

Review

Automatic extraction of ramification pattern for living plants: A review

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This paper reviews detailed methods and approaches in relation to the complex machine learning system of automatic ramification (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 paper, 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.

Key words: Pattern extraction, automatic approaches, plant ramification, machine learning, artificial intelligence.

INTRODUCTION

Plant branching pattern, depends on the nature and on the spatial arrangement of each of plant parts (that is, 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 (Figure 1) through the three main and fundamental morphogenetic processes of growth, branching and reiteration (Barthélémy and Caraglio, 2007). Repetition of these entities induces gradual or abrupt changes reflecting different stages of differentiation in the meristems (Nicolini and Chanson, 1999), which are ordered in time and correspond to the notion of physiological age of meristems (Barthélémy, 1989).

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 and 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 Figure 2, (Harris and 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

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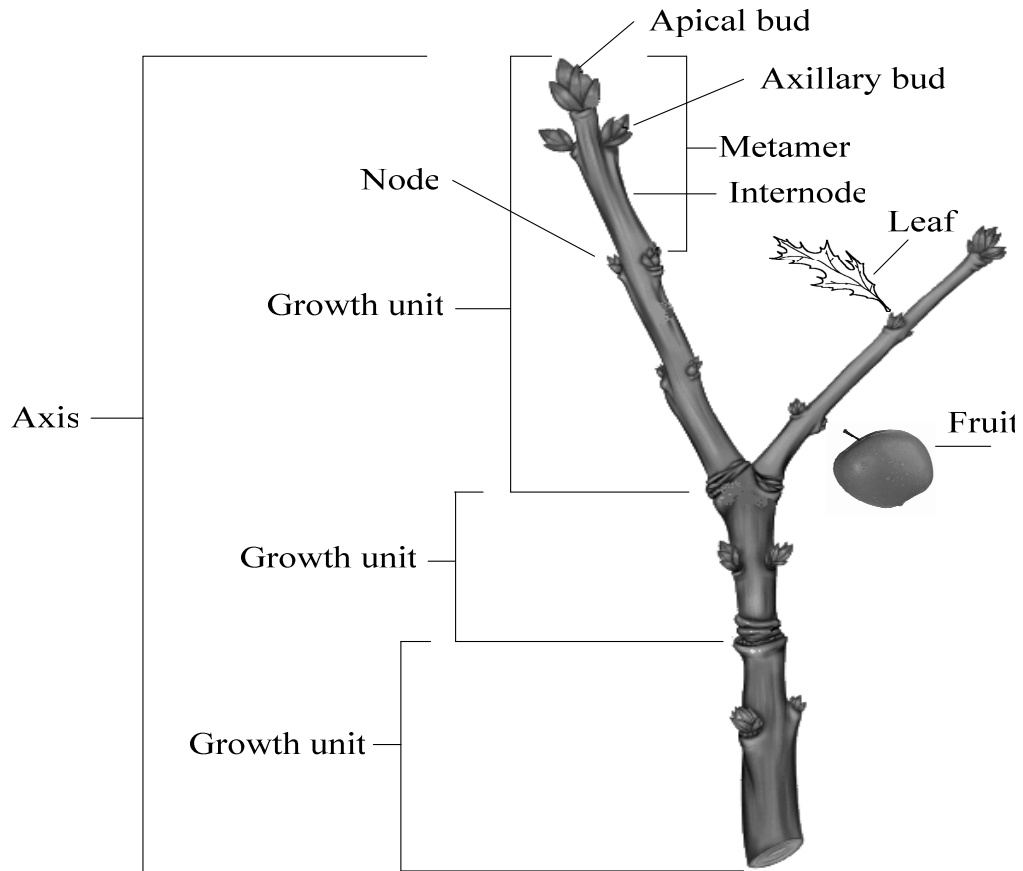


Figure 1. Schematic description of primary botanical entities of plant.

