



INSTITUT NATIONAL DE RECHERCHE EN INFORMATIQUE ET EN AUTOMATIQUE

Project-Team Virtual Plants

*Modeling plant morphogenesis from genes
to phenotype*

Sophia Antipolis

THEME BIO

Activity
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Report

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Table of contents

1. Team	1
2. Overall Objectives	2
2.1. Overall Objectives	2
3. Scientific Foundations	2
3.1. Analysis of structures resulting from meristem activity	2
3.2. Meristem functioning and development	3
3.3. A software platform for plant modeling	4
4. New Results	4
4.1. Analysis of structures resulting from meristem activity	4
4.1.1. Analysis of longitudinal count data and underdispersion	4
4.1.2. Growth synchronism between Aerial and Root Systems	4
4.1.3. Changes in branching structures within the whole plants	5
4.1.4. Growth components in trees	5
4.1.5. Markov switching models	5
4.1.6. Diagnostic tools for hidden Markovian models	5
4.1.7. Hidden Markov tree models for investigating physiological age within plants	6
4.1.8. Branching processes for plant development analysis	6
4.1.9. Self-similarity in plants	6
4.1.10. Reconstruction of plant foliage density from photographs	6
4.1.11. Fractal analysis of plant geometry	6
4.1.12. Light interception by canopy	7
4.1.13. Heritability of architectural traits	7
4.2. Meristem functioning and development	8
4.2.1. 3D surface reconstruction and cell lineage detection in shoot meristems	8
4.2.2. Simulation of auxin fluxes in the meristem	8
4.2.3. Dynamic model of phyllotaxy based on auxin fluxes	8
4.2.4. Modeling axillary root initiation	8
4.3. A software platform for plant modeling	9
5. Other Grants and Activities	10
5.1. National Grants	10
5.1.1. New interfaces of mathematics ACI grant: Arborescences	10
5.1.2. ANR NatSim Grant	10
5.1.3. ANR CarpVirtual Grant	10
5.1.4. ATP CIRAD Meristem Grant	11
5.2. UE Grants	11
5.2.1. RTN SY-STEM Grant	11
5.3. International Bilateral Relations	12
6. Dissemination	12
6.1. Services to the scientific community	12
6.2. Academic teaching	12
6.2.1. Master Biostatistics	12
6.2.2. Master Computer Science	12
6.2.3. Master Biotraçabilité, Biodétection, Biodiversité	12
6.2.4. ALEA training school	13
6.2.5. Master Course	13
6.2.6. Statistics Courses	13
6.3. Participation to workshops, seminars and miscellaneous invitations	13

6.4.	Theses and Internships	13
6.4.1.	Theses defenses	13
6.4.2.	Ongoing Theses	14
6.4.3.	Internships	14
7.	Bibliography	14

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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,
- Models for morphogenesis.

All these tools are integrated in a common software platform *V-Plants* that is available to all the partners of Virtual Plants. At a national and international level, we coordinate the development of an open software platform *ALEA* for plant modelling (based on *V-Plants*).

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. These 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 self-similarity of branching structures in order to quantify the degree of redundancy of any tree structure and to quantify in this way critical botanical notions such as the physiological states of a meristem.
- *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 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 and Markov switching linear mixed models for sequences and different families of hidden Markov tree models). A complementary approach consists in applying change-point detection 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 transitions.

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).

Designing morphogenesis models of the plant development at the macroscopic scales is a challenging problem. It is unrealistic to design models of plant development at macroscopic scales solely on the basis of biological functions since some patterns are the results of complex interactions between many functions acting at more microscopic scales. Hence, morphogenesis models should incorporate both mechanistic sub-models of plant functions and empirical sub-models of plants structures. We chose to implement such 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 equation and partial differential equations.
- models of cell development taking into account cell division and gene control (using either differential equations, finite state automata or Petri nets).

