



IN PARTNERSHIP WITH:
CIRAD

INRA

Activity Report 2017

Project-Team VIRTUAL PLANTS

Modeling plant morphogenesis at different scales, from genes to phenotype

IN COLLABORATION WITH: Amélioration génétique et adaptation des plantes (AGAP)

RESEARCH CENTER
Sophia Antipolis - Méditerranée

THEME
Computational Biology

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Project-Team VIRTUAL PLANTS

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- A1.1.13. - Virtualization
- A2.1.3. - Functional programming
- A2.1.9. - Dynamic languages
- A2.1.10. - Domain-specific languages
- A2.2.6. - Adaptive compilation
- A2.5. - Software engineering
- A3.1.1. - Modeling, representation
- A3.1.3. - Distributed data
- A3.1.8. - Big data (production, storage, transfer)
- A3.4.5. - Bayesian methods
- A5.1.1. - Engineering of interactive systems
- A5.2. - Data visualization
- A5.3.3. - Pattern recognition
- A5.3.4. - Registration
- A5.4.4. - 3D and spatio-temporal reconstruction
- A5.4.5. - Object tracking and motion analysis
- A5.5.1. - Geometrical modeling
- A5.9.2. - Estimation, modeling
- A6.1. - Mathematical Modeling
- A6.2.4. - Statistical methods
- A6.2.6. - Optimization
- A6.2.8. - Computational geometry and meshes
- A6.3. - Computation-data interaction
- A8.1. - Discrete mathematics, combinatorics
- A8.2. - Optimization
- A8.3. - Geometry, Topology
- A8.6. - Information theory
- A8.7. - Graph theory

Other Research Topics and Application Domains:

- B1.1.2. - Molecular biology
- B1.1.3. - Cellular biology
- B1.1.4. - Developmental biology
- B1.1.10. - Mathematical biology
- B1.1.11. - Systems biology
- B2.6. - Biological and medical imaging
- B9.4.1. - Computer science

B9.4.2. - Mathematics
B9.4.5. - Data science
B9.6. - Reproducibility
B9.7.1. - Open access

1. Personnel

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2. Overall Objectives

2.1. Overall Objectives

The **Virtual Plants** team is a joint team between **Inria**, **CIRAD** and **INRA** located in Montpellier. The long-term focus of the project is to study plant development, its modulation by the environment 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 develop a detailed analysis of apical meristem processes, based on advanced mathematical and computational methods and tools, 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 organization 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. Research Program

3.1. Analysis of structures resulting from meristem activity

To analyze plant growth and structure, we focus mainly on methods for analyzing 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 analyzed with combinatorial methods in order to compare them or to reveal particular types of organization. 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, generalized linear mixed models for longitudinal count data and multiple change-point models for the identification of phenological phases.
- Repeated patterns within sequences or trees: the statistical models of interest are mainly (hidden) variable-order Markov chains. Hidden variable-order Markov chains were in particular applied to characterize permutation patterns in phyllotaxis and the alternation between flowering and vegetative growth units along sympodial tree axes.
- 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 semi-Markov switching 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 latent structure models (e.g. hidden Markovian models or multiple change-point models) that consist in exploring the latent structure 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 analyze their dynamic and complex spatial interaction. To carry out this integration, we need to develop a complete methodological approach containing:

- algorithms for the automatized segmentation in 3D, and cell lineage tracking throughout time, for images coming from confocal microscopy,
- design of high-level routines and user interfaces to distribute these image analysis tools to the scientific community,
- tools for structural and statistical analysis of 3D meristem structure (spatial statistics, multiscale geometric and topological analysis),
- physical models of cells interactions based on spring-mass systems or on tensorial mechanics at the level of cells,
- models of biochemical networks of hormonal and gene driven regulation, at the cellular and tissue level, using continuous and discrete formalisms,
- and models of cell development taking into account the effects of growth and cell divisions on the two previous classes of models.

4. Highlights of the Year

4.1. Highlights of the Year

- To obtain efficient data-structures from segmented images that can be used for later physical simulations, we developed a computational tool, DRACO-STEM, that interprets cell population images as 3D cell meshes. DRACO-STEM has been released as an independent package to enable biomechanical simulations on real-world data [33].
- *Modeling cell fate decisions during Acsidian embryo development.* Canalization of developmental processes ensures the reproducibility and robustness of embryogenesis within each species. In its extreme form, found in ascidians, early embryonic cell lineages are invariant between embryos within and between species, despite rapid genomic divergence. To resolve this paradox, we used live light-sheet imaging to quantify individual cell behaviors in digitalized embryos and explore the forces that canalize their development. This quantitative approach revealed that individual cell geometries and cell contacts are strongly constrained, and that these constraints are tightly linked to the control of fate specification by local cell inductions. While in vertebrates ligand concentration usually controls cell inductions, we found that this role is fulfilled in ascidians by the area of contacts between signaling and responding cells. We propose that the duality between geometric and genetic control of inductions contributes to the counterintuitive inverse correlation between geometric and genetic variability during embryogenesis [Submitted in Dec 2017].

5. New Software and Platforms

5.1. OpenAlea

KEYWORDS: Bioinformatics - Biology

RELEASE FUNCTIONAL DESCRIPTION: OpenAlea 2.0 adds to OpenAlea 1.0 a high-level formalism dedicated to the modeling of morphogenesis that makes it possible to use several modeling paradigms (Blackboard, L-systems, Agents, Branching processes, Cellular Automata) expressed with different languages (Python, L-Py, R, Visual Programming, ...) to analyse and simulate shapes and their development.

- Participants: Christian Fournier, Christophe Godin, Christophe Pradal, Frédéric Boudon, Guillaume Baty, Julien Coste and Samuel Dufour Kowalski
- Contact: Christophe Pradal

5.2. OpenAlea.Visualea

KEYWORDS: Bioinformatics - Biology

- Participants: Christophe Pradal and Samuel Dufour Kowalski
- Contact: Christophe Pradal

5.3. VPlants

KEYWORDS: Bioinformatics - Biology

FUNCTIONAL DESCRIPTION: Computer algorithms and tools developed by the Virtual Plants team are integrated in the 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 VPlants packages are integrated into OpenAlea as Python components. General-purpose components (such as PlantGL, MTGs, L-Py) are distributed with the OpenAlea platform and usable through the visual programming environment VisuAlea.

- Contact: Christophe Pradal

6. New Results

6.1. Analysis of structures resulting from meristem activity

6.1.1. Acquisition and design of plant geometry

Participants: Frédéric Boudon, Christophe Pradal, Christophe Godin, Christian Fournier.

Virtual 3D model of plants are required in many areas of plant modeling. They can be used for instance to simulate physical interaction of real plant structures with their environment (light, rain, wind, pests, ...), 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 architectures in 3D [67], [58]. These methods are based on direct measurements of position and shape of every plant organ in space. Although they provide accurate results, they are particularly time consuming. More rapid and automated methods are now required in order to collect plant architecture data of various types and sizes in a systematic way. In this aim, we explore the use of laser scanner and pictures.

- *Reconstruction of tree structures from 3D laser scanner data.* (Bilan Yonis-Omar, Emma Carrié, Frédéric Boudon, Christophe Godin, Benoit Pallas [AFEF, AGAP], Evelyne Coste [AFEF, AGAP])

We investigate the possibility to use 3D laser scanners to automate plant digitizing. We are developing algorithms to reconstruct branching systems without leaves or foliage from scanner data or from scan simulated on plant mock-up obtained using different digitizing method.

For the branching systems, we previously proposed a reconstruction method to reconstruct plausible branching structures from laser scanner data based on the concept of space colonization [66]. Additionally, a number of automatic methods were proposed in the literature. A graphical editor has been developed and makes it possible to test these different methods and correct manually the reconstruction on laser scans. An additional validation pipeline makes it possible to compare automatic reconstruction with ground truth data using two indices of geometrical and structural similarities [53].

An application for the reconstruction of an apple tree core collection (1000 trees) has been conducted during the internships of B. Yonis-Omar and E. Carrié in a collaboration with the AFEF Team of UMR AGAP. A protocol that minimize the number of movement of the scanner has been setup. Some first method to characterize and reconstruct architectural traits from the scan has been defined.

- *Characterizing wheat canopy characteristics from LiDAR measurements.* (Shouyang Liu [Emmah,Inra], Fred Baret [Emmah,Inra], Frédéric Boudon, Christian Fournier)

Green area index (GAI) has been difficult to estimate accurately at large scales due to the cost prohibitive nature of classical in-situ methods. We propose to use LiDAR to overcome this problem. Through this work, we proposed a self-learning method to estimate GAI using LiDAR-derived metrics over a wheat field.

Specifically, we developed a LiDAR simulator to carry out scanning on digital 3D objects, mimicking the measuring principle and setups of actual LiDAR sensors. The footprint and the geometrical configuration of the LiDAR are explicitly accounted for. Comparison with measurements of actual LiDAR demonstrates that the simulator generates a 3D point cloud having the same statistical properties as those derived from the actual LiDAR measurements.

We then used a machine learning algorithm to correlate LiDAR-derived metrics and GAI over synthetic datasets. 3D wheat canopy scenes were generated with AdelWheat model for two contrasting development stages across a wide range of combination of the model parameters. The scenes were transformed into 3D point clouds using the LiDAR simulator. Results demonstrate that emerging properties, such as leaf area index (GLAI), could be retrieved with a good accuracy.