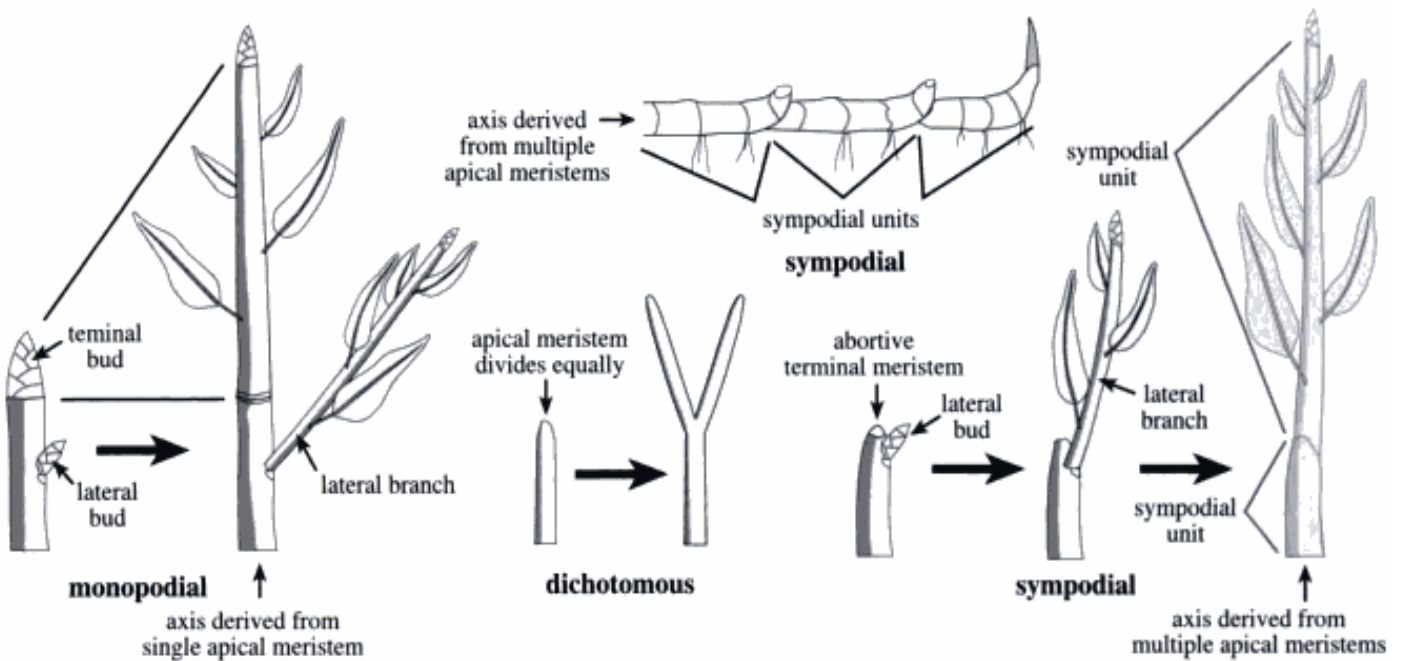


Figure 2. Stem branching patterns (Source: Harris and Woolf, 2006).

