StemGL
User guide

StemGL at a glance

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Summary

Introduction: What is StemGL ?

A tool based on a Functional Structural Plant Model (FSPM)

StemGL is a software that runs a simplified version of the GreenLab model [1] for single-stemmed plants. The tool implements stochastic simulation capabilities and biomass reallocation. Compared to the detailed model, structural aspects are strongly reduced. Eight types of organs are considered (leaf limb, leaf petiole, common pool, internode, growth rings, female fruit, male inflorescence, and roots).

StemGL provides biomass partitioning among organs

Time is discretized into growth cycles. Simple stochastics rules of growth lead to plant architecture. Organs produce biomass and grow, according to their demand and the common biomass pool availability, in the whole plant starting from the seed.

Genericity of the model but to be calibrated

The model is generic and is not targeted to a given species. However the required parameters, defined by the user expertise, differ according to the species. Using field measures, an adjustment module retrieves the parameters values corresponding to the –measured plant species and varieties in their field environmental conditions.

[1] H.P. Yan, M.G. Kang, P. De Reffye, and M. Dingkuhn, “A dynamic, architectural plant model simulating resource-dependent growth,” Annals of Botany, vol. 93, 2004, pp. 591–602.

1. Introduction: How does StemGL work ?

General Principles

All organs in a given cohort (same age and organ type) share the same chronological and physiological properties, and thus, the same fate.

Biomass production is computed from organ sources and sizes (usually the functional leaf areas).

If organogenesis occurs, the different organ cohorts are updated.

Biomass demand is then evaluated, for each organ cohort, according to its sink value.

The remaining pool of biomass is then divided among the available functioning organ cohorts.

Organ sizes are computed from their chronological age, their expansion state, and allometry rules.

The remaining biomass, if any, is kept in the biomass pool.

2. Simulation: StemGL's approach

Eight categories of parameters for plant

Eight categories of parameters are considered in StemGL. The two first concern structural aspects, the others the functional ones.

P1. The development parameters.

P2. The number of occurrences per phytomer of each organ type (the same for leaf limb and petiole)

We define for each active organ type the following functional parameters:

P3. The functioning duration and the organ expansion duration.

P4. The expansion time.

P5. The expansion delay.

P6. The sink function.

P7. The leaves and internodes allometries.

P8. The global functioning parameters, including constants radiation and climatic efficiency, production surface, seed initial weight and parameters for seed and pool emptying.

Environmental parameters

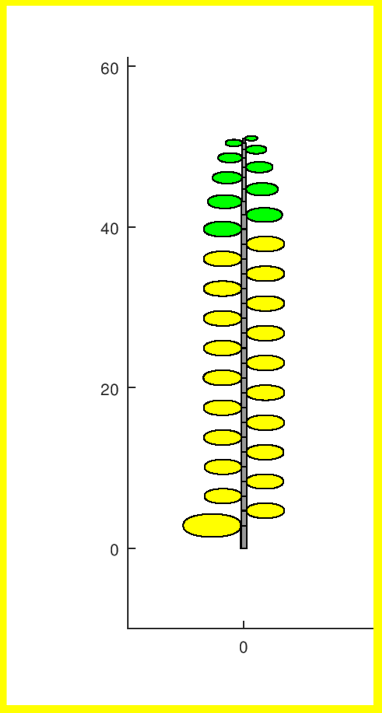
E1. Climatic variations.

E2. Water supply.

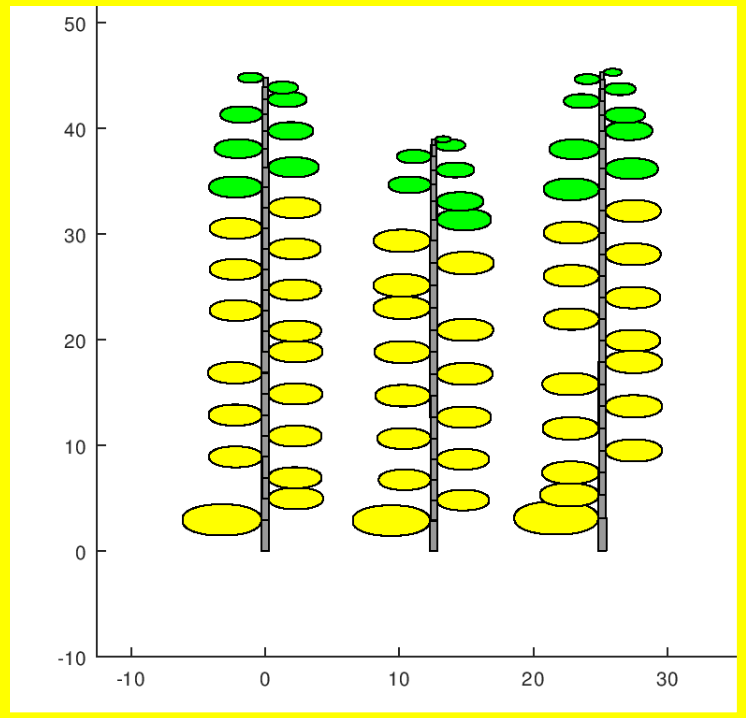
Simulation: StemGL's input – development parameters P1

