**Terrestrial Regional Ecosystem Exchange Simulator (TREES)**

**WORKSHOP**

**Instructors:** Scott Mackay (dsmackay@buffalo.edu), Diane Wang (drwang@buffalo.edu)

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**Time:** xx - xx

**Location:** xx, University of Wyoming

**PART I. Setting up your machine to run TREES**

The following are needed for the hands-on portion of this workshop:

1. TREES3 executable
2. R
3. Rstudio

*Note: for those who want to learn how to compile the model, come back after the main workshop for the afternoon Open Session.*

**PART II. Review TREES inputs and outputs**

Found inTREES\_inputs\_outputs.xlsx

1. TREES input parameter table
2. TREES output variable table
3. TREES ‘param mod’ parameter table

**PART III. Running TREES with fixed parameters:**

**An example with *Brassica rapa***

***Description of experiment:*** This exercise comes from a study on *Brassica rapa* that developed a new growth module based on the emergence and expansion of individual leaves. The main experiment was a mild drought experiment was conducted under greenhouse conditions at the University of Wyoming. Two genotypes were evaluated under mild drought and in this exercise we will be running simulations on the Chinese Cabbage (CC). There were two treatments of drought, D1 and D2, where water was completely withheld at the emergence of leaf four and emergence of leaf five, respectively, and plants were recovered just after emergence of leaf six and seven, respectively. Leaf area was measured approximately daily after the emergence of the third leaf using Easy Leaf Area (Easlon and Bloom 2014). The well-watered (WW) control treatment was watered daily in the evenings via bottom-watering. Volumetric soil water content was monitored daily in all three treatments. In this exercise, we will have a look at how to run TREES given a fixed set of parameters and see how simulations compare to empirical data. For more information on the experiment, refer to Wang *et al.,* 2019.

***Running TREES:*** We will now review the files found in the BRASSICA folder and run simulations for all three treatments (WW, D1, and D2). We will walk through the WW simulation as a group, and you will repeat steps 1-5 for D1 and D2 on your own.

1. Check that parameter and driver files are located where you expect
2. Create your ‘in’ setup files
3. In terminal, set your working directory to the BRASSICA folder
4. Run TREES by typing into terminal:

trees3 < in\_files/in\_cc\_ww.txt

1. Locate the output files in the ‘outputs’ folder

***Plotting results:*** Now that all three simulations have been run, we will have a look at our results and make some plots to compare our simulations with observed data. You will compare total leaf area (a plant variable) and soil water content (an environmental variable). Open the script Plot\_Chinese\_Cabbage\_results.R in Rstudio and follow along. Try to re-create the plots found in Figure 4A-C and 4E-G of the Wang *et al* 2019 study.

***Short discussion:*** Think about the following questions and we will discuss the answers together as a group.

1. Soil water content plots – What does the model do well? What could the model improve on? What are some parameters that you think could be varied to see if there could be better fit?
2. Total leaf area plots – Is total leaf area a direct output of TREES? Does the model capture differences in the dynamics of leaf area across the three treatments? Where could the model be improved?
3. Have a look at Figure 4D and 4H (the two sub-figures we did not plot) of Wang *et al.* 2019 study. What are you looking at in these figures? Walk through the steps of how you would create these plots using the same datasets as you have used for the exercise above.

**PART IV. Running TREES with variable parameters:**

**A sensitivity analysis with piñon pine**

***Description of experiment:*** This exercise comes from a study on *Pinus edulis* and *Juniperus monosperma* growing on a hydrologic refugia near Los Alamos, New Mexico. In this study trees were subjected to experimental drought (i.e., withholding 45% of precipitation) and heat for a five-year period. In this study all trees survived because they had roots that accessed groundwater from within bedrock fractures. We will be using a small portion of this study consisting of 180 days starting March 1, 2012, which is the first and driest year of the full study, and *P. edulis* (or piñon), with ambient (not experimentally manipulated) and drought treatments. This will give us three drought stress treatments (ambient, ambient with no groundwater access, and drought). For the ambient treatment we will run one simulation in which the roots are given access to bedrock groundwater and a second simulation in which the roots are restricted to the soil layers (down to 65 cm depth). To modify the structure of the root system we are using two parameter files, pine\_mod for the simulation with bedrock roots and pine\_mod\_noGW for the simulation with roots only in the soil layers. We will also modify the xylem vulnerability curves to resemble juniper by modifying values in the pinus\_edulis.p parameter file. For more information, refer to Mackay *et al.*, 2019.

