INRIA

Project-Team Virtual Plants

Modeling plant morphogenesis at different scales, from genes to phenotypes

Sophia Antipolis - Méditerranée

THEME BIO

Activity

Report

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2. Overall Objectives

2.1. Overall Objectives

The Virtual Plants team is a joint team between INRIA, CIRAD and INRA. It is located in Montpellier. The long-term focus of the project is to study plant development and its control by genetic processes.

Plants are branching living organisms that develop throughout their lifetimes. Organs are created by small embryogenetic regions at the tip of each axis, called *apical meristems*. In the project Virtual Plants, we are interested in studying plant apical meristem functioning and development. We believe that a detailed analysis of apical meristem processes, based on advanced mathematical and computational methods and tools, will lead us to get a deeper and better understanding of plant development.

This study is performed from two complementary perspectives.

- First, at a macroscopic level, we develop an extensive methodology to analyze *the structures produced by meristems*. This can be seen as a methodology that aims to solve an inverse problem in which one tries to infer meristem functioning from the complex structures they produce. This analysis is carried out at different spatial and temporal scales.
- Second, at a more microscopic level, we intend to exploit the recent spectacular scientific and technological progresses in developmental biology in order to understand how physiological and genetic processes control meristem growth at cell scale.

To develop these two scientific axes, we carry out research in three main categories of models and methods:

- multiscale models for the spatial (topological and geometrical) representation of structured biological objects (which range from meristem tissues to branching structures),
- methods and models for deciphering the organisation of these complex biological objects,
- and models for morphogenesis.

In order to make our methods and models available to our partners, all our tools are integrated in a common software platform *V-Plants*. Based on this platform, we coordinate the development of an open software platform *OpenAlea* for plant modeling at a national and international level.

3. Scientific Foundations

3.1. Analysis of structures resulting from meristem activity

To analyse plant growth and structure, we focus mainly on methods for analysing sequences and tree-structured data. Theses methods range from algorithms for computing distance between sequences or tree-structured data to statistical models.

- *Combinatorial approaches*: plant structures exhibit complex branching organizations of their organs like internodes, leaves, shoots, axes, branches, etc. These structures can be analysed with combinatorial methods in order to compare them or to reveal particular types of organisation. We investigate a family of techniques to quantify distances between branching systems based on non-linear structural alignment (similar to edit-operation methods used for sequence comparison). Based on these techniques, we study the notion of (topology-based) self-similarity of branching structures in order to define a notion of degree of redundancy for any tree structure and to quantify in this way botanical notions, such as the physiological states of a meristem, fundamental to the description of plant morphogenesis.
- *Statistical modeling*: We investigate different categories of statistical models corresponding to different types of structures.
  - Longitudinal data corresponding to plant growth follow up: the statistical models of interest are equilibrium renewal processes and generalized linear mixed models for longitudinal count data.
  - Repeated patterns within sequences or trees: the statistical models of interest are (hidden) variable-order Markov chains and lumped processes constructed from Markov chains. Variable-order Markov chains are in particular applied to identify complex branching patterns resulting from local inhibition phenomena.
  - Homogeneous zones (or change points) within sequences or trees: most of the statistical models of interest are hidden Markovian models (hidden semi-Markov chains, semi-Markov switching linear mixed models and semi-Markov switching generalized linear models for sequences and different families of hidden Markov tree models). A complementary approach consists in applying multiple change-point models. The branching structure of a parent shoot is often organized as a succession of branching zones while the succession of shoot at the more macroscopic scale exhibit roughly stationary phases separated by marked change points.

We investigate both estimation methods and diagnostic tools for these different categories of models. In particular we focus on diagnostic tools for Markovian and hidden Markovian models (in this latter case to explore the hidden state sequence or tree space).

- *A new generation of morphogenesis models*: Designing morphogenesis models of the plant development at the macroscopic scales is a challenging problem. As opposed to modeling approaches that attempt to describe plant development on the basis of the integration of purely mechanistic models of various plant functions, we intend to design models that tightly couple mechanistic and empirical sub-models that are elaborated in our plant architecture analysis approach. Empirical models are used as a powerful complementary source of knowledge in places where knowledge about mechanistic processes is lacking or weak. We chose to implement such integrated models in a programming language dedicated to dynamical systems with dynamical structure $(DS)^2$, such as L-systems or MGS. This type of language plays the role of an integration framework for sub-models of heterogeneous nature.

3.2. Meristem functioning and development

In this second scientific axis, we develop models of meristem growth at tissue level in order to integrate various sources of knowledge and to analyse their dynamic and complex spatial interaction. To carry out this integration, we need to develop a complete methodological approach containing:

- image processing on stacks of images coming from confocal microscopy,
- algorithms to reconstruct the meristem surface or volume (partially based on classical image processing techniques),
- lineage algorithms that automatically track cell division throughout time,
- tools for structural and statistical analysis of 3D meristem structure (spatial statistics, multiscale geometric and topological analysis),
- physical models of cell interaction based on spring-mass systems or on tensorial mechanics at the level of cells,
- models of fluxes and physiological interactions between cells based on differential equations and partial differential equations,
- and models of cell development taking into account cell division and gene control (using either differential equations, finite state automata or Petri nets).

3.3. OpenAlea: An open-software platform for plant modeling

OpenAlea is a component based, open-software platform for interdisciplinary research in plant modeling and simulation. This platform is used for the integration and comparaison of different models and tools provided by the research community. It is based on the Python language that aims at being both a *glue* language for the different modules and an efficient modeling language for developing new models and tools. *OpenAlea* currently includes modules for plant architecture analysis and modeling (*V-Plants* modules), for modeling radiative transfer, transpiration and photosynthesis (*RATP*, *Archimed*, *Canestra*) and for 3D visualization of plant architecture at different scales (*PlantGL*).

OpenAlea is the result of a collaborative effort associating 10 french research teams in plant modeling from CIRAD, INRA, INRIA, LaBRI, Laboratory Jean Kuntzmann and ENS Lyon. The Virtual Plants team coordinates both development and modeling consortiums, and are more particularly in charge of the development of the kernel and of some main data structures such as multiscale tree graph and statistical sequences.

OpenAlea is a fundamental tool to share models and methods in interdisciplinary research (comprising botany, ecophysiology, forestry, agronomy, applied mathematics and computer science approaches). Embedded in Python and its scientific libraries, the platform may be used as a flexible and useful toolbox by biologists and modellers for various purposes (research, teaching, rapid model prototyping, communication, etc.).

4. Software

4.1. V-Plants

Participants: Christophe Pradal [coordinator], Frédéric Boudon, Florence Chaubert, Jérôme Chopard, David Da Silva, Samuel Dufour-Kowalski, Jean-Baptiste Durand, Pascal Ferraro, Christophe Godin, Yann Guédon, Szymon Stoma.

Computer algorithms and tools developed by the Virtual Plants team are integrated in a common software suite *V-Plants*, dedicated to the modeling and analysis of plant development at different scales (e.g. cellular tissue, whole plant, stand). The architecture of *V-Plants* is based on the Python language and is designed to be modular and scalable.

In 2007, the *V-Plants* packages have been integrated as components of the *OpenAlea* platform (see Section 4.2). Some components are distributed with he OpenAlea platform and usable through the visual programming environment (see figure 2).

One of a key component, PlantGL [40], provides a set of graphical tools and algorithms for geometrical plant modeling and simulation at different scales. It is used by many other components to represent the geometry of biological shapes from 3D meristems (see [37], [29]), plant architectures (see [40]) to plant populations (see [12], [38]). PlantGL is built around a scene-graph datastructure and provides efficient algorithms and original geometrical shapes (parametric surfaces, dedicated envelops) usefull for plant modeling.
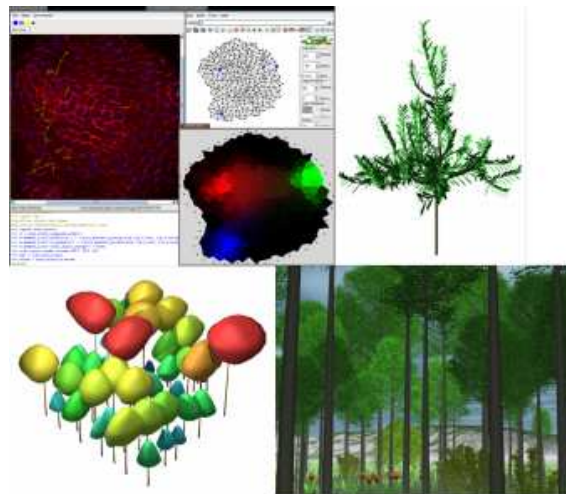
Figure 1. V-Plants components of the OpenAlea platform: simulating plant processes at different scales. Top Left: Reconstruction of a virtual meristem, analysis and simulation of the auxin fluxes inside the meristem. Top Right: Reconstruction of a virtual apple tree from digitized data. Bottom: Simulation of an ecosystem (A beech "Fagus Sylvatica L." trees forest) with a multi level approaches. On the left, explicit representation of the crown volumes that serves as input to generate the detailed representation, on the right.

