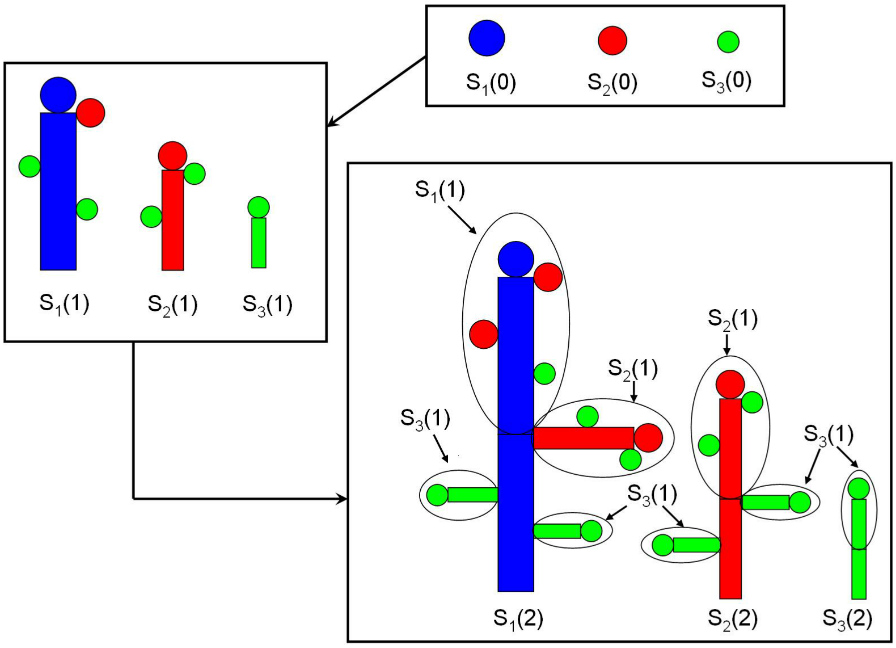


Figure 2. Substructures of physiological ages 1, 2, 3 at chronological ages 0, 1, 2 and their organization: $S_1(0)$*,* $S_2(0)$*,* $S_3(0)$ *are buds of physiological age 1, 2, 3 respectively. In this example, a growth unit of physiological age 1 is composed of 2 metamers of type* m_{13} *and 1 metamer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

This decomposition is illustrated on $S_1(2)$ in Figure 2. If we suppose that all the elements of the alphabet (set of metamers $m^t_{pq}(n)$, set of buds $b^t_p(n)$) 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:

$$S^t_p(0,k) = b^t_p(k)\ , \tag{5}$$

• and if all the substructures of chronological age $n-1$ are built, we deduce the substructures of chronological age n from Equation 4 as functions of $m^t_{pq}(n)$, $u_{pq}(t-n+1)$ 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. $m^t_{pq}(n)$ 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.

[19] 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 toplogy 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 differentation.

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 [18]. In such case, $S^t_p(n)$ 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: $S^t_p(n)$ is a stochastic variable with values in $\mathcal{S}^*$. More details are given in section [5] and in [12].
- 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 [15].

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 ([21], [18], [4], [20], [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 [72], TOMSIM [58], GRAAL [56]...). 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 [8] 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

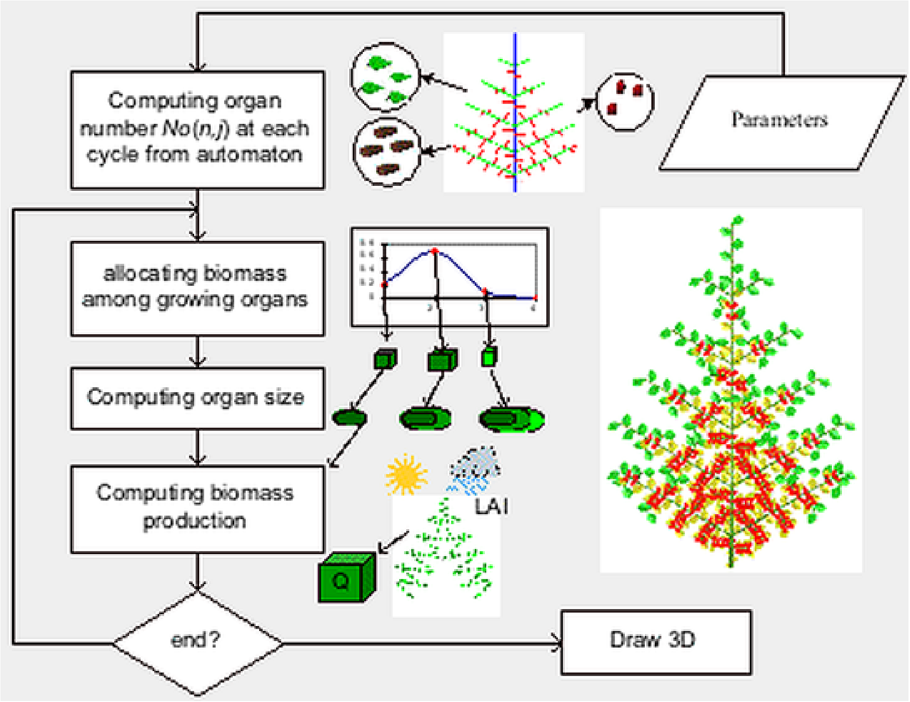


Figure 3. Flowchart of the GreenLab model.

