Tutorial on GreenLab Model using GreenScilab software

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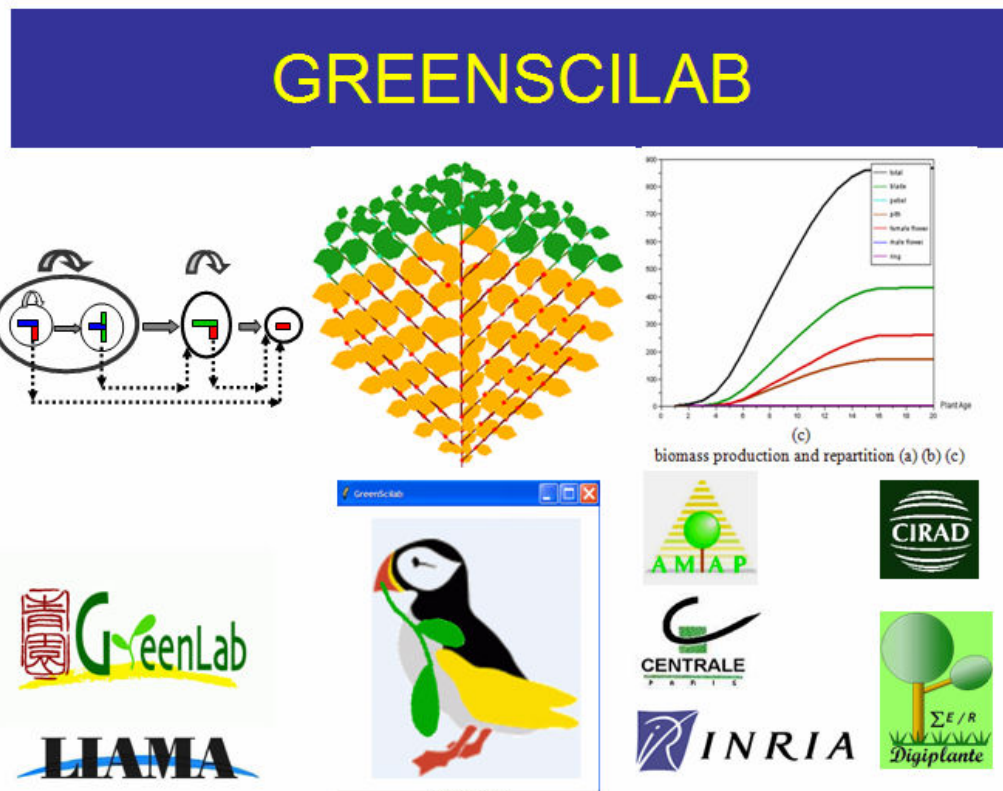
1. Introduction to GreenLab at level GL1

Scilab is versatile software developed by INRIA that shares the same philosophy as Matlab. It is useful to write easily the codes that simulate models. GreenScilab is a toolbox developed in Scilab to run the GreenLab model.

GreenLab is a Functional Structural Plant Model (FSPM), which builds the plant morphogenesis using algorithms that simulate both the organs production (plant development) and the biomass production (plant growth). The plant development is depending on an automaton that produces organs in growth cycles (GC) thank to rules of growth, branching, mutation or death. The biomass production is ensured by the source organs that are usually the seed and the leaves. Moreover GreenLab provides the biomass partitioning among the different organs according to their sink strengths and allows building their geometrical shape using allometric rules. Eventually geometric rules applied on the organ positioning and the organ orientation will complete the building of the plant architecture in 3D. GL1 is the simplest feature of GreenLab: the virtual plant is deterministic, and there is no interaction between the plant growth and the plant development. Other levels are GL2, the stochastic case (PhD Kang, 2003), and GL3, the deterministic case with retroaction between plant growth and plant development (PhD Mathieu, 2006).

2. Presentation of the toolbox

The main window of GreenScilab is as in Figure 1:

Figure 1. GreenScilab main window

File: to operate on parameter and target files.
Parameter: to set the values of the parameters that control the plant development, the plant growth, the plant geometry, environment effect, output option, *etc*.
Simulate: to launch the plant simulation, which computes the virtual plant.
Fit: to compute the hidden parameters of the model from a target file that describes the plant production.
Output: to display the results of the simulation: arrays of data, curves, or 3D display.
Option: some options for running environment.
View3D: to see plant 3D structure without simulating again the plant growth.
About: to display information about contributors, website and version info.

3. Parameters

Main options to click on are: Plant age, Physiological age.

3.1. Plant age:

It opens a dialogue with two inputs, as in Figure 2:
1) The Chronological Age (CA) N: This is the number of growth cycles for the plant development and growth, or simply plant age. The duration of a growth cycle in real time is linked to the so-called "thermal time" that is necessary to produce a growth unit (a phytomer for crops) in ecophysiology. Range of N is usually $1 \leq N \leq 100$.
2) The Maximum Physiological Age (PA) *Maxp*: it is the number of states for axis differentiations in a plant. When a bud gets aging, its PA may increase. Let PA=1 for the main stem. The PA of a branch is not less than that of the bearing axis. Plant seldom has PA higer than 5 ($1 \leq Maxp \leq 5$). For a simple branching pattern the PA is similar to the branching order.
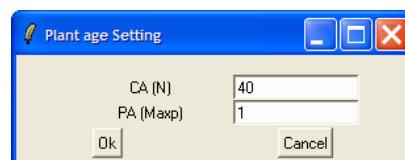

Figure 2. Dialogue for plant age

3.2. Structural parameters for axis of each PA

These parameters are done to control the plant development and the plant geometry for each physiological age. The different kinds of metamers with their associated organs and the different kinds of growth units with their associated metamers are designed, according to the physiological ages. In parallel, the geometric rules for positioning organs are recorded: branching and phyllotaxic angles, mechanical parameters. Options are:
1) Topological parameters.
2) Geometrical parameters.

3.2.1. Topological parameters of GreenLab

The topological model is a dual-scale automaton as shown in Figure 3. The automaton passes from botany towards a mathematical model to simulate the plant development.
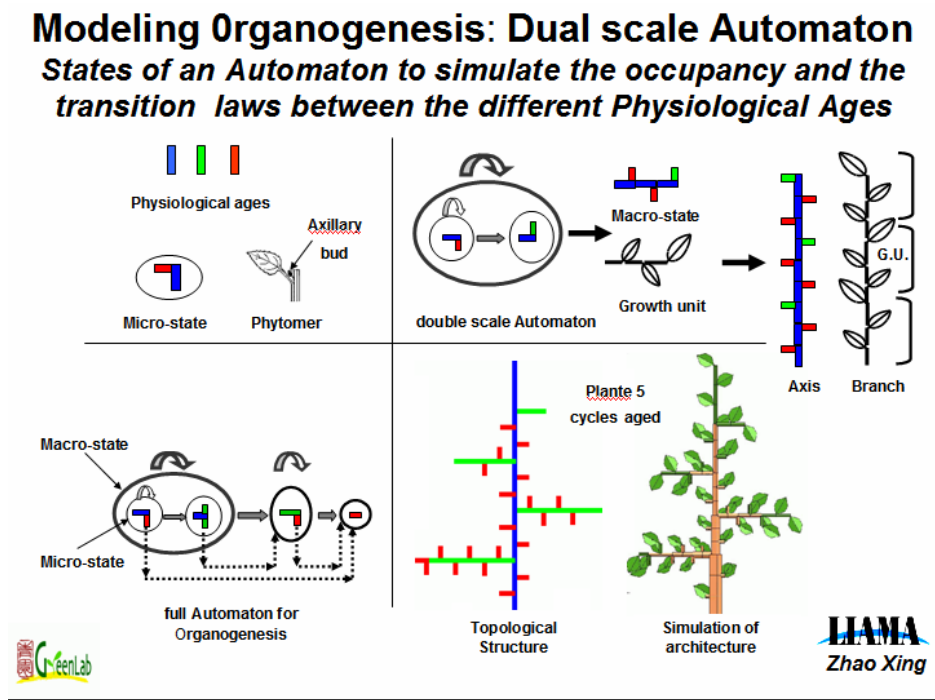

Figure 3. illustration of the dual-scale automaton

To set topological parameters in GreenScilab, choose Parameter/Physiological age k/topological parameter. Then a dialogue as in Figure 4 will appear. Remember it is setting for PA k, and the number of items in the dialogue is not the same for different PA.

Parameters for the Growth Unit

This window in Figure 4 allows building a growth unit (GU), *i.e.*, to define the number of metamers in a shoot during one growth cycle.
The PA is designed by a specific colour. Blue is for PA 1, green for PA 2, …, and purple for PA 5 etc.
Each metamer of a given PA can bear axillary buds whose PA is equal (reiteration) or higher (branch). So there are 5 types of metamers for PA 1, and $5 - k + 1$ for PA k.
The number of metamers of the same kind is to be set. The metamer kinds are sorted in a GU according to the notion *acrotony*. The metamer with reiteration (k) is in the upper part of the GU, and those that port buds of older PA locate lower.
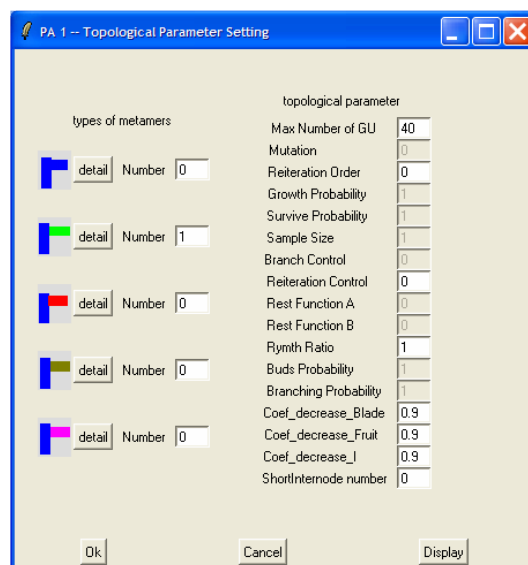
Figure 4. Dialogue for topological parameters

Clicking on display allows seeing the GU organisation, as the figure in the left in Figure 5, which gives the topology of GUs of different physiological age.

Corresponding number of metamer types are:
GU PA1   0 2 3 4 5
GU PA2   0 2 3 4
GU PA3   0 2 3
GU PA4   0 2
GU PA5   1
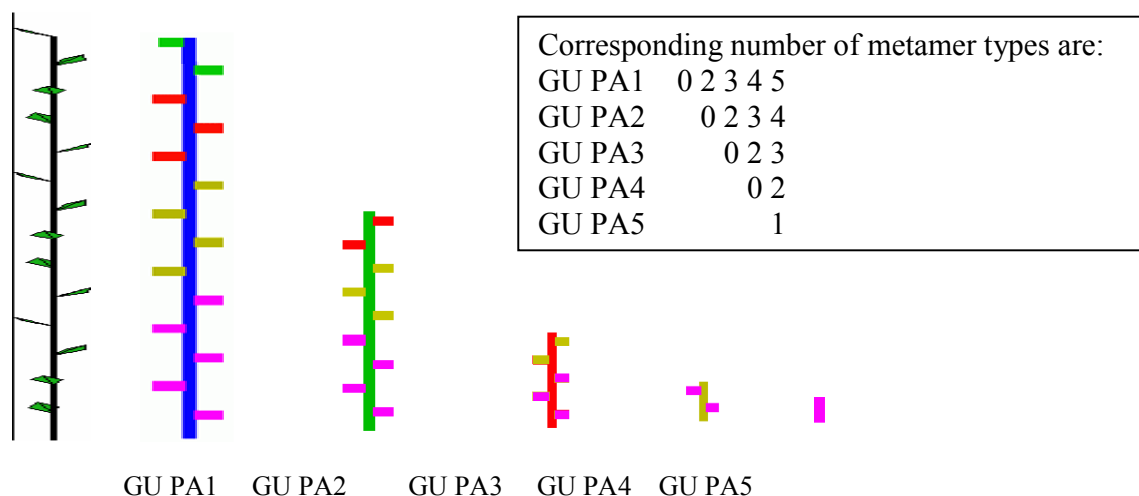
GU PA1   GU PA2   GU PA3   GU PA4   GU PA5

Figure 5. An example of topological parameters with acrotony on growth unit

Only trees have complex GU, for shrubs GU is made of a single metamer. If no reiteration occurs, the second metamer is convenient to describe a branching order if branches exist.

Parameters for the Metamer

Clicking on detail in Figure 4 allows seeing the organisation for each type of metamer.
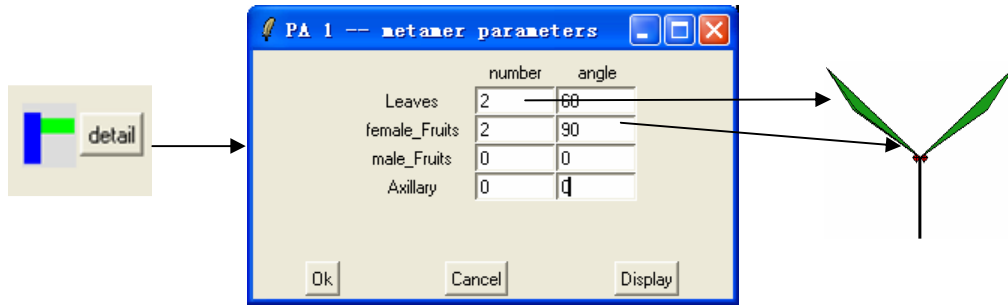
Figure 6. Dialogue for metamer parameters. 2 leaves with insertion angle 60 degree and two fruits of insertion angle 90 exist in this metamer

This dialogue in Figuer 6 designs the metamer. Each metamer can have zero or several leaves, fruits (female or male) and axillary buds. Moreover an insertion angle is given to the organs and bud. Click Display to preview the 3D of the metamer, as shown in Figure 6.

Parameters for the Bearing Axis (BA):

The Bearing axis is the part of the shoot born by buds of the same PA. It is repetition of the same kind of GU. The key parameters in Figure 4 are as follows:
Max Number of GU: Maximum number of GU on the Axis of the given PA before mutation. For example, in Figure 7, this value is 5, 3, 1 for axis of PA 1, 2, 3 separately.
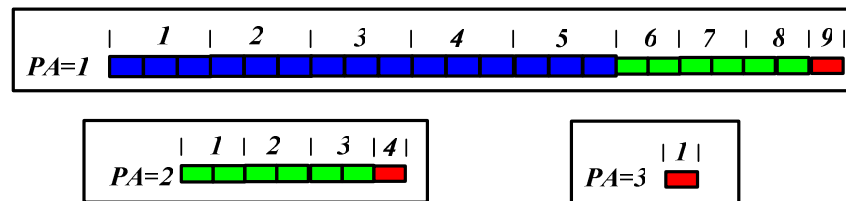

Figure 7. Illustration of the mutation of in axis

Mutation: the new PA of the terminal bud if mutation happens after cycle Max Number of GU. For example, in Figure 7, this value is 2 for PA 1, and for PA 2, this value is 3. The valid value is between 1 and Maxp, otherwise the terminal bud just die when the age of the axis is older than Max Number of GU.
Reiteration order: to control max branching order for reiteration if such metamer exist. The bigger is this value, the more the structure looks like a fractal. When this value is it means no reiteration.
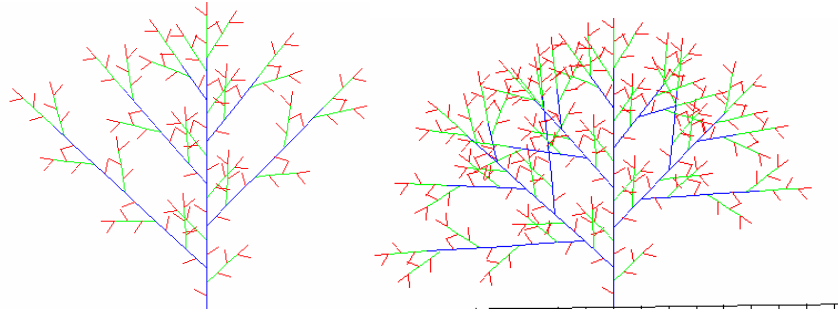
Figure 8. Reiteration on bearing axis of PA 1 with order 1 and order 2 (parameter file reiteration.sci)

Branch/reiteration control: if no control (0), each branch can reach its Max Number of GU. Otherwise (value 1), the branch development finishes when the bearing axis finishes. This is often the case of inflorescence. Example is shown in Figure 9.
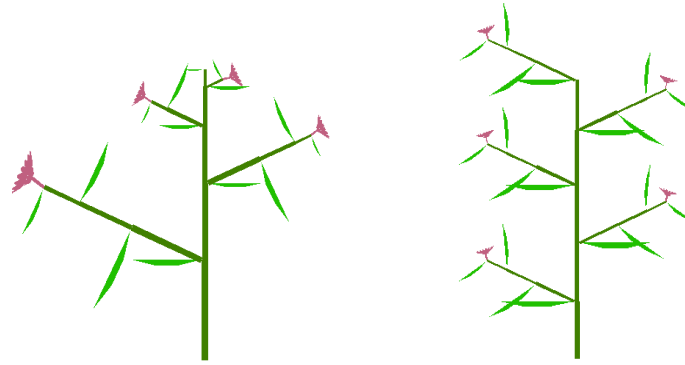

Figure 9. Simulation of branches with (left) and without (right) branch control (parameter file delay_inflo_0.sci and delay_test_0.sci)

Rest Function *A,B*: to control the delay of branch development according to the rank *i* in the bearing axis. Number of delayed cycle is *D(i)=A+B*(M-i)*, M being the Max number of GU in the stem. Examples are shown in Figure 10.
When B=0, delay does not depend on the branch position; lower flowers are heavier;
When B=1, all branches start at the same time; all flowers are of the same weight;
When B=2, the branch start from top to bottom one by one; upper flowers are heavier;

(1)   (2)   (3)
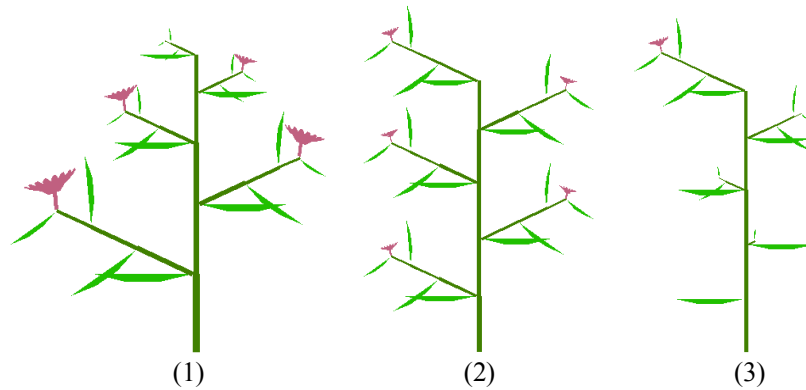
Figure 10. Delay of branch development. (1) A=1,B=0; (2)A=0,B=1(3) A=0,B=2. parameter file : delay_test_1/2/3.sci

Rhyth ratio: number of GC done for the PA *k* compared to the control clock of PA 1 as illustrated in Figure 11.

