

## AMAP2SAR AMAP SORTER V1.0: user manual

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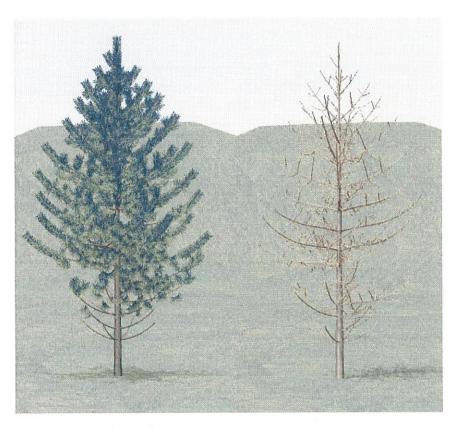
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# AMAP2SAR AMAP SORTER V1.0

User Manual

ESA ESTEC/ Contract No. 163014/96/NL



**Unité de Modélisation des Plantes (CIRAD-GERDAT)** 

&





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## 1. INTRODUCTION

Theoretical modelling of the forest backscatter is a powerful tool towards the development of quantitative forest applications such as biomass retrieval from SAR data. RT models usually describe the forest canopy as a discrete multi-layer random media containing different classes of dielectric cylinders for the vegetation elements. One of the actual major limitations of RT modelling is the difficulty to obtain a realistic and complete canopy architectural description as a function of growth stage. In particular, tree crown parameters, through which backscatter usually correlates to above-ground biomass, are very difficult to measure or estimate. Allometric equations offer an alternative but are often not available for the speciess under study and crown parameters of interest. An alternative is to develop a new approach using tree growth models to derive input parameters to RT models.

The method for canopy description presented here is based on three characterization steps implemented in the specific AMAP2SAR interface: 1) AMAP modelling of the tree architecture, 2) generic description of the tree as a collection of cylinders and 3) specific adaptation to the RT models.

The AMAP model relies on both qualitative and quantitative architectural tree growth description. Detailed botanical observations allowed to develop an architectural typology used in the modelling. Specific botanical measurements are then necessary to calibrate the model for a given speciess in its environmental conditions. They are performed on tree shoots called *growth units* (GU), which are produced by the terminal meristems and build the tree architecture (see botanical description). Parameters of theoretical distribution (binomial and geometric laws) for GU characteristics and branching process (growth, interruption or mortality) are obtained from fittings with the measurements.

Then, tree architectural simulation for a given age is realized through Monte-Carlo technique and Markov process, allowing to reproduce i) the meristem activity and ii) the branching process and associated geometry (angle, length, diameter) of GU's. The result is a realistic 3D tree (with or without needles or leafs) stored in a file.

Finally, the canopy natural variability is reproduced through successive random AMAP simulations. A set of these simulations is performed for each growth stage of interest (age).

The interface AMAP2SAR was developed to 1) simulated different tree speciess and 2) transform these 3D trees into a collection of cylinders representing the various tree elements: trunk, branches and needles, with their geometric characteristics: (x,y,z) position, diameter, length and orientation angles. A branch is considered as a collection of successive cylinders of varying dimensions and orientation, to take into account tapered and curved branches.

An additional step including in the interface is to adapt this description to the specific RT model (MIT/CESBIO, MIMICS, Karam-Fung...). It describes the canopy as a n-layer discrete random media, where the tree crown is characterized as a multi-scale cluster of dielectric cylinders. In our case, up to five scales represent the trunk, increasing orders of branches and needles.

The interface first splits the canopy into n horizontal layers, using a fixed vertical interval or a variability criteria. For each branch order, successive cylinders forming a given branch are transformed in a single approximated cylinder, since curved and tapered branches are not yet taken into account. From there, cylinders at each cluster scale (branch order BO1 to BOn) are

characterized by mean length, diameter, linear density and branching angle, after averaging over N simulated trees. In addition, histograms of all these parameters are available.
First results on the coupling <b>AMAP2SAR</b> with the MIT/CESBIO RT Model are presented in Castel et <i>al.</i> 1997; Floury et <i>al.</i> 1997 (see appendix).
Caster et al. 1997, 1 loury et al. 1997 (see appendix).

## 2. OVERVIEW

The AMAP2SAR software was created to enable simulating plant shapes and then extracting data from the 3D shapes that are relevant for SAR simulation models. It is an interactive software running on SUN Unix machines.

The three main functionnalities are:

- tree simulation
- data extracting and filtering
- data exportation to a format suited as input to SAR models.

#### 2.1. TREE SIMULATION

A tree database is provided that consists in the description of some characteristics for the different tree speciess. Those characteristics are topological and geometrical parameters describing the functioning of the buds of a species across their life. The values of the parameters were fullfilled by botanists after measurements of real trees and extraction of statistical values from those measurements. The user has no acces to this set of parameters.

A random generator reads those descriptions and generates the realistic tree shape at a given age. The output consists in a file that contains the 3D description of the different components of the computed tree (i.e. branch parts, leaves ..). The user can select the species to be simulated, the final age of the plant, a step for geometrical output and the number of simulations to be done.

The generic name of the output simulation files is: line tree. Those files are binary written, thus not directly readable (extention ".lig" and ".brc").

## 2.2. DATA EXTRACTING AND FILTERING

The user can load the characteristics of the different components described in a line tree file and then visualize it through histograms on different extracted variables. The variables are as follows:

- branching order (trunk to primary, secondary branches, etc...)
- topological position inside the branch
- length
- height
- diameter
- azimut
- direction
- death indicator
- organ type

The user can apply filter on these data consisting in min and max thresholds for the different variables, he can also apply filter on insertion angle or branched area or on trunc diameter.

After filtering, the user can save the new set of data.

The extension file name for the extracted data is ".xtr". Those files are written in ASCII.

#### 2.3. DATA EXPORTATION TO SAR FORMAT

The user can export the extracted data to a format suited as input to models that contains relevant values to describe the branches:

- ramification norder
- average height
- average diameter
- volume
- insertion angle
- direction
- length
- curving index

The generic extention for SAR files is ".sar". Those files are written in ASCII.

#### 3. SOFTWARE FUNCTIONALITIES

The name of the software is "amap2sar". It is an X11 interactive program that allows the use of the mouse. The main window consists in a drawing area and a menu bar. All options of the software can be reached through the menu bar. Here are the descriptions of the different items in the menu bar.

#### 3.1. FILE OPTION

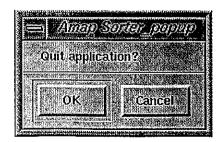
This option allow to get information on the software (Version suboption) or to quit the software (Quit suboption).

When clicking on the "Version" suboption, this message box is displayed:

You can get the actual version of the software, click on "OK" to close the box.



When clicking on the "Quit" suboption, this message box is displayed:

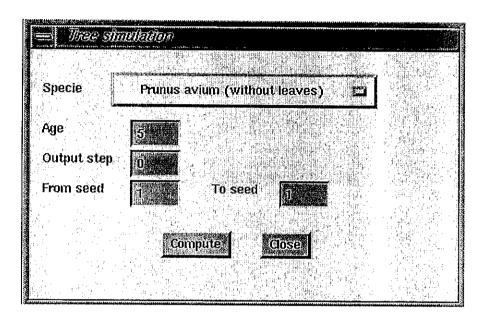


You can quit the software by clicking "OK" or close the box by clicking "Cancel".

#### 3.2. SIMULATION OPTION

This option allows to simulate trees (Simulation suboption) and to export the 3D shape to the xtr format (Extract from ligne tree suboption).

#### 3.2.1. SIMLATION SUBOPTION



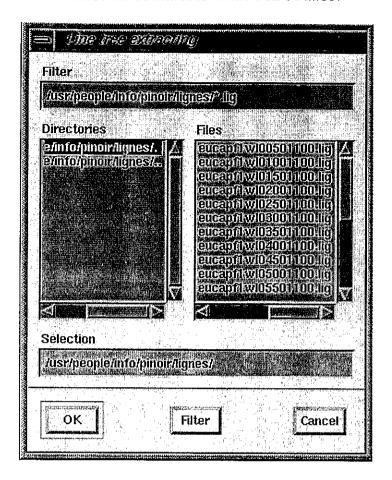
When selecting this suboption, this box is displayed. You can select the species to be computed by clicking the name button. You can enter the desired computing age (a maximal age is displayed in the name of the species).

You can enter a step for geometrical output, at each "step" of the computing geometrical output will be done (i.e. simulating a growth), a zero value means output at the end only. You can enter the number of simulations to be done by adjusting the "from seed" and the "to seed" values, the seed allows the simulator to introduce the variability between individuals into a species. The name of the files that are generated is constructed as follows:

"xxxxxnnnssaaa.lig" where xxxxx is the name of the species, nnn is the actual output step, ss is the current seed and aaa is the final age. The file are stored into the directory specifed in the ".cfg" file at the "LINE" ligne.

At the end of simulation you will be automatically prompted to extract data from ligne tree.

#### 3.2.2. EXTRACT FROM LIGNE TREE SUBOPTION



When selecting this subotion, this box is displayed. You can navigate through directories by clicking in the left window and select a file by clicking in the right window. After selecting a file you can click on "OK" to extract the data from the ligne tree (a xtr file at the same location and whith the same name except the extension will be created). Note that double-clicking on a file name has the same behaviour.

Clicking on "filter" will refresh the file list according to the filter string. Clicking on "Cancel" will close the box.

After extracting data from a ligne tree, you will be automatically prompted to load the data.

#### 3.3. SHAPE DATA OPTION

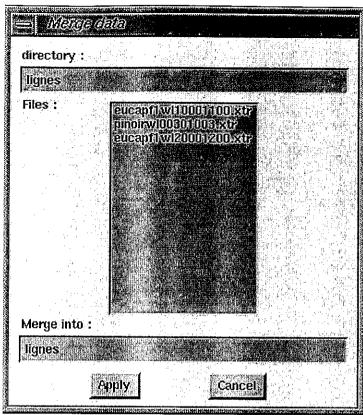
This option allows you to merge, load, filter and save data.

#### 3.3.1. MERGE DATA SUBOPTION

When clicking on this suboption you are prompted to merge several xtr files into a single one. You can navigate into directories by fullfilling the directory field and pressing the "return" key.

You can select or deselect the files to be merged by clicking in the list.

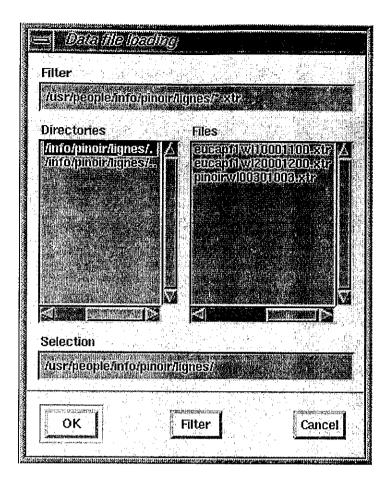
You can provide the name of the target file in the "Merge into" filed".



When clicking on "Apply", the merge will be done and the box will be closed. When clicking on "Cancel", the box will be closed.

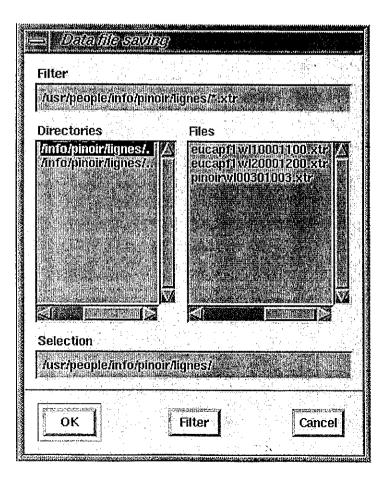
#### 3.3.2. LOAD DATA SUBOPTION

When clicking on this suboption, this box is displayed. Its behaviour is the same as in 2.2.2. The selection of an xtr file automatically prompts for filtering data.



