

Workflow for "Parameterization of PPA model using a SORTIE-ND model for the Harvard forest"

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1 Overview

This folder contains the necessary files for obtaining parameters from the SORTIE-ND files and using that to run simulations of the PPA model as described in our paper. This file contains

1. Parameter Generating Files
 - (a) Growth_LUT_Generator.R
 - (b) Sapling_generation_ LUT.R
 - (c) Morality_Calculator.R
2. The Core PPA Model
 - (a) PPA_Model.R
3. Three SORTIE-ND Outputs

4. Sortie Outputs Necessary for Individual Tree Growth
 - (a) species_growth_parameters file
5. Three Null Replicate Files Necessary to Run The Model From This Folder.
6. Data Processing scripts
 - (a) Macro_Stat_Processor.r
 - (b) Single_Species_Stat_Processor.R
7. A Graphing Package
 - (a) This also contains our raw outputs for comparison.

The following instructions describe the process by which to execute these files in order to obtain the results we found. This requires the SORTIE-ND which can be found at <http://www.sortie-nd.org/> or can be used with the outputs included here.

1. Running Necessary SORTIE-ND Model Runs
 - (a) Overall SORTIE-ND Runs
 - i. Load in SORTIE ND Parameters for Site.
 - ii. Change length of run to 500 years
 - iii. Run SORTIE-ND model
 - iv. Save output as HFrePLICATE1.csv
 - (b) Individual Trees
 - i. For each species
 - A. Load in SORTIE-ND parameters for site Remove any existing map Insert single tree of species desired Include detailed outputs for area of the single tree Run SORTIE-ND model Delinate detailed output to create seperate .csv for each life stage (Seedling, Sapling, Adult) of the single tree. Save into Species_Growth_Parameters/ as four letter tree code_life stage_full. (Ex. TSCA_adult_full.csv)

2. Creating Lookup Tables(LUT) From SORTIE-ND Data. These Scripts will create the LUTS from the Sortie-ND data, nessecary to run the PPA model.
 - (a) Mortality LUT
 - i. Open "Mortality_calculator.R" in R Studio
 - ii. Set tree data as one of the HFreplicates (ex "HFreplicate1.csv")
 - iii. Ensure species names align with 4 letter code and that time length is specified
 - iv. Run MortalityCalculator, this should create a .csv called Mortality_LUT.csv
 - v. Note for this project species (BEPA saplings and PRSE saplings eventually stopped regenerating, so a mean was taken from the years they were available). This returned values of PRSE=.06696 and BEPA=.12757 , which should be manually applied into the Mortality_LUT.csv
 - (b) Growth LUT
 - i. Open "Growth_LUT_Generator.R" in R studio and set work-drive to the species growth perimeters files. These are the files from individual tree runs in SORTIE-ND with NCI
 - ii. Ensure species names align with 4 letter code
 - iii. Ensure that in the PPA package folder you have a .csv called "Allo.lookup.csv". This is the allometry from the SORTIE-ND NCI file.
 - iv. Run Growth_LUT_Generator.R, this should create a .csv called Growth_Scenario_LUT.csv
 - (c) Sapling Mortality LUT
 - i. Open "Sapling_Generation_Rate_Generatorc.R" in R Studio
 - ii. Set tree data as one of the HFreplicates (ex "HFreplicate1.csv")
 - iii. Ensure species names align with 4 letter code and that time length is specified
 - iv. Run "Sapling_Generation_Rate_Generatorc.R" , this should create a .csv called "Time_Sapling_LUT.csv"

3. Running the PPA-model

- (a) Open the file "PPA-Model.R" in R-studio
- (b) Set w.dir to the loction of the PPA-packaging ex:w.dir("C:/Users/Johnsmith/Documents/PPA-packaging")
- (c) Set the number of time steps you wish to simulate(defaults to 0:200)
- (d) Set PPAf and SaplingPPAf coefficients (for this project PPAf=.1 and Sapling PPAf=.7 Set Number of replicates (defaults to 3) Run Sortie-PPA Mode. Run time will depend on processing speed but on average can convert 200 years in a 24-48 hours.

4. Results

- (a) Outputs of the PPA-model are put together in a time series of maps, found in each replicate. Included in this packaging is a simple script to compare SORTIE-ND outputs and PPA outputs.
- (b) Take each replicate you processed and move them to the folder in "Graphing_Package", named Sortie_PPA_outputs (There is a copy of the original data and SORTIE-ND_Outputs there currently. Make sure folders for each replicate are include
- (c) Open Macrostat_Processor.R file in R-Studio
- (d) Run each section, this will produce a .csv called Macrostats.csv. This compares the basal area, and stem density for both saplings and adults of each model.
- (e) Open Single_Species_Stat_Processor.R
- (f) Run each section, this will produce several .csv's named for each species. These compare the basal area, and stem density for both saplings and adults of each species for each model.