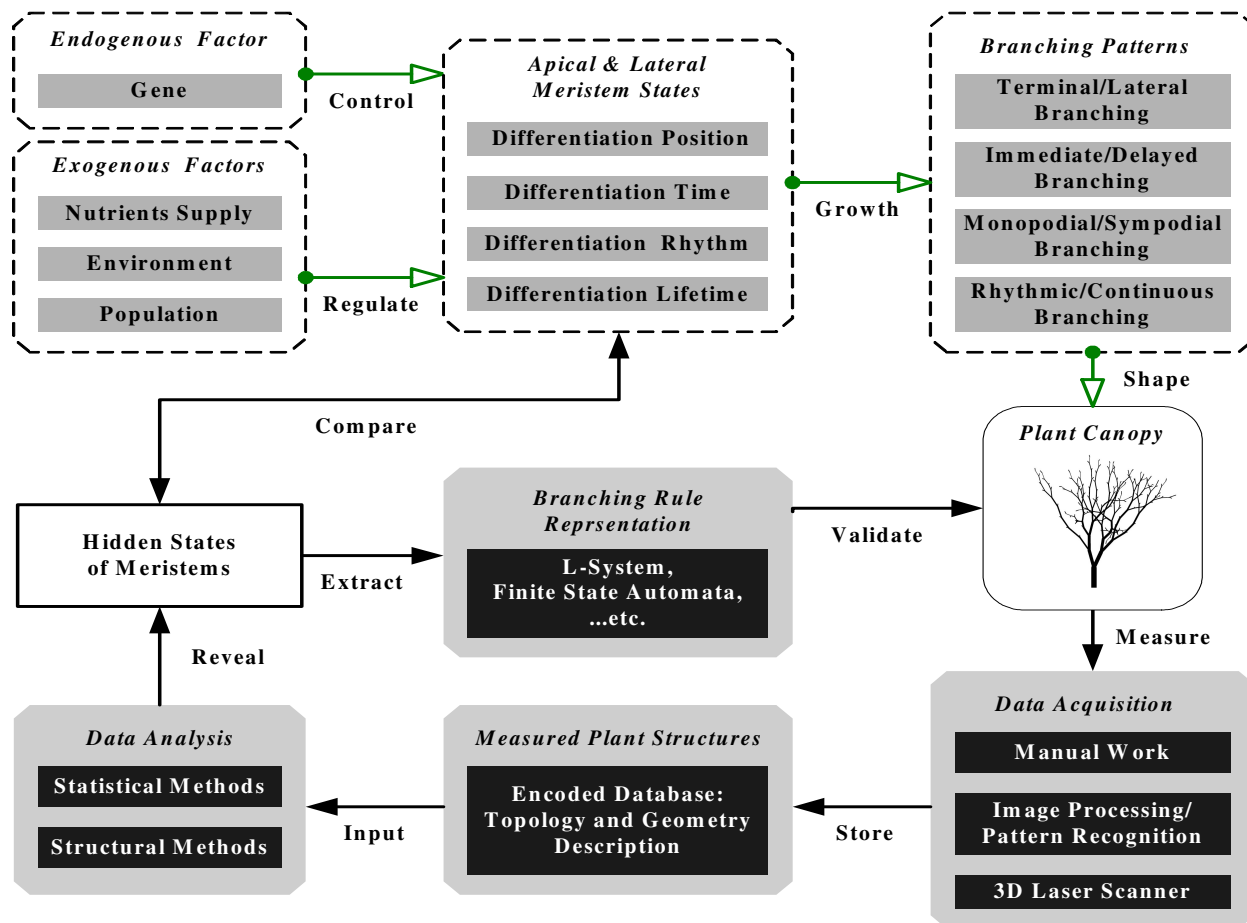


Figure 3. Schematic description of plant branching pattern extraction and meristem physiological states revelation. Dash-line marked rounded-rectangles and green arrows represent plant branching mechanism and process, while the gray rounded-rectangles and dark arrows represent the branching pattern extraction process.

process. The branching pattern analyses 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.

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 (Figure 3). 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.

PLANT DATA ACQUISITION

Data acquisition is the starting point for analyzing 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.

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 makes up the canopy consists of a set of these characteristics, and satisfies 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).

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, that is, 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 Figure 4) 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.

