

Rule-based integration of LIGNUM into GroIMP

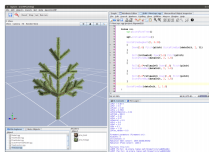
Katarína Streit (Smoleňová)

ksmolen@gwdg.de

Departement Ecoinformatics, Biometry and Forest Growth
Georg-August-University Göttingen

September 17, 2013 / Prague

“Modelling of Ecosystems by Tools from Computer Science”



Outline

Motivation

LIGNUM FSTM

XL implementation

Motivation

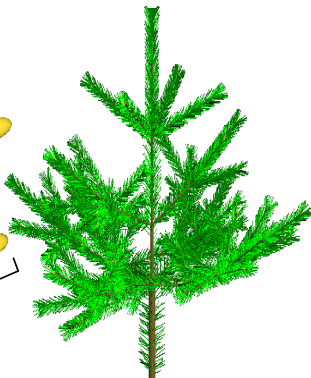
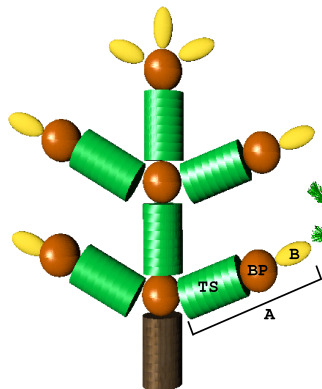
- ▶ LIGNUM - Functional-Structural Tree Model (FSTM)
- ▶ Complex model applied to several tree species
- ▶ Test case for the component framework of GroIMP and for models comparison, on the example of Scots pine
- ▶ Analysis and (partial) reimplementations into XL

LIGNUM FSTM

- ▶ Developed at METLA, Finland
- ▶ Originates from a process-based model, being developed as FSTM since 1996 (Perttunen *et al.* 1996)
- ▶ Applied to both coniferous and deciduous trees, e.g.,
 - ▶ Scots pine (*Pinus sylvestris*)
 - ▶ Jack pine (*Pinus banksiana*)

 - ▶ Sugar maple (*Acer saccharum*)
 - ▶ Eastern cottonwood (*Populus deltoides*)
 - ▶ Silver birch (*Betula pendula*)
 - ▶ Mountain birch (*Betula pubescens* subsp. *tortuosa*)
- ▶ Applied to model both individual trees and stands

Basic structural units



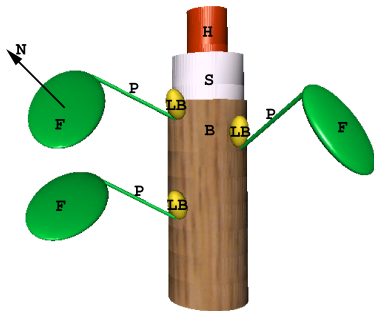
(LIGNUM manual)

- TS - tree segment
- BP - branching point
- B - bud
- A - axis

Structure of tree segment



coniferous

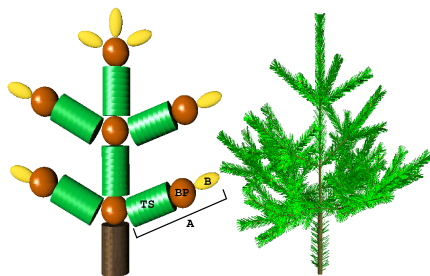


(LIGNUM manual)

deciduous

- H - heartwood
- S - sapwood
- B - bark
- LB - lateral bud
- F - foliage
- P - petiole

Tree topology

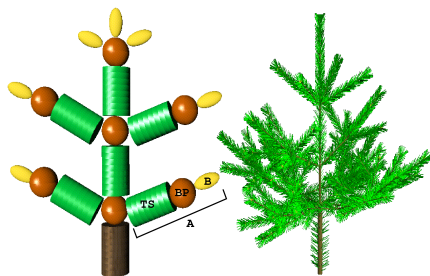


(LIGNUM manual)

- ▶ One (main) axis
- ▶ Axis - sequence of TSs, BPs & terminating B
- ▶ Each TS followed by 1 BP
- ▶ BP - list of axes

- ▶ Main axis (represented as a list):
- ▶ $A = [TS, BP, TS, BP, TS, BP, B]$
- ▶ $A = [TS, [A, A], TS, [A, A], TS, [A, A], B]$
- ▶ $A = [TS, [A, A], TS, [A, A], TS, [[B], [B]], B]$
- ▶ ...