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 (4) 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 ...

Classically, the biomass production at growth cycle t Q^t is taken as a parametric function of 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:

$$Q^t = E^t \beta \left(1 - \exp\left(-\gamma \mathcal{A}^t\right)\right) \tag{6}$$

where β and γ are empirical parameters.
It is helpful to rewrite this equation by changing the parametric structure:

$$Q^t = E^t \mu S_p \left(1 - \exp\left(-k \frac{\mathcal{A}^t}{S_p}\right)\right) \tag{7}$$

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, see Section 6.1.3 for details.
In her PhD, V. Letort [66] 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:

$$\begin{cases} q_{o,p}^{t+1}(n+1) = q_{o,p}^t(n) + \dfrac{p_{o,p}^t(n)}{D^t} Q^t \ \text{ if } 0 \leq n \leq \min\left(T_{o,p} - 1, t\right) \\ \\ q_{o,p}^t(n) = 0 \ \text{ if } n = 0 \ \text{ or } n \geq \min\left(T_{o,p}, t+1\right) \end{cases} \tag{8}$$

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)

  $$D^t = \sum_{o,p} \sum_{n=0}^{T_{o,p}} N_{o,p}^t(n) p_{o,p}^t(n) \tag{9}$$

  where $N_{o,p}^t(n)$ is the number of organs of type o, physiological age p, chronological age n at growth cycle 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 [66].

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 [69] 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).

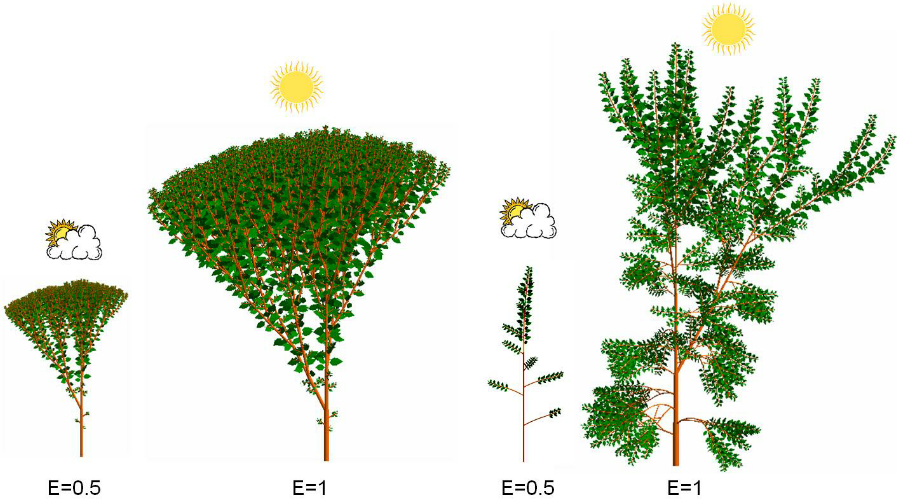


Figure 4. Effects of climatic variations on the GL1 and GL3 organogenesis models: on the left side (GL1), topology is fixed, organs are simply smaller to adjust to the environment; on the right side (GL3), toplogy is variable and the plant adapts its development to the environmental conditions.

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).

