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Plant Modeling and Developmental Biology

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ABSTRACT

The developmental biology has gained much importance due to increasing computational techniques. Whether it is acquisition, processing or any analysis of experimental data or the construction of models of organisms, computational techniques are increasingly used. In particular, models help to visualize the non-intuitive relations between local morphogenetic processes and global patterns and forms. This paper surveys the different plant modeling techniques and the key objectives and methodology for construction of appropriate model. The review is related for both botanists and mathematical modelers.

KEYWORDS - Plant Modeling, Adaptation, Growth With Stochasticity, Architectural Plant Model

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1. INTRODUCTION

Quite often, many complex biological patterns govern some simple mathematical rules. A well known example for supporting this fact is the relation between phyllotaxis and the intriguing Fibonacci sequence {1, 2, 3, 5, 8, 13 . . .}. Phyllotaxy is an arrangement of leaves on a plant stem. This example is an important historic link between observation and mathematically research problem in developmental plant biology[1]. Since old times, mathematical characters of plants had been observed like geometric regular patterns or numerically repetitious patterns (phyllotaxy). But in recent times, mathematical modeling is used for less regular patterns and forms, such as leaf venation and the branching architecture of trees. As the development of plants is a regular process so new elements and patterns are formed and incorporated into a growing plant. The geometrical models of morphogenesis explain the emergence of global patterns and forms. These models focus on the temporal and spatial coordination of development. The flower heads with spiral phyllotatic patterns or self-similar fern leaves are some examples for which their regular structures are conducive to analyze in geometric terms. In nowadays, computational modeling has become an important technique in developmental plant biology. The increased use of models is due to recent developments in computer hardware, software and modeling methodologies. There are mathematical software like Mathematica and MATLAB to develop modeling programs[2]. There are some specialized software available for plants modeling like Virtual Laboratory and L-studio[3], OpenAlea[4] and VirtualLeaf[5].

2. FUNCTIONAL STRUCTURAL PLANT MODELING (FSPM)

In recent times, many researchers developed and used a new approach called as functional–structural plant models (FSPM) in plant science by developing computer models of plant functioning and growth. FSPMs are used to understand the complex interactions between plant architecture and the physical and biological processes that drive the plant development at several spatial and temporal scales. In general, FSPMs deal with the spatial distribution of both environmental and biological processes. FSPMs are related to three dimensional plant models. In FSPMs, plant architecture is represented as a collection of plant components which are interrelated[6]. FSPMs may face various dimensions of plant architecture complexity like complexity of the biological system which is due to the high variability of plant growth, complexity of integrating various sources of knowledge into one consistent modeling framework and computer simulation to manage various dynamically changing and interacting parts[6].

3. L-SYSTEMS AND THEIR ADAPTATION TO THE PYTHON LANGUAGE

In 1968, Lindenmayer introduced L-systems as a theoretical framework for studying the development of simple multi cellular organisms and then applied to investigate higher plant organs. Lindenmayer suggested topics for study, guiding the construction of specific plant models, monitoring their correctness and participating in many discussions of biological and mathematical problems[8]. Lindenmayer systems (generally known as L-systems) were conceived as a mathematical theory of plant development[9]. L-system is a technique of rewriting. Rewriting is a technique for defining complex objects by successively replacing parts of a simple initial object using a set of rewriting rules or productions. After the induction of geometric features, plant models expressed using L-systems became detailed enough to allow the use of computer graphics for realistic visualization of plant structures and developmental processes. Functional-structural models are the models which are developed for the study of plant functioning and development[10]. These computational models make three dimensional representation of plant architecture which help to simulate different types of plant processes. These models assess the effects of these processes on plant functioning, development, and form[7]. Boudon et al[7] presented an adaptation of L-systems to the Python language which is a popular and powerful open-license dynamic language. For developing plant growth models, the use of dynamic properties is explained[7]. The methodology, which is explained, by Karwowski and Prusinkiewicz[11] to design and implement L+C is also used to adapt L-systems to the Python. Some of the example of FSPM applications in L-py are explained[7]. The first is the minimization of measurements in three dimensional plant architecture reconstructions. To digitize complex tree architectures, an intuitive idea is to exploit the redundancy of tree structures and only digitize the main branches of the tree. Boudon et al[7] assumed a reference plant as a digitized walnut tree. A simple L-Py probabilistic model was designed to generate small branches from bud modules. This example illustrated use of advanced analysis tools to parameterize a L-system that reconstructs trees from observed data. Further the use of L-Py is visualized as growth component for simulating FSPM. Boudon et al[7] illustrated the use of this approach on a real complex FSPM, MAppleT, simulating the growth of an apple tree. This model mixed stochastic topological construction with a bio-mechanical model for the geometry. Also the use of L-Py as a training tool for the classroom is suggested[7]. The use of L-Py as a tool for teaching scientific method was tested during French school in 2009–2010 in the context of a multi-disciplinary class on botany and computer science at high school level. The students were working hands on the computer and using L-Py as a modeling platform. They were explained the procedure to generate simple plant structures. First, some simple models of plant structures were created by the students. Then they easily used their knowledge of L-Py to extend and customize these models according to the measured plants. The observations made showed that the software can be used with success for training students in a multi-disciplinary context. The feedback made[7] from the classroom showed that L-Py can be adapted in various ways e.g. to simplify the visual interface, introduce debugging tools and design new language features. Vos et al[12] considered the different aspects of cereal architectural modeling: plant development, pattern formation and plant geometry. As the cereals have great the economic importance so the Gramineae is of much interested crop among non-woody plants to be modeled with the approach of FSPM. The architecture of Gramineae results from the repeated formation and expansion of the phytomer. Phytomer, a basic unit, is formed sequentially at the top of each axis by the shoot apical meristem. Shoot apical meristems (SAMs) of Gramineae are primarily based on empirical parameterization of the emergent properties of morphogenesis. There are mathematical relationships between the conservative patterns of architectural development, instead of simulating the local processes by which these patterns are built. This enables complex features of architectural development to be described with few parameters and brings new simulation capabilities to researchers[12].