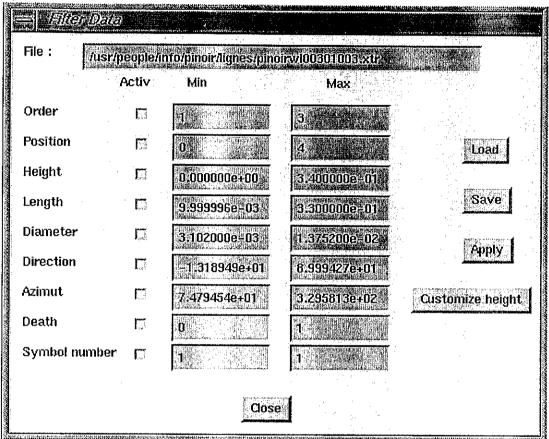
#### 3.3.3. SAVE DATA SUBOPTION

When selecting this suboption, you are prompted to save the current data. The behaviour of the box is the same as in 2.2.2.



#### 3.3.4. FILTER SUBOPTION

When selecting this suboption (or comming from the load data suboption) this box is displayed.



To activate filtering on a particular variable, click on the toggle button at the right of the name of the variable.

For each variable, you can provide a min and a max value. By default, the extremums of the file are displayed.

The variables on which you can combine filtering are:

- Order: the branching order of the branch to which behaves the element.
- Position: the topological position of the element inside the branch.
- Height: insertion height of the element (m).
- Diameter: diameter of the element (m).
- Direction: angle between vertical and principal axe of the element (deg).
- Azimut : azimut of the element compared to a virtual basis (deg).
- Death: death indicator of the element (0 or 1).
- Symbol number : organ identifier of the element.

You can customize the height threshold by clicking on the "Customize height" button.

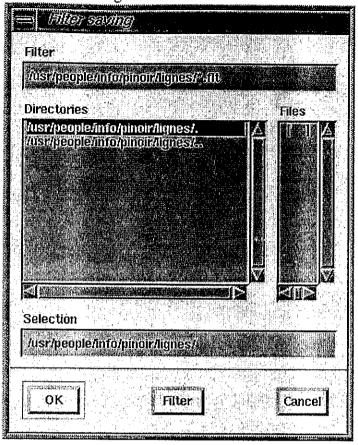
You can save the current settings on filter by clicking on the "Save" button.

You can load filter settings by clicking on the "Load" button.

When clicking on "Apply", the filtering will be done and the distribution on the avalaible elements will be displayed for each variable. The display is done whith histograms.

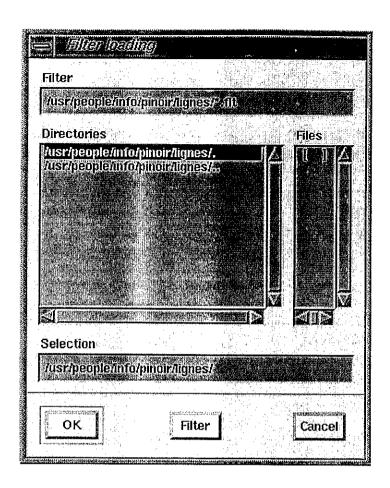
When clicking on the "Close" button, the box will be closed.

When clicking this button, this box is displayed. Its bbehaviour is the same as in 2.2.2. The generic extension for filter configuration is "flt".



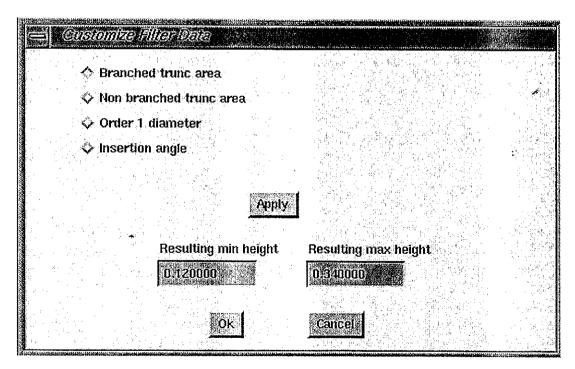
3.3.4.2. LOAD FILTER CONFIGURATION BUTTON

When clicking this button, this box is displayed. Its bbehaviour is the same as in 2.2.2. The generic extension for filter configuration is "flt".



3.3.4.3. CUSTOMIZE HEIGHT BUTTON

When clicking on the "Customize height" button, this box is displayed.



By clicking on a toggle button you select a criteria on which you want to compute height thresholds. This criteria are as following:

- Branched trunc area: the height threshold will correspond to extremas heigh of the crown.

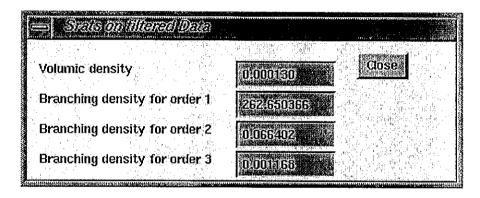
- Non branched trunc area: the heigh threshold will correspond to extremas heigh under the crown.
- Order 1 diameter: You are prompted to provide a min and a max branch diameter (m) of order 1. The height threshold will correspond to the part of the tree where these branches are found.
- Insertion angle: You are prompted to provide a min and a max angle (deg). The height threshold will correspond to the part of the tree where this branches are found.

When clicking on the "Apply" button the heigh threshold are computed and displayed. When clicking on the "OK" button, the box is closed and the heigh threshold are updated in the filter box.

When clicking on the "Cancel" button, the box is closed whithout update.

#### 3.3.5. STATS SUBOPTION

When selecting this suboption, this box is displayed.



The volumic density is displayed (i.e. ratio between wood volume and tree-occupied volume). For each branch order in the tree, the branching density is displayed (i.e. ratio between borne branch and global length of bearing branch).

When clicking on "Close" the box is closed.

#### 3.4. HISTOGRAMS OPTION

This option allows to configure the histograms displaying and to save the values to a file.

#### 3.4.1. CONFIGURATION SUBOPTION

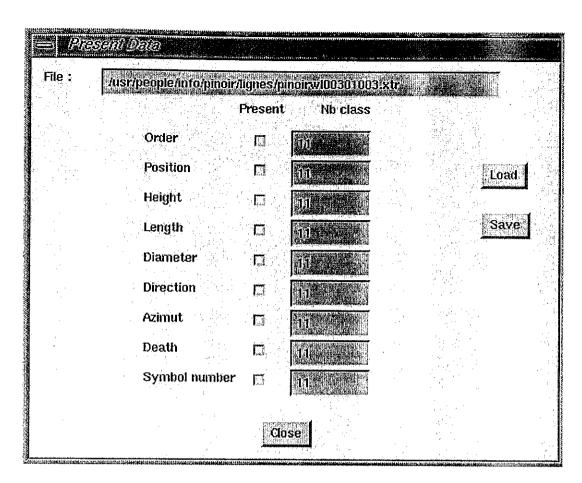
When selecting this suboption, this box is displayed.

By clicking on the toggle button, you select which histogram to display or not.

By providing a value into the "Nb class" fields and pressing "enter", you adjust the number of clas to be displayed for that histogram.

By clicking on the "Load" button you can load a histogram configuration.

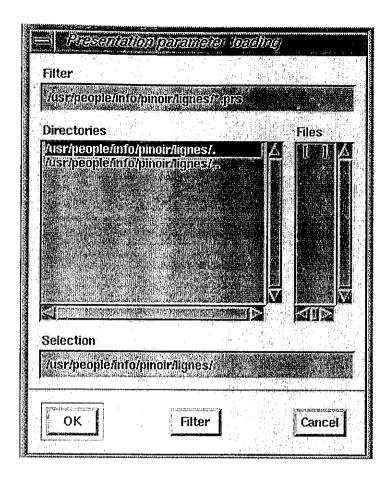
By clicking on the "Save" button you can save a histogram configuration.



When clicking on "Close" the box is closed.

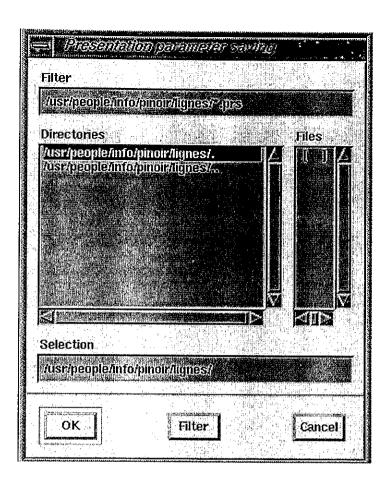
## 3.4.1.1. HISTOGRAM LOAD CONFIGURATION SUBOPTION

When clicking this button, this box is displayed. Its behaviour is the same as in 2.2.2. The generic extension for histogram configuration is "prs".



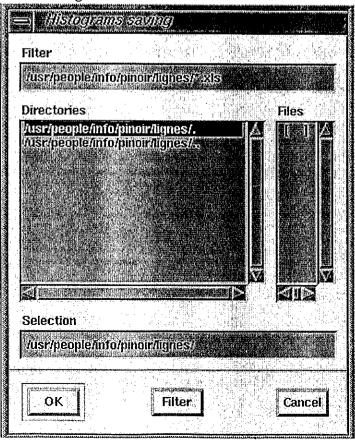
3.4.1.2. HISTOGRAM SAVE CONFIGURATION SUBOPTION

When clicking this button, this box is displayed. Its behaviour is the same as in 2.2.2. The generic extension for histogram configuration is "prs".



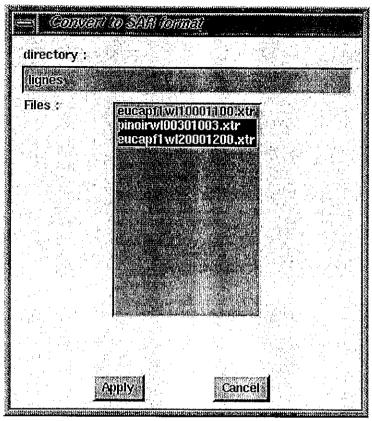
#### 3.4.2. SAVE HISTOGRAMS SUBOPTION

When clicking this button, this box is displayed. Its behaviour is the same as in 2.2.2. The generic extension for histogram is "xls".



## 3.5. MODEL DATA OPTION

When selection this option, you are prompted to select several xtr files to be converted in sar format.



You can navigate into directories by fullfilling the directory field and pressing the "return" key.

You can select or deselect the files to be exported by clicking in the list. Each selected file will be exported whith the same name and an extention "sar".

When clicking on "Apply", the merge will be done and the box will be closed.

When clicking on "Cancel", the box will be closed.

#### 4. FILE FORMATS

#### 4.1. DATA FILES

The data files are ASCII files that are tiled in two different parts. The first part is a header that contains some global information on the file content. The second part contains information on each tree element. Their extension is "xtr".

Every information concerning position or length are expressed in meter, every information concerning an angle is expressed in degree.

The header has the following structure:

#file /home/thierry/touille/trans/pinoir/lignes/pin1001.xtr #Thu May 15 14:48:25 1997

#maxorder 3
#maxportee 9
#height min +1.200000e-01 max +1.980000e+00#length min +9.999995e-03 max +1.970000e+00
#diameter min +3.101998e-03 max +5.292000e-02
#direction min -6.067527e+01 max +8.999427e+01
#azimut min +5.646362e-01max +3.570171e+02
#symbol min 1 max 1

Where the first two lines contain the name of the file and its creation date, and the next lines contain min and nax values for some variables.

- order: the branching order of the branch containing that element.
- portee : the position of that element inside the branch
- height: height of the beginning of the element
- length: length of the element
- diameter : diameter of the element
- direction : angle between element principal axis and vertical
- azimut : angle between a virtual horizontal reference and the horizontal projection of the principal axe of the element
  - symbol : index to identify the different organs

The second part contains as many lines as number of elements in the tree. Each line consists in 17 values that are :

- num: number of the branches element
- prec: number of the bearer branch of the element
- order: the branching order of the branch containing that element
- portee : the position of that element inside the branch
- height: height of the beginning of the element
- length: length of the element
- diameter : diameter of the element
- direction : angle between element principal axis and vertical
- azimut : angle between a virtual horizontal reference and the horizontal projection of the principal axe of the element
  - death : death index (0 dead, 1 alive)
  - symbol: index to identify the different organs

- xorig: x coordinate of the origin of the element
- yorig: y (height) coordinate of the origin of the element
- zorig: z coordinate of the origin of the element
- xext : x coordinate of the end of the element
- yext : y (height) coordinate of the end of the element
- zext : z coordinate of the end of the element

#### 4.2. SAR FILES

The SAR files are ASCII files that contain relevant informations for SAR models. Their extension is "sar".