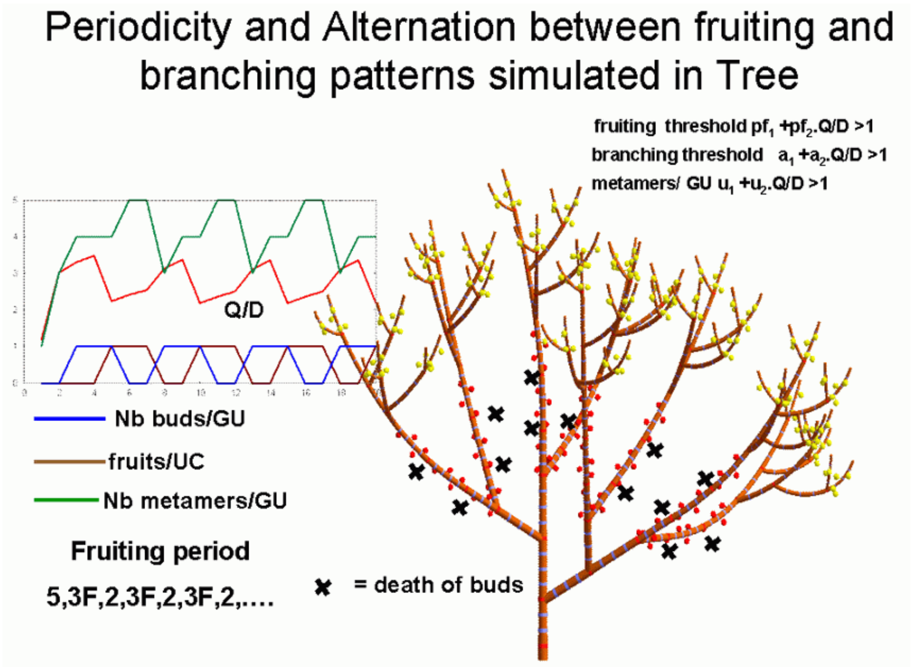
The behaviour of the system was studied by A. Mathieu during her PhD. The conditions of the growth stabilisation were determined according to the parameters. Moreover, an interesting emerging property was obtained: under some conditions, rhythmic phenomena may be generated by the system (Biomass production, 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 :



Periodicity and Alternation between fruiting and branching patterns simulated in Tree

fruiting threshold $pf_1 + pf_2.Q/D > 1$
branching threshold $a_1 + a_2.Q/D > 1$
metamers/ GU $u_1 + u_2.Q/D > 1$

Fruiting period

5,3F,2,3F,2,3F,2,....

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

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 [15].

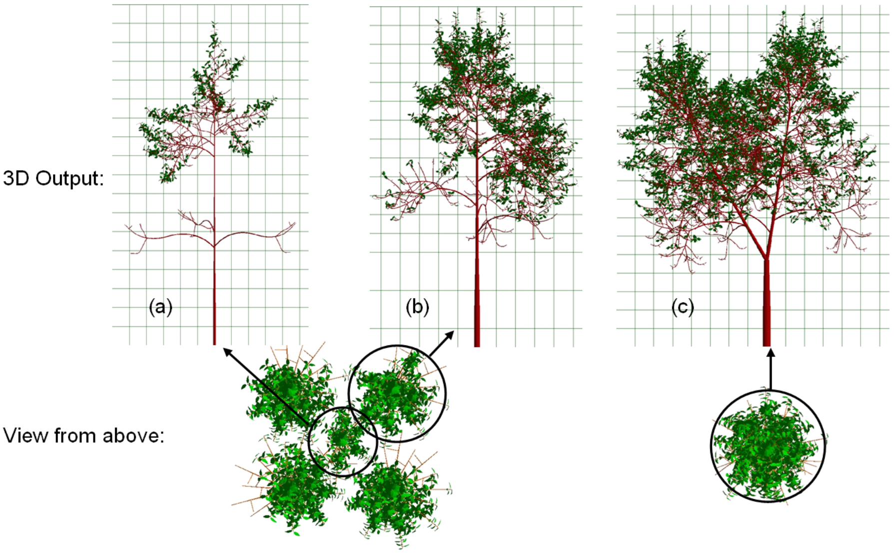


Figure 6. Simulation of tree growth in heterogeneous conditions: view from above and detailed architectures of the individuals. In the upper right corner of the figure, Tree 1 grows in open-field like conditions. In the lower left corner, Tree 3 surrounded by its four neighbours (including Tree 2) severely 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 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.
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) [59]. 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 multiscal models to implement. After some prelimnary works carried out at LIAMA, it is now the PhD subjet of V. Le Chevalier, under the supervision of Marc Jaeger.

Two successive prototypes were developped. The first prototype, voxel based, was a simple simulator synchronizing all events at a daily schedule (water rain, run-of, diffusion, plant growth). Models were basic, and run-of simulated as a diffusion process on the land surface [64]. The second prototype, is surface based. 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 (see Computer Graphics section). The system was tested on synthetic cases (see Figure9), with real climate conditions and published in JCST journal [8].

Both prototypes show strong conceptual limitations. Since end 2006, concepts to develop the design of landscape functional simulators are extensivily studied. A new formalism of resource containers is designed, leading to a new software architecture, with an improvement of the underlying models (the PILOTE model developed by CEMAGREF [68] is used for water budget, the complete version of the GreenLab model is implemented for crops or trees).

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. [75] 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 [13], Arabidopsis [54], Pine saplings [57], Cucumber [70], Sugar-Beet [65], Cotton [76], Beech[9], Chrysanthemum [63], Grapevine [71]...

