LANDIS-II Root Rot v1.0
Extension User Guide

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1 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.* This extension is only compatible with the PnET-Succession extension due to its reliance on soil moisture and temperature variables that are currently only provided by this version of succession.

The Root Rot extension described here is the model first presented 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.

1.1 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 Uninfected (U), 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, temperature). Cells that are Infected (I) or Diseased (D) only revert to a status of Uninfected (U) 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 air temperature falls below the lethal temperature, the pathogen is eliminated. Those cells can subsequently be re-infected when the temperature returns 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 applied as proportions of the cohort biomass to be removed when the site is Diseased.

1.1.1 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 air 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).

$$p(Presence) = \frac{(ExtremeTmin - LethalTemp)}{ABS(LethalTemp)}$$

where ExtremeTmin is the extreme minimum monthly air 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.

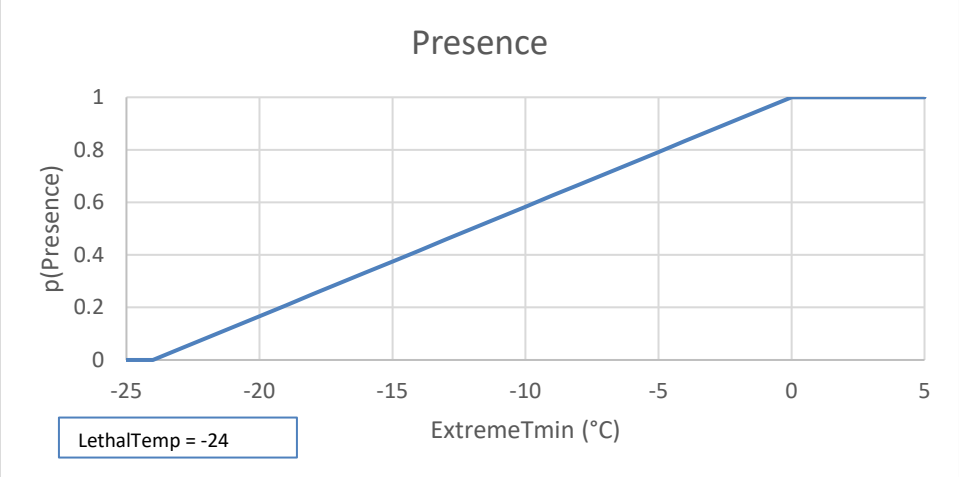

Figure 1. Example p(Presence) curve given a LethalTemp of -24°C.

1.2 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, and can also be influenced by soil temperature.

The soil moisture impacts are determined by evaluating the current soil moisture condition (averaged across months with air temperature above 0°C) relative to threshold values defined by the user. The soil moisture condition is represented by soil water pressure head (Ψ, 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.

The soil temperature impacts are determined by evaluating the temperature at a soil depth of 10 cm, where soil temperature is a function of air temperature, and soil thermal conductivity, as modeled within the PnET-Succession extension. The soil temperature impact on the pathogen uses the monthly soil temperature at the defined depth across all months within the timestep that have average air temperatures above 0°C.

1.2.1 Uninfected (U) Cells

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

1.2.1.1 Uninfected (U) to Infected (I)

Under moist conditions (pressure head (Ψ) < phDry) it is possible for a site to progress from U to I. The probability of U converting to I [p(U->I)] is an average of the monthly growing season (air temperature > 0) probabilities $p_m(U \rightarrow I)$, which are calculated from a monthly Wetness Index.

Wetness Index

Cook (1973) reported optimal growth for *P. cinnamomi* at soil water potentials of - 5 bars, and Weste and Ruppin (1977) found that soils with water potential lower than -5 bars began to limit populations, and soils with potentials of -10 or lower reduced populations to zero. A wetness index (WI) is calculated as 1.0 for water potential greater than -5 bars (wetter), and 0.0 for water potential less than -10 bars (drier). WI decreases linearly from 0 to 1 for water potential between -10 (102 m) and -5 bars (51 m).

