We are IntechOpen, the world's leading publisher of Open Access books Built by scientists, for scientists

6,900
Open access books available

185,000
International authors and editors

200M
Downloads

Our authors are among the

154
Countries delivered to

TOP 1%
most cited scientists

12.2%
Contributors from top 500 universities



WEB OF SCIENCE™

Selection of our books indexed in the Book Citation Index in Web of Science™ Core Collection (BKCI)

Interested in publishing with us?
Contact book.department@intechopen.com

Numbers displayed above are based on latest data collected.
For more information visit www.intechopen.com



23

Automatic Approaches to Plant Meristem States Revelation and Branching Pattern Extraction: A Review

Hongchun Qu and Qingsheng Zhu
College of Computer Science, Chongqing University
P.R. China

1. Introduction

Plant branching pattern, depends on the nature and on the spatial arrangement of each of plant parts (i.e. botanical entities, metamers or growth units, etc.), at any given time, is the expression of an equilibrium between endogenous genetic controlled growth processes and exogenous stimulations exerted by the nutrients supply and the micro-environmental climate, as well as the competition or cooperation from population (community). From botanical perspective, this expression can be viewed as the result of the repetition of elementary botanical entities through the three main and fundamental morphogenetic processes of growth, branching and reiteration (Barthélémy & Caraglio, 2007). Repetition of these entities induces gradual or abrupt changes reflecting different stages of differentiation in the meristems (Nicolini & Chanson, 1999), which are ordered in time and correspond to the notion of physiological age of meristems (Barthélémy & Caraglio, 2007).

Due to both endogenous control and exogenous effects, the development of meristem leads to some basic branching patterns that make the whole plant exhibits complex structures (Barthélémy & Caraglio, 2007). These basic branching patterns can be roughly divided into four types: 1) terminal or lateral branching, no branching (depends on the position of the active meristem, is the apical or axillary one), 2) monopodial or sympodial branching (depends on the indeterminate or determinate growth pattern of meristem, as shown in Fig. 1, Harris & Woolf, 2006), 3) immediate or delayed branching (depends on immediately or delayed initiation of meristem), and 4) rhythmic or continuous branching (depends on whether all the axillary meristems of a stem develop into lateral axes, or whether lateral axes are grouped as distinct tiers with an obvious regular alternation of a succession of unbranched and branched nodes on the parent stem).

As an intelligent organism (Trewavas, 2005), plant exhibits some kinds of intelligent behavioral capabilities through phenotypic plasticity (e.g. phototropism) other than movement, which is the nature of animals or human beings. This phenomenon demonstrates that the development of plant results from the mutual effect between structure and endogenous physiological process. The branching pattern analysis make it possible to identify these endogenous processes and to separate them from the plasticity of their

expression resulting from external influences by means of observation and sometimes experimentation. Applicable to any kind of plant, branching pattern analysis has proved to be one of the most efficient means currently available for the study of the organization of complex arborescent plants. Therefore, the study of plant pattern and revelation of the corresponding meristem states will lead us to get a deeper and better understanding of plant development and also provide a convenient tool for growth rules construction for functional-structural plant modelling (virtual plants), which emerged as a new scientific discipline in the last decades.

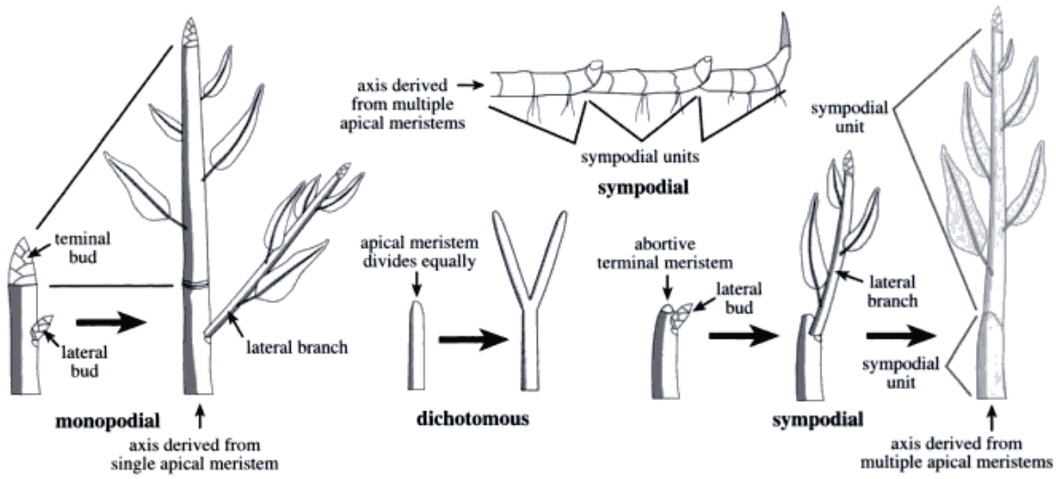


Fig. 1. Stem branching patterns (Source: Harris & Woolf, 2006).

Nevertheless, plant branching pattern extraction and the corresponding meristem states revelation by no means a simple task. The extensive methodology used for analyzing the structures produced by meristems needs to be investigated. 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 (Fig. 2). Moreover, this analysis needs to be carried out at different spatial and temporal scales. Generally, the implementation of plant pattern extraction is usually composed of three steps: first, acquiring plant topological and geometrical data via manual work, image processing and pattern recognition, or 3D laser digitizing; second, analyzing these data to reveal hidden relations between plant entities (metamers or growth units) through statistical computing or topological operation; third, extracting the evolutionary rule set that reflecting the variation of meristem states from the second step to validate analysis and to guide the plant modelling. Therefore, the plant branching pattern extraction could be regarded as a complex machine learning system, in which many software and hardware tools as well as artificial intelligence methods are involved.

This chapter reviews detailed methods and approaches in relation to the complex machine learning system of automatic branching pattern extraction. First, we will introduce plant topological and geometrical description, encode database or structure used for storage of measured plant structure. And then, the most important part of this chapter, we will discuss recent methods and theories used for plant topology and geometry acquisition, statistical and structural analysis as well as branching rule extraction for any species of plant. Finally,

some unsolved problems and challenges need to be addressed in future research are outlined.

