Luberon2 quick tutorial using the installer *capsis-luberon2-18624.jar*

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This is a simple guide to the graphical interface, see general information in the Luberon2 user manual. Luberon2 was developped by Claire Godineau[1*], Victor Fririon[1*], Nicolas Beudez[2], François de Coligny[2], François Courbet[1], Gauthier Ligot[3], Sylvie Oddou-Muratorio[1,4], Leopoldo Sanchez[5], François Lefèvre[1§].

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Capsis installation guide from the installer

Follow the instructions on https://capsis.cirad.fr/capsis/documentation/installation_guide

To start Capsis in english, the command is "*capsis –l en*" or "*sh capsis.sh –l en*"

Create a Luberon2 project and load inventory

Here, we will create a new project called *demo* and load the inventory file "*cedrus_Sault.txt*" to initiate a 2.25ha *Cedrus atlantica* even-aged stand, 27-years old in 2027, with 5625 trees (2500 trees/ha), in a low fertility site (dominant height 18m at 50 years).

- ✓ The *New Project* pop-up window should appear, otherwise in the top menu: *Project > New*
- ✓ Give a name to your project and *Initialize*
- ✓ Then in the Model initialization pop-up (the one on the left below): *Browse* and choose your inventory file
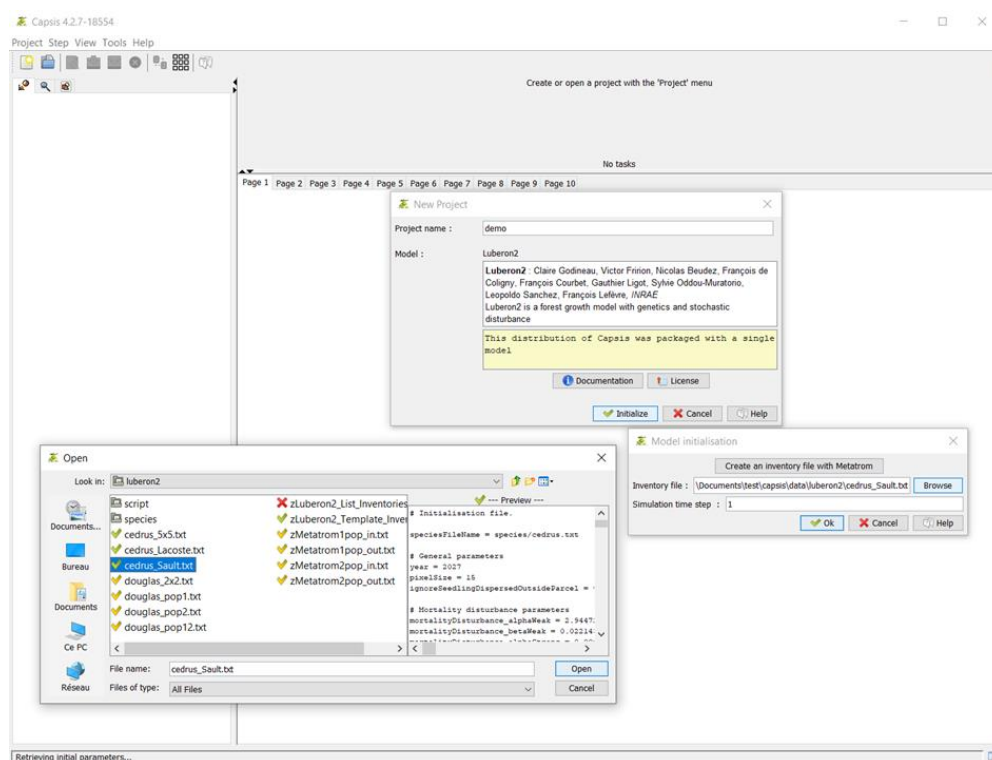
Visualize the scene

In Capsis' lateral bar on the left, select the *Scene Viewer* menu (2nd position) and choose *Complexe Scene Viewer*. The stand can now be seen from above with circles proportional to individual tree dbh.