Bernoulli probability for developing (b)

Bernoulli parameter (b) for stochastic development of stems is characteristic of species and varieties. Default: b=1 (case of most single-stemmed plants).



b=1



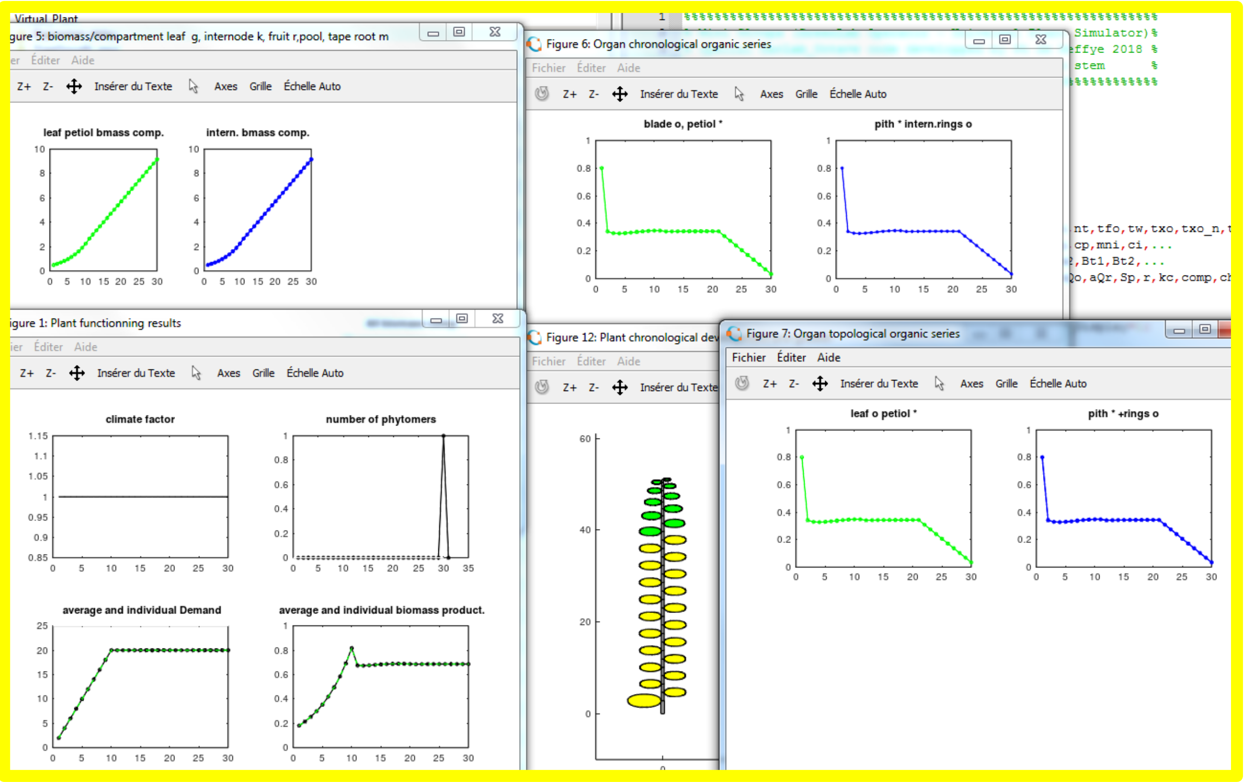
Several (N) stochastic realization with b=0.8 (in this example N=3) it means that for each cycle, stem grows with a probability of 0.8

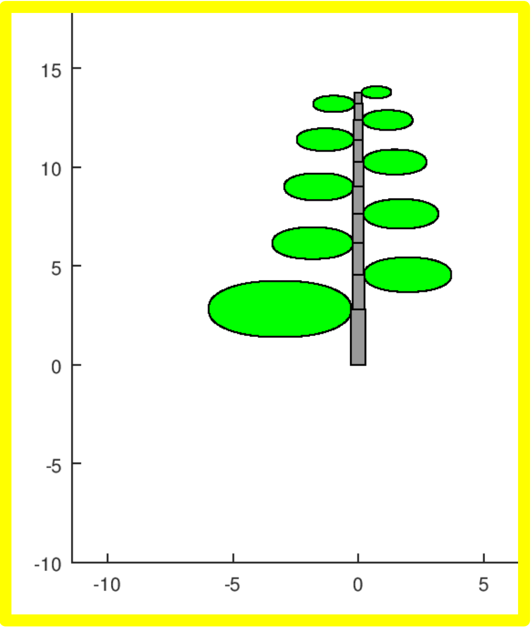
StemGL gives the user the possibility to represent the simulated plants with the variability induced by the Bernoulli parameter.