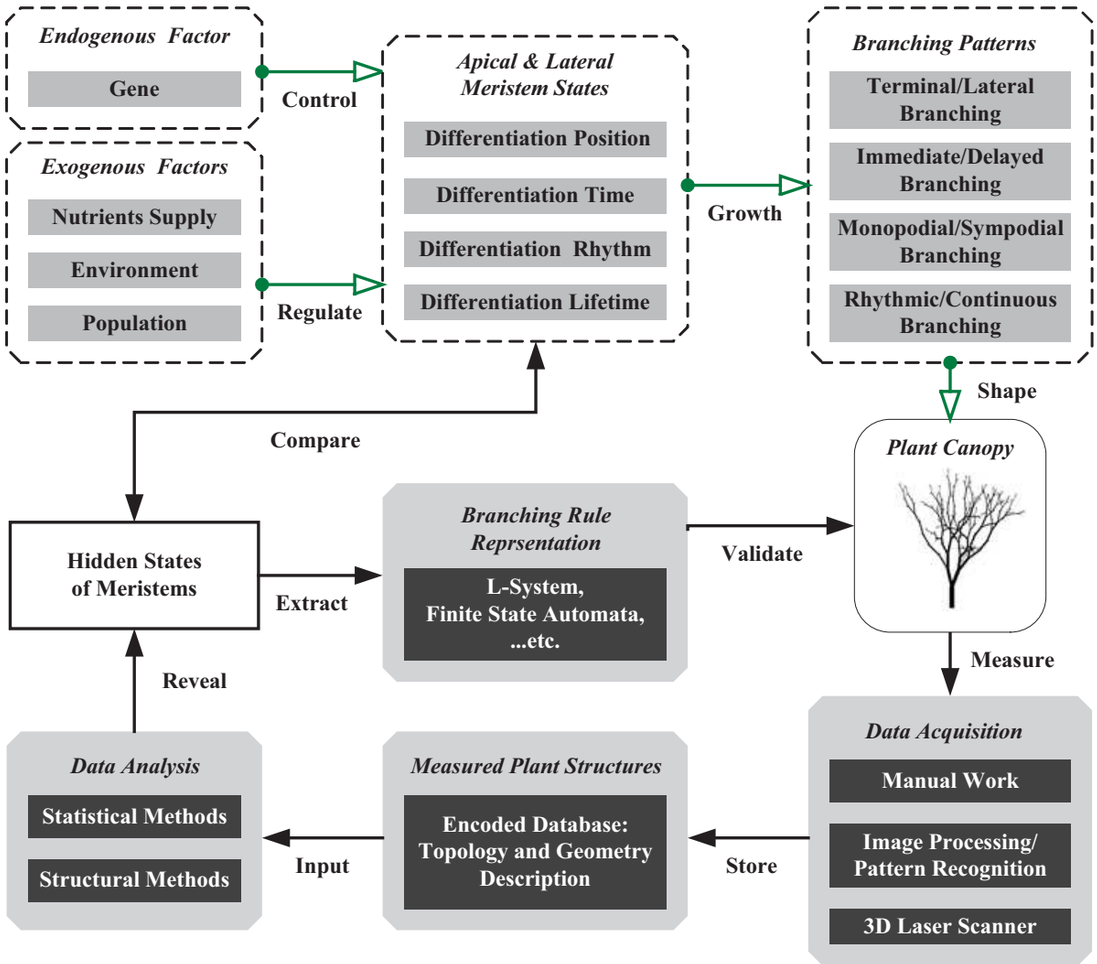


Fig. 2. Schematic description of meristem physiological states revelation and plant branching pattern extraction. Dash-line marked rounded-rectangles and green arrows represent plant branching mechanism and process, while the gray rounded-rectangles and dark arrows represent the branching pattern extraction process.

2. Plant Data Acquisition

Data acquisition is the starting point for extraction of plant branching patterns, yet the type of data used may vary greatly. The description of plant architecture therefore must be investigated and the corresponding architecture model or data structure for recording measured data needs to be established prior to the process of plant architecture measurement.

2.1 Description of plant architecture

As discussed by Prusinkiewicz (1998), on the most qualitative end of the spectrum, the architectural unit (metamer or growth unit) introduced by Edelin (1977) is well-suited to characterize plants within the conceptual framework of architectural models proposed by Hallé et al. (1978). The morphological characteristics incorporated into an architectural unit must be directly observed, estimated or measured. They include: the orientation of branches (e.g. orthotropic or plagiotropic), type of branching (monopodial or sympodial), persistence of branches (indefinite, long or short), degree of lateral shoot development as a function of their position on the parent branch (acrotony, mesotony or basitony), type of meristematic activity (rhythmic or continuous), number of internodes per growth unit, leaf arrangement (phyllotaxis), and position of reproductive organs on the branches (terminal or lateral). An authoritative description of these and other notions used to specify plant architecture was presented by Bell (1991) and Caraglio and Barthélémy (1997). The architectural unit acting as the basic component that make up the canopy consist of a set of these characteristics, and satisfy with all branch orders. Examples of architectural description of specific plants in terms of architectural units also have been investigated by Atger and Edelin (1995).

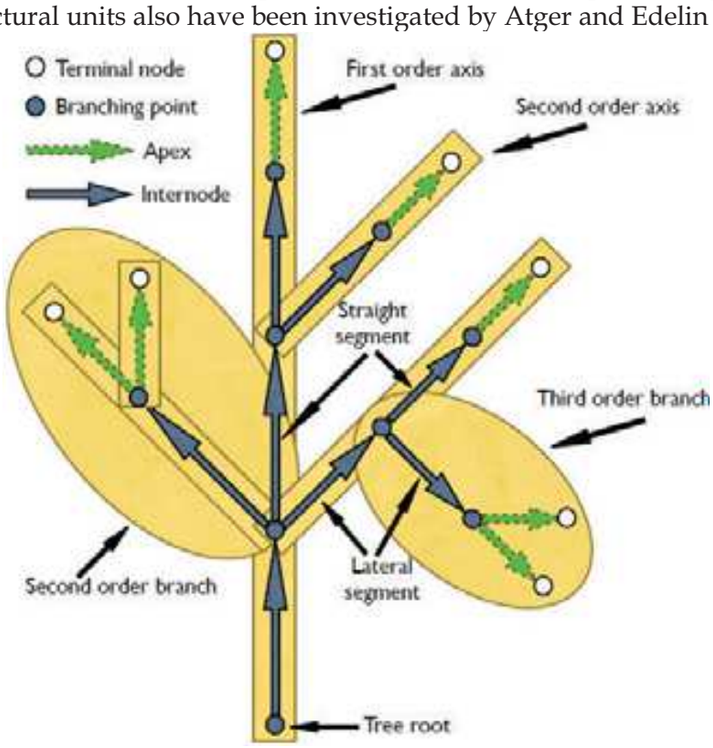


Fig. 3. Plant architecture representation: the multiscale tree graph (MTG). (Source: Godin and Caraglio, 1998).

Nevertheless, this qualitative characterization of architecture unit is insufficient to construct a spatial structure for a plant. The relations among architecture units are exact needed to be taken into consideration. Plant architecture is a dynamic expression of these basic architecture units, in the sense that the observed structural features reflect plant development over time. As stated by Hallé et al. (1978), "The idea of a form implicitly contains also the history of such a form." Correspondingly, the architecture of plant canopy

may be viewed as a sequence of branch patterns created over time, rather than merely a set of branch patterns. "In this sequence, leading from axis 1 to the ultimate axes following the specific branching pattern, each branch is the expression of a particular state of meristematic activity and the branch series as a whole can be considered to be tracking the overall activity" (Barthélémy et al., 1991).

Plant maps (McClelland, 1916; Constable, 1991) may be considered the first attempt to characterize the structure for particular plants. This method of description captures the branching topology, i.e. the arrangement of branches, organs, and other features with no respect to the plant's geometry (e.g. the lengths of internodes and the magnitudes of the relative branching angles: the azimuth and the inclination). Plant maps can be recorded using different notations, e.g. Hanan and Room (1996) adapted the idea of plant maps using the bracketed string notation introduced by Lindenmayer (1968), which can be regarded as one of the most notable characters of the L-System (Prusinkiewicz et al., 1990). A different notation was presented by Rey et al. (1997). A refinement of the topological description of plants, named multiscale tree graphs (MTG, as shown in Fig. 3) has been proposed by Godin and Caraglio (1998). This makes it possible to specify plant topology at different scales and levels of detail, and incorporate temporal aspects into a single framework. Multiscale tree graphs form the basis of a coding language implemented in AMAPmod, an interactive program for analyzing the topological structure of plants (Godin et al., 1997a,b). The advantages and detailed descriptions for multiscale representation of plant architecture have also been discussed by Remphrey and Prusinkiewicz (1997).

For each species of plants, at each stage of development and in each environmental condition, the qualitative and quantitative topology and geometry can be measured via manual labour, depending on the complexity of the architecture. Small plants can be observed, manipulated and measured directly but this work is hardly accomplished when plants reach several metres high, furthermore it can be extremely time consuming. Therefore, automatic acquisition methods are preferred, e.g. image processing and pattern recognition, 3D magnetic-scan based digitizing as well as 3D laser scanning techniques.

2.2 Image-based Approaches

Varjo et al., (2006) proposed a digital camera based method for estimating the stem diameters of growing trees for forest inventory purposes. The imaging system consists of a single camera, a laser distance measurement device and a calibration stick placed beside the tree to be measured. To carry out the task, the camera geometry parameters are first determined using linear pinhole camera and nonlinear lens distortion models. In addition of the accurate camera calibration, the viewing geometry has to be determined for 3-D measurement purpose with the help of the calibration stick. The estimation of the stem diameters is carried out by combining the stem curve information from the image with a priori stem form model.

Lin et al. (2001) reported capturing top-view and lateral images taken from two color CCD cameras to measure several geometric features, such as seedling height, average projection area, leaf area index, leaf and stem node number, coordinates of stem nodes and leaf endpoints. The position and approximate shape of overlapped seedling leaves were initially located using elliptical Hough transform. Based on this information, the hidden leaf boundary can be further reconstructed and the total leaf area can be calculated without pre-determined calibration relationship. This image-processing algorithm is incorporated into a

stereo machine vision system to dynamically measure selected vegetable seedlings. However, this approach is better for small plant such as vegetables and bushes, not well-suited for large woody plants because of the difficult of image capturing.

