

GreenScilab-Crop, An Open Source Software For Plant Simulation And Parameter Estimation

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Abstract—GreenLab is a mathematical model simulating the dynamics of plant organogenesis, biomass production and allocation, and plant three-dimensional structure. Being a functional–structural model, its software implementation and test are costly. On the other hand, software is a necessary tool to understand, analyze and apply the model. With increasing scientific publications on GreenLab, need for a freely-accessible software increased in the community of plant modeling.

Implementation of GreenLab has been done in Scilab, named *GreenScilab*, which simulates generic plant structures from trees to crops. In this paper, a new version of GreenScilab dedicated to herbaceous plants, called GreenScilab-Crop, is presented. It allows flexible control on plants, especially the position-dependent organ growth delay. A case study is made on tomato plant for simulation and parameter identification.

Index Terms—GreenLab, plant modeling, inflorescence, FSPM, model calibration, open-source

I. INTRODUCTION

The functional-structural plant model (FSPM) aims at simulating both plant and plant growth [1]. Basically there are two components in a FSPM: one simulates plant organogenesis, the other simulates plant functioning, mainly biomass production and biomass repartition. The notion of FSPM appeared since mid 1990's, indicating a new multidisciplinary subject including computer science, botany, ecophysiology, applied mathematics, etc. Examples in the FSPM family include LIGNUM [2], L-system based approaches (such as L-peach [3]), AMAPHydro, GreenLab [4][5], etc. FSPMs are generally complex in model structure and hard to develop without team work. Implementation of FSPMs is time and labor consuming [6], and the resulting software is often vulnerable to bugs.

Currently there are several softwares for FSPMs. L-studio (<http://algorithmicbotany.org>) is a L-system based commercial plant simulator written in c++, with tools for plant rendering and interacting with environment. GroIMP (<http://sourceforge.net/projects/groimp/>) is growth grammar-related interactive modeling platform written in Java. LIGNUM (<http://www.metla.fi/metinfo/kasvu/lignum/index-en.htm>) software implements the model of the same name. AMAPSim [7], written in c++, simulates plant based on botanical rules using reference axis, and it can incorporate external functional modules. Besides, OpenAlea (http://jeudi.inrialpes.fr/2007/Raweb/virtual_plants/uid30.html), written in Python, is claimed to be an

open-source platform for the integration of heterogeneous FSPM components. These softwares aim at designing and simulating plant. Softwares that provide tools to calibrate the model is rather few. Based on the GreenLab model, Cornerfit is a pioneer software for both plant simulation and parameter identification from real experimental data [8]. While CornerFit was limited to plants of single stem, DigiPlante software, also written in c++, can simulate and fit target data of generic plant structure from crops [4] to trees [9]. An open-source member of GreenLab softwares is GreenScilab (<http://www.greenscilib.org>), started by Matlab code and then implanted to Scilab. It can simulate generic plant structures [10] including both crops and trees and do calibration for plants of simple branching structure [5].

Trees are more complex in terms of structure than crops. There can be different kinds of metamers in a single growth unit of a tree [11], while for crop there is only one. Substructure algorithm [11] has been applied in GreenScilab for speeding up the computation on tree structure, but this brought little advantage for crops. Moreover, for trees, organs of the same physiological age and chronological age are regarded as the same, while for crops, it is not necessary the case, especially when the positional information need to be taken into accounted, e.g., simulation of basipetal flowering sequence [12]. Therefore, a new version of GreenScilab dedicated to crops, namely GreenScilab-Crop, is developed, where plant structure is explored in prefix-order to get the positional information. The new version needs less source code and has clearer software structure.

II. PRESENTATION OF GREENSCILAB-CROP

A. GreenLab methodology

There are different levels of the GreenLab model, namely the deterministic model GL1 [11] as in most GreenLab applications, the stochastic model GL2 [10] where bud behavior is probabilistic, and feedback model GL3 [13] where bud behavior is dependent on plant growth. The common feature among different GreenLab versions is that there is an organogenesis model providing the number and types of organs, and a functional model providing the biomass and size of organs. The detailed description of GreenLab model can be found in