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

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 [81], 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 :

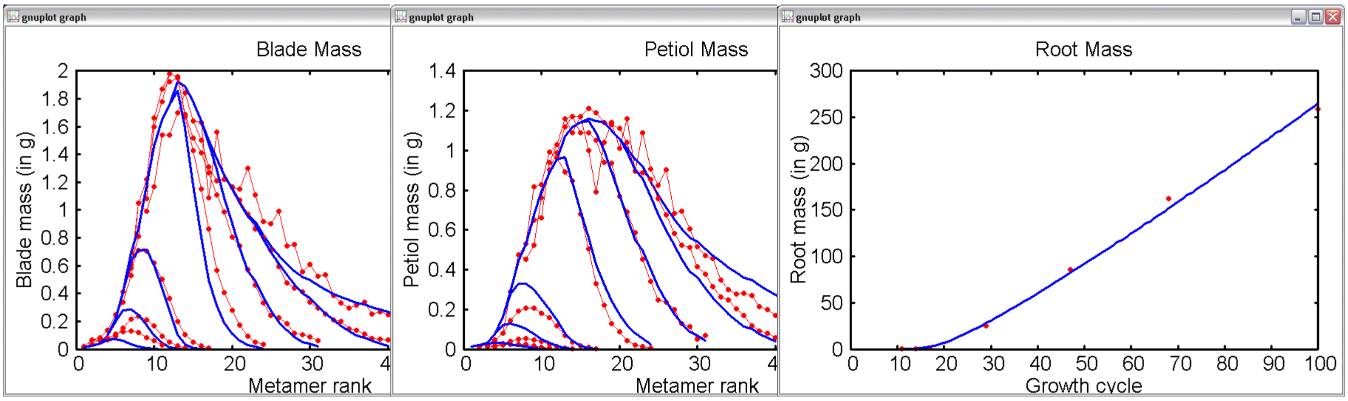


Figure 7. Fitting results: Average plants at organ level: experimental data (in red) and simulated data (lines) (a) Blade dry masses and (b) petiole dry masses according to phytomer ranks, at 7 different growth stages; (c) root dry mass as a function of the growth cycle (with experimental measures at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

Plant simulated visualization in DigiPlante project is still based on the AMAP prinicples [81], characterized by a high level, device independant simulation output, called the line-tree. Geometrical ouput 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, refered by basic indetification 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 scalled, story thus internode diameter/length and other organ sizes. These geometrical informations are stored in a 3 by 4 mattrix, similar to a classical OpenGl Mattrix 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 componant with its orientation
- The structure is flat, no hierarchy or topology information is given. However, extension were developped, using a separated structure storing the componant father-son relations. From these, pruning operatin are available as well as branch per branch output or other hierarchical tree based data exploring schemes.
- The structure cannot be displayed directly; each componant must be given an exhaustive geometrical description, build from instance from CAD-CAM tools. On the other side, the tree skeletton is obvious to be extracted and displayed; each componant can be simply represented by a simple line linking its origin to the end point of its main direction (which is scalled). 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 cilinder 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 independant for the line tree, since define at the organ geometry descrition level.
- The structure allows Level of Details approaches and simplifications. According to componant sizes (length / diameter) selection can be done in order to extract componants of interest (trunk and main axis). Coupled to statistical selection of leaves/flower, fruits, lower graphical model can be generated, without losing the global sahpe of the simulated plant. On branches, successive componants can be

concatanete d, remplacing list of internodes by a straith 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 developped 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. Prior is thus given to approaches keeping biological consistency (for instense leaf area) to appraoches 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 developped 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 diagramm 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 [77]. 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 as shown in Figure8.

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. On this topic, two set of studies are further explored; the intensive use of GPU for folliage drawing (see new results) and the use of adaptative billboards.

3.4.2. Functional Landscape Visualisation

Functional Landscape visualisation, i.e. visualisation of function landscape simulation (cf. Section 3.2.5), aiming to simulate the evolution of the biomass under resource constraints (water) is a recent field in the project, quite original (not developped in literrature so far). 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 as shown in Figure9. The orginality of the developped tools lays in the fact that all these maps are dynamic (daily change), and thus not compatible with classical approaches (all in memory). Vegetation representation is so far rougth; limited to a simple color definition merged with the relief texture (or any othe colorized parameter value). A "pseudo realistic" landscape visualisation can be preformed representing the cumulated biomass by spheres those area are proportional to the cumulated biomass, converting some how the crop production to a "tree crow".

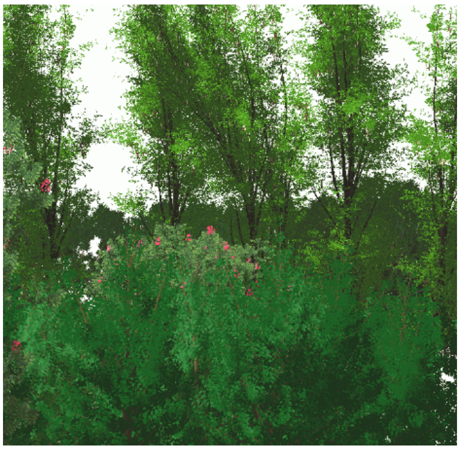


Figure 8. Real time view (close-up) on forest scene including conifers and broadleaves. From [55].

