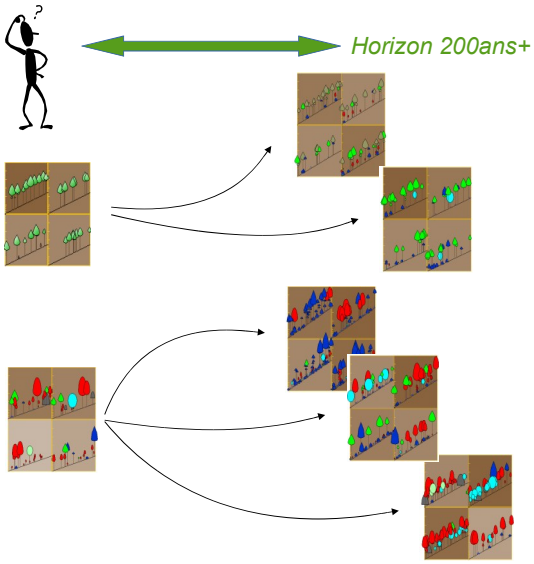
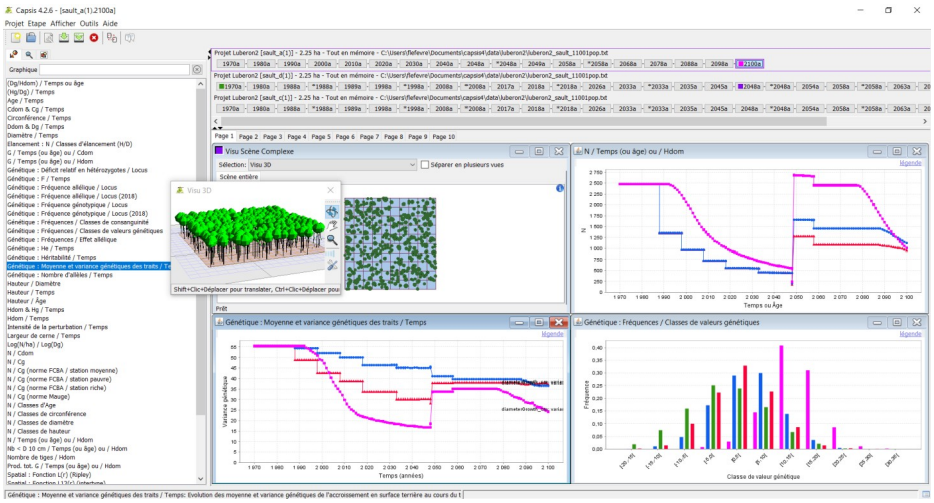
# LUBERON2 : a model of forest dynamics with genetic diversity to simulate the impacts of silvicultural practices and disturbance.



## What is it ?

- It is a model of forest dynamics with natural regeneration that allows to simulate different initial genetic compositions, different silvicultural treatments and disturbance regimes.
- It provides graphical representation of the evolution of dendrometric, demographic and genetic characteristics of a forest stand, allowing to compare the response to different silviculture and disturbance regimes.
- It is a demo-genetic model, i.e. demographic processes and genetic diversity are integrated :
  - the genetic diversity has an impact on stand dynamics and on the response to silviculture
  - stand dynamics and silviculture have an impact on the evolution of genetic diversity
- It offers the possibility to simulate stochastic disturbance events
- It is aimed at simulating the evolution of a stand of individual spatialised trees over several generations.

## What for ?

- The simulator can be used for different objectives :
  - for management, to compare different silviculture options;
  - for research, to analyse the effects of interactions between silviculture and disturbance on stand dynamics, genetic quality and evolutionary potential;
  - for teaching and communication, to raise awareness on the potential impacts of silviculture and disturbance on the genetic quality and adaptive capacity of the forests.