2. Simulation: StemGL's input – development parameters P1

Number of growth cycles (T)

Number of cycles realization by the software, defined by the last observation date. (T > 0)





Number of growth cycles
T = 10
Ten internodes are produced

Number of growth cycles T = 30
Visualization of graphical results provided by StemGL (under Octave©)

2. Simulation: StemGL's input – development parameters P2

Rhythm parameters (W, W0 and tw)
The defaut rhythm ratio is W.
A change in rhythm parameter is allowed, W0 change in W at cycle tw

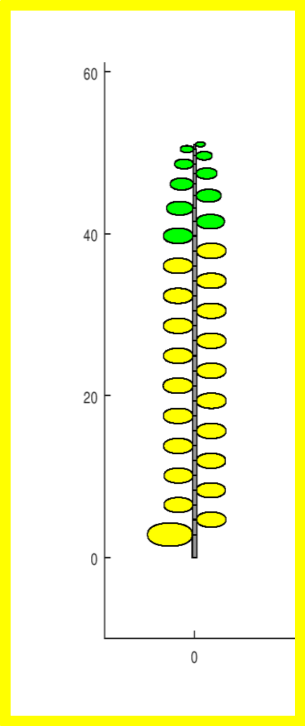
Except particular cases, in StemGL, the rhythm parameter W should be set to 1.
In all cases $0 < W <= 1$
Default values: W=1, W0=1, tw=0

Interest of rhythm ratios

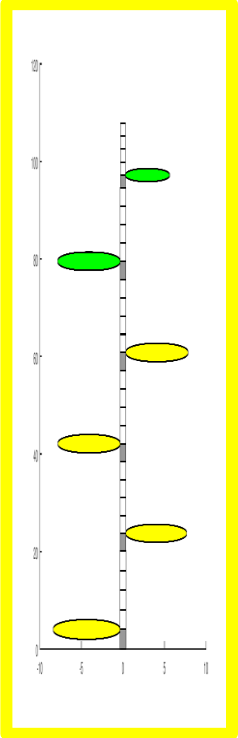
In GreenLab, the rhythm parameter (W) allows to take into account different growth rates between branches and trunk. If rhythm parameter of branches is 0.5, it means that branches grows every two cycles. As a consequence, the trunk grows twice as fast as the branches.

Interest within StemGL: taking into account variation of climatic data during one cycle

In the single-stem case (StemGL), the ratio W is not necessary. On a single stem, W alternates growth period that build phytomer and break period that make void entities. The rhythm parameter W induces pauses during which the simulation may use detailed input data (such as climate variations) impacting the plant production.



W=1

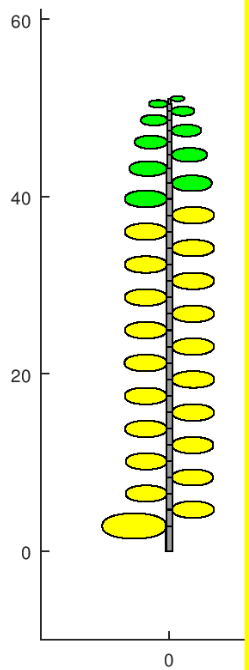


W=0.2

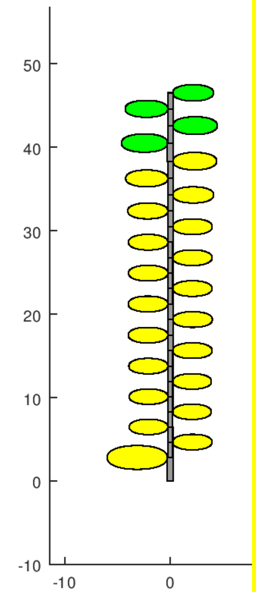
2. Simulation: StemGL's input – development parameters P2

Final age of organogenesis (Tm)

After Tm cycles, no new organ is created but the existing ones continue to grow and function.



(a) T= 30 growth cycles
Final age of organogenesis
Tm=30



(b) T = 30 growth cycles
Final age of organogenesis
Tm=24

Case (a): Tm ≥ T
30 internodes are created. The last leaf is small because it was created within the last cycle.

Case (b): Tm < T
24 internodes are created. The last leaf is as big as older ones because it was created 6 cycles ago.