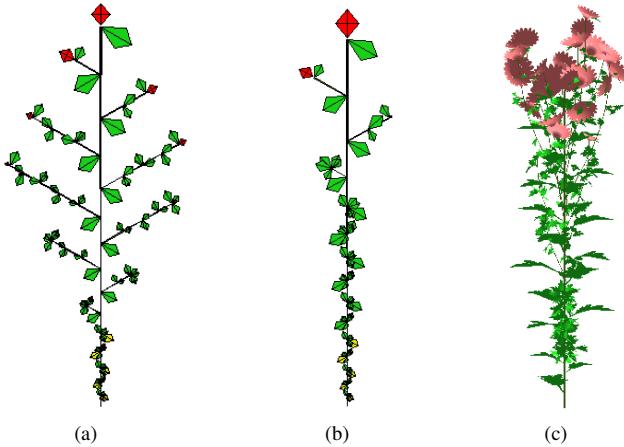


Fig. 1. Simulating plants with basipetal (top-down) inflorescence by applying delay function in GreenScilab-Crop. (a),(b) virtual plants with growth delay of different dependency on sink-source ratio; (c) simulation of a chrysanthemum plant.

publications focusing either on the theoretical or application aspects [11][14][15][16].

In GreenScilab-Crop, which implements a deterministic GreenLab model for crops, at each cycle (corresponding to a phyllochron), all the buds produce a phytomer until the plant structure is complete. A phytomer is a botanical unit containing one internode, one or more axillary leaves, buds and sometimes flowers. Each expanding organ has a (relative) sink strength as a function of its age and branching order. The type of organs are blade, sheath, internode, female organ, male organ, and the root system. Based on a common biomass pool hypothesis, the biomass available at each cycle is partitioned among all expanding organs according to their sink strength. By accumulating the biomass since its appearance, the biomass and consequently size of an organ are computed, including leaf area, from which the biomass production for next cycle is computed using empirical formula. Finally, geometrical parameters, such as organ insertion angle and phyllotaxy, are used to build plant 3D structure.

Compared to previous GreenLab model, in the current GreenScilab-Crop, the growth delay function is introduced for simulating the basipetal flowering sequence in plants with inflorescence of any branching order. The growth delay of a branch is modeled as a function of its position. In building plant topological structure in prefix-order, the position of each branch is noted using the its phytomer rank on its mother axis, being one number in main stem, two numbers in first-order branches, etc. Fig. 1 shows an example of simulated inflorescence structures with an application on chrysanthemum plant. More detailed description can be found in [12].

B. Model calibration

Model calibration is an important issue in application. Some parameters are directly measurable, such as specific leaf weight, leaf functioning time, organ allometry parameters, etc. Other hidden sink-source parameters are to be identified by

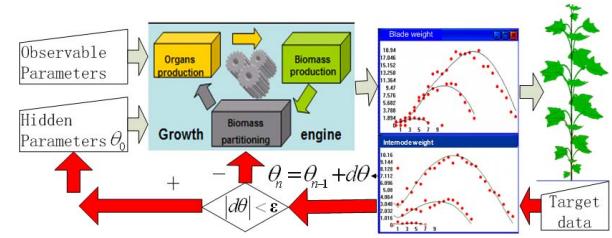


Fig. 2. Illustration of GreenScilab-Crop flowchart. For simulation (in gray arrow), the software loads parameters and outputs plant data (lines) with 3D structure; for calibration (in red arrow), the software minimizes weighted root-mean-square error between the model output and the measured data (dots), by searching for optimal values of hidden parameters (θ).

minimizing the weighted square root between the measured plant (target) data with the corresponding model output. It is important to add weight to each data as those of different types and sampling stages may have significant difference in data scale. The *lsqrsolve* Scilab function has been chosen as solver for the non-linear fitting between model output and target data, which is based on levenberg-marquardt algorithm.

C. Software architecture

An illustration of the software architecture is shown in Fig. 2. The kernel of the software is a GreenLab-based growth engine responsible for organ production and expansion. There are two ways of running the software. One is from plant parameters to plant data including 3D structure (simulation), the other is from plant data to achieving plant hidden parameters (calibration), by minimizing the weighted root-mean-square error between the model output and the measured data. In the latter case, the growth engine will be called iteratively to update the parameters from their initial values.