4.2. OpenAlea

Participants: Christophe Pradal [coordinator], Samuel Dufour-Kowalski, Frédéric Boudon, Florence Chaubert, Jérôme Chopard, David Da Silva, Christophe Godin, Yann Guédon, Szymon Stoma, Christian Fournier [INRA], Nicolas Donès [INRA], Hervé Sinoquet [INRA], Frédéric Théveny [CIRAD].
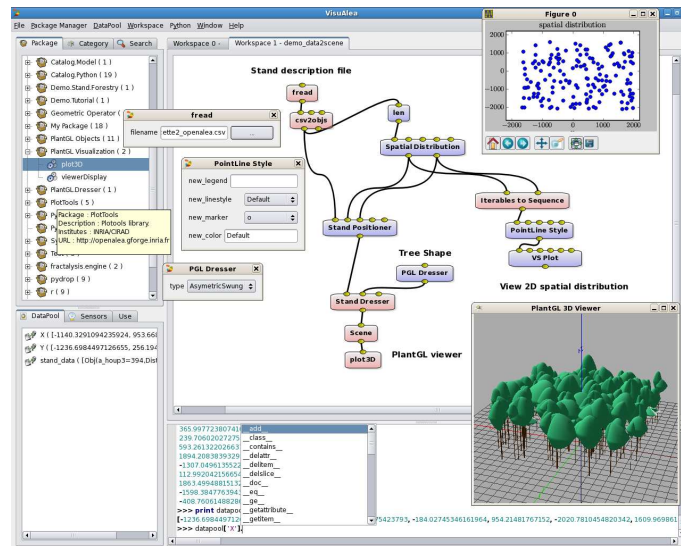
Figure 2. OpenAlea.Visualea: Visual programming interface. The package manager shows the available components. The components can be interconnected on a workspace to form a dataflow. The python interpreter allows low level interaction with the system.

This research theme is supported by an INRIA ODL Grant.

OpenAlea is an open source project primarily dedicated to the plant research community, with a particular focus on plant architecture and ecophysiology. It is a distributed collaborative effort to develop Python libraries and tools which address the needs of current and future work in plant architecture.[33], [32], [22].

OpenAlea is designed as a component framework to dynamically glue together models from different plant research labs, and to enhance reusability of existing models in the plant research community.

In 2007, the following steps have been performed:

1. Develop and extend the component platform architecture
   – OpenAlea.Core is the kernel of OpenAlea. It provides a component architecture, a package manager and a dataflow to build models by interconnecting components in a directed graph.
   – OpenAlea.Visualea is a visual programming application allowing to build intuitively new models by connecting available components together. For each component, a graphical user interface is automaticaly generated based on the type of its interfaces (see figure 2).
   – OpenAlea.Deploy : Deploy extends the python setuptools package to simplify the deployment and the installation of the different OpenAlea packages. It is able to research available OpenAlea packages on different web repositories (like GForge), and provides an uniform way to the user to install and update components on different platforms.

2. Integrate existing models and provide functionalities
   – Provide common tools (basic data structure, statistics, visualization...)
   – Integrate ecophysiological models (Caribu, Drop [INRA],).
   – Integrate V-Plants models (meristem, plant structure analysis, 3D modeling)

3. Animation and diffusion
    – Developers and modelers of different teams start collaboration and work together in pairs on a common objective during coding and modeling sprint sessions. In 2007 three coding sprint and two modeling sprints have been organised.
    – Software demonstration have been held in the FSPM conference [22] and in the INRIA 40 ans, presenting a set of plant modeling scenarii provided by differents modelers of the OpenAlea community.

5. New Results

5.1. Analysis of structures resulting from meristem activity

5.1.1. *Analysis of longitudinal count data and underdispersion*
Participants: Catherine Trottier, Mariem Zouch [Master student], Yann Guédon, Christian Lavergne.

The elongation of leafy axes is influenced by environmental conditions such as rainfall for instance. In the context of plant growth follow-up, measurement is made of the number of newly elongated leaves during successive observation periods. These count data are often underdispersed with reference to the Poisson distribution and are repeated along time. We are studying dedicated models based on the weighted Poisson distribution, which is defined by 3 parameters (λ, r, a), r expressing the under- or over-dispersion, and the effects of explanatory variables being introduced in λ. With a fixed, these weighted Poisson distributions belong to a two-parameter exponential family for which we designed an estimation algorithm based on Fisher's scoring. This algorithm has been compared to a direct Marquardt algorithm. We are now working on the estimation of parameter a and the introduction of random effects in these models in order to take into account the longitudinal aspect of the measurement and thus the dependence in the data.

5.1.2. *Quantitative analysis of the phenotypic variability of shoot architecture in grapevine cultivars*
Participants: Yann Guédon, Gaétan Louarn [INRA, LEPSE], Eric Lebon [INRA, LEPSE], Jérémie Lecoeur [Montpellier SupAgro, LEPSE].

Plant architecture and its interaction with agronomic practices and environmental constraints are determinants of the structure of the canopy, which is involved in carbon acquisition and fruit quality development. A framework for the quantitative analysis of grapevine (*Vitis vinifera*) shoot architecture, based on a set of topological and geometrical parameters, was developed for the identification of differences between cultivars and the origins of phenotypic variability; see [16]. Shoot topology was analysed for two cultivars ("Grenache N", "Syrah"), using a hidden semi-Markov chain and variable-order Markov chains to identify deviations from the normal pattern of succession of phytomer types (P0-P1-P2), together with kinematic analysis of shoot axis development. Shoot geometry was characterized by final internode and individual leaf area measurements. The main factors leading to differences in leaf area between the cultivars were: (a) slight differences in main shoot structure, with the supplementary P0 phytomer on the lower part of the shoot in "Grenache N", which bears a short branch; and (b) an higher rate and duration of development of branches bearing by P1-P2 phytomers related to P0 ones at the bottom of the shoot in "Syrah". Differences in axis length were accounted for principally by differences in individual internode morphology, with "Syrah" having significantly longer internodes. This trait, together with a smaller shoot diameter, may account for the characteristic "droopy" habit of "Syrah" shoots. This study highlights the architectural parameters involved in the phenotypic variability of shoot architecture in two grapevine cultivars. Differences in primary shoot structure and in branch development potential accounted for the main differences in leaf area distribution between the two cultivars. By contrast, shoot shape seemed to be controlled by differences in axis length due principally to differences in internode length.

5.1.3. *Predicting the vertical location of branches along Atlas cedar stem in relation to annual shoot length*

Participants: Yann Guédon, François Courbet [INRA, URFM, Avignon], Sylvie Sabatier [CIRAD, AMAP, Montpellier].

A model for the vertical location of whorl and interwhorl branches was constructed for Atlas cedar (*Cedrus atlantica* Manetti); see [13]. The vertical location of branches in the crown partly governs their further growth and mortality from which depend (i) the stem growth and form and (ii) the quality of lumber and veneer, including wood knots. Each annual shoot was considered as a sequence of successive positions, unbranched or branched with two types of branch: short or long shoot. Branching sequences were analyzed using hidden semi-Markov chains. A wide range of annual shoot lengths was sampled in order to determine the relationships between sequence length and the characteristics of every zone identified (frequency of every type of axillary production, probability of zone occurrence and probability of transition to the following zone). The model predicts branch vertical position which can be used as inputs for branch diameter and mortality models.

5.1.4. *Semi-Markov switching models*

Participants: Florence Chaubert, Yann Guédon, Christian Lavergne, Catherine Trottier, Yves Caraglio [CIRAD, AMAP].

Incorporating both the influence of explanatory variables and inter-individual heterogeneity in a hidden Markovian model is a challenging problem. We are studying different families of semi-Markov switching models including semi-Markov switching linear mixed models, i.e. models that combine linear mixed models in a semi-Markovian manner and semi-Markov switching generalized linear mixed models [19]. In the case of a semi-Markov switching linear mixed model, the underlying semi-Markov chain represents the succession of growth phases while the linear mixed models attached to each state of the semi-Markov chain represent both the influence of the explanatory variables (mainly climatic variables which are time-dependent explanatory variables) and the inter-individual heterogeneity within a given growth phase; see [18]. The EM algorithm which is the standard algorithm for estimating hidden Markovian models cannot be applied for estimating semi-Markov switching linear mixed models. We are thus investigating alternative solutions which extend the EM algorithm and incorporate simulation steps either for the hidden state sequences or for the random effect. Another family of semi-Markov switching linear mixed models is also investigated where, instead of individual-wise random effects, random time effects are incorporated in order to model the synchronous fluctuations between individuals.

5.1.5. *Diagnostic tools for hidden Markovian models*

Participants: Yann Guédon, Jean-Baptiste Durand.

This research theme is partially supported by the ACI "Arborescences".

Once a hidden Markovian model has been estimated, it is generally of interest to understand the hidden state sequence (or tree) structure underlying each observed sequence (or tree). Questions of interest are:

- Is the most probable state sequence most probable by a large margin or are there other state sequences with near-optimal probability?
- Do these near-optimal sequences have state structures very similar to the most probable state sequence or do they greatly differ?