The first lines contains comments and the next one contains informations for each branch of the tree. From the xtr file branches element are concatenated into a single segment whose extremities fit the extremities of the branch. Each branch is described with 10 values:

Num: branch number Ordre: ramification order Hauteur (m): average height Diametre (m): average diameter

Volume (m3)

Beta\_eq (deg): branching angle

Beta2 (deg): angle between element and vertical

Longueur\_eq (m): real branch length

Indice de courbure (m) : Difference between real length and vector length

niveau de simplification : not used

#### 4.3. HISTOGRAM FILES

Histogram files are the files that containes information on the histograms that were displayed. These are Excel compatible files and their extension is "xls".

The header consists in the name and date of the file followed by statistic values on the data.

#file /home/thierry/touille/trans/pinoir/lignes/pin1001.xls #Thu May 15 14:48:55 1997

volumic density 0.000313 m3/m3 linear branching density, order 1 10.215054 linear branching density, order 2 0.543358

The histograms are then displayed variable by variable into the standard Excel format.

## 4.4. FILTER CONFIGURATION FILES

The filter configuration files are ASCII files that have the "flt" extension.

They have the following structure:

```
1 1.000000 5.000000
1 0.000000 7.000000
1 1.940762 7.732135
1 0.004605 7.593878
1 0.001599 0.103990
1 -87.583710 89.999990
1 0.167955 359.872100
1 0.000000 1.000000
1 1.000000 1.000000
0 0.000000 0.000000
```

For each variable, the activation flag, the min and max values are written.

#### 4.5. HISTOGRAM CONFIGURATION FILES

The histogram configuration files are ASCII files that have the "prs" extension.

They have the following structure:

For each variable the visualization flag and the number of class are written.

## 5. REFERENCES

- Castel, T., Beaudoin, A., Barczi, J. F., Caraglio, Y., Floury, N., and Le Toan, T. "On the Coupling of Backscatter Models with Tree Growth Models:1) A Realistic Description of the Canopy using the AMAP Tree Growth Model, , Singapore, August 4-9 1997." *Proceedings IGARSS'97 Symposium*, Singapore.
- Floury, N., Picard, G., Le Toan, T., Kong, J. A., Castel, T., Beaudoin, A., and Barczi, J. F. "On the coupling of backscatter models with tree growth models: Part 2: RT modelling of forest backscatter." *Proceedings IGARSS'97 Symposium*, Singapore.

## 6. AMAPsim : Species modelling description

Modelling tree architecture requires both a qualitative and a quantitative assessment.

The first step is the qualitative aspect, which consists in botanical observations, in order to provide an accurate description of the architecture and growth pattern of a tree. With this approach, homogeneous groups of growth-units and/or axes can be identified within the tree, according to morpho-genetical gradients.

Quantitative measurements are then necessary for building up the model. In order to facilitate the subsequent coding, measurements are recorded and concerns:

- growth processes: length, number of inter-nodes, polycyclism, state of the apex (living, dead, broken), nature of the axis (dominant, dominated, forked),
- branching process: nature and position of lateral buds, axes or floral buds,
- geometric aspects: diameters, angle of insertion.

From the botanical observation of growth units and their classification into different classes (axis order, physiological age, long/short axis), and after a coding phase of every information, the static frequency distributions of number of inter-nodes per growth unit are computed and fitted to theoretical distributions. The dynamic growth and interruption processes which generate these distributions are estimated and validated with the help of mathematical routines. The parameters of branching processes (Markov chains) are then calculated.

In order to build the architecture of a tree with AMAPsim, it is then necessary to know how the successive growth units are stacked. The meristems, as well as the growth units they produce can be characterised according to their physiological age. It is therefore possible to establish a classification of the growth units, by grouping them into classes representative of each particular type of functioning: in each class the growth units have the same physiological age and the same type of growth and branching process. A single theoretical graduated axis can thus be defined, which successively takes into account all the possible morphological differentiation stages of growth units according to their physiological age. This « reference axis » formalize the changes in meristem functioning.

The laws governing bud activity are expressed as progression along the reference axis.

The branching processes are expressed as a jump in the reference axis between carried and carrying growth units.

The progression is usually a step by step forward progression, but it can take various forms according to the state of differentiation of a given axis. According to the morphogenetical gradients, the apical meristem of an axis can have different behaviour relative to the reference axis: a mature order-1 shoot may have the same behaviour as an order-3 or order-4 shoot, or an axis with order-3 or order-4 behaviour can appear on an order-1 axis.

Short shoots and flowering are direct jumps up to the terminal stage.

This concept of reference axis, fundamental for the description of bud activity, can also be extended to geometric properties of the elements resulting from growth (angle, phyllotaxy, length), and can be numerically deduced from architectural data taken on a given tree.

AMAPsim software manages simultaneously the two ages (temporal and physiological) during the simulation of tree development, according to the reference axis.

#### It integrates:

- the data of the growth process of the growth units, where bud activity is simulated by the Monte Carlo process in which random numbers are combined with stochastic laws of mortality, interruption and branching,
- the measurable geometry (angles, length, diameter) in order to allow the creation of realiztic three-dimensional models.

The reference axis is simulated by a finite « left to right automaton », where each state is characterised by three sets of parameters:

- topological parameters (growth, branching and death laws),
- geometric parameters (length, angle),
- transition parameters (from one state to another).

Examples of the reference axes for the trees presented in this work are described in the following pages. They formalize:

- 1- the structure of the reference axis, with the correspondence between the stages of the reference axis and the nature of the growth units,
- 2- the structure of the model, with the topology of the plant and the jumps according to the different axes resulting from the architectural analysis,
- 3- the structure of the jumps describing the branching process.

# Pinus nigra nigricans

## Pinaceae

#### Growth

Image 1.: Pinus nigra at 5, 10 and 20 years, side view.

Image 2.: Pinus nigra at 20, 30 and 40 years, side view.

Image 3.: Pinus nigra at 30 years, top view of a forest.

Image 4.: Pinus nigra at 30 years, bottom view of a forest.

Image 5.: Pinus nigra at 5, 10 and 20 years, side view, without leaves.

Image 6.: Pinus nigra at 20, 30 and 40 years, side view, without leaves.

Image 7.: Pinus nigra at 30 years, top view of a forest without leaves.

Image 8.: Pinus nigra at 30 years, bottom view of a forest without leaves.

#### **Variability**

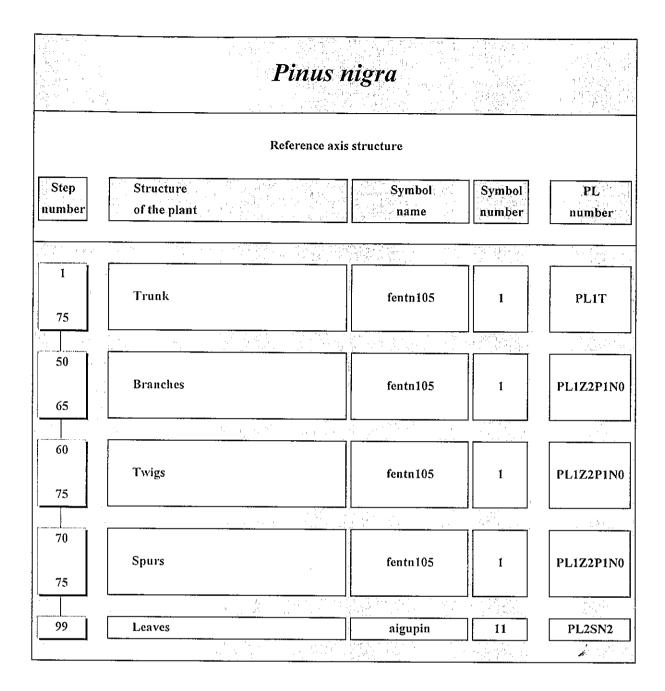
Image 9.: Pinus nigra at 10 years, 5 realizations, side view.

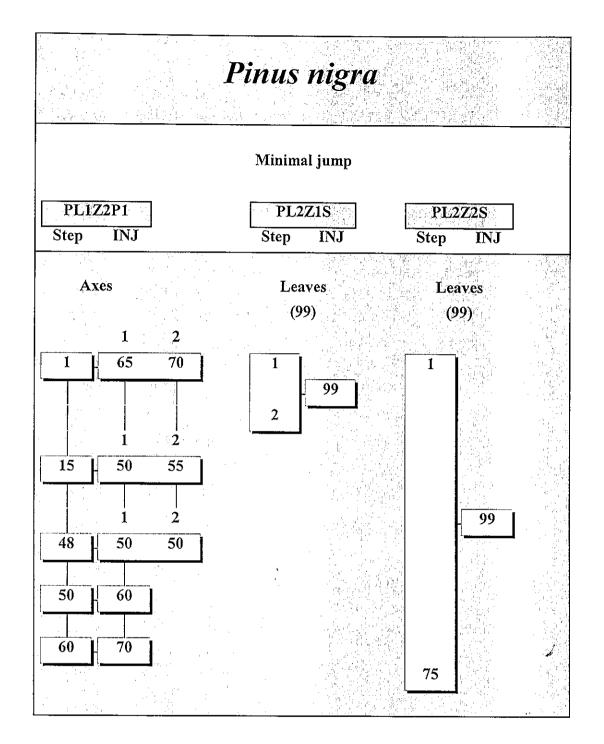
Image 10.: Pinus nigra at 30 years, 5 realizations, side view.

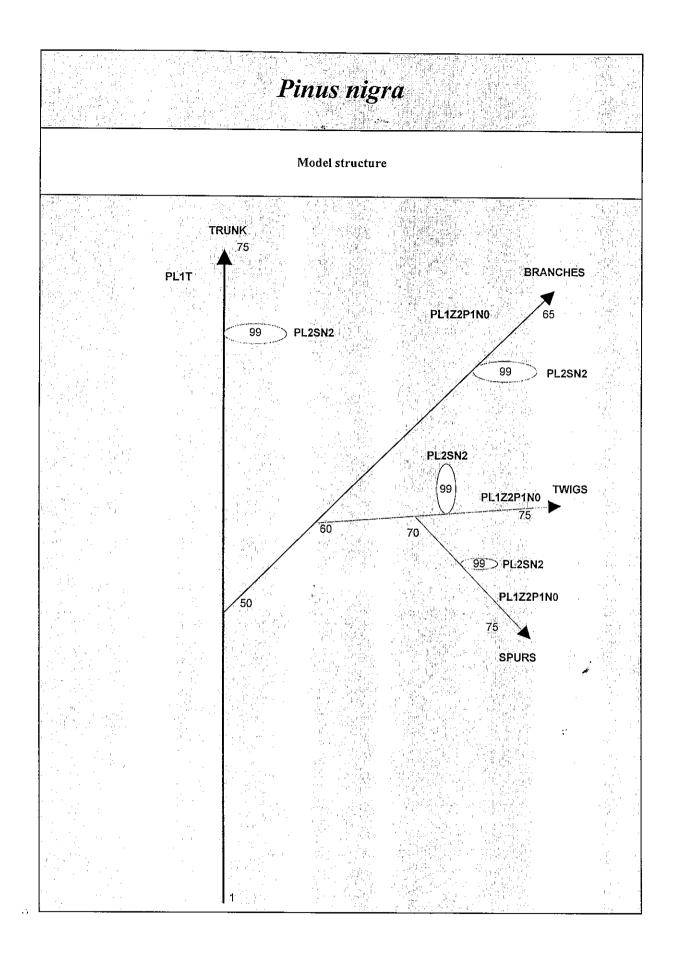
Image 11.: Pinus nigra at 30 years, 5 realizations, side view, without leaves.