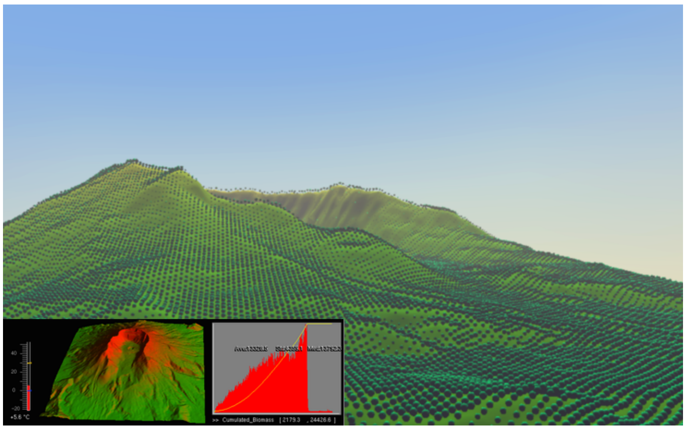


Figure 9. Functional Landscape simulation and visualisation. Biomass values map to colors (red, left) or to sphere radii.

4. Application Domains

4.1. Application Domains

Keywords: *Agriculture*, *Computer Graphics*, *Ecology*, *Ecosystem Management*, *Forestry*, *Landscape Planning*.

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 [7] 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 Digiplant 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

P.H. Cournède has developed the Digiplant 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, Digiplant is used in the partner institutions for research: CAU, INRA Montpellier, INRA Grignon, ITB, Univ. of Wageningen, China Academy of Forestry, CIRAD, IRD

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.

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 [6]. 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.

In 2008, these preliminray 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 architectural development 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.

6.1.2. Parameter identification of trees and of the GL3 model

After some important theoretical advances concerning the GL3 model (model of interaction between growth and development), the year 2008 brought some key results in the validation process. e validation results of validation on experim The theoretical advances in modelling and the development of new tools allowed confronting the model to new plant species, with more complex architectures than the previous versions.

Trees :

The first preliminary results on trees were found in 2007, when fitting the experimental data of pine saplings [57]. The set of data used was a complete description of eight young pines (*Pinus tabulaeformis*) with ages ranging from 1 to 5 years and grown in similar environmental conditions. In 2008, the parametric identification of the model was achieved for adult beech trees (21 and 46 year old), with complex topologies [9]. Contrary to the previous work, only partial descriptions of the trees were available. Data on tree topology were recorded for first-order branches only (along the trunk) and data on biomass weights were agregated by compartments (wood/leaves) at the same level. The main particularities of this work were:

- estimation of the GL3 parameters ruling the structural development in interaction with the functional growth
- combining different levels of data collection (detailed, sparse, and aggregated) and analyzing them with a multiscale approach
- the implementation of a new model of cambial growth and the estimation of its parameters

These two trees were grown in contrasting local environments. The environmental control was represented through a single variable, E, that was found twice higher for one tree than for the other one. All other parameters of the model were set identical for the two trees and fitted in parallel. Owing to the retroactive interactions between topological development and physiological processes, the growth dynamics of the simulated trees resulting from the identification procedure were really different as well in terms of architectural development as in terms of biomass production and allocation. Thus this work was a first demonstration the ability of the model to capture tree plasticity in response to different environmental conditions.

Rhythmic fructification :

A. Mathieu [14] has shown that a consequence of the GL3 model (with retroaction of plant growth on its structural development) was the possible appearance of rhythmic patterns in plants, for exemple in terms of fructification [14]. Such behavior is observed for cucumber plants, with an alternation of zones bearing fruits, and others without fruits. Experiments were conducted at the China Agriculture University (Pr. Zhang Bao Gui) and analyzed with the GreenLab model of interaction between growth and development (GL3). The functional parameters of source-sink balance were estimated and the ratio of available biomass to demand was shown to control the abortion of fruits, cf. Figure 10.