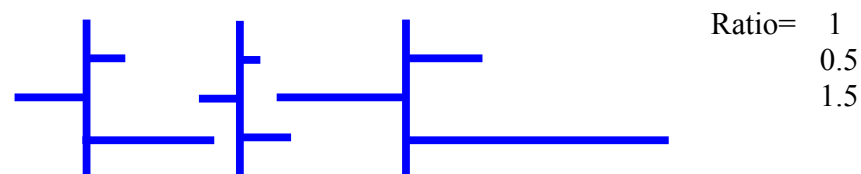Ratio= 1
       0.5
       1.5

Figure 11. Diagram on rhythm ratio

ShortInternode number: to set number of short internodes in the bottom of the stem like for maize and wheat. Their sink strength is very small, and a coefficient can be set in Functional Parameter.

Most fields in grey colour are not yet available (features for GL2)

An example

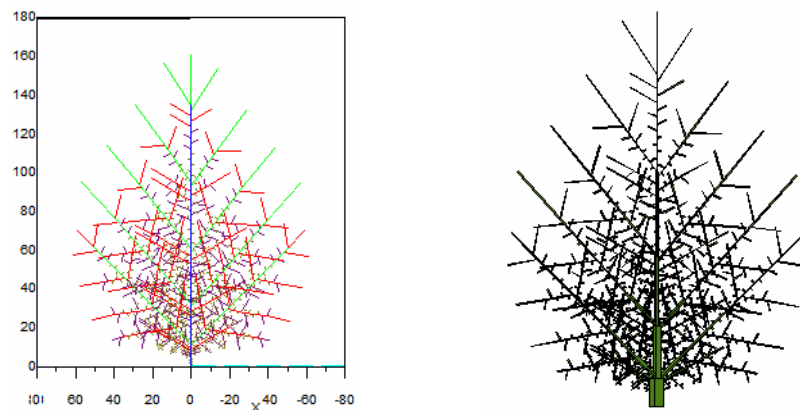An example of complex structure is given, as in Figure 12.

Figure 12. Plant topology and 3D display (parameter file topo_file.sci)

Choose "Number of Organs" in Output (main window) gives the organ production for each physiological age and their sum.

For this tree, at plant age 6, it is:
  Number of Growth units, Internodes, Leaves in plant...
phy_age   1
       1   14   14
       2   28   28

```
            3       42      42
            4       56      56
            5       70      70
            5       70      70
    Number of Growth unit, Internodes, Leaves in plant...
phy_age         2
            0       0       0
            2       18      18
            6       54      54
            12      108     108
            20      180     180
            29      261     261
    Number of Growth unit, Internodes, Leaves in plant...
phy_age         3
            0       0       0
            3       15      15
            13      65      65
            34      170     170
            67      335     335
            114     570     570
    Number of Growth unit, Internodes, Leaves in plant...
phy_age         4
            0       0       0
            4       8       8
            24      48      48
            76      152     152
            179     358     358
            347     694     694
```

The results are computed with substructure method (Yan, 2002; Cournède, 2006), which is very efficient for tree structure.

3.2.2. Geometrical parameters

These parameters are done to control nicely the plant shape by setting the curvature of the axis, the leaf direction, *etc.* The bending of axis is set using theory from mechanics, as shown in Figure 13.
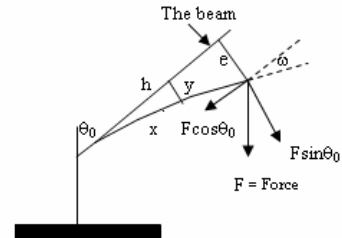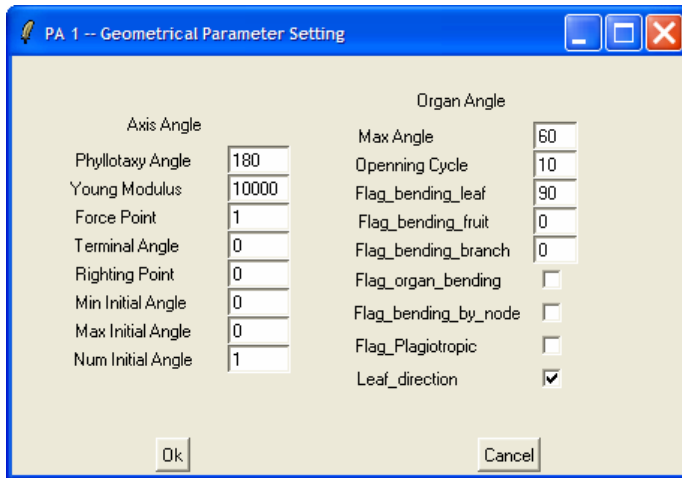
Figure 13. Geometrical parameters and illustration on stem bending

Phyllotaxy Angel: it designs the spiral that controls the insertion of axillary buds on the bearing axis. They are 180 degree for the example is Figure 12.

Young Modulus: it gives the stiffness to the branch. The bigger this value is, the more stiff is the stem.

Force Point: a force is applied with range 0 – 1, which means a position between 0% and 100% of length of the axis. The value is near 1 in graph in Figure 13. The bending is positive before the force point and this mimics the effect of gravity.

Terminal Angle: the end angle of an axis, as the θ in Figure 14.

Righting Point: the number of GU in the top of axis that begins to change to its original trace to mimic the righting of branches with given terminal angle, illustrated in Figure 14, where this value is 4. When this value is 0, the terminal angle will not function.
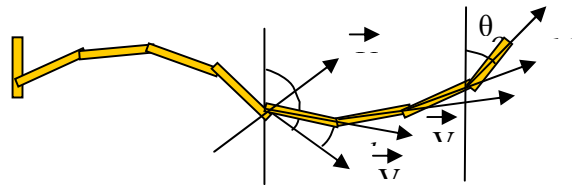

Figure 14. The bending and righting up of branches

Min/Max Initial Angle: the initial angle is the beginning angle between the beam and the vertical direction (θ_0). It must not be 0, otherwise bending can not take place. However, we can set several possible initial angles to have different curvature of the axis.

Num Initial Angle: this gives number of different initial angles. Normally it is 1. It can be more than if plants like weeping willows are to be simulated.

Max Angle: the insertion angle of axillary branches and organs may change from the top to bottom until Max Angle.

Opening cycles: changes of insertion angles mentioned above take place in certain number of growth units in the top of the bearing axis. If this value is 0, the Max Angle does not function.
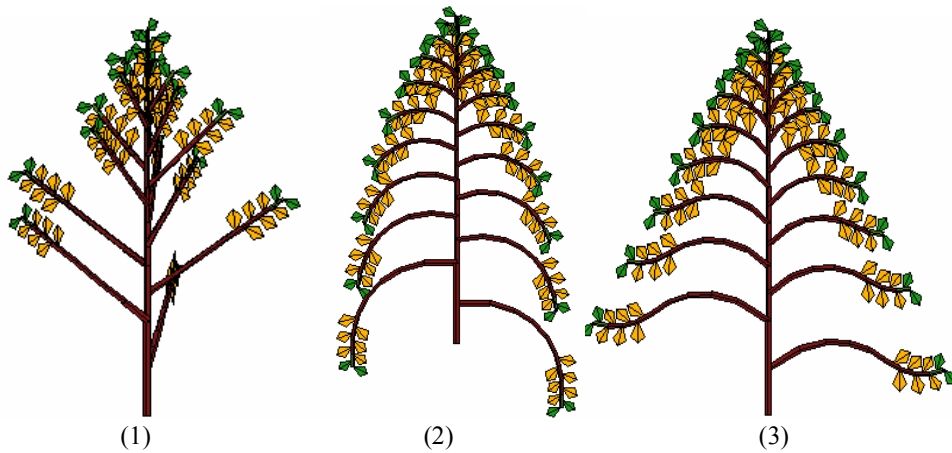
Effects of these parameters are shown in Figure 15.

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Figure 15. Examples on geometrical parameters. (1) Phyl(PA 1) =144.5, Young Mod(PA 2) = 10000 (2) Phyl(PA 1) =180, Young (PA 2) = 800, Force point (PA 2)= 0.6, Max Angle (PA 1)=90, Opening cycle=10, (3) same to (2) except the righting point (PA 2) =5. (parameter file test_bending1,2,3.sci)

3.3.   Inflorescences and Plant Architectural Models.

The Dual-Scale Automaton authorized easily multiple combinations that enable to mimic a lot of inflorescences and architectural models (F. Hallé 1978), as shown in Figure 16. They are the result of different branching patterns, growth and death process, and repetition and transition laws upon the automaton control. Running GreenScilab gives the organs production for each GC and each PA according to the selected Automaton.
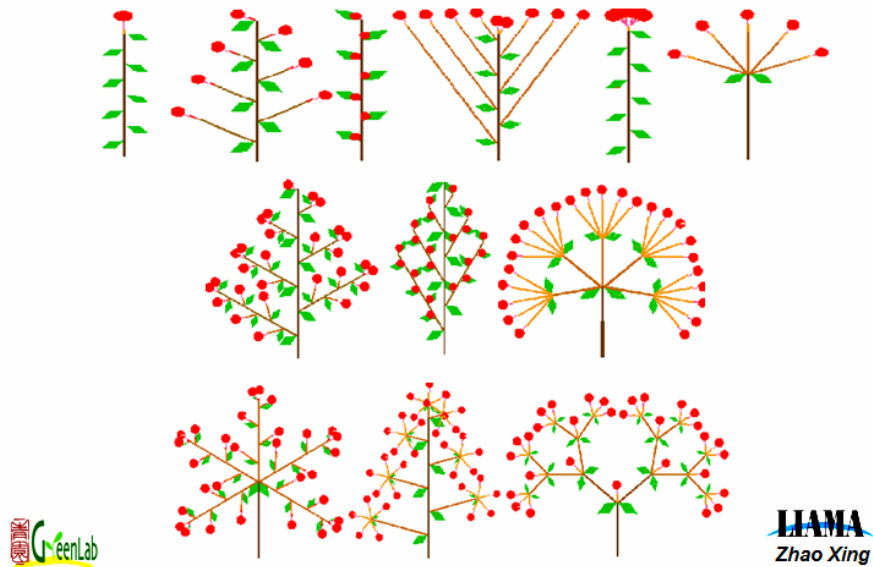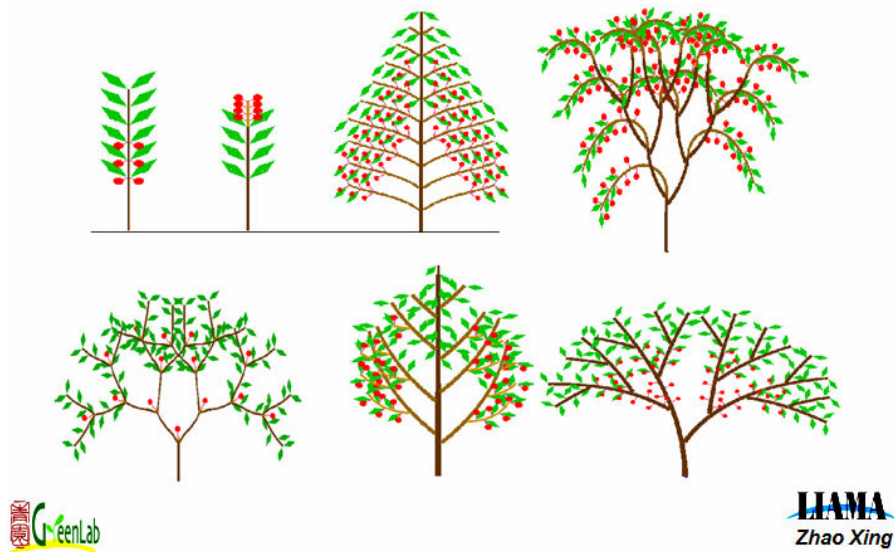
Figure 16. The inflorescence and architectural models simulated with GreenLab model

Several parameter files in folder 'Gallery' show different plant architectures, as shown in Figure 17.

Figure 17. Plant structures simulated in GreenScilab

Plant visualization can be speeded up using *tree_visu* software, developed with OpenGL in LIAMA by PhD students TENG Jun (滕军) and WANG Ning (王宁)。This software is distributed together with GreenScilab, but it is executable only in Window environment. It is very useful for visualizing complex structures like for trees, with good speed. Users can rotate, zoom and move the 3D graphics easily, and three display modes are possible: skeleton, wireframe, mesh. It is also possible to generate animated 3D if a

series of 3D files are prepared. The interface is shown in Figure 18. An example of visualization of tree in shown in Figure 19.
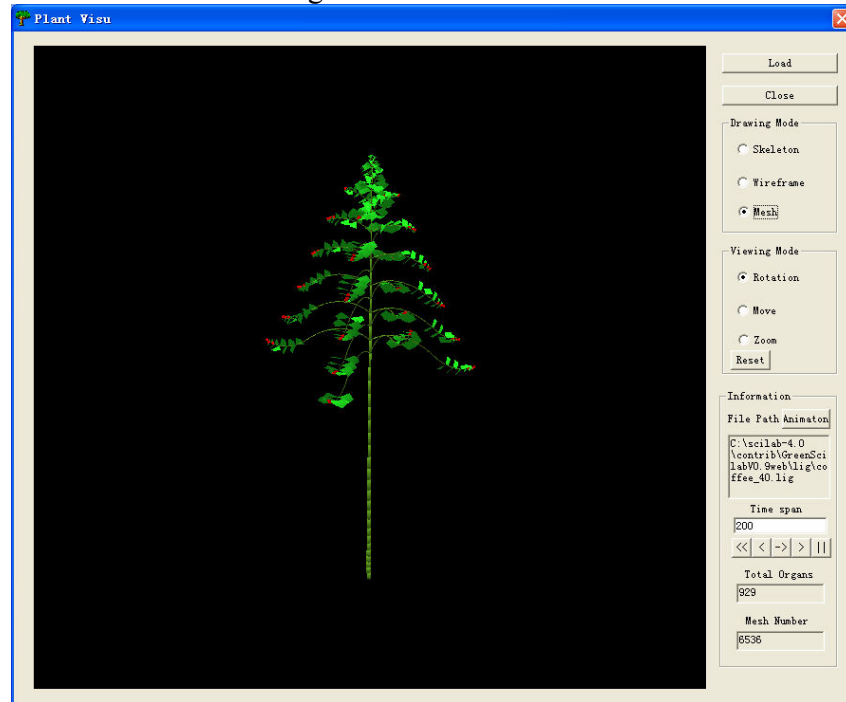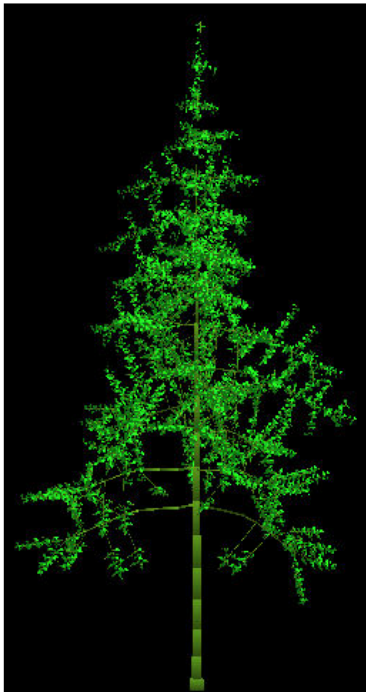

Figure 18. Interface of tree_visu software

The input file of this software is created by clicking Output/export 3D File from simulated plant. Then click View3D/plant in tree_visu.exe to start this software. Click Load to open the file. A display setting file (.dsw) is created to give the shape and color of the organs.

Figure 19. Visualization of a tree in tree_visu

3.4. Parameters for Plant Growth

Once the organ generation is done thanks to the Dual Scale Automaton (DSA, *Zhao et al.*), we have to make them play their roles as source organs and sink organs. Source organs are for now the seed and the leaves. They provide their biomass production to a common pool of biomass that is shared by all the organs that will compete to catch their part of biomass according to their sink strength, and thus carry out the biomass partitioning in the whole plant architecture. The process is shown in Figure 20. Note that GreenLab works as a Process Based Model (PBM). Here compartments are single organs and the pool of biomass feeds them by means of an allocation at each GC. There is no need of a topological structure at this step. No diffusion process or exploration of the topological structure is needed here, which makes the computation much faster.
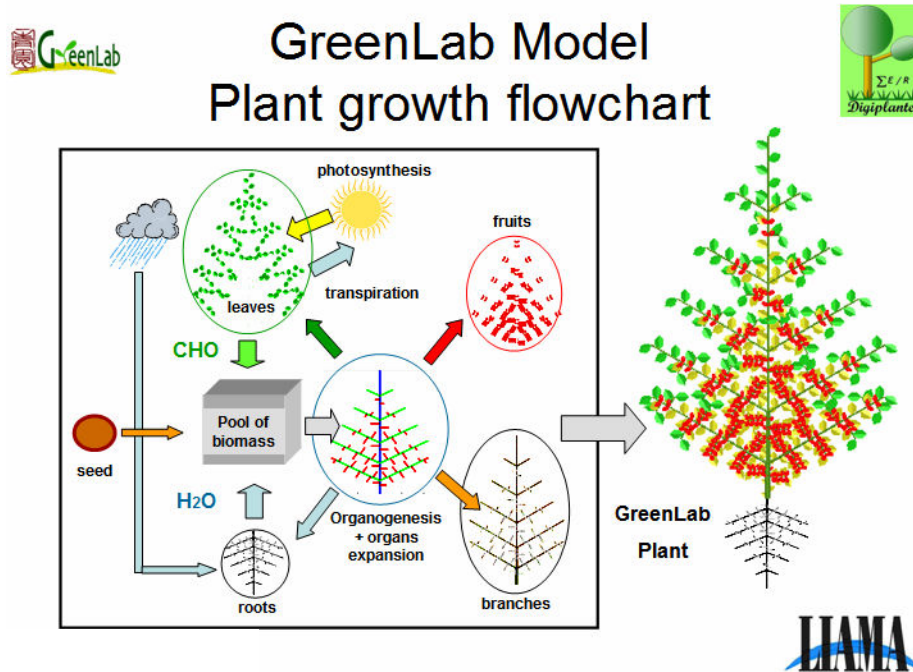

Figure 20. Flow chart of GreenLab model

3.4.1. Equations for biomass production:

Seed is made of a biomass Q_0 that is used at the first cycle to build the first metamer and the root compartment. The seed can empty during several GC into the pool of biomass:

$$dQ_n = Q0 * (1 - dQ_0)^n$$

Functioning of leaves in GreenLab uses transpiration. The water transpiration of a single leaf is proportional to its surface and to the potential evapo-transpiration ET0 and inverse of the leaf resistance. Eventually the incoming biomass inside the leaf is a fraction of the water coming out. The so called Water Use Efficiency (WUE) will be the rate of fresh or dry mater compared to the amount of water transpiration.