1) Parameter file: The principle input file is the parameter file (*.sci) under folder *parafiles*\ of GreenScilab-Crop folder. This file specifies the parameters for organogenesis, sink and source, geometry and output information. Most of the parameters are accessible through the user interface, see an example in Fig.3. Besides, an external functioning file (*.txt) is specified in case some parameters are not constant, such as the expansion duration of organs, specific leaf weight, etc. The user needs to use reserved keywords for such specification. The content of a functioning file can be empty. If the task is calibration, the parameter file need to include also the list of target data files (see below) and their corresponding functioning files. There are parameters indicating which subset of the target data should be included into the fitting, and which hidden parameters need be identified. When a parameter is chosen for fitting, its value in parameter file will be taken as the initial value for optimization algorithms.

2) Target file: The type of data in the target file are of several levels of detail. Each target file (*.txt) contains some key words indicating the data type and contents. The most simplified data type is at plant level, where organ data of the same type are all gathered, for example, the total fruit mass. This kind of data is typically used in process based model. On

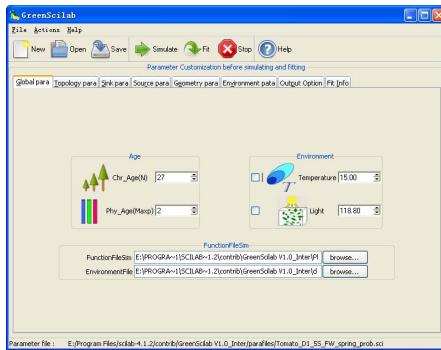


Fig. 3. Illustration of GreenScilab-Crop interface.

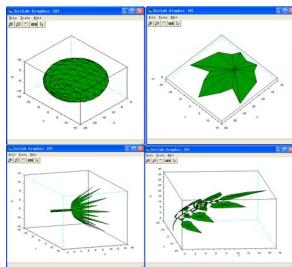


Fig. 4. Examples of organ geometrical shapes described by .smb files.

the other hand, the most detailed data type is at organ level, where the exact plant topology is recorded, and the information (biomass and size) is described for each organ in axis. An intermediate data type contains detailed organ description for main stem, and summed biomass for all branches at each phytomer rank of main stem. More detailed data description gives more information on plant architecture, but it also means more labor needed to obtain the original data. Choice can be made according to prior knowledge on the plant. Each data file can contain data from destructively measurement at one or more stages. If the plant topology is different, their data need to be written in separate data file.

3) *Geometrical file*: GreenScilab-Crop computes the position and orientation of each individual organ in 3D space. To visualize the plant geometrical shape, each type of organ is represented by a specific file (*.smb) denoting its geometrical shape. These binary files are under folder smb\|. In this file, the size of organ is normalized, and the organ shape is scaled according to its actual size when building plant geometrical shape. To plot an organ from a .smb file, the following command can be used.

```
exec('GSL_DIR\smb\gl_draw_organ.sc')
```

where GSL_DIR is the path of GreenScilab folder. Fig.4 shows the example of .smb files in software. The constructed geometrical link of plant organs can be output to a linear tree file (*.lgi), saved under the folder of the same name. Combined with .smb file, the resulting geometrical model of plant can be converted to other file format to be rendered in commercial or free software like Povray.

D. Tour of software

To design and simulate a plant from a parameter file, users can create a new parameter file or modify from an existing one through the interface. When the parameter file is ready, the user can click the button with label 'Simulate' to run simulation. Numerical results regarding the number of organs, plant demand and biomass production at each cycle, will be displayed in the command window of Scilab, if the corresponding output options are on. Some Scilab graphic windows will appear, indicating leaf area index, organ size and biomass (Fig.5a), etc., depending on the output option. Similarly, the plant 3D shape can be plotted directly in Scilab (Fig.5b), or output to a .lgi file.

To identify parameters, the plant data files need to be prepared. The user may choose though the interface not only the data to be included in fitting target, but also the hidden parameters to be identified. The user can click the button with label 'Fit' to start the fitting process. Once it is done, the fitting result, both in figures for plant data and model output (Fig.6), and the final parameter values, will be displayed.

Besides the interface, user can also choose command line way to start the job, being

```
exec('GSL_DIR\gl_simulate.sce');
exec('GSL_DIR\gl_fit_para.sce');
```

for simulation and fitting respectively. However, for the unexperienced users, it will be difficult to modify the parameters without interface.