Biskup et al. (2007) presented an area-based, binocular field stereo system to measure structural canopy parameters such as leaf angle distribution by using techniques such as calibration of cameras and stereo rig, epipolar rectification, colour segmentation of foliage and stereo matching.

Recently, Qu et al. (2009) proposed an image-analyzing-based method to analyze tree structure. In their method, any hand-held cameras with enough resolution (megapixels) can be employed to capture the image sequences of the unfoliaged deciduous plant of interest from a number of different overlapping views. Usually, about 30 to 45 images need to be taken, with coverage 360° around each plant. Then the camera parameters and a collection of 3D cloud points were recovered and extracted from point correspondences and running structure from motion on the captured image sequences. Standard computer vision methods (Hartley & Zisserman, 2000) have been used to estimate the point correspondences across the images and the camera parameters. Moreover, the method proposed by Lhuillier and Quan (2005) was used to compute a semi-dense cloud of reliable 3D points in space. Their image-based process shows a reasonable results for 3D skeleton extraction (Fig. 4).

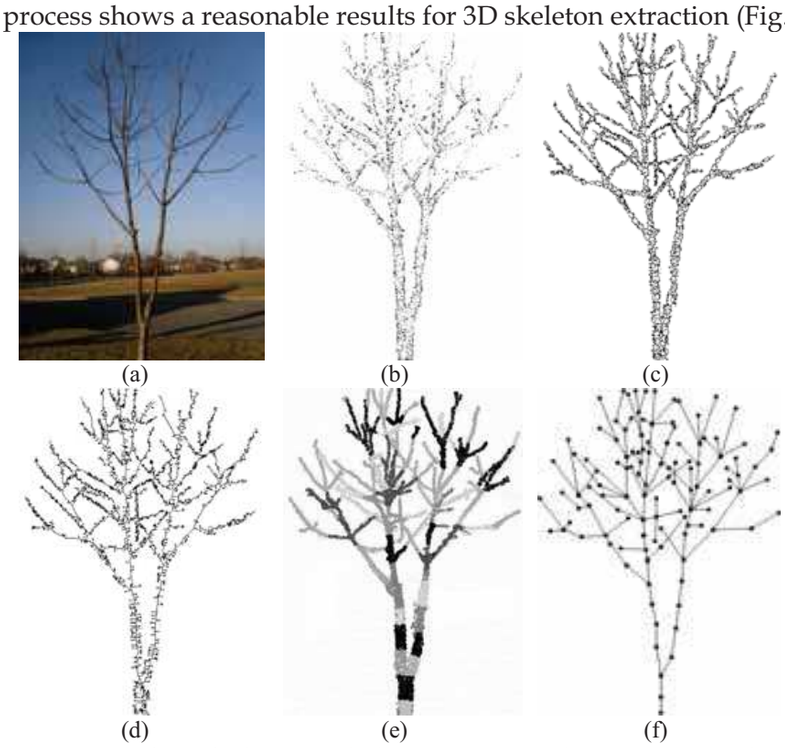


Fig. 4. Image-processing-based plant 3D skeleton recovery. (Source: Qu et al, 2009).

2.3 3D digitizing Approaches

Sinoquet and Rivet (1997) proposed a method for the measurement of the 3D architectural of a 20-year-old and 7-meter-high walnut tree. Their approach combines a 3D digitizing device (3SPACE FASTRAK, Polhemus) associated with the software DiplAmi designed for digitizer control and data acquisition management. It works at the shoot level and

simultaneously measures the plant topology, geometry and the shoot morphology. Di iorio et al. (2005) used a low-magnetic-field digitizing device (Fastrak, Polhemus) to measure the geometry and topology of structural root with a diameter of 1cm for a single-stemmed Quercus pubescens tree. In their method, several root architecture characteristics are extracted by macros, including root volume, diameter, length, number, spatial position and branching order.

The algorithms proposed in (Gorte & Pfeifer, 2004) and (Pfeifer et al., 2004) took laser data as input, and created a voxel-based occupancy grid represetentation of the data. Morphological operations were used to find the underlying branching structure and fit cylinders to the branches. Moreover, these algorithms can be used to extract metric parameters of the tree, such as branch length, radius and rotation angles. Xu et al. (2007) proposed a method to reconstruct realistic looking trees from laser scan data. The laser data is first converted to a points cloud, a graph-based technique is used to find the 3D skeleton, and then the 3D information is used to measure the relative geometric parameters of plant branching structures. A similar approach was employed by Tan et al (2008) to find overall branch structures, but images instead of laser range scans are used as input, a structure from motion algorithm is used to create a 3D point cloud from the images. The 3D point cloud and the raw images are then used to find the branching structures.

However, aforementioned methods being developed for digitization of plant architecture are based on direct measurements of position and shape of every plant organ in space. Although they provide accurate results, these methods are particularly time consuming. More automatized methods are now required in order to collect plant architecture data of various types and sizes in a systematic way, i.e. these processes need to be completely implemented by hardware (3D scanner) instead of software.

3. Data Analysis

From botanical perspective, plant architecture is the result of repetitions that occur through growth and branching processes. During plant ontogeny, changes in the morphological characteristics of botanical entities exhibit either similar or very contrasted characteristics, which can be characterized as homogeneous zones. These homogeneous zones were discovered in most plant species with diverse characteristics (length, number of nodes, number of growth units, number of branches, non-flowering/flowering character) attached to the elementary botanical entities, these botanical entities being either built by the same meristem or derived from one another by branching. These results can be related to the notion of "physiological age of a meristem". The physiological age of a meristem may be defined by a particular combination of morphological, anatomical and functional characteristics of a given botanical entity produced by this meristem (Barthélémy et al., 1997; Barthélémy & Caraglio, 2007). For identifying the physiological age of plant entities, it seems at first sight the most relevant to analyze directly the whole plant structure described at a given scale is to use appropriate analysis methods.

In the last two decades, coupled with precise morphological observations, architectural analysis of several plant species (Caraglio & Edelin, 1990) revealed that, under given environmental conditions, the structure and features of a particular elementary botanical entity are predictable and strongly dependent on both (1) its topological location in the comprehensive architecture of a plant and (2) the ontogenetic stage of the organism. At the

level of the whole plant, the "morphogenetic gradients" notion was defined (Barthélémy et al.,1997) in order to take into account the intrinsic organization rules of plant structure and branching pattern and was shown to be a powerful concept (Prusinkiewicz et al., 2001) to explain the observed structure and series of modifications of botanical entities during the ontogeny of any plant species.
In order to enhance the understanding of this filed, some frameworks of investigation are required to reveal the hidden effects (the morphogenetic gradients) of the ontogenetic growth behavior, which should rely on appropriate analysis methods (most being statistical approaches). One challenge of this work is the complexity of the data which are tree-structured with variables of heterogeneous types (binary, count, quantitative, etc.) attached to each botanical entity. In the following section, we will focus on the discussion of statistical approaches to plant architecture and branching pattern, which are organized as the order of structural complexity: from axis to the entire shoot system.

3.1 Statistical Approaches

As discussed by Costes and Guédon (2002), it has been shown that over several growth periods, the growth and consequently the number of lateral, decreases rapidly with ageing (Ouellette & Young, 1995). Such a decrease in the growth and branching characteristics with plant development and ageing has been represented by Gatsuk et al. (1980) and Barthélémy et al. (1997) and has been discovered in most woody plants. As a consequence, when growing conditions are keeping optimal, the first annual growth of the stem developing from the grafted bud is the longest in the tree and bears the limbs which will later make up the plant architecture. This make it possible that evaluate plant growth and branching habits by analyzing the branching pattern of the first annual shoot of the trunk.
To test the aforementioned assumption, Costes and Guédon (2002) proposed a method of branching pattern analysis on 1-year-old trunks of six apple cultivars (Malus domestica Borkh.) using the AMAPmod software (developed by Godin et al., (1997,1999). Before the analysis procedure, the number of metamers (White, 1979), the location and the length of the sylleptic shoots were recorded from the shoot that had developed from the retained bud at the end of the first year of growth. Furthermore, at the end of second year of growth, three other types of axillary bud fate which led to proleptic development were recorded, they include: 1)spur or short shoot consisting of preformed organs only, with no or little elongation of the internodes, 2)long shoot, where the corresponding internodes are elongated and 3) bourse, resulting from the differentiation of the meristem into an inflorescence after the development of a few preformed leaves. Then the branching model on the trunks of these 1-year-old apple cultivars was established using the Hidden semi-Markov chain (HSMC, as shown in Fig. 5), which is particularly useful for identifying homogeneous zones within sequences and detecting transitions between zones (Ephraim & Merhav, 2002). In the model each state corresponding to a branching zone is denoted as a circle and the possible transitions between states are represented by arcs associating with probabilities. The occupancy distributions are listed above the corresponding states, as are the possible lateral types (denoted by symbol: 0, latent bud; 1, proleptic spur; 2, proleptic long shoot; 3, bourse; 4, sylleptic shoot) observed in each state.