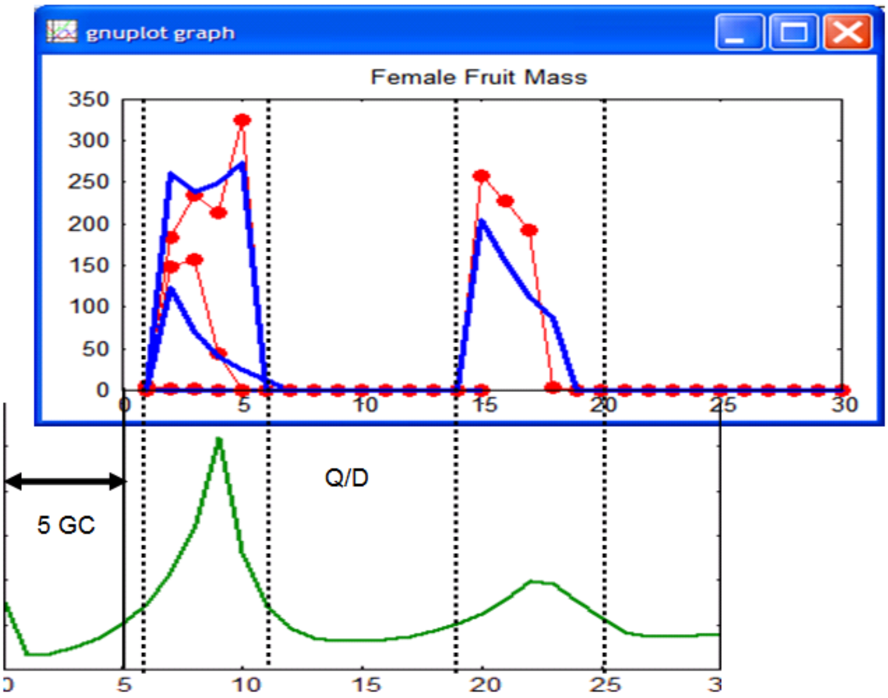


Figure 10. Mass of the fruits according to their positions on the stem and correlation with the ratio of available biomass to demand

These results are submitted to publication. A new experiment is also conducted on several cultivars of sweet pepper at the Univeristy of Wageningen since this plant shows the same cyclic behavior.

Effects of trophic competition on the development rate of axillaries in Grapevine :

Experiments were conducted on several cultivars in SupAgro Montpellier (MAPI team, J. Lecoeur, B. Pallas) and analyzed with the GreenLab model. The functional parameters of grapevine source-sink dynamics were estimated. The probability of maintaining secondary axis development, expressed as a function of Q/D ratio, indicated that an increase in trophic competition inside the shoot led to a progressive stop in their development.

6.1.3. Analysis of the effects of density on crop production

In 2008, the theoretical model of competition [3] recalled in Section 3.2.5, was confronted to real experimental data for Sugar Beet [65], Maize[13] or tomato.
As shown in [3], for high-density crops, our model is strictly equivalent to the classical formula of field crop production given by Howell and Musick [59]. On cultivated crops the optimized S_p (cf. Equation 7) is close

to the inverse of the density $S_p \approx 1/d$ provided that thee density d is big enough, $d > 3$ plantes$/m^2$. Let us denote $S_d = 1/d$.

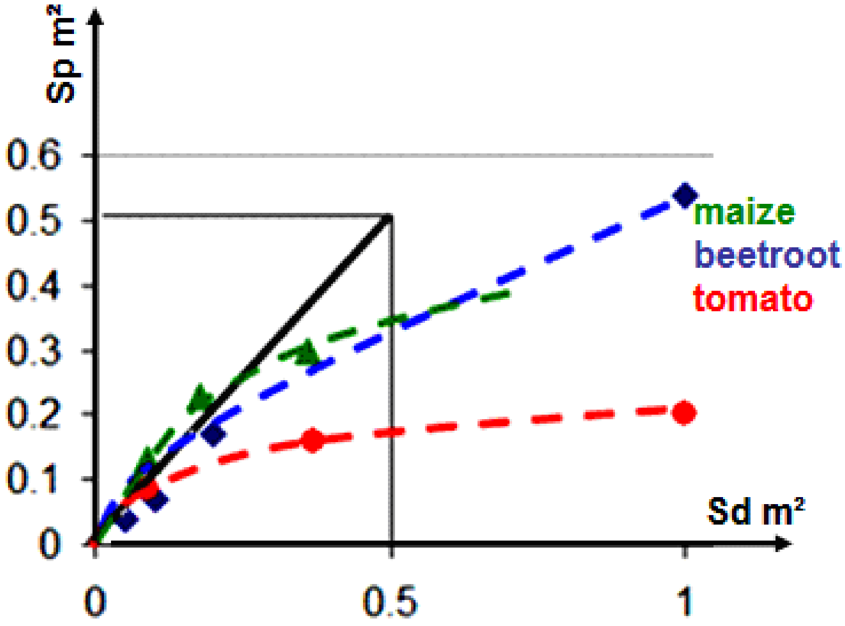


Figure 11. Relationship between S_p and $S_d = 1/d$ for several crops. S_p is estimated from experimental data for several densities.

6.1.4. Plant - soil interactions: coupling GreenLab to a hydric model

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 (M. Puech) has started on this subject, with the first objective of coupling the GreenLab model with a model of soil water budget. This work is done in collaboration with CEMAGREF Montpellier (J.C. mailhol). The first result is the combination of the GreenLab model of plant production to the PILOTE model [68]. A proper study of the model is in process and experiments on wheat and maize (2009) will help estimate the model parameters.

