LANDIS-II v

Extension User Guide

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# Introduction

This document describes the **Root Rot** extension for the LANDIS-II model. For information about the model and its core concepts, see the *LANDIS‑II Conceptual Model Description.*

The Root Rot extension described here is the model that was first published in Gustafson et al. (*In Prep*). This extension was initially designed for the specific purpose of modeling Root Rot disease caused by *Phytophthora cinnamomi* in the eastern United States. However, most parameters are user-defined, making it possible to adapt to other *P*. *cinnamomi* systems, or even other pathogens that are cold-limited and influenced by soil moisture. This could include *P*. *cinnamomi* and European chestnut or other *Phytophthora* spp. that cause root diseases, though we provide no guidance on how this extension should be applied to those other pathogens.

## Root Rot Disturbances

Mortality caused by root rot infection is modeled by tracking the infection status of each cell, with probabilistic transitions between states. Each active cell has a mutually exclusive status of Susceptible (S), Infected non-symptomatic (I) or Diseased symptomatic (D). The probability of each transition between states is a combination of presence (controlled by temperature) and conducive environment (controlled by soil moisture). Cells that are Infected (I) or Diseased (D) only revert to a status of Susceptible (S) when pathogen is absent (Presence == 0). Cells that are Diseased (D) can revert to a status of Infected (I), and will always revert to I if all susceptible tree hosts are eliminated. It is assumed that the pathogen can disperse anywhere on the landscape.

The presence of the pathogen is controlled by a user-defined parameter of lethal temperature. On cells where a minimum temperature falls below the lethal temperature, the pathogen is eliminated. Those cells can subsequently be re-infected when the temperature stays above the lethal temperature.

Partial or complete mortality of tree cohorts can occur on cells that are Diseased (D). The rate of mortality is controlled by two species parameters of susceptibility, the first applying to the initial impact on a cohort, and the second controlling the impact of re-infection, which can be lower for cohorts that survived the first infection (selection pressure). These susceptibility indices are implemented as proportions of the cohort biomass to be removed when the site is Diseased.

### Pathogen Presence

The model assumes no limitation on the dispersal of the pathogen, that it can equally reach all cells in the landscape. Presence of the pathogen on a cell is therefore only controlled by its ability to survive on that cell. Survival of the pathogen is determined by the extreme minimum temperature compared to the input lethal temperature (LethalTemp) for the pathogen. Minimum temperatures that remain above 0°C are assumed to be optimal for pathogen presence. The presence status on a cell is a binary value, which is probabilistically determined to be ‘present’ if a uniform random number is greater than p(Presence), or ‘absent’ if <= p(Presence).

where ExtremeTmin is the extreme minimum monthly temperature across years in the timestep, and p(Presence) is constrained to be between 0 and 1. Extreme minimum temperature must be provided by the succession extension, with this capability currently enabled in PnET-Succession. The minimum extreme temperature is estimated within the succession extension as the monthly average temperature minus three times the winter standard deviation.

Figure 1. Example p(Presence) curve given a LethalTemp of -24°C.

## Cell Transitions between Infection States

The probability of each transition between infection states is a combination of presence (see 1.1.1) and environment conducive to the transition. The conducive environment is primarily controlled by soil moisture conditions, but varies for each type of state transition.

The soil moisture impacts are determined by evaluating the current soil moisture condition relative to threshold values defined by the user. The soil moisture condition is represented by soil water pressure head (m). Pressure head equals 0 when soil is saturated and increases as water is reduced. A pressure head of approximately 3.37m equates to soil field capacity, and 153m equates to soil wilting point. The user-defined parameters of phWet, phDry and phMax represent the pressure head values (m) that define when the soils are considered ‘wet’, ‘dry’ and ‘extremely dry’, respectively, in terms of conditions conducive to the pathogen.

### Susceptible (S) Cells

Cells that are Susceptible (S) can transition to either Infected (I) or Diseased (D) states.