Tree topology

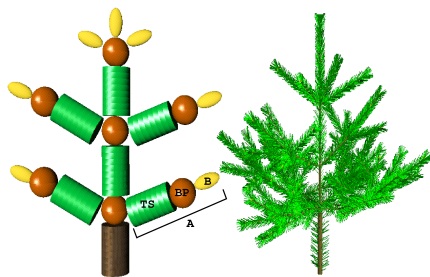


(LIGNUM manual)

- ▶ One (main) axis
- ▶ Axis - sequence of TSs, BPs & terminating B
- ▶ Each TS followed by 1 BP
- ▶ BP - list of axes

- ▶ Main axis (represented as a list):
- ▶ $A = [TS, BP, TS, BP, TS, BP, B]$
- ▶ $A = [TS, [A, A], TS, [A, A], TS, [A, A], B]$
- ▶ $A = [TS, [A, A], TS, [A, A], TS, [[B], [B]], B]$
- ▶ ...

Tree topology

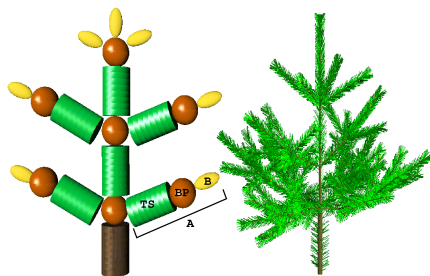


(LIGNUM manual)

- ▶ One (main) axis
- ▶ Axis - sequence of TSs, BPs & terminating B
- ▶ Each TS followed by 1 BP
- ▶ BP - list of axes

- ▶ Main axis (represented as a list):
- ▶ $A = [TS, BP, TS, BP, TS, BP, B]$
- ▶ $A = [TS, [A, A], TS, [A, A], TS, [A, A], B]$
- ▶ $A = [TS, [A, A], TS, [A, A], TS, [[B], [B]], B]$
- ▶ ...

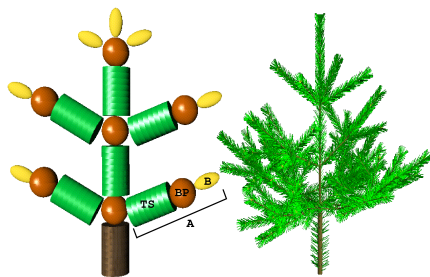
Tree topology



(LIGNUM manual)

- ▶ One (main) axis
 - ▶ Axis - sequence of TSs, BPs & terminating B
 - ▶ Each TS followed by 1 BP
 - ▶ BP - list of axes
- ▶ Main axis (represented as a list):
 - ▶ $A = [TS, BP, TS, BP, TS, BP, B]$
 - ▶ $A = [TS, [A, A], TS, [A, A], TS, [A, A], B]$
 - ▶ $A = [TS, [A, A], TS, [A, A], TS, [[B], [B]], B]$
 - ▶ ...

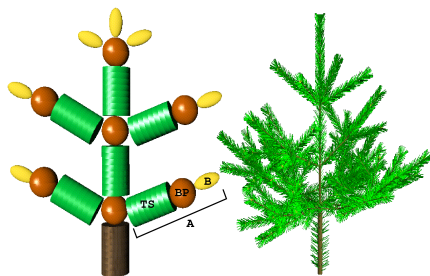
Tree topology



(LIGNUM manual)

- ▶ One (main) axis
 - ▶ Axis - sequence of TSs, BPs & terminating B
 - ▶ Each TS followed by 1 BP
 - ▶ BP - list of axes
- ▶ Main axis (represented as a list):
 - ▶ $A = [\text{TS}, \text{BP}, \text{TS}, \text{BP}, \text{TS}, \text{BP}, \text{B}]$
 - ▶ $A = [\text{TS}, [A, A], \text{TS}, [A, A], \text{TS}, [A, A], \text{B}]$
 - ▶ $A = [\text{TS}, [A, A], \text{TS}, [A, A], \text{TS}, [[B], [B]], \text{B}]$
 - ▶ ...