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

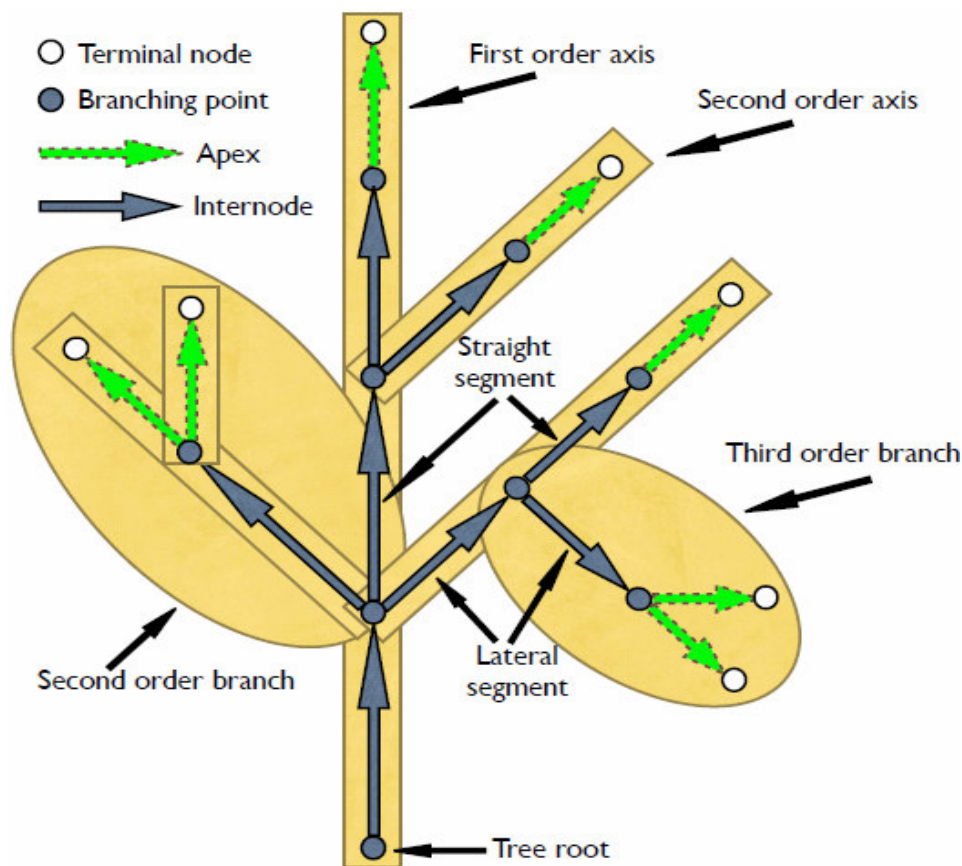


Figure 4. Plant architecture representation: the multiscale tree graph (MTG) (Source: Godin and Caraglio, 1998).

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 unfoliated 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 and 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 reasonable results for 3D skeleton extraction (Figure 5).

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 DiplAme designed for digitizer control and data acquisition management. It works at the shoot level and simultaneously measures

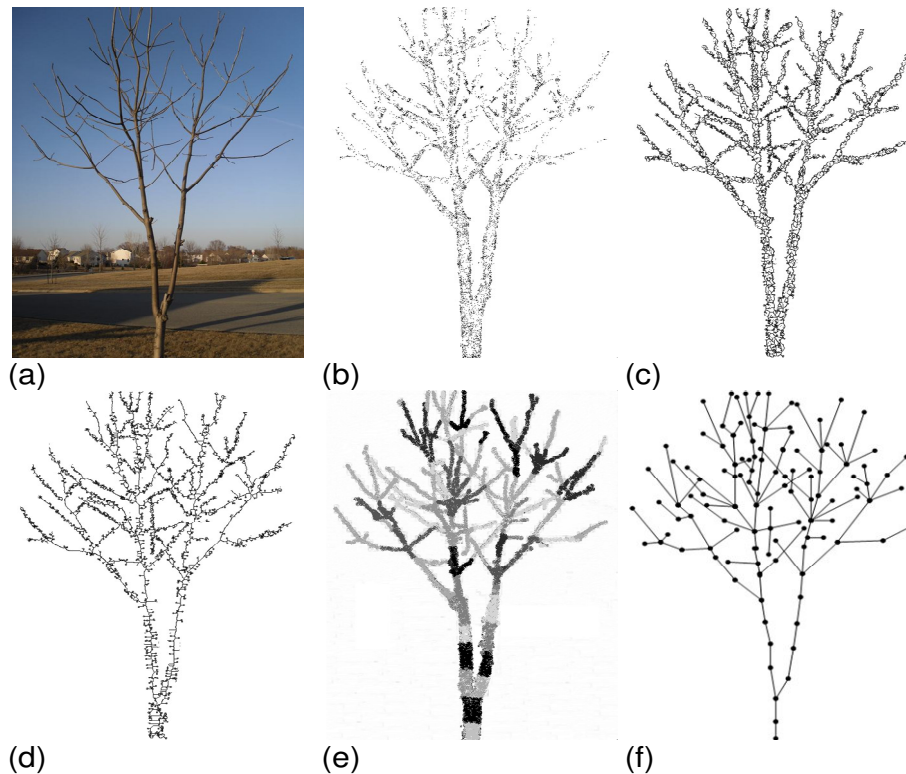


Figure 5. Image-processing-based plant 3D skeleton recovery (Source: Qu et al., 2009).

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 1 cm 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 and Pfeifer, 2004) and (Pfeifer et al., 2004) took laser data as input, and created a voxel-based occupancy grid representation 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 tree models 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 have been developed to digitize 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, that is, these processes need to be completely implemented by hardware (3D scanner) instead of software.

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 much 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 and 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 and 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 field, some frameworks of investigation are required to reveal the hidden effects (the morphogenetic gradients) of the ontogenetic growth behaviour, 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.

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 and 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 makes it possible to 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 has been established using the Hidden semi-Markov chain (HSMC, as shown in Figure 6), which is particularly useful for identifying homogeneous zones within sequences and detecting transitions between zones (Ephraïm and 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.