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For a single leaf we have: $Q = \dfrac{E}{R} = E.\dfrac{S}{r}$, where r is the resistance to transpiration of 1 cm^2 of surface and S the leaf surface.

The plant has N_B leave blades; each one has a surface S_i.

If we consider a homogeneous density of population of plants, each plant occupying a surface Sp, then according to ecophysiology and Leaf Area Index (LAI), the single plant production will be (GreenLab assumes $LAI = \dfrac{\sum_{i=1,n} S_i}{Sp}$)

$$Q_n = \frac{E.Sp}{r.k}\left(1 - \exp\left(-\frac{k}{Sp}.\sum_{i=1,N_B} S_i\right)\right)$$
Equation (1)

- k a coefficient for light extinction (related to Beer-Lambert law)
- Sp the leaf projection area that design the LAI per plant.
- E the growth potential for biomass production (it is up to the user (for example ETP)
- ΣS the functioning leaves area per plant.

The parameter E is the driving force of the plant growth. It is up to the user and according to the field conditions, can integrate ETP, PAR, …

Once the plant biomass production Q is computed, the biomass partitioning has to be performed. The Dual Scale Automaton computes the organ production of the plant at each GC. This provides what we call the plant demand D that is the scalar product between the organs and their associated sinks. We can write:

$$D(i) = \sum_{o=a,e} p_o \cdot \sum_{j=1}^{i} N_0(i,j).f_o(j)$$
Equation (2)

O is the type of organ: leaf, internode, fruit, root system, layer for girth;

p_o is the sink strength of the organ;

$f_o(j)$ is the function of sink variation strength of the organ j GC aged; In GreenLab Beta law is chosen for this function, as shown in Figure 21.

$N_0(i,j)$ is the number of organs of type O created at the cycle i-j+1; they are j-aged in current cycle.

So the demand looks like a convolution between the organ numbers and the sink function.

In GreenLab the flux of biomass incoming into an organ at plant cycle "i" is:

$$\Delta q_o(i,j) = \frac{p_o \cdot f_o(j)}{D(i)} \cdot Q(i-1)$$
Equation (3)

This flux of biomass depends instantaneously on the sink function and the ratio *Q/D* for the GC *i*. Finally the weight of the organ $q_0(i)$ is the sum of the fluxes along the growth duration.

$$q_o(i) = \sum_{j=1}^{i} \Delta q_o(i,j)$$

Equation (4)

Shape of the sink variation function

$P(i) = P.f(i)$ is the sink function

$P(i)$ is the sink value for an organ *i* cycles aged

P is the sink strenght.

$f(i)$ is the sink variation function with $Max(f(i)) = 1$

f(i) is a Beta Law, T is the expansion duration of Organ

Parameters *a* and *b* are computed by optimization

$$\begin{cases} f(i) = \dfrac{(x_i)^{a-1} \cdot (1-x_i)^{b-1}}{\sum_{k=1}^{T} (x_k)^{a-1} \cdot (1-x_k)^{b-1}} : & (1 \le i \le T) \\ x_i = \dfrac{i-0.5}{T} \end{cases}$$

The mean of normalized law is : $m = \dfrac{a}{a+b}$
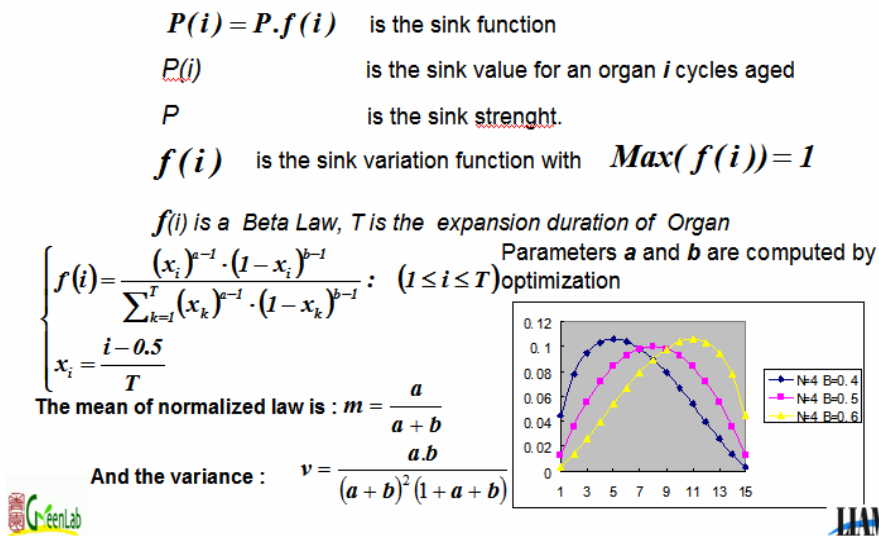
And the variance : $v = \dfrac{a.b}{(a+b)^2(1+a+b)}$

Figure 21. Sink variation function (Beta law) in GreenLab

The Beta Law choice is related to the plasticity of its shape. It can be J, I, U, constant, or Bell shaped. It is assumed that parameters *a* and *b* will catch the sink variation as long as possible. The source functions and the sink functions are hidden inside the plant architecture and cannot be assessed separately. The role of optimization is to compute by model inversion the parameters of GreenLab from a target file built with the organ weights at different CA and PA, as done in PhD thesis on GreenLab (Zhan, 2002; Ma, 2006 and Dong, 2006).

3.4.2. Allometry parameters for organ sizes

These parameters are to control the shape of organs. To enter the parameters click the "Physiological age / allometry parameters", then a dialogue as in Figure 22 appears. This allows giving the shape coefficients (*b, α,* see below) and the densities (*d*) of the organs. The biomass of the organ *q* divided by its density *d* gives the organ volume $v = q/d$. The volume through the organ densities and allometric parameters (*b* and *α*) give the sizes.
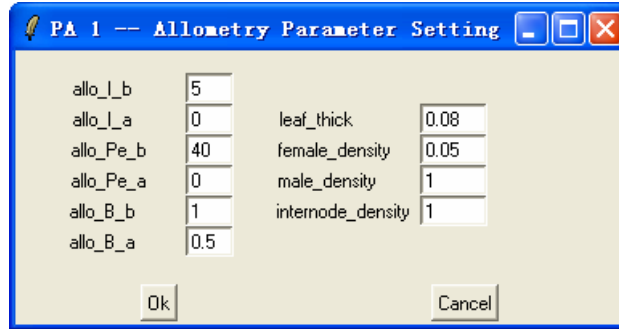
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Figure 22. Dialogue for allometry parameters

For the leaf we assume constant thickness *e* whatever is its contour, so the leaf surface is: $S = v/e$. Some kinds of plant blades have quite stable width, vary more in length for different area, thus its length and width is computed as:

$L = b.s^{\alpha}, W = s/L$

When $b = 1, \alpha = 0.5$, it is general case for leaves;

When $b = 0.1, \alpha = 1$, width will have fixed value 10 (cm). This is almost the case for the Chinese maize;

For internodes and petioles a cylinder is required. Its shape is controlled by parameters *b* and *α*:

Length: $L = \sqrt{b}.v^{\frac{1+\alpha}{2}}$, Section: $\sigma = \sqrt{\frac{1}{b}}.v^{\frac{1-\alpha}{2}}$

For fruit the basic volume shape can be a cube so the size *l* is: $l = \sqrt[3]{v}$

Special features are related to parameter α here (allo_i_a or allo_p_a):

$\alpha = 1$ means constant diameter, the length is proportional to the volume;

$\alpha = -1$ means constant length;

$\alpha = 0$ means constant ratio L/σ;

$\alpha = 2/3$ means constant ratio length/diameter;

The bigger *b* is, the thinner the shape is.

3.4.3. Functional parameters of GreenLab

To get access to the functional parameters click physiological age/functional parameters. The dialogue is shown in Figure 22. The meaning of the indexes are: B- blade; P- Petiole; I - Internode ; Ff - Female fruit; Fm - Male fruit; L - Layers (for girth); R - Roots; Br - branches.

PA 1 -- Functional Parameter Setting

	B	P	I	Ff	Fm	L	R	Br
Time_function	15	1	5	5	1	1	1	1
Time_appearance	1	1	1	1	1	1	1	1
Time_disappearance	99	99	99	99	99	99	99	99
Sink	1	0.0	0.4	3	0.0	0.5	0.0	
Time_expansion	12	1	12	12	1	1	1	
Para_expansion_1	1	1	1	1	1	1	1	
Para_expansion_2	1	1	1	1	1	1	1	
	curve	curve	curve	curve	curve	curve	curve	

Sp 250   rp 30   kp 1   ShortInternode RelaSink 1
Q0 1   dQ0 0.0   coef_layer 1

Ok   Cancel

Figure 23. Dialogue for functional parameters

Time functioning:

For now in GreenLab only leaf is functioning. Its functioning time is related to its photosynthetic duration in GC. Different colours can be used for the 3D representation when organs function or do not (yellow and green). This is convenient to visualize in 3D the functioning state of the plant. Note that internodes or fruit do have a photosynthetic functioning, but often it is often negligible.

Time appearance, Time disappearance: It is convenient to control the metamers on which the organ apparition is authorized on the bearing axis.
Normally for leaves, internodes and roots, the range is 1 – 99, which means that they appear at all growth cycles.
It may be different for fruits, it often needs several metamers before their apparitions (*eg*. range: 6-99)
The position can be at the tip, like for sunflower. If the bearing axis is finite (*eg*. parameter Max number of GU= 20) then the range can be: (range 20, 21). This means that the fruit appears at the position 20, and disappears at position 21.
Sometimes there is an isolated fruit, *eg*. cob on maize, the range can be 15, 16.
For now GreenLab proposes simple positioning. It can be extended to periodic or stochastic series (GL2).

Sink

Each organ, according to its index B, P, I…, gets a sink strength value. Some sink can be very big (case of fruits). Conventionally the blade sink is set to 1, because sink are relative and the blade always exists and can be measured. The sink strength of other organs are usually to be found by inverse the model based on measured data (see the tutorial on fitting).

Time expansion

Each organ, according to its index B, P, I…, gets expansion in weight during GCs. Root compartment expansion duration is indefinite, but other durations are finite. If the expansion duration is 1 it is called immediate expansion. In that case parameters for expansion have no effect.

Para expansion 1 and 2
Those 2 parameters are *a* and *b* of the *Beta* Law *f*.

The *Beta* Law can provide versatile shapes. Note that the skewness is controlled by $a+b$ and the shift by $a/a+b$. Examples are shown from Figure 24-26.
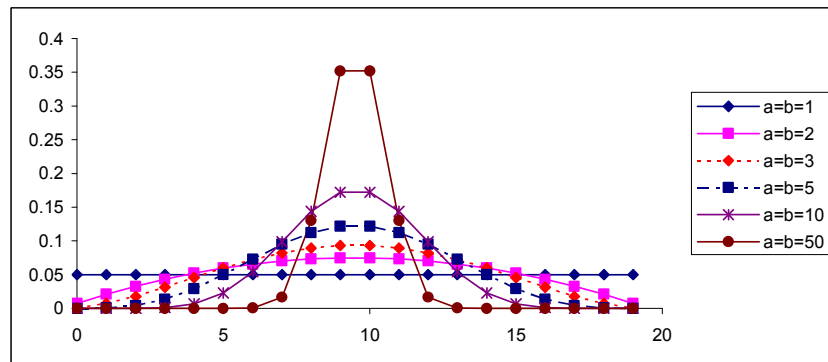
Figure 24. Different shapes of Beta law in case *a= b*
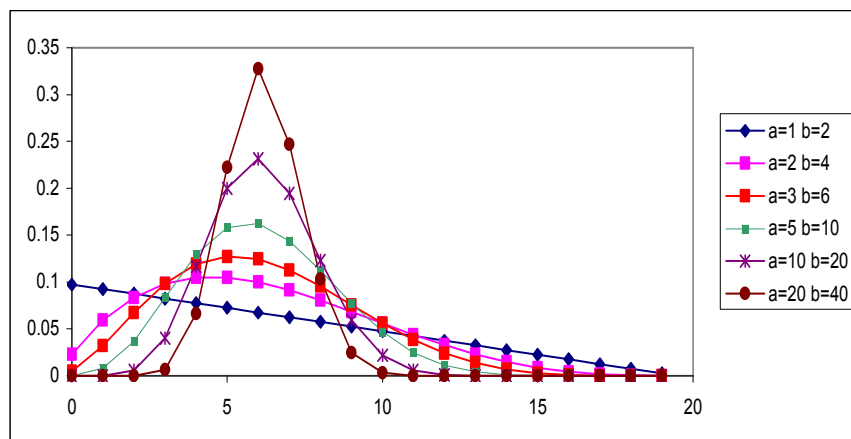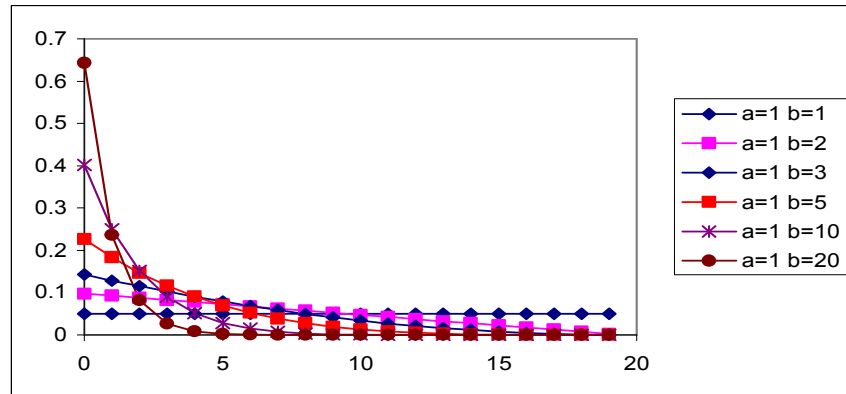
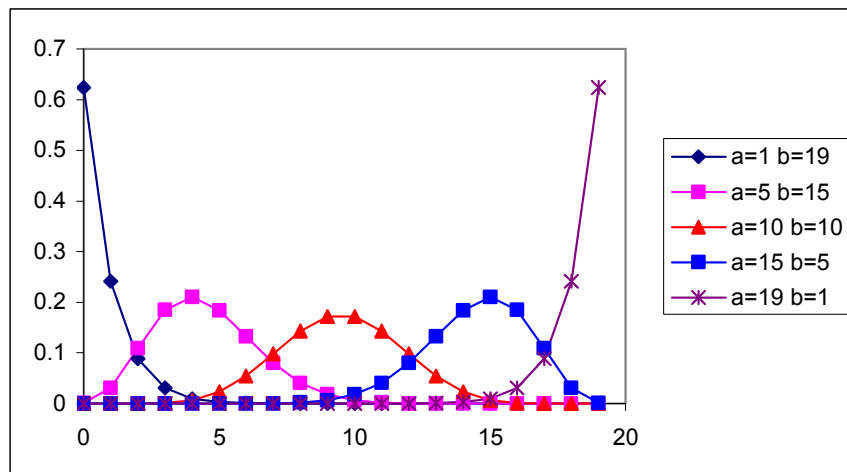Figure 25. Different shapes of Beta law in case *a < b*

Figure 26. Miscellaneous *a & b*

By clicking on "curve", we can see the Beta Law display according to its parameters.

3.4.4. Output options

These parameter control what will be output from the model. To get access to the output parameters click physiological age/output parameter. A dialogue in Figure 27 will appear.
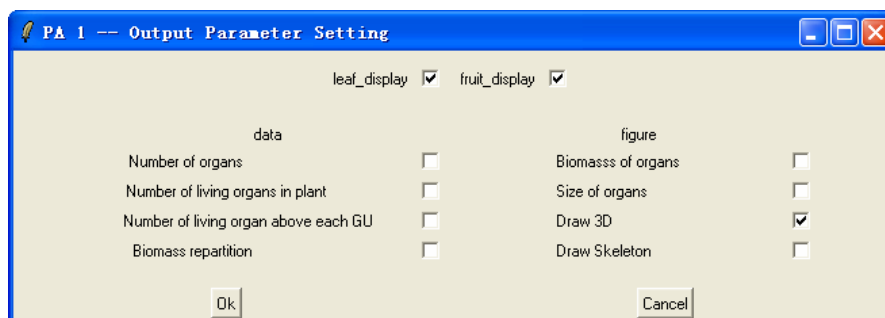
Figure 27. Dialogue for output parameters for each PA

One can see either numerical data or figures, or 3D shape of the plant. Click the checkbox to choose to output. Then when choosing corresponding item in menu output, these results will displayed.
Number of organs: total number of organs produced by the DSA;
Number of living organs in plant: number of functioning organs;
Number of living organs above each GU: this is used for computing layer for each growth unit.
Biomass repartition: total biomass produced in each cycle and its repartition to each kind of organs;
Biomass/size of organs: weight and size of individual organs of each PA.
Draw_3D: to display 3D shape of organs in Scilab graphics window; menu output/3D can function only if it is selected. Leaf_display and Fruit_display are controlling visibility of these organs in 3D output.
Draw_Skeleton: to display 3D shape of plant structure in Scilab graphics window. Internodes of different PA are distinguished by colors.