4. PLANT CELLULAR GROWTH WITH STOCHASTICITY

Stochastic means relating to or characterized by random, chance or probability[14]. A Stochastic model is a mathematical model involving random variables in order to estimate probability distributions of potential outcomes. In recent times, to describe biological events, particularly noise in gene expression, stochasticity has been used[15]. For investigating stochasticity in biological systems, there are two main approaches. In the first approach, experimental results and the results obtained by a stochastic computational model are compared. If the results of the experiments and stochastic model are same then it means that stochasticity is someway useful in plant process. In the second approach, the behaviors of two identical systems due to stochastic noise are tested experimentally. This approach is used to study stochasticity of gene expression in single cells. It is a natural phenomenon of plants to develop continuously. It has specialized mechanisms to carefully control organ size and structure. But there is a high degree of variability in growth and division in plant cells which implies that stochasticity is there in the plant tissues. The epidermis of an expanding dicot leaf is a mosaic of cells which are different in identity, size and differentiation stage. Elsner et al[16] tested the hypotheses that in such a cell, mosaic growth is heterogeneous and changes with time and that this heterogeneity is not dependent on the cell cycle regulation *per se*. The growth of leaf epidermis exhibits spatiotemporal variability[16]. Quite often, cells differentiate and form highly organized patterns during its development to determine the finalized function of a tissue. There are a lot of examples to demonstrate that stochasticity facilitates reproducible phenotypic outcomes. Plant growth depends upon on increased cell number and cell size. The understanding of the link between regulatory genes and the growth and shape of plant organs is still a considerable challenge[17]. Schiessl et al[17] discussed how growth regulators direct the growth of organ primordia at the cellular level. The analysis suggested that JAG is required for the transition from meristem to primordium growth patterns, including a shift from isotropic to anisotropic growth, increased cell proliferation and cell enlargement. JAGGED is needed to uncouple the cell cycle from cell volume leading to substantial variability in sepal cells. But still, there is a lot more to learn about how this cellular heterogeneity contributes to the regularity of organ growth[13]. As stochasticity is a behavior, not a gene function so the techniques that enhance stochastic behavior must be developed to study the consequences of stochasticity during development[13].

5. TREE MODELING

Procedural tree models is very much used in computer graphics as these have ability to generate a variety of output trees from a set of input parameters and to simulate plant interaction with the environment for a realistic placement of trees in virtual scenes[18]. The researchers from computer graphics has not been addressed the problem of finding the parameters of a given stochastic procedural model of biological trees. Stava et al[18] introduced a framework for stochastic inverse procedural modeling of biological trees. This approach detects the parameters that generate a tree by maximizing similarities between the input trees and generated tree. The suggested model can be used to obtain the procedural representation of different species of trees by using inputs ranging from developmental models. As the basis of this model is stochastic so it generates a set of similar trees for a given set of parameters. Hence the inverse system cannot reproduce exactly the same structure of the input tree. To achieve this, there should be control on the stochastic growth of the procedural model so that all random parameters generated during application of the rules are replaced by fixed values[18]. Pirk et al[19] suggested a method for creating growth models from a static input tree. To create branches, the tree is analyzed and self-similarity is used. Growth parameters are determined and interpolated to create convincing animations. Based on these parameters, the tree can be edited as a whole or in parts. The method allows the production of time lapse animations of tree development, providing plausible interpolation of branching angles and growth rates at the same time.