Methods for exploring the state sequences that explain a given observed sequence for a known hidden Markovian model may be divided into three categories: (i) enumeration of state sequences, (ii) state profiles i.e. state sequences summarized in a $J \times \tau$ array where J is the number of states and τ the length of the sequence, (iii) computation of a global measure of the state sequence uncertainty (entropy of the state sequence that explains an observed sequence for a known hidden Markovian model). Various methods belonging to these three categories have been developed for different families of hidden Markovian models including hidden semi-Markov chains, hidden hybrid model combining Markovian and semi-Markovian states [15] and different
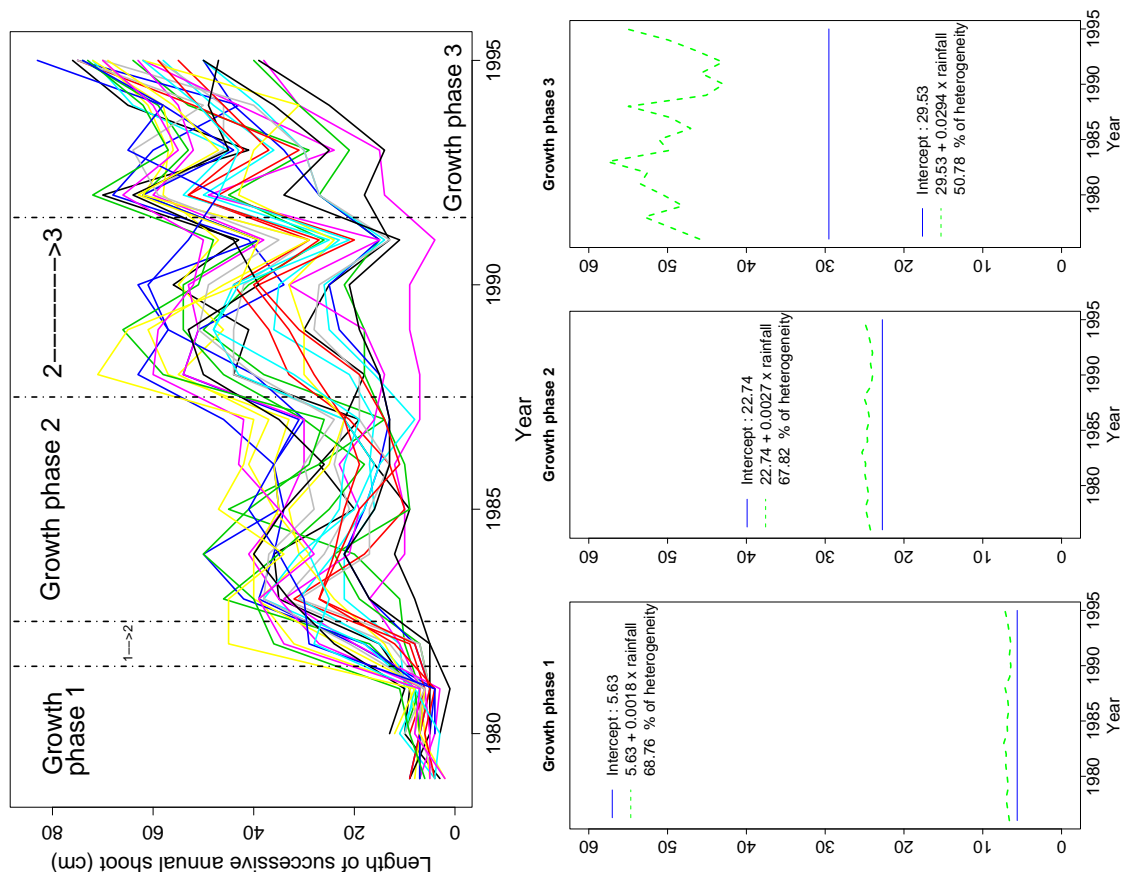
Figure 3. Segmentation of sequences of annual shoot lengths along 17-year-old Corsican pine trunks using a 3-state semi-Markov switching linear mixed model. The phase change years (two first growth phases : between 1982 and 1983; two last growth phases : between 1987 and 1992) are specifics to each tree. The inter-individual heterogeneity is greater at the beginning of the plant life (more than 67% on the two first growth phases). On the two first growth phases, the cumulated rainfall has a moderate influence on the length of annual shoots. On the phase of strongest growth, the annual shoot lengths is markedly influenced by the cumulated rainfall.

categories of hidden Markov tree models. Due to their multidimensional nature, state profiles are difficult to visualize and interpret on trees. Hence, we propose to compute in a first stage a unidimensional profile of conditional entropies that summarize for each vertex the state uncertainty. In a second stage, the usual state profiles are visualized on selected paths of interest within the tree.

5.1.6. *Methods for exploring the segmentation space for multiple change-point models*
Participant: Yann Guédon.

The retrospective or off-line change-point detection problem is addressed. From an algorithmic point of view, this research theme is closely connected to the preceding theme restricted to hidden semi-Markov chains. The studied algorithms share a common structure with similar algorithms recently proposed for exploring the state sequence space structure for hidden semi-Markov chains [15]. The independence between segments in multiple change-point models corresponds to conditional independence at jump times for hidden semi-Markov chains. A key difference between a hidden semi-Markov chain and a multiple change-point model lies in the fact that the hidden semi-Markov chain parameters are fixed parameters (previously estimated) for state sequence or state profile computation while change-point model parameters (for instance mean and variance for each segment in the Gaussian case) are "'contextual"' parameters that depend on the change points. This explains the specific behaviour of the proposed diagnostic tools in connection with the determination of the optimal number of change points. Methods for exploring the segmentation space structure for a fixed number of segments may be divided into two categories: (i) enumeration of segmentations, (ii) summary of the possible segmentations in change-point or segment profiles. Concerning the first category, a forward dynamic programming algorithm for computing the top L most probable segmentations and a forward-backward algorithm for sampling segmentations are studied. Concerning the second category, a forward-backward dynamic programming algorithm and a smoothing-type forward-backward algorithm for computing two types of change-point and segment profiles are studied. The proposed methods are mainly useful for exploring the space of possible segmentation for successive numbers of segments; see [25]. Change-point and segment profiles may help to predict supplementary change points, highlight overestimation of the number of segments and a specific type of change-point profiles summarizes the uncertainty concerning the location of change points.

5.1.7. *Growth components in trees*
Participants: Florence Chaubert, Yann Guédon, Yves Caraglio [CIRAD, AMAP], Patrick Heuret [INRA, AMAP], Emilie Lebarbier [AgroParisTech], Céline Meredieu [INRA EPHYSE, Cestas].

Observed growth, as given for instance by the length of successive annual shoots along the main axis of a plant, is mainly the result of two components: an ontogenetic component and an environmental component. An open question is whether the ontogenetic component along an axis at the growth unit or annual shoot scale takes the form of a trend or of a succession of phases. Various methods of analysis ranging from exploratory analysis (symmetric smoothing filters, sample autocorrelation functions) to statistical modeling (multiple change-point models, hidden semi-Markov chains, hidden hybrid model combining Markovian and semi-Markovian states and semi-Markov switching linear mixed model) were applied to extract and characterize both the ontogenetic and environmental components using contrasted examples; see [18] for the application of semi-Markov switching linear mixed models in this context. This led us in particular to favor the hypothesis of an ontogenetic component structured as a succession of stationary phases and to highlight phase changes of high magnitude in unexpected situations (for instance when growth globally decreases); see [14], [26]. These results shed light in a new way on botanical concepts such as "phase change" and "morphogenetic gradient". We are now studying multiple change-point models that incorporate a random time effect for the joint segmentation of multiple sequences. In this way, the synchronous fluctuations between individuals, mainly of climatic origin, are explictly modeled.

5.1.8. *Hidden Markov tree models for investigating physiological states within plants*
Participants: Jean-Baptiste Durand, Yann Guédon, Evelyne Costes, Yves Caraglio [CIRAD, AMAP], Patrick Heuret [INRA, AMAP].

This research theme is supported by the ACI "Arborescences".

Plant architecture is the result of repetitions that occur throughout growth and branching processes. During plant ontogeny, changes in the morphological characteristics of plant entities such as growth units or annual shoots, are interpreted as the indirect effect of the meristems being in different physiological states. Thus, connected entities can exhibit either similar or very contrasted characteristics. We designed a statistical model to reveal and characterise homogeneous zones and transitions between zones within tree-structured data: the hidden Markov tree (HMT) model. This model enables to assign the entities to classes sharing a same "physiological state" [4]. The ability of hidden Markov tree models (HMTs) to discriminate classes of entities that make biological sense was investigated using diverse temperate and tropical forest species.

(i) The analysis of branches from Aleppo pines led to a characterization of the changes in the length, branching intensity, and in the presence/absence of male and female sexuality, according to the entity position within the branch.

(ii) The analysis of *Symphonia globulifera* (Clusiaceae) (a tree species of the rain forest in French Guyana) individuals highlighted well-separated and clearly interpretable classes of entities that structure these individuals (see Figures 4, 5). To assess the architectural variability within this species, trees growing in a greenhouse were compared with forest trees using HMT models. The individual heterogeneity was also investigated using hierarchical clustering - based on an edit distance between trees [43] - and also statistical tests to discriminate individuals growing under different controlled light conditions [27], [23].

(iii) To investigate the status of flowering in the architecture of centenary beech trees, HMT models were identified. The results suggest that flowering is involved in two well-separated successive patterns of entities with different levels of vigor. Synchronicity of the development of annual shoots was assessed by resorting to tree comparison methods [43]. As for the *Symphonia globulifera* dataset, classes of individuals with similar levels of development were inferred using either the vector of state frequencies computed at individual scale, or using tree comparison methods [23]).

5.1.9. *Branching processes for plant development analysis*

Participants: Jean Bérard [U. Lyon I], Anne Perrut [U. Lyon I], Didier Piau [U. Grenoble I], Evelyne Costes, Yann Guédon, Yves Caraglio [CIRAD, AMAP], Patrick Heuret [INRA, AMAP].

This research theme is supported by the ACI "Arborescences".

We are investigating multitype branching processes with dependences as a new analysis tool for plant structures. This research theme is closely connected to the preceding one concerning hidden Markov tree models since, in most cases, the types are the states restored for each entity using a previously estimated hidden Markov tree model. Our objective is twofold: First, we are testing various sub-families of branching processes (with different parameterizations and dependencies) using a set of reference data sets (apple tree, Aleppo pine, *Symphonia globulifera*) in order to determine the most useful ones. Second, branching processes focus on an unusual way of studying plant development and this generates new biological questions concerning the rules governing the generation of offspring entities from a parent entity.

5.1.10. *Self-nested structure of plants*

Participants: Christophe Godin, Pascal Ferraro.

This research theme is supported by the ACI "Arborescences".