On the graphic display window, bottom right, in the menu *Selection*, you can choose *Viewer 3D* and then select with a right click the zone you want to visualize in 3D, which will appear in a separate window with its own display tools (in blue below, with the *best rendering* option of the 3D toolbox).
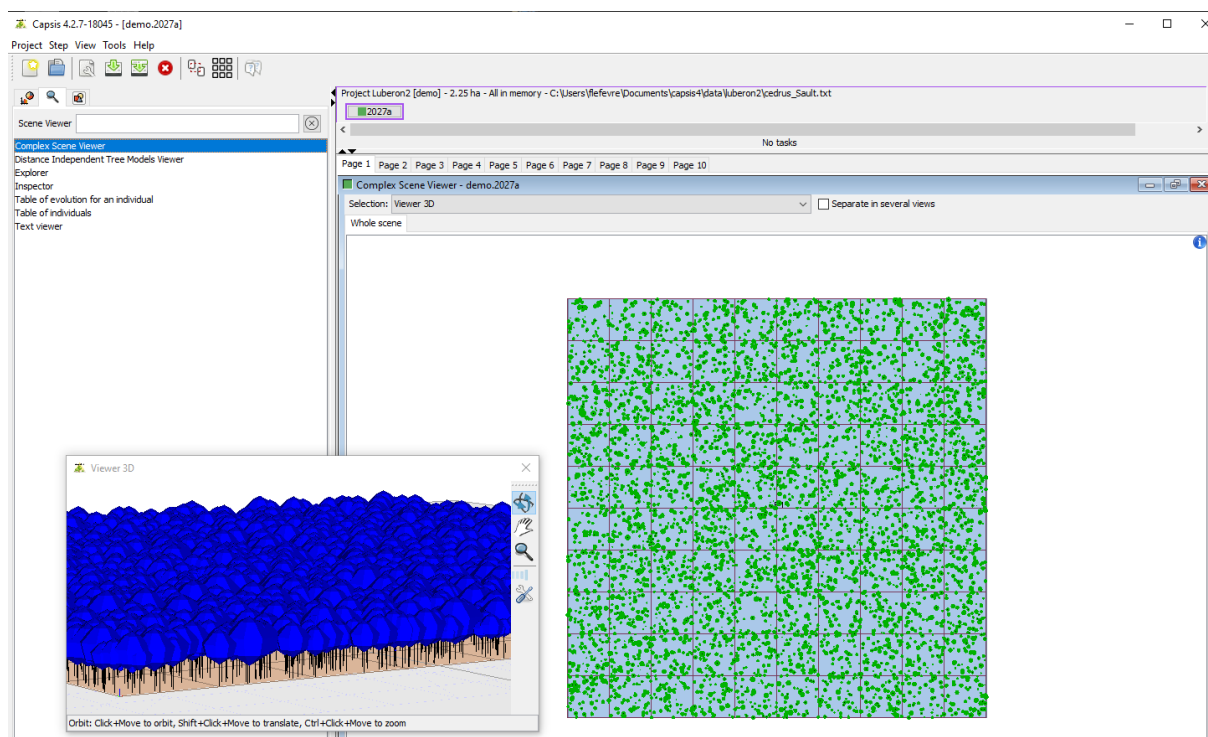
Choosing *Table of Individuals* in the *Scene Viewer* menu, instead of *Complexe Scene Viewer*, will display a table with all individuals and their attributes.

In this demo, the stand consists of a single square *Parcel* (P1, written in the center). A regular grid of *Pixels*, automatically created, is used for the regeneration steps. We will simulate two silviculture scenarios suited for low fertility sites adapted from Ladier et al. (2012)[1], as follows :

|	Scenario 1		Scenario 2	
	Year	Target density N/ha	Year	Target density N/ha
clearing	-	-	2027	1100
1st thinning	2060	800	2050	600
2nd thinning	2080	430	2060	430
3rd thinning	2100	320	2075	320
4th thinning	2120	245	2090	245
5th thinning	-	-	2105	200
Seed trees	2140	80	2120	80
Final cut	2150	-	2130	-

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[1] J. Ladier, F. Rei, P. Dreyfus (2012) Guide des sylvicultures de montagne Alpes du Sud françaises, ONF-Irstea Eds, 301p.