3.3. A software platform for plant modeling

The *ALEA* platform, initially sponsored by the Réseau d'Ecophysiologie de l'Arbre from INRA, aims at providing modellers and biologists with a homogeneous software platform, integrating various tools and models for studying plant architecture and morphogenesis. This platform is intended to have the following features: it should

- allow the integration of tools and models that currently exist in different laboratories within a unique software framework. These modules, possibly written in different languages (Python, C, C++, Fortran) should be integrated in *ALEA* without rewriting them,
- provide a set of general-purpose tools (3D plant representation, data structure standards, ...) that can be reused by every modeller,
- provide a common high-level language interface to all tools and models,
- provide an open-software kernel, developed by a community of people from interested institutes,
- define a user-friendly graphic interface to the different modules,
- be available on Linux and Windows operating systems,
- be able to communicate with other main softwares about plant architecture (like L-Studio, Grogra, Lignum, ...).

The first kernel of *ALEA* was developed in 2003-2004. It is based on the Python language that aims at being both a "glue" language for the different modules and an efficient modelling language for developing new models and tools. *ALEA* currently includes modules for plant architecture analysis and modelling (*V-Plants* modules), modules for modelling radiative transfer, transpiration and photosynthesis (RATP, Archimed, Canestra), modules for 3D visualization of plant architecture at different scales (PlantGL). Integration of other modules and development of connections with other softwares are planned in 2006.

4. New Results

4.1. Analysis of structures resulting from meristem activity

4.1.1. Analysis of longitudinal count data and underdispersion

Participants: Yann Guédon, Tessa Pierre-Joseph, Catherine Trottier.

The elongation of leafy axes is influenced by environmental conditions such as for instance rainfall. 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. Incorporating the rainfall covariate within a statistical model requires to take into account both the delayed response of the plant to a water stress and the difference in time step between the rainfall covariate (daily data) and the plant response (observation period of several days). Statistical models studied for analysing these longitudinal count data belong to the classes of generalized linear mixed models.

4.1.2. Growth synchronism between Aerial and Root Systems

Participants: Evelyne Costes, Yann Guédon, Eduardo Garcia-Villanueva, Christophe Jourdan, Jean-Luc Regnard.

In several species exhibiting a rhythmic aerial growth, the existence of an alternation between root and shoot growth has been demonstrated. We investigated the respective involvement of the emergence of new organs and their elongation in this phenomenon and its possible genotypic variation in young apple plants. We proposed a biological model of dynamics that summarises the interactions between processes and includes the assumption of a feedback effect of lateral root emergence on leaf emergence [14].

4.1.3. Changes in branching structures within the whole plants

Participants: Evelyne Costes, Yann Guédon, Christophe Godin, Michael Renton.

The objective of this study is to model the changes in growth unit branching structures during tree ontogeny. A single statistical model was estimated from around 700 branching sequences measured on two six-year-old apple trees, cultivar "Fuji". This statistical model is a hidden semi-Markov chain where the underlying semi-Markov chain represents the succession and the lengths of branching zones along the growth units while the observation distributions represent the branching type composition within each zone. The main output of this study is to show that while the succession and the lengths of branching zones change during ontogeny, the compositions of branching zones remain unchanged. In particular the composition of the flowering shoot zone is not affected by the alternation of flowering and non-flowering years.

4.1.4. Growth components in trees

Participants: Yves Caraglio, Yann Guédon, Patrick Heuret, Emilie Lebarbier, Céline Meredieu.

The observed growth as given for instance by the lengths of successive annual shoots along a tree trunk is mainly the result of two components: an ontogenic component and a climatic component. An open question is whether the ontogenic 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 (change-point detection models, hidden semi-Markov chains and hidden hybrid model combining Markovian and semi-Markovian states [19]) were applied to extract and characterize the ontogenic growth component. This has led us to highlight phase changes in unexpected situations (for instance in the decreasing growth phase).

4.1.5. Markov switching models

Participants: Florence Chaubert, Yann Guédon, Christian Lavergne, Carine Véra.