#### Susceptible (S) to Infected (I)

Under ‘wet’ conditions (pressure head < phWet) it is possible for a site to progress from S to I. The probability of S converting to I [p(S->I)] decreases linearly from 1 when saturated (ph = 0) to 0 at phWet:

p(S→I) = IF(ph < phWet, -1/phWet \* ph + 1, 0)

Figure 2. Example of probability of transition from Susceptible to Infected, given a phWet value of 3.

#### Susceptible (S) to Diseased (D)

The probability of S converting to D [p(S→D)] is the product of the probabilities p(S→I) and p(I→D) (see 1.2.2), that is, it must successfully make both transitions.

p(S→D) = p(S→I) \* p(I→D)

### Infected (I) Cells

Cells that are Infected (I) can transition to Susceptible (S) or Diseased (D) states.

#### Infected (I) to Susceptible (S)

The probability of I converting to S [p(I→S)] is binary depending on the presence of the pathogen. If the pathogen is ‘absent’, then p(I→S) = 1. If the pathogen is ‘present’, then p(I→S) = 0. This relationship assumes that the absence of the pathogen always reverts a cell to a Susceptible status, and that a cell will sustain Infected status as long as the pathogen remains present.

#### Infected (I) to Diseased (D)

The probability of I converting to D [p(I→D)] is bimodal. Probability decreases from 1 when soil moisture is saturated (ph = 0) to a minimum value when pressure head is phWet. The minimum probability of I converting to D is set by the parameter minProbID. At moderate pressure head, the probability of disease development can be greater than 0. Probability also increases from minProbID at phDry to 1 at phMax.:

p(I→D) = IF(ph < phWet, (minProbID – 1)/phWet \* ph + 1, IF(ph > phDry, IF(ph > phMax, 1, m1 \* ph + b1),minProbID));

m1 = (1-minProbID)/(phMax - phDry);

b1 = minProbID – (phDry \* m1)

Figure 3. Example probability of transition from Infected to Diseased, given phWet = 3, phDry = 150, phMax = 250, and minProbID = 0.1.

### Diseased (D) Cells

Cells that are Diseased (D) can transition to either Susceptible (S) or Infected (I) status.

#### Diseased (D) to Susceptible (S)

The probability of D converting to S [p(D→S)] is binary depending on the presence of the pathogen. If the pathogen is ‘absent’, then p(D→S) = 1. If the pathogen is ‘present’, then p(D→S) = 0. This relationship assumes that the absence of the pathogen always reverts a cell to a Susceptible status.

#### Diseased (D) to Infected (I)

Cells that are Diseased convert to Infected any time no cohorts are present with susceptibility > 0, and with probability [p(D→I)] when pressure head is between phWet and phDry. The probability increases towards the midpoint between phWet and phDry. Maximum probability is capped at a user defined parameter (maxProbDI).

If all Susceptibility(i) == 0, then p(D→I) = 1;

Else, p(D→I) = MIN(maxProbDI,IF(ph < phWet, 0, IF(ph > phDry, 0, IF(ph <= (phDry – phWet)/2, m2 \* ph + b2, m3 \* ph + b3))));

m2 = 1/((phDry – phWet)/2 - phWet);

b2 = -1\*phWet \* m2;

m3 = 1/((phDry – phWet)/2 - phDry);

b3 = -1\*phDry \* m3

Figure 4. Example probability of transition from Diseased to Infected, given values of phWet = 3, phDry = 150, and maxProbDI = 0.85.

## Damage

After updating the cell infection status, any cell with a status of Diseased (D) receives damage.

For each cohort on the cell, damage is determined as a proportional removal of cohort biomass (representing the death of individual trees), based on the user-input susceptibility of the species to the pathogen (i):

Damage = Susceptibility(i)

The model utilizes two susceptibility values for each species, representing the rate of mortality for the first time the cohort is diseased and for subsequent disease impacts. The secondary mortality rate provides the ability to represent differential survival among cohorts that survived a previous infection of the pathogen. The extension determines whether a cohort was previously diseased by comparing the cohort’s age to the time that the last disease impact occurred on the cell.

## Major Releases

This is the first major release of this extension.