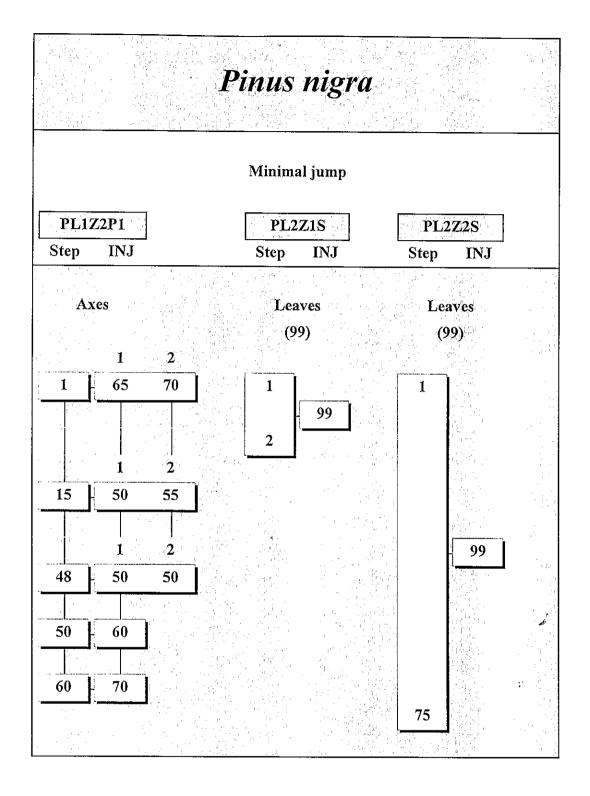
Image 12.: Pinus nigra at 30 years, 5 realizations, side view, without leaves

Simulations come from measurements realized in an artificial stand in the south of France.









# Pinus pinaster

## Pinaceae

#### Growth

Image 13.: Pinus pinaster at 5, 10 and 20 years, side view.

Image 14.: Pinus pinaster at 20, 30 and 40 years, side view.

Image 15.: Pinus pinaster at 30 years, top view of a forest.

Image 16.: Pinus pinaster at 30 years, bottom view of a forest.

Image 17.: Pinus pinaster at 5, 10 and 20 years, side view, without leaves.

Image 18.: Pinus pinaster at 20, 30 and 40 years, side view, without leaves.

Image 19.: Pinus pinaster at 30 years, top view of a forest without leaves.

Image 20.: Pinus pinaster at 30 years, bottom view of a forest without leaves.

#### **Variability**

Image 21.: Pinus pinaster at 10 years, 5 realizations, side view.

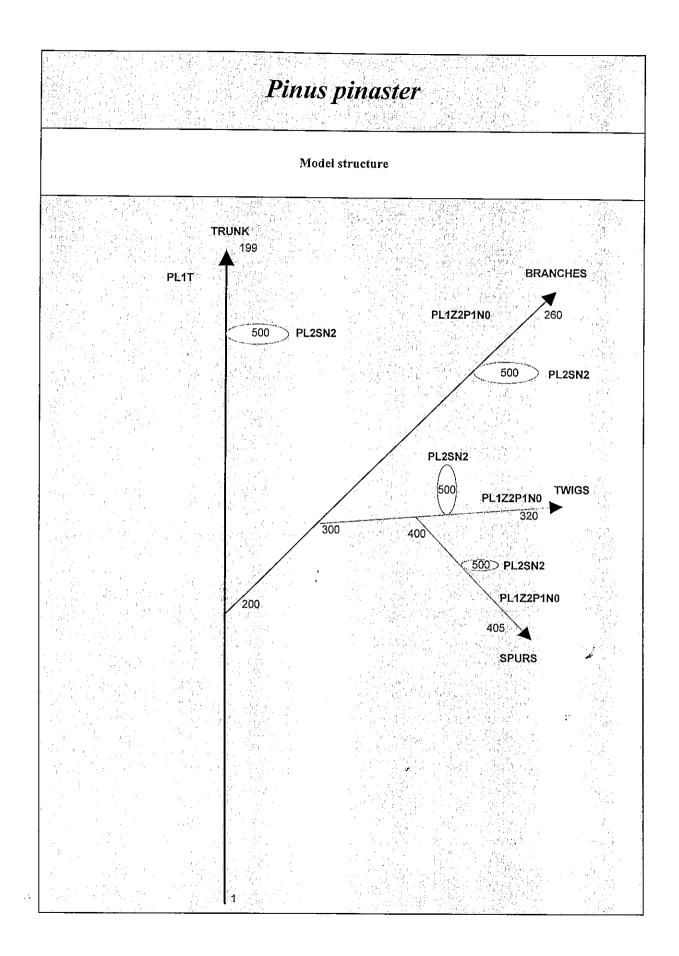
Image 22.: Pinus pinaster at 30 years, 5 realizations, side view.

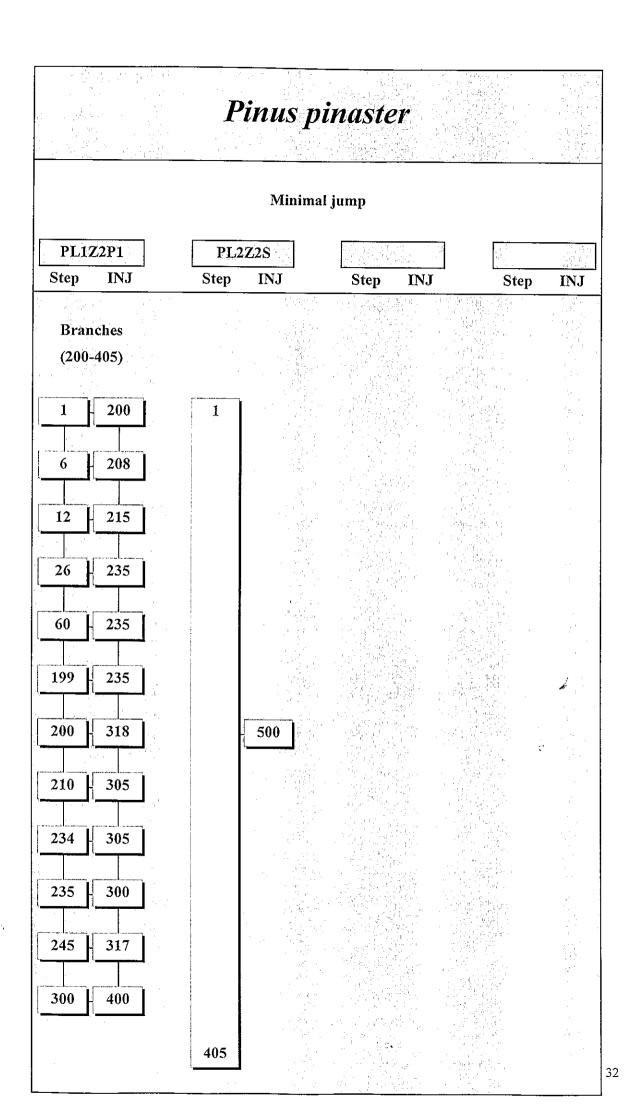
Image 23.: Pinus pinaster at 30 years, 5 realizations, side view, without leaves.

Image 24.: Pinus pinaster at 30 years, 5 realizations, side view, without leaves

Simulations come from measurements realized in an artificial stand in the south-west of France.

	Pinus pinaster (	oin maritim							
	Reference axis structure								
Step number	Structure of the plant	Symbol name	Symbol number	PL number					
199	Trunk	fentn105	1	PL1T					
				1 11 1					
260	Branches	fentn105	1	PL1Z2P1N0 et PL1Z2CN0					
300	Twigs	fentn105	1	PL1Z2P1N0					
400	Spurs	fentn105	1	PL1Z2P1N0					
500	Leaves	aigupin	11	PL2Z2SN2					
600	Fruit								
				<u> </u>					





			TRONG	BRANCHES	SEIMU	SPURS	
		SPURS	184 199	255 260	315 320	400 405	
Pinus pinaster	Typology and reference axis	TWIGS	169	240			
	Typok	BRANCHES	129	210		j.	
		TRONC	1	200			

# Prunus avium

#### Rosaceae

#### Growth

Image 25.: Prunus avium at 5, 10 and 20 years, side view.

Image 26.: Prunus avium at 20, 30 and 40 years, side view.

Image 27.: Prunus avium at 30 years, top view of a forest.

Image 28.: Prunus avium at 30 years, bottom view of a forest.

Image 29.: Prunus avium at 5, 10 and 20 years, side view, without leaves.

Image 30.: Prunus avium at 20, 30 and 40 years, side view, without leaves.

Image 31.: Prunus avium at 30 years, top view of a forest without leaves.

Image 32.: Prunus avium at 30 years, bottom view of a forest without leaves.

#### **Variability**

Image 33.: Prunus avium at 10 years, 5 realizations, side view.

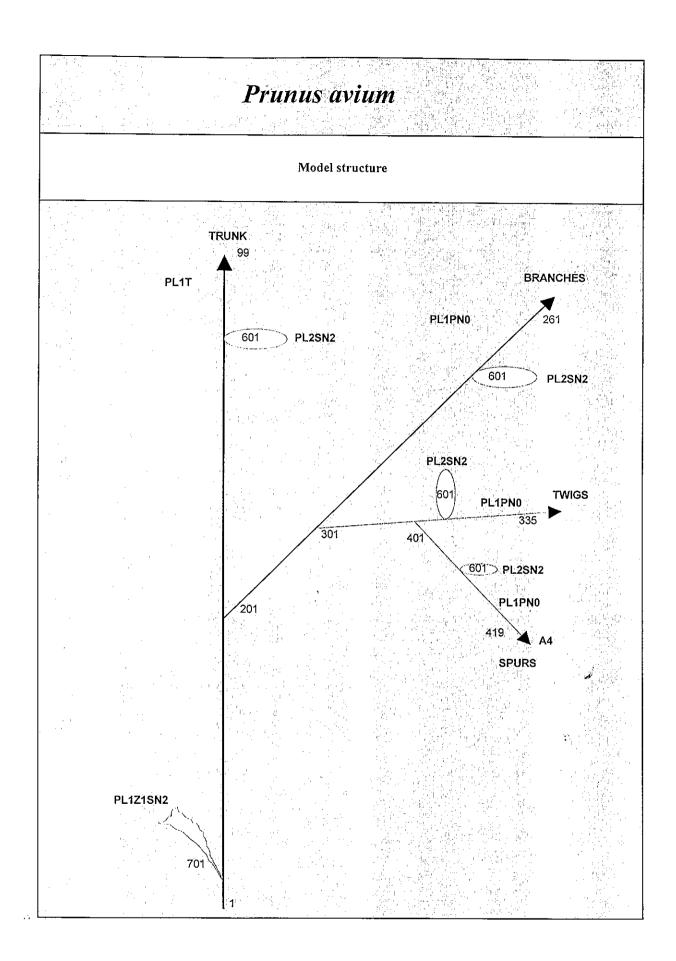
Image 34.: Prunus avium at 30 years, 5 realizations, side view.

Image 35.: Prunus avium at 30 years, 5 realizations, side view, without leaves.

Image 36. : Prunus avium at 30 years, 5 realizations, side view, without leaves

Simulations come from measurements realized in a natural stand in the north-east of France.