2. Simulation: StemGL's input – functioning parameters P2

Number of organs no (na, nf, nm)
Organ notations
a: leaves, p: petiole, i: internode,
c: rings, f: female fruit, r: root,
m: male inflorescence

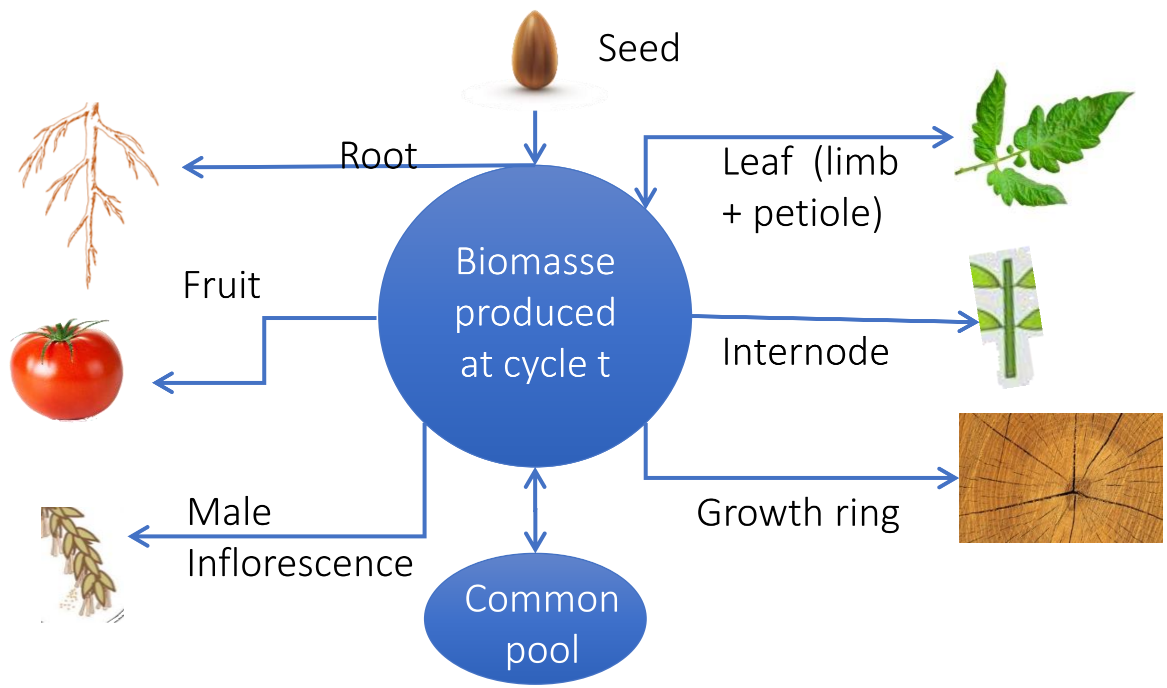
The user sets the number of leaves, na, (same for limb and petiole), the number of fruit, nf, and the number of male inflorescence, nm, per internode.
The internode, growth ring and root are considered present if their relative sink is not zero.

<u>Organs contributing to biomass production</u>

The leaf limb is an organ contributing to biomass production. In StemGL, the petiole and internodes can also contribute to biomass production, thanks to remobilization. The seed is a stock of biomass, released in one or several cycles. Common pool is a virtual organ that stocks biomass and may release it.

<u>Organs where biomass is allocated</u>
Except seed, biomass production is allocated to all organs depending of their sink.

In StemGL, the number of leaves per phytomer is not limited, except for the plant display (limited to 2).



2. Simulation: StemGL's input – functioning parameters P3

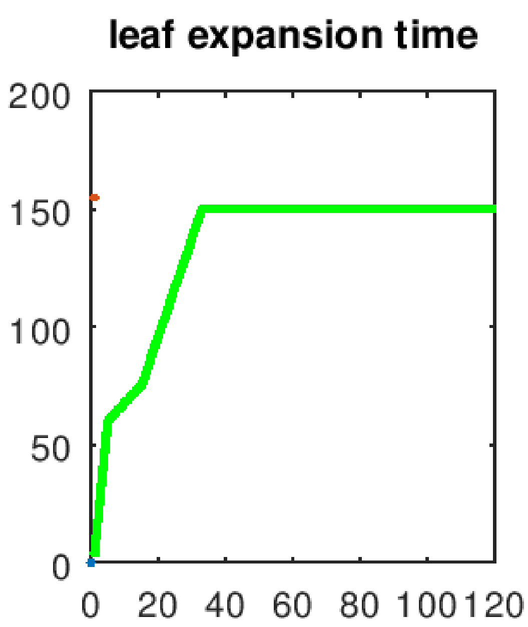
The functioning duration (tfa, tfp, tfi, tfc, tff, tfm, tft) and the organ expansion duration (txa, txp, txi, txc, txf, txm, txt) for respectively leaves, petiole, internode, growth ring, fruit, male inflorescence and root.

The functioning duration correspond to the number of cycles during which the organ is alive (this is of importance when the organ may produce or remobilize biomass).

The organ expansion duration correspond to growth duration (in cycles)

2. Simulation: StemGL's input – function. parameters P4&P5

The organ expansion duration may vary according to the age of the plant at organ apparition (ontogenic age). Four variation steps are allowed in StemGL.