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 plant 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 < 5 cm),

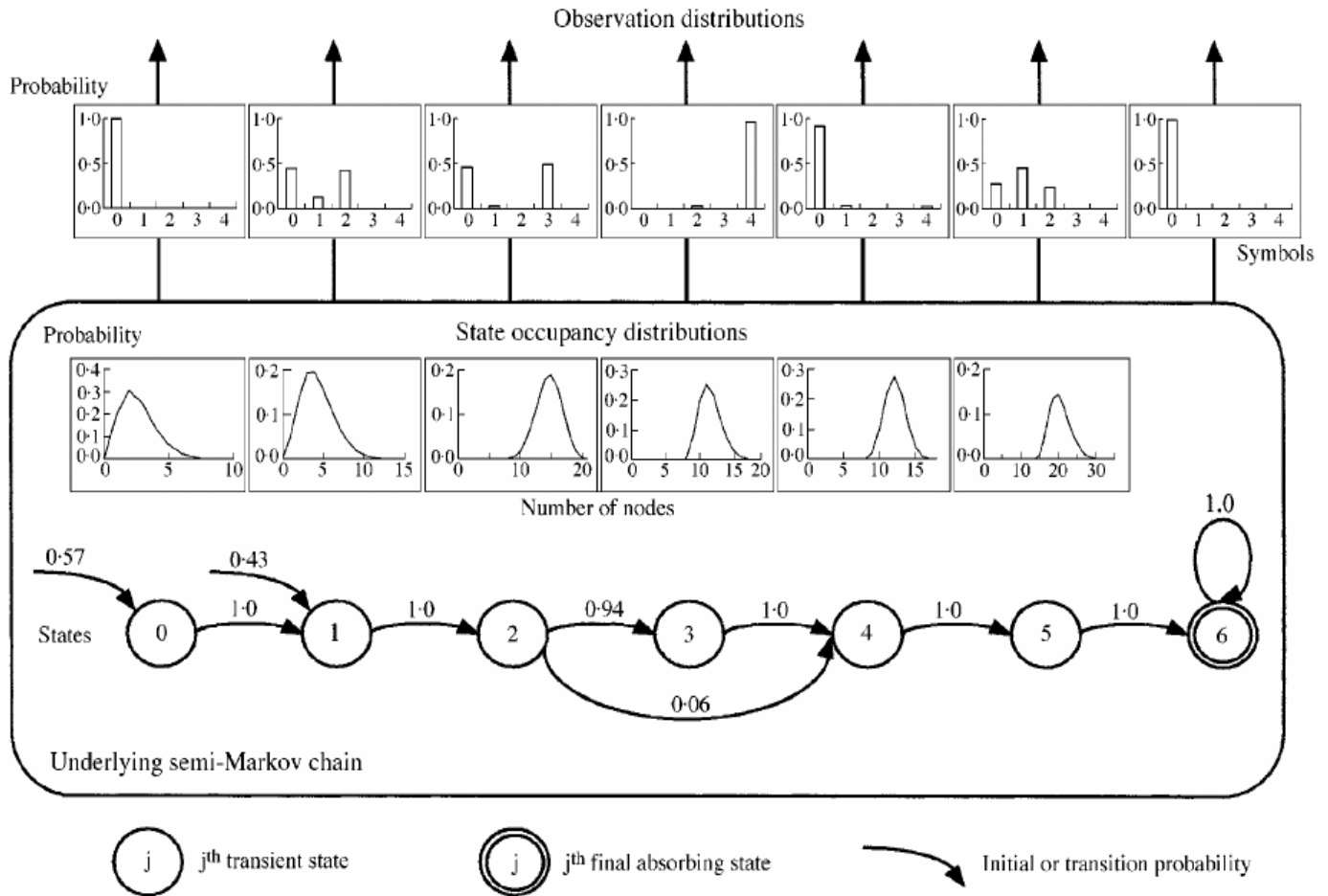


Figure 6. Modelling branching on 1-year-old trunks using a hidden semi-Markov chain (Source: Costes and Guédon, 2002).