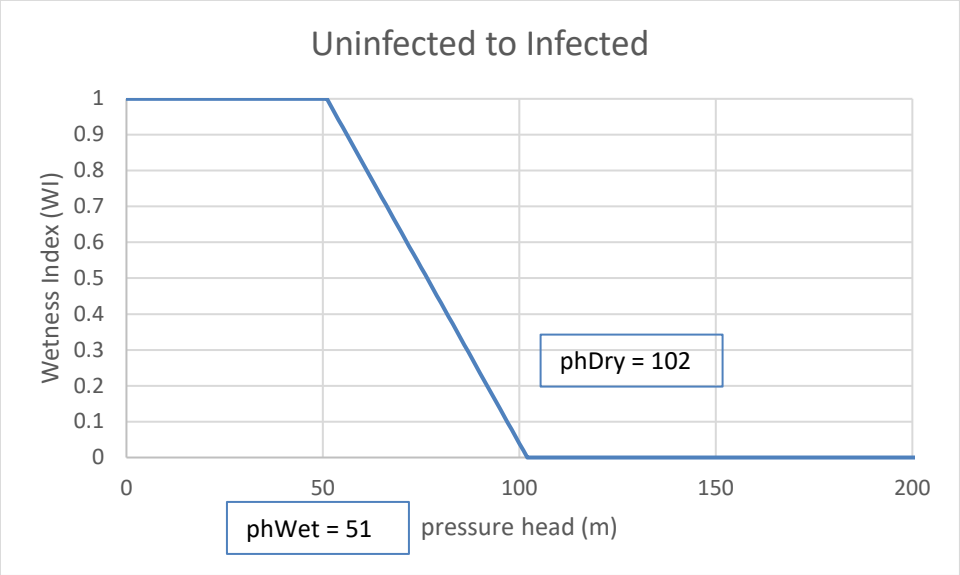

Figure 2. Example of the Wetness Index (WI), given a phWet value of 51 and phDry value of 102.

The phWet and phDry parameters are set within the extension input file, and the values presented here (phWet = 51 and phDry = 102) are not hardcoded in the model, but provided as suggestions based on Weste and Ruppin (1977).

Soil texture is believed to impact the soil moisture conditions that influence pathogen populations through differing abilities to hold water in the soil (Weste and Ruppin 1977). A soil modifier is used along with WI to account for differences in soils. The data from Weste and Ruppin (1977; Figures 4-6) were fit with a linear regression model relating the population density index (PDI, rescaled to range 0-1) to estimated WI (from water potential) and soil field capacity (FC), estimated from site soil descriptions including soil depth and texture. Calculations from Saxton and Rawls (2004) used texture class and percent clay to estimate soil field capacity (cm water) for the Weste and Ruppin (1977) study sites: Wilson's Promontory = 6.53 cm, Brisbane Ranges = 1.96 cm, Narbethong = 44.64 cm. The fitted relationship between rescaled PDI, WI and FC (with an interaction between WI and FC) had an adjusted-R^2 of 0.3134 and p-value of 0.0001999.

$$PDI = 0.006711 + 0.556566 \times WI + 0.013227 \times FC - 0.008511 \times WI \times FC$$

PDI as a relative population index is used in this extension to represent the monthly probability of transition from U to I ($p_m(U \rightarrow I)$).

Average p(U→I)

An average transition probability (p(U→I) is calculated for each succession timestep, across all cohorts for all growing season months in the timestep, with limitations based on soil temperature. A minimum infection temperature parameter (MinSoilTemp) defines a soil temperature below which pathogen populations drop and do not cause infection. For any month with soil temperatures below MinSoilTemp, the p_m(U→I) value used in averaging is 0. This limitation denotes conditions when soils are too cold to support pathogen growth.

Soil Temperature

Soil temperature, at depth *z* (10 cm), is estimated using the same methods presented in Gustafson et al. (In Review). T_{soil} at month *m* is estimated as described for the LPJ DGVM in the appendix of Sitch et al. (2003):

$$T_{soil}(m) = T_{ave} + A \times exp\left(\frac{-z}{d}\right) \times \sin\left(\Omega m - \frac{z}{d}\right)$$

where T_{ave} is average air temperature for month *m*, *A* is the amplitude of air temperature over the previous 12 months, *d* is the damping depth (m), and **Ω** is the angular frequency of oscillation (radians/month). The damping depth, *d*, and angular frequency of oscillation (**Ω**) are calculated as:

$$d = \sqrt{\frac{2k}{\Omega}} \qquad [2]$$

$$\Omega = \frac{2\pi}{12} \qquad [3]$$

where *k* is the thermal diffusivity ($mm^2\ mo^{-1}$) of the soil.

Thermal diffusivity (*k*) is estimated using the methods of Jong van Lier and Durigon (2013) and Farouki (1986), with inputs of total porosity (m^3/m^3), water content (m^3/m^3) and fraction clay (proportion), which make it dynamically dependent on the soil texture and its water content each month.

1.2.1.2 Uninfected (U) to Diseased (D)

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

p(U→D) = p(U→I) * p(I→D)

1.2.2 Infected (I) Cells

Cells that are Infected (I) can transition to Uninfected (U) or Diseased (D) states.