- *Reconstruction of annual plants from multi-view images.* (Simon Artzet, Jerome Chopard, Christian Fournier, Christophe Pradal, Christophe Godin, Xavier Sirault [CSIRO-HRPPC, Canberra], Tsu-Wei Chen[Inra, LEPSE])

Image-based phenotyping platforms in semi-controlled conditions offer large possibilities to perform genetic analyses of plant growth, architecture, light interception, and biomass accumulation over large time series for thousands of plants. However, methods for image analysis currently available are still very crude and need improvement and robustness to process huge amount of data. We are developing a python software framework dedicated to the analysis of high throughput phenotyping data and models named Phenomenal. This software framework currently consists of 2D and 3D image analysis workflow which ranges from 2D organs segmentation, 3D multi-view reconstruction, image-base meshing transformation, 2D/3D morphological thinning/skeletonization, 3D segmentation and tracking of plant organs maize (under development). We have processed images from phenoarch platform of the last four years and have built for each plant (maize, cotton, etc.) a voxel point cloud and image-base meshing representation and also for 725 maize plants a voxel point cloud automatically segmented (currently stem and mature leaf). Each process is run on distant server (private or virtual machines on FranceGrille cloud) and results can be viewed via a jupyter notebook server. Furthermore, 3D FSPM model for maize architectural development (named Cereals), is used to help segmenting plant images and to automate the mapping between segmented 3D objects and plant organs defined in the model. The 3D reconstructed model is combined with meteorological data to feed a light distribution model and estimate light use efficiency or establish response curve of morphogenetic processes to light environment [37]. This software framework was presented to “BMVA technical meeting: Plants in Computer Vision”.

This research theme is supported by the PIA Phenome.

- *Tracking the growth of maize ear and silks in a high-throughput phenotyping platform using a robot-assisted imaging pipeline* (Simon Artzet, Jerome Chopard, Christian Fournier, Christophe Pradal, Nicolas Bricet [LEPSE, INRA], Llorenç Cabrera-Bosquet [LEPSE, INRA])

In maize, silks are hundreds of filaments that simultaneously emerge from the ear for collecting pollen over a period of 1–7 days, which largely determines grain number especially under water deficit. Silk growth is a major trait for drought tolerance in maize, but its phenotyping is difficult at throughputs needed for genetic analyses.

We have developed a reproducible pipeline [31] that follows ear and silk growths every day for hundreds of plants, based on an ear detection algorithm that drives a robotized camera for obtaining detailed images of ears and silks. We first select, among 12 whole plant side views, those best suited for detecting ear position. Images are segmented, the stem pixels are labelled and the ear position is identified based on changes in width along the stem. A mobile camera is then automatically positioned in real time at 30 cm from the ear, for a detailed picture in which silks are identified based on texture and colour. This allows analysis of the time course of ear and silk growths of thousands of plants. The pipeline was tested on a panel of 60 maize hybrids in the PHENOARCH phenotyping platform. Over 360 plants, ear position was correctly estimated in 86% of cases, before it could be visually assessed. Silk growth rate, estimated on all plants, decreased with time consistent with literature. The pipeline allowed clear identification of the effects of genotypes and water deficit on the rate and duration of silk growth.

The pipeline presented here, which combines computer vision, machine learning and robotics, provides a powerful tool for large scale genetic analyses of the control of reproductive growth to changes in environmental conditions in a non invasive and automatized way. It is available as Open Source software in the OpenAlea platform.

- *Review on morphological plant modelling.* (Christophe Pradal, Mathilde Balduzzi, Alexander Bucksch [Georgia Univ., USA], Daniel H. Chitwood [Donald Danforth Plant Science Center, USA], Erin E Sparks [Univ. of Delaware, USA])

Plant morphology is inherently mathematical. The geometries of leaves and flowers and intricate topologies of the root have fascinated plant biologists and mathematicians alike. Beyond providing aesthetic inspiration, understanding plant morphology has become pressing in an era of climate change and a growing population. Gaining an understanding of how to modify plant architecture

through molecular biology and breeding is critical to improving agriculture, and the monitoring of ecosystems and global vegetation is vital to modeling a future with fewer natural resources. In this review [8], we begin by summarizing the rich history and state of the art in quantifying the form of plants, mathematical models of patterning in plants, and how plant morphology manifests dynamically across disparate scales of biological organization. We then explore the fundamental challenges that remain unanswered concerning plant morphology, from the barriers preventing the prediction of phenotype from genotype to modeling the fluttering of leaves in a light breeze. We end with a discussion concerning the education of plant morphology synthesizing biological and mathematical approaches and ways to facilitate research advances through outreach, cross-disciplinary training, and open science. Never has the need to model plant morphology been more imperative. Unleashing the potential of geometric and topological approaches in the plant sciences promises to transform our understanding of both plants and mathematics.

- *Qualitative and Quantitative Descriptors for Plant Morphology.* (Christophe Pradal, Mathilde Balduzzi, Alexander Bucksch [Georgia Univ., USA], Erin E Sparks [Univ. of Delaware, USA])

An emerging challenge in plant biology is to develop qualitative and quantitative measures to describe the appearance of plants through the integration of mathematics and biology. A major hurdle in developing these metrics is finding common terminology across fields. In this review, we define approaches for analyzing plant geometry, topology, and shape, and provide examples for how these terms have been and can be applied to plants. In leaf morphological quantifications both geometry and shape have been used to gain insight into leaf function and evolution. For the analysis of cell growth and expansion, we highlight the utility of geometric descriptors for understanding sepal and hypocotyl development. For branched structures, we describe how topology has been applied to quantify root system architecture to lend insight into root function. Lastly, we discuss the importance of using morphological descriptors in ecology to assess how communities interact, function, and respond within different environments. This review [30] aims to provide a basic description of the mathematical principles underlying morphological quantifications.

6.1.2. Modeling the plant ontogenic program

Participants: Christophe Godin, Yann Guédon, Jean-Baptiste Durand, Pierre Fernique, Marc Labadie, Christophe Pradal, Jean Peyhardi.

This research theme is supported by one PhD program.

The remarkable organization of plants at macroscopic scales may be used to infer particular aspects of meristem functioning. The fact that plants are made up of the repetition of many similar components at different scales, and the presence of morphological gradients, e.g. [47], [59], [60], [57], provides macroscopic evidence for the existence of regularities and identities in processes that drive meristem activity at microscopic scales. Different concepts have been proposed to explain these specific organizations such as "morphogenetic program" [65], "age state" [56] or "physiological age" [50]. All these concepts state that meristem fate changes according to position within the plant structure and during its development. Even though these changes in meristem fate are specific to each species and lead to the differentiation of axes, general rules can be highlighted [56], [50]. Here we develop computational methods to decipher these rules.

- *Relating branching structure to the shoot properties.* (Jean Peyhardi, Yann Guédon, Evelyne Coste [AGAP, AFEF team], Catherine Trottier [I3M], Yves Caraglio [AMAP], Pierre-Eric Lauri [AGAP, AFEF team])

Shoot branching structures often take the form of a succession of homogeneous branching zones and have been analyzed using segmentation models such as hidden semi-Markov chains. Axillary meristem fates are influenced by local properties of the parent shoot such as for instance its growth rate or local curvature. The objective of this work is to develop statistical models that generalize hidden semi-Markov chains with the capability to incorporate explanatory variables that vary along the parent shoot (e.g. leaf growth rate, leaf surface, internode length, local curvature of the parent shoot). More precisely, the simple multinomial distributions that represent the axillary productions

observed in the different branching zones are replaced by multinomial generalized linear models (GLMs). Since the two classical categories of multinomial GLMs that correspond either to nominal or ordinal categorical response variables were not appropriate, we chose to develop a new family of multinomial GLMs called partitioned conditional GLMs [21] that enable to tackle hierarchically-structured categorical response variables. Typically, we need to distinguish different timing of branching events (e.g. immediate shoot, one-year-delayed shoot and latent bud), different categories of offspring shoots (e.g. among one-year-delayed shoots, vegetative short shoot, vegetative long shoot and flowering shoot) and to specialize the explanatory variables for certain categories of offspring shoots (e.g. the growth of the parent shoot influence the immediate offspring shoots but not the one-year-delayed offspring shoots). The resulting integrative models are called semi-Markov switching partitioned conditional GLMs and have been applied to apple and pear tree branching structures [20].

- *Genetic determinisms of the alternation of flowering in apple tree progenies.* (Jean-Baptiste Durand, Alix Allard [AGAP, AFEF team], Evelyne Costes [AGAP, AFEF team])

A first study was published to characterize genetic determinisms of the alternation of flowering in apple tree progenies. Data were collected at two scales: at whole tree scale (with annual time step) and a local scale (annual shoots, which correspond to portions of stems that were grown during the same year). One or several replications of each genotype were available.

Three families of indices were proposed for early detection of alternation during the juvenile phase. The first family was based on a trend model and a quantification of the deviation amplitudes and dependency, with respect to the trend. The second family was based on a 2nd-order Markov chain with fixed and random effect in transition probabilities. The third family was based on entropy indices, in which flowering probabilities were corrected from fixed effects using Generalized Linear Models.

This allowed early quantification of alternation from the yearly numbers of inflorescences at tree scale. Some quantitative trait loci (QTL) were found in relation with these indices [43], [35].

New data sets were collected in other F1 progenies. Ancestral relationships between parents of different progenies were taken into account to enhance the power of QTL detection using Bayesian methods. Other QTLs are expected to be found using these new indices and genetic material. However, the amount of replicate per genotype and of data per replicate is quite reduced compared to those of our previous work. This is why we will investigate the loss of power in QTL detection due to a degraded amount of data, by simulating data deletion in our reference results.

- *Characterizing tree patchiness using a tree segmentation/clustering approach.* (Pierre Fernique, Anaëlle Dambreville, Jean-Baptiste Durand, Christophe Pradal, Yann Guédon, Frédéric Normand [CIRAD, HortSys, Réunion Island], Pierre-Eric Lauri [INRA, System]).