To study the redundancy of structure embedded at various levels in tree architectures, we investigated the problem of approximating trees by trees with particular self-nested structures. Self-nested trees are such that all their subtrees of a given height are isomorphic. We show that these trees present remarkable compression properties, with high compression rates. In order to measure how far a tree is from being a self-nested tree, we introduced a quantitative measure of the degree of self-nestedness for any tree. For this, we construct a self-nested tree that minimizes the distance of the original tree to the set of self-nested trees that embed the initial tree. To solve this optimization problem, We designed a polynomial-time algorithm that makes it possible to
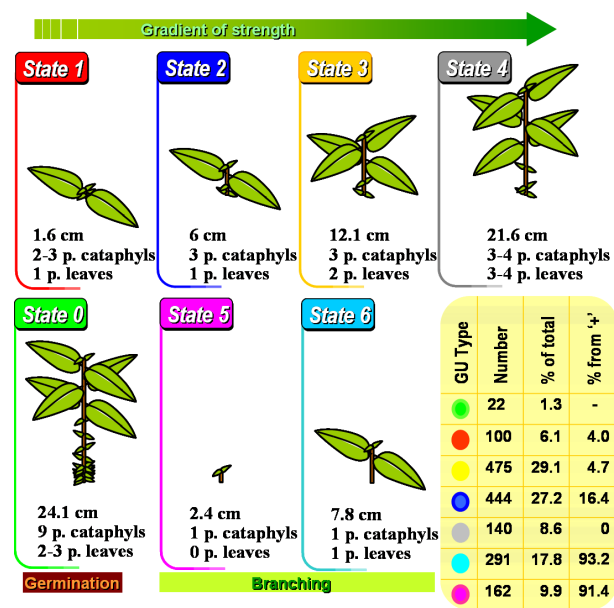
Figure 4. Symphonia globulifera. Representation of the different types of Growth Unit (GU) identified by the HMT model. Mean length, number of pairs of cataphylls and leaves are provided. The total number and the associated frequency of GUs in each state is indicated on lower-right corner as well as the proportion of GUs issued from branching (+).
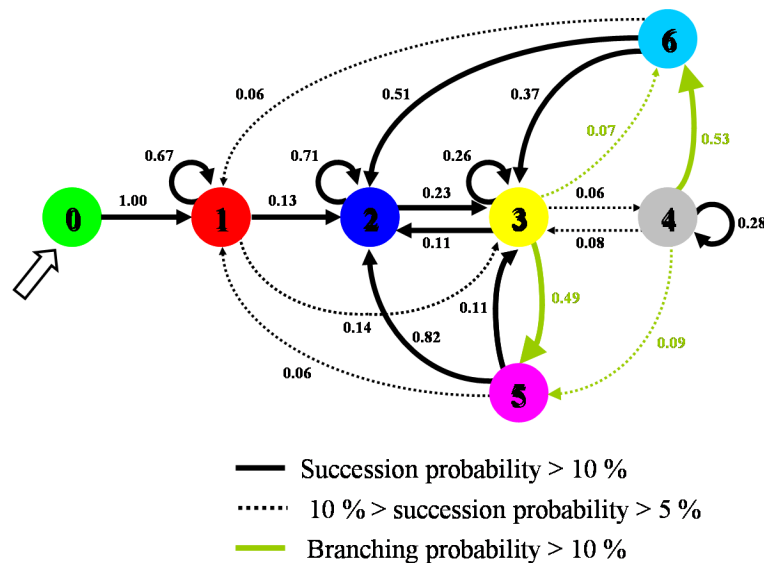
Figure 5. Symphonia globulifera. Transition graph with information on succession (black arrows) or branching (green arrows) between successive states. The dotted arrows correspond to transition probabilities. Only the transitions with probability > 0.05 are represented. .

quantify the degree of self-nestedness of a tree in a precise manner. The distance to this nearest embedding self-nested tree (NEST) is then used to define compression coefficients that reflect the compressibility of a tree. In the context of the structural analysis of botanical plants, it is possible to give a strong biological interpretation of the NEST of a tree based on the hypothesis that isomorphic tree structures at macroscopic levels are actually produced by meristems in identical physiological states (scaling hypothesis). This makes it possible to show that the reduction graph of the NEST of a plant may be interpreted as the maximum sequence of differentiation states that any meristem of a plant may go through. We characterized this approach on both a database of artificial plants with degraded degree of self-nestedness and on a real plant (a rice panicle) whose structure was completely measured 6. We showed that the NEST of this plant may be interpreted in biological terms and reveals important aspects of the plant growth. This work was presented at the 5th workshop of functional-structural models in Napier [24], New-Zealand, Nov 2007 and will be submitted in December 2007 to IEEE Transactions on Pattern Analysis and Machine Intelligence (PAMI).

5.1.11. Reconstruction of plant architeture from 3D laser scanner data

Participants: Frédéric Boudon, Jean-Christophe Chambellan [UMR PIAF, Clermont-Ferrand], Christophe Godin, Hervé Sinoquet.

3D digitized computer images of real plants are required in many areas of plant modelling. They can be used for instance to simulate physical interaction of real plant structures with their environment (ligth, rain, wind, pest, ...), to set up initial conditions of growth models or to assess their output against real data. In the past decade, methods have been developed to digitize plant architecture in 3D [51], [45]. These methods are based on direct measurements of position and shape of every plant organ in space. Although they provide accurate results, these methods are particularly time consuming. More automatized methods are now required in order to collect plant architecture data of various types and sizes in a systematic way. In this work, we investigate the possibility to use 3D laser scanners to automate plant digitizing. We consider different levels of complexity: i) reconstruction of organs ii) reconstruction of branching systems without leaves iii) reconstruction of branching

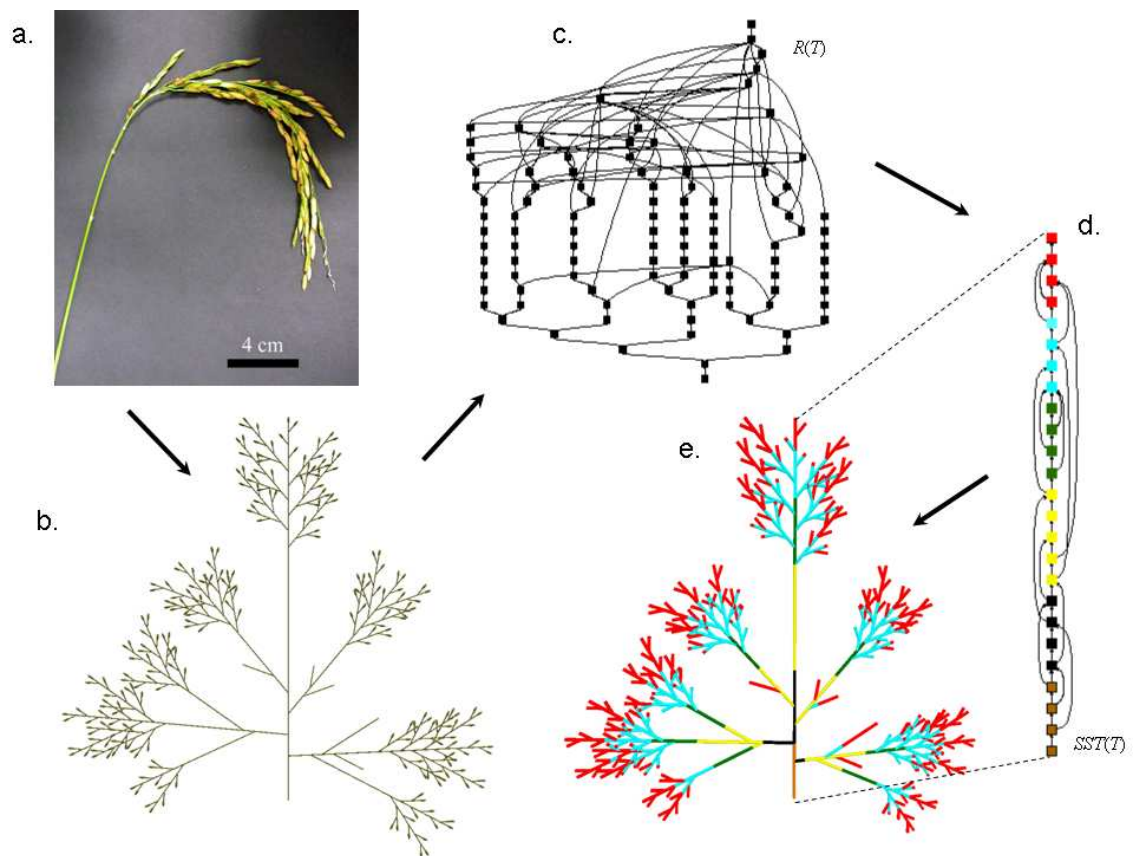*Figure 6. (a) Photo of a rice panicle (b) tree representing the topological structure of the panicle (c) Reduced graph of the panicle tree (d) Corresponding NEST that can be interpreted as the maximal sequence of differentiation states that a meristem can go through when building the panicle (e) color map of the meristem differentiation states obtained by projecting the NEST states back to the original topological tree*

systems with leaves. Point i) has been recently addressed by the PIAF team and led to design a first generic method for simple leaf reconstruction. We are currently designing algorithms to reconstruct branching systems without leaves from scanner data simulated on plant mock-up obtained using different digitizing method. These methods are based on the study of shape continuity bewteen horizontal sections of 3D images. This preliminary work has lead us to submit a proposal to the 2007 ARC INRIA call, where several reconstruction methods will be investigated in collaboration with the project-teams Galaad (based on algebraic geometry) and Geometrica (based on mesh reconstruction and processing).

5.1.12. A multiscale model of light interception

Participants: David Da Silva, Frédéric Boudon, Hervé Sinoquet, Christophe Godin.

Light capture by plants is an essential process for plant growth and survival since light provides plants with energy which can be used for transpiration and carbon fixing. In particular, the local light environment in the canopy during plant development is a major component of the meristem fate.

In ecophysiology, the most common approach to model light interception abstracts the plant canopy as a turbid medium, i.e. a medium made of infinitely small foliage particles randomly dispersed in the vegetation volume. In such medium, light penetration can be expressed by the Beer-Lambert law, which defines the probability p_0 that a photon crosses the vegetation volume without any interception as:

$$p0 = exp(G.LAD.l)$$

where LAD is the leaf area density of the canopy, l is the distance travelled by a ray of light in the canopy ad G is a geometric constant. This equation is only valid for homogeneous and random foliages. For clumped foliages, that augment the self-shading effect, or for foliages whose regularity decreases the self shading effect, a correction has to be introduced in the original Beer-lambert equation by adding a new empirical coefficient μ that depends on the foliage dispersion. This modification is usually sufficient to adapt the initial model satisfactorily. However, how the coefficient μ is related to the plant architecture is still unknown.