Besides the output option of each PA, there is a global output option in menu/global output parameters, which has higher priority.
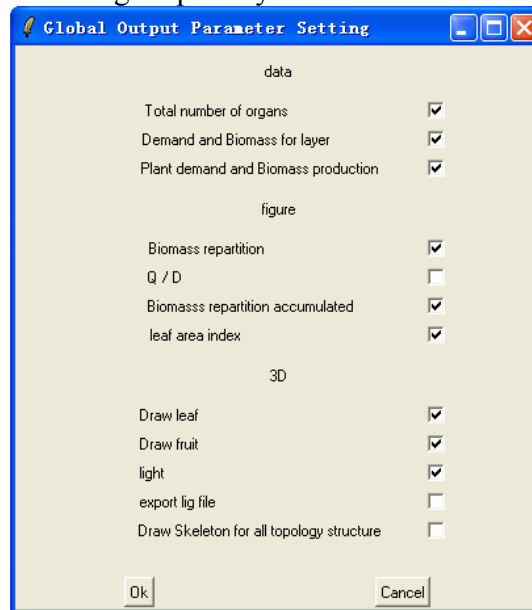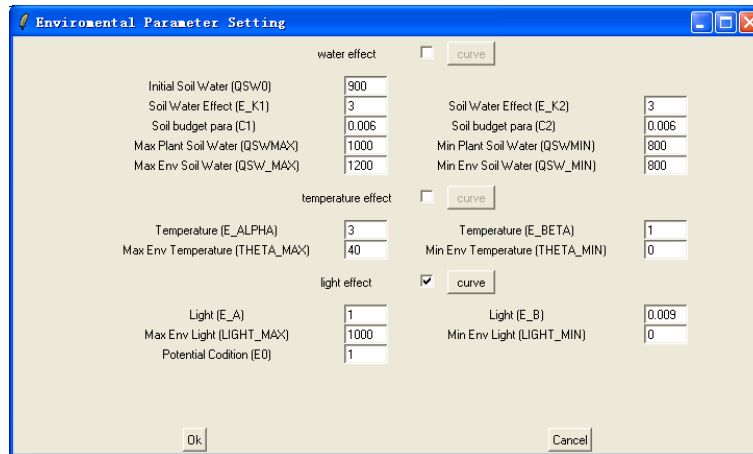

Figure 28. Global output parameters

3.5.   **Environmental Parameters**

Click parameter/Environmental parameters for setting, as shown in Figure 29. If any of the three climate condition is chosen, a dialogue will pop out asking the user to choose a environmental file (.env) when simulating the plant. It defines the water, light and

temperature condition in each cycle. Optimal climate control based on GreenLab formula has been studied (Wu, 2005).

Figure 29. Environmental parameter setting

4. Running GreenLab Model with GreenScilab

First load the parameter file by clicking file/load parameters. It is cautious that you save this file as test, not to destroy the original one (to have a backup). One can modify parameters and then launch simulation to see theis effect without changing the original file, except if one choose File/Save.

Click on Simulate, it beging computing. Whenit is done then a dialogue as in Figure 30 appear:

Figure 30. Dialogue for showing the simulation message

Click ok.

Results of the simulation can be displayed in miscellaneous ways using Output. Remember the results available depend on the output parameters, for each PA and global.

Number of Organs: Display arrays of numbers of organs produced for each PA and CA.
Demand and Biomass: Display the plant demand and the biomass of compartments and organs for each GC
Figures: Display curves for the biomass production, (compartments, and organs weights)
Skeleton: skeleton of the plant structure;
3D: Display the 3D architecture of the Plant.

Export 3D: output 3D description file so that it can be read in *tree_visu* or other standalone software for visualization.

Environmental factors: it output E value at each cycle. It is constant when no climate effect is chosed parameter/environment parameters. Otherwise it output the climate condition and the E value. Here is an example when light level is decreasing in each cycle.
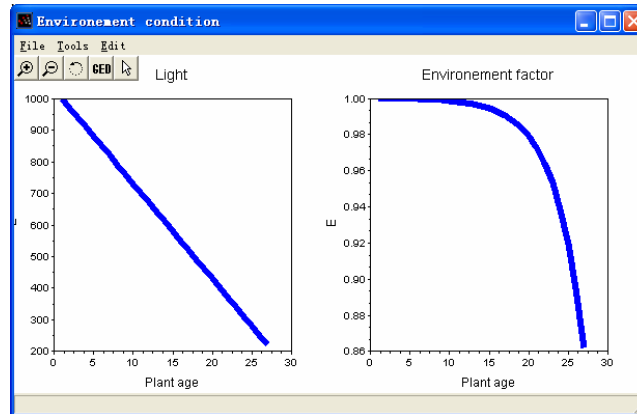

Figure 31. The light level and resulting E value in each cycle

Choose Output/Close all window one can close all graphics window.s

5. Study on Corner model

Plants that follow Corner Model are monoculm as Palm trees, Carica Papaya. Starting from a seed, the growth is indefinite. The terminal bud sets in place metamers continuously whose composition is internode, leaf and fruit. This is the simplest plant architectural model and it allows studying the sources-sinks relationships in the best conditions. Figure 32 displays a drawing by botanist of the this model.
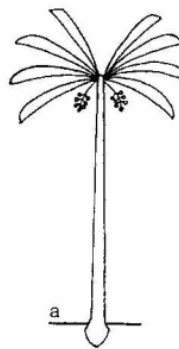

Figure 32. Corner architectural model (F. Halle *et al. 1978*)

5.1.   The simulated control plant

We simulate the Corner model by open file 'Model_Corner.sci' under folder 'Function'.

From the test file we can see that the plant age is 20 and the number of PA is 1. We can see that each metamer has got 1 leaf, 1 internode, and one fruit. From the organs colours we assess obviously the functioning time. From a glance more accurate, we can see that there is a secondary growth (layers for girth). The increasing sizes of the organs from the tip shows the phenomena of expansion. The first leaf is the biggest. This comes here from a seed effect. The following leaves increase their final size gradually until a maximum. This is typically the result of the exponential growth that characterize the plant youth. Later competition for light stabilizes the growth. On the Figure 33 we can see cycle by cycle where the biomass goes into the plant compartment, the exponential starting and the stabilization of the biomass production.

This figure is a normal result of PBM, but it is nice to have the corresponding architecture. Both are necessarily.
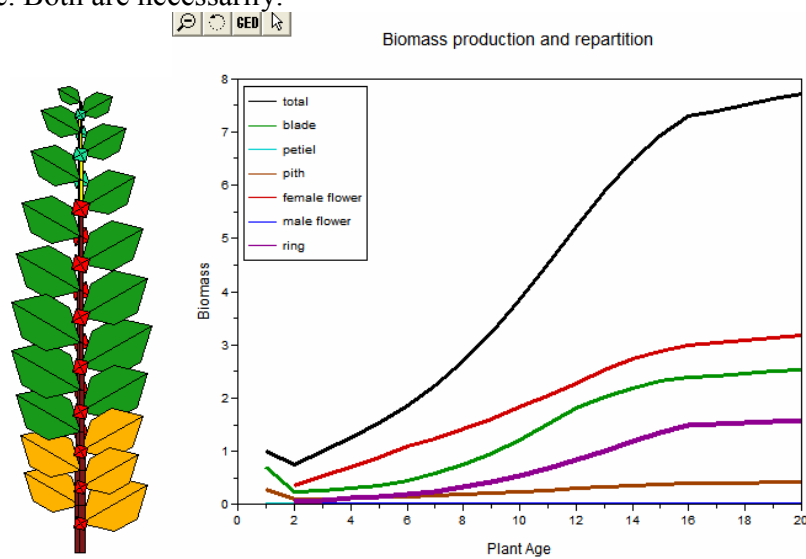

Figure 33. The biomass production and repartition, and the final 3D at age 20 for the Corner model

At the level of the organs we can watch the increasing of the organ size and weight, for leaf, internode, fruit, as in Figure 34 and 35.
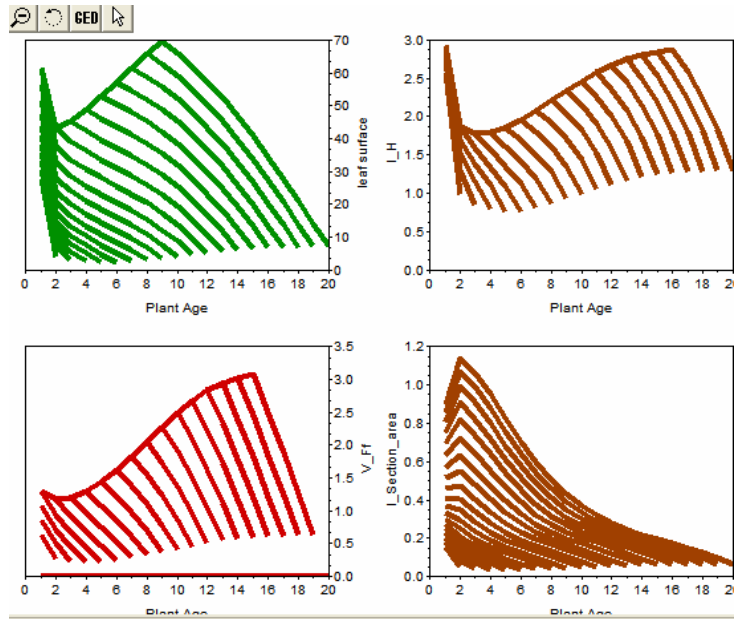
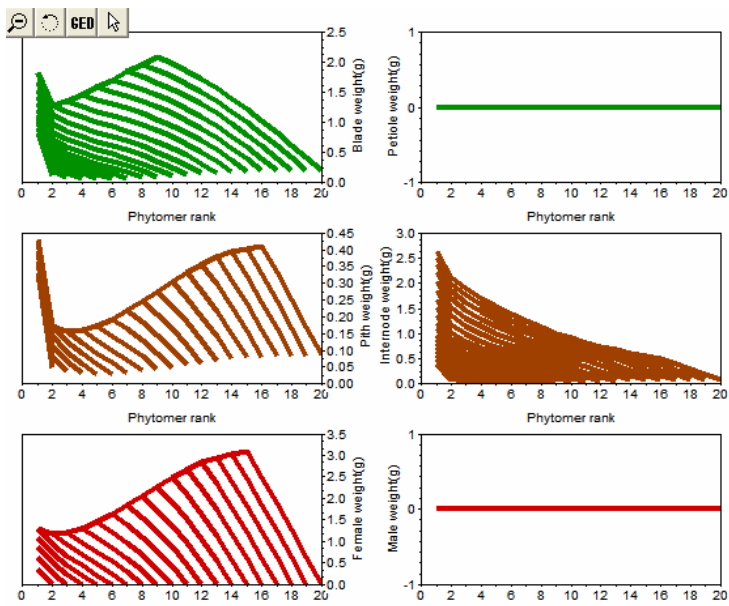Figure 34. Size of individual organs in Corner Model

Figure 35. Weight of individual organs in Corner Model

GreenScilab output also the LAI or total leaf area (in case of single plant), as in Figure 36:
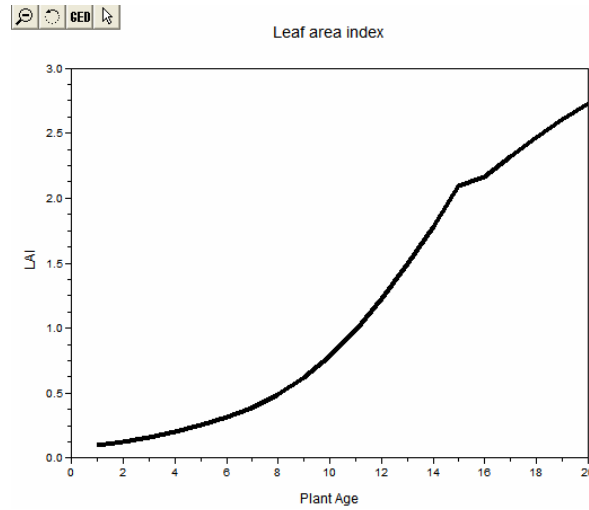
Figure 36. Leaf Area Index of this Corner model plant

5.2. Effect of source organs:

5.2.1. Effect of seed parameters Q0, dQ0

To see the effect of the seed we can set the value of the resistance at a high value (*rp* =100000). This will stop the leaf photosynthesis. The plant will grow only on the seed reserves. The flux of biomass from the seed is according to the empirical formula:

$$\boldsymbol{\Delta q = Q_0 \cdot (dQ_0)^n}$$. We take here dQ_0=.9. Both parameters are to be set in Parameter/Physiological age 1/Functional parameter. The result is shown in Figure 37.
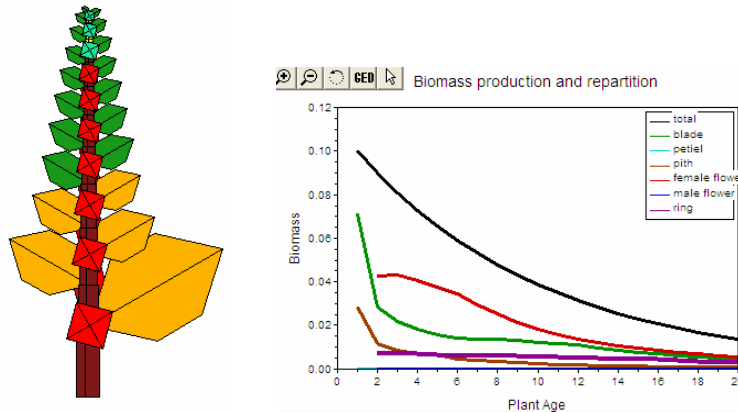

Figure 37. Case of plant growth depanding on the seed reserve

We can see that the plant run out the reserves of the seed and will died.

5.2.2. Effect of leaf functioning parameters rp, Sp, ta

We have seen the general formula for biomass production in GreenLab for one plant.

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The functional parameters drive the photosynthesis. But the surface itself is a result of the biomass production as a result of the combination of the sources and sinks functioning through the leaf allometry. By elimination of *S* the Equation (1) becomes Equation (5):

$$Q(n) = \frac{E}{r.k^{'}}\left(1-\exp\left(-k^{'}\frac{p_B}{e}\sum_{i=1}^{t_a}N_L(n,i)\sum_{j=1}^{i}\frac{f_B(j)Q(n-(i-j)-1)}{D(n-(i-j))}\right)\right)$$

Equation (5)

Here ta is the leaf functioning duration for photosynthesis. $k^{'} = k / Sp$. The shape of this formula is a recurrent equation. The biomass production *Q(n)* at CA *n*, depends on the **ta** previous layers of leaves combined with the values of the corresponding *Q/D*.

p_B is the leaf blade sink strength (set to 1) and *e* the leaf thickness. $N_L(n,i)$ is the number of leaves produced at CA *n-i*+1 and we can see the apparition of the ratio *Q/D* on all the concerned active growth cycle between ***n*** and ***n-ta +1. f_B(j)*** is the sink value for the leaf blade *j* aged.

The behaviour of this formula will be studied in another tutorial. Simply some important results can be summarized.

5.2.2.1. Case of immediate expansion

This means that the expansion of organs is immediate (See Parameter/Physiological age 1/functional parameter). In that case the link between growth and architecture is clearly visible.

- if the leaf area is small then :

$$Q_n = \frac{E.\sum_{i=1,N_B}S_i}{r}$$

This means that the biomass production depends only on leaf surface, the resistance, and the growth potential. In the normal case it gives an exponential growth as it is the case at the beginning of growth. If we take the immediate organ expansion, then the exponential growth is directly visible on the organ sizes (see Figure 38).
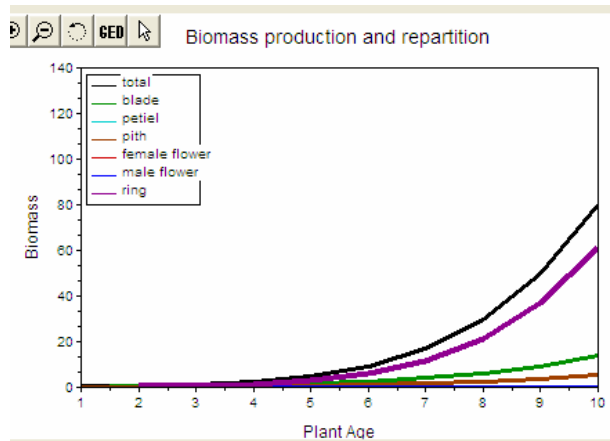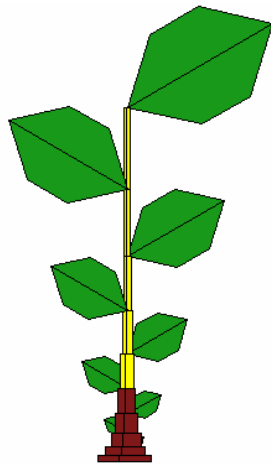
Figure 38. Exponential growth without expansion (parameter file Model_Corner_ta1_1.sci)

The exponential growth is clearly visible due to the immediate expansion in one cycle.

- if the LAI is big, i.e., Sp is very small, then the field canopy is covered then equation becomes:

$$Q_n = \frac{E.Sp}{rp.k}$$

This means that the plant photosynthesis has reached its maximum related to the plant projection area *Sp*. At this level we have reach the field production. And the effect of the plant architecture disappears, see Figure 39.
Normally the plant growth will follow a sigmoid shape between the initial and the final conditions, as it can be seen previously on the results for the control plant.
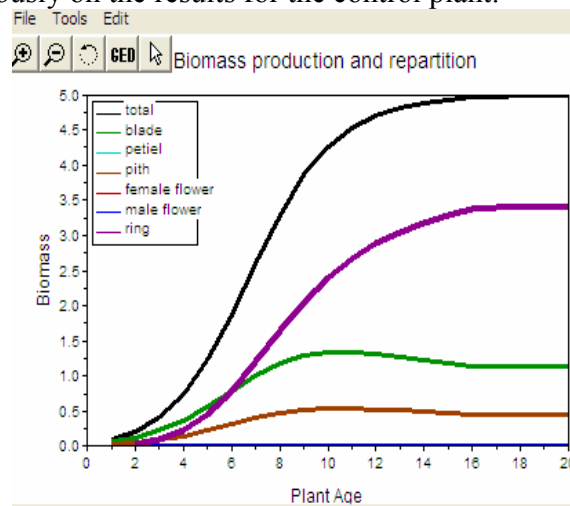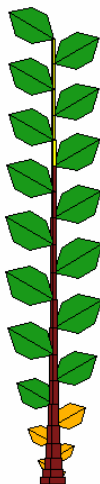
Figure 39. Case of big LAI without expansion (parameter file Model_Corner_ta1_2.sci)

The plant biomass production is stabilized because the LAI is high inside the *Sp* surface. The plant reproduces always the same metamers.