Many tropical trees are affected by strong phenological asynchronisms entailing patchiness. Patchiness is characterized by clumps of homogeneous botanical entities (e.g. a clump of flowering growth units) within tree canopy. It is therefore assumed that there are subtrees within which the characteristics of the botanical entities follow the same or nearly the same distribution, and between which these characteristics have different distributions. The detection of such subtrees can thus be stated as tree-indexed data segmentation. We therefore transposed multiple change-point models to tree-indexed data. The output of the segmentation procedure is a partition of trees such that two non-adjacent subtrees can be very similar in terms of botanical entity characteristics. We thus incorporated a second stage of clustering of subtrees based on a mixture model in order to group non-adjacent similar subtrees. Finally, directed acyclic graphs we built for summarizing the succession of patches over time within the canopy. This statistical modeling framework was applied to young mango trees [11].

- *Simulating fruit tree phenology.* (A.S. Briand, Frédéric Boudon, Frédéric Normand [CIRAD, HortSys, Réunion Island], Anaëlle Dambreville, Jean-Baptiste Durand, Pierre Fernique, Yann Guédon, Christophe Pradal, Pierre-Eric Lauri [INRA, System])

Mango is a tropical tree characterized by strong asynchronisms within and between trees. To study more precisely the interplay between the plant structural components, we built an integrative model to simulate the plant development based on the L-system formalism and GLM to model the dependencies between events. With such model, we showed the importance of architectural and temporal factors in the development of the units of the trees, see 1. The model also simulates the phenology of shoots and inflorescences. For this, the sizes of the different organs is modelled by statistical laws estimated from measurements that depends on their locations in the architecture. The growth speed of organs is modulated by the temperature. The model has been then coupled with an ecophysiological model of fruit growth [62], [63]. The global aim is to have a crop simulation model to predict fruit yield and quality on mango tree.



Figure 1. Simulation of the development of a mango tree over two cycles [52]. The first and last image corresponds to the end of the vegetative period of the 3rd and 5th growing cycle (June), respectively while the second and third images correspond to the flowering phase (August) of the 3rd and 4th cycles, respectively. The different colours of the inflorescences of the 3rd image show different developmental stages and the flowering asynchronism over the tree.

In the context of the PhD of S. Persello, we aim at extending this model with the effect of agricultural practices. For this, a number of experiment has been conducted this year with some mango trees being pruned with different intensity (global mass removed) and severity (depth of the removed elements). Analysis and characterization of the effect of pruning on the subsequent vegetative development of the tree is currently under investigation.

- *Characterizing the successive flowering phases of strawberry in relation to genetic determinants.* (Yann Guédon, Marc Labadie, Béatrice Denoyes [INRA, UMR BFP, Villenave d'Ornon], Justine Perrotte)

Our aim was to characterize the phenology of various strawberry genotypes, which is of particular importance for better predicting fruit production. We applied multiple change-point models for the synchronous segmentation of the individuals of a given genotype in successive flowering phases [19]. A multivariate generalization of the synchronous segmentation approach was developed in the context of Marc Labadie's PhD [14], the idea being to characterize not only the flowering pattern as in our first study but more generally the developmental pattern combining vegetative development, branching and flowering.

- *Self-nested structure of plants.* (Christophe Godin, Romain Azais, Farah Ben Naoum, Jean-Baptiste Durand, Alain Jean-Marie)

In a previous work [13], we designed a method to compress tree structures and to quantify their degree of self-nestedness. This method is based on the detection of isomorphic subtrees in a given tree and on the construction of a DAG (Directed Acyclic Graph, equivalent to the original tree, where

a given subtree class is represented only once (compression is based on the suppression of structural redundancies in the original tree). In the compressed graph, every node representing a particular subtree in the original tree has exactly the same height as its corresponding node in the original tree.

The class of self-nested trees presents remarkable compression properties because of the systematic repetition of subtrees in their structure. In a collaboration with two other Inria project-teams (MISTIS and BIGS), studied methods to approximate a tree with a tree in the class of self-nested trees. We first provided a better combinatorial characterization of this specific family of trees. We then showed that self-nested trees may be considered as an approximation class of unordered trees. We finally compared our approximation algorithms with a competitive approach of the literature on a simulated dataset [4].

6.1.3. Analyzing the influence of the environment on the plant ontogenic program

Participants: Jean-Baptiste Durand, Christian Fournier, Christophe Godin, Yann Guédon, Christophe Pradal, Jean Peyhardi, Pierre Fernique, Guillaume Garin.

This research theme is supported by three PhD programs.

The ontogenetic programme of a plant is actually sensitive to environmental changes. If, in particular cases, we can make the assumption that the environment is a fixed control variable (see section 6.1.2), in general the structure produced by meristem results from a tight interaction between the plant and its environment, throughout its lifetime. Based on observations, we thus aim to trace back to the different components of the growth (ontogenetic development and its modulation by the environment). This is made using two types of approaches. On the one hand, we develop a statistical approach in which stochastic models are augmented with additional time-varying explanatory variables that represent the environment variations. The design of estimation procedures for these models make it possible to separate the plant ontogenetic programme from its modulation by the environment. On the other hand, we build reactive models that make it possible to simulate in a mechanistic way the interaction between the plant development and its environment.

- *Investigating how architectural development interfere with epidemics and epidemic control.* (Christian Fournier, Corinne Robert [Ecosys, INRA], Guillaume Garin [ITK, Montpellier], David Claessens [ENS ULM, Paris], Christophe Pradal)

Sustainable agriculture requires the identification of new, environmentally responsible strategies of crop protection. Modelling of pathosystems can allow a better understanding of the major interactions inside these dynamic systems and lead to innovative protection strategies. In particular, functional–structural plant models (FSPMs) have been identified as a means to optimize the use of architecture-related traits. A current limitation lies in the inherent complexity of this type of modelling, and thus the purpose of this work is to provide a framework to both extend and simplify the modelling of pathosystems using FSPMs. Complex models are disassembled into separate *knowledge sources* originating from different specialist areas of expertise and these can be shared and reassembled into multidisciplinary models. Following the PhD of Guillaume Garin, we finalised a sensitivity analysis of the response of the severity of septoria to architectural traits, and an analysis of the influence of the wheat architecture on the competition between septoria and brown rust. These studies allowed to populate the framework with consistent example of application, and lead to the development of operational modules that allows the fitting and validation of pathosystem models with experimental data.

- *Investigating how hydraulic structure interfere with gas-exchange dynamics of complex plants canopies under water deficit* (Christophe Pradal, Christian Fournier, Rami Albasha [LEPSE, Inra], THierry Simmoneau [LEPSE, Inra] and Eric Lebon [LEPSE, Inra])

Individual leaves positioning within a plant canopy is a major determinant of the spatial distribution pattern of gas-exchange rates and energy budget within that canopy. Under water deficit, this distribution may be altered since soil drying affects stem hydraulic conductivity and, consequently, leaves stomatal conductance, suggesting that the hydraulic structure of the shoot may shape the intra-canopy variability of gas-exchange rates under water deficit. In this project, we design HydroShoot

[1], a functional-structural plant model which allows simulating the hydraulic structure, energy budget and gas-exchange fluxes of complex plant canopies under water deficit. Model parameters are calibrated and validated using sapflow and entire plant gas exchange data collected in 2009 and 2012 from grapevine (*Vitis vinifera* L. cv. Syrah) experiments under three training systems (Lyre, GDC and VSP) having contrasted canopy structures. The model is then used to evaluate the role of the hydraulic structure in predicting the intra-canopy variability of temperature and intrinsic water use efficiency of trained grapevines. The resulting HydroShoot model allows to capture the effect of the different training systems on the spatial distribution of temperature and foliar photosynthesis within the canopy. We show that the intra-canopy variability of gas-exchange dynamics were mainly explained by the variability of local climate conditions, while the role of the hydraulic structure appeared only as secondary. Finally, the proposed HydroShoot model has been implemented for grapevine in the OpenAlea platform and will be extended to other plant architectural systems.

- *Eucalyptus development in response to different water stress and fertilization levels* (Yann Guédon, Charlène Arnaud (CIRAD AMAP and BioWooEB), Yves Caraglio, Sylvie Sabatier (CIRAD AMAP))

Eucalyptus grandis has been grown successfully in plantations in many tropical regions including southern Brazil. The objective of the PhD of Charlène Arnaud (CIRAD AMAP and BioWooEB) is to study the modulation of the development of Eucalyptus main stems in response to water stresses and different levels of potassium or sodium fertilization. Eucalyptus main stem is characterized by a three-scale growth pattern with (i) at coarse scale, roughly stationary growth phases with phase changes often corresponding to cold seasons (ii) at intermediate scale, some growth fluctuations corresponding to the influence of the climatic factors (mainly temperature and cumulated rainfall) and (iii) at fine scale, more or less systematic alternation of short and long internodes as a consequence of the phylotactic pattern. We thus developed a pipeline of statistical models that incorporates specific multiple change-point models (piecewise 1st-order stationary autoregressive models) for characterizing this three-scale growth pattern.

6.2. Meristem functioning and development

In axis 2 work focuses on the creation of a *virtual meristem*, at cell resolution, able to integrate the recent results in developmental biology and to simulate the feedback loops between physiology and growth. The approach is subdivided into several sub-areas of research.