Incorporating both the influence of explanatory variables and inter-individual heterogeneity in a hidden Markovian model is a challenging problem. We are studying Markov switching linear mixed models, i.e. models that combine linear mixed models in a Markovian manner. The underlying Markov chain represents the succession of growth phases while the linear mixed models attached to each state of the Markov chain represent both the trend, the influence of the explanatory variables (mainly climatic variables which are time-dependent explanatory variables measured at a scale different from the scale of the plant response) and the inter-individual heterogeneity within a given growth phase. The EM algorithm cannot be applied for estimating Markov switching linear mixed models. As an alternative to the EM algorithm, we are studying iterative algorithms which decompose in three steps: restoration, maximization and prediction. The restoration step can be viewed as a Markovian restoration step (restoration of the state sequences) while the prediction step can be viewed as a restoration step for the linear mixed models (restoration of the random effects).

4.1.6. Diagnostic tools for hidden Markovian models

Participants: Yann Guédon, Jean-Baptiste Durand.

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 long way 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? The knowledge of state sequences that explain a given observed sequence for a known hidden Markovian model is the basis of diagnostic tools that may be divided into two categories: enumeration of state sequences and 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. Various diagnostic tools belonging to these two 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 [19] and different categories of hidden Markov tree models. In particular, we propose a new type of state profiles that can be viewed as the superposition of all the state sequences from the less probable to the most probable.

4.1.7. *Hidden Markov tree models for investigating physiological age within plants*

Participants: Jean-Baptiste Durand, Yann Guédon, Yves Caraglio, Evelyne Costes.

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 design 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 leads to a clustering of the entities into classes sharing a same "physiological state" [15]. This research theme is supported by the ACI "Arborescences".

4.1.8. *Branching processes for plant development analysis*

Participants: Jean Bérard, Anne Perrut, Didier Piau, Yann Guédon, Patrick Heuret, Yves Caraglio, Evelyne Costes.

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

4.1.9. *Self-similarity in plants*

Participants: Pascal Ferraro, Christophe Godin.

Self-similarity of plants has attracted the attention of biologists for at least 50 years, yet its formal treatment is rare, and no measure for quantifying the degree of self-similarity currently exists. In this work, we introduce a formal definition and measures of self-similarity, tailored to branching plant structures. To evaluate self-similarity, we make use of an algorithm for computing topological distances between branching systems, developed in computer science. The formalism was illustrated using theoretical branching systems, and applied to analyze self-similarity in two sample plant structures: inflorescences of *Syringa vulgaris* (lilac) and shoots of *Oryza sativa* (rice) [16]. Quantification of self-similarity leads to a new method to formalize the notion of physiological state. This research theme is supported by the ACI project "Arborescences".

4.1.10. *Reconstruction of plant foliage density from photographs*

Participants: Jessada Phattaralerphong, Christophe Godin, Hervé Sinoquet.

Methods have been developed in the past decade to digitize plant architecture in 3D. 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. In this work, we design a method to reconstruct the 3D leaf density of the plant based on horizontal photographs of the plant crown and on foliage aggregation assumptions. The problem is formulated as an inverse problem where the model is based on different variants of Beer-Lambert model for light interception. This results in a large number of non-linear equations, which depends on several structural parameters (discretization of the image, discretization of the canopy, number of "black zones" on the image, etc.). The huge set of equations is solved using the optimization algorithm L-BFGS-B with simple bounds. This algorithm is based on the gradient projection method and uses a limited memory BFGS matrix to approximate the Hessian of the objective function. Comparisons were made between the actual leaf foliage density of plants digitized leaf by leaf and results of our methods. They show that optimal experimental parameter can be defined depending on the type of plant crown (number of photographs, size of the image zones used for discretization, size of the voxels, ...).

