GreenScilab version 1 for chrysanthemum

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This version is derived from a standard GreenScilab version 1 for simulation, calibration and validation of GreenLab model on chrysanthemum.

In this version, the basipetal flowering sequence is simulated by introducing a delay function for branches, which can be organ-specific. Growth rhythm is allowed to simulate different treatments using the same time step, see corresponding functioning files. Data of chrysanthemum from 16 treatments are included.

To start, first load the toolbox by running the 'loader.sce', e.g.,

Then the GreenScilab functions are loaded, and you will see info in SCilab window like:

exec('…\GreenScilab_Herbaceous_2011_H_RR\loader.sce');

Two main kinds of scripts are provided for fitting and simulation respectively. For fitting flower number, run

exec('…\ GreenScilab_Herbaceous_2011_H_RR \ Gl_fit_Para_NoF_PSO.sce');

A dialogue will appear asking which file to select. Choose corresponding parameter file for fitting flower number, such as 'chrys_T24L51**_NoF**.sci'.

For fitting organ biomass, run

exec('…\ GreenScilab_Herbaceous_2011_H_RR \Gl_fit_Para.sci');

There are list of parameter files (under folder 'parafiles') to choose. Choose corresponding parameter file for fitting organ biomass, such as 'chrys_T24L100_H1.1_DW', 'chrys_T24L100_H2.1_DW.sci', 'chrys_T24L100_H4_DW.sci'. Notice that for each treatment, calibration was done stepwise.

Each parameter file is a text file including all the information for description of initial parameters, which parameters to be fitted, and which functioning files to be loaded. The fitting target can be biomass and/or plant height. Target data for fitting are under folder 'targetfiles'.

```
//TargetFlag(C_Tar_Com)_compartment
Leaf_Mass       1 1 1
Leaf_Area       1 1 1
In_Mass         1 1 1
FeFr_Mass       0 0 1
MaFr_Mass       0 0 0
```

1 mean this target will be fit. First column is total organ biomass, second column corresponds to

organ biomass in main stem, the third one refers to organ biomass in side shoots.

PlantHeight(P_H) 1

There are another list of 0/1 to tell which parameters are to be fitted, such as:
Allom_Internode(c_a_bI) 1 0 0 0 0 0
(c_a_aI) 1 0 0 0 0 0

After fitting on biomass is done, it is possible to output the target data and model output into a file for plot, by running

exec('…\GreenScilab_Herbaceous_2011_H_RR\bin\gl_output_FitResult_File.sce');d

To interpolate parameters from the eight treatments, run

exec('…\GreenScilab_Herbaceous_2011_H_RR\bin \Para_Analysis_fitting.sce');

This file contains the seven parameter values for each of eight treatments.

For validation treatments, the result can also be seen by running "**Gl_fit_Para.sci'**". No parameters are to be fit, but one can compare the predicted and target data. The parameter values are from interpolation. The result can saved a text file by running

exec('…\GreenScilab_Herbaceous_2011_H_RR\bin\gl_output_FitResult_File_Validation.sce')

For simulation you may run

exec('…\GreenScilabV2_Pine\Gl_simulate.sci');

Here you need only to choose the parameter file. Choose such parameter files like 'chrys_T15L40_H4_DW**_sim**.sci', whose geometrical parameters are normally properly set.

M.Z. Kang, P.-H. Cournède, Ph. de Reffye, B.G. Hu. 2008. Analytic Study of a Stochastic Plant Architectural Model: Application to the GreenLab Model. *Mathematics and Computers in Simulation*. *Mathematics and Computers in Simulation*, Vol. 78, pp. 57-75, 2008.
M.Z. Kang, de Reffye P, Barczi JF, Hu BG, and Houllier F. 2003. Stochastic 3d tree simulation using substructure instancing. In: Hu BG and Jaeger M, eds. *PMA03 (The First International Symposium on Plant Growth Modeling, Simulation, Visualization and Applications)*. Beijing: Tsinghua University Press/Springer-Verlag, 154–168.