Tree topology



(LIGNUM manual)

- ▶ One (main) axis
 - ▶ Axis - sequence of TSs, BPs & terminating B
 - ▶ Each TS followed by 1 BP
 - ▶ BP - list of axes
- ▶ Main axis (represented as a list):
 - ▶ $A = [TS, BP, TS, BP, TS, BP, B]$
 - ▶ $A = [TS, [A, A], TS, [A, A], TS, [A, A], B]$
 - ▶ $A = [TS, [A, A], TS, [A, A], TS, [[B], [B]], B]$
 - ▶ ...

Structure development

- ▶ Described by rules (species specific), written in the language L

```
// initial structure
```

```
Start:
```

```
{
```

```
...
```

```
produce
```

```
  F(0.30)
```

```
  SB() Down(1.0) Pitch(pitch) B(data,2,0.9) EB()
```

```
  SB() Roll(rollmain4) Down(1.0) Pitch(pitch) B(data,2,1.0) EB()
```

```
  SB() Roll(2.0*rollmain4) Down(1.0) Pitch(pitch) B(data,2,1.0) EB()
```

```
  SB() Roll(3.0*rollmain4) Down(1.0) Pitch(pitch) B(data,2,1.0) EB()
```

```
  B(data,1,1.0);
```

```
}
```

Metabolic processes

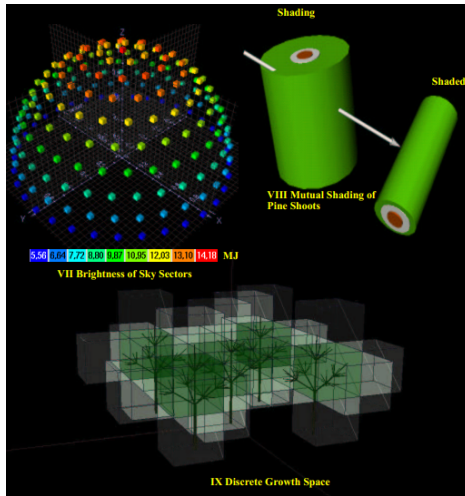
- ▶ Two categories (w/o or w flow of information):
 - ▶ Photosynthesis
 - ▶ Respiration
 - ▶ Mortality

 - ▶ Length growth
 - ▶ Diameter growth
 - ▶ Up flow
 - ▶ Down flow

- ▶ Iterative allocation of new photosynthates into the organs

$$P - M = \Delta W_n + \Delta W_o + \Delta W_r \quad \text{and} \quad P - M > 0$$

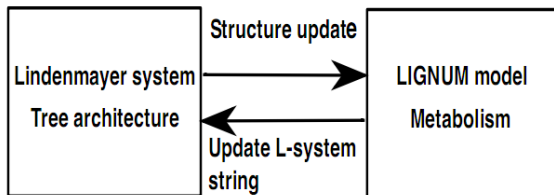
Light distribution



(Perttunen *et al.* 2002)

Implementation background

- ▶ Implemented in C++ (metab. processes), L (architecture)
- ▶ Two-way communication



4 generic algorithms

- ▶ For traversing the model tree, quering the status of the tree or passing information between tree compartments
- ▶ Sufficient to cover the computation of modelled metabolic processes
 - ▶ **ForEach** (e.g., calculate photosynthesis for each segment)
 - ▶ **Accumulate** (e.g., sum up photosynthates of all segments)
 - ▶ **AccumulateDown** (e.g., diameter growth)
 - ▶ **PropagateUp** (e.g., signal/data passing)

```
Tree<ScotsPineSegment, ScotsPineBud> scotspine;  
ForEach(scotspine, Photosynthesis<ScotsPineSegment,  
ScotsPineBud> ());
```