Simulate scenarios of stand evolution

In the ProjectManager bar, top right, right click on the current step (here, 2027) and choose *Evolution*, which opens the menu *Criteria of evolution*.

Choose the year to reach and activate/disactivate the annual processes of regeneration, mortality disturbance and growth disturbance with their own options as indicated on the screen shot beside (see Luberon2 user manual on these processes).

Using a right click on the *ProjetManager*, display options can be used to facilitate visualization of the evolution scenario, e.g. show only *One step out of 5*.
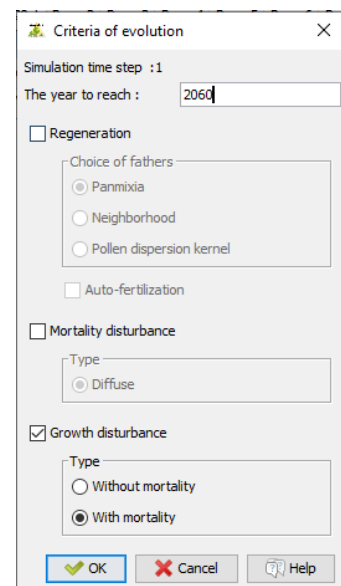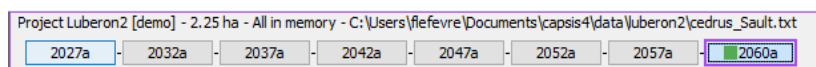
Then, right click on the step 2060 and choose *Intervention*, which opens the *Intervention* menu (left panel below). Different methods can be used to perform the thinnings, with their specific options. For each method proposed, a pop-up window guides the user. Here we illustrate the *Thinning diagram* method. The pop-up window shows the current distribution of dbh classes (right panel). Thinning rules are defined by reducing the number within each class (either absolute values or per ha), either graphically or numerically, while a table shows the result of the intervention (bottom of right panel). Once satisfied, click on OK.
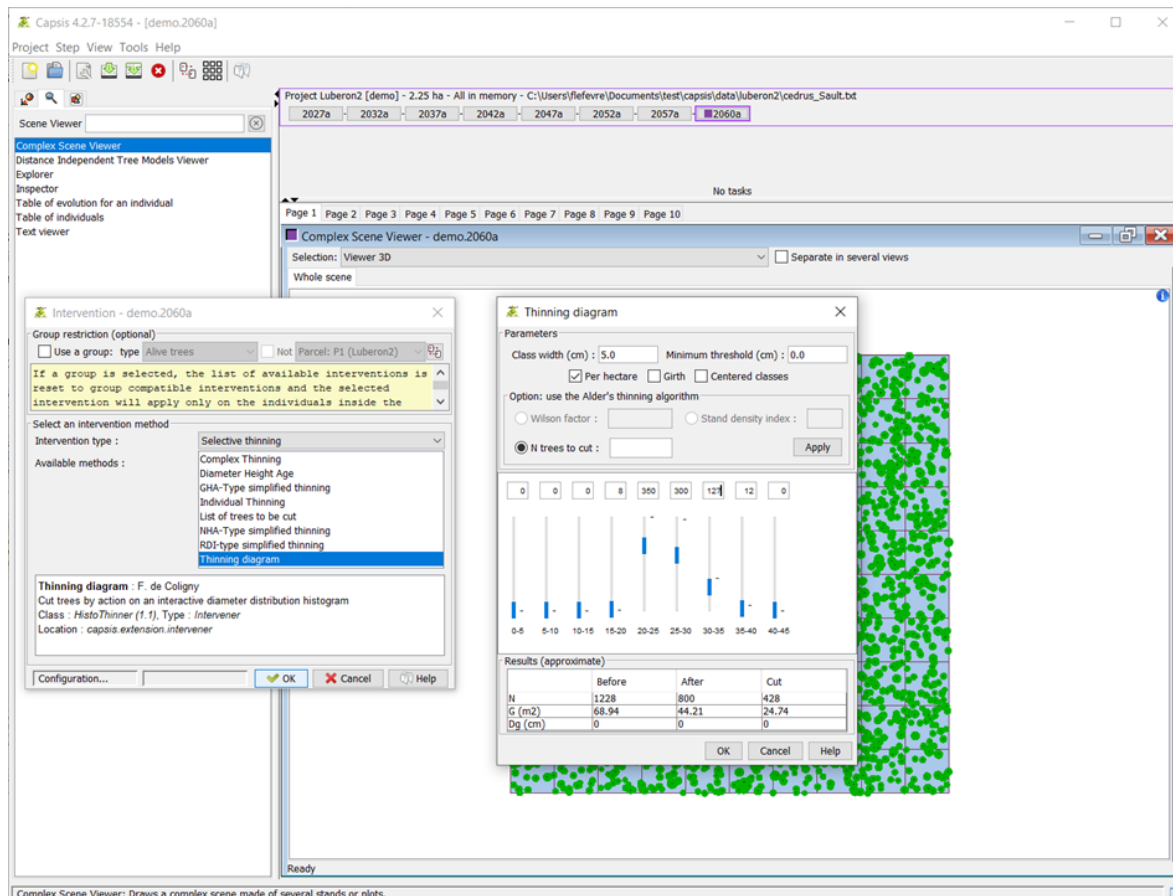
Then, a new step appears for year 2060 marked with a * indicating that an intervention happened:

Project Luberon2 [demo] - 2.25 ha - All in memory - C:\Users\flefevre\Documents\capsis4\data\luberon2\cedrus_Sault.txt

| 2027a | 2032a | 2037a | 2042a | 2047a | 2052a | 2057a | 2060a | ■*2060a |
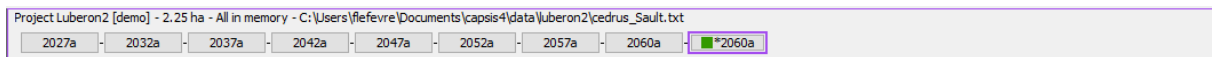
Repeat the process to simulate succesive thinnings as indicated for scenario 1, with an alternance of evolutions and interventions. For this scenario, in the following graphs, thinnings were conducted from below, while biggest trees were kept as seed trees. Once seed trees have been selected (year 2140), make an evolution until 2150 with regeneration activated. Then make an intervention using the *Diameter Height Age* method to remove seed trees based on the age criteria.
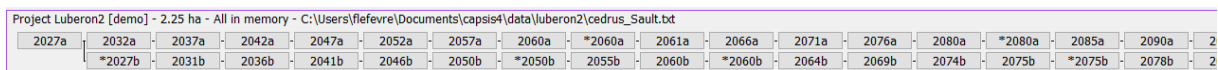
Note: pixels with 4 or more seed trees cannot receive any regeneration and appear as empty once seed trees are removed.

Proceed the same way to simulate the second scenario, starting with a clearing at the initial step in 2027. The second scenario appears with index "b":

Project Luberon2 [demo] - 2.25 ha - All in memory - C:\Users\flefevre\Documents\capsis4\data\luberon2\cedrus_Sault.txt

| 2027a | 2032a | 2037a | 2042a | 2047a | 2052a | 2057a | 2060a | *2060a | 2061a | 2066a | 2071a | 2076a | 2080a | *2080a | 2085a | 2090a | 2 |
| | *2027b | 2031b | 2036b | 2041b | 2046b | 2050b | *2050b | 2055b | 2060b | *2060b | 2064b | 2069b | 2074b | 2075b | *2075b | 2078b | 2 |

Visualize the simulation results with available charts

In Capsis' lateral bar, select the *Chart* menu (1st position) to see the list of proposed graphical tools, in alphabetical order. The barred ones are not currently available for Luberon2. See the description of the objects in the documentation manual to better understand the meaning of these charts.