6.2.1. Data acquisition and design of meristem models

- *Improvement of the MARS-ALT pipeline robustness.*

Meristem, laser microscopy, image reconstruction, cell segmentation, automatic lineaging

Participants: Léo Guignard, Christophe Godin, Christophe Pradal, Grégoire Malandain [Morpheme, Inria], Gaël Michelin [Morpheme, IPL Morphogenetics, Inria], Guillaume Baty, Sophie Ribes [IBC, UM], Jan Traas [RDP, ENS Lyon], Patrick Lemaire [CRBM, CNRS], Yassin Refahi [RDP, ENS-Lyon / Sainsbury Lab, Cambridge, UK].

This research theme is supported by a PhD FRM grant, Jan Traas's ERC, Inria ADT programme and the Morphogenetics Inria Project Lab.

The MARS-ALT (Multi-Angles Registration and Segmentation - Automatic Lineage Tracking) software pipeline [10] automatically performs a segmentation at cell resolution from 3D or 2D voxel images where the membranes/walls are marked (by a die for example) and makes it possible to follow the lineage of these cells through time.

We finalized the development of a new segmentation and tracking pipeline, ASTEC (Adaptive Segmentation and Tracking of Embryonic Cells). ASTEC is a one-pass algorithm (in contrast to MARS-ALT, that perform first the segmentation and then the tracking in two-passes) that is best suited for movies with numerous close time-points acquired at high spatio-temporal resolution. This

pipeline takes advantage of information redundancy across the movies and biological knowledge on the segmented organism to constrain and improve the segmentation and the tracking. We used this one-pass algorithm to segment and track all cell shapes of a developing embryo of the marine invertebrate *Phallusia mammillata*. As a result we obtained the full track of the shapes of all the cells from the 64 cell stage up to the early tailbud stage (1030 cells undergoing 640 division events followed across 180 time-points through 6 hours of development imaged every 2 minutes, Figure 2). To our knowledge, it is the first time that such high-resolution 4D digital tissues have been generated taking into account the cell shapes.

Based on this quantitative digital representation, we systematically identified cell fate specification events up to the late gastrula stage. Computational simulations revealed that remarkably simple rules integrating measured cell-cell contact areas with spatio-temporal expression data for extracellular signalling molecules are sufficient to explain most early cell inductions. This work suggests that in embryos developing with stereotyped cell shapes and positions (like *Phallusia mammillata* embryos), the genomic constraints for precise gene expression levels are relaxed, thereby allowing rapid genome evolution. A paper describing the whole approach has been submitted in December 2017.

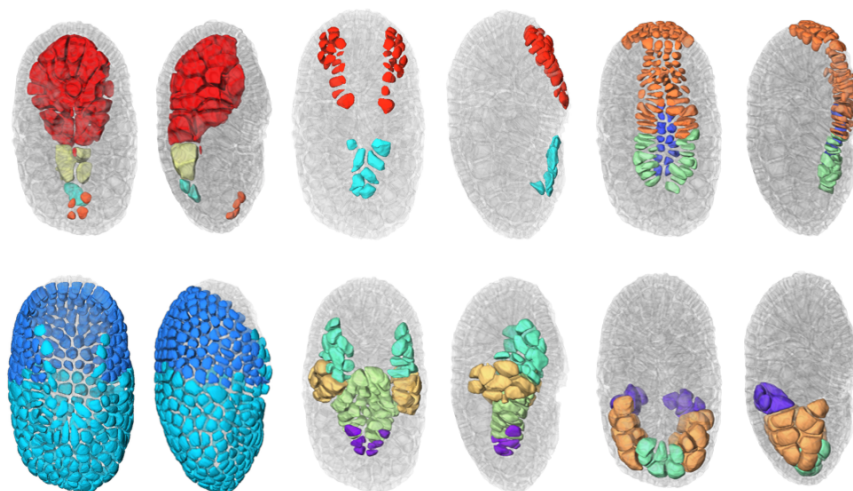


Figure 2. 3D projection of the segmented embryo at the early tailbud stage. The cells are colored by tissue type. The cells are slightly rounded to allow their distinction. The other cells of the embryo are in transparent grey. The dorsal and lateral sides are shown.

- *Creating mesh representation of cellular structures.*

Participants: Guillaume Cerutti, Sophie Ribes, Christophe Godin, Géraldine Brunoud [RDP, ENS], Carlos Galvan-Ampudia [RDP, ENS], Teva Vernoux [RDP, ENS], Yassin Refahi [RDP, ENS, Sainsbury Lab].

This research theme is supported the HFSP project Biosensors.

To produce a more efficient data structure accounting for the geometry of cellular tissues, we studied the problem of reconstructing a mesh representation of cells in a complex, multi-layered tissue structure, based either on membrane/wall images segmented using MARS or on nuclei images of shoot apical meristems. The construction of such mesh structures for plant tissues is currently a missing step in the existing image analysis pipelines.

We developed tools to reconstruct a 3D cell complex representing the tissue, based on the dual simplicial complex of cell adjacencies. This set of tetrahedra is optimized from a reasonable initial guess to match the adjacencies in the tissue, which proved to produce a very faithful reconstruction [55]. We also developed a set of methods to triangulate such reconstructions, and enhance the quality of triangular mesh representations of plant tissue, simultaneously along several criteria [54].

These tools are integrated in the DRACO-STEM computational pipeline released as an independent package to enable biomechanical simulations on real-world data.

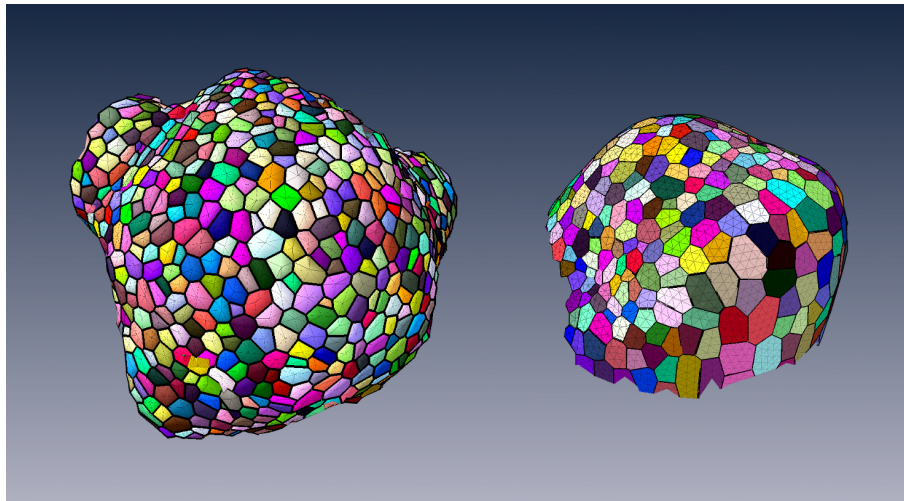


Figure 3. Triangular mesh representations of shoot apical meristem and flower meristem tissues obtained from MARS segmentations

- *Design of 3D digital atlases of tissue development.*

Participants: Sophie Ribes, Yassin Refahi [RDP, ENS, Sainsbury Lab], Guillaume Cerutti, Christophe Godin, Christophe Pradal, Frédéric Boudon, Gregoire Malandain [RDP, ENS], Gaël Michelin [RDP, ENS], Jan Traas [RDP, ENS], Teva Vernoux [RDP, ENS], Patrick Lemaire [CRBM, CNRS].

This research theme is supported the Inria Project Lab Morphogenetics, the ADT Mars-Alt and the HFSP project Biosensors.

To organize the various genetic, physiological, physical, temporal and positional informations, we build a spatialized and dynamic database [61]. 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 visually retrieve and manipulate the information, 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 polarization (transporters, microtubules), and gene expression patterns. Such 3D digital atlas is mainly descriptive. However, like for classical databases, specific tools make

it possible to explore the digital atlas 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 3D virtual atlas. Current developments of this tool consist in using directly the segmented images produced from laser microscopy to build the atlas. To better represent the development of a biological population, a method to compute an "average" structure is being investigated (a manuscript is in preparation).

6.2.2. *Shape analysis of meristems*

Participants: Jonathan Legrand, Guillaume Cerutti, Pierre Fernique, Frédéric Boudon, Yann Guédon, Christophe Godin, Pradeep Das [RDP, ENS], Arezki Boudaoud [RDP, ENS].

The MARS-ALT pipeline provides rich spatio-temporal data sets for analyzing the development of meristems, since it allows to perform 3D cell-segmentation and to compute cell-lineage. This enables the extraction and study of spatio-temporal properties of a tissue at cellular scale. To facilitate the analysis and to structure the obtained data we have implemented a dedicated temporal graph structure. In this graph, vertices are cells and edges are spatial or temporal relationships, thus proposing a natural representation of the growing tissue. Various variables can be attached either to the vertices (e.g. cell volume, inertia axes) or the edges (e.g. wall surface, distance between cell centroids). This graph may be augmented by new variables resulting from various spatial or temporal filtering (e.g. cell volumetric growth). Looking at homogeneous regions in the variable space, cellular patterns can be identified, by clustering methods for instance.

Considering the highly-structured nature of our data (time and space structuring) and the potential diversity and heterogeneity of possible cell descriptors, we developed two complementary approaches:

- A first one that favours the spatial structuring: In this approach, the cell neighbourhood and the cell descriptors are jointly taken into account in a clustering approach whose objective is to identify a small number of clusters corresponding to well-defined cell identities. Once the cells have been labelled using the clustering algorithm, cell generation distributions may be estimated on the basis of the labelled lineage trees.
- A second one that favours the temporal structuring: In this approach, the data of interest are lineage forest and the only spatial structuring taken into account corresponds to siblings with respect to a given parent cell. In a first step, cell identities are inferred on the basis of the cell descriptors taking into account lineage relationships using hidden Markov tree models and the spatial regions that emerge from the cell identity labelling are then characterized. This second approach is supported by the fact that cell topology is only affected by division which makes highly relevant the local spatial information taken into account in this approach.