To address this issue, we designed a multiscale model of light interception based on the Beer-Lambert original equation. In this model, we consider that a plant canopy may be recursively decomposed into sub-canopies corresponding to clusters at different scales. The probability that a ray is stopped by the vegetation volume is then expressed recursively as a function of the multiscale structure of the plant:

$$p_{i,j} = 1 - p_{0i,j} = 1 - \prod_{k=1}^{n_j} [1 - p_{i+1,k}] \tag{1}$$

where $p_{i,j}$ is the opacity of the jth subcanopy at scale i. This expression generalizes the Beer-Lamber equation to multiscale structures and makes it possible to interpret the μ coefficient. The approach was illustrated and tested on the multiscale structure of digitized plants (mango trees). This model will be submitted in December 2007 to the journal Multiscale Modelling and Simulation.

5.1.13. Modeling of light transmission under heterogeneous forest canopy

Participants: David Da Silva, Philippe Balandier, Frédéric Boudon, Hervé Sinoquet, Christophe Godin.

A major factor for heterogeneous forest management is the control of light microclimate. Indeed growth and survival of regeneration saplings and understorey vegetation development is closely related to light available below the forest trees. Manipulating the forest structure by thinning adult trees is therefore a major tool to control light transmission to the understorey.

The transmission is related to the attenuation of light which is usually estimated with the Beer-Lambert law assuming homogeneous foliage within the canopy. However forest canopies are far from homogeneous, which requires models that can take into account the effect of clumping between and within trees. In this work we develop a model that can be readily used with both coarse or detailed parameterization to generate any type of stand and compute the distribution of light transmitted below the canopy. This work is a made in collaboration with the INRA - ONF - CEMAGREF project *ECOGER*.

5.1.14. Heritability of architectural traits

Participants: Christian Cilas, Evelyne Costes, Pascal Ferraro, Christophe Godin, Vincent Segura [INRA, Montpellier], Charles-Eric Durel [INRA, Angers], Aïda Ouangroua [LaBRI, Bordeaux].

This research theme is partially supported by the ACI "Arborescences".

Plant development is controlled by the combined effect of gene activity and environmental constraints, which in turn combine with ontogenetic gradients. At a given date, a plant architecture is thus the outcome of this complex combination. The phenotype dissection into its genetic, ontogenetic and environmental components thus requires specific experimental design to be addressed. We investigated this issue in an agronomic context, on an apple tree progeny segregating for architectural traits ([42]; [50]). On the basis of a staggered-start experimental design, observation protocols for describing the architecture, including both topological and geometric traits, were collected at different scales (trees, branching systems, axes and nodes), and over four and three consecutive years for experimental plots planted in 2003 and 2004 respectively. They were included in architectural databases which were explored using the *V-Plants* software. Both spatial repetitions, i.e. different axis types, and temporal repetitions, i.e. successive ages of trees, were considered in a linear mixed model for repeated data. A significant genotype effect was found for most studied traits and interactions between genotypes and years or/and ages were also detected. For each studied trait, predicted values (BLUPs) of the genotypic (G) effect or its interaction with tree age (GxA) and climatic year (GxY) were extracted from linear mixed models for repeated data, and used for QTL mapping, on the basis of a genetic map that was built in UMR GenHort in Angers. For each architectural process, numerous QTL were detected and some particularly robust co-localized in common genomic regions, for internode lengthening, top diameter, and number and percentage of axillary shoots. QTL detected by BLUPs for GxY effects were interpreted as resulting from the interaction between genetic maximal potential of growth and climatic factors, while those for GxA effects were interpreted in relation to tree ontogeny. Most of them were found to be concomitant with key development stages.

As a complement, in order to characterize the architectural variability within the progeny, distances were estimated between the architectures of these hybrid apple trees when 2-year old by exploring a set of edit distance algorithms. These algorithms, developed by Aïda Ouangroua, are currently available to compare plants with different topological representations in the tree_matching module of *V-Plants* software. For a given formal representation, i.e. considering non-ordered and semi-ordered trees, both global and local comparison methods can be applied depending on the biological context and goal. However, each method is more or less appropriate depending on (i) the heterogeneity of the number of entities of the compared plants; (ii) the traits that must be taken into account. From an applied point of view, this exploration revealed the preponderant weight of the number of plant entities in the estimated distances with the global methods while, in the local methods, relatively small plants defined sub-parts that aligned in larger plants. From a theoretical point of view, this analysis opens new perspectives to improve and extend the plant architecture comparison methods, especially the local comparisons or for dealing with more than two scales in the formal representation.

5.1.15. Multivariate dynamic model for ordinal outcomes

Participants: Florence Chaubert, Frédéric Mortier [CIRAD], Laurent Saint-André [CIRAD].

Individual or stand-level biomass is not easy to measure. The current methods employed, based on cutting down a representative sample of plantations, make it possible to assess the biomasses for various compartments (bark, dead branches, leaves, ...). However, this felling makes individual longitudinal follow-up impossible. In this context, we propose a method to evaluate individual biomasses by compartments when these biomasses are

taken as ordinals. Biomass is measured visually and observations are therefore not destructive. The technique is based on a probit model redefined in terms of latent variables. A generalization of the univariate case to the multivariate case is then natural and takes into account the dependency between compartment biomasses. These models are then extended to the longitudinal case by developing a Dynamic Multivariate Ordinal Probit Model. The performance of the MCMC algorithm used for the estimation is illustrated by means of simulations built from known biomass models. The quality of the estimates and the impact of certain parameters, are then discussed [41].

5.1.16. *An integrated model of apple tree development*

Participants: Colin Smith, Evelyne Costes, Yann Guédon, Christophe Godin.

This research theme is supported by an INRA Grant (post-doc).

A new type of structure-function model has been developed by the integration at tree level of stochastic and mechanistic models [36]. This approach has been carried out to model the development of apple trees (over the first six years of the growth). The simulation was based on two submodels. The first one, which is inspired by the hierarchical hidden Markov model proposed by [44], models the tree topology, *i.e.* both the succession of GUs along axes and the branching structures of GUs at node scale. The second submodel is a biomechanical model that simulates the bending of branches under fruit and branch weight. The global model, called MappleT, thus attempts to capture in an integrated developmental framework both the apple tree topology and its form (the shape of the branches, as determined dynamically by the gravity and the wood properties). The core simulation is specified using a L-system implemented with the Ł+C language [47] with which the sequence_analysis module of V-Plants has been coupled. The statistical analysis was done using the sequence analysis module of *V-Plants* [49]. To assess the simulation ouputs quantitativelly with respect to observed tree architectures, geometrical descriptors such as fruiting branch enveloppes were calculated with the module PlantGL and compared with observations. Following this first integration of advanced stochastic processes for modeling tree topology with mechanistic processes, the approach was extended through the integration of Markovian models with the carbon-based model L-Peach [21] previously developed by Ted DeJong at U.C. Davis.

5.1.17. *Compression of plant geometry*

Participants: S. Mondet [IRIT, Toulouse], Frédéric Boudon, Jean-Christophe Hoelt [IRIT, Toulouse], Géraldine Morin [IRIT, Toulouse], Romuls Grigoras [IRIT, Toulouse], Christophe Pradal.

This research theme is supported by ANR project NatSim.

In collaboration with the IRIT lab from Toulouse, we are working on progressive compression of plant models based on generalized cylinders. We adapted the multi-scale representation of plants developed in Virtual Plants to direct-acyclic graph representations previously proposed by IRIT that allows a progressive streaming. We proposed a method for differential coding of plants: an average branch is computed for any chosen group of branches and then, for each branch, we only need to code some transformations for instantiation and differences for geometry refinement. To be able to stream, we identify and take advantage of two types of dependencies: topological and dependencies due to differential coding. We obtain a progressive model that makes it possible to select a lightweight representation of a plant while preserving branch density. This work has been presented at the 20th workshop of the Association Francophone d'Informatique Graphique, Marne la Vallée, Nov. 2007 [30].

5.1.18. *Sketching plants*

Participants: Frédéric Boudon, Jamie Whiter [INRIA, Evasion], Marie-Paule Cani [INRIA, Evasion], Christophe Godin.

This research theme is supported by ANR project NatSim.
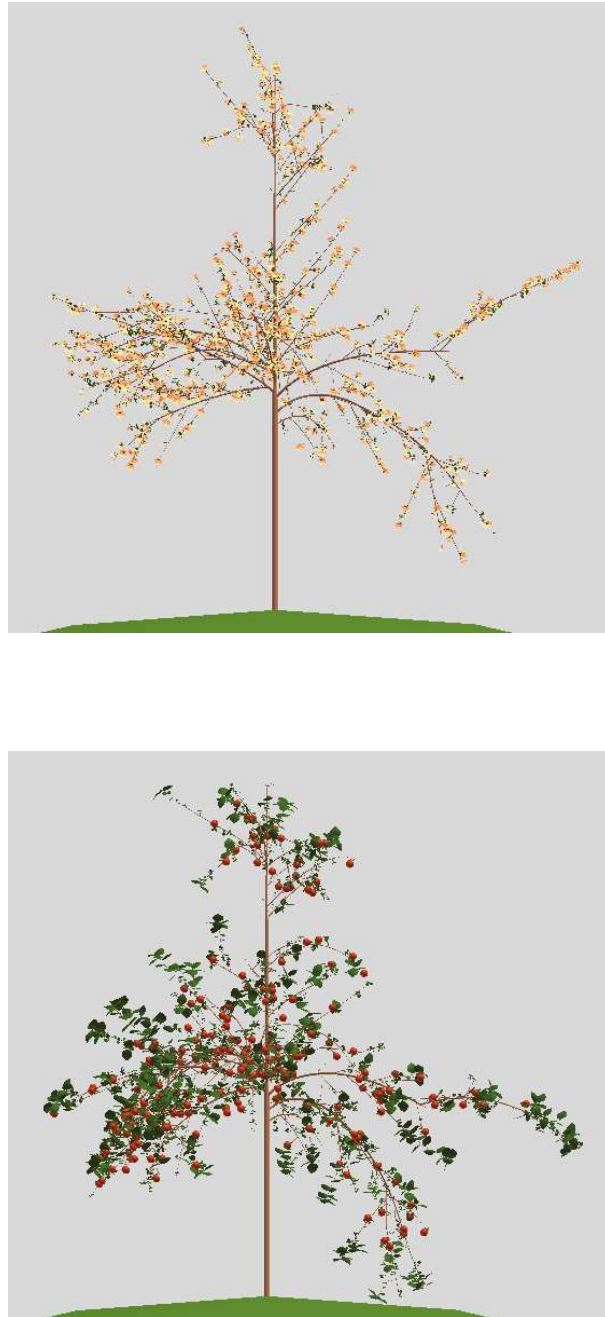
Figure 7. Simulation of the growth of an apple tree over one year. At the beginning of spring flowers are located in the tree according to the markovian model describing pattern of flowers on branches. Later, leaves and fruits appear, which contribute to the bending of axes.