6. ARCHITECTURAL PLANT MODEL SIMULATING RESOURCE-DEPENDENT GROWTH OF PLANTS

Although physiological plant models and architectural plant models are developed for different reasons yet there is an increasing demand for crop models that simulate the genetic and resource-dependent variability of plant geometry and architecture[20]. Yan et al[20] presented GREENLAB which is a mathematical plant model that simulates interactions between plant structure and function. Earlier, architectural plant models were entirely descriptive and built from mathematical algorithms as these models needed computer graphics. Architectural plant models describe structure based on topological principles like sympodial or monopodial structure and plant geometry like organ shape, its size and phyllotaxy. Modelling of plants and software for constructing three dimensional plant models originated in 1968 with the concept of L-systems proposed by Lindenmayer. Plant growth and architecture models mainly depend upon biological assumptions of plants. Yan et al[20] suggested a new mathematical plant growth model which combines complex architectural and morphological features with biomass production and allocation. Although this model is extremely simple in terms physiological components yet it has the potential as a complete quantitative tool. In this model, to simulate plant organogenesis, dual scale automaton is used. Plant fresh biomass production is computed from transpiration. The fresh biomass is then distributed among expanding organs according to their relative demand. This model is able to reproduce the dynamics of plant growth, architecture and geometry of different plants along with their 3D visualization. This plant model also simulated the variability of leaf size on the plant and compensatory growth following pruning.

7. MULTI RESOLUTION ORGAN GEOMETRICAL MODELS OF PLANTS WITH COMPLEX ORGANS

In nowadays, plants are necessary for our living and working environment. Today agronomy, forestry and environmental defense are the industries which are plant centered[21]. Further landscape image synthesis, computer simulation, theoretical biology, botany, ecology, horticulture, plant-environment interaction modeling etc are the areas which are plant based. Interactive visualization of virtual trees and forests is an important challenge in computer graphics. A lot of plants modeling softwares are developed for plant modeling and simulation. Using these softwares, one can simulate plant species with fine geometric details. Tree modeling has been widely investigated and its representation is very realistic[22]. However, tree models are formed by such a vast number of polygons that real-time visualization of scenes with trees is practically impossible. Remolar et al[22] suggested Foliage Simplification Algorithm (FSA) which decreases the number of polygons in the crown while maintaining the appearance. In FSA, two leaves disappear to create a new one. The leaves obtained after collapsing preserved an area similar to that of the collapsed leaves. Further Remolar et al[22] suggested the geometric simplification of foliage, accepting the results of the simplification algorithms on the structure of the trunk and the branches. Zhang et al[23] suggested a leaf polygon decimation method, Progressive Leaves Union (PLU to gradually diminish the number of sparse polygons while approximately keeping the spatial occupation and colour distribution of the foliage[23]. The results suggested that PLU keeps visual effect of original foliage. It is very effective for multi-resolution representation and view dependent plant community visualization. Zhang et al[21] suggested an upgrades and modified FSA and PLU. Zhang et al[21] also tested their model with error control algorithms on different tree species with needle-like leaves, broad leaves or complex shapes, thin leaves with complex shapes, flowers with complex shapes, and fruits. It seems to be a novel approach to construct multi resolution organ geometrical models under spatial error control. This approach extended FSAs to complex shapes describing leaves, flowers and fruits. Also knowledge of organ phyllotaxy is used to define plant organ clusters. This approach allowed multi resolution geometrical representation of trees with very significant compression ratios, up to a single leaf for a whole crown.

8. CONCLUSION

Plant morphology attracts both mathematical and plant biology researchers alike. Cross-disciplinary training of researchers is inevitably first step to develop the interface between mathematical-driven and plant biology-driven sciences. Further for unleashing the potential of geometric and topological approaches in the plant sciences, we need an interface familiar to both plants and mathematical approaches so that the challenges posed by a future with uncertain natural resources as a consequence of climate change can be met. Mathematical and computational models help to unveil the non-intuitive relations between local morphogenetic processes and global forms. This review tries to unite diverse emergent phenomena of plant morphogenesis. The study of various models (mathematical or simulation) may provide a unifying insight into the mechanisms of development so that developmental biology can be visualized as transformation into an experimentally based deductive science.

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