1.2.2.1 Infected (I) to Uninfected (U)

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

1.2.2.2 Infected (I) to Diseased (D)

The probability of I converting to D [p(I→D)] is bimodal. The probability at pressure head values below phDry follow the value of WI as used above (see 1.2.1.1), except with the minimum probability constrained to be at or above the parameter minProbID. At moderate pressure head, the probability of disease development can be greater than 0, which is set by minProbID. Unlike p(U→I) above, probability p(I→D) increases from minProbID at phDry to 1 at phMax.:

p(I→D) =

If ($\Psi \leq$ phDry): Maximum(WI, minProbID);

If($\Psi >$ phMax): 1;

If(phDry $< \Psi \leq$ phMax): m1 * ph + b1;

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

b1 = minProbID – (phDry * m1);

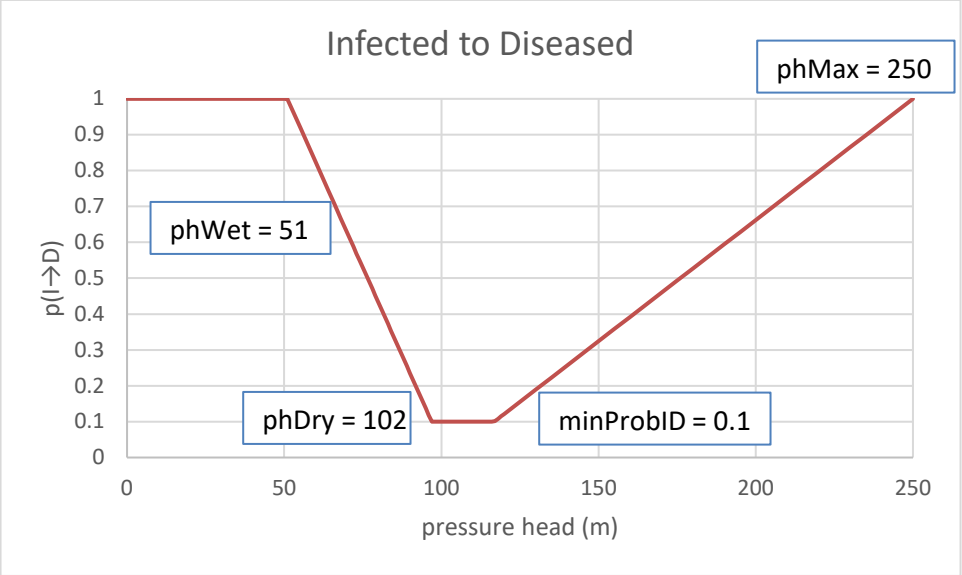

Figure 3. Example probability of transition from Infected to Diseased, given phWet = 51, phDry = 102, phMax = 250, and minProbID = 0.1.

1.2.3 Diseased (D) Cells

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

1.2.3.1 Diseased (D) to Uninfected (U)

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

1.2.3.2 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).

p(D→I) =

If all Susceptibility(i) == 0: 1;

If (Ψ < phWet): 0;

If (Ψ > phDry): 0;

If($\Psi \leq$ (phDry – phWet)/2): m2 * Ψ + b2;

m2 = 1/((phDry – phWet)/2 - phWet);

b2 = -1*phWet * m2;

If(Ψ > (phDry – phWet)/2), m3 * Ψ + b3;

m3 = 1/((phDry – phWet)/2 - phDry);

b3 = -1*phDry * m3

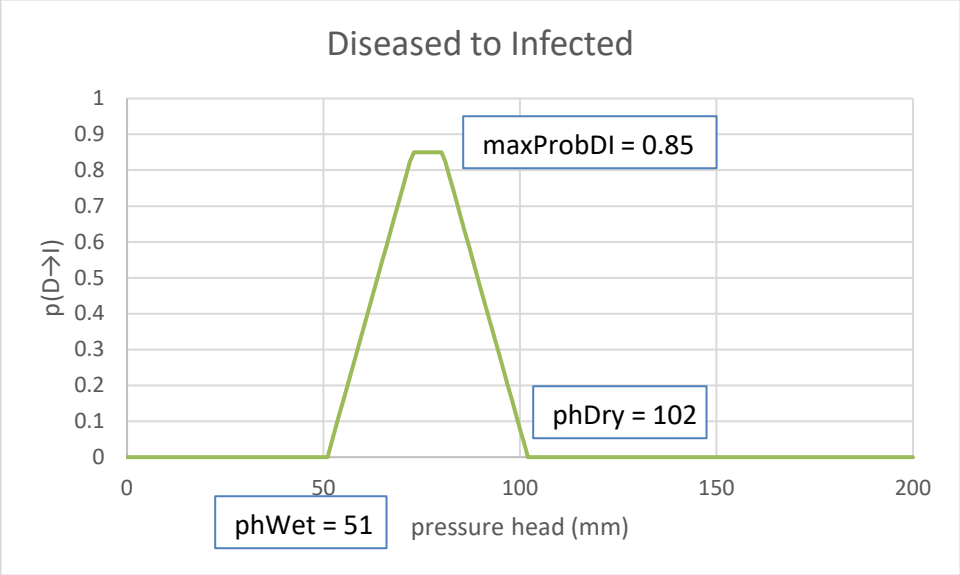

Figure 4. Example probability of transition from Diseased to Infected, given values of phWet = 51, phDry = 102, and maxProbDI = 0.85.