Variation is control by "txo_n_control", the number of control points for variation in expansions (same for all organs), step1 to step4, number of cycles at which change 1 to 4 occurs.

User set up, for each step, organ expansion duration multiplier coefficients that applies to usual txo for leaves, petiole, internode, fruit and male inflorescence. The final expansion duration is the usual coefficient txa, txp, txi, txf, txm.

Steps must be age sorted 0 < step1 <…< step4 < txo
Defaut are: txo_n_control = 0;

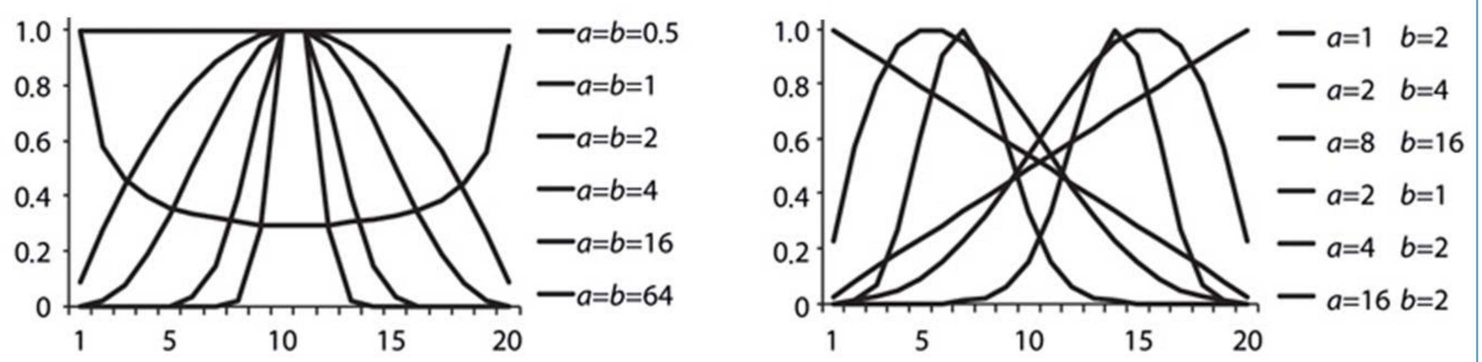
2. Simulation: StemGL's input – functioning parameters P6

Sink functions

<u>To take into account biomass demand of organs</u>

The demand of organs is defined by organ category (fruit, leave, growth ring, root, …). They can be constant but generally they are considered as varying during organ development and modelled with a generic function, the beta function in StemGL. An organ sink function is thus defined for each kind of organ and plant by the two Beta curve parameters.

Sink functions are proportional to the leaf one. By convention, leaves sink function mode is set to 1.



Sink function shapes varying Beta function parameters with an expansion on 20 cycles

In StemGL, sink functions are assumed being the same during the whole plant development

2. Simulation: StemGL's input – functioning parameters P7

Organ allometries (e, b, a, f parameters)

<u>To link the organ fresh biomass to organ dimensions</u>

Organs dimensions are inferred from its biomass increase. Fresh biomass is first converted to a volume. The relation between this volume and the organ dimensions is defined by an allometry, supposed to be stable during growth.

$s = \frac{v_l}{e}$	$Leaf: simple\ area\ s\ of\ thickness\ e$
$r = f\sqrt[3]{\frac{3v_f}{a\,b\,\pi}}$	$Fruit: ellipsoïd\ shape\ (r, ra, rb)$
$height = \sqrt{b}\,(v_i)^{\frac{1+a}{2}}$ $section = \sqrt{\frac{1}{b}}\,(v_i)^{\frac{1-a}{2}}$	$Internode: cylinder\ with\ lengthening\ b$ $and\ allometry\ \frac{height}{section} = b\,v_i{}^a$

Leaf thickness : e leaf biomass -> leaf area

Fruit density coefficient : f
Fruit biomass -> fruit radius r (a=b=1)

Lengthening (b) and shape (a) coefficients :
internode biomass -> internode height and section

2. Simulation: StemGL's input – functioning parameters P8

Functioning parameters at plant level (Eo,Qo,aQo,aQr)

Eo: overall environmental conditions

Eo qualifies the environmental pressure (default is 1). Decreasing it limits the production in proportion. *Eo* can be defined at various cycles in an external file or expressed as a function (see further)

Qo, aQo : Plant seed

Qo defines the seed biomass (i.e. must be > 0, typical values are 0.2 to 1) . Parameter *aQo*, when ≠ 1, specifies a exponential seed biomass decay . The biomass released by the seed *dQo* at cycle *t* is expressed as follow: $dQo(t) = Qo \cdot aQo \cdot (1 - aQo)^{(t-1)}$

aQr : Reserve Common Pool

aQr defines the proportion the reserve common pool mobilizes. Default value is 0 (no reserve pool). Example: with *aQr* = 0.75, only ¾ of the common pool are available for organs

2. Simulation: StemGL's input – functioning parameters P8

Functioning parameters at plant level (r,Sp,kc)

<u>r: leaf resistivity</u>

R stands for the reversed Water use efficiency. Typical values belong to interval [5-20]. This value must be set by inverse method (fitting)

In practice, set Sp according to your stand characteristics, keep kc value set to 1, and define r from fitting,

<u>Sp: Production area</u>

Sp defines the production area (in cm2).