4.1.11. *Fractal analysis of plant geometry*

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

Plant geometry is a key factor of the modelling of plant ecophysiological interaction with the environment. To capture and analyse the irregular nature of plant shapes we develop tools based on fractal geometry. For this purpose, a range of fractal methods is applied to various 3D digitized tree databases and on theoretical plants generated from fractal rules (Iterated Function Systems). We determined the fractal dimension of tree crowns using two different methods. The first one is based on the classical box-counting estimator, adapted here to 3D scenes. The method was extensively analysed and various features and drawbacks were discussed. Possible variants of the box counting estimators of the fractal dimension with better properties are currently investigated. Other estimators of the fractal dimension were also considered, based on the so called "two-surface" method and on mass estimators. These latter estimators are connected with the notion of lacunarity, used in fractal geometry to characterize the texture of the studied object as a function of scale. Here, we defined a notion of "centered" lacunarity that can be used to characterise the typical size of gaps at different scales in the object.

4.1.12. *Light interception by canopy*

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

Light models for vegetation canopies based on the turbid medium analogy are usually limited by the basic assumption of random foliage dispersion in the canopy space. The objective of this work was to assess the effect of three possible sources of non-randomness in tree canopies on light interception properties. For this purpose, four three-dimensional (3D) digitized trees and four theoretical canopies - one random and three built from fractal rules - were used to compute canopy structure parameters and light interception, namely the sky-vault averaged STAR (Silhouette to Total Area Ratio). STAR values were computed from (1) images of the 3-D plants, and (2) from a 3-D turbid medium model using space discretization at different scales. For all trees, departure from randomness was mainly due to the spatial variations in leaf area density within the canopy volume. Indeed STAR estimations, based on turbid medium assumption, using the finest space discretization were very close to STAR values computed from the plant images. At this finest scale, foliage dispersion was slightly clumped, except for one theoretical fractal canopy, which showed a marked regular dispersion. Taking into account a non-infinitely small leaf size, whose effect is theoretically to shorten self-shading, had a minor effect on STAR computations. STAR values computed from the 3-D turbid medium were very sensitive to plant lacunarity, a parameter introduced in the context of fractal studies to characterize the distribution of gaps in porous media at different scales. This study shows that 3-D turbid medium models based on space discretization are able to give correct estimation of light interception by 3-D isolated trees, provided that the 3-D grid is properly defined, that is, discretization maximizes plant lacunarity.

4.1.13. *Heritability of architectural traits*

Participants: Christian Cilas, Evelyne Costes, Vincent Segura, Christophe Godin.

Plant development is controlled by the combined effect of gene activity and environmental constraints. At a given date, a plant architecture is thus the outcome of this combination. The question of identifying the genetic and environmental components of plant development can be addressed by studying the heritability of architectural traits. We started to investigate this issue in the context of two agronomic applications, respectively on coffee and apple tree ([26]; [27]). In these studies, architectural parameters were used to predict target traits for breeding programs: (i) yield capacity for coffee trees; (ii) adequate forms for an easy and low cost training in the field and regular bearing behaviour, for apple trees. Observation protocols for describing the architecture were applied to six clones of *Coffea canephora* in a comparative trial on the one hand, and on an apple progeny whose parents were chosen for their contrasted architecture, on another hand. Architectural traits, including both topological and geometric traits, were collected at different scales (trees, branching systems, axes and nodes) and were included in architectural databases which were explored using the *V-Plants* software (formerly AMAPmod). Several traits exhibited high heritability values, for instance branching, internode length and branch orientation in apple tree. In the case of coffee tree, some of the traits displayed strong genetic correlations with cumulated yield over two cycles (14 years). In the apple tree progeny, since a genetic map was built in UMR GenHort in Angers, correlations between the phenotypic variation of a given

trait and allelic variations observed in the population are currently under investigation to seek for quantitative trait loci (QTL).

4.2. Meristem functioning and development

4.2.1. 3D surface reconstruction and cell lineage detection in shoot meristems

Participants: Pierre Barbier de Reuille, Christophe Godin, Isabelle Bohn-Courseau, Jan Traas.