6.2.3. *Mechanical models of plant tissues*

Participants: Olivier Ali, Hadrien Oliveri, Christophe Godin, Jan Traas [ENS-Lyon].

This research theme was supported, between 2012 and 2017, by the Inria Project Lab Morphogenetics and Jan Traas's ERC.

During the previous years, we set up a multi-scale mechanical model of a growing *shoot apical meristem* (the specific tissue at the very tip of plants where stem cells are active and produce new organs such as branches, leaves and flowers) with sub-cellular resolution, a detailed description of the core elements of this modelling approach has been developed in our previous reports. The aim of this project is to provide a computational framework for simulating growth of multicellular plant tissue. Several papers (and a review) have been published over the past few years on this work, in close collaboration with biologists: [51], [3], [26], [2].

Last year, our simulations pointed out that cell wall remodelling and growth initiation have to be co-regulated in order to initiate young organs formation. Biologists unraveled a biochemical signaling pathway that could explain this synergy. This joint work is currently under submission in a high impact factor journal.

Two years ago, we started to work on the integration of a feedback loop between mechanical stresses and growth (PhD work of Hadrien Oliveri started in Oct. 2015). A close study of this feedback mechanism made us refine several aspects of our modelling approach (tensor formalism to quantify cell polarity, ...). Ever since, Hadrien Oliveri has been studying the influence of this feedback loop on the morphogenesis of an epithelium. FEM-based simulations have been carried out on simple structures as proof of concept. This first step of the work is currently being submitted. This year, we also started to study the influence of such a mechanical-based feedback mechanism on the morphogenesis of real tissues. The specific question we want to investigate concerns flatness: How can plants produce flat organs such as leaves of sepals ? We investigate this question in the context of the sepal formation, always in close collaboration with biologists doing experiments on the very same topic.

This year, we also started to investigate to a quantitative manner the mechanical influence of inner tissues in the morphogenesis process. Indeed, up to now, our modelling approach was focused on the mechanics of the epidermis, known to be the main load-bearing layer. However, new experimental evidence suggest that inner tissues may influence and/or trigger morphogenesis processes. In order to investigate such mechanisms, our strategy relies on the use of high quality digitized tissues in 3D. Such structures, composed of triangular meshes, are produced through a workflow based on the updated version of the MARS pipeline and the DRACO-STEM module, developed within the team. Currently, numerical simulations are being carried out to analyse the mechanical equilibrium of the structures loaded with pressurized forces, see 4. Preliminary results tend to confirm the leading mechanical role of the epidermis. Interestingly, sharp differences in the mechanical characteristics emerge between epidermal cells and inner ones.

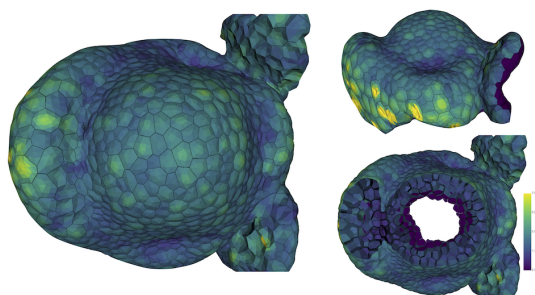


Figure 4. Heatmap of the stress tensor amplitude in a digitalized flowerbud.

6.2.4. Mechanical modelling of embryo morphogenesis.

Participants: Bruno Leggio, Emmanuel Faure, Patrick Lemaire [CRBM, CNRS], Christophe Godin.

A work on data analysis and modelling of morphogenesis and development in embryos of ascidians has been started this year. It comprises two main branches: starting from segmented data at cellular resolution, global and local symmetries of embryo development were analyzed. An analysis in terms of entropy of conserved embryonic properties was developed in order to characterise different stages of development as well as different tissues. In parallel, a mechanical and topological analysis of cell-cell interactions was carried out. This lead us to develop a new and original physical model of cleavage-plane determination in different tissues, with the goal of understanding the role of purely mechanical interactions in shaping ascidian embryos.

6.2.5. Gene regulatory networks: Design of a genetic model of inflorescence development.

Participants: Eugenio Azpeitia, Christophe Godin, François Parcy, Etienne Farcot.

This research theme is supported by the Inria Project Lab Morphogenetics.

Modeling gene activities within cells is of primary importance since cell identities correspond to stable combination of gene expression. We studied the regulatory network that controls the flowering transition during morphogenesis. To overcome the network complexity and integrate this regulation during ontogenesis, we have developed a first model of the control of floral initiation by genes, and in particular the situation of cauliflower mutants, in which the meristem repeatedly fails in making a complete transition to the flower. The network was validated by multiple analyses, including sensibility analyses, stable state analysis, mutant analysis, among others. Once the network was validated, it was coupled with an architectural model of plant development using L-systems. The coupled model was used to study how does changes in gene dynamics and expression could change the architectural properties of plants and produce cauliflowers instead of flowers. Finally, the architectural model without the network was used to study how changes in certain parameters could generate different curd morphologies, including the normal cauliflower and the romanesco one.

We have three main types of predictions. (1) How does gene expression is modified from WT to cauliflower organisms. (2) How gene regulate plants shape in order to produce curds instead of flowers. (3) The main parameter regulating curds shapes. The predictions made using the model are currently being experimentally tested. All our results could provide a comprehensive understanding of how does genes and plant architecture are linked in a dynamical way.

6.2.6. Model integration

Participants: Frédéric Boudon, Christophe Godin, Guillaume Cerutti, Jean-Louis Dinh, Eugenio Azpeitia, Jan Traas.

This research theme is supported by the Morphogenetics Inria Project Lab.

One key aspect of our approach is the development of a computer platform dedicated to programming virtual tissue development, TissueLab. This platform, based on *OpenAlea*, will be used to carry out integration of the different models developed in this research axis. In the past year, progress has been made in defining a generic tissue data structure that would be visualized, manipulated and updated through this platform. Currently, robust geometric operations such as division are implemented and tested. Moreover, a redesign of the structure based on more elaborated formalisms such as combinatorial maps is being investigated. A 2D version is being developed in the context of Jean-Louis's Dinh PhD thesis, and will be described in a forthcoming book chapter.

Our approach consists of building a programmable tissue which is able to accept different modeling components. This includes a central data structure representing the tissue in either 2-D or 3-D, which is able to grow in time, models of gene activity and regulation, models of signal exchange (physical and chemical) between cells and models of cell cycle (which includes cell division). An introduction to the modeling of some main components of such integrated system was published as a book chapter in the series of Ecole de Physique des Houches [12]. For each modeling component, one or several approaches are investigated in depth, possibly at different temporal and spatial scales, using the data available from the partners (imaging, gene networks, and expression patterns). Approaches are compared and assessed on the same data. The objective of each sub-model component will be to provide plugin components, corresponding to simplified versions of their models if necessary, that can be injected in the programmable tissue platform. This work is developed in collaboration with the RDP group at ENS-Lyon [64] and the CPIB group in Nottingham, UK [49].

6.3. Multi-scale models and analysis: from cells to plant architecture (and back)

6.3.1. Modeling water transport in roots

Participants: Mikaël Lucas [IRD], Christophe Pradal, Christophe Godin, Yann Boursiac [BPMP], Christophe Maurel [BPMP].

This research theme is supported by the ANR project HydroRoot.

A model of *Arabidopsis thaliana* root hydraulics at the cellular level was developed in the OpenAlea modeling platform. The model relies on the integration throughout root architecture of elementary hydraulic components. Each component integrates local radial and axial water flows. Axial hydraulic conductivity is calculated according to Poiseuille's law, based on local size of xylem vessels. Radial hydraulic conductivity is determined in part by aquaporin activity and was set constant throughout root architecture in the first model versions. In its current state, the model is parameterized using architectural, tissular and physiological data that were experimentally determined in the Aquaporin group at UMR BPMP. The architectural reconstruction of the root system is based on a tridimensional multi-scale tree graph (MTG). The current model is capable of predicting the water flow that is transported by a root system in the standard experimental conditions used in the Aquaporin group. This model was used to perform sensitivity analyses and determine the respective contributions to root hydraulic dynamics of various biological parameters (axial and radial hydraulic conductivities, root architecture). One major finding is that the root hydraulic conductivity (L_{pr}) computed from the model is highly dependent on root architecture. This is due to the limiting role of axial (xylem) conductance, one feature that had been neglected in previous representations of root water transport. The radial hydraulic conductivity may primarily be limiting in conditions of L_{pr} inhibition, since its increase from values in control roots has marginal effects on L_{pr} . A new set of experimental data including root diameter repartitions in wild-type plants, and xylem vessel diameters in mutants with altered xylem morphology (*irx3*, *esk1*) will be used to challenge the model. Root cell hydraulic conductivities will also be measured in these and aquaporin mutant phenotypes. Our aim is to check whether, based on anatomical and morphological data, the model can properly predict the radial hydraulic conductivity of these genotypes.

As the simulations may be time consuming and results sometimes difficult to interpret on complex branching systems, we started to investigate new methods to compute efficiently hydraulic conductivities and corresponding flows on complex root systems using architecture compression technics developed in the 1st axis of the project. First results show that very efficient computations of complex hydraulic architectures can be derived from the use of these compression techniques on idealized root architectures. These encouraging results provide a new abstraction that will be used in combination with the detailed modeling approach described above to break down the complexity of the analysis these huge branching systems.

6.3.2. Functional-Structural Root System Models in the Context of Drought Tolerance Breeding

Participants: Mikaël Lucas [IRD], Christophe Pradal.

