Multiscale Functional-Structural Plant Modelling at the Example of Apple Trees

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Introduction

This is a description of an ongoing project which aims at understanding the development and functioning of apple trees by modelling them at several spatial and temporal scales. Dependence of growth and carbon allocation upon genotype, environmental variables, fruit load and experimental manipulation of carbon transport is investigated and simulated. For the required functional-structural models, new tools are developed, especially for handling multiple-scale representations of the same organism in a user-friendly way. This joint project (French-German) brings together expertise in botany, eco-physiology, horticultural tree modelling, mathematics and computer science. The following gives short outlines of the research, planned and partially completed, in the four work packages which correspond to the principal partners (University of Göttingen, Göttingen, Agrocampus Ouest, Angers, INRA, Montpellier, and CentraleSupélec, Paris).

Work Packages Outline

WORK PACKAGE 1

A. *Provide tools for working with multiple scales*
- development of software tools for simultaneous handling of fruit trees at several structural scales within FSPMs
- methods for upscaling (aggregating microscale information to a macroscale) and downscaling (the reverse information flow) for plant structures and for processes affecting plants
- meta-modelling - the aggregated description of the output of a fine-scale model by a simpler model at a coarser scale

B. *Case studies*
- tools evaluated at an integrated multiscale model of apple branch physiology and organ development
- compare several, alternative components for light interception, water and carbon transport at different scales
- evaluate the benefits and drawbacks of modelling at finer scales

C. *Platform interfacing*
- interfaces between GroIMP and OpenAlea and between GroIMP and PYGMALION are currently being developed and tested

WORK PACKAGE 2

A. *Branch model – concept*
- aims at the conceptualization and subsequent implementation of a functional-structural plant model of the bearing branch of apple, with a strong emphasis on combined carbon and water flows between sources (leaves) and sinks (developing fruits) within the same branch (cf. [1]).

B. *Branch model – development*
- to elucidate and quantify the influence of the topological and geometrical distribution of source and sink organs within a branch, by achieving a better description of combined sugar and water transport

Fig. 1 Experiments used to follow C transport in the branch of apple tree: $^{13}CO_2$ labelling with LI-6400XT portable photosynthesis system.

WORK PACKAGE 3

A. *Analysis and modeling source-sink relationships under water stress (WS)*
- experimental measurements of source (photosynthesis) and sink activities (growth) and of non structural carbohydrate contents under well watered and WS conditions for three apple tree cultivars
- aims at providing MappleT with new ecophysiological formalisms to simulate the impact of WS on plant architecture

B. *Integrating genome information in FSPM*
- a genome wide prediction model was used to estimate SNP makers effects on the rate of leaf emergence and the probability of sylleptic branching along 1yr old trunk, depending on thermal time, on 116 genotypes issuing from a F1 cross
- MappleT parameter values were estimated for each genotype based on SNPs polymorphisms and effects
- accuracy of this model prediction was evaluated on integrated variables (e.g. trunk length) by a k fold cross-validation
- first simulations with MAppleT gave promising results even if further works are needed to better simulate genotype-environment interactions

WORK PACKAGE 4

A. *Parameter estimation by Bayesian methods*
- translate the models in the framework of hidden Markov models
- state of the art methods for parameter inference are currently being tested in the context of FSPM

B. *Sensitivity analysis*
- use of 'Factor Fixing Setting' for non-influential parameters
- development of variance decomposition methods for sensitivity analysis, adapted to correlated inputs

Bayesian estimation and sensitivity analysis are implemented in the modelling platform PYGMALION

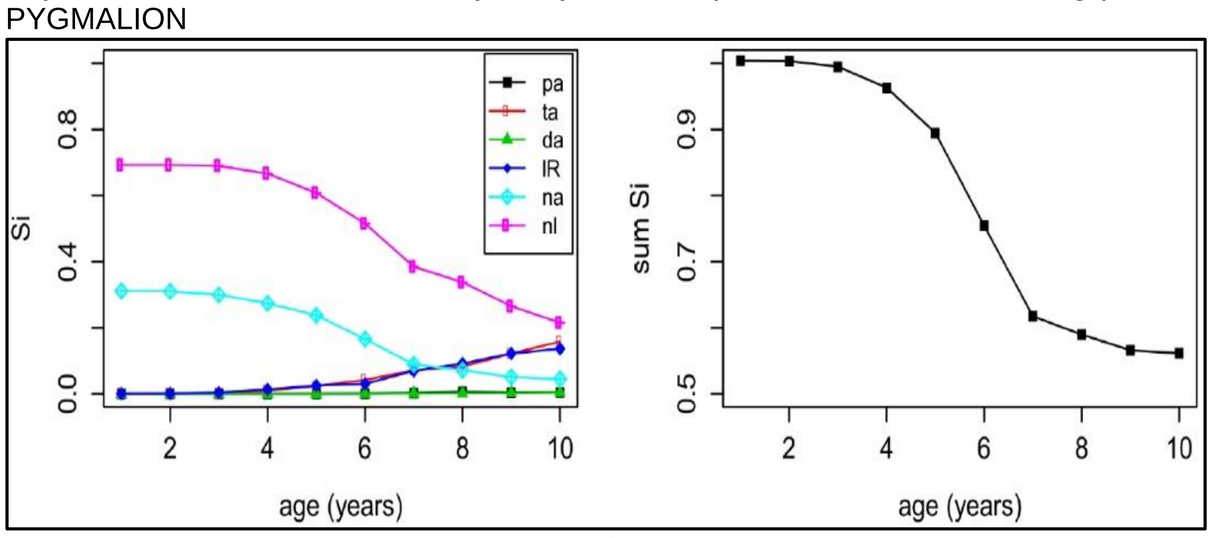

Fig. 2 Sensitivity analysis run on PYGMALION based on a GroIMP model. The colors correspond to different parameters of the model.

GROIMP OPENALEA INTERFACE

- development of an interface for data exchange using a file format compliant with the generic XML syntax [3]
- design of a web-based communication workflow adopting the standardized HTTP protocol
- the design includes the creation of two interfacing packages on top of both GroIMP and OpenAlea [3,4,5].
- it consists of a communication layer and an information transformation layer
- the GroIMP-OpenAlea interface could serve as a prototype for a general framework for communication and data exchange among diverse modelling platforms, e.g. cross-platform modelling with different FSPMs

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