	Pr	unus	avium		
Reference axis structure					
Step number	Structure of the plant		Symbol name	Symbol number	PL number
		1 1 A 1		to the second	
1 30 99	Trunk	base max old	fentn105	1	PL1T
201 205 261	Branches	base max old	fentn105	1	PL1P1-2N0
301 305 335	Twigs	base max old	fentn105	1	PL1P1-2N0
		7 (8)			
401 404 419	Spurs	base max old	fentn105	1	PL1P1-2N0
601	Leaves		feumeri2	4	PL2SN2
701	<b>T</b>				D. 1710
701	Fruit		frumeri	9	PL1Z1S
1.4					



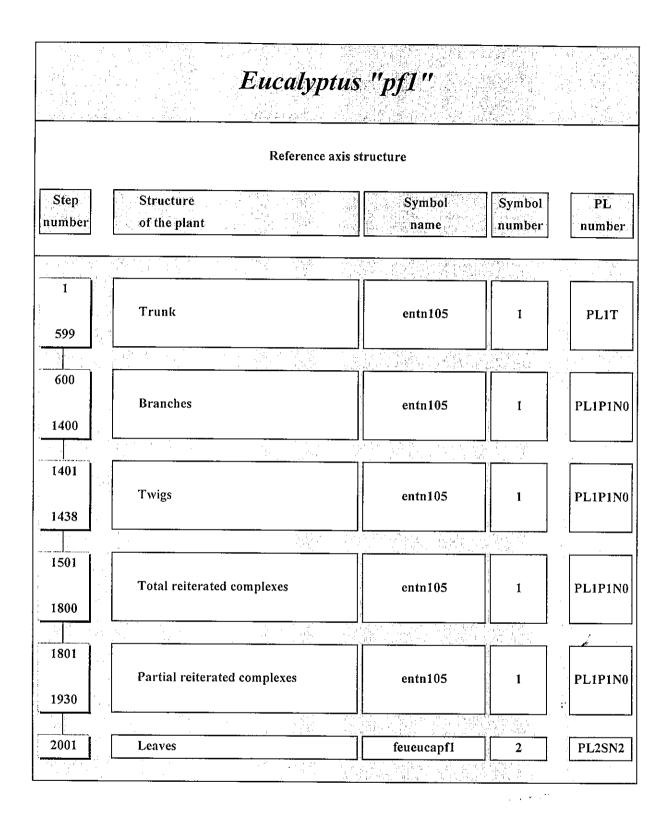
		Prunus avium		
		Minimal jump		
PL1Z1P1-2N0		PL2Z1SN2	PL2Z2SN2	PL1ZISN2
Step INJ	Step INJ	Step INJ	Step INJ	Step INJ
Spurs (401)	Branches (201 Twigs (301) Spurs (401)	Leaves (601)	Leaves (601)	Fruit (701)
1 417	237			
		。 一种的人。 一种, 一种, 一种, 一种, 一种, 一种, 一种, 一种,		
6 417				
415				
414 8 415				8
	1	12 235 9		
	25 401	406		

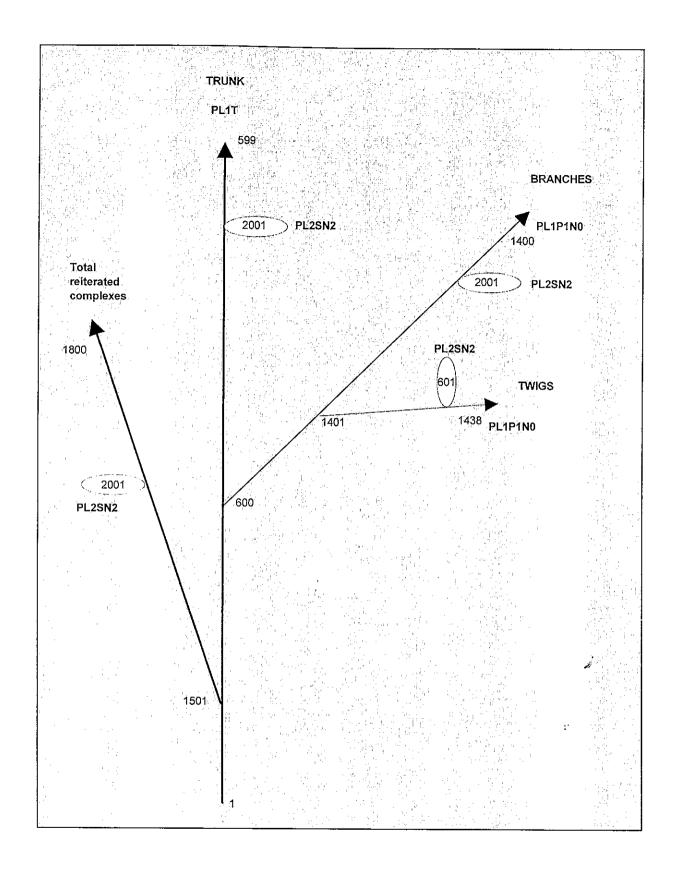
			TRUNK	BRANCHES	Twics	Shuks	
		SPURS	84 99	240 261	320 335	404 419	
Prunus avium	Typology and reference axis	TWIGS	74	235	305	401	
	Typol	BRANCHES	09	205	301	j.	
				200			

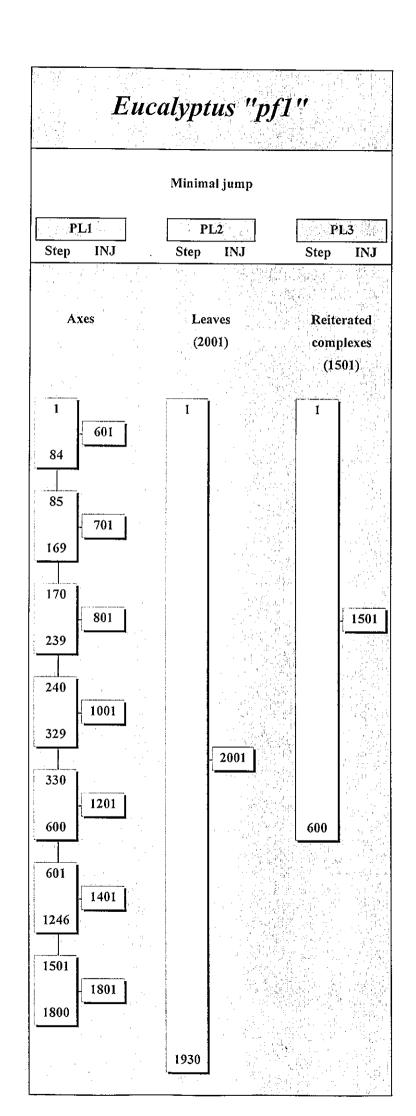
# Eucalyptus x platiphylla F1-41

## Myrtaceae

	Myrtaceae					
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Image 38. :	Eucalyptus x platiphylla F1-41 at 3, 4 and 5 years, side view.					
Image 39. :	Eucalyptus x platiphylla F1-41 at 3 years, top view of a forest.					
Image 40. :	Eucalyptus x platiphylla F1-41 at 3 years, bottom view of a forest.					
Image 41.:	Eucalyptus x platiphylla F1-41 at 1, 2 and 3 years, side view, without leaves.					
Image 42. :	Eucalyptus x platiphylla F1-41 at 3, 4 and 5 years, side view, without leaves.					
Image 43.:	Eucalyptus x platiphylla F1-41 at 3 years, top view of a forest without leaves.					
Image 44. :	Eucalyptus x platiphylla F1-41 at 3 years, bottom view of a forest without leaves.					
	£*					
<u>Variability</u>						
Image 45. :	Eucalyptus x platiphylla F1-41 at 2 years, 5 realizations, side view.					
Image 46. :	Eucalyptus x platiphylla F1-41 at 4 years, 5 realizations, side view.					
Image 47. :	Eucalyptus x platiphylla F1-41 at 2 years, 5 realizations, side view, without leaves.					
Image 48. :	Eucalyptus x platiphylla F1-41 at 4 years, 5 realizations, side view, without leaves					
Simulations Congo.	come from measurements realized in an artificial stand in Pointe-noire,					







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Image 1: Pinus nigra at 5, 10 and 20 years, side view.



Image 2: Pinus nigra at 20, 30 and 40 years, side view.



Image 3: Pinus nigra at 30 years, top view of a forest.



Image 4: Pinus nigra at 30 years, bottom view of a forest.



Image 5: Pinus nigra at 5, 10 and 20 years, side view, without leaves.



Image 6: Pinus nigra at 20, 30 and 40 years, side view, without leaves.



Image 7: Pinus nigra at 30 years, top view of a forest without leaves.



Image 8: Pinus nigra at 30 years, bottom view of a forest without leaves.

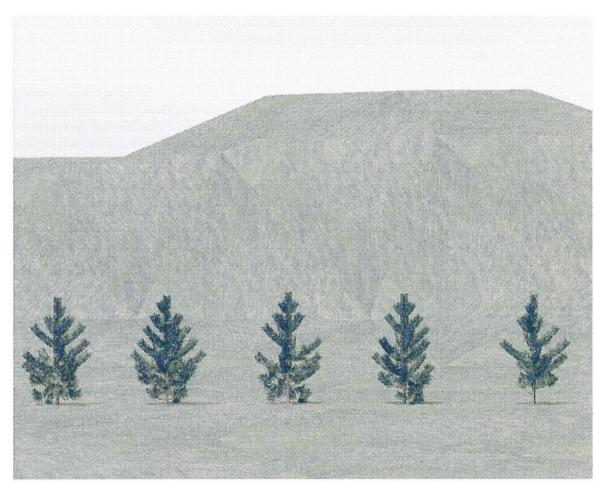


Image 9: Pinus nigra at 10 years, 5 realizations, side view.



Image 10: Pinus nigra at 30 years, 5 realizations, side view.



Image 11: Pinus nigra at 10 years, 5 realizations, side view, without leaves.



Image 12: Pinus nigra at 30 years, 5 realizations, side view, without leaves.



Image 13: Pinus pinaster at 5, 10 and 20 years, side view.

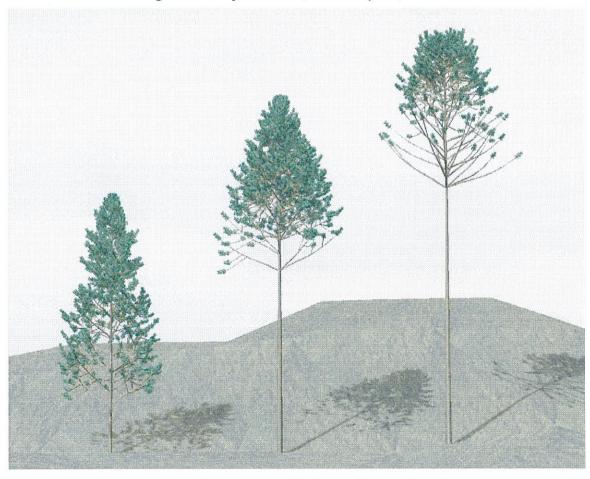


Image 14: Pins pinaster at 20, 30 and 40 years, side view.



Image 15: Pinus pinaster at 30 years, top view of a forest.



Image 16: Pinus pinaster at 30 years, bottom view of a forest.

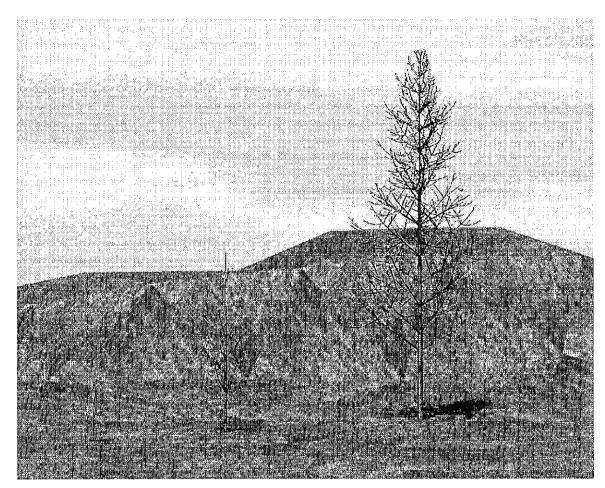


Image 17: Pinus pinaster at 5, 10 and 20 years, side view, without leaves.

