

Ph.D. in computer science and modeling applied to agronomy

Titre : Semantic and modular representation of plant growth models using a declarative metalanguage.

Summary : Plant growth simulation models are commonly used to predict and analyze the response of plants to their environment. The intercomparison and improvement of these models remains difficult because of their monolithic structure and the diversity of the programming languages of the modeling platforms. The objective of the thesis is to develop a high-level language, allowing to describe mathematically and to annotate semantically each model and its assembly independently of the programming languages and the formalisms of each modeling platform. The operational objectives concern the interoperability of the modeling tools, as well as their links with the information systems collecting the data. A modularity of models in the level of biological processes is aimed to allow a better integration of knowledge in agronomy and plant biology and to facilitate links with data. The thesis will be a major contribution to the international initiative for the exchange of models in agriculture (AMEI).

Several communities in biology have defined declarative languages for the representation and exchange of models of biological processes. For instance, [SBML](#) in systems biology (Hucka et al., 2003), [CellML](#) in cellular physiology (Miller et al., 2010) or [NeuroML](#) in neuroscience (Gleeson et al., 2010) have become standards. However, the expressiveness of these declarative languages is limited to their domain of application. In particular, the mathematical representation in the form of an algebraic differential equation or of reactions is interesting as a high-level universal representation but is not sufficient to describe crop and soil process-based models. It is necessary to extend and adapt these languages to have an explicit representation of time, and that formalism can describe difference equations and fine control structures. Moreover, the information associated with each model (e.g. biological processes, name of the variables) are not semantic in nature. It is therefore difficult to compose models between them by having only a scientific knowledge of the processes without knowing their fine mathematical representation (formalism, names of the variables and their meaning). The thesis aim to integrate various models describing at different scales (from the organ to the community) the biological processes at work during the development of the plant. This temporal and spatial integration requires a language, as well as a multi-scale coupling formalism between these different process models, which is the most adapted to the plant object within a plant stand and its environment.

Profil recherché : We are looking for a candidate strongly motivated by difficult research subjects in a multidisciplinary environment. The candidate must have a Master (or equivalent) in computer science applied to modeling and / or agronomy. A double competence in these two disciplines is ideally sought.

Funding : A three-years Ph.D. grant is co-funded by the National Research Agency ([ANR](#)) and the National Institute for Agricultural Research ([INRA](#)) within the framework of the Digital Agriculture Convergence Laboratory ([#DigitAg](#)).

Doctoral School : ED 584, Biodiversité, Agriculture, Alimentation, Environnement, Terre, Eau ([GAIA](#)), Université de Montpellier.

Main place of work : Montpellier.

Starting date : 1 November 2017.

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How to apply : Send a CV and a cover letter to Pierre Martre (pierre.martre@inra.fr), Frédéric Garcia (frederick.garcia@inra.fr), and Christophe Pradal (christophe.pradal@cirad.fr). Application deadline 1 October 2017.