In collaboration with the project-team Evasion, we currently work on a multiscale plant design system based on multi-resolution sketch interface and on botanists experience. We designed a sketch-based system in which the user can specify a complex plant shape by incremental sketching. (S)he first draws the large scale outline, enabling the automatic inference of the branching structures inside. The user then zooms in and designs a refined outline of one branch that is automatically generalized to the other ones. The user goes on by progressively zooming in on a given branch, until (s)he finally draws outlines at the level of leaves. A python module of a 3D gui toolkit enabling interactions has been developed based on the libQGLViewer library. A first coarse sketching system has been implemented. Specific interactions for plant design are currently being investigated.

5.1.19. *Generation of plant communities*
Participants: Frédéric Boudon, Gilles Le Moguedec [INRA, LERFoB].

This research theme is supported by ANR project NatSim.

In previous work, we exploit a method for specifying plant geometry using multiscale procedure [Boudon et al. 2003]. This method enables the user to define abstractions of branching systems of the plant based on volumetric representations at different scales. We recently extended this to the generation of realistic natural plant communities. We coupled this procedure with a stochastic stand model based on Gibbs process that defines distributions of plant species on a terrain using coarse representations. A key contribution of this work was to take into account crown plasticity during the distribution by considering deformable asymmetric crown shapes and simulating plant-plant interactions. Realistic stand model can thus be achieved with high variability. Using this methodology, we present in this work a realization of such a process with beech tree forest [12].

5.2. Meristem functioning and development

5.2.1. *3D reconstruction of shoot and root meristems from confocal microscopy*

Keywords: *3D segmentation*, *Meristem*, *cells*, *plants modelling*.

Participants: Romain Fernandez, Grégoire Malandain [INRIA, Asclepios], Christophe Godin, Christophe Perin [CIRAD], Jean-Luc Verdeil [CIRAD], Pradeep Daas [ENS-Lyon], Jan Traas.

This research theme is supported by the European RTN project SY-STEM and a CIRAD ATP Meristem Grant.

In order to extend the insight of the biologists and to improve plant growth models, there is a growing need to design algorithms to process new 3D images of vegetal cells from microscopy. Actual geometric models only describe the surface of the meristem [1] and protocols to analyse cellular dynamics in the surface layer during plant development. Here, we try to construct automatically a 3D model of meristem cells from images of Arabidopsis (shoot and root) and rice (root only) meristems. These meristems are collected in-vivo with a confocal microscope at ENS-Lyon or with a multiphoton laser scanning microscope at PHIV (first multiphoton used on vegetal tissues in France, CIRAD Montpellier, which allows 3D imaging with deep penetration in the tissue).

Our goal is to achieve automatic segmentation of shoot/root meristem cells during plant growth and to build geometric and topologic models of the meristem structure.

This year, we worked on the customization of acquisition parameters and we designed a method for 3D images processing based on watersheds. Then, we constructed algorithms to build automatically 3D models (abstract simplicial complex or simplex mesh), which will permit simulation of the activity of stem-cells and a better understanding of plants' behaviour.

5.2.2. *Canalization as a plausible mechanism of auxin transport in the meristem*
Participants: Szymon Stoma, Jérôme Chopard, Christophe Godin, Jan Traas.

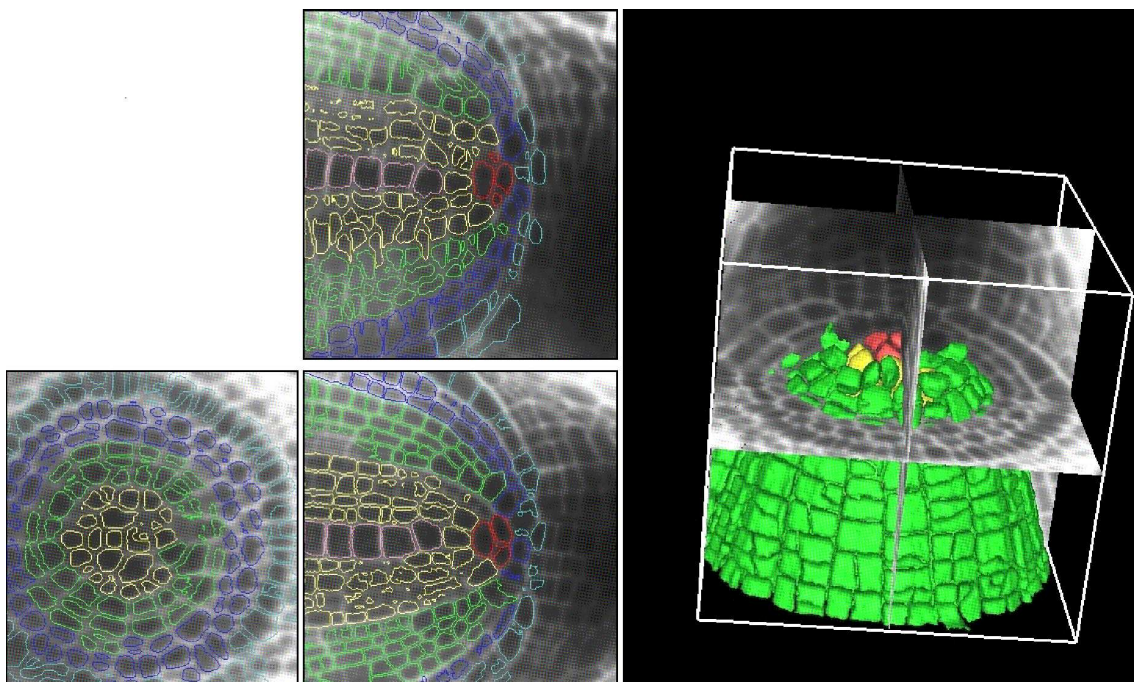*This research theme is supported by the European RTN project SY-STEM.*

Figure 8. On the left, the 3 orthogonal views of the 3D optical stack from multiphoton microscope, with the superimposed segmentation of meristem's layers of cells. On the right, the volume rendering of the segmentation.

The active transport of the plant hormone auxin plays a major role in the initiation of organs at the shoot apex. Polar localized membrane proteins of the PIN1 family facilitate this transport and recent observations and models suggest that the coherent organization of these proteins in the L1 layer is responsible for the creation of auxin maxima, which in turn triggers organ initiation close to the meristem centre [48] [1].

While the regulation of PIN polarization is thus a key determinant of primordia formation, very little is known about its biological or physical nature. However, two recent models have shown that such a polarization may be due to a simple mechanistic hypothesis, called "up the hill" hypothesis, which states that in each cell, PIN proteins are preferentially located on cell walls separating this cell from neighbouring cells with maximum auxin concentration. PIN proteins may thus transport auxin against the concentration gradients.

Although this hypothesis was shown to be a plausible explanation of phyllotaxy by two teams independently [46], [52], it is not consistent with an other hypthesized auxin transport mechanism that has been proposed in the 70's by Sachs to explain the development of vascular vessels during leaf development and that is now recognized as a fairly plausible mechanism of vein formation. This hypothesis suggests that PIN proteins are polarized in the direction of the auxin flux through the cell, and thus reinforce the flux. This positive feedback mechanism is called 'canalization'.

During the last year, we investigated the possibility that canalization could be an alternative plausible mechanism for auxin transport in the L1 layer of the meristem. If true, it could unify the models used for leaves and meristems and the mechanisms creating primordia at the meristem surface and provascular strands in the inner parts of the meristem, below the primordia. To show that canalization may generate phyllotactic patterns in the L1 layer, we showed this process can create an inhibitory field around each primordium of a meristem. This was shown by Snow and Snow and later confirmed by Douady and Couder to be a suffcent condition for the generation of phyllotactic patterns. We could thus show that 'canalization' is a plausible unifying concept for auxin transport in the shoot apical meristem.
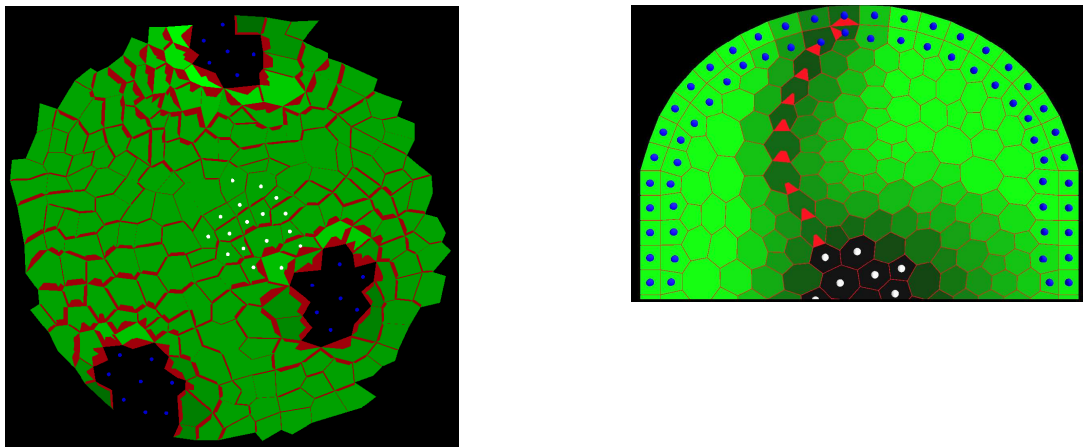
(a)   (b)

Figure 9. (a) Simulation of the orientation of PIN proteins (red) in the L1 layer during meristem growth: Pumps are oriented towards primordia and create a deplation of auxin (inhibition) in their neighbourhood (b) The same transport model is able to create vascular patterns in the inner layers of the meristem, below the young primordia.