## Minor Releases

## References

Gustafson, E. J., B. R. Miranda, T. J. Dreaden, D. F. Jacobs, C. C. Pinchot. In Prep. Forecasting the limiting effects of *Phytophthora* root rot on restoration of the American chestnut in the eastern United States.

## Acknowledgements

# Input File

The input parameters for this extension are specified in one input file. This text file must comply with the general format requirements described in section 3.1 Text Input Files in the LANDIS-II Model User Guide.

## LandisData

This value of this parameter must be "Root Rot".

## Timestep

This parameter is the timestep of the wind extension. Value: integer > 0. Units: years.

## InputMap (optional)

The path and filename to a raster map that indicates the infection status of all cells at the start of the simulation (Year 0). The map values represent Susceptible (1), Infected (2) and Diseased (3) status. If an input map is not provided, the model assumes all cells begin as Susceptible (1).

## SpeciesSusceptibility

The SpeciesSusceptibility table defines the initial and secondary susceptibility of each species. Each row of the table lists one species followed by its initial susceptibility and its secondary susceptibility. The species names must match the species names in the core species text file. Both susceptibility values must range between 0 and 1, inclusive. Species that are not listed are assumed to have susceptibilities of 0, but for any species listed, both susceptibility values must be provided (they can be the same).

## LethalTemp

The minimum temperature below which the pathogen cannot survive. Numeric value ≤ 0.

## PhWet

The pressure head threshold (m) below which the soil is considered ‘wet’. Under wet conditions it is possible for a cell to transition from Susceptible to Infected and from Infected to Diseased. Pressure head equals 0 when soil is saturated, and increases as soil moisture is reduced. A pressure head of approximately 3.37m equates to soil field capacity, and 153m equates to soil wilting point. Numeric value > 0.

## PhDry

The pressure head threshold (m) above which the soil is considered ‘dry’. Under dry conditions it is possible for a cell to transition from Infected to Diseased. Pressure head equals 0 when soil is saturated and increases as soil moisture is reduced. A pressure head of approximately 3.37m equates to soil field capacity, and 153m equates to soil wilting point. Numeric value > 0.

## PhMax

The pressure head threshold (m) above which the soil is considered ‘extremely dry’ and optimal for cell transitions from Infected to Diseased. Pressure head equals 0 when soil is saturated and increases as soil moisture is reduced. A pressure head of approximately 3.37m equates to soil field capacity, and 153m equates to soil wilting point. Numeric value > 0.

## MinProbID

The minimum probability of Infected cells transitioning to Diseased. At moderate pressure head, the probability of disease development can be low, but might be greater than or equal to 0. Numeric value between 0 and 1, inclusive.

## MaxProbDI

The maximum probability of Diseased cells transitioning to Infected. At moderate pressure head, the probability of disease symptoms disappearing can be high, but might be less than or equal to 1. Numeric value between 0 and 1, inclusive.

## OutputMapName (optional)

The path and filename template for the root rot infection status map output. The filename must include the {timestep} template, which will be replaced by the numeric simulation year when the maps are written, and the file extension must be an acceptable raster map format (i.e., ‘.gis’ or ‘.img’).

## TOLPMapName (optional)

The path and filename template for the Time of Last Pathogen (TOLP) map output. The filename must include the {timestep} template, which will be replaced by the numeric simulation year when the maps are written, and the file extension must be an acceptable raster map format (i.e., ‘.gis’ or ‘.img’).

## LethalTempMapName (optional)

The path and filename template for the LethalTemperature map output. The filename must include the {timestep} template, which will be replaced by the numeric simulation year when the maps are written, and the file extension must be an acceptable raster map format (i.e., ‘.gis’ or ‘.img’).

## TotalBiomassRemovedMapName (optional)

The path and filename template for the TotalBiomassRemoved map output. The filename must include the {timestep} template, which will be replaced by the numeric simulation year when the maps are written, and the file extension must be an acceptable raster map format (i.e., ‘.gis’ or ‘.img’).

## SpeciesBiomassRemovedMapName (optional)

The path and filename template for the SpeciesBiomassRemoved map output. The filename must include both the {species} template and the {timestep} template, which will be replaced by the species name and numeric simulation year, respectively, when the maps are written, and the file extension must be an acceptable raster map format (i.e., ‘.gis’ or ‘.img’).