We developed a general protocol for observing and reconstructing in 3D and 4D the surface of shoot apical meristems from confocal microscopy at cell scale. This includes: acquisition of images, preprocessing of the images, image segmentation, three- and four-dimensional reconstruction of the meristem surface and quantitative analysis. This protocol uses both classical techniques from image processing (topological closure, watersheds) and specially designed algorithms, in particular to automate the detection of cell lineage throughout time in temporal series corresponding to meristem development [25]. These tools were integrated the software platform *ALEA* for plant modelling and analysis and are freely available for the scientific community.

4.2.2. Simulation of auxin fluxes in the meristem

Participants: Pierre Barbier de Reuille, Christophe Godin, Isabelle Bohn-Courseau, Jan Traas.

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 suggest that auxin maxima created by these proteins are at the basis of organ initiation. This hypothesis is based on the visual, qualitative characterization of the complex distribution patterns of the PIN1 protein in *Arabidopsis Thaliana*. To take these analyzes further, we investigated the properties of the patterns using computational modeling and extensive sensitivity analysis of the model. The simulations reveal novel aspects of PIN1 distribution. In particular they suggest an important role for the meristem summit in the distribution of auxin and the emergence of phyllotactic patterns. We confirm these predictions by further experimentation and propose a detailed model for the dynamics of auxin fluxes at the shoot apex [13].

4.2.3. Dynamic model of phyllotaxy based on auxin fluxes

Participants: Pierre Barbier de Reuille, Christophe Godin, Isabelle Bohn-Courseau, Jan Traas.

We integrated the previous results (organization of the PIN transporters, auxin fluxes, accumulation of auxin in the meristem center) in a dynamic model of the meristem development. The meristem structure is represented by a Voronoi diagram and the changes over time of the meristem structure were described using declarative rules using the *MGS* language (language dedicated to the modeling of dynamic systems with dynamic structures (DS)², developed at the University of Evry by J.L. Giavitto and O. Michel). The complete model relies on i) a model of cell growth and division, ii) a spring-mass description of the mechanical interaction between cells, iii) a magnetic polarisation of PIN transporters towards the primordia and the center iv) assumptions for auxin transport identical to the static case. Based on these models and assumptions, we showed that phyllotactic patterns emerge from cell growth and cell-cell interactions [11]. This cell-centered model is a first step towards the development of a 3D mechanical and dynamic model of the *Arabidopsis Thaliana* meristem based on cell-cell interaction.

4.2.4. Modeling axillary root initiation

Participants: Mikael Lucas, Christophe Godin, Yann Guédon, Christian Jay-Allemand, Laurent Laplaze.

In this work, our aim is to understand the genetic and physiological determinants of axillary root initiation in *Arabidopsis Thaliana*. As in the case of primordia initiation of the shoot apical meristem, auxin plays a crucial role in root initiation. Organ initiation is correlated to high concentrations of auxin. However, in both systems, organ initiation is very different. In particular, in the root development, lateral organs initiation is observed at a long distance from the root meristem, with no apparent spatial or temporal structure. Our main assumption is that this system is governed by a mechanism of competition for auxin while the root system

is developing. To understand this complex dynamic interaction, we develop a sink-source dynamic model of the root system development in which the transport of auxin is controlled by active carriers of the PIN family (a first prototype has been developed using L-Systems). First experimental protocols were carried out on *Arabidopsis Thaliana*, with accuracy ranging from macroscopic to cellular levels. We obtained complete data about the developmental sequence in the primary root and its laterals. This extensive database is explored using tools for sequence analysis (distance between sequences, different types of Markovian models). First results show structures and correlations between positions and stages of development of lateral organs which can now be exploited for the design of the dynamical model.

4.3. A software platform for plant modeling

Participants: Christophe Pradal, Pierre Barbier de Reuille, Christophe Godin, Yann Guédon, Frédéric Boudon, Nicolas Donès, Hervé Sinoquet, Hervé Autret, Frédéric Théveny.