5.2.2.2. Case of organ expansion on several cycles

- If the leaf area is small:

The effect of the exponential growth is hidden on the architecture, because the organ expansion on several cycles, see Figure 40.

Figure 40. Exponential growth with expansion duration bigger than 1. (parameter file Model_Corner_ta10_1.sci)
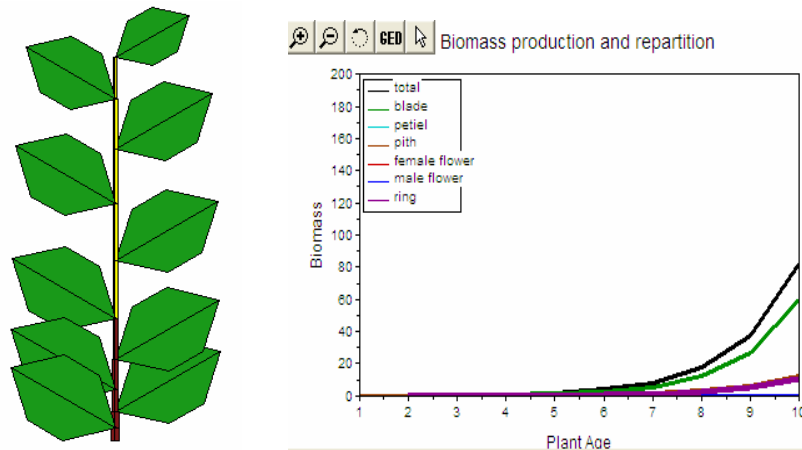
- If LAI is big, the results are as in Figure 41:
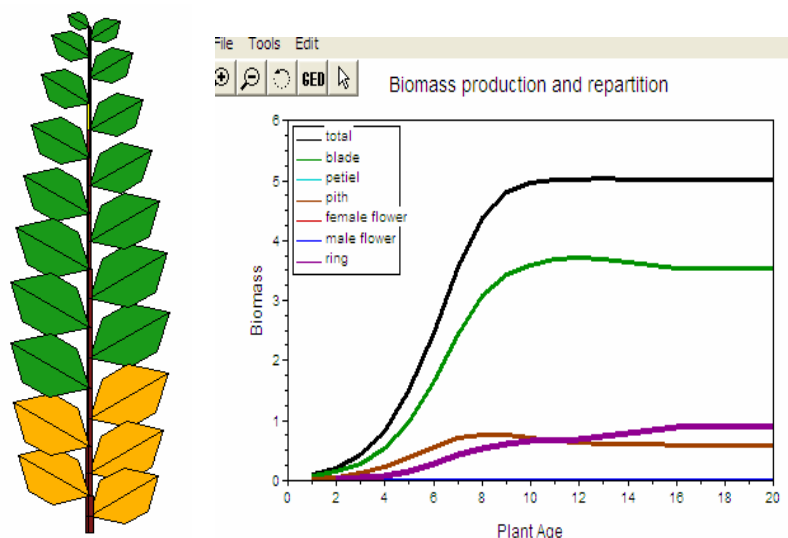
Figure 41. Case of big LAI with expansion (parameter file Model_Corner_ta10_2.sci)

Here we can see also the effect of a high LAI. The plant production is stabilized after 10 growth cycles. It is because the expansion duration hide the behaviour of the growth in the plant architecture.

5.3. Effect of sink organs

All the organs even leaves are sinks and enter into the plant demand equation. Nevertheless we will focus here on fruits and layers.

5.3.1. Effect of fruits

Increasing sink strength of fruits can prevent the plant growth, and increase the allocation of biomass to the fruits. Above a sink threshold the growth will decrease indefinitely. There is an optimal sink for the fruit yield that can be computed by optimization. One can change sink strength in functional parameters with file 'Model_Corner.sci'.

Figure 42. Effect of sink strength on the Corner model plant

 Optimization of sink strength has been studied (Wu, 2006).
- Effect of the fruit positioning

Some plants will have deterministic positions for the fruit apparition. It can be at the middle of the stem (cob of maize) or at the end (cap of sunflower). Usually the sink of fruit in that case is very strong and captures all the biomass.
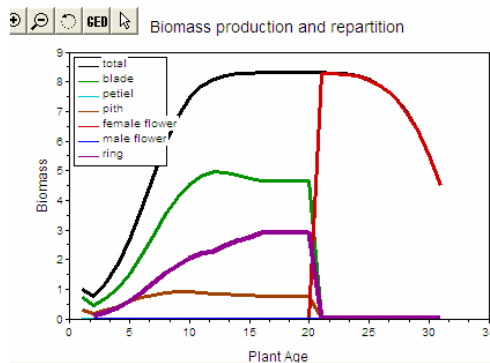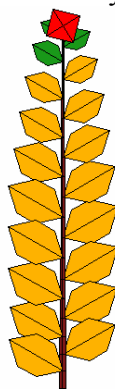
Figure 43. Effect of fruit appearance on the sink competition (parameter file Model_Holtum.sci)

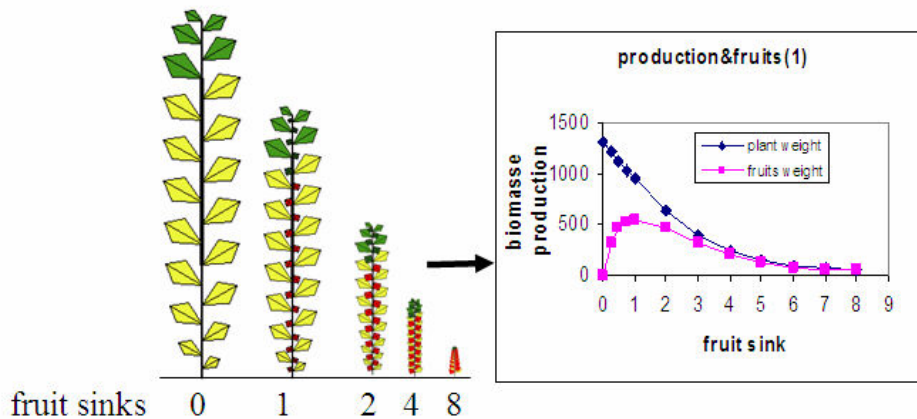Here in the case of terminal flower we can see that the fruit takes all the biomass once it appears, expansions of other organs stop.

5.3.2. Effect of layers (girth)

The sink of the layers for secondary growth can also prevent the growth. There is an optimal sink for wood production. We can load the original Model_Corner.sci, set the sink strength of fruit to 0, and play with the sink strength of the layer.
Here 2 simulations are done for *pc* = 2 and *pc* =10, as shown in Figure 44
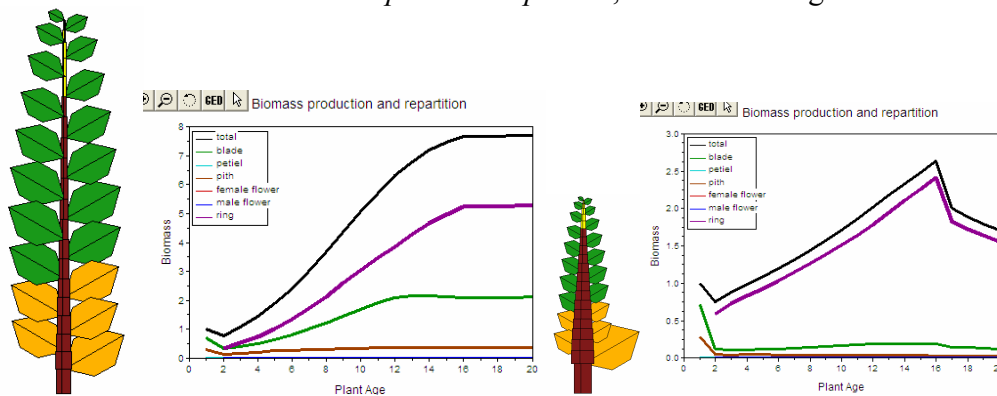
Figure 44. Effect of sink strength of layer on the plant growth

In the second case the secondary growth is too heavy for the plant and the growth decreases when CA > *ta*.

6. Study on Roux Model

Plants that follow such kind of architecture are shrubs like coffee tree that have 2 kinds of PA. Branching system is monopodium. Orthotropic trunks that are vertical and plagiotropic branches that are always horizontal without righting at the end. Growth Unit are made with a single metamer. Figure 45 illustrates this model.
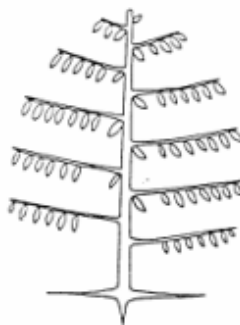
Figure 45. Roux architectural model (F. Halle *et al. 1978*)

All the previous studies on the parameters effect about Corner model remain true here. So we will not repeat them. New features of that kind of plants are related to branch control: branches duration, branch rhythm ratio, and branch time apparition. Often only the branches bear the fruits.

One can simulation in GreenScilab by loading parameter file 'Model_Roux.sci', giving the output at in Figure 46.
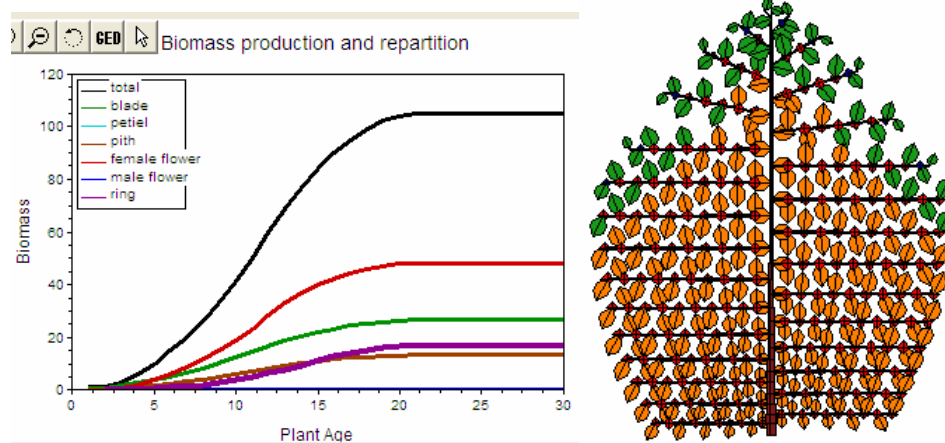
Figure 46. The biomass production and repartition, and the final plant shape for the Roux model

The first branches have a final size smaller because at the beginning Q/D is smaller. When the growth is stabilized, the branches will get a maximum size.

The organs sizes depend on the branch span duration. The less it is the biggest they are. This effect can be easily shown with pruning branches at their apparition. The control parameter is the Max Number of GU for PA 2. Sample results are shown in Figure 47.

(1)   (2)   (3)
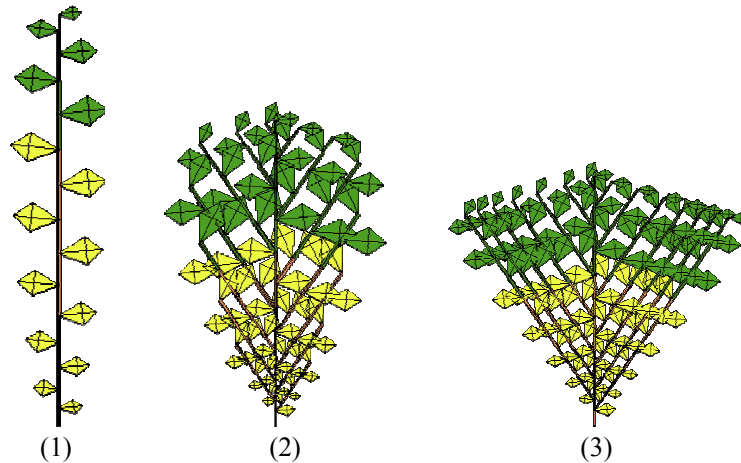
Figure 47. Effect of branch span duration Max Number GU (PA 2): (1) 0, no branch (2) 5, and (3) a big value (indefinite). The biomass production increases with increasing Max Number of GU (PA 2), but the organs sizes decrease because too many organs compete for biomass.

7. Study on Leeuwenberg model

Plants that follow this kind of model are trees like Plumeria. Branching system is sympodial. The entire axis gets a terminal flowering after setting in place several growth units. Branches appear after the flowering process and relay the development of the architecture. Figure 48 illustrate this model:
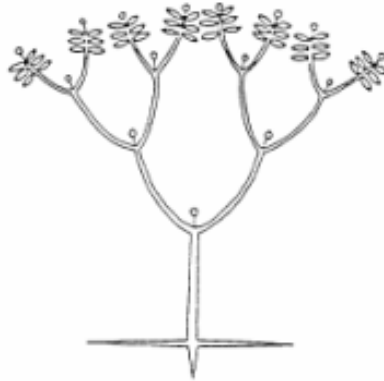
Figure 48. Leeuwenburg architectural model (F. Halle *et al. 1978*)

New features of that kind of trees are the number of axillary branches that take the relay and the number of metamers of an axis before it ends with an inflorescence. The behaviour of this tree is quite complicated.
GreenScilab simulation can be done by loading parameter file Model_Leeuwenberg.sci:
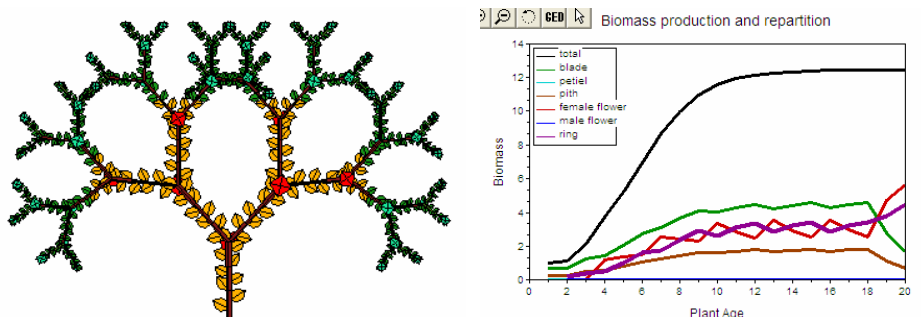
Figure 49. The biomass production and repartition, and the final plant shape for the Leeuwenburg model

There is an intermittent biomass partitioning due to the cyclic fruit apparition that create oscillations in the different biomass compartments.

8. Conclusion

Here ends then first part of the tutorial. Normally the GreenScilab user should understand the mechanisms of the sources and sinks balance inside the plant architecture during the plant development and the plant growth for a first qualitative point of view. For a deeper understanding on the behaviour of the GreenLab model see other tutorials.

9. References

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Building and Fitting a Maize Plant with GreenLab model

Data coming from prof Guo Yan and Phd Student Ma Yuntao(China agricultural university, CAU)

10. Botanical description of a Maize Plant

Here are 4 development stages of a Maize Plant.

Fig.1 Four development stages of a maize plant

11. Maize study in CAU

Chinese researchers (professor Guo Yan and his students Ma Yuntao) from the Key Laboratory of Plant-Soil Interactions of China Agriculture University(CAU) have done a consequent work on the Maize development and growth. We present here their results.

For a given genotype the number of metamers is quite stable, but there is an important genetic variation between different genotypes. For example, the maize plant studied has 21-22 metamers in CAU-China, but the maize studied in Inra-France only has 16 metamers.

Here, we just use Chinese maize as an example to illustrate.The cobs appear in the middle of the stem and the tassel at the end. Cobs were produced on several metamers(between the 10th and the 15th) , but those last two carried by meatmers 14 and 15 were the most productive, contributing >80% to cob yield. To simplify simulation, henceforth cob production is attributed to metamer 15 only.

In order to permit a dynamic, 3D representation of maize plant, a digitizer was used to measure the 3D co-ordinates of maize organs (GUO *et al*, 2006). This 3D representations can be used to calculate precise light interception and energy balances, for single plants as well as for uniform or mixed plant populations that grow under conditions of inter-plant competition for light and ultimately, for water. Fig. 2 is the different kinds of digitizer. Fig. 3 is the light distribution within established virtual maize canopy using such kind of apparatus to measure the plant architecture.