The charts are generally displayed for the whole scene, except the ones with a name followed by *(Luberon2)* that draw a line for each *Pixel* within a chosen *Parcel*.
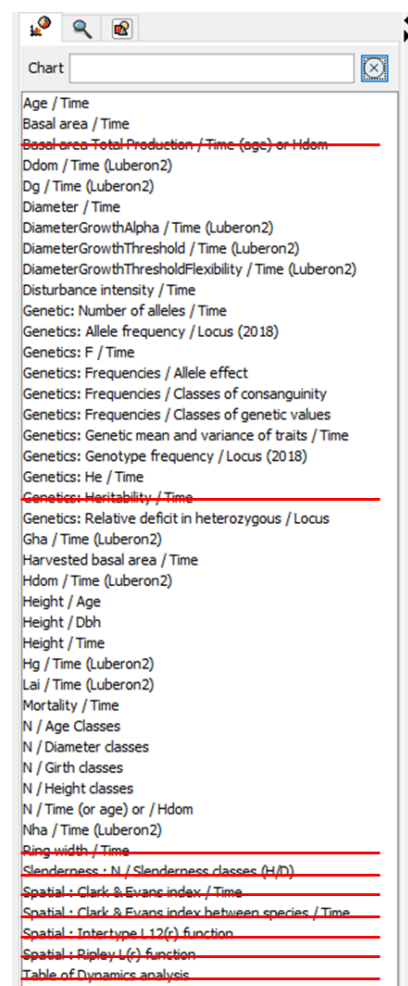
Click on the final step of scenario 1 (or any other step) to make it "current": the current step is the one with a colored mark.

| ■*2150a |
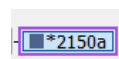
Then, double click on the charts *Basal area / Time* and *Genetics: Frequencies / Classes of genetic values*

The charts refer to the current step: either showing the evolution of stand-level variables until this step (e.g. basal area), or showing the distribution of tree-level variables at the time of the current step (e.g. distribution of genetic values).

Each chart has its own specific configuration options. The configuration menu opens after a right click anywhere in the chart. Each chart can be displayed graphically or in table format.

Chart

Age / Time
Basal area / Time
Basal area Total Production / Time (age) or Hdom
Ddom / Time (Luberon2)
Dg / Time (Luberon2)
Diameter / Time
DiameterGrowthAlpha / Time (Luberon2)
DiameterGrowthThreshold / Time (Luberon2)
DiameterGrowthThresholdFlexibility / Time (Luberon2)
Disturbance intensity / Time
Genetic: Number of alleles / Time
Genetics: Allele frequency / Locus (2018)
Genetics: F / Time
Genetics: Frequencies / Allele effect
Genetics: Frequencies / Classes of consanguinity
Genetics: Frequencies / Classes of genetic values
Genetics: Genetic mean and variance of traits / Time
Genetics: Genotype frequency / Locus (2018)
Genetics: He / Time
Genetics: Heritability / Time
Genetics: Relative deficit in heterozygous / Locus
Gha / Time (Luberon2)
Harvested basal area / Time
Hdom / Time (Luberon2)
Height / Age
Height / Dbh
Height / Time
Hg / Time (Luberon2)
Lai / Time (Luberon2)
Mortality / Time
N / Age Classes
N / Diameter classes
N / Girth classes
N / Height classes
N / Time (or age) or / Hdom
Nha / Time (Luberon2)
Ring width / Time
Slenderness : N / Slenderness classes (H/D)
Spatial : Clark & Evans index / Time
Spatial : Clark & Evans index between species / Time
Spatial : Intertype L12(r) function
Spatial : Ripley L(r) function
Table of Dynamics analysis

To add the result of the second scenario on the same chart for comparison (or any other step to compare), click on the final step of the second scenario · ■*2130b

then right click on the chart and choose the option *Add demo.*2130b*. A legend on top of the chart indicates the colors and symbols of each step (can be changed).

Below are the comparisons of basal area per ha through time in two scenarios (left panel) and three distributions of genetic values for the trait *growthVigor* (right panel): the initial stand 2027a (in grey) and the final steps of the two scenarios. When there are multiple comparisons, the legend appears in a pop-up window upon request.

It is possible to zoom on a graph with mouse drag to the right. For instance, in the graph below, He values for neutral loci (5 alleles each) and QTL (diallelic) are not on the same scale, which makes the raw chart *Genetics: He / Time* uninformative (left panel), zooming helps (right panels). De-zooming is obtained with mouse drag to the left.

… you should now be ready to continue exploring the tool by yourself.