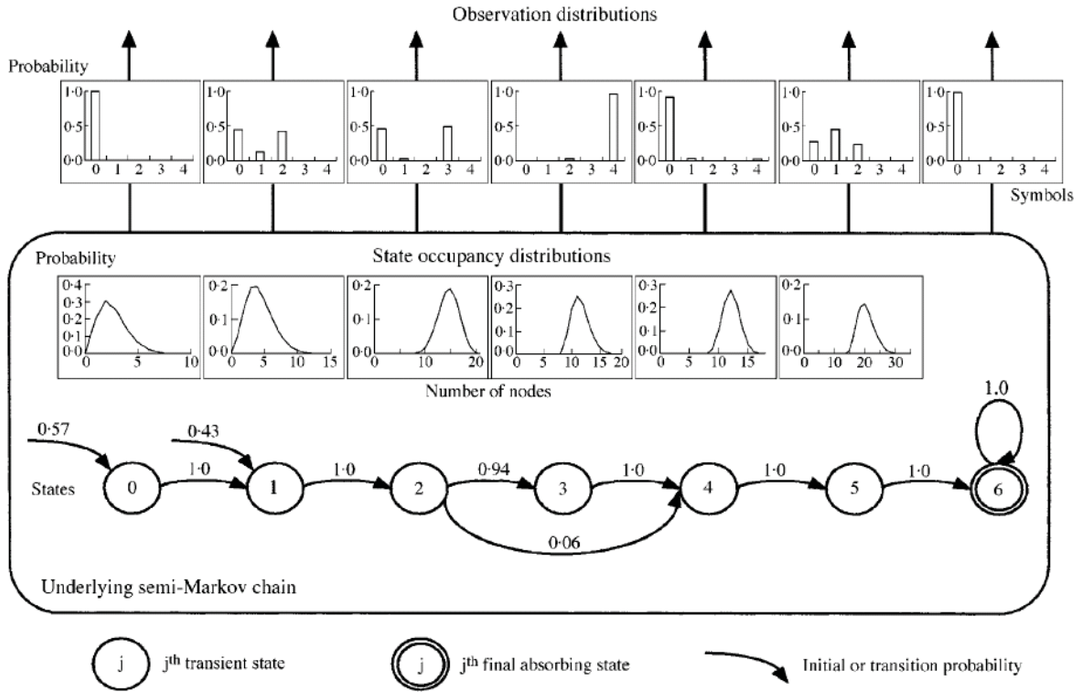


Fig. 5. Modelling branching on 1-year-old trunks using a hidden semi-Markov chain. (Source: Costes and Guédon, 2002)

Their analysis results show that the succession of lateral types along trunks as discrete sequences highlighted the existence of successive zones within which the lateral type composition was homogeneous, but changed between zones. The five zones that were common to and located in the same position in all cultivars studied demonstrate that successive developmental stages occur in the same order over a growing season and can be used to explain the fate of meristems.

Although plant architecture are composed of repetition of growth units (White, 1979; Barlow, 1994), these growth units always show diversity on length with plant age and branching order (Gatsuk et al., 1980; Barthélémy et al, 1997). Plant branching patterns are likely to change with the length of growth units depending on plat growth stage (Costes et al. 2003) . To investigate this phenomenon, Renton et al. (2006) use the Hidden semi-Markov chain model to explore the similarities and gradients in growth unit branching patterns during plant ontogeny. Their experimental data (two 6-year-old Fuji apple trees) were encoded into a database corresponding to entire plant described at the node scale. Within this database, four types of growth units were measured: short (length < 5cm), medium (length between 5 and 20 cm), long (length > 20 cm) and floral growth units. And accordingly, five types of lateral growth were identified: latent buds, short lateral growth units, medium lateral growth units, long lateral growth units and floral growth units. Their Hidden semi-Markov chain model relies on three assumptions: 1) the branching types within a different zones (i.e. hidden states) are independent of growth unit length, year of growth and branch order, 2) each branching zone may be present or absent depending on

growth unit length, year of growth and branch order, and 3) some branching zones may be longer or shorter, depending on growth unit length.

Analysis results of Renton et al. (2006) show that growth branching patterns exhibited both similarities and gradients during plant ontogeny. The degree of similarity of growth units over the years depends on their sharing certain zones, the floral and the short-lateral zones. Complex branching structures with more than one median branching zone tended to decrease in number towards the periphery, while the percentage of unbranched medium growth units progressively increased. Two phenomena also have been discovered: first, the two median zones disappeared with increasing plant age and branch order and second, the floral zone length decreased with the parent growth unit length.

The aforementioned statistical analysis of sequential data from plant architecture are mainly based on Markovian model, for instance the Hidden semi-Markov chains for investigating homogeneous zones of botanical entities (e.g. growth units). These models, although accurately accounting for the structure contained along remarkable paths in the plant (e.g. a plant trunk), are not suited for identifying tree-structured zones, because the dependencies among botanical entities of disjoint sequences are eluded. The complete topology has to be included in the investigation for the existence of multiple dependent successors or descendants to be considered in the distribution of zones. The statistical framework of the Hidden Markov tree (HMT) introduced by Crouse et al. (1998) in the signal-processing engineering just provides the appropriate solution for the analysis of tree-structured data.

Durand et al. (2005) proposed the Hidden Markov tree model to label the homogeneous zones in plant, which architecture is modelled by assigning one hidden state to each growth unit. The hidden state represents the class of the growth units. Each class contains growth units that have similar statistical properties or attributes such as the number of internodes, connection type (succession or branching), etc. Although the HMT is quite close to the Hidden Markov chains, both of which have the same parameter set and are based on local dependency assumptions between hidden states, the parameter estimation (EM algorithm, refer to Arthur Dempster et al. 1977) for HMT is different from Hidden Markov chains (Durand et al. 2004). Two successive steps: the parameter estimation from the measured entities and state tree restoration are executed in Durand et al. (2005) proposed approach. The state tree restoration makes the underlying zones (i.e. the hidden states) directly apparent : different zones in a same state have equivalent attribute distributions. The different distributions can be interpreted as an underlying stage of differentiation: the physiological age of the meristems. The plant is therefore automatically segmented into comparable parts, whereas states changes highlight where the ruptures (physiological states of meristems) are (as shown in Fig. 6). This HMT model assume that the transitions of hidden states conform to the first-order semi-Markov dynamics, because the first-order model is enough to reflect the statistical properties of plant and is easy to be learned. However, from a biological point of view, it is as yet a simplified assumption.

Plant development is controlled by the combined effect of gene activity and environmental constraints, which in turn combine with ontogenetic gradients. At a given date, a plant architecture is thus the outcome of three complex combination: 1) an endogenous component which is assumed to be structured as a succession of roughly stationary phases separated by marked change points asynchronous between individuals (Guédon et al., 2007), while the 2) environmental component which regulate the plant development are mainly of climatic origin such as light, rainfall or temperature, 3) the individual component

corresponds to the local environment of each individual such as pathogen infestation or competitions between trees for light or nutrient resources. These factors are rarely measurable and not considered by aforementioned approaches.