Sp can be understood as the ground projection available for the plant growth. When Sp decreases (competition is high), Sp tends to the reversed density (Sd ≈1/d) area defines the seed biomass (i.e. must be > 0, typical values are 0.2 to 1) . Typical values belong to interval [100-10000]

<u>kc: LambertBeer law extinction coeficient</u>

The kc parameter is supposed to be constant during plant's life. Default value is 1.

Detailed Environmental parameters E1

<u>climate global parameters (modE, Ec, cor, wE, bE, Lmax, Lmin)</u>

modE stands for the environmental modes ; *Ec* is a global scaling factor, *cor* is a correlation factor, *wE* is a rhythm, *bE* a probability and *Lmax* and *Lmin* are light limit values.

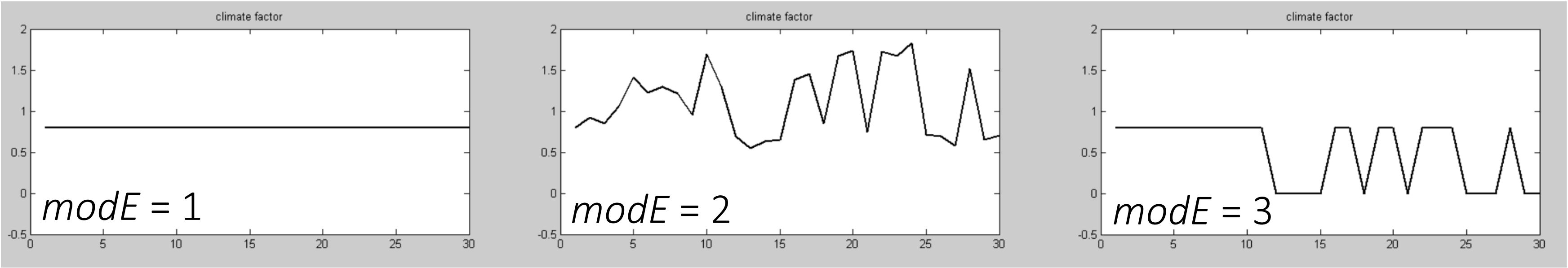
for *modE* = 1 we have $E(t) = Eo$ (constant, default), for each cycle t

for *modE* = 2 we have $E(t)$ is random with autocorrelation :

$$E(1) = Ec \text{ and then } E(t>1) = cor * E(t-1) + (1-cor) * (Lmin + \text{random} *(Lmax-Lmin));$$

for *modE* = 3 we have $E(t)$ is periodic with values 0 and *Ec* with rhythm *wE* and probability *bE*

Example (mode comparison) with   *Ec* = 0.8, *cor* = 0.2,*Lmax* = 2.5, *Lmin* = 0.5, *wE* = 3, *bE* = 0.25



Detailed Environmental parameters E2

<u>Water supply parameters (modH, c1, c2, Hmx, Hmn, H1,_psi,_pH20,_dH20)</u>

modH, c1, c2, Hmx, Hmn, H1,_psi,_pH20,_dH20

modH stands for the water supply mode and frequencies

for modH = 0 we have no irrigation DH(1:T) = 0

for modH = -1 we have random irrigation DH(1:T) = random*dH20 (if random < pH20)

for modH > 0 we have regular irrigation DH(1:T) = dH20 * (1 - sign(mod(t,modH)))

The water availability model:

H(1) = H1: water availability at first cycle;

then H(i) = H(i-1) - (Sf/Sp) * c1 * (H(i-1) -Hmn) + c2 * (Hmx- H(i-1)) * DH(i,1)

c1 and c2 are two coefficients standing for the plant water uptake and the soil absorption respectively

2. Simulation: StemGL's output.

Information in the command console

<u>During simulation</u>

Files loaded names (parameters, mask, ...) and eventually an error message (file error or data error)

At each growth cycle, Cycle, Biomass (cumulated, increment, leaf, internode, fruit) are given.

Example (with 28 cycles):

C:1 Biomass:0.046236(0.046236) leaf:0.015082 internode:0.002558 fruit:0.000000

....

