


VISmaF: Synthetic Tree for Immersive Virtual Visualization in Smart Farming

Mariano Crimaldi ^{1,†,*} , Fabrizio Carteni ¹, Francesco Giannino ¹

¹ University of Naples Federico II, Department of Agricultural Sciences, Portici (NA), Italy;

* Correspondence: mariano.crimaldi@unina.it

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Abstract: A 3D geometric model helps researchers to visually validate biological processes like the interaction of plants with changing ambient light, competition, or changing temperature. This work has the goal to create a synthetic tree in a real-time 3d environment that grows according to mathematical biological rules, reacting to changes in the external virtual environment, such as changes in direction and amount of light. To obtain a 3D structure from system dynamics model, a link has been created between a system of ordinary differential equations (ODEs) and a real-time 3D rendering engine. The ODEs system calculates the internode elongation at each time-step which will be the input for the 3D engine; the input parameter for the ODEs system is calculated in the 3D environment and can be the amount of light, temperature, or other species-specific growth parameters. On the other side, the elongation rate is calculated according to the amount of light in the 3D environment using a custom shader. The independence of the 3D rendering from the biological mathematical part allows the change, optimization, or improvement of the mathematical model. This can provide an at-a-glance view if a certain model is related to reality, modeling future trends of plantations for productive purposes, and display the results in a clear way for end-users. Further studies are underway to improve both biological modeling and 3D engine rendering.

Keywords: biological models; smart farming; 3d tree; ordinary differential equations; system dynamics; virtual plant

1. Introduction

Computer simulations of plant growth have a story long over fifty years [1,2]. The first method for branching structure simulation using a computer, named cellular automaton, was proposed by Ulam [3] in 1966. Simple models, without fundamental factors such as branch collisions, were developed later. Lindenmayer [4] proposed a string rewriting system for cellular interaction commonly called the L-system, later adopted to generate plants and trees with the contribution of Prusinkiewicz [5]. Approximate models, such as the one proposed by Weber and Penn [6], were introduced later, focusing more on geometric generation rather than biological rules. Other models were developed during the years, following the needs of both 3D artists or professionals and botanists [7]. The integration with mathematical-biological models has been introduced in the last two decades thanks to scientists that developed plant models capable of describe both functional and structural parts of plant with the so-called Functional-Structural Plant Models (FSPMs) [8]. On the other hand, the complexity of digital design has reached elevated levels of quality standards allowing to use the 3D structure as output of FSPMs in order to characterize plant phenotypes [9], or as feedback to assess and calculate light partitioning [10]. A synthetic 3D tree can be used in different scientific applications, such as synthetic silviculture [11], generic digital representation of real world [12], flow dynamics [13,14] and in botany to

determine physiological parameters [15]. In botany, these models are used to determine physiological parameters [16–18]. A 3D plant structure allows researchers to visually validate biological processes, such as the interaction of plants with light and environment. In ecology, these models are used to visualize plant reactions to diseases, stress or pruning [19,20]. Another critical aspect to study is the competition of plants for light to estimate field crop canopy photosynthesis [21–23], or carbon and water flows [24] making an observer aware of systems mechanism. In this paper, we provide a proof of concept for a link between a biological mathematical model based on Ordinary Differential Equations (ODE) and a 3D real-time rendering engine. This link can operate in both ways, i.e., by rendering a tree using parameters from ODE solutions, or by considering geometrical 3D data (e.g. the amount of light from the virtual scene) as input to solve the ODEs. In Section 2 we present the results of first experiments with the model, showing how a synthetic tree reacts to different light amount into 3D real-time environment, first with a simple simulation of an internode growing in different light conditions (different growing rate), then expanding the model to the whole tree, showing how it grows differently under different virtual environmental light conditions. In Section 4 we explain how we started from the mathematical biological model in *Simile* and how we linked this model to the real-time 3D rendering engine, thanks to object-oriented programming (OOP) paradigm. In Section 3 we analyze the results and discuss further experiments.

2. Results

The results of the first tests with the model described in Section 3 are shown in Figure 1. A first simulation was performed with a simple one-child internode model at two different light conditions. In figure 1a it can be seen that internodes grow differently depending on the amount of ambient light in which they grow. The left internode has a shorter total length than the right internode as it grew in a low light environment. As shown in the model in figure 2, the ambient light parameter calculated in the 3d environment, directly influences the calculation of the internode length. The result will be different with different amount of light in terms of single internode length and total length. In the presence of branches, as shown in figure 1b and figure 1c, even a simple tree behaves differently. Again, tests were performed with different amount of light, but setting a branching parameter. Specifically, it was set as number of children equal to 2 and branching angle of 30° (the model allows to set species-specific parameters depending on the tree to be modeled, number of children and branching angle are some of them). From figure 1b and figure 1c, it can be seen that the amount of light affects the total length of the tree and the lengths of individual internodes. Branching is triggered when the calculation of the inhibitor concentration, referred to the individual branch, reaches its maximum value. Once the maximum concentration is reached, the tree enters a seasonal growth stop phase until the inhibitor concentration reaches a minimum value. Upon reaching the minimum value, the tree resumes growth by generating the number of new branches set oriented according to the branching angle (Figure 3b). In addition, the length of the single internode decreases as the total height of the tree increases, in accordance with the model described in Section 4. Internodes at the top of the tree will be shorter than those on the main trunk (the first to grow from seed) because they are closer to the maximum height of the tree.

