LANDIS-II v

Extension User Guide

Brian R. Sturtevant1

Eric J. Gustafson1

Hong S. He2

Robert M. Scheller3

Brian R. Miranda1

1USFS North Central Research Station

2University of Missouri-Columbia

3University of Wisconsin-Madison

Last Revised:

# Table of Contents

[1 Introduction 2](#_Toc318707049)

[1.1 Modifications to Budworm BDA 2](#_Toc318707050)

[2 Biological Disturbance Agents 4](#_Toc318707051)

[2.1 Overview of BDA 4](#_Toc318707052)

[2.2 Site resource dominance 5](#_Toc318707053)

[2.2.1 Site resource modifiers 5](#_Toc318707054)

[2.3 Neighborhood resource dominance 6](#_Toc318707055)

[2.4 Regional outbreak status 6](#_Toc318707056)

[2.5 BDA effects 6](#_Toc318707057)

[2.6 BDA dispersal 8](#_Toc318707058)

[2.6.1 Epicenters 8](#_Toc318707059)

[2.6.2 Spatial outbreak zones 9](#_Toc318707060)

[2.7 References 11](#_Toc318707061)

[2.8 Acknowledgements 11](#_Toc318707062)

[3 Input Files 12](#_Toc318707063)

[3.1 Input File Rules 12](#_Toc318707064)

[3.2 Input File Parameters 12](#_Toc318707065)

[3.2.1 Extension title, time step 12](#_Toc318707066)

[3.2.2 Output map names 12](#_Toc318707067)

[3.2.3 SRD map names (Optional) 12](#_Toc318707068)

[3.2.4 NRD map names (Optional) 12](#_Toc318707069)

[3.2.5 Vulnerability map names (Optional) 13](#_Toc318707070)

[3.2.6 Log file 13](#_Toc318707071)

[3.2.7 BDA entries 13](#_Toc318707072)

[3.3 Individual BDA Parameter Files 13](#_Toc318707073)

[3.3.1 Regional Outbreak Status parameters 14](#_Toc318707074)

[3.3.2 Dispersal Parameters 15](#_Toc318707075)

[3.3.3 Neighborhood Resource Dominance parameters 16](#_Toc318707076)

[3.3.4 Budworm Model Inputs 16](#_Toc318707077)

[3.3.5 Ecoregion Modifiers 17](#_Toc318707078)

[3.3.6 Disturbance Modifiers 17](#_Toc318707079)

[3.3.7 Species parameters 17](#_Toc318707080)

[3.3.8 Ignored species (Optional) 18](#_Toc318707081)

[4 Output Files 20](#_Toc318707082)

[4.1 BDA Severity Map 20](#_Toc318707083)

[4.2 BDA Site Resource Dominance (SRD) Map (Optional) 20](#_Toc318707084)

[4.3 BDA Neighborhood Resource Dominance (NRD) Map (Optional) 20](#_Toc318707085)

[4.4 BDA Site Vulnerability Map (Optional) 20](#_Toc318707086)

[4.5 BDA Log file 20](#_Toc318707087)

# Introduction

This document describes the extension for the LANDIS-II model. For information about the model and its core concepts, see the *LANDIS‑II Conceptual Model Description.* This is a modified version of the Biological Disturbance Agent v2.0 extension, with features specific to the spruce budworm. The Budworm BDA extension will work with both age-only and biomass succession. However, it only uses cohort age information. Partial cohort removal and growth reductions are not possible. Much of this documentation has been copied directly from the Biological Disturbance Agent v2.0 User Guide.

## Modifications to Budworm BDA

The major modifications from the original Budworm BDA extension are listed here.

* + 1. User-defined suitability class thresholds

New user inputs now define the vulnerability thresholds to reach the different severity classes (1-3).

* + 1. Balsam fir advanced regeneration survival

Balsam fir (‘abiesbals’) cohorts are all removed from a disturbed site, except those below a user-defined age limit can be allowed to survive an outbreak. The intent is to account for the advanced regeneration strategy of balsam fir, where small, young cohorts exist under the main canopy and are able to survive a budworm outbreak, but older cohorts are highly susceptible.

* + 1. User-defined Site Resource Dominance

The user can now define the Site Resource Dominance (SRD) value for each host class (Minor, Secondary, Major). These were previously hard-coded to be 0.33, 0.66, and 1.0, respectively.

* + 1. Stochastic mortality

If a site is disturbed (based on biological disturbance probability [BDP], described in 2.1 below) the mortality of individual cohorts is now a probabilistic function of the vulnerability probability (VulnProb) of the corresponding susceptibility class for the cohort. The user defines which species and ages fall into each susceptibility class (1-3), and the probability of cohort mortality for each class.