This research theme is supported by a PhD program at IRD.

In this work, we study the impact of hydraulic architecture on water fluxes, and we review the conception and use of functional-structural root models in the broader context of research on root-driven drought tolerance, on the basis of root system architecture (RSA) phenotyping [40]. Such models result from the integration of architectural, physiological and environmental data. Here, we consider the different phenotyping techniques allowing for root architectural and physiological study and their limits. We discuss how QTL and breeding studies support the manipulation of RSA as a way to improve drought resistance. We then go over the integration of the generated data within architectural models, how those architectural models can be coupled with functional hydraulic models, and how functional parameters can be measured to feed those models. We then consider the assessment and validation of those hydraulic models through confrontation of simulations to experimentations. Finally, we discuss the up and coming challenges facing root systems functional-structural modeling approaches in the context of breeding.

6.3.3. Mechanical modeling of fruit growth

Participants: Ibrahim Cheddadi [Inra, Avignon], Mik Cieslak [U. Calgary], Frédéric Boudon, Valentina Baldazzi [Inra, Avignon], Nadia Bertin [Inra, Avignon], Michel Genard [Inra, Avignon], Christophe Godin.

This research theme is supported by the Agropolis project MecaFruit3D.

Fruits and plants in general are large scale hydraulic systems in which growth is closely linked to water fluxes: thanks to osmotic pressure difference, the cells are able to absorb water from their environment and therefore increase their volume; as the cells are bounded by rigid walls, this results in both hydrostatic pressure (the so-called turgor pressure) in the cell and tension in the cell walls; above a threshold, synthesis of new cell wall material occurs and relaxes the tension. This process allows cells to grow, and along with cell division, is responsible for plant growth. In fruits, phloem and xylem vascular networks provide the water fluxes necessary for growth, while the osmotic pressure is mainly regulated by sugar intake from the phloem. The goal of this project is to combine a description of water and sugar fluxes at the fruit scale with a modelling of growth at cell level, as described above.

As a first step in this direction, we have developed a bidimensional multicellular model that couples, on the one hand, water fluxes between cells (symplastic pathway) and between cells and intercellular space (apoplastic pathway), and on the other hand, mechanical properties of the cell walls and mechanical equilibrium of this complex system. Existing multicellular models for plant growth overlook this coupling. From a mathematical point of view, it corresponds to a coupling between (1) the ordinary differential equations that describe fluxes and cell walls properties and (2) the highly non linear system of equations that describes the mechanical equilibrium of the cell walls.

We have developed a numerical method for this coupled system, that allows to simulate in a reasonable amount of time a hundred of connected cells. Numerical simulations exhibit a highly non linear behaviour with respect to the governing parameters. Thanks to the detailed analysis of a simplified setup, we have identified two clearly distinct growth regimes: one regime that allows large growth heterogeneities by amplifying the effect of differences between cells, and conversely another regime that smoothes differences out and yields a homogeneous growth. On the biological level, the first regime is well adapted to morphogenesis, whereas the second one is well adapted to homothetic growth after the differentiated tissues have been created. A publication of these completely new results is in preparation.

We have developed a collaboration with biophysicists in RDP laboratory in Lyon (Arezki Boudaoud and Yuchen Long) in order to compare the results of this model to experiments at the microscopic scale of the meristem. A publication is in preparation.

In the longer term, we plan extend this model to the larger scale of tissues and organs in order to model fruit growth.

6.3.4. Analyzing root growth and branching

Participants: Beatriz Moreno Ortega, Sixtine Passot, Yann Guédon, Laurent Laplaze [IRD, DIADE], Mikael Lucas [IRD, DIADE], Bertrand Muller [INRA, LEPSE].

This research theme was supported by two PhD programmes.

New 2D and 3D root phenotyping platforms are emerging with associated image analysis toolbox (e.g. SmartRoot, RhizoScan) and the identification of developmental patterns within these complex phenotyping data requires new approaches. Here, we aim at developing a pipeline of methods for analyzing root systems at three scales:

1. tissular scale to identify and characterize the division, elongation and mature zones along a root apex using piecewise heteroscedastic linear models for segmenting epidermal cell length profiles [17].
2. individual root scale to analyze the dynamics of lateral root elongation. We in particular applied semi-Markov switching linear models for classifying roots on the basis of the identification of phases within growth rate profiles,
3. root system scale to analyze the primary root branching structure using variable-order Markov chains.

This pipeline of analysis methods was applied to different species (maize, Pearl millet [18]) with contrasting biological objectives (study of genetic diversity for Pearl millet and of metabolic and hormonal controls of morphogenesis for maize).

6.3.5. *The role of auxin and sugar in rose bud outgrowth control*

Participants: Jessica Bertheloot [INRA, Angers], Frédéric Boudon, Christophe Godin.

Auxin in the stem is known to be a key regulator of apical dominance. Over the last decades, many studies have been undertaken to understand its action mode, which is indirect because auxin in the main stem does not enter into the bud. Recently, apical dominance over basal buds in pea has been related to low sugar availability caused by high sugar demand of growing apical organs. Auxin and sugar are two signals regulating the entrance of bud into sustained growth in opposite ways. In the last year, it has also been demonstrated that sugar effect on bud outgrowth was preceded by a modification of the hormonal levels involved in bud outgrowth, which suggests that auxin and sugar pathways do interact in a non-trivial way. However, auxin and sugar effects have been studied separately until now. In this work, we investigate what is the combined effect of sugar and auxin on bud outgrowth, and how they integrate to regulate bud entrance into sustained growth. For this, a series of experiments has been carried out on a single-node cuttings of *Rosa hybrida* grown in vitro in which different combinations of sugar and auxin levels have been tested. A model of the regulatory networks controlling stem-bud molecular interaction has been developed.

6.4. Generic methodological results

6.4.1. *OpenAlea scientific workflows and grid computing*

Participants: Christophe Pradal, Sarah Cohen-Boulakia, Christian Fournier, Didier Parigot [Inria, Zenith], Patrick Valduriez [Inria, Zenith].

This research theme has been supported by IBC.

Plant phenotyping consists in the observation of physical and biochemical traits of plant genotypes in response to environmental conditions. Challenges, in particular in context of climate change and food security, are numerous. High-throughput platforms have been introduced to observe the dynamic growth of a large number of plants in different environmental conditions. Instead of considering a few genotypes at a time (as it is the case when phenomic traits are measured manually), such platforms make it possible to use completely new kinds of approaches. However, the data sets produced by such widely instrumented platforms are huge, constantly augmenting and produced by increasingly complex experiments, reaching a point where distributed computation is mandatory to extract knowledge from data. We design the infrastructure InfraPhenoGrid [42] to efficiently manage data sets produced by the PhenoArch plant phenomics platform in the context of the French Phenome Project. Our solution consists in deploying *OpenAlea* scientific workflows on a Grid using a middleware, SciFloware, to pilot workflow executions. Our approach is user-friendly in the sense that despite the intrinsic complexity of the infrastructure, running scientific workflows and understanding results obtained (using provenance information) is kept as simple as possible for end-users.

6.4.2. *Reproducibility in the Life Science with Scientific workflows*

Participants: Christophe Pradal, Sarah Cohen-Boulakia, Jerome Chopard.

This research theme has been supported by IBC and the GDR MADICS/ReproVirtuFlow.

With the development of new experimental technologies, biologists are faced with an avalanche of data to be computationally analyzed for scientific advancements and discoveries to emerge. Faced with the complexity of analysis pipelines, the large number of computational tools, and the enormous amount of data to manage, there is compelling evidence that many if not most scientific discoveries will not stand the test of time: increasing the reproducibility of computed results is of paramount importance. In the context of the project 7.2.5.3, we study how scientific workflows can help to improve the reproducibility of computational experiment in the domain of life science [34]. We characterize and define the criteria that need to be catered for by *reproducibility-friendly* scientific workflow systems, and use such criteria to place several representative and widely used workflow systems and companion tools within such a framework.

6.4.3. Statistical modeling

Participants: Yann Guédon, Jean Peyhardi, Pierre Fernique, Jean-Baptiste Durand Peyhardi, Catherine Trottier [IMAG, Montpellier].

We develop statistical models and methods for identifying and characterizing developmental patterns in plant phenotyping data. Phenotyping data are very diverse ranging from the tissular to the whole plant scale but are often highly structured in space, time and scale. Problems of interest deal with the definition of new family of statistical models specifically adapted to plant phenotyping data and the design of new methods of inference concerning both model structure, model parameters and latent structure. This is illustrated this year by [41].

6.4.4. Lossy compression of tree structures

Participants: Christophe Godin, Romain Azaïs, Jean-Baptiste Durand, Alain Jean-Marie.

In in [13], we defined the degree of self-nestedness of a tree as the edit-distance between the considered tree structure and its nearest embedded self-nested version. Indeed, finding the nearest self-nested tree of a structure without more assumptions is conjectured to be an NP-complete or NP-hard problem. We thus introduced a lossy compression method that consists in computing in polynomial time for trees with bounded outdegree the reduction of a self-nested tree that closely approximates the initial tree. This approximation relies on an indel edit distance that allows (recursive) insertion and deletion of leaf vertices only. We showed in a conference paper presented at DCC'2016 [48] with a simulated dataset that the error rate of this lossy compression method is always better than the loss based on the nearest embedded self-nestedness tree [13] while the compression rates are equivalent. This procedure is also a keystone in our new topological clustering algorithm for trees. In addition, we obtained new theoretical results on the combinatorics of self-nested structures and their ability to approximate complex trees in a costless manner [4].