5.2.3. *Design of a structural database for specifying gene expression patterns*
Participants: Jérôme Chopard, Christophe Godin, Jan Traas.

This research theme is supported the ANR Virtual Carpel project.

To organise the various genetic, physiological, physical, temporal and positional informations, we build a spatialised and dynamic database. This database makes it possible to store all the collected information on a virtual 3D structure representing a typical organ. Each piece of information has to be located spatially and temporally in the database. Tools to retrieve and manipulate the information visually, quantitatively through space and time are being developed. For this, the 3D structure of a typical organ has been created at the different stages of development of the flower bud. This virtual structure contains spatial and temporal information on mean cell numbers, cell size, cell lineages, possible cell polarisation (transporters, microtubules), gene expression patterns. Such a database is mainly descriptive. However, like for classical databases, specific tools make it possible to explore the database according to main index keys, in particular spatial and temporal keys. Both a dedicated language and a 3D user interface are being designed to investigate and query the database.
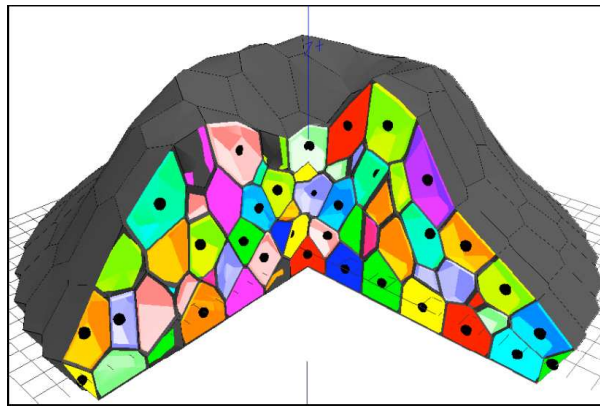

Figure 10. Prototype of a 3D database represented as a cell-based volumic tissue that can contain different types of information (cell lineage, cell size, cell identity,...)

A prototype version of such a database is currently being built and is integrated in *V-Plants*. Algorithms to explore such database at various levels of abstraction will have to be developed. Queries such as: get the number of cell of the L1 layer, get the volume ratio between two zones with different gene expression identities, make the intersection of two expression zones, compute the curvature at the topmost cell, find the lineage of cells descending from this region, etc. would typically be carried out efficiently with such a database. The prototype of a 3D database presented on figure 10 shows a cell-based volumic tissue that can contain different types of information (cell lineage, cell size, cell identity,...)

5.2.4. *Mechanical model of vegetal tissues*

Participants: Jérôme Chopard, Szymon Stoma, Christophe Godin, Olivier Hamant [ENS-Lyon], Jan Traas.

This research theme is supported by the ANR project Virtual Carpel project and the RN SY-STEM project.

The rigid cell walls that surround plant cells is responsible for their shape. These structures are under constraint due to turgor pressure inside the cell. To study the overall shape of a plant tissue and morphogenesis, its evolution throughout time, we therefore need a mechanical model of cells.

We developed such a model, in which walls are characterized by their mechanical properties like the Young modulus which describes the elasticity of the material. Wall deformation results from forces due to turgor pressure. If this deformation is too high, cells actively synthesize material to augment their wall size, which enables cell growth. their are computed and the final shape of the cell in the tissue corresponds to the minimum strain of each wall that accounts for these constraints.

To model this process, we used a tensorial approach to describe both tissue deformation and stresses. Deformations were decomposed into elementary transformations that can be related to underlying biological processes. These processes can then be individually tested to study their role in plant morphogenesis. Different numerical approaches have been tested to solve the integration problem associated with the model simulation. In 2D cases, transversal cut of the meristem or representation of the surface of the meristem only, walls are treated as linear 1D elements. An efficient way to solve the problem uses a mass-spring solver in which each wall is a spring whose stiffness depends on its mechanical properties. However, for large deformations or 3D systems, this approach is no longer efficient enough. In these particular cases we use finite elements methods to integrate the local constraints at tissue scale and find overall tissue growth. This work have been presented at IPCAT (August 2007, UK) [20] and at FSPM (Napier 2007, New Zealand) [37].

5.2.5. *Modeling axillary root initiation: effect of gravistimulation*
Participants: Mikaël Lucas, Christophe Godin, Christian Jay-Allemand, Laurent Laplaze.

This research theme is supported by an ENS-Lyon PhD Grant.

Root architecture plays an important role in water and nutrient acquisition and in the ability of the plant to adapt to the soil. Lateral root development is the main determinant of the shape of the root system and is controlled by external factors such as nutrient concentration. Here it is shown that lateral root initiation and root gravitropism, two processes that are regulated by auxin, are co-regulated in Arabidopsis. To understand patterns of lateral root initiation along the main root and their control by auxin fluxes, we designed a mathematical model that simulates the effects of gravistimulations on lateral root initiation density. This model, based on non-linear differential equations, suggests that lateral root initiation is controlled by an inhibitory fields mechanism, in a way similar to what occurs for the generation of primordia at the shoot apical meristem. The model made it possible to predict the number of lateral root initiations on root systems submitted to arbitrary gravitropic signals with a fairly good accuracy. Moreover, gene transactivation experiments suggested a mechanism involving a single auxin transport route for both responses [17].

6. Other Grants and Activities

6.1. National Grants

6.1.1. *New interfaces of mathematics ACI grant: Arborescences*
Participants: Yann Guédon, Evelyne Costes, Jean-Baptiste Durand, Christophe Godin, Christophe Pradal.

(Contractor for Virtual Plants: CIRAD. From November 2004 until November 2007)

Arborescences: Mathematical and computer methods for the study of plants structure and development. The aim of this project is to propose a set of consistant methods for analyzing tree-structured data and to apply these methods to plant structures. Three main categories of methods or models are investigated: algorithms for computing distances between tree structures, hidden Markov tree models for finding homogeneous zones (or change points) within tree structures and multi-type branching processes with dependencies for analysing the generative growth process. This three-year grant started in November 2004. This project is coordinated by Yann Guédon (UMR DAP) and the participants are the Institut Camille Jordan (University Claude Bernard Lyon 1), the LaBRI (Bordeaux), the UMR AMAP (Montpellier) and the Laboratory Jean Kuntzmann (University Joseph Fourier, Grenoble). See Sections 5.1.8, 5.1.9, 5.1.10 and 5.1.14.

6.1.2. *ANR NatSim Grant*
Participants: Frédéric Boudon, Christophe Pradal, Christophe Godin.

(Contractor for Virtual Plants: CIRAD. From December 2005 until December 2008)

Nature simulation (NATSIM) : hybrid representation for modeling, simulation, visualisation and streaming of animated natural scenes. In this project, our goal is to create models of natural scenes containing vegetals (trees, forests, prairies), watercourses (rivers, rivulets, waterfalls) and clouds (clouds, mist, fog). On the one hand, the botanic, biologic and physics communities acquire and store huge data sets representing each single natural entity with a dedicated model. On the other hand, the user community is willing to smoothly navigate in realistic virtual environments or to easily create complex virtual landscapes. The project NatSim addresses this huge amount of data in terms of data structure, techniques and algorithms, in a unifed framework able to adapt both to the content (e.g. the internal representation) and to the navigation context (e.g. view point, devices etc.). We focus on the models, the evolution, the adaptive transmission and the visualization, but also on the composition of several natural entities in a complex virtual environment. The project gathers partners whose expertise covers botany, modeling and simulation (DAP: CIRAD-INRIA-SophiaAntipolis in Montpellier, LIAMA : Academy of Sciences of China, INRIA, CIRAD, Evasion: INRIA-Rhône Alpes), graphics (Evasion, IRIT: Univ.Toulouse-CNRS, Iparla: INRIA-Futur) as well as adaptive streaming (IRIT, Iparla).

6.1.3. ANR CarpVirtuel Grant

Participants: Jérôme Chopard, Christophe Godin.

(Contractor for Virtual Plants: INRIA. From December 2005 until December 2008)

The virtual carpel (CarpVirtuel): building of a predictive model of the development of the female sexual organ of the flower. The carpel is the precursor of the fruit in the flowering plants and is therefore of capital socio-economic importance. The early phase of carpel development is crucial regarding final morphology. The objective of the project is to understand cellular and molecular mechanisms behind the early phase of carpel development. For this purpose, we combine experimental and modeling approaches. During the first year we have gathered first quantitative morphometric data of carpel growth using live imaging to build a 3D computer model and even a 4D model if we include developmental stages: the virtual carpel. In parallel, transcriptomic data have been collected in such a way to have homogeneous samples of tissues and stages of development. Information will be extracted from these data to construct a gene interactions network controlling carpel development. These analyses will be achieved in both wild type and mutant plants affected in carpel development. All these data will be processed and integrated into the virtual carpel model, which will then in turn, help to predict the effect of a given gene or of a defined cellular process on carpel development in planta. For this model, we are currently studying a mechanical model of cell-cell interaction in 3 dimensions. The project is carried out in collaboration with teams of biologists and computer scientists from ENS-Lyon (Jan Traas and Michel Morvan).