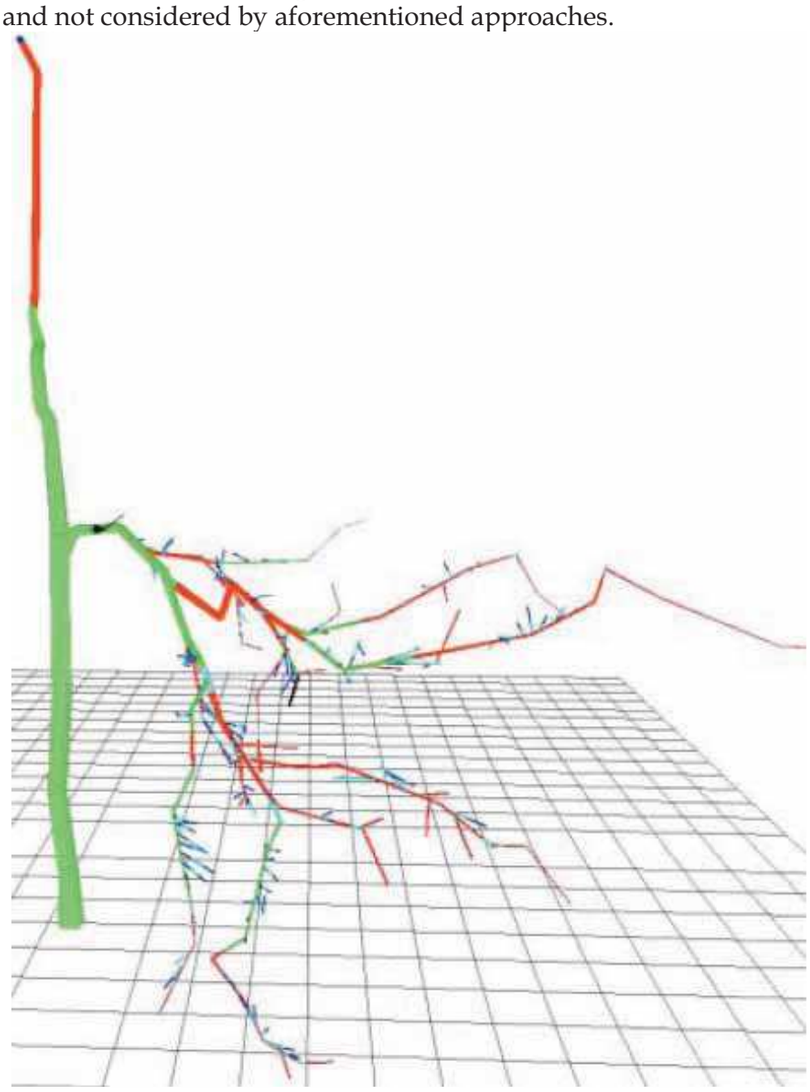


Fig. 6. Restored hidden state tree for the apple tree data set. Each growth unit is coloured according to its hidden state. (Source: Durand et al. 2005).

Incorporating both the influence of environmental variables and inter-individual heterogeneity in a hidden Markovian model is a challenging problem. Guédon et al. (2007) proposed a set of methods for analyzing the endogenous and the exogenous components. In particular, hidden semi-Markov chains with simple observation distributions were applied to plant growth data. In this case, the underlying semi-Markov chain represents the succession of growth phases and their lengths while the environmental component is characterized globally. Hidden semi-Markov chains (Guédon, 2003) generalize hidden Markov chains (Ephraim and Merhav, 2002) with the distinctive property of explicitly modeling the sojourn time in each state. Based on above works, Chaubert-Pereira et al.

(2008) introduced semi-Markov switching linear mixed models that generalize both Markov switching linear mixed models and hidden semi-Markov chains. These models can be regarded as a finite mixture of linear mixed models with semi-Markovian dependencies and make it possible to identify and to characterize the different growth components (e.g. endogenous, exogenous effects and competition or cooperation from population) of plants. The utilization of climatic covariates and individual-state-wise random effects renders the endogenous growth component more synchronous between individuals than with a simple Gaussian hidden semi-Markov chain. Moreover, the behavior of each plant within the population can be explored on the basis of the predicted individual-state-wise random effects.

Up to now, approaches we discussed merely focus on the topological relations among botanical entities of plant. However, the geometry of plant entities and spacial architecture of them are equally important to the revelation of meristems' hidden states, and furthermore, these information also make great help to plant architecture 3D modelling and reconstruction. Wang et al. (2006) proposed a novel tree modeling approach, efficiently synthesizing trees based on a set of tree samples captured from the real world. They designed a two-level statistical model for characterizing the stochastic and specific nature of trees. At the low level, the plantons, which are a group of similar organs, to depict tree organ details statistically. At the high level, a set of transitions between plantons is provided to describe the topological and geometrical relations between organs. The authors designed a maximum likelihood estimation algorithm to acquire the two-level statistical tree model from single samples or multi- samples.

3.2 Structural Analysis-based Approaches

As reviewed as Barthélémy and Caraglio (2007), most plants repeat their architectural unit during their development, late in ontogeny. Oldeman (1974) named this process "reiteration" and defined it as a morphogenetic process through which the organism duplicates its own elementary architecture, i.e. its architectural unit at different scale (node, metamer, growth unit, etc.). The result of this process is called a "reiterated complex" (Hallé et al., 1978; Barthélémy et al., 1988, 1991) or a "reiterate" (Millet et al.,1998). This property of plant architecture can be also called the "self-similarity" and consequently, provides an alternative to investigate the plant architecture and branching pattern.

Plant structures are usually represented by either ordered or unordered rooted tree (Prusinkiewicz & Lindenmayer, 1990; Godin & Caraglio, 1998). The intrinsic property of self-similarity make plant structure has some kind of redundancy, in some sense, that is the tree structure (graph) can be reduced to a minimum structure (graph) with the isomorphic structure to the previous one. The graph isomorphism can be defined as the edit-distance between two structures, as stated by Ferraro and Godin (2000). To study the redundancy of structure embedded at various levels in tree architectures, Godin and Ferraro (2009) investigated the problem of approximating trees by trees with particular self-nested structures. Self-nested trees are such that all their subtrees of a given height are isomorphic. Their investigation show that these trees present remarkable compression properties, with high compression rates. In order to measure how far a tree is from being a self-nested tree, a quantitative measure of the degree of self-nestedness for any tree has been introduced. For this, a self-nested tree has been constructed to minimize the distance of the original tree to the set of self-nested trees that embed the initial tree. To solve this optimization problem, a

polynomial-time algorithm has been designed to make it quantify the degree of self-nestedness of a tree in a precise manner. The distance to this nearest embedding self-nested tree (NEST) is then used to define compression coefficients that reflect the compressibility of a tree.
From the view point of the structural analysis of botanical plants, one therefore can give a biological interpretation of the NEST of a tree based on the hypothesis that isomorphic tree structures at macroscopic levels are actually produced by meristems in identical physiological states. This makes it possible to show that the reduction graph of the NEST of a plant may be interpreted as the maximum sequence of differentiation states that any meristem of a plant may go through. Analysis results showed that the NEST of one plant may be interpreted in biological terms and reveals important aspects of the plant growth (Barthélémy and Caraglio, 2007).

4. Results Utilization

The statistical and topological analysis approaches discussed above make it possible to formally reveal the sequences of meristem physiological state differentiation corresponding to each axis of a given plant. These open up the perspective to use such an analysis on various plant species as a guiding principle to develop some applications or functional-structural plant models, and even to further explore the notion of meristem state and differentiation at a bio-molecular and genetic levels, in the spirit of the pioneering work described in (Prusinkiewicz et al., 2007).



Fig. 7. Simulated apple trees using the MAPPLET model. (Source: Costes et al. 2008).

A new type of structure-function model named MAPPLET (Markov Apple Tree) has been developed by Costes et al. (2008). In MAPPLET, the statistical approach, which is inspired by the hierarchical Hidden Markov model has been carried out to model the development of apple trees (over the first six years of the growth). The tree topology of MAPPLET, i.e. both the succession of growth units along axes and the branching structures of growth units at node scale are controlled by the hidden states and spatial transitions between them, which are the results of the statistical approach: the Hidden Markov model. Moreover, the biomechanical model of MAPPLET simulates the bending of branches under fruit and branch weight. Therefore, from the global perspective, the MAPPLET is an integrated developmental framework can capture both the apple tree topology and its form (the shape of the branches, as determined dynamically by the gravity and the wood properties). The core simulation of MAPPLET is implemented using a L-system implemented with the L+C language (Karwowski & Prusinkiewicz, 2003) with which the statistical analysis module of

V-Plants (Renton et al., 2006) has been integrated. The simulation results of MAPPLET are shown in Fig. 7.