6.4.5. Version climber

Participants: Christophe Padal, Dennis Shasha, Sarah Cohen-Boulakia, Patrick Valduriez.

This research has been supported by the Inria International Chair of Dennis Shasha.

Imagine you are a data scientist (as many of us are/have become). Systems you build typically require many data sources and many packages (machine learning/data mining, data management, and visualization) to run. Your working configuration will consist of a set of packages each at a particular version. You want to update some packages (software or data) to their most recent possible version, but you want your system to run after the upgrades, thus perhaps entailing changes to the versions of other packages.

One approach is to hope the latest versions of all packages work. If that fails, the fallback is manual trial and error, but that quickly ends in frustration.

We advocate a provenance-style approach in which tools like *ptrace* and *reprozip*, combine to enable us to identify version combinations of different packages. Then other tools like *pip* and *VirtualEnv* enable us to fetch particular versions of packages and try them in a sandbox-like environment.

Because the space of versions to explore grows exponentially with the number of packages, we have developed a memorizing algorithm that avoids exponential search while still finding an optimum version combination.

Experimental results have been tested (with full reproducibility) on well known packages used in data science to illustrate the effectiveness of our approach as well as life science computational experiment.

6.4.6. Automatic generation of python bindings for C++ libraries

Participants: Pierre Fernique, Christophe Padal.

This research has been supported by the Inria ADT SCOOP

Most of Python and R scientific packages incorporate compiled scientific libraries to speed up the code and reuse legacy libraries. While several semi-automatic solutions exist to wrap these compiled libraries, the process of wrapping a large library is cumbersome and time consuming. In this paper, we introduce AutoWIG, a Python package that wraps automatically compiled libraries into high-level languages using LLVM/Clang technologies and the Mako templating engine. Our approach [46] is automatic, extensible, and applies to complex C++ libraries, composed of thousands of classes or incorporating modern meta-programming constructs.

7. Partnerships and Cooperations

7.1. Regional Initiatives

7.1.1. *New pearl*

Participants: Sixtine Passot, Yann Guédon, Soazig Guyomarc'h [Montpellier University, DIADE], Laurent Laplaze [IRD, DIADE].

Funding: Labex Agro (Contractor for Virtual Plants: CIRAD, from 2014 to 2017)

Pearl millet is an orphan crop regarding research effort despite its key role for food safety in Sub-Saharan Africa. The objective of the New Pearl project is to develop basic biological knowledges concerning Pearl millet development and genetic diversity. We are more specifically involved in the study of the root system development and the genetic diversity on the basis of root phenotypic traits.

7.1.2. *Integrated model of plant organ growth*

Participants: Yann Guédon, Christine Granier [INRA, LEPSE], Garance Koch [INRA, LEPSE], Nadia Bertin [INRA, PSH], Valentina Baldazzi [INRA, PSH].

Funding: Labex Agro (Contractor for Virtual Plants: CIRAD. From 2015 to 2018)

The objective of this project is to develop a generic model which will predict interactions among the main processes controlling the development of source and sink organs in tomato, i.e. cell division, cell expansion and endoreduplication in relation to carbon and water fluxes under fluctuating environment. To achieve this objective we will i) capitalize on expertise, multi-scale phenotyping tools and genetic resources already compiled on the fruit model tomato and the model plant *Arabidopsis thaliana*; ii) perform new experiments to collect phenotyping data currently missing in this field, especially concerning the early phase of fruit and leaf development in tomato and the interactions between genes and environment; iii) develop a process-based model of organ growth which will integrate knowledge collected at the different scales.

Partners: PSH, INRA, Avignon; LEPSE, INRA, Montpellier, Biologie du fruit et Pathologie INRA, Bordeaux;

7.2. National Initiatives

7.2.1. *HydroRoot*

Participants: Mikaël Lucas [IRD], Christophe Pradal, Christophe Godin, Yann Boursiac [BPMP], Christophe Maurel [BPMP].

Funding: ANR (Contractor for Virtual Plants: Cirad, From 2012 to 2016)

The HydroRoot project proposes a unique combination of approaches in the model plant *Arabidopsis thaliana* to enhance our fundamental knowledge of root water transport. Accurate biophysical measurements and mathematical modeling are used, in support of reverse and quantitative genetics approaches, to produce an integrated view of root hydraulics. The HydroRoot project will address as yet unknown facets of root water transport. It will lead to an integrated view of root hydraulics that considers both tissue hydraulics and root architecture and explains how these components are controlled at the molecular level by physiological and/or environmental cues. Because of its strong physiological and genetic background, this research may also directly impact on breeding programs, for production of crops with optimised water usage and stress responses.

7.2.2. *Phenome*

Participants: Christian Fournier, Christophe Pradal, Yann Guédon, Sarah Cohen-Boulakia, Christophe Pradal, Pierre Fernique, Jerome Chopard, Patrick Valduriez.

Funding: ANR-Investissement d'avenir (Contractor for Virtual Plants: INRA, From 2015 to 2018)

The goal of Phenome is to provide France with an up-to-date, versatile, high-throughput infrastructure and suite of methods allowing characterisation of panels of genotypes of different species under climate change scenarios. We are involved in the methodological part of the project, that aims at developing a software framework dedicated to the analysis of high throughput phenotyping data and models. It will be based on the OpenAlea platform that provides methods and softwares for the modelling of plants, together with a user-friendly interface for the design and execution of scientific workflows. We also develop the InfraPhenoGrid infrastructure that allows high throughput computation and recording of provenance during the execution of Workflows.

7.2.3. *DigEM*

Participants: Christophe Godin, Grégoire Malandain, Patrick Lemaire.

Funding: ANR (Contractor for Virtual Plants: Inria, From 2015 to 2019)

In this project, we will use advanced light-sheet imaging of live embryos to quantitatively describe embryonic morphogenesis in ascidians, a class of animals that undergo very rapid genomic divergence, yet show an extraordinary stasis of embryonic morphologies, based on invariant early cell lineages shared by all studied species. The global aims of the proposal, which will bridge micro- and macroevolutionary scales of analysis, are: i) to provide a global systems-level description at cellular resolution of an animal embryonic program; ii) to use this description to characterize intra-specific and inter-specific patterns of morphogenetic variations; iii) to analyze possible molecular mechanisms explaining the unusual robustness of this program to environmental and genetic perturbations. To achieve these aims, we will combine advanced live light-sheet microscopy, computational biology, functional gene assays and evolutionary approaches.

7.2.4. *Leaf Serration*

Participants: Christophe Godin, Eugenio Azpeitia.

Funding: ANR (Contractor for Virtual Plants: Inria, From 2014 to 2019)

Leaf growth and development result from the coordination in time and space of cellular divisions and cellular expansion, and expansion of certain plant cells reaches up to one thousand times their size when living in the meristem. Transcription factors belonging to the CUP-SHAPED COTYLEDON (CUC) genes and homeodomain genes of the KNOTTED-LIKE (KNOXI) family were shown to be essential for the control of leaf size and shape. In addition, the phytohormone auxin is a critical regulator of growth and development, involved in the regulation and coordination of cell division and cell expansion. The mechanisms of auxin signalling are based on a complex set of co-receptors exhibiting high to low affinity for auxin and an even more complex modular network of transcriptional repressors and activators tightly controlling the expression of a large set of genes.

The SERRATIONS project is based on recent data relative to key transcription factors regulating leaf morphogenesis and advanced knowledge on the generic signalling mechanisms of the phytohormone auxin that plays a critical role in the control and coordination of cellular responses sustaining leaf size and shape. The goal of the project is to identify auxin signalling modules involved in leaf morphogenesis and to integrate these data in mathematical modelling to provide new insights into complex regulatory networks acting on leaf morphogenesis and to further test model-derived hypotheses.

7.2.5. *Other national grants*

7.2.5.1. *Morphogenetics*

Participants: Christophe Godin, Olivier Ali, Frédéric Boudon, Jean Phillippe Bernard, Hadrien Oliveri, Christophe Pradal, Guillaume Cerutti, Grégoire Malandain, François Faure, Jan Traas, François Parcy, Arezki Boudaoud, Teva Vernoux.

Funding: Inria Project Lab (From 2013 to 2017)

Morphogenetics is an Inria transversal project gathering 3 Inria teams and two Inra teams. It aimed at understanding how flower shape and architecture are controlled by genes during development. Using quantitative live-imaging analysis at cellular resolution we will determine how specific gene functions affect both growth patterns and the expression of other key regulators. The results generated from these experiments will be integrated in a specially designed database (3D Atlas) and used as direct input to new predictive computational models for morphogenesis and gene regulation. Model predictions will then be further tested through subsequent rounds of experimental perturbation and analysis. A particular emphasis will be put on the modeling of mechanics in tissues for which different approaches will be developed.

Partners: RDP ENS-Lyon; Imagine Inria Team (Grenoble); Morpheme Inria Team (Sophia-Antipolis), UMR PCV (Grenoble).

7.2.5.2. *Rose*

Participants: Christophe Godin, Frédéric Boudon.

Funding: INRA - PhD project (From 2016 to 2019)

In this project we want to quantify and understand how sugars interfere with hormonal signals (auxin, cytokinins) to regulate lateral bud outgrowth of aerial stems of roses. Experiments will be made on Rose stems to test different levels of sugar conditions and hormonal concentrations on bud outgrowth. An extension of the recently published hormonal model of apical dominance will be made to take into account the role of carbon as a signaling molecule.

Partners: UMR SAGAH, Angers

7.2.5.3. *ReProVirtuFlow*

Participants: Christophe Pradal, Sarah Cohen-Boulakia, Jerome Chopard.