- In particular, it allows :
  - to compare different sylviculture treatments in a genetically diverse forest stand;
  - to visualize the combined impacts of silviculture and disturbance;
  - to test the evolution of different initial genetic compositions;
  - etc.
- WARNING : the simulator should be used for comparative analyses, not for quantitative predictions, because this would require further calibration of the coupled demo-genetic model (see below).

## For whom ?

- The simulator is mainly for R&D services of public and private forest entreprises, as well as scientists using the CAPSIS platform : these users will have the capacity to use all the library of tools offered by the platform.
- A simpler use is possible, based on default options or just as a demo.
- A more advanced used by all CAPSIS modelers is possible, to integrate new features into the code, or to extract part of the code and re-use it in other models of the CAPSIS platform.

## How does it work ?

- LUBERON2 relies on an individual-based, even-aged, growth model of *Cedrus atlantica*.
- On this basis, several processes and functionalities have been added to allow demo-genetic coupling : trees are spatialized, the stand is composed of independent even-aged sub-plots to simulate multiple cohorts, reproduction as well as pollen and seed dispersal have been added, demographic performance traits (currently growth and mortality, may be extended to reproduction) may be genetically determined. Coupling processes that are individually calibrated can still affect the quantitative predictions of the integrated model: the model can be used for comparative analyses but quantitative predictions still require validation.
- On top of the demo-genetic model, a « generator of genotypes » allows to simulate initial individual genotypic data that fit with population-scale genetic diversity parameters and quantitative genetic parameters defined by the user (or default values). Individual genotypes currently include quantitative trait loci coding for growth performance and susceptibility to disturbance, as well as neutral loci with no effect, in the nuclear and cytoplasmic genomes.
- During the annual cycles of stand evolution, individual tree growth, survival and reproduction is driven by the demographic processes. The genotypes of new recruited seedlings are determined by the reproduction processes between its two parents. Thus, both demographic and genetic processes drive the evolution of the stand.
- The user can simulate different types of interventions at each annual step, manually.
- Stochastic disturbance defined by intensity and frequency patterns can be switched on/off during stand evolution (currently one type of disturbance, to be extended to several types).

## How to use it ?

- The simulator runs on a PC, it requires installation of the CAPSIS software and appropriate Java version.
- Simulations start with an initial stand inventory made of individual trees spatialized in one or several parcels characterized by their site index. Each tree has initial dendrometric

characteristics and a genotype. Individual genotypes can be provided directly or simulated using the generator of genotypes.

- A user-guide is in preparation, proposing different levels of utilisation, from the use of default options, menu options, to possible changes in the model parameters themselves.
- WARNING: with the most expert user mode, many options can be changed but a smart choice might require information difficult to obtain.

## Who did it ? contact ?

- LUBERON2 was developed at INRA by Claire Godineau et Nicolas Beudez, with the help of François de Coligny, Sylvie Muratorio, Leopoldo Sanchez, François Courbet, Christine Deleuze, Christian Pichot and François Lefèvre ; within the project *Assessment of the genetic impacts of adaptation-oriented sylviculture practices*, funded by RMT AFORCE and Conseil Général de Vaucluse
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## And now ?

- Thanks to the modularity of the CAPSIS platform, the integration of demo-genetic coupling with disturbance regime and control of the initial genetic composition of the stand will be extended to other forest dynamics models, for other species and other forest systems.

## Two references


- Introduction to the evolution-oriented forest management approach :
    - Lefèvre F, Boivin T, Bontemps A, Courbet F, Davi H, Durand-Gillmann M, Fady B, Gauzere J, Gidoin C, Karam MJ, Lalagüe H, Oddou-Muratorio S, Pichot C (2014) Considering evolutionary processes in adaptive forestry. Annals of Forest Science, 71:723-739.
- A literature review, in french, on the potential genetic impacts of silviculture :
    - Valadon A (2009) Effets des interventions sylvicoles sur la diversité génétique des arbres forestiers : Analyse bibliographique. Office National des Forêts, Collection dossiers forestiers, n° 21, Juin 2009, 160p.


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