Computer algorithms and tools developed by the Virtual Plants team are integrated in a common software platform *V-Plants*, dedicated to the modeling and analysis of plant development at different scales. The architecture of *V-Plants* is based on the Python script language and is designed to be modular and scalable. Based on *V-Plants* architecture, the Virtual Plants team coordinates the development of an open-software platform, *ALEA* (Open Source Software for Ecophysiology and Modeling of Plant Architecture). In 2005, the following steps have been performed:

1. Set up of the collaborative infrastructure of ALEA:
 - Software engineering tools (use of gforge at INRIA),
 - E-tools for communication (Instant Messaging for distant meetings),
 - Coordination (e-meetings, e-forum, organisation of Coding Sprints for developers),
 - Training session for developers and modelers on the intergration of components in ALEA.
2. Finalization of a graphic library to model and render 3D plant architecture: PlantGL
3. Assistance to the development and integration of new components in ALEA:
 - Module for digitizing root systems grown in rhizotrons (collaboration with C. Jourdan, CIRAD),
 - Module for the simulation of maize architecture and light interception computation. Integration of components ADELE-maïs and Caribu (collaboration with C. Fournier, M. Chelles, INRA).

5. Other Grants and Activities

5.1. National Grants

5.1.1. *New interfaces of mathematics ACI grant: Arborescences*

Participants: Yann Guédon, Yves Caraglio, Evelyne Costes, Jean-Baptiste Durand, Christophe Godin, Patrick Heuret.

Mathematical and computer methods for the study of plants structure and development. The aim of this project is to propose a set of consistent 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 AMAP) and the participants are the Institut Camille Jordan (University Claude Bernard Lyon 1), the LaBRI (Bordeaux), the UMR BEPC (Montpellier) and the LMC (University Joseph Fourier, Grenoble). See Sections 4.1.7, 4.1.8 and 4.1.9.

5.1.2. *ANR NatSim Grant*

Participants: Christophe Pradal, Christophe Godin, Post-doctoral Student 2 years.

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

Nature simulation: hybrid representation for modelling, simulation, visualisation and streaming of animated natural scenes. In this project, we propose the study of natural scenes through vegetals (trees, forests, prairies), watercourses (rivers, rivulets, waterfalls) and clouds (clouds, mist, fog). On 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 will treat this huge amount of data in terms of data structure, techniques and algorithms, in a unified 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 will hence 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. In order to efficiently address this complex problem, the project is proposed by a group of partners whose expertise covers botany, modeling and simulation (AMAP: CIRAD-INRIA-SophiaAntipolis in Montpellier, LIAMA : Academy of science of China, INRIA, CIRAD, EVASION: INRIA-Rhône Alpes), graphics (EVASION, IRIT: Univ.Toulouse-CNRS, IPARLA: INRIA-Futur) as well as adaptive streaming (IRIT, IPARLA).

5.1.3. *ANR CarpVirtual Grant*

Participants: Christophe Godin, Post-doctoral Student 2 years.

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

The virtual carpel: 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 proposed project is therefore to understand cellular and molecular mechanisms behind the early phase of carpel development. For this purpose, we will combine experimental and modeling approaches. We will first gather 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, we will gather transcriptomic data 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. The project will be carried

out in collaboration with teams of biologists and computer scientists from ENS-Lyon (Jan Traas and Michel Morvan).

5.1.4. ATP CIRAD Meristem Grant

Participants: Christophe Pradal, Christophe Godin, PhD Student 3 years, Jean-Luc Verdeil, Grégoire Malandain, Jean-Daniel Boissonnat.

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

3D imagery and geometrical modeling of meristems. The aim of this Action Thématique Programmée of CIRAD is twofold. Our first goal is to design 3D visualization technics of the meristem and of its molecular components. Second, we aim at developing a generic geometric model of the meristem able to support various treatments and modelling processes at cell scale (characterization of meristem geometry, cell growth, mechanical forces, circulation of hormone fluxes, ...). This methodology will be carried out and tested on the 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.