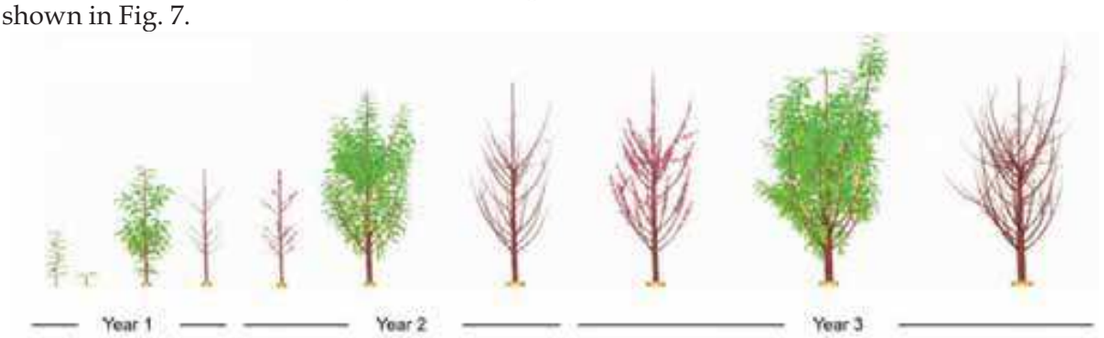


Fig. 8. L-Peach model output shows the development of the structure of a 3-year-old unpruned peach tree. (Source: Lopez et al., 2008).

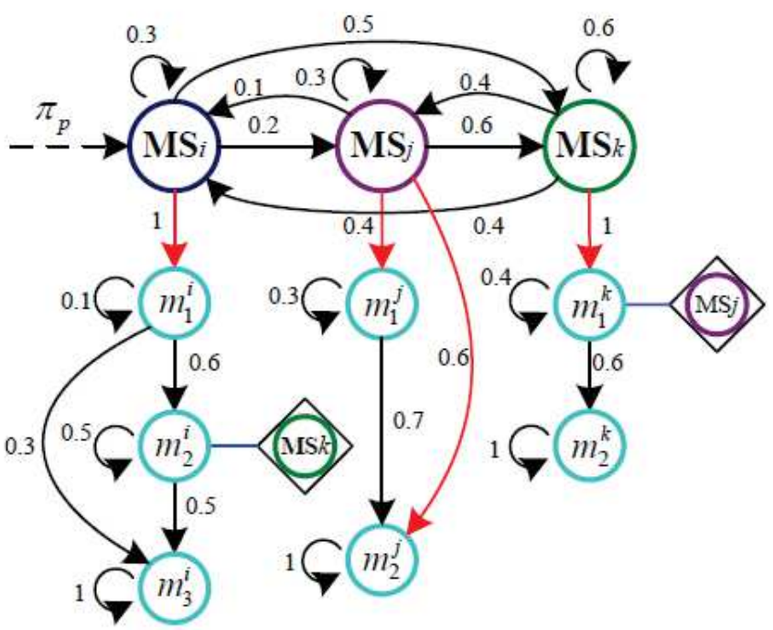


Fig. 9. Schematic structure of the Bidimensional Hierarchical Automaton (BHA), where cycles marked with $MS_{i,j,k}$. etc. represent the physiological states of meristems (hidden states of the Hidden Markov tree model), while the light blue cycles denote the different types of metamers (with different length of internodes). (Source: Qu et al., 2008).

Following this first integration of advanced stochastic processes for modeling tree topology with mechanistic processes, the approach was extended through the integration of Markovian models with the carbon-based source-sink model L-Peach (Lopez et al., 2007), which was developed from the original version of L-Peach (Allen et al., 2005). In the newest version of L-Peach, the Hidden semi-Markov chain is used to control the branching structure, it successfully reproduced peach trees that were similar to the peach trees observed in the real world (Fig. 8).

The branching patterns of plants not only can make convenience to the functional-structural plant model, but also open up the new perspective to plant architecture 3D reconstruction (Wang et al., 2006) as well as growth rule extraction (Qu, et al., 2008), which emerges a new scientific attempt. Over the last decades, L-System has been widely used as a powerful tool in plant modeling, in particular the plant branching control. However, it is really a difficult work to manually develop a L-System for a given plant species depending only on imagination or experience. Qu, et al. (2008) proposed a novel approach of automatic L-System discovery via branching pattern analysis of unfoliaged trees. In their approach, three steps are involved for L-System extraction: 1) image processing as well as pattern recognition methods are employed to recover topological and geometrical information for growth units and metamers from multiple images of unfoliaged trees, 2) Markovian methods are used to further analyze data which have been extracted in the first step for capturing the hidden relations between plant entities and, 3)the L-System has been generated via the runtime of a Bidimensional Hierarchical Automaton (BHA), which is constructed from the analysis result of the second step for describing plant branching structure, as shown in Fig. 9.

5. Conclusion

This chapter reviewed the approaches and theories in relation to the plant branching pattern extraction, those include plant architecture description, measurement and acquisition for topology and geometry of plant botanical entities, statistical and structural analysis for the revelation of physiological states of meristem as well as the utilization of these analysis results for plant modelling and 3D structure reconstruction.

The study of plant branching pattern requires detailed metric data about the plant architecture. Acquiring these metric information can be extremely time conuming when using manual labor. To address this issue, many researches contributed to the theoretical and applied approaches to automatically acquire plant topology and geometry, such as 3D laser scanning as well as image recognition. However, there are still some deficits in data acquisition need to be overcome. For instance the image processing based approaches, in which usually several images have been taken, if branch is not seriously occluded, a reasonable 3D branching structure can still be generated, but it will be obviously failed when a branch is fully occluded by other branches or leaves. Moreover, regarding the 3D digitizing approach, more automatized methods are now required in order to collect plant architecture data of various types and sizes in a systematic way, i.e. these processes (including laser scanning, 3D cloud computation and branching skeleton extraction) need to be completely implemented by hardware (3D scanner) instead of software.

Plant branching structure can be interpreted as the indirect transformation of different physiological states of the meristems, thus connected entities may exhibit either similar or very contrasted characteristics. During the last decades, some statistical models (e.g. Hidden semi-Markov chain, Hidden Markov tree, semi-Markov switching linear mixed model, etc.) have been employed by botanists and statisticians to discover and characterize homogeneous entity zones and transitions between them in different temporal scales within plant topological and geometrical data. These analytical methods and models lead to a clustering of the entities into classes sharing the similar statistical properties that help to find the tendency of the differentiation of meristems. One limitation of these stochastic methods

must be mentioned is that one assume that the transitions of botanical entities conform to the first-order Markov dynamics, because the first-order model is enough to reflect the statistical properties of plants and also is easy to be learned. However, from the perspective of botany, it is as yet a simplified assumption. As an alternative approach, analysis of structural similarity has been explored to reduct a complex structure to a simplest one that may be interpreted as the maximum sequence of differentiation states that any meristem of a plant may go through.

In addition, Computer scientists proposed theoretical methods to integrate these hidden relations as growth rules into some classic complex systems such as parametric probabilistic L-System, Bidimensional Hierarchical Automaton, etc. Naturally, the mapping between plant growth process and these complex systems used for plant branching rules description are built. Moreover, these complex systems provide an open interface so that any virtual plants models can access it easily as long as they are compatible with this interface.

6. Acknowledgement

The authors are grateful to the Virtual Plants team (a joint team between INRIA, CIRAD and INRA, France, European Union) for their valuable comments. This research is supported by the National Natural Science Foundation of China (60773082), the National "863" Hi-Tech Research and Development Project of China (2006AA10Z233), the National Study-abroad Project for Joint PhD Program of Key Constructed High Level Universities in China (CSC-2008605048).

7. References

Allen, M. T.; Prusinkiewicz, P. & DeJong, T. M. (2005). Using L-systems for modeling source-sink interactions, architecture and physiology of growing trees: the L-PEACH model. *New Phytologist* 166, 869-880.

Atger, C. & Edelin, C. (1995). Un cas de ramification sympodiale à déterminisme endogène chez un système racinaire. *Platanus hybrida Brot. Acta. Bot.* Vol. 142, 23-30, Gallica.