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 (that is, 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 them sharing certain zones, especially the latent bud 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

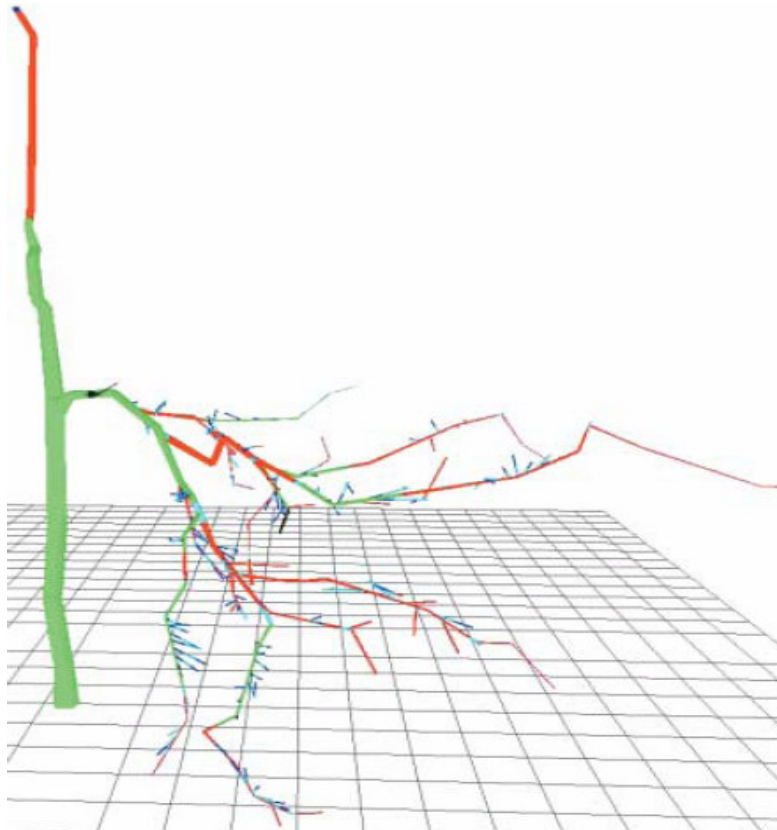


Figure 7. Restored hidden state tree for the apple tree data set. Each growth unit is colored according to its hidden state. (Source: Durand et al., 2005).

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 (that is, 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 Figure 7). 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.

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, Florence 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.

Structural analysis-based approaches

As reviewed by 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, that is, its architectural unit at different scale (node, metamer, growth unit, etc.). The result of this process is called a "reiterated complex" (Hallé 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 and Lindenmayer, 1990; Godin and 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 (1998). 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 investigations 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).

RESULTS UTILIZATION

The statistical and topological analysis approaches discussed 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

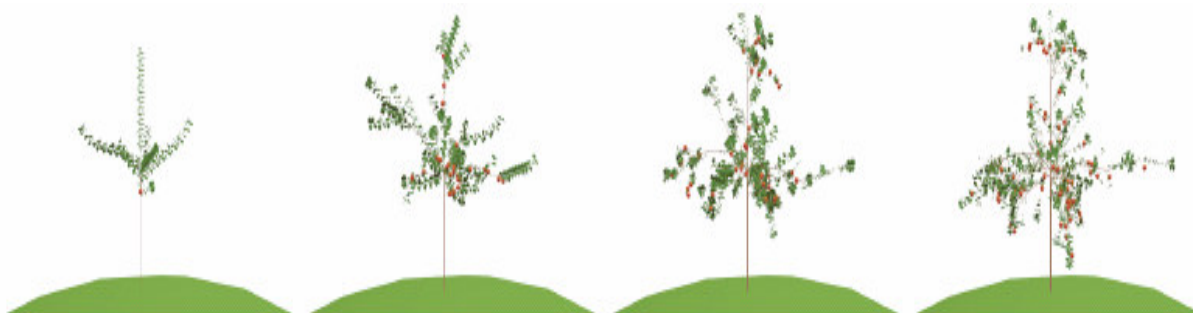


Figure 8. Simulated apple trees using the MAPPLET model (Source: Costes et al., 2008).