C:28 Biomass:148.344551(2609.407942) leaf:273.070718 internode:207.233293 fruit:1784.252201

<u>Computing time performances (at end of simulation, for each task).</u> Example:

TOTAL CPU TIME 3.984375 Total simulation 0.187500

Parameter loading 0.031250 Development Axis 0.015625

Mask load & apply 0.015625 Climate model 0.000000

Organ durations 0.000000 Sink Organ Beta laws 0.015625

Plant Organ demand 0.015625 Plant Organ growth 0.109375

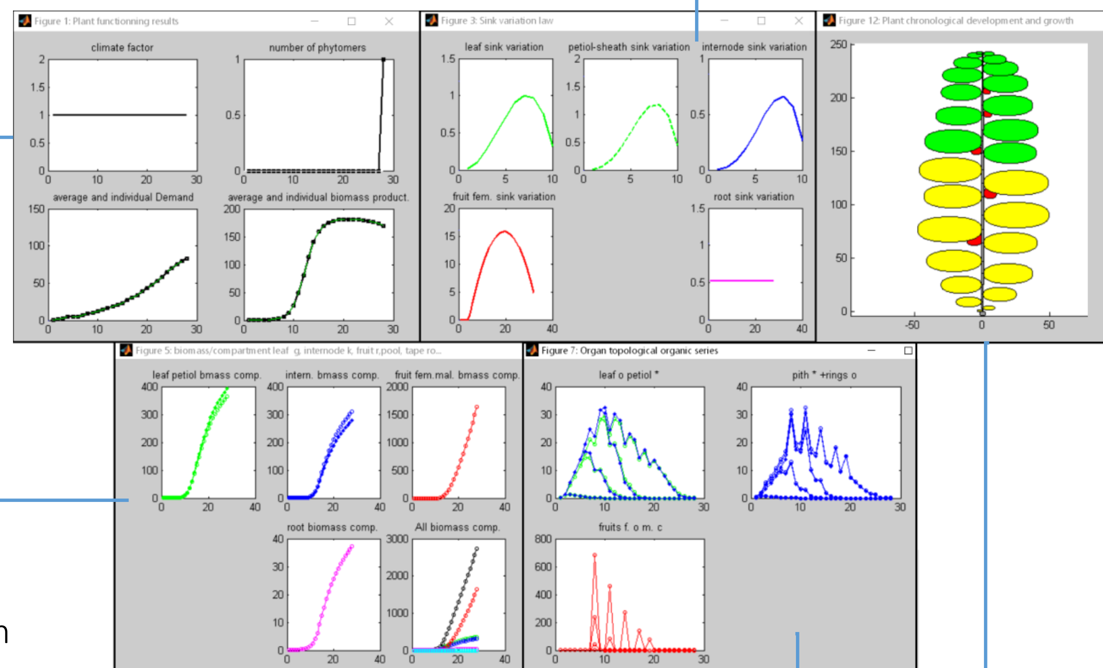
Organic series 0.031250 Plotting results 0.968750

Plant Display 0.250000 Target & Mask save 0.015625

2. Simulation: StemGL's output. Curves

Graphical diagrams (displayed at end of simulation)

Organ expansion and sink functions



Plant functioning results (cycle)

Climate factor, number of phytomers, demand, biomass production

Biomass allocated to organ componants

Organ chronological and topological series

biomass curves, including those at observation

Plant chronological and topological structure representations

3. Fitting: Principles

Given parameters and fitted parameters

Structural development parameters

Structural parameters (development probability, rhythm ratio, viability, ...) must be given. They can be estimated from field internode distribution statistical analysis. Typically, the mean variance ratio is used to estimate Bernoulli parameter b.

Functional parameters to be given

The following parameters must be given : Expansion and functioning times, Surface of production and Organ allometries

Functional parameters to be fitted

Global functioning parameters (Qo, r)

Organ sink functions (beta law parameters)

3. Fitting: StemGL's input – Parameters F1

Data collection modes & fitting parameters

Data collection modes (comp, phyt)

Measures can be given per compartment or/and per phytomer

At least one collection mode must be active

Comp=1 stands for global organ compartment level (default 1)

Phyt=1 stands for local organ compartment level, (phytomer level) (default 1)

Fitting parameters are predefined (they can be changed in the interpreted code)

The fitting method is the generalized least square method

The number of iterations is set to 10 (by default)

3. Fitting: StemGL's input – Parameters F2

Parameter selection

Selected parameters have their selector set to value 1

Unselected parameters have their selector set to value 0

Trick: the parameter selector name is the parameter name prefixed by letter 'x'
Example : xSp is the selector of Parameter Sp

<u>Parameter that can be fitted</u>

xQo, xaQo, xr, xSp : global functional parameters

Xpp, xpi, xpc, xpf, xpm, xpt, kpc, kpa, kpi Sink functions

xBa1, xBp1, xBi1, xBf1, xBm1, xBt1, xBa2, xBp2, xBi2, xBf2, xBm2, xBt2 Expansion Beta law parameters (two parameter per organ type)

At least one parameter selector must be active

3. Fitting: StemGL's output. Console window

Information in the command console

<u>During simulation</u>

Files loaded names (parameters, mask, …) and eventually an error message (file error or data error)