LIGNUM's structural components as XL modules

- ▶ Main structural units:
TreeSegment, Bud
(*BranchingPoint* and *Axis*, inevitable in LIGNUM, inherently expressed in XL)
- ▶ Modules for trees in general:
Tree, TreeCompartment
- ▶ Modules specific for conifers, pine and Scots pine:
CfTreeSegment, PineSegment, PineBud, ScotsPineTree, ScotsPineSegment, ScotsPineBud
- ▶ Modules to control branch orientation:
Pitch, Roll, Turn, Down, HDir

Structure development (XL)

- Straightforward translation of L rules into XL rules

LIGNUM	GroIMP	Description
$Start : \{ produce\ A(); \}$	$Axiom ==> A;$	Start symbol
$A() : \{ produce\ B() A(); \}$	$A ==> B\ A;$	L-system rule
$SB()$	$[$	Branch start
$EB()$	$]$	Branch end

Structure development (XL)

```

Start:
{
...
produce
  F(0.30)
  SB() Down(1.0) Pitch(pitch) B(data,2,0.9) EB()
  SB() Roll(rollmain4) Down(1.0) Pitch(pitch) B(data,2,1.0) EB()
  SB() Roll(2.0*rollmain4) Down(1.0) Pitch(pitch) B(data,2,1.0) EB()
  SB() Roll(3.0*rollmain4) Down(1.0) Pitch(pitch) B(data,2,1.0) EB()
  B(data,1,1.0);
}

```

Axiom ==>

```

...
ScotsPineSegment(0.30)
[ Down(1.0) Pitch(pitch) ScotsPineBud(data, 2, 0.9) ]
[ Roll(rollmain4) Down(1.0) Pitch(pitch)
  ScotsPineBud(data, 2, 1.0) ]
[ Roll(2.0*rollmain4) Down(1.0) Pitch(pitch)
  ScotsPineBud(data, 2, 1.0) ]
[ Roll(3.0*rollmain4) Down(1.0) Pitch(pitch)
  ScotsPineBud(data, 2, 1.0) ]
ScotsPineBud(data, 1, 1.0)
;

```

Metabolic processes (XL)

LIGNUM	GroIMP	Example
<i>ForEach</i>	execution rule (::>)	<i>sps:ScotsPineSegment</i> ::> <i>sps.photosynthesis()</i> ;
<i>Accumulate</i>	aggregators (<i>sum, count, max, ...</i>), with queries ((* *))	<i>sum((* ScotsPineSegment *)</i> <i>.getP())</i> <i>// sum up photosynthates</i>
<i>AccumulateDown</i> <i>PropagateUp</i>	path patterns with directed relations (-r->, <-r-), with <i>r = minDescendants,</i> <i>descendants, ancestor,</i> shortcuts: -->, <-- = any edge, >, <= successor, +>, <+= branch	<i>sps:ScotsPineSegment</i> ::> <i>if (sps.getAge() == 0) {</i> <i>sps.setQin(</i> <i>(* sps -ancestor-></i> <i>ScotsPineSegment *)</i> <i>.getQin()</i> <i>);</i> <i>}</i> <i>// propagate up incoming radiant flux</i> <i>// to new segments</i>

Light distribution

- ▶ Sky model and two (presented) light models used in LIGNUM were adapted into GroIMP
- ▶ Their code is hidden from the user
- ▶ Light models called using execution rules

```
sps:ScotsPineSegment ::> radiation.eval(sps);
```

Comparison



Summary

- ▶ Partial translation of both, the structural and the functional part of LIGNUM into the rule-based language XL
 - ▶ Architecture, radiation distribution, photosynthesis, respiration, senescence, allocation, elongation
- ▶ Focus on Scots pine
- ▶ Future work
 - ▶ Translation of missing parts - pruning
 - ▶ Model comparison
 - how will the final structure look like if different light models, photosynthesis, etc., are used
 - simulation of a same species with LIGNUM and GreenLab, comparison of outputs

Thank you for your attention!