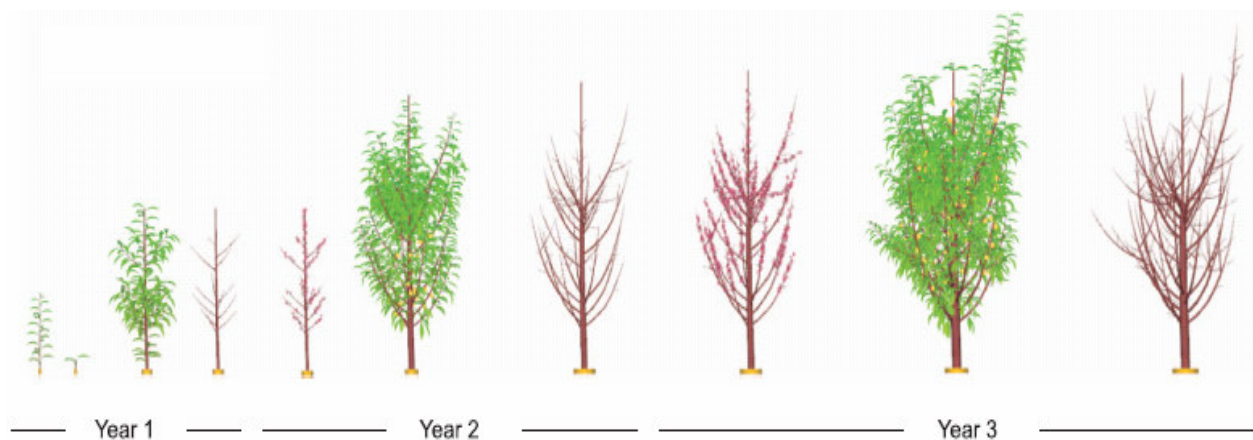


Figure 9. L-Peach model output shows the development of the structure of a 3-year-old unpruned peach tree. (Source: Lopez et al., 2008).

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).

A new type of structure-function model named MAPPLET (Markov Apple Tree) has been developed by Costes et al. (2007). 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, that is, 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 and 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 Figure 8.

Following this first integration of advanced stochastic processes for modelling 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 real peach trees (Figure 9). 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 modelling, in particular the plant branching control.

However, it is really a difficult work to manually develop an L-System for a given plant species depending only on

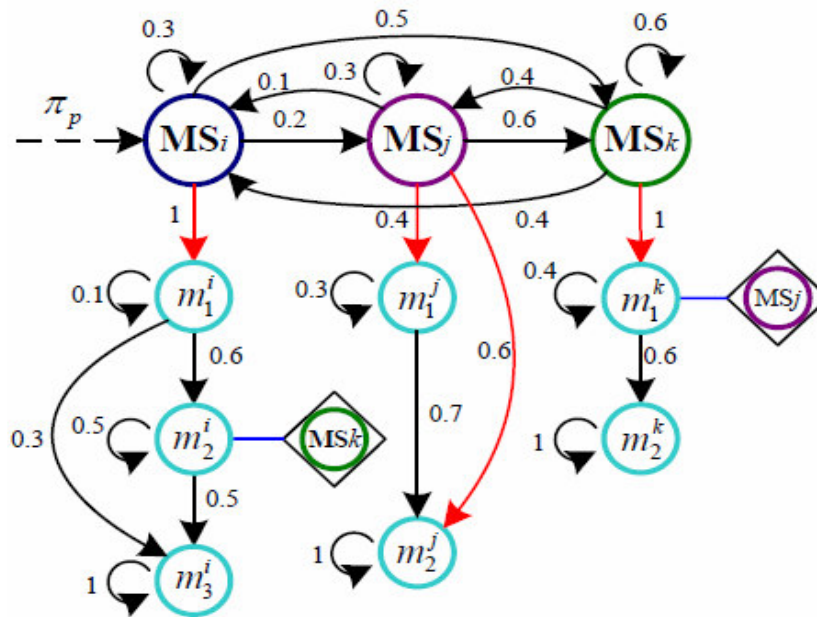


Figure 10. Schematic structure of the Bidimensional Hierarchical Automaton (BHA), where cycles marked with $MS_{i,j,k}$. etc. represent the physiological states of meristems (hidden states of the Hidden Markov tree model), while the light blue cycles denote the different types of metamers (with different length of internodes) (Source: Qu et al., 2010).

imagination or experience. Qu et al. (2010) proposed a novel approach of automatic L-System discovery via branching pattern analysis of unfoliated trees to address this issue. 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 unfoliated 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 Figure 10.

CONCLUSION

This paper 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 this

metric information can be extremely time consuming when using manual labour. 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 intelligent methods are now required in order to collect plant architecture data of various types and sizes in a systematic way, that is, 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 analyses 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 reduce 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.

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