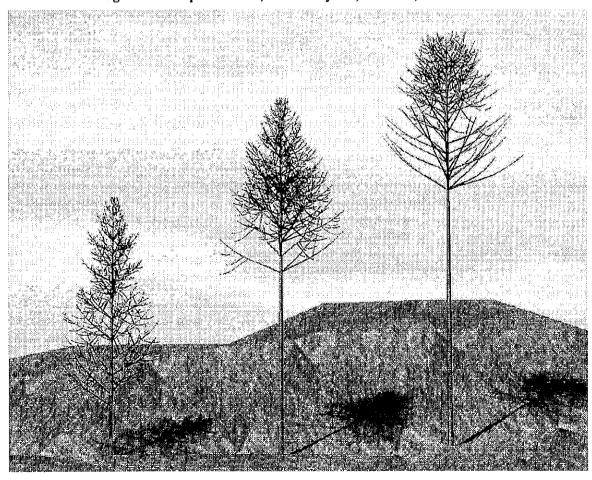


Image 18: Pinus pinaster at 20, 30 and 40 years, side view, without leaves.



Image 19: Pinus pinaster at 30 years, top view of a forest without leaves.



Image 20: Pinus pinaster at 30 years, bottom view of a forest without leaves.

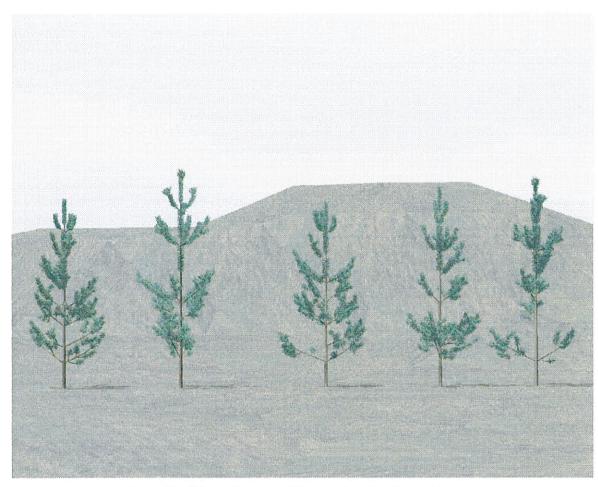


Image 21: Pinus pinaster at 10 years, 5 realizations, side view.

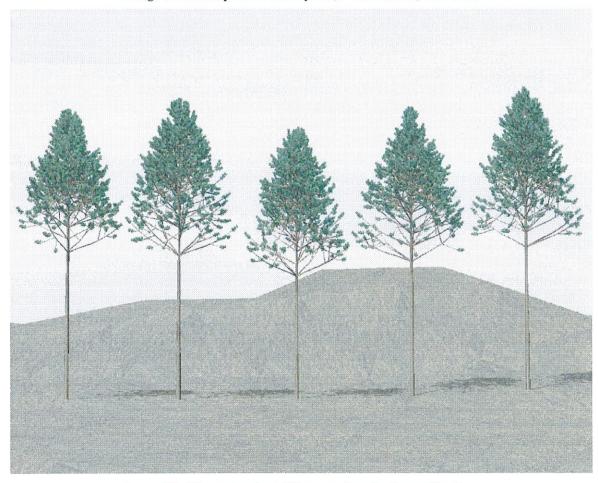


Image 22: Pinus pinaster at 30 years, 5 realizations, side view.

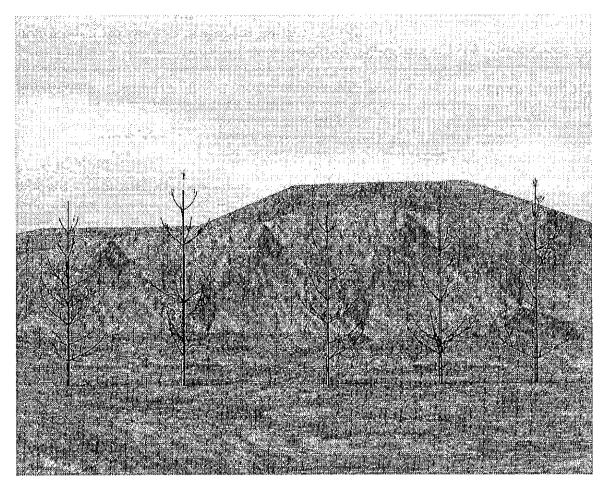


Image 23: Pinus pinaster at 10 years, 5 realizations, side view, without leaves.

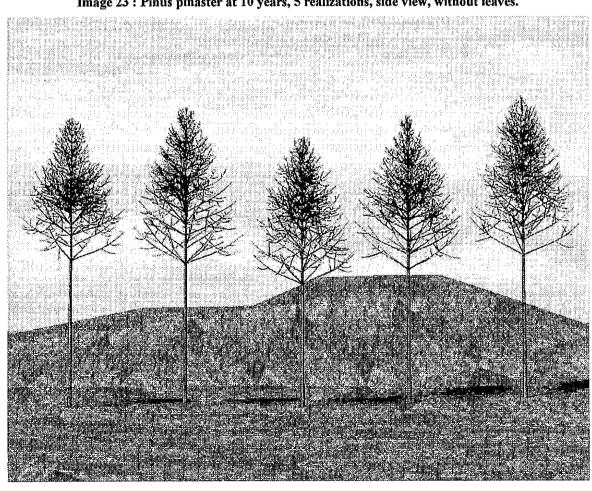


Image 24: Pinus pinaster at 30 years, 5 realizations, side view, without leaves.



Image 25: Prunus avium at 5, 10 and 20 years, side view.

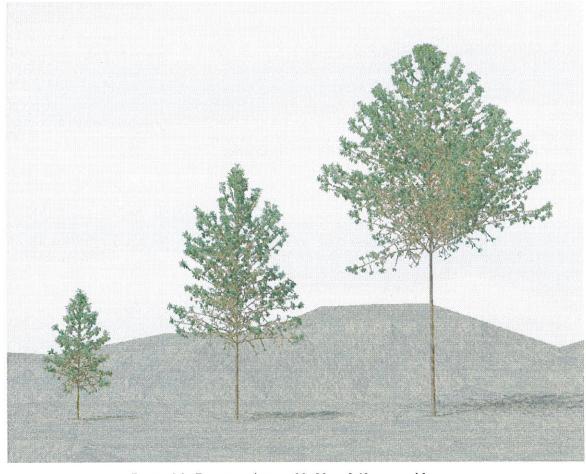


Image 26: Prunus avium at 20, 30 and 40 years, side vew.



Image 27: Prunus avium at 30 years, top view of a forest.



Image 28: Prunus avium at 30 years, bottom view of a forest.

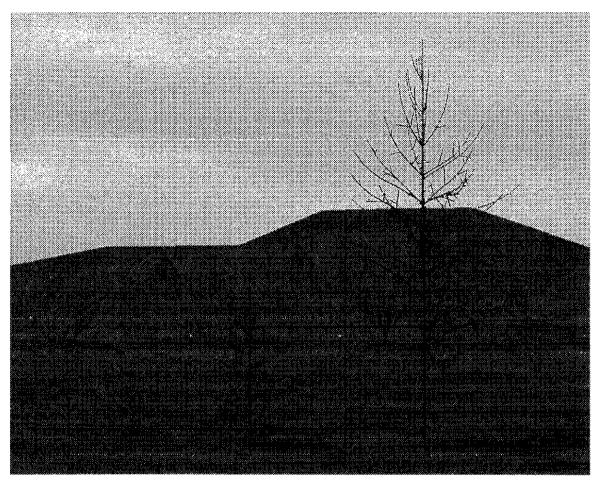


Image 29: Prunus avium at 5, 10 and 20 years, side view, without leaves.



Image 30: Prunus avium at 20, 30 and 40 years side view, without leaves.



Image 31: Prunus avium at 30 years, top view of a forest without leaves.



Image 32: Prunus avium at 30 years, bottom view of a forest without leaves.



Image 33: Prunus avium at 10 years, 5 realizations, side view.

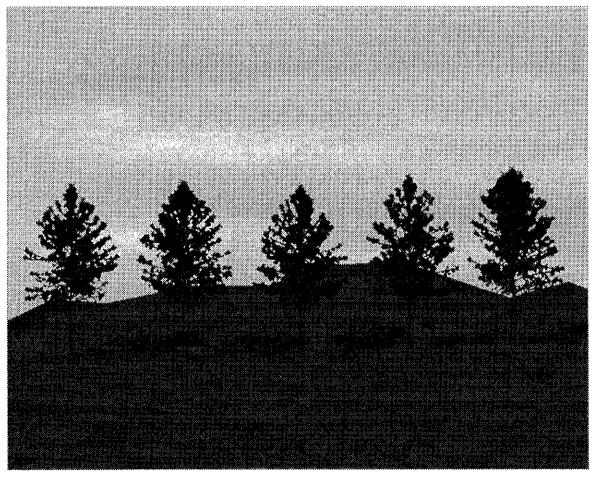


Image 34: Prunus avium at 30 years, 5 realizations, side view.

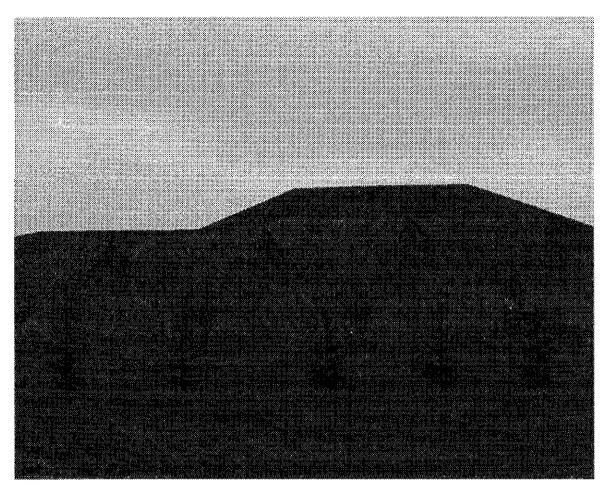


Image 35: Prunus avium at 10 years, 5 realizations, side view, without leaves.



Image 36: Prunus avium at 30 years, 5 realizations, side view, without leaves.

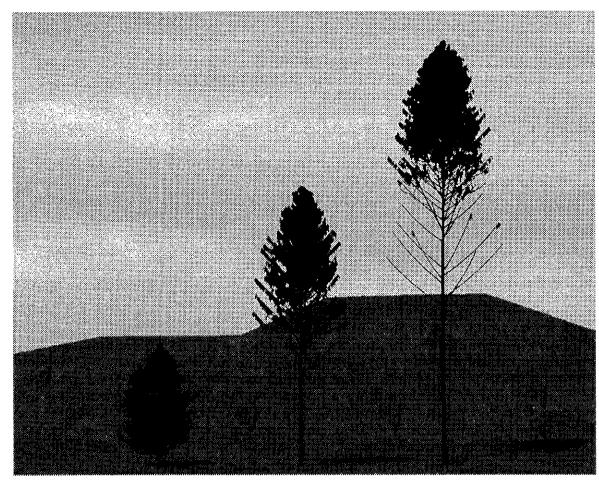


Image 37: Eucalyptus x platiphylla F1-41 at 1, 2 and 3 years, side view.

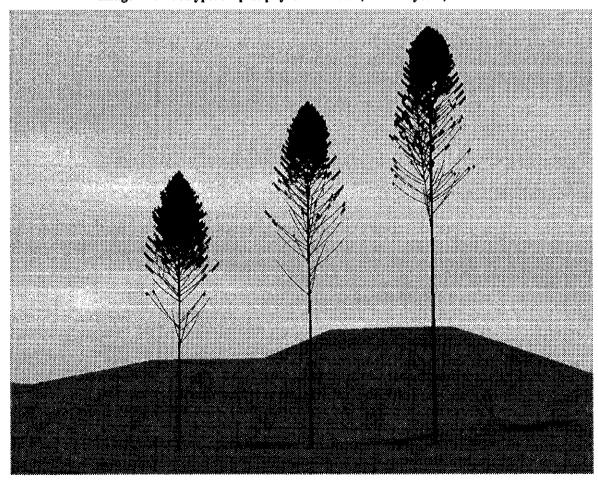


Image 38: Eucalyptus x platiphylla F1-41 at 3, 4 and 5 years, side view.