Fig.2 Different kinds of 3D digitizer
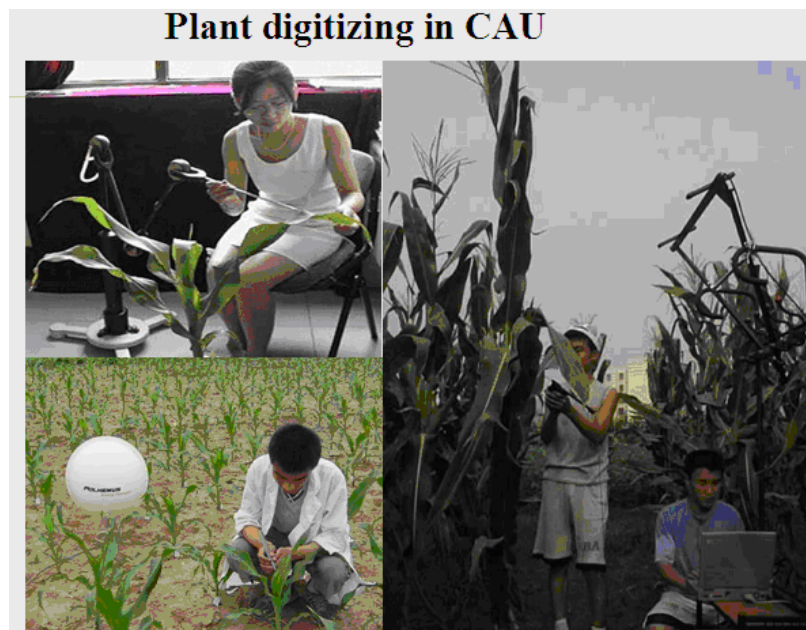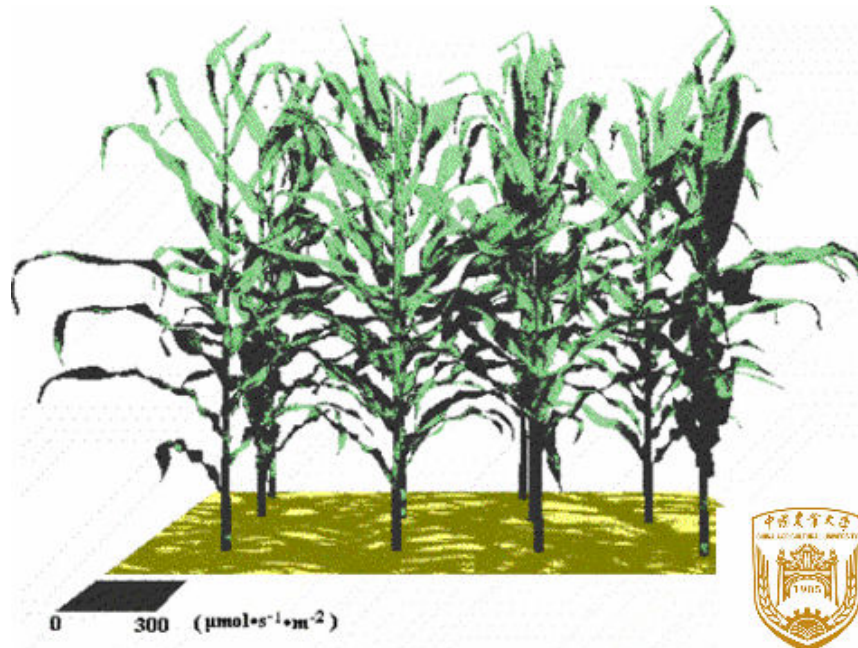
Fig.3 Virtual maize canopy and light interception by each organ within this canopy

12. Instruments for plant measurements

In GreenLab model, organ weight(fresh matter or dry matter) and dimension are needed to compute hidden parameter values.
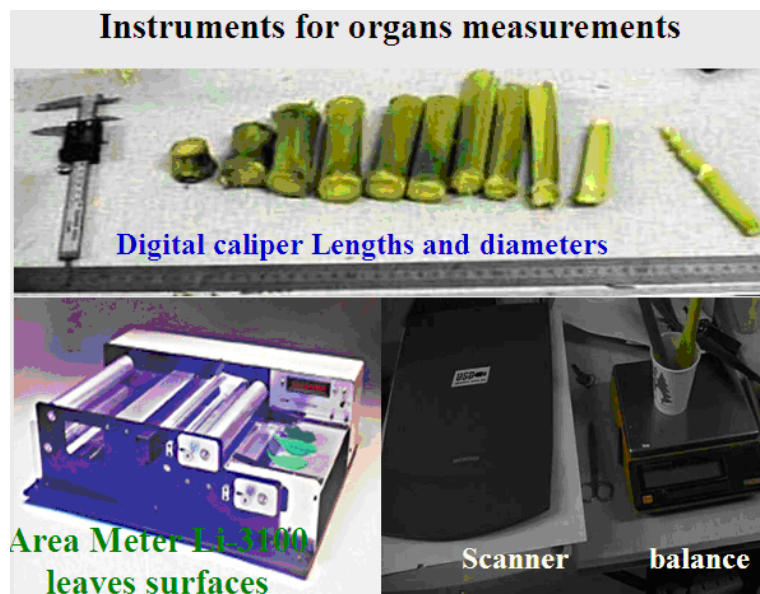
Fig.4 Instrument to measure internode length and diameter, leaf surface and organ weight.

13. Simulating the maize architecture

The GreenLab model dynamically represents the morphogenesis and architecture of a plant based on a few recurrent mathematical equations and generic metamorphic rules. It is executed at time steps corresponding to organogenetic growth cycles(GC), corresponding to the thermal time it takes to generate a new metamer(the architectural unit comprising a node, internode and leaf, or the metamorphic variations of these organs).

The plant architecture is generated by an automaton(Guo et al, 2006), providing compartments(organs; Fig.5) that represent sinks for biomass in the course of their development which can span several GCs.
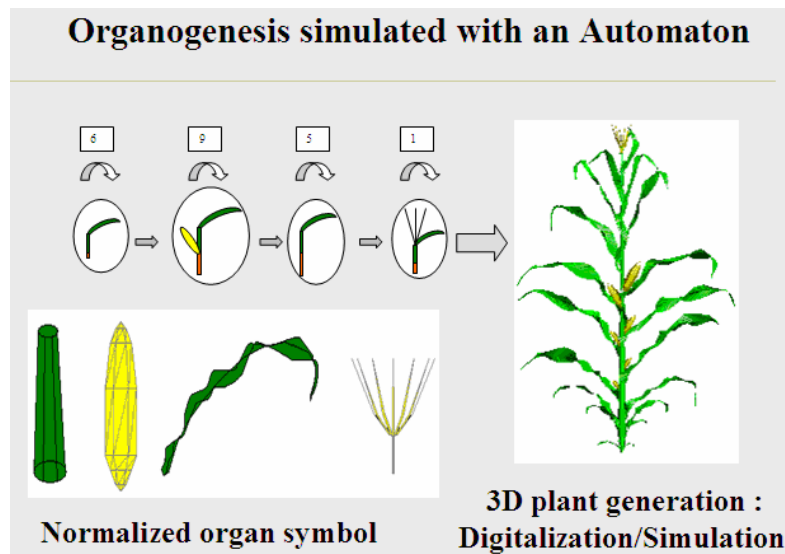
Fig.5 Organogenesis simulated with an automaton

To simulate correctly the different types of metamers we have to consider 4 steps that correspond to 4 physiological ages.
1. Metamer 1-6 produce leaves(consisting of blade and sheath)with short internode.
2. Metamer 7-15 produce leaves with long internodes and may carry cobs. Only the last one will bear a cob in our case.
3. Metamer 16-20 produce leaves with longer and thinner internodes but no cobs(female flower).
4. Metamer 21(the last) produces a leaf, an internode and a tassel(male flower).

For a realistic display of the virtual plant, it is convenient to design the organs (leaves, sheaths, cob, tassel) with 3D architecture model. A lot of work has been done on collecting the 3D shape of the leaves at each metamer rank with 3D digitizer in CAU. So once the fitting is done, the difference between the simulated plant and the digitalized one is few (Fig. 6).
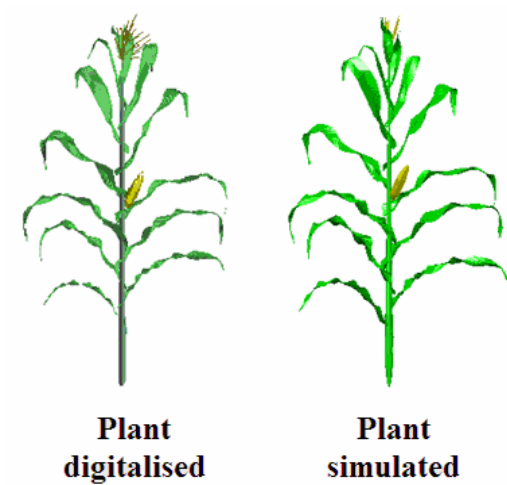
Fig.6 Comparison between simulated and digitized maize plant.

14. Parameters within the reach of the researchers

Throughout crop development, destructive sampling was periodically done on individual plants in order to characterize growth and organogenesis, thus will provide us the fitting file (target file) and also allometric rules for the organs.

15. What is a target file?

Recording the information about metamers according to their position provides the description of the plant architecture by the mean of an array(Table 1). The weights and dimensions of all existing organs belonging to the metamer rank are recorded in the array. We call it a TARGET FILE because this array must be fitted by the model later.

Table 1 Record of measurement data, called target file for later parameter optimization

N_inter	N_group	T_leaf	D_inter	L_inter	W_inter	D_petiole	L_petiole	W_petiole	W_blade	S_blade	W_female	W_male
1	1	9	1.9	0.7	2.0	0.6	4.8	0.1	0.1	5.7	0	0
2	2	9	1.9	0.7	2.0	1.0	6.2	0.2	0.2	12.8	0	0
3	3	9	1.9	0.7	2.0	1.5	6.6	0.3	0.4	14.3	0	0
4	4	9	1.9	0.7	2.0	2.6	7.9	1.0	1.0	45.3	0	0
5	5	9	1.9	0.7	2.0	6.0	16.0	2.8	4.5	178.4	0	0
6	6	9	2.8	3.7	26.2	7.9	18.8	7.8	8.2	315.2	0	0
7	7	9	2.9	6.3	44.2	8.8	20.0	10.3	11.5	409.8	0	0
8	8	9	2.8	8.9	52.5	9.9	20.5	13.2	15.5	535.4	0	0
9	9	9	2.7	10.4	53.3	10.3	20.4	15.3	19.8	670.3	0	0
10	10	9	2.5	11.8	50.7	10.2	19.4	16.2	23.6	792.3	0	0
11	11	9	2.4	12.7	44.3	10.8	18.2	17.2	26.5	908.1	0	0
12	12	9	2.3	13.8	39.9	10.9	17.7	17.6	28.4	977.9	0	0
13	13	9	2.2	14.2	34.5	10.5	16.9	17.3	28.1	1007.9	0	0
14	14	9	2.1	14.6	26.8	10.1	16.8	17.1	26.8	987.7	0	0
15	15	9	1.9	14.2	20.9	9.3	16.9	15.8	24.8	912.7	895.4	0
16	16	9	1.6	14.2	16.2	9.1	16.8	14.4	22.2	855.3	0	0
17	17	9	1.4	14.6	12.4	8.2	16.5	12.4	18.9	739.3	0	0
18	18	9	1.2	14.1	8.9	7.5	16.0	10.1	14.4	597.5	0	0
19	19	9	1.1	14.5	6.7	6.2	15.6	7.7	9.3	422.0	0	0
20	20	9	0.8	11.5	3.9	4.3	11.0	4.0	4.2	205.9	0	0
21	21	9	?	?	1.11	?	?	1.1	0.2	9.1	0	29.1

16. Parameters of the Maize development

Regular observations on maize plants provide the date of appearance of the new metamer. For these dates, there is an associated average temperature. The concept of thermal time used here is the sum of the daily average temperatures for a given date of observation from germination. Thermal time is computed as the additive accumulation of mean, daily, air temperature minus a crop specific base temperature (8°C in this study as recommended for maize by Ritchie and NeSmith, 1991). Other cardinal temperatures such as Topt and Tmax are not considered. The relation between the number of metamers and the corresponding thermal time is quasi linear (although there are 4 types of metamers) and can describe the plant development.

Use of sum of temperature to control organogenesis and organ expansion

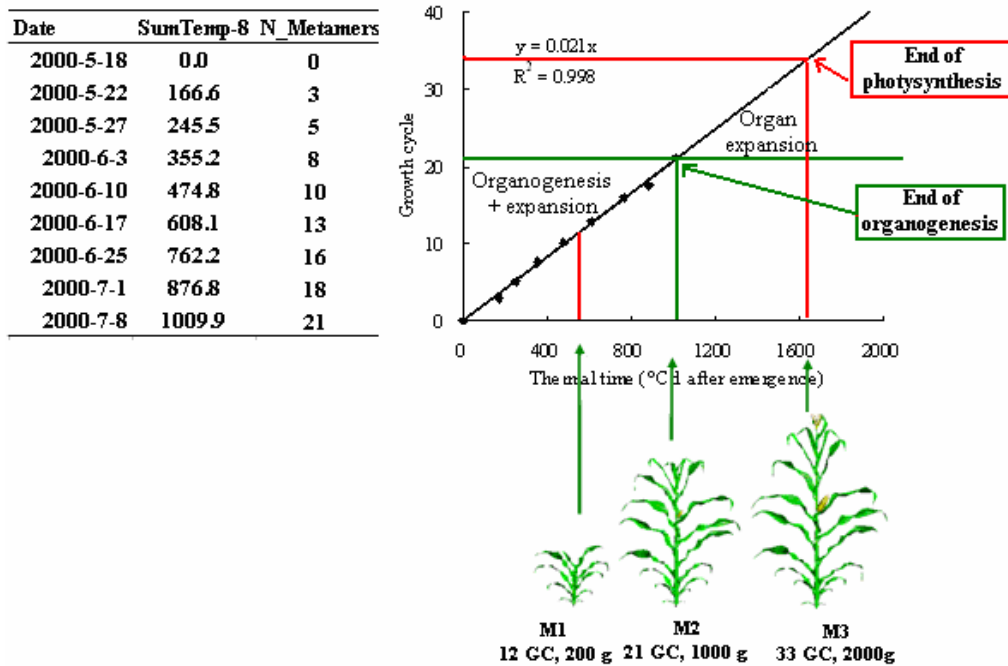| Date	SumTemp-8	N_Metamers
2000-5-18	0.0	0
2000-5-22	166.6	3
2000-5-27	245.5	5
2000-6-3	355.2	8
2000-6-10	474.8	10
2000-6-17	608.1	13
2000-6-25	762.2	16
2000-7-1	876.8	18
2000-7-8	1009.9	21

Fig.7 Number of metamers on maize plants developed as a function of thermal time.

We can consider 3 phenological stages.
1. M1: 12th GC, end of the vegetative growth period. It corresponds to 500 °Cd.
2. M2: 21th GC, end of the organogenesis, no more metamer will appear. It corresponds to 1200 °Cd.
3. M3: 33th GC, maturity. It corresponds to 1800 °Cd.

Note that after 21 metamers no obvious signs on the plant allowed to follow the growth. But we can extend the linear relationship between the thermal time and the development beyond 21th GC. So thermal time is thus used to simulate the plant development and growth cycle by cycle. Each cycle is used to create a new metamer and to expand the organs biomass. The linear relationship between thermal time and metamer number is quite stable for a certain genotype(Guo et al, 2006).

17. Measurement on Organs and computation of organ's allometry

The allometry here is the relationship between organ biomass and its dimension. So according to this relationship, we can easily translate from biomass to organ geometry.

18. Leaf blade

We measure both weight and surface for each existing leaf blade. So we can easily compute the leaf blade thickness, which is defined as the ratio between the leaf blade volume (that is the leaf blade weight if the organ density is 1), and the leaf blade surface. From Fig.8 we can see that the linear relationship was found between leaf blade fresh weight and its surface if we gathered all the leaves together to analyze.
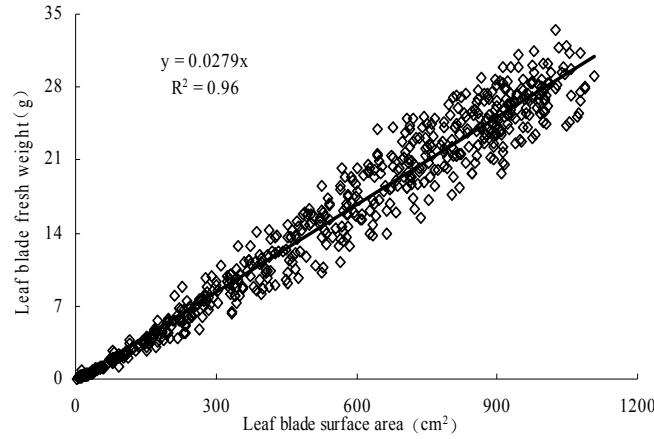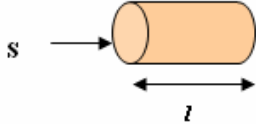
Fig.8 The linear relationship between leaf blade fresh weight and leaf blade surface area

19. Sheath

We measure weight, length and width of leaf sheath, because it is an important source and sink organ. As the leaf sheath rolling around its internode in maize, we didn't consider its architecture in such detail. So we neglect to draw leaf sheath.

20. Internode

The length, the diameter and the weight of internode was obtained during the measurement. The allometry of a cylinder is defined as follows:

$$\begin{cases} l_e(j,i) = \sqrt{b_e} \cdot \left(\dfrac{q_e(j,i)}{\rho_e(j,i)}\right)^{\frac{1+\alpha}{2}} \\ s_e(j,i) = \sqrt{\dfrac{1}{b_e}} \cdot \left(\dfrac{q_e(j,i)}{\rho_e(j,i)}\right)^{\frac{1-\alpha}{2}} \end{cases}$$

The length l and the section s depends on the parameter b and α that control the shape of the cylinder for a given volume ($v = q/\rho$ where q is the weight of the cylinder and ρ its density). We have $l*s = q/\rho$. The bigger is b, the thinner is the cylinder. For $\alpha = 1$, the internode section is constant. For $\alpha = 0$, the ratio l/s is constant.

For maize we can take $\beta = 0.3$ for the internode, but the b value changes a lot after the 15th internode. We chose to give the value b= 2 for the first PA and b =12 for the second PA

Practically speaking the relationship between the internode lenght and section can be written as follows:

$$l = ks^{\beta}$$

This equation is easy to assess (here, no secondary growth occurred)

This allows to compute $\alpha = \dfrac{\beta - 1}{\beta + 1}$ and $b = k^{1-\alpha}$

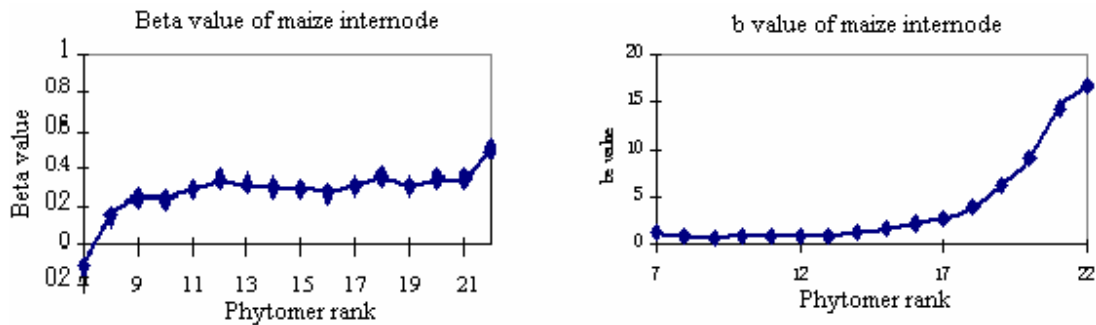The following data are the results on maize for each internode rank are.

