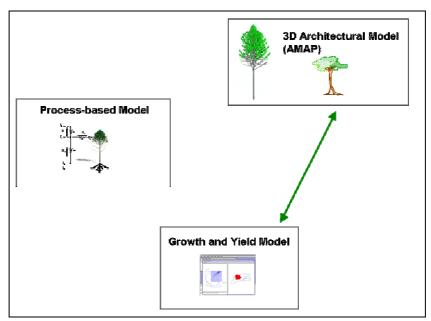
# The advantages of coupling stand description from growth models to tree description from architectural models

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#### Introduction

There is now a wide variety of models available to predict growth of forest stands. Common classifications distinguish process-based, architectural and growth and yield models, each of them dealing with a particular aspect of the forest production (Fig. 1).



**Figure 1:** Three types of models to predict growth of forest stands.

Process-based models (PBM) focus on forest ecosystems functioning (H2O, Carbon, and nutrients flows). Some examples are BIOMASS, McMurtrie *et al.*, 1990; 3-PG, Landsberg and Waring 1997; CENW, Kirschbaum 1999; G'DAY Dewar and McMurtrie 1996; TRIPLEX, Peng *et al.* 2002. These models describe the interactions between water, Carbon and nutrient cycles. They are mainly used to simulate (i) water and CO2 exchanges between the stand and the atmosphere, and (ii) gross and net primary production, using meteorological input (e.g. rainfall, incident radiation, air temperature, ...), and other information about the soil (e.g. soil texture), the canopy structure and physiological properties.

Architectural models (or Geometric models) deal with the botanical individual tree growth. They focus on bud growth, ramification, and mortality. Resulting models are mainly stochastic and they can accurately simulate the 3D architecture of plants (AMAP, L-SYSTEMS; a review is given by Godin 2000). They are used for different applications such as biomechanics (Fourcaud *et al.* 1996) or landscape studies (Auclair *et al.* 2001).

Growth and yield models are designed to simulate tree and stand growth under different silviculture regimes. They are based upon a series of basic relationships where diameter increments, height growth, and mortality are a function of site potentiality and silvicultural practices (Dhôte 1990,

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1996; Dreyfus 1993; Meredieu 1998; Tomé et al. 2001; Saint André et al. 2002; García and Ruiz 2003).

Several connections have been reported between the aforementioned approaches: functional-structure models (FSMs) are defined by Sievänen *et al.*, 2000 as a combination between process-based models and geometrical models. FSMs offer the opportunity of simulating plant growth as a result of the interaction between the plant architecture and its physiological processes. Some examples are Lignum (Perttunen *et al.*, 1998) and Greenlab (de Reffye and Hu, 2003) for the tree species. Connections between process-based models and growth and yield models have also been explored: for example, Battaglia *et al.* 1999, connected ProMod (a PBM) to an empirical growth projection model (Nitgro). Mäkelä *et al.* 2000 also emphasized that many process-based models embedded empirical components (especially for the Carbon allocation and competition). To our knowledge, the connection between growth and yield models and architectural models has not yet been explored. Hence we propose, in this paper, a first attempt to make possible this interaction.

A generic computer platform was designed to host a wide variety of forest growth or dynamics models and stand intervention mechanisms to study the evolution of forest ecosystems: the *Capsis* platform (Coligny *et al.* 2003). Different growth and yield models are implemented as modules. The main interest of these models lies in their simplicity and robustness and in the fact that they are designed to explicitly take into account silvicultural practices and competition between trees. These models generally give information on the global dimensions of trees like diameter at breast height, total height, total volume... We think that integrating architectural description into growth and yield models could be a useful way to get a more precise tree description. This could also result in various improvements for connection with wood properties modules either concerning knottiness through position and vital status of branches or by providing a basis for improved compartment biomass assessment.

The AMAPsim plant architectural software (Barczi *et al.*, 1996), computes realistic 3D trees relying on both qualitative and quantitative tree architecture description. Tree growth process is mainly driven by tree age. Diameter of axes is computed according to Shinozaki's pipe model (Shinozaki *et al.*, 1964). Calibration of model parameter values is estimated from sample measurements on stands at various ages. However, because architectural measurements are time-consuming, the number of sampled stands was generally limited (especially for the oldest stands). To improve the probabilistic methods used to generate the 3D simulated trees, it would be interesting to use the growth and yield models which have been calibrated using a larger range of silvicultural trials and/or temporary plots. Simulating several silvicultural scenarios should then help tuning the architectural models parameters to get trees closer to reality.

This paper proposes the methodology to connect these tools and discuss the potentials and limits of such an approach.

## Synthetic description of the connection

Such a connection implies to constrain AMAPsim (tree architecture) simulation by Capsis (tree growth models) computed parameters. The following method was implemented: (i) connection between the two software, (ii) adjust AMAPsim simulations from Capsis parameters, (iii) compute AMAPsim trees, (iv) extract data from the simulated trees, (v) send back these information to Capsis. Two types of connections were created: Mode 1 is a free simulation and mode 2 is a synchronised simulation.

In mode 1, Capsis provides to AMAPsim a dataset for site and stand description (fertility defined by the dominant height at a given age, the number of stems within the stand, the number of trees to be simulated by Amapsim) and a set of target values (age, average and standard deviation of diameters and heights). From these information, AMAPsim calculates a set of trees that respect the target values. This mode 1 is useful to test the ability of AMAPsim in generating realistic stands.