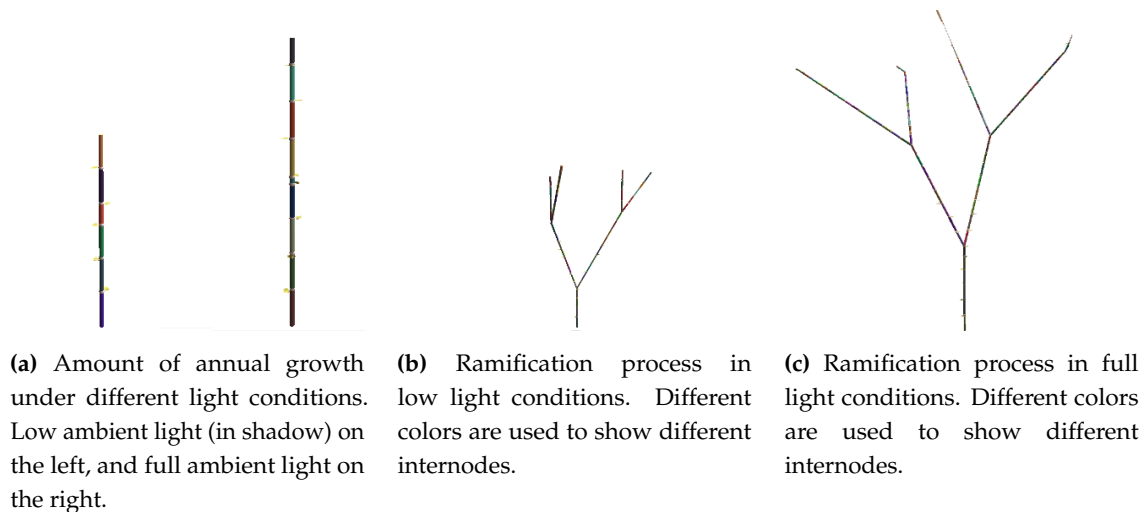


Figure 1. Different growing rate and ramification of internodes under different light conditions. (a) different amount of annual growth, (b) growth under low light, (c) growth under full light. Different internodes are rendered in different colors for showing purpose.

3. Discussion

The results show how it is possible to create a synthetic tree in a 3d real-time modeling environment from a mathematical biological model. The flexibility of the model is given by the use of interconnected modules according to the object-oriented programming (OOP) paradigm. The use of a proprietary shader for calculating the amount of light in the virtual environment provides further flexibility to the model. Other solutions have been used in literature, such as the use of global illumination, radiosity or ray-tracing algorithms, but the solution proposed in this work presents a further alternative to the subject. It is possible, in fact, to use the calculated amount of light to modify the main growth parameters such as branching angles and amount of growth. In this way it is also possible to model the competition for light between near trees in addition to the change in branching direction caused by tree's own shadow. Further studies are underway to improve the tree modeling by introducing secondary growth and other environmental parameters that can change the growth model such as temperature.

4. Materials and Methods

In the rendering system, all mathematically modeled parts have been made independent following object-oriented programming (OOP) paradigms. In particular, the final tree is made up of several independent and interconnected modules.

- A biological mathematical model to simulate the internode and branch growth
- A 3D structure module to render the tree

The mathematical model is a set of ordinary differential equation able to simulate the internode elongation and the rules for stopping growth. In particular, the internode elongation is a function of environmental parameters (temperature and light) and some species parameters (growth rate and max length). The rules for stopping the internode growth are instead simulated according to the concentration of an inhibitory substance produced during the internode elongation. The internodes grow until a given concentration of inhibitor is reached, then the tree enters a seasonal growth stop and then starts growing again after the inhibitor concentration reaches a minimum (Figure 3). Restarting the growth, the system will generate one or more branches depending on the species-specific parameters set. Figure 2 shows the stock and flow model representation in the system dynamics tool *Simile* [25]. The 3D module is composed by two different sub-modules:

(a) internode module, finalized to the creation of the internode geometry (length and width) thanks to

the data calculated by the integrator. It contains the stop-growth rules (maximum length reached) and the positioning of the apical bud;