6.2. Computer Graphics (in collaboration with LIAMA)

6.2.1. Simple plant LOD models and real time plant rendering

Level of Detail single plant models, based on simulator Line Tree output has reached a state of maturity within the collaboration with Dr. Xiaopeng Zhang and its team in LIAMA.

In year 2008 many works and publications were finalized on both structure (branch) LOD models and organ union collapse. Especially foliage compression algorithms were adapted to intensive GPU use. The principles are the following:
- in order to avoid multiple exchanges between GPU and CPU, scenes are rendered according to tree species and individuals (forestry scenes are supposed to involve widely instanciations)

- for a given instanciation group, first the full foliage lod models are stored in a simple table, compressed and send to the GPU
- then, while rendering, CPU computes according to viewer parameters the adequate LOD model. From this information only the corresponding indexes of the table are sent to the GPU

An extensive summary paper covering many aspects developped in the past four years has been accepted to Computer Anination and Virtual Words journal CAVW08 Deng QingQiong Jun did successfully succeed her Phd Defense mid summer 2007 on Lod foliage models. She joined the Laboratory of Virtual Reality of Beijing Normal University, working on volume imaging and virtual fossil remedy.

On this subject, two kind of works are currently going on:

- exploring the potential of substructures, that may multiply the use of instanciations inside a single plant.
- valorise existing algoritms, coupling the LOD model generator to different landscape viewer. With SLE tool developped by S. Griffon at Cirad. And Web dedicated tools, in the frame of new projects linking Tongji University to CIRAD AMAP and LIAMA.

6.2.2. 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 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 [80] shows also a high interest on simulated plants, generating thus simplified shapes of crowns

Another related summary work as also been hold in cooperation with Prof. Hu Baogang. It aims to propose new methods to evaluate 3D reconstruction from images base on an image base metrics. The paper accepted to Cyberworlds 2008 [60], "Objective Evaluation of 3D Reconstructed Plants and Trees from 2D Images" shows the application of such an evaluation on reconstructed plants branch structure from laser point clouds, and on LOD models synthetic models

3D reconstruction from laser range point becomes a hot topic in forestry sciences. Both LIAMA GreenLab team and Digiplante were sollicited to participate to an ANR Bioenergy project "EMERGE", planning to evaluation wood ressource for energy (project is accepted and will start early 2009)

Dr Zhang Xiaopeng and PhD Student Zhu Cao came to France in October-November, in the frame of the ANR (MMDA) NATSIM project. M. Jaeger went 2 weeks November/december 2008 in LIAMA, in Zhang Xiaopeng's team.

6.2.3. Volume imaging

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

Mid 2008, M. Jaeger gave a presentation [61] at Interdisciplinary Workshop on 3D Paleo-Anthropology in Toulouse on past work hold at LIAMA in the frame of LIAMA Project 2001-08: Virtual Paleao-antropology. Late 2008, a publication to VRCAI conference (an is related journal IJVR) [78] was published, in which these modules where applied with LIAMA partners (2006) . The paper is a collaborative work hold on voxel image tree data hierachical segmentation.

7. Contracts and Grants with Industry

7.1. Contracts and Grants with Industry

Running contracts

- 3rd year of industrial contract with ITB (French Research Institute for Sugar Beet).
- 3rd year of the Terra Data project in the context of the “Pôle de compétitivité” Cap Digital.
- 1st year of the ANR project (07-CIS) 3Worlds project linking INRIA-DigiPlante with ENS, CNRS, IRD (Geodes), IFI Hanoi, Australian National University. Co-ordinator: ENS
- 1st year of the Terra Magna project in the context of the “Pôle de compétitivité” Cap Digital.

New contracts accepted in 2008

- Agreement between LIAMA, Digiplante and BJFU, for poplar modeling, signed in April 2008
- ANR Emerge (involved M. Jaeger, and Zhang Xiaopeng) Bio-Energy. Co-ordinateur C. Deleuze (ONF). Estimating French Wood resource for Bio-Energy. 750 KEuros. Starts January 2009
- RTRA-INRIA Computational Plants and Ecosystems project: 0803-007. Title: Vers une approche de recherche fédérative pour les plateformes de modélisation et de simulation. (Involved M. Jaeger, Le Chevalier Vincent) Functional Landscapes. 37 KEuros. Co-ordinators J.P Muller (CIRAD), J.C. Fabre (INRA). Starts January 2009
- RTRA-INRIA Computational Plants and Ecosystems project: No 0803-021. Title: Modélisation intégrative de l’écosystème et du paysage (Involved M. Jaeger, Le Chevalier Vincent) Functional Landscapes. 64 KEuros. Co-ordinators M. Jaeger, X. Louchart (INRA). Starts January 2009