In mode 2, Capsis sends the dataset for site and stand description and a list of trees to AMAPsim. For each Capsis tree, AMAPsim should return one tree of similar size (height and diameter at breast height). This mode is slightly different from the previous one because, in this case, the target values

are tree-specific. This mode was created either to complete information on trees that are not calculated by the module in Capsis (e.g. the leaf area index), or to compare some tree properties that are simulated by both AMAPsim and Capsis (e.g. the branch biomass).

The two software are connected in a client-server way connection. In the Capsis platform, the tree description is module (or model) specific. A generic extension of Capsis, AMAPsim client, was created. It can be potentially used by each of the hosted growth and yield model in Capsis, provided that the module tree description has a detectable additional AMAPsim data description (to ensure that the information returned by AMAPsim can be integrated in Capsis). The client establishes a connection network with the AMAPsim server. It builds, sends and memorizes the pending requests and processes the received answers. It uses transaction numbers in order to manage the possibility of deferred responses in case of long AMAPsim simulations.

After the creation of a Capsis project (silvicultural scenarios), the connection tool is launched (in mode 1 or 2). Capsis sends data for the selected step in the simulation history. The information returned by AMAPsim is stored in Capsis throughout two main procedures depending on the chosen mode for the connection: in mode 1, a new Capsis project is created using a specific technical module that carries the tree data calculated by AMAPsim; in mode 2, the tree description is stored in the simulation in progress using the additional Amapsim data description. The AMAPsim tree description can then be analysed by all Capsis tools (viewers and graphics) or used in the growth and yield model.

### Managing the constraints under AMAPsim

Four parameters can be used to drive the tree architecture simulation: age, total stem height, diameter at breast height and crown size. In mode 1, the target values can be described as a mean (arithmetic or quadratic) or a dominant value with (or without) a deviance criteria. Each constraint can be used independently and all the combinations are available. In this last case, we consider that age has to be the first target, height the second, crown size the third, and finally the diameter which is supposed to be a natural consequence of the present architecture:

Age is normally considered and corresponds to the main entry of AMAPsim software (a tree is computed at a given age).

For a given target *age*, the *total stem height* is linked to the site fertility (and the stand density for some tree species). The stem height, from a meristematic point of view, is the result of two growth processes in tree architecture, i.e. organogenesis (number of leaves and number of shoot internodes) and extension phase (of each internode). In order to get the target *total stem height*, we decided to tune firstly the number of internodes and secondly the length of internodes. This action is applied on all the successive growth units of the stem. As the number of internodes of a growth unit relies on the branching ability of a growth unit, the branching is automatically affected by height adjustment.

From Capsis point of view, *stem diameter* is controlled by site fertility, density and tree diameter. In AMAPsim, diameter of axes is computed according to Shinozaki's pipe model from the number and structure complexity of branches and elementary leaf production. As branching is automatically affected by height adjustment, we considered that the only parameter to be changed in order to get the target *stem diameter*, is the elementary leaf production.

*Crown size* is related to stand density, and for now, crown shape is considered as a cylinder, so that AMAPsim has to simulate branches not longer than the ray cylinder.

Many limitations occurred as we built this connection between Capsis and AMAPsim. The first one is the biological knowledge about the growth- and branching-process changes according to growth conditions. If some general considerations can be solved, when algorithms have to be produced, very fundamental questions appeared. For example, are branching and extension similarly affected by density? If we want to respect crown size, how do we manage branch extension? How the basal height part of the crown is modified along with increasing fertility? Studies dedicated to some of theses questions are still in progress.

### **Preliminary results**

This approach offers numerous possibilities. Expected use is to extract biomass features, which are distinguished according to branching order (stem, branches and others) and diameter classes. Such accurate parameter extraction managed by tree size characteristics could be very useful for fire

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propagation models; in this case, fuel parameters could be adjusted according to land changes. Furthermore, this project offers the opportunity to investigate the links between a new generation of process-based models and constraints on plant architecture (Fig. 1).

Some results can be shown for one species: *Pinus pinaster* Ait. The first one deals with the evolution of the relationship between the height and the diameter for simulated populations of AMAPsim trees at different target ages (Fig.2).

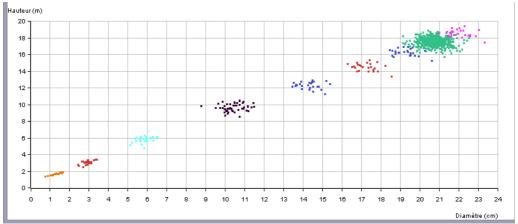
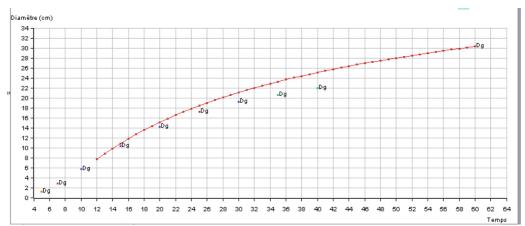


Figure 2: Individual height versus diameter at breast height for simulated Amapsim trees.



**Figure 3:** Simulated mean diameter of a 'Maritime pine' stand obtained with Pp3 growth model (curve) and mean diameter of a population of AMAPsim trees (dots) generated at different target ages.

Secondly, we can compare the evolution of the mean diameter of a stand during a period and the value of the mean diameter of a population of AMAPsim trees generated at different target ages (Fig. 3).

Our project is under development: the connection between the two software is in progress and we begin tests on different species: Eucalyptus, Maritime Pine and Black Pine.

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