## EventLog (optional)

The path and filename for the event log file output. The file extension must be ‘.csv’.

## SummaryLog (optional)

The path and filename for the summary log file output. The file extension must be ‘.csv’.

# Output Files

The extension generates two types of output files: a) maps of infection status, time of last pathogen damage, lethal temperature, total biomass removed, and biomass removed by species for each time step, and b) logs of root rot events and a summary for the entire scenario.

## Root Rot Infection Output Maps

Root Rot infection status maps are produced at each extension timestep.

Map values:  
0 = Non-active  
1 = Susceptible  
2 = Infected  
3 = Diseased

## Time of Last Pathogen (TOLP) Maps

Time of Last Pathogen maps are produced at each extension timestep if a path and filename are provided for the TOLPMapName parameter.

Map values represent the simulation year in which each cell was most recently disturbed (damaged) by the pathogen. Cells that have not been disturbed during the simulation have a value of -9999, and non-active cells have a value of 0.

## Lethal Temperature Output Maps

Lethal Temperature maps are produced at each extension timestep if a path and filename are provided for the LethalTempMapName parameter.

Map values represent the extreme low temperature (°C) that caused the absence of the pathogen on each cell in each timestep. Because the determination of presence is probabilistic (based on p(Presence)), cells with the same climate data may not have the same value on the Lethal Temperature map, except when the extreme minimum temperature is above 0 or below LethalTemp. Cells where the temperature did not cause the absence of the pathogen have a value of 99 in the maps.

## Total Biomass Removed Output Maps

Total Biomass Removed maps are produced at each extension timestep if a path and filename are provided for the TotalBiomassRemovedMapName parameter.

Map values represent the total biomass removed due to disease across all cohorts on a cell in each timestep. Units of biomass are g/m2.

## Species Biomass Removed Output Maps

Species Biomass Removed maps are produced at each extension timestep if a path and filename are provided for the SpeciesBiomassRemovedMapName parameter.

Map values represent the biomass removed due to disease across all cohorts on a cell for each species in each timestep. A separate map is produced for each species. Units of biomass are g/m2.

## Event Log

An event log is produced with records for each extension timestep if a path and filename are provided for the EventLog parameter. The event log provides information about the mortality for each tree species by timestep. The columns represent Time (simulation year), Species (species name) and MortalityBiomass (sum of landscape species biomass removed due to disease; g/m2).

## Summary Log

A summary log is produced with records for each extension timestep if a path and filename are provided for the SummaryLog parameter. The summary log provides landscape summaries of the pathogen status and impact at each extension timestep. The columns represent Time (simulation year), InfectedSites (number of cells with status of Infected), DiseasedSites (number of cells with status of Diseased), DamageSites (number of cells that had some cohort damage), CohortsDamaged (number of cohorts damaged due to disease), CohortsKilled (number of cohorts completely removed due to disease), MortalityBiomass (sum of cohort biomass removed due to disease), and Absent (proportion of landscape with absent pathogen due to LethalTemp).

# Example File

LandisData "Root Rot"

Timestep 5

>>InputMap rootrot\_init\_map.img << Optional

SpeciesSusceptibility

>> species 1st 2nd

pinustro 0.5 0.05

pinubank 0.5 0.05

pinuresi 0.5 0.05

LethalTemp -24

PhWet 3

PhDry 150

PhMax 250

MinProbID 0.10

MaxProbDI 0.85

OutputMapName "RootRot/RootRot-{timestep}.img"

TOLPMapName "RootRot/TOLP-{timestep).img"

LethalTempMapName “RootRot/LethalTemp-{timestep}.img:

TotalBiomassRemovedMapName “RootRot/TotalBiomassRemoved-{timestep}.img”

SpeciesBiomassRemovedMapName “RootRot/BiomassRemoved-{species}-{timestep}.img”

EventLog "RootRot/RootRot-events.csv"

SummaryLog "RootRot/RootRot-summary.csv"