III. A CASE STUDY ON TOMATO

The tomato plant (*Solanum lycopersicum L.*) is chosen for a case study to show how to simulate and fit plant data using GreenScilab-Crop. It is part of our research work on studying plant behavior in reacting to different population density [17].

A. Simulation

To create a parameter file for tomato, all of the topological parameters, sink-source parameters and geometrical parameters need to be given. The tomato plant in our study has a main stem with trusses distributed along it. Taking into account the development of individual fruits in the truss, the truss is regarded as a branch instead of a single organ as in [16], thus the physiological age (equivalent to branching order for crops) of plant is set to two. Numbers of fruits in each truss are given in the functional file using keyword (Axis). For example, to indicate there are two trusses at phytomer rank eight and eleven on main stem respectively, each having six fruits, one may write:

```
(Axis)      1  8
(Phy_Age)  2
(Length)   6
```

```
(Axis)      1  11
(Phy_Age)  2
(Length)   6
```

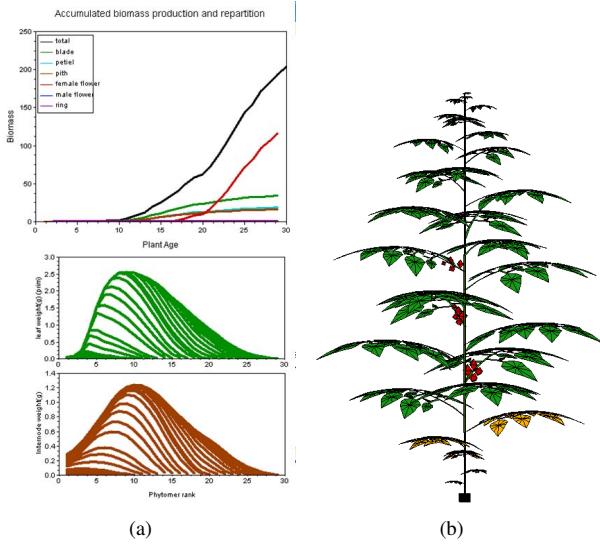


Fig. 5. Simulation results of a tomato plant. (a) numerical results on organ biomass and biomass repartition at plant level; (b) simulated plant geometrical shape.

where the keyword (Axis) indicates the position of an axis, (Phy_Age) is one for main stem, and two for first-order branch, (Length) is the number of phytomers per branch.

Some functional parameters can be obtained directly from the data, such as the specific leaf weight (SLW). If a parameter varies with time instead of being constant, it can be written in the functional file using the corresponding keyword. For example, for SLW, keyword (Thickness) is used, as below:

```
(Thickness)
(Cycle) 10 0.0023
(Cycle) 15 0.003
(Cycle) 19 0.003
```

where the integers after keyword (Cycle) indicates plant age in phyllochron, and the last number is the measured specific leaf weight at these plant ages. Linear interpolation will be made for other plant ages. In this way, the organ expansion duration and the leaf functioning time can be given.

For the hidden sink-source parameters, to start, users can specify their values arbitrarily, but the simulation results can be bizarre if the values are not reasonable. Identification of parameters will give realistic simulation. In the example of Fig.5, the sink-source parameters resulted from fitting the model output with experimental data. To get the 3D shape of plant as in Fig.5, geometrical parameters are also needed. For tomato, they are mainly the insertion angles of organs, name of their .smb shape files, etc.

B. Parameter identification

The plant data were obtained from a solar greenhouse experiment in spring 2007, with population density three plants m^{-2} . Samplings were made at five dates during cultivation period. The target data include both those of plant level and

intermediate level. An example of plant level data in target file is shown below, where text between () are all reserved keywords. For example, the two integers after the keyword (Cible) mean the age of plant and the type of target data, respectively; for plant of a given age, it is possible to have more than one types of target data. The following keywords indicate the biomass of different components of plant (blade, petiole, internode, fruit).

```
(Cible) 27 2
```

(Blade_Mass)	31.239
(Pet_Mass)	16.514
(In_Mass)	18.789
(FeFr_Mass)	102.47

For tomato, the parameters to be assessed inversely including eight sink parameters and two source parameters. Fig.6 shows the plant data and the corresponding output from GreenScilab-Crop, when the fitting process finish. Notice that all data were fit simultaneously by optimizing the hidden parameters.