5.2. UE Grants

5.2.1. RTN SY-STEM Grant

Participants: Szymon Stoma, Pierre Barbier de Reuille, 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 modelling 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 modelling 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). Christophe Godin is deputy coordinator of the project for the modelling and computational aspects of the project.

5.3. International Bilateral Relations

Within the framework of a bilateral collaboration between HortResearch and INRA that concerns the analysis of dwarfing rootstock on the aerial development of apple tree, E. Costes was invited in Palmerston North in March 2005 to meet A. Seleznyova and H. Tustin (HortResearch), J. Hanan (Univ. Brisbane, Australie), and Pr T. DeJong (Univ. Davis, USA).

Christophe Godin invited Pr. Prusinkiewicz from the University of Calgary (Canada) in the context of an long-going collaboration between both teams (visits, exchange of students, joint projects and publications) in April 2005.

6. Dissemination

6.1. Services to the scientific community

Christophe Godin is member of two expert scientific commissions (CSS): at INRA (CSS Ecophysiologie, génétique et biologie intégrative des plantes) and of the university of Montpellier III (CSS mathematics, statistics and computer sciences). He was a member of the UMR-AMAP board and headed the Mathematics and Computer Science group (MIA) at UMR AMAP. He is a member of the INRA Tree Ecophysiology Network (REA) advisory board since 2001. He was a member of Jury for the selection of 3 attachés scientifiques contractuels (ASC) of INRA. He was an expert for the Dutch Technology Foundation STW and for the Royal Society of England (excellence in science program). He is a member of the board of the new Fédération de Recherche DAPHNE, coordinating joint actions of UMRs working in Plant Sciences in the region Languedoc Roussillon. He received the Plaque of Appreciation of Great Contribution from the University of Kasetsart (Aug. 2005, Bangkok, Thailand).

Yann Guédon is a member of the editorial board of Annals of Botany. He was a member of the evaluation commission of the UMR INA-PG/ENGREF/INRA Mathématiques et Informatique Appliquées.

Christophe Pradal was member of a Jury for the selection of a post-doctoral position at CIRAD on Ecophysiological modelling of plants.

Evelyne Costes is the scientific manager of "Fruit tree Architecture and Functions" (AFEF) team composed of 13 scientists (8 INRA researchers, 2 Agro.M professors and 3 assistant-professors). She participates to the scientific board of the **UMR BEPC** where she represents the AFEF team which is associated to other institutions (CIRAD, IRD and UMII). Since 2004, she participates to the scientific board of the INRA center in Montpellier. At the national level, E. Costes is involved in the scientific coordination of the working group "Architecture" for the "Genetics and Breeding" Department (DGAP) of INRA. She also participates to the scientific board of this department. Since 2000, Evelyne Costes represents DGAP in the scientific board of an INRA transversal program on Tree environmental physiology. At an international level, she is member of the International Society for Horticultural Research.

6.2. Academic teaching

6.2.1. Master Biostatistics

Jointly with Montpellier I, Montpellier II Universities and Agro-Montpellier.

Yann Guédon teaches the **stochastic modelling** course.

6.2.2. Master Computer Science

University Montpellier II.

Christophe Godin teaches jointly with Guy Mélançon (Professor at Lirimm) the course on **Multiscale structures and their algorithms**.

6.2.3. Master Biotraçabilité, Biodétection, Biodiversité

Montpellier II University.

Christophe Godin and Yann Guédon jointly teach a course on Modelling in the context of plant biology.

6.2.4. ALEA training school

University of Kasetsart, Thailand.

Christophe Pradal taught a one week course on the use of plant modelling tools based on the platform *ALEA*.

6.2.5. Master Course

Agro-Montpellier and Horticultural National School in Angers.

Evelyne Costes teaches a Master course in the optional module "Tree".