Barlow, P. (1994). From cell to system: repetitive units of growth in the developement of roots and shoots. In: *Growth patterns in vascular plants* (I. M., ed.), pp. 19-58. Dioscorides Press, Portland.

Barthélémy (1988). Architecture et sexualité chez quelques plantes tropicales: le concept de floraison automatique, University Montpellier II.

Barthelemy, D. (1989). Levels of Organization and Repetition Phenomena in Seed Plants. *Seminar of the French Soc of Theoretical Biology*, pp. 309-323, Solignac Abbaye, France.

Barthélémy, D.; Edelin, C. & Hallé, F. (1991). Canopy architecture. *Physiology of trees* (A. S. Raghavendra, ed.), pp. 1-20, Wiley, London.

Barthélémy, D. & Caraglio, Y. (2007). Plant architecture: A dynamic, multilevel and comprehensive approach to plant form, structure and ontogeny. *Annals of Botany* 99, 375-407.

Barthélémy, D.; Caraglio, Y. & Costes, E. (1997). Architecture, gradients morphogénétiques et âge physiologique chez les végétaux. In: *Modélisation et simulation l'architecture*

des végétaux (d. R. P. Bouchon J, Barthélémy D, ed.), pp. 89-136. Science Update, Paris: INRA Editions.

Bell, A. D. (1991). Plant Form: An Illustrated Guide to Flowering Plants. Oxford Univ. Press, Oxford.

Biskup, B.; Scharr, H.; Schurr, U. & Rascher, U. (2007). A stereo imaging system for measuring structural parameters of plant canopies. *Plant Cell and Environment* 30, 1299-1308.

Caraglio, Y., Barthélémy, D. (1997). Revue critique des termes relatifs à la croissance et à la ramification des tiges des végétaux vasculaires. In: *Modélisation et simulation de l'architecture des végétaux* (D. R. P. Bouchon Jean, Barthélémy Daniel, ed.), pp. 11-87. INRA, Paris.

Caraglio, Y. & Edelin, C. (1990). Architecture et dynamique de la croissance du platane, Platanus hybrida Brot. (Platanaceae) fsyn. Platanus acerifolia (Aiton) Willd.g. In: *Bulletin de la Société Botanique de France, Lettres Botaniques* 137, 279-291.

Constable, G. A. (1991). Mapping the Production and Survival of Fruit on Field-Grown Cotton. *Agronomy Journal* 83, 374-378.

Costes, E. & Guédon, Y. (2002). Modelling branching patterns on 1-year-old trunks of six apple cultivars. *Annals of Botany* 89, 513-524.

Costes, E.; Sinoquet, H.; Kelner, J. J. & Godin, C. (2003). Exploring within-tree architectural development of two apple tree cultivars over 6 years. *Annals of Botany* 91, 91-104.

Costes, E.; Smith, C.; Renton, M.; Guedon, Y.; Prusinkiewicz, P. & Godin, C. (2007). MAppleT: simulation of apple tree development using mixed stochastic and biomechanical models. *5th International Workshop on Functional Structural Plant Models*, pp. 936-950, Napier, New Zealand.

Crouse, M. S.; Nowak, R. D. & Baraniuk, R. G. (1998). Wavelet-based statistical signal processing using hidden Markov models. *IEEE Transactions on Signal Processing* 46, 886-902.

Dempster, A. P.; Laird, N.M. & Rubin, D.B. (1977). Maximum Likelihood from Incomplete Data via the EM Algorithm. *Journal of the Royal Statistical Society. Series B* (*Methodological*) 39, 1-38.

Di Iorio, A.; Lasserre, B.; Scippa, G. S. & Chiatante, D. (2005). Root system architecture of Quercus pubescens trees growing on different sloping conditions. *Annals of Botany* 95, 351-361.

Durand, J. B.; Goncalves, P. & Guédon, Y. (2004). Computational methods for hidden Markov tree models - An application to wavelet trees. *IEEE Transactions on Signal Processing* 52, 2551-2560.

Durand, J. B.; Guédon, Y.; Caraglio, Y. & Costes, E. (2005). Analysis of the plant architecture via tree-structured statistical models: the hidden Markov tree models. *New Phytologist* 166, 813-825.

Edelin, C. (1977). Images de l'architecture des coniferes, Université de Montpellier II.

Ephraim, Y. & Merhav, N. (2002). Hidden Markov processes. *IEEE Transactions on Information Theory* 48, 1518-1569.

Ferraro, P. & Godin, C. (1998). A distance measure between plant architectures. *2nd International Workshop on Functional-Structural Tree Models*, pp. 445-461, Clermont Ferra, France.

Florence Chaubert-Pereira, Y. G.; Christian Lavergne & Catherine Trottier (2008). In: *Markov and semi-Markov switching linear mixed models for identifying forest tree growth components*.

Gatsuk, L. E.; Smirnova, O. V.; Vorontzova, L. I.; Zaugolnova, L. B. & Zhukova, L. A. (1980). Age States of Plants of Various Growth Forms - a Review. *Journal of Ecology* 68, 675-696.

Godin, C. & Caraglio, Y. (1998). A multiscale model of plant topological structures. *Journal of Theoretical Biology* 191, 1-46.

Godin, C.; Costes, E. & Caraglio, Y. (1997a). Exploring plant topological structures with the AMAPmod software: an outline. *Silva Fennica* 31, 357-368.

Godin, C.; Costes, E. & Sinoquet, H. (1999). A method for describing plant architecture which integrates topology and geometry. *Annals of Botany* 84, 343-357.

Godin, C. & Ferraro, P. (2009). In: *Quantifying the degree of self-nestedness of trees. Application to the structural analysis of plants* .

Godin, C.; Guédon, Y. & Costes, E. (1999). Exploration of a plant architecture database with the AMAPmod software illustrated on an apple tree hybrid family. *Agronomie* 19, 163-184.

Godin, C.; Guédon, Y.; Costes, E. & Caraglio, Y. (1997b). Measuring and analyzing plants with the AMAPmod software. In: *Advances in computational life sciences sciences, Vol I : Plants to ecosystems* (P. Michalewicz Maillard, ed.), pp. 63-94, Australia: CSIRO.

Godin, C.; Guédon, Y.; Costes, E. & Caraglio, Y. (1997). measuring and analyzing plants with the amapmod software. In: *Plants to ecosystems-advances in computational life sciences* (M. MT., ed.), Vol. 1, pp. 53-84. CSIRO Publishing, Collingwood.

Godin, C. & Sinoquet, H. (2005). Functional-structural plant modelling. *New Phytologist* 166, 705-708.

Gorte, B. & Pfeifer, N. (2004). Structuring laser-scanned trees using 3d mathematical morphology. *Proceedings of 20th ISPRS Congress*, pp. 929-933.

Guédon, Y. (2003). Estimating hidden semi-Markov chains from discrete sequences. *Journal of Computational and Graphical Statistics* 12, 604-639.

Guédon, Y.; Caraglio, Y.; Heuret, P.; Lebarbier, E. & Meredieu, U. (2007). Analyzing growth components in trees. *Journal of Theoretical Biology* 248, 418-447.

Hallé, F. (1978). Architectural variation at specific level of tropical trees. In: *Tropical trees as living systems* (Z. M. Tomlinson PB, ed.), pp. 209–221. Cambridge University Press, Cambridge.

Hallé, F. O.; R.A.A. & Tomlinson, P.B. (1978). Tropical trees and forests : an architectural analysis Springer Verlag, Heidelberg.

Hanan, J. S. & Room, P.M. (1996). *Virtual plants. A hypertext document and digitizing software distribution*. Cooperative Research Centre for Tropical Pest Management, Brisbane.

Harris, J. & Woolf, M. (2006). Systematic evidence and descriptive terminology. In: *Plant systematics* (M. G. Simpson, ed.). Amsterdam ; Boston : Elsevier/Academic Press, Burlington MA. U.S.A.

Hartley, R. I. a. Z., A. (2000). *Multiple View Geometry in Computer Vision*, Cambridge University Press, ISBN: 0521623049.

Jari Varjo, H. H.; Juha Lappi; Jukka Heikkonen and & Juujärvi (2006). In: *Digital horizontal tree measurements for forest inventory*.

Lhuillier, M. & Quan, L. (2005). A quasi-dense approach to surface reconstruction from uncalibrated images. *IEEE Transactions on Pattern Analysis and Machine Intelligence* 27, 418-433.