***Running TREES:*** We will now review the files found in the PINON\_PINE folder and run simulations for the three drought stress treatments (ambient, ambient with no groundwater access, and drought). We will walk through all three simulations as a group, and then you will modify the vulnerability curve parameters and re-run the ambient simulation with the new parameters.

1. Check that parameter and driver files are located where you expect
2. In terminal, set your working directory to the PINON\_PINE folder
3. Run TREES for the three treatments as follows:
   1. trees3 < in\_files.in\_pinon\_ambient.txt
   2. trees3 < in\_files.in\_pinon\_drought.txt
   3. trees3 < in\_files.in\_pinon\_ambient\_noGW.txt
4. Make a backup copy of pinus\_edulis.p as follows:
   1. cp pinus\_edulis.p pinus\_edulis\_original.p
5. Using a text editor, open pinus\_edulis.p and locate the following lines and delete the first number of each row (highlighted in blue):

3.43 14.1 3.43 ax\_Shoot-b\_value\_(weibull)

1.65 3.55 1.65 ax\_Shoot-c\_value\_(weibull)

3.43 14.1 3.43 lat\_Shoot-b\_value\_(weibull)

1.65 3.55 1.65 lat\_Shoot-c\_value\_(weibull)

3.57 10.1 3.57 ax\_Root-b\_value\_(weibull)

4.07 6.96 4.07 ax\_Root-c\_value\_(weibull)

3.57 10.1 3.57 lat\_Root-b\_value\_(weibull)

4.07 6.96 4.07 lat\_Root-c\_value\_(weibull)

1. Save the modified pinus\_edulis.p file and run TREES using the in\_pinon\_ambient\_run2.txt input file
2. Locate the output files in the ‘outputs’ folder

***Plotting results:*** Now that all three treatment simulations have been run, we will have a look at our results and make some plots to compare results. The first part of the code will convert half-hourly simulation output to daily variables to make the plots less dense and therefore easier to compare treatments. Open the script Aggregate\_to\_Daily.R in Rstudio and follow along. This will save some new files with the aggregated variables. Open the script Plot\_Pinon\_Pine\_results.R in Rstudio and follow along. How do the leaf water potential plots here compare to those in Figure 2 of the Mackay *et al* 2019 study?

***Short discussion:*** Think about the following questions and we will discuss the answers together as a group.

1. Leaf water potential plots – What are some of the main differences in these plots among the four simulations? Why do these plots change so much when the parameters for the vulnerability curves are altered?
2. Critical and actual transpiration – What happens to the difference between critical transpiration and actual transpiration when leaf water potential is low (more negative)? Why is this difference less pronounced with the second set of vulnerability curves (simulation with in\_pinon\_ambient\_run2.txt)?
3. Have a look at Figure 2 in Mackay *et al.* 2019. What are some notable differences between the simulation results we just generated and those in this figure? In the last simulation (in\_pinon\_ambient\_run2.txt ) we actually used parameters for observed juniper vulnerability curves. Compare our leaf water potential simulation results to Figure 2 SUMO juniper ambient (blue curve). Why are they so different? Can you think of parameters one might change to match the results obtained for juniper in Figure 2?

**PART V. Wrap-up**

We will take the next 5-10 minutes to complete a workshop survey. There should be some free time to ask any remaining questions.

Thank you for attending our TREES hands-on workshop! If you are interested in deeper understanding of TREES, come back for the afternoon Open Session.

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**References**

Easlon HM, Bloom AJ. Easy Leaf Area: Automated digital image analysis for rapid and accurate measurement of leaf area. Applications in plant sciences. 2014 Jul 1;2(7).

Mackay DS, Savoy PR, Grossiord C, Tai X, Pleban JR, Wang DR, McDowell NG, Adams HD, Sperry JS. Conifers depend on established roots during drought: results from a coupled model of carbon allocation and hydraulics. New Phytologist. 2019 Jul 5.

Wang DR, Guadagno CR, Mao X, Mackay DS, Pleban JR, Baker RL, Weinig C, Jannink JL, Ewers BE. A framework for genomics-informed ecophysiological modeling in plants. Journal of experimental botany. 2019 Mar 2;70(9):2561-74.