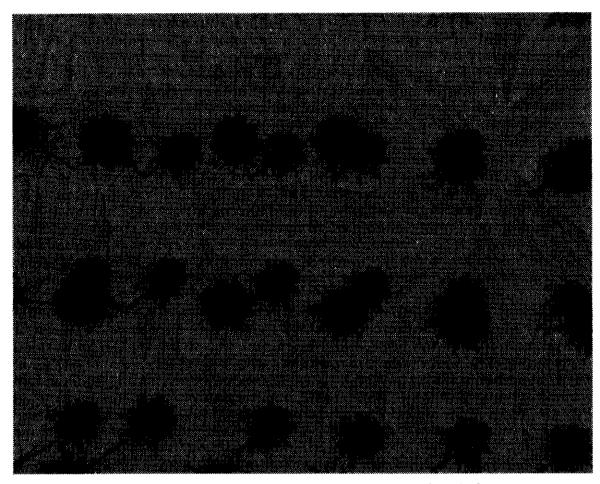


Image 39: Eucalyptus x platiphylla F1-41 at 3 years, top view of a forest.

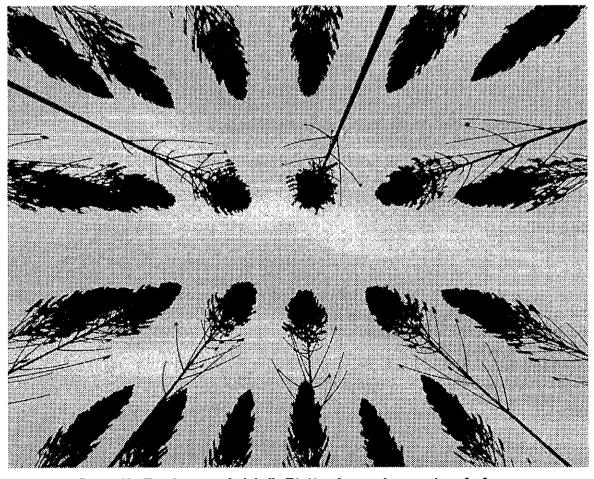


Image 40: Eucalyptus x platiphylla F1-41 at 3 years, bottom view of a forest.

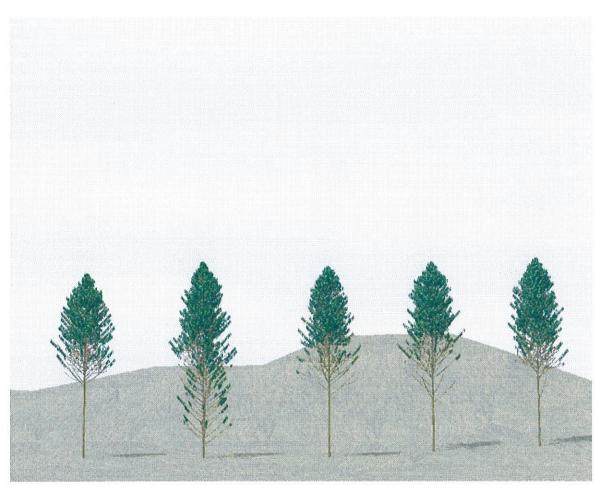


Image 45: Eucalyptus x platiphylla F1-41 at 2 years, 5 realizations, side view.

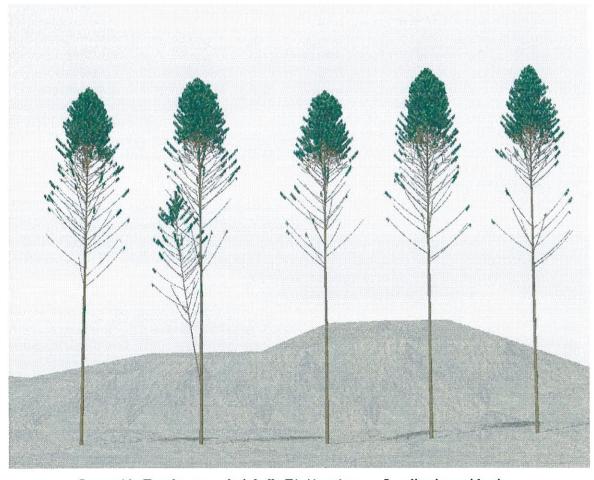


Image 46: Eucalyptus x platiphylla F1-41 at 4 years, 5 realizations, side view.

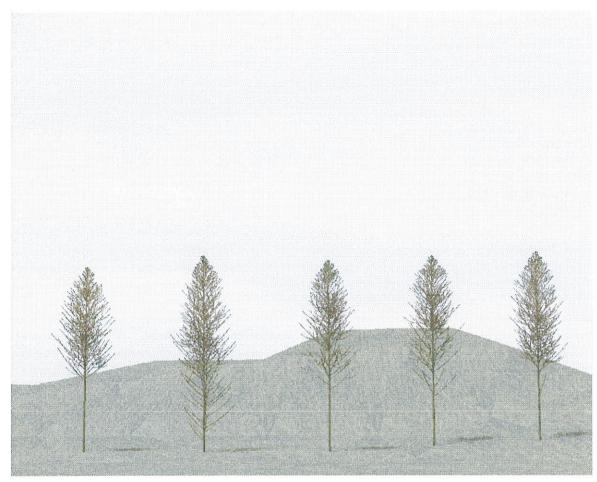


Image 47: Eucalyptus x platiphylla F1-41 at 2 years, 5 realizations, side view, without leaves.

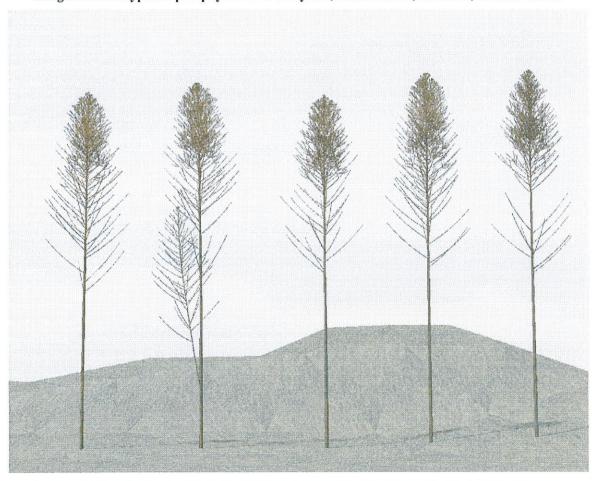


Image 48: Eucalyptus x platiphylla F1-41 at 4 years, 5 realizations, side view, without leaves.

### 8. APPENDIX

On the Coupling of Backscatter Models with Tree Growth Models:

Part 1: A Realistic Description of the Canopy using the AMAP Tree Growth Model

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Abstract- In this paper, we present a method using the AMAP architectural tree growth model to describe the 3D canopy architecture, towards forest backscatter modelling. This method allows to 1) fully describe a tree as a collection of dielectric cylinders and 2) obtain histograms and statistics of the cylinder parameters within the canopy layers. The usefulness of this method is illutrated in southern France on Austrian pine trees, where the parameters in the crown layer show a variability with age and canopy depth that should be considered in RT modelling.

#### 1. INTRODUCTION

Biomass retrieval is a promising application of SAR remote sensing, considering the numerous results recently reported in the literature. In particular, we conducted an experiment in southern France (Mende forest, Lozère) on Austrian pine plantations, towards the assessment of biomass retrieval over hilly terrain. The experimental set-up along with significant relationships between relief-corrected SIR-C L-band forest backscatter and forest parameters were reported in [1].

In a joint paper [2], radiative transfer (RT) modelling is considered to interpret the link between the L-band  $\sigma^{\circ}$  and the pine forest biomass. It requires a detailed description of the canopy as a collection of dielectric cylinders embedded within a multi-layer discrete random media. Even though part of this characterization can be obtained from *in situ* measurements of usual forest parameters (tree and crown height, trunk diameter and density), the crown characterization through measurements and/or allometric equations (see for example [3]) is tedious, time-consuming and usually destructive. Therefore, other realistic description methods and associated tools are needed to get proper input parameters to RT models.

To this aim, we present a method based on an architectural tree growth model called AMAP [4]. It is illustrated on homogeneous even-aged Austrian pine (pinus nigra nigricans) plantations

found in various topographic situations (Mende state forest). Stand ages extend from 0 to 140 years, with bole volume reaching up to 800 m<sup>3</sup>/ha.

#### 2. METHOD FOR CANOPY DESCRIPTION

The method is based on three characterization steps: 1) AMAP modelling of the tree architecture, 2) generic description of the tree as a collection of cylinders and 3) specific adaptation to the MIT/CESBIO RT model.

1) The AMAP model relies on both qualitative quantitative architectural tree growth description. Detailed botanical observations allowed to develop an architectural typology used modelling [5]. Specific botanical measurements are then necessary to calibrate the model for a given species in its environmental conditions. They are performed on tree shoots called growth units (GU), which are produced by the terminal meristems and build the tree architecture. Parameters of theoretical distribution geometric (binomial and laws) characteristics and branching process (growth, interruption or mortality) are obtained from fittings with the measurements.

Then, tree architectural simulation for a given age is realized through Monte-Carlo technique and Markov process, allowing to reproduce i) the meristem activity and ii) the branching process and associated geometry (angle, length, diameter) of GU's. The result is a realistic 3D tree stored in a file, such as the 40 years old Austrian pine (without needles) in Fig. 1a.

Finally, the canopy natural variability is reproduced through successive random AMAP simulations. A set of these simulations is performed for each growth stage of interest (age).

2) An interface was developed to transform these 3D trees into a collection of cylinders representing the various tree elements: trunk, branches and needles, with their geometric characteristics: (x,y,z) position, diameter, length and orientation angles. A branch is considered as a collection of successive cylinders of varying dimensions and

orientation, to take into account tapered and curved branches (Fig. 1b).

3) An additional step is to adapt this description to the specific MIT/CESBIO RT model, including the branching model [6]. It describes the canopy as a n-layer discrete random media, where the tree crown is characterized as a multi-scale cluster of dielectric cylinders. In our case, up to five scales represent the trunk, increasing orders of branches and needles.

The interface first splits the canopy into n horizontal layers, using a fixed vertical interval or a variability criteria. For each branch order, successive cylinders forming a given branch are transformed in a single approximated cylinder, as sketched in Fig. 1c, since curved and tapered branches are not yet taken into account. From there, cylinders at each cluster scale (branch order BRI to BR4) are characterized by mean length, diameter, linear density and branching angle (Fig.1c), after averaging over 20 simulated trees. In addition, histograms of all these parameters are available.

#### 3. RESULTS AND DISCUSSION

For validation purposes, AMAP-derived parameters such as tree height, diameter and length of primary branches (10 and 20 years old stands) are compared to those measured at the whorl level (mean values). This is illustrated in Fig. 2 where a satisfactory agreement is reached, although some observed dispersion still has to be explained. Also, this validation will need to be extended to all other parameters.

Fig. 3 includes vertical profiles of cylinder parameters (4-scale cluster for branches): number, diameter and length averaged over twenty 40 years old trees (as in Fig. 1a). Number of branches is quite constant for 1<sup>st</sup> order whereas it is high for 2<sup>nd</sup> and 3<sup>rd</sup> orders. Branch length and diameter, which are highly correlated, increase rapidly in the first top meters to reach a relatively constant value within the deeper layers (except for the 2<sup>nd</sup> order). From these profiles, it is obvious that more than one layer should be considered in RT modelling.

Fig. 4 includes the histogram of branching angle within the crown layer. Considering the sensitivity of L-band backscatter to this structural parameter [6], the use of such histograms should improve the computation of averaged scattering amplitudes in RT models. This could be useful also for other cylinder parameters.