At each iteration, the list of parameters values issued and the error. The two last lines print the estimated parameter values (A) and their standard deviation (sA). Example:

```
13.047  2421.442   1.000   0.500  25.003   0.700   1.500   3.000   3.000   3.000        iter = 3  error = 67.4794
 ……
12.013  2221.031   1.024   0.612  22.673   0.768   1.738   3.460   3.037   3.372        iter = 10  error = 15.1926
   'xr____xSp___xpp___xpe___xpf___xkpa__xkpe__xBa1__xBp1__xBi1__'
 A 1=12.01  A 2=2221.0  A 3=1.024  A 4=0.6118  A 5=22.67  A 6=0.7682  A 7=1.738  A 8=3.459  A 9=3.036  A 10=3.371
sA 1=0.8969 sA 2=226.1 sA 3=0.0539 sA 4=0.0479 sA 5=1.671 sA 6=0.03414 sA 7=0.0967 sA 8=0.2151 sA 9=0.2132 sA 10=0.2456
```

<u>Computing time performances (at end of simulation, for each task).</u> Example:

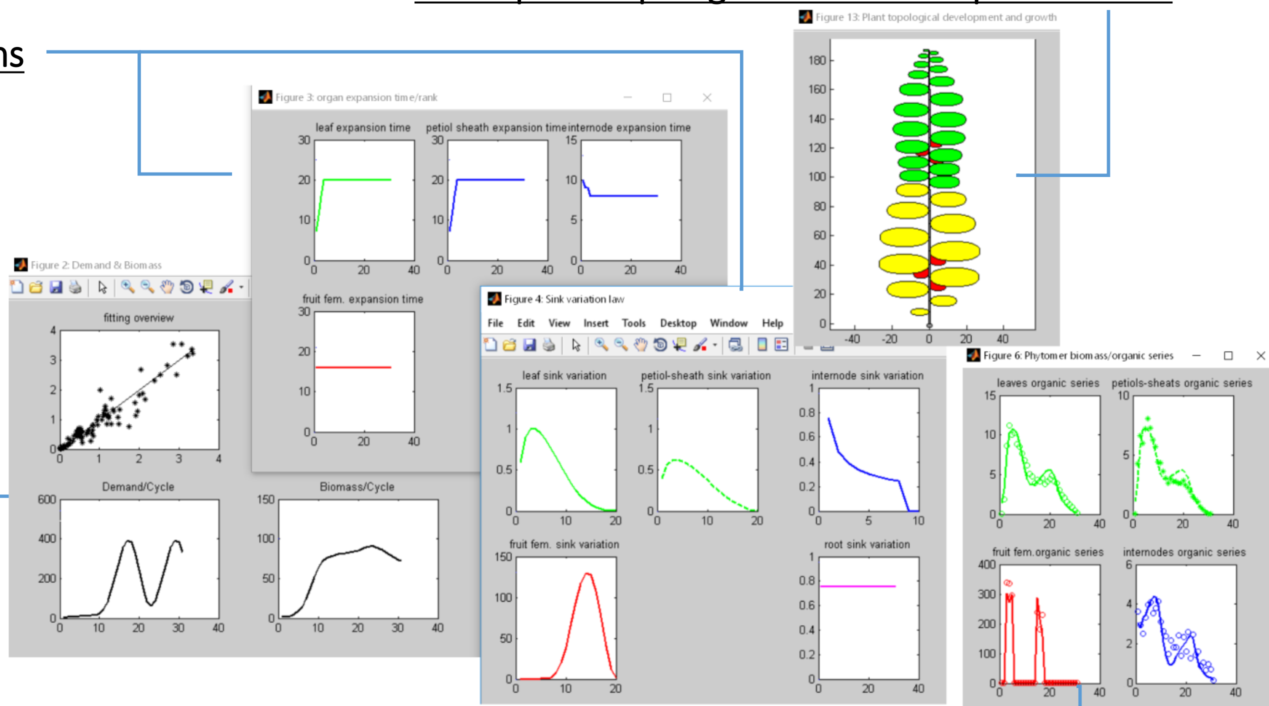
```
TOTAL CPU TIME    3.937500      Total simulation  1.687500
Parameter loading 0.015625      Target loading    0.062500
Development Axis  0.031250      Mask load & apply 0.031250
Organ durations   0.015625      Climate model     0.000000
Parameter fitting 1.609375      Plotting results  0.765625
Parameter saving: 0.015625      Plant Display     0.093750
```

3. Fitting: StemGL's output. Curves

Graphical diagrams (displayed at end of simulation)

<u>Fitted plant topological structure representation</u>

<u>Organ expansion and sink functions</u>



<u>Plant functioning results (cycle)</u>

fitting overview

demand, biomass production

<u>Organ chronological and topological series</u>

biomass curves, including those at observation times