6.2.6. Statistics Courses

Institut National Polytechnique de Grenoble (INPG) - Ecole Nationale Supérieure d'Informatique et de Mathématiques Appliquées de Grenoble (ENSIMAG).

Jean-Baptiste Durand teaches the probability theory and applications course, the statistical principles and methods course and the computational statistics course.

6.3. Participation to workshops, seminars and miscellaneous invitations

Christophe Godin was invited to give seminars at INRA Avignon, U. Lyon, U. Gent, ENS Lyon, INRIA-Rocquencourt (Thématiques conférences, cycle "modéliser le vivant"). He was an invited speaker at the XVII International Botanical Congress (Vienna, Austria), at the XLIX congress of the Italian Society for Genetics and Agriculture (Potenza, Italy). He was co-organizer (with Franck Molina, CNRS) of the spring school: "[Modélisation et simulation de processus biologiques dans le contexte de la génomique](#)", Montpellier, Avril 2005.

He is member of the international board of the Functional-Structural Plant Models conference (he was chair of this board between 2001-2005).

Yann Guédon was invited to give seminars at INA-PG, Joseph Fourier University (Grenoble) and Montpellier II University. He was an invited speaker at the workshop "statistical models with missing data" (Marne La Vallée).

Christophe Pradal was invited to participate to Les Causeries d'Intech'Sophia (June 2005): "[Quelle place pour le logiciel libre ? Dans l'entreprise, la recherche publique, les services publics](#)".

Evelyne Costes participated to the XVII International Botanical Congress (Vienna, Austria).

Jean-Baptiste Durand was invited to give a seminar at INRA, Avignon. He was an invited speaker at the workshop "statistical models with missing data" (Marne-La-Vallée) and presents a communication at the first workshop for young statisticians (Aussois).

Patrick Heuret obtained the Medal from the French National Academy of Agriculture for his thesis on the analysis and modeling of botanical sequences.

Carine Véra presented a communication at the first workshop for young statisticians (Aussois).

6.4. Theses and Internships

6.4.1. Theses defenses

- Pierre Barbier de Reuille, "[Vers un Modèle Dynamique du Méristème caulinaire apical d'Arabidopsis Thaliana](#)", Université Montpellier II, December, 2005

6.4.2. Ongoing Theses

- Florence Chaubert, "*Modèles linéaires généralisés mixtes multiphasiques*", Université Montpellier II.
- David Da Silva, "*Quantification de la structure autosimilaire des plantes par des méthodes de la géométrie fractale*", Université Montpellier II.
- Mikaël Lucas, "*Etude et modélisation des déterminismes de mise en place et de développement des racines latérales chez Arabidopsis Thaliana*", Université Montpellier II.
- Szymon Stoma, "*A mechanical based model of Arabidopsis Thaliana meristem development*", Université Montpellier II.

6.4.3. Internships

- Loïc Clavino, "*Développement d'une application pour digitaliser et analyser l'architecture de systèmes racinaires d'arbres tropicaux*", Université Montpellier II.
- David Da Silva, "*Evaluation des caractéristiques géométriques d'une structure végétale dans le cadre de l'analyse fractale*", Université Montpellier II.
- Mikaël Lucas, "*Approche intégrative du déterminisme de la ramification de la racine chez Arabidopsis Thaliana*", Université Montpellier II.
- Tessa Pierre-Joseph, "*Analyse de données longitudinales de comptage: Modélisation de l'effet de la pluviométrie sur la croissance de caféiers*", Université Montpellier II.

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- [11] P. BARBIER DE REUILLE. *Vers un Modèle Dynamique du Méristème caulinaire apical d'Arabidopsis thaliana*, Ph. D. Thesis, Université Montpellier II, December 2005.
- [12] Y. GUÉDON. *Méthodes et Modèles Statistiques pour l'Analyse de la Croissance et de la Structure des Plantes*, Habilitation Thesis, Université Montpellier II, October 2005.

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