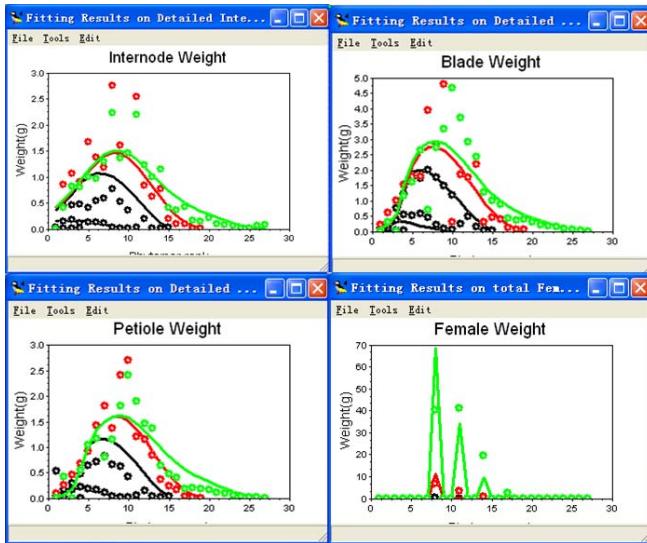
In the end of fitting process, the final values of parameters will be displayed in the command window of Scilab. Part of the results are shown as follows, with the initial values of parameters displayed in the right. The final parameter values can be used to simulate the plant by the calibrated model.

```
x_S_P(1) = 0.5415120 (init = 0.670000)
x_S_I(1) = 0.4313699 (init = 0.460000)
x_S_Ff(2) = 13.483729 (init = 25.900000)
x_rp = 0.0011776 (init = 0.001980)
```

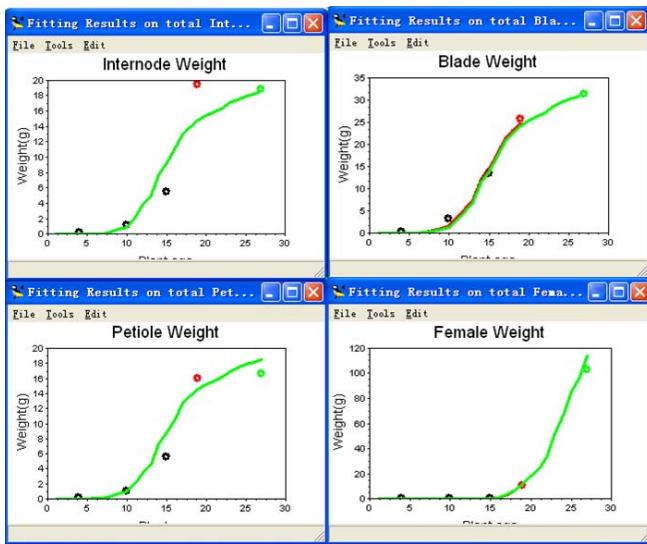
IV. REMARKS

GreenScilab-Crop provides a free software for crop simulation and parameter identification. This open-source member in family of FSPM softwares can serve for deep understanding and testing of the GreenLab model. It has actually already served in teaching activity. The new version GreenScilab-Crop makes it more feasible to fit data of agronomic and horticultural plants. The introduction of delay function make it possible to simulate the basipetal flowering sequence for herbaceous plant with inflorescence. Example parameter and target files, better interface and user manual are provided to help users.

Scilab itself is a free software for scientific computation, whose programming language is easy to be grasped by modelers. Moreover, Scilab provides functions for optimization, matrix manipulation and visualization, which can save a lot of coding work. It is easy to translate code from Matlab, a commercial software commonly used in modeling. Aiming at sharing knowledge from among people from different domain, GreenScilab-Crop can play a role as an open platform for linking with other modules such as photosynthesis model, plant biomechanics model, genetic model or ecophysiological model.



(a)



(b)

Fig. 6. Fitting results on tomato data for four types of organs (blade, petiole, internode and fruit) at five sampling dates, from simulation (symbols) and measurement (lines). (a) organ level data for main stem and summed data for branches; (b) plant level data.

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