#### 4. CONCLUSION

The results show that the AMAP model can provide a realistic and complete 3D canopy description as a collection of dielectric cylinders. The AMAP model has been calibrated up to a tree age of 50 years (close to the L-band saturation level) and will be extrapolated to older trees. Further measurements and improvements are needed for the needle modelling found on various orders of branches.

Most backscatter models can not yet fully accommodate such a detailed description, a degradation of the architectural information is necessary to feed them. Hopefully, this description should be very helpful to point out future modelling improvements related to scattering from curved branches, layered canopy, 2<sup>nd</sup> order effects, etc.

In a joint paper [2], encouraging RT modelling results obtained at L-band after the coupling with the AMAP model are presented over the Mende forest.

#### ACKNOWLEDGMENTS

We would like to thank various French institutes for their financial support: CNES, PNTS and ADEME. Special thanks go to the CIRAD-AMAP team and the French forestry board (ONF) for their contribution.

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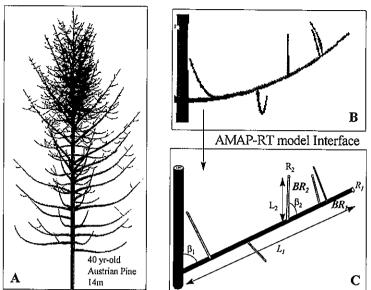


Fig. 1: A) 3D AMAP simulation, B) zoom on a single branch and
 C) description as a cylinder collection, with cylinder length L,
 diameter R and branching angle β for 2 branch orders.

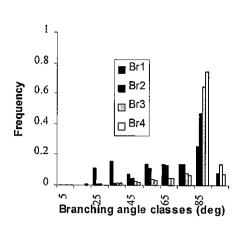


Fig 4: Histogram of branching angle  $\beta$  for the 4 branch orders in the crown.

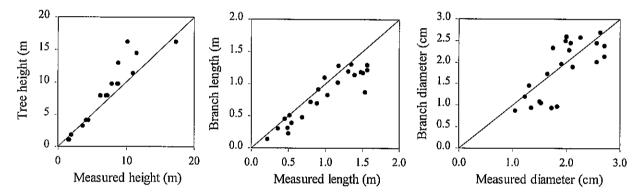


Fig. 2: Comparison of AMAP-derived forest parameters with measurements (10 and 20 year-old trees).

Diameter and length are for primary branches (comparison at the whorl level).

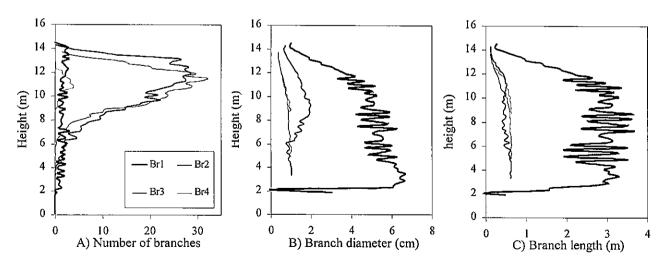


Fig. 3: Vertical profiles within the canopy of mean cylinder parameters for RT modelling: A) number of branches, B) diameter and C) length, representing the 4 branch orders in the crown layer of a 40 years old stand of Austrian pine.

# ON THE COUPLING OF BACKSCATTER MODELS WITH TREE GROWTH MODELS: 2) RT MODELLING OF FOREST BACKSCATTER

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#### **ABSTRACT**

In this paper, the use of an architectural tree growth model as a generator of input parameters for a forest backscatter model is investigated. This is shown to be a useful method to (1) provide input data which are otherwise tedious to obtain, (2) describe the canopy with an enhanced precision which may be useful to explain physical mechanisms involved in the interaction between the electromagnetic wave and the forest.

#### 1. INTRODUCTION

Theoretical modelling of the forest backscatter is a powerful tool towards the development of quantitative forest applications such as biomass retrieval from SAR data. RT models usually describe the forest canopy as a discrete multi-layer random media containing different classes of dielectric cylinders for the vegetation elements. One of the actual major limitations of RT modelling is the difficulty to obtain a realistic and complete canopy architectural description as a function of growth stage. In particular, tree crown parameters, through which backscatter usually correlates to above-ground biomass, are very difficult to measure or estimate. Allometric equations offer an alternative but are often not available for the species under study and crown parameters of interest. An alternative is to develop a new approach making use of the available tree growth models to derive input parameters to RT models.

In this paper, we illustrate a new approach based on the coupling of a RT model to an architectural tree growth model providing a detailed 3D canopy description. We present preliminary results applied to SIR-C L-band backscatter (HH and HV at 55° incidence angle) of Austrian pine (*Pinus nigra*) plantations over hilly terrain in southern France. The experimental set-up along with significant relationship between relief-corrected forest backscatter and forest parameters were reported [1].

In this study, the RT branching model [6] is used and coupled to the AMAP architectural tree growth model [7], through an interface allowing to extract the tree architecture as multi-scale clusters of dielectric cylinders [2].

#### 2. CANOPY DESCRIPTION FROM AMAP

The Mende forest under investigation is composed of 500 large stands (5-15 ha) of homogeneous evenaged Austrian pine plantations found in various topographic situations. Stand age extend from 0 to 140 yr-old, with bole volume reaching up to 800 m<sup>3</sup>/ha. 60 stands were sampled for basic forest parameters: age, dbh, tree and crown height, tree density and bole volume. In addition, the AMAP tree growth model was validated for this site through specific botanical calibration measurements, allowing to reconstruct 1) the 3D tree architecture, as in Fig. 1 for a 40 yr-old tree (needles not represented), and 2) to extract forest geometric parameters according to the following canopy description used in the MIT RT model.

For a stand at a given age, the canopy is described as a 2-layer discrete random media (crown and trunk) over a rough surface, as sketched in Fig. 1. At this stage, we consider only one crown layer but according to the vertical variability of the simulated tree

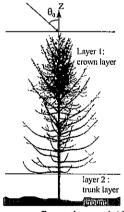


Fig. 1: 2-layer configuration and 40 yr-old tree simulation (17m high) from AMAP

architecture in Fig. 1, it is clear that probably at least 2 layers will be considered later.

In the top layer, the tree is described as a 5-scale cluster of dielectric cylinders, where the different scales account for the vegetation element of increasing order (1: primary branches, 2: secondary branches, etc.), up to the 5<sup>th</sup> scale being the needle clusters. Cylinders at each scale are described by mean length, diameter, linear density and branching angle relative to the lower scale. Pdf of these parameters can also be considered. At this stage, we consider only the pdf of the branching angle of the primary branches.

Statistics of cylinder parameters were obtained in the following manner using the AMAP interface. For each age, 20 independent 3D trees were simulated using the AMAP model to account for natural architectural variability. Then, a specific interface absorption, and can be obtained through the optical theorem in terms of forward scattering functions. The phase matrix  $\overline{\overline{P}}(\theta,\varphi,\theta',\varphi')$  characterises the scattering of the Stokes vector from  $(\theta',\!\varphi')$  direction into  $(\theta,\!\varphi)$ 

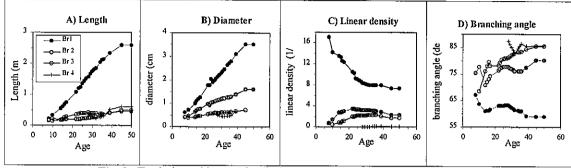


Fig. 2: Evolution with age of cylinder parameters within the 4-scale cluster, describing the 4 branch orders (Br1 to Br4) within the tree crown (mean values)

allows to describe a given tree as a collection of (x,y,z) positioned cylinders for each order of branch, in addition to trunk and needles. For example, the 40yr-old tree in Fig. 1 includes more than 80000 cylinders (without the needles). Then, 1<sup>st</sup> order statistics of these parameters are obtained from averaging over the 20 trees.

Fig. 2 includes the evolution with stand age of the geometric parameters of cylinders for increasing order of branches. Diameter and length are correlated and linearly increase with age, whereas linear density and branching angle have a more complex behaviour. Needle clusters are the most difficult to characterise; at this stage, a mean cluster is used with needle diameter, length, density and branching angle respectively of 1 mm, 8 cm, 16 / cm and 33°.

In addition to geometric parameters, dielectric constant of the soil, trunk, branch and needles were derived from field measurements of water content WC. These were found quite stable as a function of growth stage.

#### 3. RT MODEL DESCRIPTION

The RT model developed at MIT [6] includes three layers: a crown layer, a trunk layer and a ground surface. The trunks, branches and needles are modelled as circular cylinders where finite cylinder approximation is used [4]. The bottom rough surface is described by its rms height and its correlation length. The Kirchhoff approximation is used to calculate the scattering from the random rough surface. The scattering properties of structured pine trees are taken into account by incorporating the branching model [5] into the phase matrix of the RT equation (1).

$$\cos\theta \frac{d\overline{I}(\theta,\phi,z)}{dz} = -\overline{\kappa}_{e}(\theta,\phi,z) \cdot \overline{I}(\theta,\phi,z) + \int_{d\pi} d\Omega' \overline{\overline{P}}(\theta,\phi,\theta',\phi') \cdot \overline{I}(\theta',\phi',z) \qquad (I)$$

Where the Stokes vector  $\overline{I}$  contains information regarding field intensity and phase relation of the two orthogonal polarisations. The extinction matrix k represents the attenuation due to both scattering and

direction. The phase matrix can be formulated in terms of the scattering functions of the randomly distributed discrete scatterers

#### 4. RESULTS

In the following, modelling results are compared to backscatter measurements at L and C-band obtained from SIR-C data acquired over the Mende test-site during the SRL-2 mission in October 94, in dual-pol mode (HH and HV) at 55° incidence angle. The data set was radiometrically corrected for slope effects and ortho-rectified in the Lambert II projection [3].

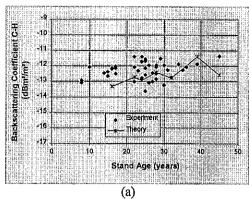
The overall agreement between experiment and theory is good. Fig. 4 presents the experimental and simulated backscattering coefficients at C-HH and L-HV. These preliminary results do not include simulated values of young stands, due to the lack of appropriate soil surface characterization. The RT model can be used to identify the major scattering mechanisms. Fig. 5 presents the main contributions of the tree element classes at C-HH.

Some differences remain between experimental and simulated results. For example, L-HV simulated values decrease for stands older than 24 years whereas a slight increase is observed experimentally. One of the possible causes is the assumption of homogeneity whithin the crown layer by a RT model. As an example, fig. 6 shows the histogram of primary branches angle vs the stand age (high values are bright, low values are dark). It can be observed that at about 24 years there is a change of the dominant angle from 70° to 80°, and also appearance of lower angles of about 30°. This indicates the need to take into account the vertical variability within the canopy by using the AMAP output to increase the number of layers in the RT model.

#### CONCLUSION

This study has shown the usefulness of using a tree growth model such as AMAP to provide input parameters for a backscatter model. The tree growth

model can provide missing data or measurements difficult to acquire.



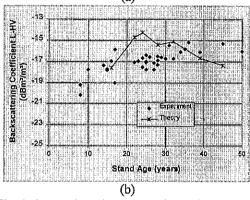


Fig. 4: Comparison theory-experiment for (a) CHH and (b) LHV

Moreover, the flexibility of AMAP to provide information on any part of the canopy may help providing inputs to more detailed description improved backscatter models, such as considerating more layers in the crown canopy or curved branches.

#### **ACKNOWLEDGMENTS**

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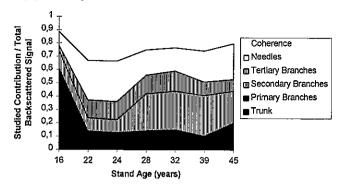


Fig. 5: Relative contributions of the scattering elements in the total backscattered signal, C-HH configuration.

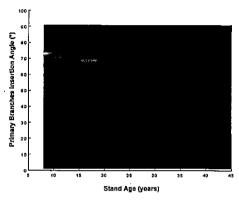


Fig. 6: Histogram of the primary branches angle vs stand age

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