Fig.9 The allometric parameters β and b of maize internode at different growth stages

21. Cob and Tassel

We measure the weight of these organs(dry weight and fresh weight).

22. Parameters out of the reach of the researchers

Biomass acquisition is simulated by applying atmospheric, evaporative demand(potential evapotrannspiration PET according to FAO guidelines; Allen et al, 1998) to the exposed green leaf area, and by linearly converting the resulting transpiration rate into biomass assimilation using an empirical value for transpiration efficiency.

The model is parameterized by optimization procedures using botanical and morphological observations measured on a sample plant at maturity(case of single fitting) or in the course of its development(multi-fitting), and subsequently is able to construct identical or divergent phenotypes by implementing the same rules and parameters for the same or different environments.

GREENLAB, in contrast to most crop models, is mathematical in the sense that it uses one single, aggregate, recurrent equation that generates, in combination with the automaton system, the entire plant structure. No non-linear behaviour resulting from 'if-then loops' and no changes in parameter values occur during the simulation. As a consequence, the equation uses a relatively small number of crop parameters whose values are 'hidden'(not accessible to direct measurements because they do not describe a specific physiological process or morphological feature) but are well suited to statistical optimization procedures(exceptions are parameters involved in the topological structure, allometric rules and leaf longevity that are set manually before the optimimzation process).

As well, GREENLAB does not allocate biomass to organs or organ groups according to fixed partitioning tables, but according to the current, relative sink strength of the organs that are expanding at any given point in time. For a given organ type, this relative sink strength is the same regardless of organ position, but varies in time according to the organ type's expansion law. The term 'sink strength' for different organ classes is relative because it is normalized against that of one specific organ class (the leaf blade), which is set to 1. This value is distributed over an organ specific period of thermal time according to the organ type's expansion law. The total, normalized sink strength of the plant is the

sum of all sinks that are active simultaneously, which may for example include several leaves, sheaths, internodes and a cob. Thus, an individual organ's absolute share the currently available resource depends on the number, type and expansion status of other organs competing for the same pool. Using this principle, GREENLAB simulates the increasing size of subsequently appearing leaves not with an explicit, empirical function, but instead, on the basis of sink and source dynamics resulting from the organogenetic process.

The set of GreenLab parameters

Directly Measurable Parameters
- Organs Allometry, Angles …
- Functioning span-time of leaves
- Organ's expansion time
- Automaton for Metamers production

GreenLab Parameters

Hidden Parameters to compute
- Sink Function $\{ P_o, a, b\}$
- Source Function $\{r, k\}$

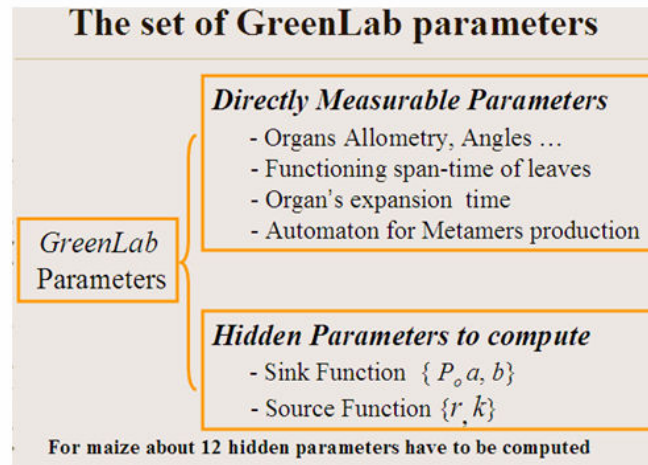For maize about 12 hidden parameters have to be computed

Fig. 10 Two kinds of GreenLab parameters

Parameter optimization of the model uses the Generalized Least Square Method (GLSM), an approach suited to curvi-linear parameter behaviour(Press *et al.*, 1992). The application of this method to GREENLAB was described by Zhan *et al.*(2003). The process is repeated until the solution is stabilized and an optimal solution is found for parameter values. Advantages of the method are its rapid convergence(ten iterations are often sufficient) and that it provides the standard deviation linked to the parmeter values thus indicating the accuracy of the solution.

Fitting in parallel with GLSM

Variables Initialization $\theta(0)$

$\theta(n) = \theta(n-1) + d\theta$

Organs production → Biomass production

Growth ← Biomass partitioning → engine

$|d\theta| < \varepsilon$

Sources & Sinks hidden functions to optimize

Convergence
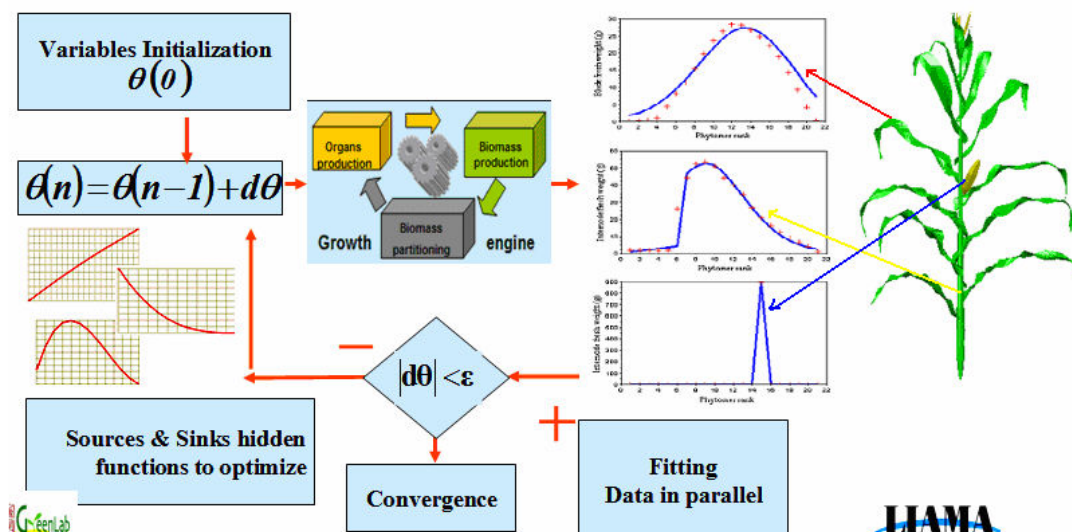
Fitting Data in parallel

Fig. 11 Fitting in parallel with GLSM method

23. Modelling results using single and multi-fitting

Once the plant architecture is defined for each metamer, it provides the format of a target file that can be filled with observed values. Fitting the architecture can be dong on a single plant for a given phonological stage(single fitting). Several plants of different phonological stage and/or experiments can also be fitted at the same time for the same set of parameters, along the trajectory of the dynamic system(multi-fitting).

24. Single fitting

Analyzing only one growth stage is single fitting. We find a set of parameters that reconstruct the plant organs at the good dimension according to their chronological ages.

For a single fitting exercise of the model, observations on mature plants of Exp.2000 were used(Fig.12). According to model time steps(thermal time elapsing between the production of two metamers), the crop age at maturity is 33th GC. The observations at 33th GC permit reconstructing the entire morphogenetic process of the crop because, at maturity, almost all organs ever produced are still present, and their time and sequence of initiation are determined by the known plant architecture and the duration of the crop cycle, assuming that metamers were produced at regular intervals of thermal time(Fig.7).

The model reproduced well the data in the target file used for parameter optimization. The increase and subsequent decrease of organ weight is entirely generated by competition among sinks and by assimilate supply, and not forced with growth stage-specific function. But there is no guarantee about the accuracy on the previous stages (Guo *et al*, 2006).
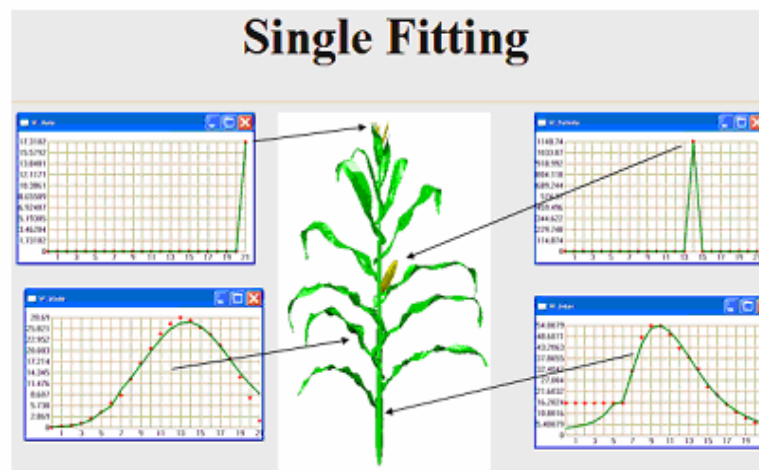

Fig. 12 Explanation of single fitting excise on target file

25. Multi fitting

For multi-fitting, three target files as presented in Table1 were established, representing observations made at vegetative stage, flowering stage and grain maturity, Fig.13 presents simulation results analogous to Fig.12, but here, intermdediate situations with

some organs still growing and others not yet appeared are shown. Although the fit is not absolute, observations are well approximated.
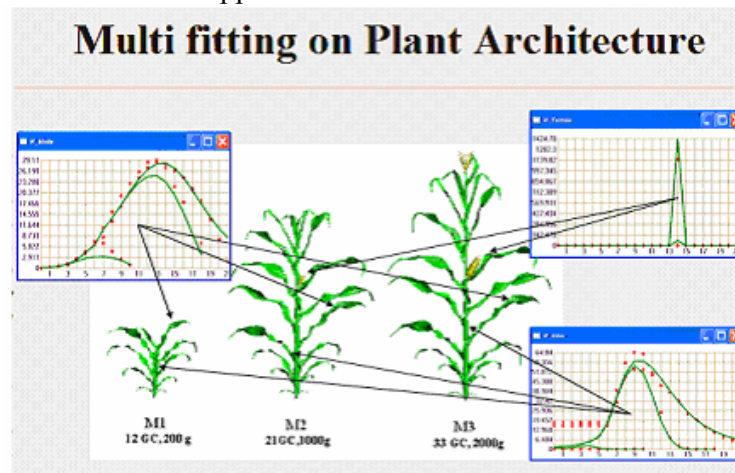

Fig.13 Explanation of multi-fitting excise on target file

One advantage of multi-fitting is that the accuracy of parameter estimation is better. Another advantage of multi-fitting as compared with single fitting emerges from the analysis of simulated sink variation kinetics. In the course of the parameter optimization process, the shape of organ sink kinetics is set by calibration of a beta function that can assume vastly different forms. If single fitting is conducted on the basis of the final plant morphology, little information on the expansion laws governing organ development is available. The model thus picks the function shape that equilibrates best biomass assimilation with the succession of demand functions. If several developmental stages of the crop are considered in a multi-fitting process, however, data on expanding organs are available and are taken into account in the fitting of expansion laws. In fact, multi-fitting dramatically changed leaf blade and internode sink kinetics(Fig.8 in Guo, *et al*, 2006).

For multi-fitting, the number of growth stages to fit is up to the researcher. The more are the data, the more tedious are the measurements.
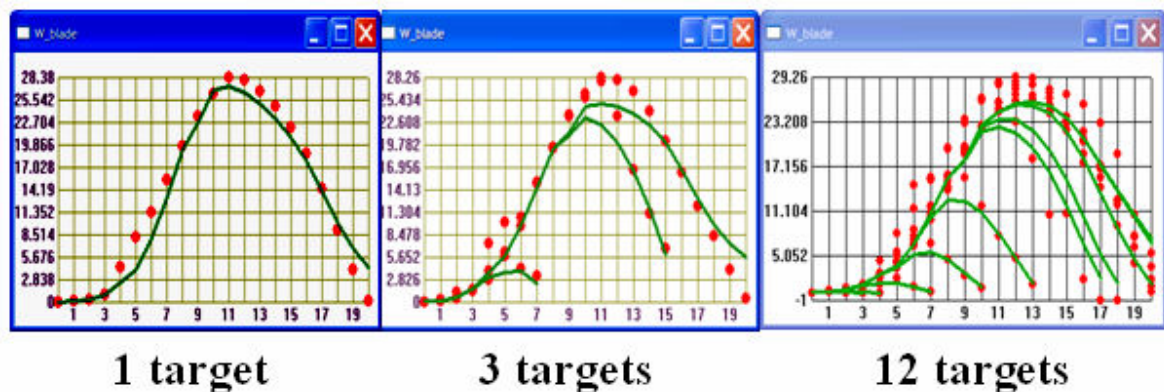

Fig.14 From single fitting to multi-fitting(take leaf blade as an example)

26. Fitting the maize data with GreenScilab (Single fitting and Multi-fitting)

27. The format of target file in GreenScilab

In calibrating the model parameters, we try to fit the model output with the measurement data.

<center>Table 2 the format of target file in GreenScilab</center>

//*********************Target*data*********************
NumberPlant(NumPlt) 1   [Number of target plant]

[Plant age]   [Physiological age]

[0 Complete dataset / 1 Compartment dataset]

InfoPlant(CA,PA,LoD) 33 1 0   [Missing data]

Root(Q_R) -1

//-GU--NbSub--IDSub--Q_B--Q_P--Q_I--Q_Ff--Q_Fm-S_B--S_I--H [Lowest rank of GU in target data]

InfoAxis(ID,PA,CA) 0 1 33 1

GU	ID	NbSub	IDSub	Q_B	Q_P	Q_I	Q_Ff	Q_Fm	S_B	S_I	H
GU	1	0	-1	0.09	0.09	2.01	0	0	5.7	2.01	0.65
GU	2	0	-1	0.23	0.19	2.01	0	0	12.8	2.01	0.65
GU	3	0	-1	0.41	0.34	2.01	0	0	14.34	2.01	0.65
GU	4	0	-1	1.03	0.95	2.01	0	0	45.26	2.01	0.65
GU	5	0	-1	4.5	2.75	2.01	0	0	178.38	2.01	0.65
GU	6	0	-1	8.22	7.76	26.23	0	0	315.23	26.23	3.73
GU	7	0	-1	11.46	10.29	44.21	0	0	409.82	44.21	6.33
GU	8	0	-1	15.46	13.23	52.53	0	0	535.42	52.53	8.88
GU	9	0	-1	19.78	15.26	53.34	0	0	670.34	53.34	10.43
GU	10	0	-1	23.58	16.24	50.71	0	0	792.32	50.71	11.75
GU	11	0	-1	26.45	17.17	44.32	0	0	908.06	44.32	12.73
GU	12	0	-1	28.38	17.63	39.92	0	0	977.94	39.92	13.75
GU	13	0	-1	28.11	17.25	34.48	0	0	1007.87	34.48	14.18
GU	14	0	-1	26.75	17.14	26.82	0	0	987.71	26.82	14.58
GU	15	0	-1	24.77	15.84	20.86	895.4	0	912.65	20.86	14.2
GU	16	0	-1	22.22	14.36	16.2	0	0	855.31	16.2	14.23
GU	17	0	-1	18.86	12.42	12.43	0	0	739.27	12.43	14.55
GU	18	0	-1	14.35	10.1	8.94	0	0	597.45	8.94	14.08
GU	19	0	-1	9.25	7.65	6.7	0	0	421.99	6.7	14.48
GU	20	0	-1	4.18	3.99	3.88	0	0	205.85	3.88	11.53
GU	21	0	-1	0.2	1.12	1.11	0	29.11	9.11	1.11	-1

end

28. How to fit the target data in GreenScilab

To begin fitting process, two files should be loaded sequentially: the parameter file that includes the initial and default values of parameters (.sci) under folder 'parafiles', and the target file (.dat) under folder 'targetfiles'. But these two files often had similar names (eg. maize.sci, maize.dat).
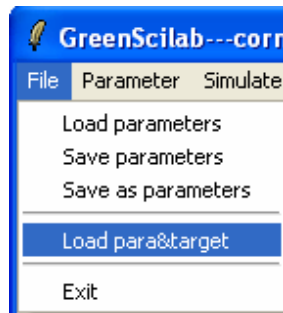
Fig.15 Menu for loading initial parameter value and target file

Once they are loaded, one can check the initial values and control of the parameters from the menu:
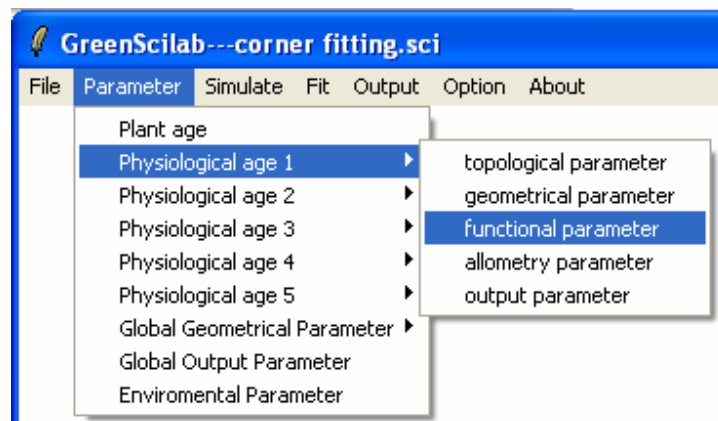
Fig.16 Menu for modifying the parameter values

We can modify the initial values of the parameters and whether this parameter needed to be fit or not:

Fig.17 Dialog for modifying the settings of functional parameters

Usually the sink strength of the blade is not to be fit because it is the reference value. Only hidden parameters with a checkbox beside are to be fit. For example, sink strength of the petiole(for maize called sheath) and one of its expansion coefficients are to be fit, as indicated in the red rectangle; while the expansion duration can be observed directly, thus they are regarded as known parameters that will not be fit.