8. Other Grants and Activities

8.1. Visiting Scientists

Main overseas visits :

- Short stay of P de Reffye in China (8 weeks): Partners CAU, BJFU, CAF, LIAMA (Beijing)
- Short stay of M Jaeger in China (3 weeks): Partners CAU, BJFU, CAF, LIAMA (Beijing), Tongji (Shanghai)
- Short stay of V Letort in China (3 weeks): Partners CAU, BJFU, CAF, LIAMA (Beijing)

Visitors Hosted in Digiplante team (ECP MAS and Cirad Amap locations) :

- Guo Yan, 1 month, 1 stay, may, Professor at CAU in China (DIGITEO Funding).
- Hu Baogang, 2 weeks, 1 stay, december, Professor at Liama-Casia in China.
- JIA Jinyuang, 2 weeks, 1 stay, december, Professor at Graphics and image Research Center at Tongji University, in China.
- Zhang Xiaopeng, 1 month, 1 stay, October-November, Associate-Professor at Liama-Casia in China
- Zhu Cao, 1 month, 1 stay, october, Doctorate student at Liama-Casia in China
- Xiang Bo, 1 month, 1 stay, october, Master student at Liama-Casia in China
- Liu Jia, 1 month, 1 stay, october, Doctorate student at Liama-Casia in China

9. Dissemination

9.1. PhD

V. Letort, Multi-scale analysis of source-sink relationships in plant growth models for parameter identification. Case of the GreenLab model, Ecole Centrale Paris, May 2008

Q.Q. Deng, Level of Detail and multi-resilution Foliage geometrical models. (in Chinese), Institute of Automation, Chinese Academy of Sciences, Dec. 2008.

J.F. Barczi, Une Contribution Logicielle dédiée la simulation de l’architecture et de la croissance des plantes, Ecole Centrale Paris, Dec. 2008.

9.2. Conference and workshop committees, invited conferences

Invited speakers :

P. de Reffye was an invited speaker to the international 8th China's Conference on Virtual Reality (CCRV08, Fuzhou, September)

Seminars :

- P. de Reffye gave several talks in China at Beijing Forest University (April 08), Nanjing Institute of Agriculture (April 08), Fuzhou Univ. f Agriculture (Sept. 08), Xian University of Agriculture (Sept. 08), Institute of Genetics of Shengzen (Sept. 08).
- M. Jaeger gave several talks in China on plant fast visualisatin and functional landscapes at China Academy of Forestry, Beijing University of Forestry, University of Tongji, LIAMA; and 2 talks on Volume Imaging and its applications in life sciences at Beijing Normal University.
- M. Jaeger gave a talk at 11eme Caquofolies; INRA-SupAgro, Montpellier (March 08)
- M. Jaeger gave a talk at the Interdisciplinary Workshop on 3D Paleo-Anthropology, Anatomy, Computer Science and Engineering - Synergies for the Future . Toulouse, (June 08)
- M. Jaeger organized the Digiplante-GreenLab-Amap Software Engineering workshop at CIRAD Montpellier (November 08) - P.H. Cournède organized the international seminar "Conversation between Plant Biology and Mathematics", Paris, (May 2008)
- P.H. Cournède, "Système dynamique de la croissance des plantes", Journée thématique sur la modélisation de la croissance des plantes, Lyon, Institut des Systèmes Complexes (Avril 08)
- P.H. Cournède, "Mathematical Models of Plant Growth and their Applications in Agriculture Forestry and Ecology", Seminar Princeton - Bell Labs - Centrale - Supélec : Information, Energy and Environment (June 08)

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
- Marc Jaeger was member of Executive Commitee of Edutainment 2008, June 4-5, Nanjing, China

9.3. Courses and Tutorials - Media

The GreenLab model is used in several laboratories in China, in Holland and in France. GreenSciLab, the free GreenLab model implementation running under Scilab environment is now available with tutorial pages and study cases on LIAMA web site with a new easy to use interface and simple case demos.

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.
- In the frame of an ERASMUS project led by Wageningen University: 7 hours course on the GreenLab model (A. Mathieu, P. de Reffye) at Orsay University.
- 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.

Digiplante senior and students were involved in several communications open for public or dissemination activities:
- Participation to the 8ème Salon des Jeux Mathématiques (Paris, May 2008)
- Participation to Agropolis-INRIA Movie Computation Plants and Eco-systems
- Participation to "Fête de la Science" (Saclay, November 2008)
- P.H. Cournède was interviewed by "Banque des Savoirs de l'Essone" for a file on numerical simulation http://www.savoirs.essonne.fr/dossiers/les-technologies/informatique/in-vivo-in-vitro-in-silico/creer-des-organismes-numeriquement-modifies/

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