1.3 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 (2.4), 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.

1.4 Major Releases

This is the first major release of this extension.

1.5 Minor Releases

1.6 References

Cook, J. R. 1973. Influence of low plant and soil water potentials on diseases caused by soil-borne fungi. Phytopathology 63, 451-7.

Farouki, O.T. 1986. Thermal properties of soils. California, Trans. Tech. 136p. (Series on Rock and Soil Mechanics, 11)

Gustafson, E. J., B. R. Miranda, T. J. Dreaden, C. C. Pinchot and D. F. Jacobs. In Prep. Beyond blight: *Phytophthora* root rot under climate change limits populations of reintroduced American chestnut.

Jong van Lier, Q. de and A. Durigon. 2013. Soil thermal diffusivity estimated from data of soil temperature and single soil component properties. Revista Brasileira de Ciência do Solo, 37(1), 106-112. https://doi.org/10.1590/S0100-06832013000100011

Saxton, K. E. and W. J. Rawls. 2004. Soil water characteristic equations.xls. Online database (http://hrsl.arsusda.gov/SPAW/SPAWDownload.html)

Weste, G. and P. Ruppin, 1977. *Phytophthora cinnamomi* population densities in forest soils. Australian Journal of Botany, 25:461-475.

1.7 Acknowledgements

2 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.

2.1 LandisData

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

2.2 Timestep

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

2.3 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 Uninfected (1), Infected (2) and Diseased (3) status. If an input map is not provided, the model assumes all cells begin as Uninfected (1).

2.4 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).

SpeciesSusceptibility values are used to determine the damage caused to species when a site is diseased (see 1.3). Initial susceptibility is applied the first time a cohort is damaged by disease, and secondary susceptibly is applied each time a cohort is damaged by disease after the first instance.

2.5 LethalTemp

The minimum air temperature (°C) below which the pathogen cannot survive. Numeric value ≤ 0.

2.6 MinSoilTemp

The minimum soil temperature below which the pathogen cannot transition from Uninfected to Infected. Value: Numeric. Units: degrees C.

2.7 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 Uninfected 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. Units: meters water.

2.8 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. Units: meters water.

2.9 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. Units: meters water.

2.10 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.

2.11 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.

2.12 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').

2.13 TOLDMapName (optional)

The path and filename template for the Time of Last Disease (TOLD) 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').

2.14 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').

2.15 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').

2.16 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').

2.17 EventLog (optional)

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

2.18 SummaryLog (optional)

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

3 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.

3.1 Root Rot Infection Output Maps

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

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

3.2 Time of Last Disease (TOLD) Maps

Time of Last Disease maps are produced at each extension timestep if a path and filename are provided for the TOLDMapName 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.

3.3 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.

3.4 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/m^2.

3.5 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/m^2.

3.6 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/m^2).

3.7 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), UninfectedSites (proportion of active cells with status of Uninfected), InfectedSites (proportion of active cells with status of Infected), DiseasedSites (proportion of active cells with status of Diseased), DamageSites (proportion of active cells that had some cohort damage), ColdKilledSites (proportion of active cells where the pathogen is absent due to LethalTemp), 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).

4 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      -30     <<degrees C
MinSoilTemp     10      <<degrees C
PhWet           51      <<units=pressure head
PhDry           102     <<units=pressure head
PhMax           250     <<units=pressure head
MinProbID       0.10
MaxProbDI       0.85

OutputMapName       "RootRot/RootRot-{timestep}.img"  << Optional
TOLDMapName             "RootRot/TOLD-{timestep).img"  << Optional
LethalTempMapName       “RootRot/LethalTemp-{timestep}.img:  << Optional
TotalBiomassRemovedMapName      “RootRot/TotalBiomassRemoved-{timestep}.img”  << Optional
SpeciesBiomassRemovedMapName    “RootRot/BiomassRemoved-{species}-{timestep}.img”  << Optional
EventLog        "RootRot/RootRot-events.csv"  << Optional
SummaryLog  "RootRot/RootRot-summary.csv"
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