In the life science domain, scientists are facing the deluge and the size of available data, the composition of a myriad of existing tools, and the complexity of computational experiment. In this context, reproducing an experiment is particularly difficult, as evidenced by numerous recent studies. The aim of this GDR CNRS project is to make a complete review of existing approaches in this field, considering in priority as elements of solution: (i) scientific workflows, (ii) data provenance, and (iii) virtual machines. This project brings together experts in data bases, algorithms and virtual environments, working in the domain of life science.

Funding: GDR - CNRS

7.3. European Initiatives

7.3.1. *Collaborations in European Programs, Except FP7 & H2020*

Program: H2020

Project acronym: ROMI

Project title: RObotics for MIcrofarms

Duration: November 2017 - October 2021

Coordinator: Sony

Other partners: Iaac, (Spain), FEI (France), Inria (France), CNRS (France), UBER (Germany), Chatelain (France)

Abstract: All over Europe, young farmers are starting small market farms and direct sales businesses. These farms can be found both in rural, peri-urban and urban areas. They grow a large variety of crops (up to 100 different varieties of vegetables per year) on small surfaces (0.01 to 5 ha) using organic farming practices. These farms have proven to be highly productive, sustainable and economically viable. However, a lot of work is done manually, resulting in physically challenging work conditions. ROMI will develop an open and lightweight robotics platform for these microfarms. We will assist these farms in weed reduction and crop monitoring. This will reduce manual labour

and increase the productivity through advanced planning tools. Thanks to ROMI's weeding robot, farmers will save 25 percents of their time. This land robot will also acquire detailed information on sample plants and will be coupled with a drone that acquires more global information at crop level. Together, they will produce an integrated, multi-scale picture of the crop development that will help the farmer monitor the crops to increase efficient harvesting. For this, ROMI will have to adapt and extend state-of-the-art land-based and air-borne monitoring tools to handle small fields with complex layouts and mixed crops. To achieve this, we will: (i) develop and bring to the market an affordable, multi-purpose, land-based robot, (ii) develop a weeding app for this robot that is adapted for organic microfarms, (iii) apply advanced 3D plant analysis and modelling techniques to in-field data acquisition, (iv) integrate these analysis techniques in the robot for detailed plant monitoring, (v) integrate these techniques also in the aerial drone N-E-R-O for multi-scale crop monitoring, (vi) extend the robot with novel, adaptive learning techniques to improve sensorimotor control of the plant monitoring app, and (vii) test the effectiveness of our solution in real-world field conditions.

This project was accepted in July 2017 and started Nov. 2017.

7.4. International Initiatives

7.4.1. Inria International Partners

7.4.1.1. Informal International Partners

An important collaboration with the CIRAD research unit HortSys at the Reunion island and in particular Frédéric Normand and Isabelle Grechi has been established for several years. The topic of the collaboration is the study of the phenology of mango tree. This is a tripartite collaboration that also involves Pierre-Eric Lauri of the System research unit (INRA, Montpellier).

7.5. International Research Visitors

7.5.1. Research Stays Abroad

In the context of the project on mango modelling and the PhD of S. Persello, F. Boudon was positioned in the Reunion island in the Hortsys unit for one year until August. He developed there a project on Mango modelling in collaboration with F. Normand.

8. Dissemination

8.1. Promoting Scientific Activities

8.1.1. Journal

8.1.1.1. Member of the Editorial Boards

- C. Godin is a member of the Editorial Board of *Frontiers in Plant Sciences*.
- Since February 2017, Yann Guédon is an Associate Editor of *Frontiers in Plant Science*, section Technical Advances in Plant Science.
- Since March 2017, Christophe Pradal is Associate Editor of *BMC Plant Methods*.

8.1.1.2. Reviewer - Reviewing Activities

- C. Godin has been reviewing for several journals in plant sciences and modelling: *PNAS*, *PLoS Computational Biology*, *Annals of Botany*, *Frontiers in Plant Science*.
- Y. Guédon has been reviewing for several journals: *Agricultural and Forest Meteorology*, *Annals of Botany*, *Frontiers in Plant Science* and *Statistics and Computing*.

- F. Boudon has also been reviewing for several journals: International Journal of Computer Games Technology, Computer and Graphics, Frontiers in Plant Science, Plant Methods, PLoS One, Presence, Annals of Botany, Biology Open, Developmental Dynamics.
- O. Ali has been reviewing papers submitted in Scientific Report and Development.
- C. Pradal has been reviewing papers submitted in SoftwareX and Frontiers in Plant Science.

8.1.2. Invited Talks

- C. Godin has been invited to give a talk at the Mathematics for Developmental Biology meeting, held at the BIRS Center for Mathematics in Banff, Canada.
- C. Pradal has been invited to give talks about Multiscale Plant Hydraulics in the kickoff meeting of the ANR-DFG Project FSPM Apple, about Modularity in FSPM in the national meeting of the INRA MFPC network, and about Reproducibility of computational experiments in high-throughput phenotyping in the GDR MADICS at Paris-Saclay.

8.1.3. Leadership within the Scientific Community

8.1.3.1. Christophe Godin:

- is member of the Board of the Functional Structural Plant Models series of conferences.
- is co-coordinator with Patrick Lemaire of the 4th Research Axis on Imaging in Biology and Modeling of the Institute for Computational Biology (IBC) of Montpellier.

8.1.3.2. Yann Guédon:

- is a member of the committee board of the CIRAD/INRA/Montpellier SupAgro AGAP research unit and the scientific lead of the Models and Methods for Plant Phenotyping (M2P2) team.
- is member of the ERCIM working group on Computational and Methodological Statistics.

8.1.3.3. Christophe Pradal:

- is a member of the INRA expert scientific commissions (CSS Ecophysiologie, géométrie et biologie intégrative des plantes) that assesses INRA individual researcher activities.
- is a member of the HCERES expert scientific commissions that assesses national research organisations.

8.1.3.4. Christian Fournier:

- is a member of the INRA engineer evaluation commission (CEIMÉthodes Pour la Recherche : Biologie végétale / Domaine Informatique, bio-informatique, statistiques et calcul scientifique) that assesses INRA individual engineer activities.

8.1.4. Scientific Expertise

- C. Godin is a member of the International Scientific Advisory Committee of the new Plant Phenotyping and Imaging Research Centre (P2IRC), Saskatchewan, Canada.
- C. Godin is a member of the Review and Mentoring committee of James Lock's group in Sainsbury Lab, Cambridge, UK.

8.1.5. Research Administration

- C. Godin is a member of the project committee board at Sophia-antipolis Méditerranée Reacher Center.
- C. Godin is a member of the Scientific board of the modeling axis of Labex NUMEV and a member of the direction board of the institut de biologie computationnelle (IBC) in Montpellier.

8.2. Teaching - Supervision - Juries

8.2.1. Teaching

Master : C. Godin, Computer & Discrete Geometry & Graphics, 9h, (M1), universit  de Montpellier, Fr

Master : C. Godin, Introduction to Plant Modeling, 25h, (M2), universit  de Montpellier, Fr

Master : C. Godin, Mathematical Modelling of Phyllotaxis, 4h, (M2), universit  de Montpellier, Fr

Master : Y. Gu don , Stochastic processes, 16h, (M2) universit  de Montpellier, Fr

Master : F. Boudon, Computer Graphics, 18h, (M2) universit  de Montpellier, Fr

Master : C. Pradal, Curves & Surfaces, 4.5h, (M2) universit  de Montpellier, Fr

Master : P. Fernique, Stochastic processes, 16h, (M2) universit  de Montpellier, Fr

Doctorat : C. Godin, Animal & Vegetal Morphogenesis, 35h, ENS Paris, Fr

Doctorat : C. Godin, Modelling Plant Development, 6h, E  cole de Physique des Houches, Fr

8.2.2. Supervision

PhD in progress : Anne Schneider, "*Modeling branching in Roses*", Angers University, Jessica Bertheloo, C. Godin, F. Boudon.

PhD in progress : Hadrien Oliveri, "*Mechanical modeling of organ growth*", Montpellier University, C. Godin, J traas and O. Ali.

PhD in progress : Jean-Louis Dinh, "*Coupling flux and growth models in plant development*", Nottingham University, C. Hodgman, C. Godin.

PhD in progress : Jean-Philippe Bernard, "*Meshless methods for organ development*", Montpellier University, C. Godin, B. Gilles.

PhD in progress : Severine Persello, "*Structural-Functional modeling of yield and fruit quality build-up of the mango, and integration of the effects of cultural practices*", Montpellier University, F. Normand, I. Grechi, F. Boudon.

PhD in progress : Marc Labadie, Study of the alternation between vegetative and floral development in strawberry: spatio-temporal architecture and analysis of key flowering genes, Bordeaux University, B atrice Denoyes, Yann Gu don.

8.2.3. Juries

C. Godin was president of the CR-concours at Inria for the Sophia-Antipolis Me  diterrane  e center.

C. Godin was president of a Professor concours at ENS de Lyon.

C. Godin was the President of the Jury of Elise Laruelle's defence (AgroParitech).

8.3. Popularization

- C. Godin gave an invited 2 hours seminar to 4 classes of high-school students for the Math week (March) at the Lyce  e International de Valbonne, France.
- C. Godin gave a couple of 2h classes at Lyce  e Pompidou (Montpellier).
- C. Godin participated to the writing of a collective book reviewing the recent discoveries in Biology and dedicated to a wide audience including politicians and medias.
- O. Ali is a member of the Sam & You newsletter (the newsletter of the SAM Inria research center) writing committee.
- H. Oliveri took part in the Class'Code Initiative, a Mooc produced by Inria and OpenClassRoom providing supports and guidelines for people wanting to teach computer science to young childrens.

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