(b) bud module, modeled as a particular internode of unitary length, it stores information about the number of children to be generated, the branching angle and the state of the bud (asleep/awake). In addition, a particular bud module called seed, stores species-specific information about the tree and is hierarchically the first bud from which all subsequent buds, branches and internodes descend; Using this modular approach, it is possible to make the modeling mathematical part independent from the rendering part. This way, if there is a need to change the mathematical model, it is possible to do it without affecting the 3D generation other than parameter calculation. The main part of the simulation is the calculation of the amount of light in the virtual environment to be used as a parameter in the mathematical model of growth. Different solutions have been studied (global illumination, radiosity, ray-tracing), each with its own precision and computational performance. In this work it has been decided to use a custom shader for the calculation of the amount of light. This solution is a balance between accuracy and computational performance sufficient for the purpose of simulation. In particular, an ambient light sensor has been programmed that renders a temporary texture on the surface of the sensor itself, extracting an array of RGB values and converting them into brightness values (lux). In our work, tests have been performed by placing the brightness sensor at the top of the tree (a single sensor) and at the ends of the internodes (as many sensors as the number of active growing internodes) and at the position where a leaf is present and rendered, which in this case will act as light sensor itself. It has been observed that by placing the sensors at the ends of the internodes there is no performance decay such that a single sensor placement at the top of the tree is preferred. In addition, using leaves as sensors for light makes the calculation more accurate and realistic. The calculated value of the amount of light is used as a parameter in the calculation of the length of the internode in the relative module. Higher light amount leads to higher internode growth and vice versa lower light amount leads to lower internode growth as shown in the results of the Section 2.

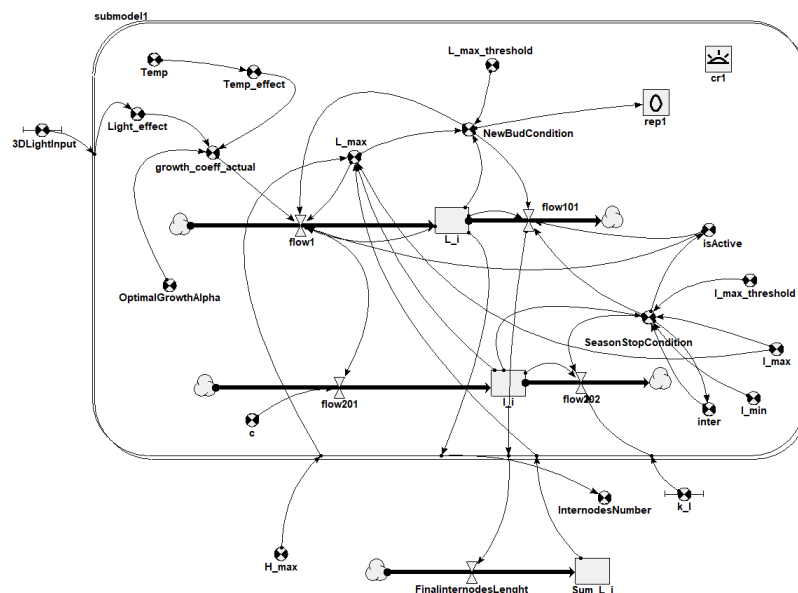


Figure 2. Stock and flow model of internode growth in the system dynamics tool SIMILE

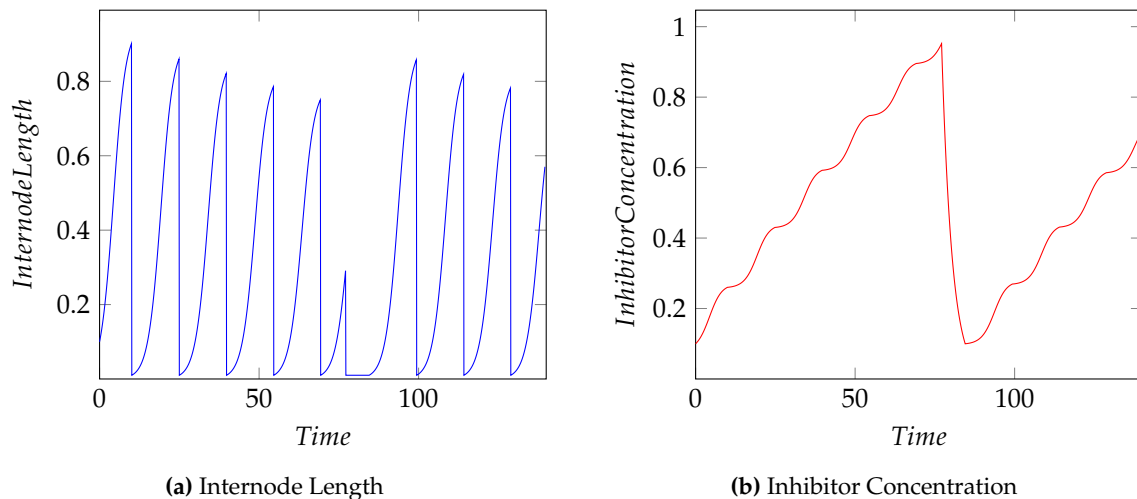


Figure 3. Internode length and Inhibitor concentration simulations

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