6.1.4. ATP CIRAD Meristem Grant

Participants: Romain Fernandez, Christophe Godin, Jean-Luc Verdeil [CIRAD], Grégoire Malandain [INRIA], Olivier Devillers [INRIA].

(Contractor for Virtual Plants: CIRAD. From December 2005 until December 2008)

Meristem : 3D imagery and geometrical modeling of meristems. The aim of this Action Thématique Programmée of CIRAD is twofold. We first intend to design 3D visualization technics of the meristem architecture cellular and molecular levels. Second, we aim at developing a generic geometric model of the meristem able to support various treatments and modeling processes at cell scale (characterization of meristem geometry, cell growth, mechanical forces, circulation of hormone fluxes, ...). Data will be collected from bi-photon microscopy at CIRAD (in the context of the RIO imaging platform) on rice, a model plant for agronomy, and on other perennial species to characterize the state of the meristem at different phenological states or for different environmental constraints. The project includes several teams from CIRAD, INRA and IRD and 3 INRIA projects Asclepios, Geometrica and Virtual Plants.

6.2. UE Grants

6.2.1. RTN SY-STEM Grant

Participants: Szymon Stoma, Christophe Godin.

SY-STEM: Systems biology of stem cell function in Arabidopsis Thaliana. SY-STEM is a Marie Curie european Research Training Network (RTN) from the 6th European Framework Research Program. Significant progress has been made in the understanding of meristem development during the last few years, but the complexity and lack of completeness of the available data is such, that an integrated view of meristem function is not yet possible. Therefore, not only additional data, but also adapted mathematical and informatics approaches are now required to integrate the growing body of knowledge in such a way that it can advance the level of understanding in the field. To address these issues, SY-STEM will pursue the following objectives:

- provide extensive training in biological sciences, informatics and mathematics and create an environment that favours the interaction and integration of these disciplines,
- provide new technology platforms to study meristem function,
- address key questions on meristem function and plant developmental biology using novel systems biology and modeling approaches.

The integration of the unprecedented amount of data generated in this way will involve the expertise of the participating mathematicians and computing scientists, who will create new modeling tools. This network started in January 2005 and gathers 10 european research groups that will use genetic, molecular and cellular approaches, imaging techniques, as well as large-scale genomic techniques applied to the reference plant *Arabidopsis Thaliana* for 4 years. In the project, Virtual Plants is responsible for the development of a 3D dynamic model of the meristem integrating knowledge obtained by the other teams in a coherent picture of the meristem growth and functioning. The project is offering 360 fellow-months for PhD students (36 for INRIA).

6.3. International Bilateral Relations

After E. Costes's visit to Ted DeJong's lab at the U.C. Davis (USA) last year, a joint project has started on the simulation of peach tree development. Based on MappleT development, Markovian models were integrated in the carbon-based model L-Peach, and this project was presented in FSPM07. A PhD student from Ted DeJong's lab will visit Virtual Plants in 2008 for estimating Markovian models in a Californian peach cultivar.

Christophe Godin was visiting Pr. Prusinkiewicz at the University of Calgary (Canada) to work on multiscale models of plants in November 2006. This work is carried out in the context of an long-going collaboration between both teams (visits, exchange of students, joint projects and publications).

7. Dissemination

7.1. Services to the scientific community

Christophe Godin is a member of the Steering Committee of UMR DAP. He is a member (for 4 years) of two expert scientific commissions (CSS): at INRA (CSS Ecophysiologie, génétique et biologie intégrative des plantes) and of Montpellier 3 University (CSS mathematics, statistics and computer sciences). Since 2006, he has been the team leader of the joint INRIA-CIRAD-INRA Virtual Plant project-team located in UMR DAP, Montpellier. He is a member of the board of the Fédération de Recherche (IFR) DAPHNE, coordinating joint actions of UMRs working in Plant Sciences in the region Languedoc Roussillon. He is the representant of the IFR at the doctoral school of the University of Montpellier II, SIBAGH, in Plant Biology. He is member of the international advisory board of the Functional-Structural Plant Models conference since 2001 (he was chair of the conference in 2004). In 2007, he was a member of the evaluation committee of UMR SAGAH in Angers and he was member of an INRA committee for the selection of 5 researchers in plant science at INRA, referee for 2 PhD thesis in plant modeling (from U. Bordeaux and U. Of Queensland, Australia). He participated in a working group leaded by F. Kepes for studying actions that should be undertaken between CNRS and the Max Planck Institutes (MPI, Germany) in systems biology. He was a reviewer for several journals (Eurographics, Transactions on Graphics, Human Frontier Programme Journal, Silva Fennica, Computers and Electronics in Agriculture, Annals of Botany) and one book chapter.

Yann Guédon is vice-head of the Virtual Plants project-team. He was a member of the program committee of the 5th International Workshop on Functional-Structural Plant Models (FSPM07) held in Napier, New Zealand. In 2007, he was a referee for a PhD thesis in forest science and an jury member for another PhD thesis in statistics. He is a member of the editorial board of Annals of Botany and a member of the ERCIM working group on mixture models. He was a referee for papers submitted to Annals of Botany, Applied Stochastic Models in Business and Industry and Notebooks on Geology.

Christophe Pradal coordinates the national platform for plant modeling *OpenAlea*.

Evelyne Costes is the scientific leader of "Fruit tree Architecture and Functions" (AFEF) team composed of 8 scientists (5 INRA researchers, 2 Montepllier SupAgro professors and 1 assistant professor). She participates to the scientific board of the UMR DAP where she represents the INRA AFEF team and acts as "chargée de mission" in the direction board. At the national level, E. Costes is involved in the scientific coordination of the working group "Achitecture" for the "Genetics and Breeding" Department (DGAP) of INRA. She also participates to the scientific board of this department. At an international level, she is member of the International Society for Horticultural Research. She is member of the Genomics Database for Rosaceae network (GDR).

7.2. Academic teaching

7.2.1. *Master Biostatistics*

Jointly with Montpellier 1, Montpellier 2 Universities and Agro-Montpellier.

Yann Guédon teaches the stochastic modeling course.

7.2.2. *Master Computer Science*

University Montpellier 2.

Christophe Godin teaches a course on computational plant modeling.

7.2.3. *Master Biotraçabilité, Biodétection, Biodiversité*

Montpellier 2 University.

Yann Guédon teaches a course on statistics in the context of plant biology.

7.2.4. *Master Classes*

Evelyne Costes taught a Master class in the optional module "Tree" at Agro-Montpellier and at the Horticultural National School in Angers

Christophe Godin taught a Master class 'an introduction to plant modelling' of the module 'Systems biology and plant development' coordinated by Jan Traas in the BioScience Master of ENS-Lyon.

7.2.5. *High School class*

Lycée Pompidou, Castelnau le Lez.

Christophe Godin, Yann Guédon, Christophe Pradal and Frédéric Boudon gave 5 3-hours classes to pupils with scientific option on plant modelling, plant structure analysis and fractals (jointly with Yves Caraglio [CIRAD, AMAP]).

7.3. Participation to workshops, seminars and miscellaneous invitations

- Christophe Godin was invited to give seminars at the Colloquium of University Joseph Fourier in Grenoble, and at the conference of the National Network on Complex Systems, organized by the CNRS in Paris. He was also invited to give a talk on meristem modelling in a joint CNRS-MPI workshop held in Paris. He presented a communication at FSPM07 (Napier, New Zealand)

- Yann Guédon was invited to give seminars at the Universities Henri Poincaré Nancy 1 and Montpellier 2 and presented communications at 39èmes Journées de Statistique (Angers) and FSPM07 (Napier, New Zealand). He organized the annual internal workshop of Virtual Plants (June 2007).

- Christophe Godin, Christophe Pradal, Frédéric Boudon and Evelyne Costes gave two 4-hours classes on plant modelling to high school teachers from the Languedoc-Roussillon region in the context of a workshop organized by CNRS, CIRAD, INRA and IRD institutes.

- Evelyne Costes presented a communication at FSPM07 (Napier, New Zealand).

- Frédéric Boudon was invited to give a seminar at Bordeaux 1 University.

- David Da Silva presented a communication at FSPM07 (Napier, New Zealand).

- Jérôme Chopard presented communications at FSPM07 (Napier, New Zealand) and at IPCAT (Oxford, UK).

- Christophe Pradal presented a communication at FSPM07 (Napier, New Zealand).

- Samuel Dufour-Kowalski presented a communication at EuroPython (Vilnius, Lithuania) and at FSPM07 (Napier, New Zealand).

- Mikael Lucas presented a communication at FSPM07 (Napier, New Zealand).

- Florence Chaubert has presented a communications at 39èmes Journées de Statistique (Angers)

- Samuel Dufour-Kowalski, and Christophe Pradal have presented a software demonstration at FSPM07 (Napier, New Zealand) and at Forum INRIA 40 ans (Lille, France).

7.4. Theses and Internships

7.4.1. *Ongoing Theses*

- Florence Chaubert, *"Modèles linéaires généralisés mixtes multiphasiques"*, University Montpellier 2.

- David Da Silva, *"Quantification de la structure autosimilaire des plantes par des méthodes de la géométrie fractale"*, University Montpellier 2.

- Romain Fernandez, *"3D Reconstruction of meristems from+ bi-photon images"*, University Montpellier 2.

- Mikaël Lucas, *"Etude et modélisation des déterminismes de mise en place et de développement des racines latérales chez Arabidopsis Thaliana"*, University Montpellier 2.

- Mohamad Saad, *"Impact des opérations sylvicoles sur les broussins et picots du chêne. Modélisation statistique de la séquence de différenciation et de la répartition le long des troncs"*, University Henri Poincaré Nancy 1.

- Szymon Stoma, *"A mechanical based model of Arabidopsis Thaliana meristem development"*, University Montpellier 2.

7.4.2. *Internships*

- Mariem Zouch, *"Loi de Poisson pondérée et famille exponentielle bidimensionnelle"*, Master2 Recherche Biostatistique, Montpellier 2 University.

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