Lin, T. T.; Liao, W.C. & Chien, C.F. (2001). 3D graphical modeling of vegetable seedlings based on a stereo machine vision system. *ASAE Annual Meeting*, Sacramento, California,U.S.A. Paper No:01-3137.

Lindenmayer, A. (1968). Mathematical models for cellular interaction in development, Parts I and II. *J. Theor.Biol.* 18, 280-315.

Lopez, G.; Favreau, R. R.; Smith, C.; Costes, E.; Prusinkiewicz, P. & DeJong, T. M. (2007). Integrating simulation of architectural development and source-sink behaviour of peach trees by incorporating Markov chains and physiological organ function submodels into L-PEACH. *5th International Workshop on Functional Structural Plant Models*, pp. 761-771, Napier, New Zealand.

McClelland, C. K. (1916). On the regularity of blooming in the cotton plant. *Science* 44, 578-581.

Millet J, B. A. & Edelin C. (1998). Plagiotropic architectural development and successional status of four tree species of the temperate forest. *Canadian Journal of Botany* 76, 2100-2118.

Nicolini E, C. B. (1999). La pousse courte feuillée, un indicateur du degré de différenciation chez le Hêtre (Fagus sylvatica L.). *Canadian Journal of Botany* 77, 1539-1550.

Oldeman, R. (1974). L'architecture de la forét guyanaise. *Mémoire no.* Vol. 73, Paris: O.R.S.T.O.M.

Pfeifer, N.; Gorte, B. & Winterhalder, D. (2004). Automatic reconstruction of single trees from terrestrial laser scanner data. *Proceedings of 20th ISPRS Congress*, pp. 114-119.

Prusinkiewicz, P. (1998). Modeling of spatial structure and development of plants: a review. *Scientia Horticulturae* 74, 113-149.

Prusinkiewicz, P.; Erasmus, Y.; Lane, B.; Harder, L. D. & Coen, E. (2007). Evolution and development of inflorescence architectures. *Science* 316, 1452-1456.

Prusinkiewicz, P.; Karwowski, R.; Mech, R. & Hanan, J. (1999). L-studio/cpfg: A software system for modeling plants. *International Workshop on Applications of Graph Transformations with Industrial Relevance* (ACTIVE 99) (M. Nagl, A. Schurr and M. Munch, eds.), pp. 457-464, Kerkrade, Netherlands.

Prusinkiewicz, P. & Lindenmayer, A. (1990). In: *The algorithmic beauty of plants*, Springer Verlag, New York.

Prusinkiewicz, P.; Mundermann, L.; Karwowski, R. & Lane, B. (2001). The use of positional information in the modeling of plants. *Siggraph 2001*, pp. 289-300, Los Angeles, Ca.

Prusinkiewicz, P. & Aristid, L. (1990). In: *The Algorithmic Beauty of Plants*, Springer-Verlag.

Qu, H. C.; Zhu, Q. S.; Guo, M. W. & Lu, Z. H. (2009). An Intelligent Learning Approach to L-Grammar Extraction From Image Sequences of Real Plants. *International Journal on Artificial Intelligence Tools*, To be published.

Qu, H. C.; Zhu, Q. S.; Zeng, L. Q.; Guo, M. W. & Lu, Z. H. (2008). Automata-Based L-Grammar Extraction from Multiple Images for Virtual Plants. *3rd International Conference on Bio-Inspired Computing - Theories and Applications* (D. Kearney, V. Nguyen, G. Gioiosa and T. Hendtlass, eds.), pp. 89-96. IEEE, Adelaide, Australia.

Quellette DV, Y. E. (1995). lateral shoot development in six diverse seedling populations of apple. *Fruit Varieties Journal* 49 248-254.

Radoslaw Karwowski & Prusinkiewicz, P. (2003). Design and Implementation of the L+C Modeling Language. *Electronic Notes in Theoretical Computer Science* 86, 1-19.

Radoslaw Karwowski & Prusinkiewicz, P. (2004). The L-system-based plant-modeling environment L-studion 4.0. *Proceedings of the 4th InternationalWorkshop on Functional-Structural PlantModels*, pp. 403-405, Montpellier, France.

Remphrey, W. R.; Prusinkiewicz, P. (1997). Quantification and modeling of tree architecture. In: *Plants to Ecosystems. Advances in Computational Life Sciences I*. (M. T. Michalewicz, ed.), pp. 45-52, CSIRO Publishing,Melbourne.

Renton, M.; Guedon, Y.; Godin, C. & Costes, E. (2006). Similarities and gradients in growth unit branching patterns during ontogeny in 'Fuji' apple trees: a stochastic approach. *Journal of Experimental Botany* 57, 3131-3143.

Rey, H.; Godin, C. & Guédon, Y. (1997). Vers une représentation formelle des plantes. In: *Modélisation et Simulation de l' Architecture des végétaux* (J. Bouchon, Reffye, P.D., Barthélémy, D., ed.), pp. 139-171. INRA Editions,Paris, .

Room, P. M.; Maillette, L. & Hanan, J. S. (1994). Module and Metamer Dynamics and Virtual Plants. *Advances in Ecological Research*, Vol. 25, 105-157.

Sinoquet, H. & Rivet, P. (1997). Measurement and visualization of the architecture of an adult tree based on a three-dimensional digitising device. *Trees-Structure and Function* 11, 265-270.

Tan, P.; Fang, T.; Xiao, J. X.; Zhao, P. & Quan, L. (2008). Single Image Tree Modeling. *ACM SIGGRAPH Conference 2008*, Singapore.

Trewavas, A. (2005). Plant intelligence. *Naturwissenschaften* 92, 401-413.

Van den Berg, C.; Willemsen, V.; Hage, W.; Weisbeek, P. & Scheres, B. (1995). Cell fate in the Arabidopsis root meristem determined by directional signalling. *Nature* 378, 62-65.

Wang, R.; Hua, W.; Dong, Z. L.; Peng, Q. S. & Bao, H. J. (2006). Synthesizing trees by plantons. *Visual Computer* 22, 238-248.

White, J. (1979). the plant as a metapopulation. *Annual Review Ecological Systems* 10, 109-145.

Xu, H.; Gossett, N. & Chen, B. Q. (2007). Knowledge and heuristic-based modeling of laser-scanned trees. *ACM Transactions on Graphics* 26.



Pattern Recognition
Edited by Peng-Yeng Yin

ISBN 978-953-307-014-8
Hard cover, 568 pages
Publisher InTech
Published online 01, October, 2009
Published in print edition October, 2009

For more than 40 years, pattern recognition approaches are continuingly improving and have been used in an increasing number of areas with great success. This book discloses recent advances and new ideas in approaches and applications for pattern recognition. The 30 chapters selected in this book cover the major topics in pattern recognition. These chapters propose state-of-the-art approaches and cutting-edge research results. I could not thank enough to the contributions of the authors. This book would not have been possible without their support.

How to reference
In order to correctly reference this scholarly work, feel free to copy and paste the following:

Hongchun Qu and Qingsheng Zhu (2009). Automatic Approaches to Plant Meristem States Revelation and Branching Pattern Extraction: A Review, Pattern Recognition, Peng-Yeng Yin (Ed.), ISBN: 978-953-307-014-8, InTech, Available from: http://www.intechopen.com/books/pattern-recognition/automatic-approaches-to-plant-meristem-states-revelation-and-branching-pattern-extraction-a-review

INTECH
open science | open minds

InTech Europe
University Campus STeP Ri
Slavka Krautzeka 83/A
51000 Rijeka, Croatia
Phone: +385 (51) 770 447
Fax: +385 (51) 686 166
www.intechopen.com

InTech China
Unit 405, Office Block, Hotel Equatorial Shanghai
No.65, Yan An Road (West), Shanghai, 200040, China
中国上海市延安西路65号上海国际贵都大饭店办公楼405单元
Phone: +86-21-62489820
Fax: +86-21-62489821

© 2009 The Author(s). Licensee IntechOpen. This chapter is distributed under the terms of the Creative Commons Attribution-NonCommercial-ShareAlike-3.0 License, which permits use, distribution and reproduction for non-commercial purposes, provided the original is properly cited and derivative works building on this content are distributed under the same license.

IntechOpen

IntechOpen