

GreenScilab_Crop, an open source toolbox for plant simulation and parameter estimation

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Abstract

GreenLab is a mathematical model for simulating plant organogenesis, biomass production and allocation, as well as 3D plant structure. Being a functional–structural model, its implementation and test usually take a lot of time and human resource. Several softwares have been developed, but it is difficult for external users to access to them or make modification according to their own knowledge. In past years, the community of plant modeling was increasing in China, both from agronomy and computer science domain. With increasing international publications on GreenLab model [1][2][3][4], there is more need from the community of plant modeling to apply GreenLab-based software, therefore a free-accessible software is desirable.

Scilab is a free software for scientific computation. Implementation of GreenLab in Scilab started several years ago, their combination giving a toolbox named GreenScilab. This toolbox kept on evolution since its appearance with updating of both Scilab software and GreenLab theory. Its demo version has been used several times in graduate student course in France. The source code and user manual can be downloaded from web site www.greenscilab.org.

Previous GreenScilab version was able to simulate both tree and crop. Trees are more complex in structure than crops, allowing several metamers in one growth unit, while in crop there is only one. Substructure algorithm was applied in the code for speeding up the computation of trees, but this brought little advantage for crops, and even limited the application of some specific features. Because of importance of agronomic plants, a new version of GreenScilab dedicated to crops was thus developed, named GreeScilab_Crop In this version, features that are necessary for crops have been introduced. The amount of source code has been significantly reduced, and structure is clearer to be understood. Until now, it has been applied and been tested for simulation and parameter estimation of several crops of various architectures: tomato[5], chrysanthemum[6], maize[3] and wheat[7].

Currently, new interface is being developed and online

help is to be done to be better user-friendly. A user manual is being prepared, which aims at not only guiding the users with case study from data measurement to parameter estimation, but also providing an analysis of code so that new functions can be understood and modified if needed. The new version is expected be online before this September.

References

- [1] A. Christophe, V. Letort, I. Hummel, P.-H. Cournède, P. de Reffye, and J. Lecoœur, “A model-based analysis of the dynamics of carbon balance at the whole-plant level in *Arabidopsis thaliana*,” *Functional Plant Biology*, vol. 35, pp. 1–16, 2008.
- [2] Q.-X. Dong, G. Louarn, Y.-M. Wang, J.-F. Barczi, P. de Reffye, and 2008, “Does the structurefunction model greenlab deal with crop phenotypic plasticity induced by plant spacing? a case study on tomato,” *Annals of Botany*, pp. 1195–1206, 2008.
- [3] Y.-T. Ma, M.-P. Wen, Y. Guo, P.-H. Li, B.-G. Cournède, and P. de Reffye, “Parameter optimization and field validation of the functional structural model greenlab for maize at different population densities,” *Annals of Botany. Plant Growth Modelling, Simulation, Visualization and Applications Special Issue.*, vol. 101, pp. 1185–1194, 2008.
- [4] R. Qi, V. Letort, M.-Z. Kang, P.-H. Cournède, P. de Reffye, and T. Fourcaud, “Application of the greenlab model to simulate and optimize wood production and tree stability: a theoretical study,” *Silva Fennica*, 2009, accepted.
- [5] L.-L. Yang, G. Kang, M.-Z. Louran, P. de Reffye, Y.-M. Wang, and Q.-X. Dong, “Link between tomato flower abortion and trophic competition: a modelling approach,” in *PMA09: The Third International Symposium on Plant Growth Modeling, Simulation, Visualization and Applications*, L. Marcelis, G. van Straten, C. Stanghellini, and E. Heuvelink, Eds., Wageningen, Netherlands, 2009, accepted.
- [6] M.-Z. Kang, E. Heuvelink, and P. de Reffye, “Building virtual chrysanthemum based on sink source relationships: preliminary results,” in *Acta Horticulturae*, L. Marcelis, G. van Straten, C. Stanghellini, and E. Heuvelink, Eds., vol. 718. Wageningen, Netherlands: III International Symposium on Models for Plant Growth, Environmental Control and Farm Management in Protected Cultivation, 2006, pp. 129–136.

- [7] M.-Z. Kang, J.-B. Evers, J. Vos, and P. de Reffye, “The derivation of sink functions of wheat organs using the greenlab model.” *Annals of Botany. Plant Growth Modelling, Simulation, Visualization and Applications Special Issue.*, vol. 101, pp. 1099–1108, 2008.