To begin the fitting process, choose Fit/Begin. Then in the command window one can see the iteration of parameters.
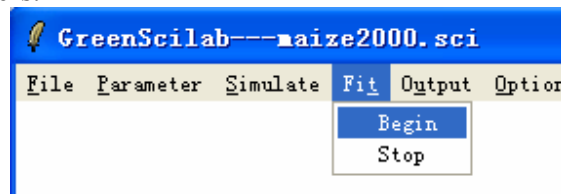
Fig.18 Menu for fitting of the target file

The process will end with the following dialogue when the one of the criteria is reached.
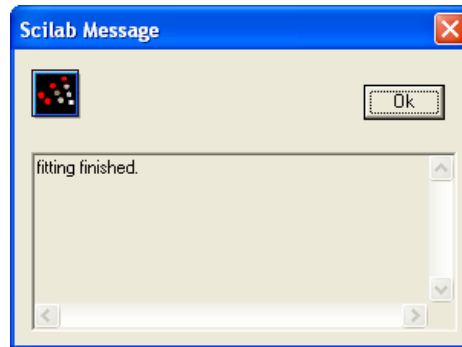
Fig.19 Dialog representing the finishing of the fitting

When the fitting is finished, the result will be shown at the time (single fitting or multi-fitting).
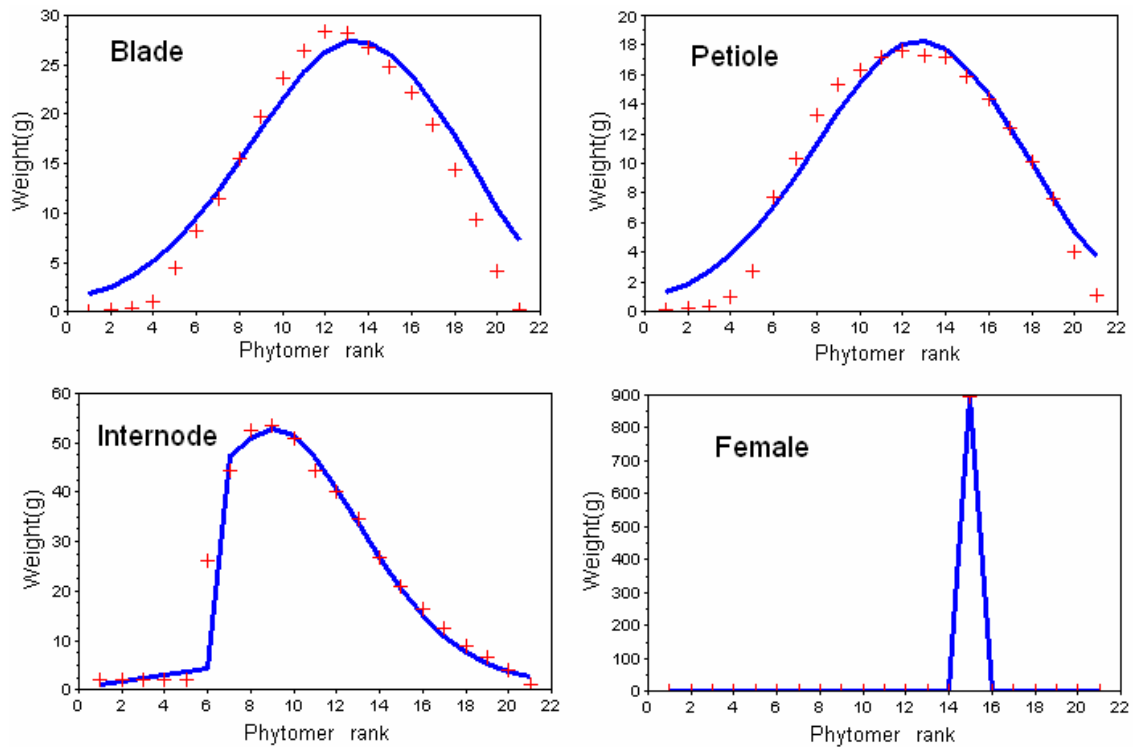
Fig. 20 Results of single-fitting exercise using observations on mature plants
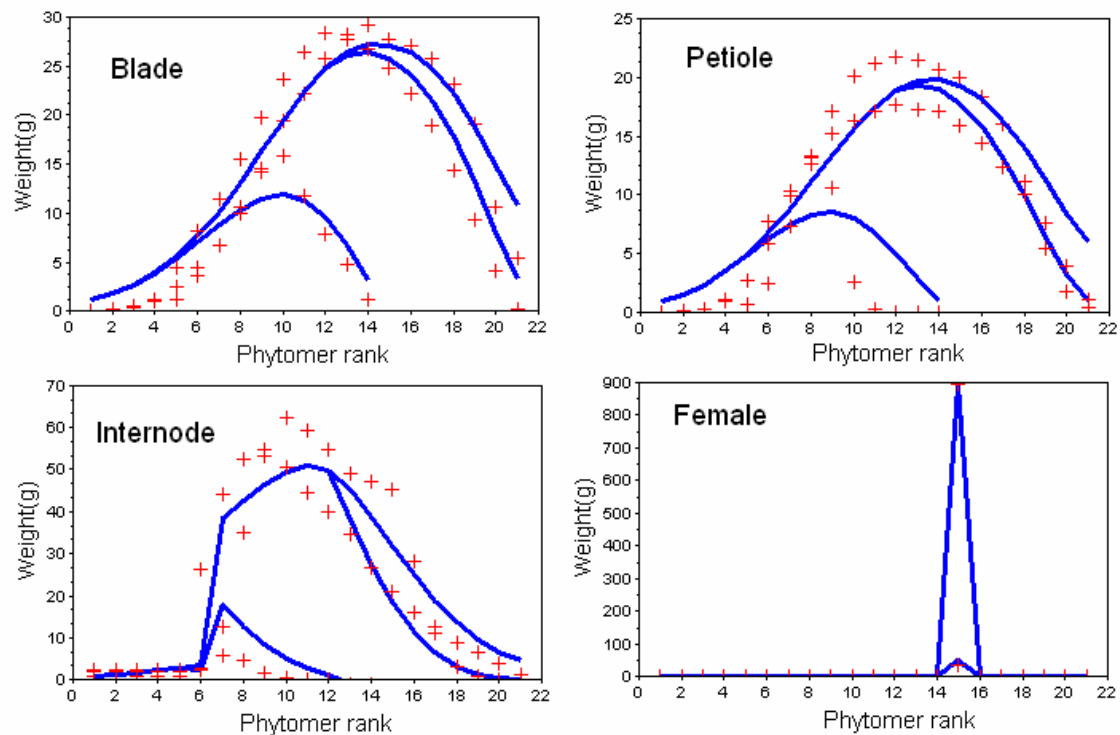
Fig. 21 Results of a multi-fitting exercise using observations on plants observed at three different growth stages

Click 'Ok' in Fig.19 to finish fitting. The result will be shown in a new window which showing the fitted parameters. The user will be asked whether the results are satisfying or not. If the result is good, we can press the 'Accept the results' button to save the results.
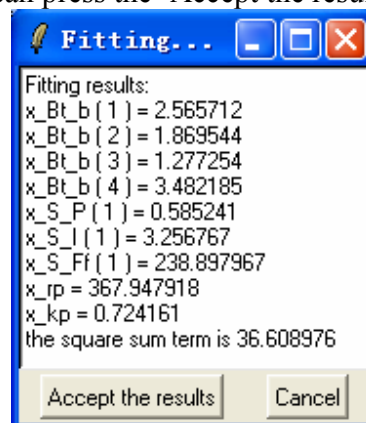
Fig.22 Fitting result window

If people want to have a look of the model output, first choose Simulate/Begin.
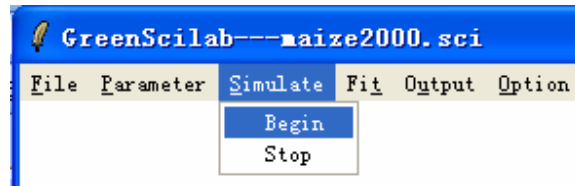
Fig.23 Menu for simulating with the computed parameter values

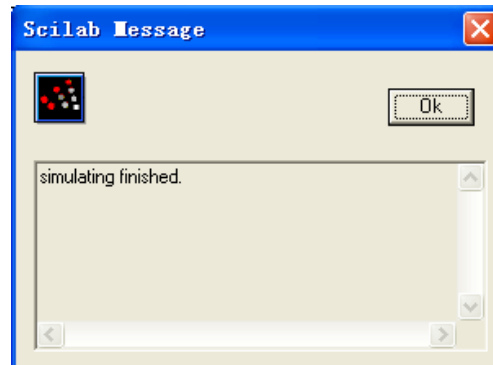The simulation process will end with appearing of the following dialogue.

Fig.24 Dialog representing the finishing of the simulation

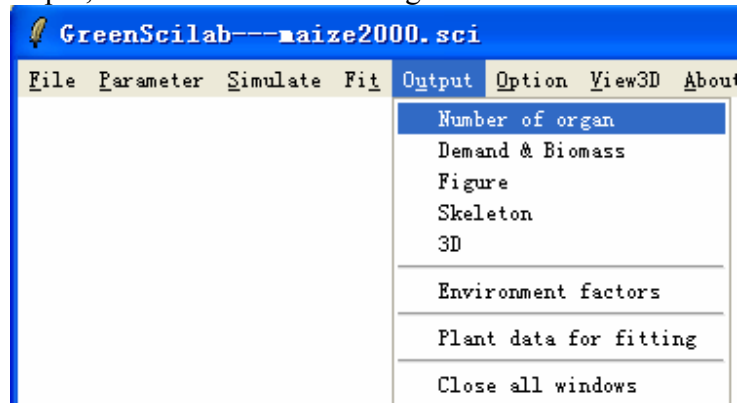Then click the Output, we can have a look on figure and data.

Fig.25 Menu for the model output

As a result of the model functioning we can display for each growth cycle the biomass production and the biomass partitioning (Fig. 26). And also the simulation of organ biomass and geometry varied with growth stages(Fig.27)
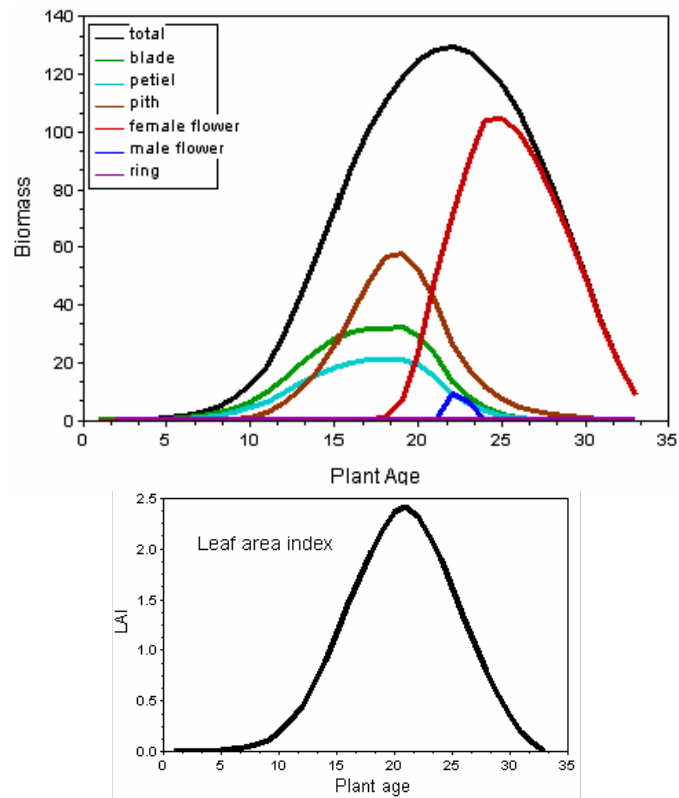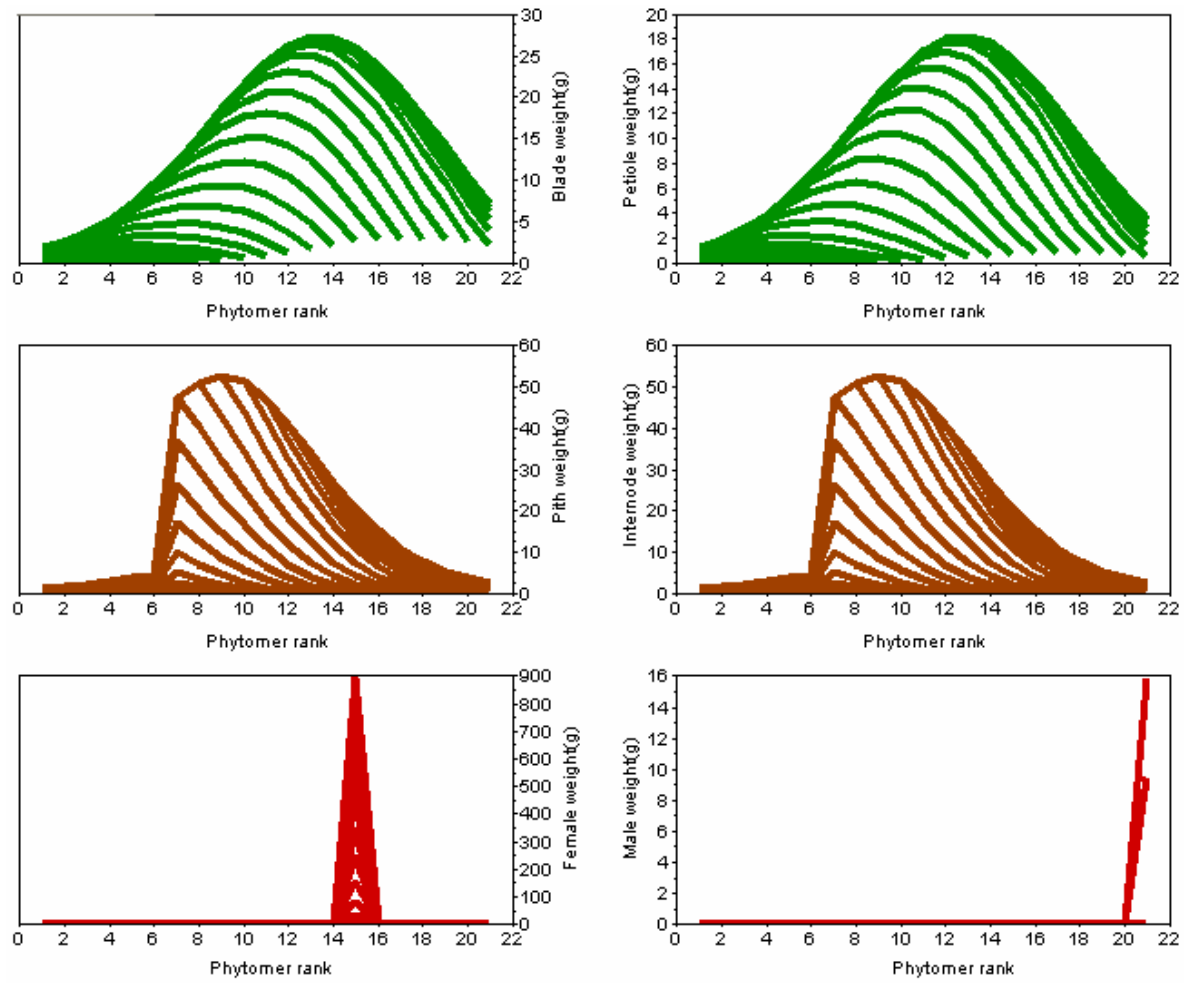
Fig.26 Left: Incremental, fresh biomass gain and partitioning during per organogenetic growth cycle(thermal time between production of two metamers) of maize as simulated with the multi-fitted model. Right: Prediction of leaf area index (LAI).
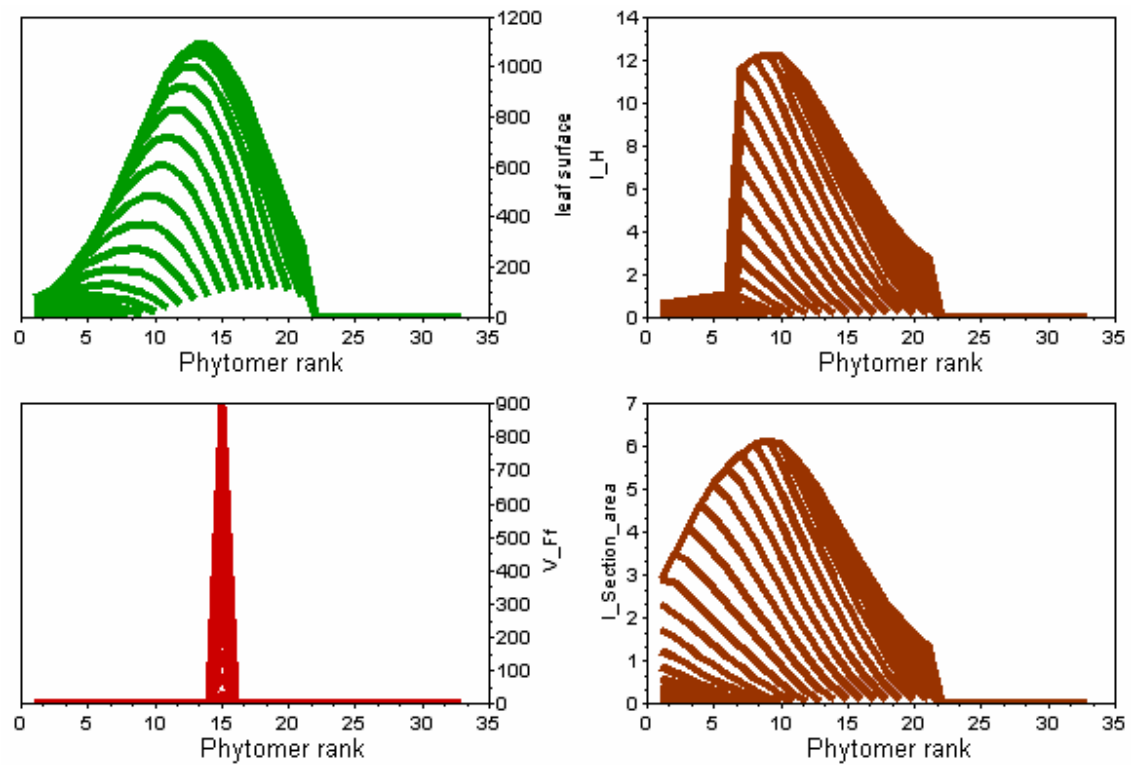
Fig.27 Simulation of organ biomass and geometry varied with growth stages

The Maize can be simulate in 3D with GreenScilab because all the necessarily parameters have been measured or assessed.

Fig. 28 3D model output for maize plants simulated at 33th growth cycle