* + 1. Dynamic fuel system interaction

Host species can now be flagged as Canadian Fuel System (CFS) conifers, which allows the dead cohorts to be considered when the Dynamic Fire and Fuel System extensions determine fuel types. The presence of dead conifers allows the use of specific budworm-kill fuel types from the CFS.

# Biological Disturbance Agents

## Overview of BDA

Biological disturbances, such as insect and disease outbreaks, are critically important agents of forest change that cause tree mortality at scales ranging from individual trees of a single SPP to entire regions. The BDA module is designed to simulate tree mortality following major outbreaks of insects and/or disease, where major outbreaks are defined as those significant enough to influence forest succession, fire disturbance, or harvest disturbance at landscape scales.

Biological disturbances in LANDIS are probabilistic at the site (i.e., cell) scale, where each site is assigned a probability value called ***biological disturbance probability (BDP)*** and compared with a uniform random number to determine whether the site is disturbed or not. Disturbance causes species- and cohort-specific mortality in the cell. In the simplest case, BDP equals *Site Resource Dominance*, a number that ranges from 0 (no host) to 1 (most preferred host) based on the tree species and age cohorts present on the site. Four additional optional factors may also modify BDP:

1) Environmental and/or other disturbance-related stress (*Site Resource Modifiers*).

2) The abundance of host in the neighborhood surrounding the site (*Neighborhood Resource Dominance*).

3) User-defined temporal functions (e.g., cyclic, random, or chronic) that affect the temporal pattern of disturbances across the entire spatial domain of the simulation (*Regional Outbreak Status*).

4) Spatial epidemic zones defined via simulated dispersal of a BDA through a heterogeneous landscape (*Dispersal*).

The above combinations of optional factors allow the BDA module to accommodate several types of destructive insect and disease species, and more than one BDA may be simulated concurrently to examine their interactions.

More detail on the BDA module and its behavior can be found in Sturtevant *et al.* (2004). In this users guide, we use the term BDP for site vulnerability, all references to “vulnerability” or “susceptibility” been changed to either tolerance class (for species) or susceptibility class (for species age cohort). The rank order of these two classes is also consistent with the design of the other disturbance modules. Finally, all references to the “severity” class of a disturbance have been changed to “intensity” class.

## Site resource dominance

Site resource dominance (SRD) indicates the relative quantity/quality of food resources on a given site and is a combined function of tree species composition and the age cohorts present on that site. The relative resource value of a given species cohort is defined by its host preference class, where preferred host = 1.0, secondary host = 0.66, minor host = 0.33, and nonhost = 0. The BDA module compares a look-up table with the species cohort list generated by LANDIS to calculate SRD using one of two methods: 1) the maximum host preference class present, and 2) an average resource value of all tree species present, where the resource value of each species is represented by the cohort with the oldest host preference. Species identified as “ignored” do not contribute to the calculation of average resource value; whereas nonhost species that are not ignored contribute a value of 0.

### Site resource modifiers

Site resource modifiers are optional parameters used to adjust SRD to reflect variation in the quality of food resources introduced by both site environment (i.e., land type) and recent disturbance. Both land type modifiers (LTMs) and disturbance modifiers (DMs) can range between –1 and +1, and will be added to the SRD value of all active sites where host species are present. LTMs are assumed to be constant for the entire simulation, while DMs decline linearly with the time since last disturbance. Disturbances that may affect a given BDA include fire and wind. Disturbance effects from another BDA and user-specified harvest prescriptions are currently not implemented. SRD is then modified by LTM and the sum of all DMs:

SRDm = SRD + LTM + (DMwind + DMfire + ...) (1)

The user should calibrate the above modifiers to reflect the relative influence of species composition/age structure, the abiotic environment, and recent disturbance. For example, an LTM value of 0.33 is equal to a full step increase in disturbance intensity above that calculated using species composition alone.

## Neighborhood resource dominance

Several recent studies suggest that the landscape context of a site also influences the probability and intensity of disturbance (Cappuccino *et al.* 1998; Radeloff *et al.* 2000). A neighborhood effect is modeled in LANDIS as the mean SRDm of each cell within a user-defined radius *R*, using one of three radial distance weighting functions listed in increasing order of local dominance: uniform, linear, and Gaussian (Orr 1996; see Sturtevant *et al.* 2004). Neighborhood resource dominance (NRD) is calculated for all sites containing host species (i.e., SRD > 0). An optional subsampling procedure calculates the NRD for every other site, and the NRD of the remaining sites are estimated by the mean NRD of adjacent sites in the four cardinal directions. For large neighborhoods, this subsampling routine can increase the processing speed of the BDA by over 40% (Sturtevant *et al.* 2004).

## Regional outbreak status

Several simple temporal patterns may be simulated in the BDA module to represent general outbreak trends for the entire study landscape. Temporal patterns in a given BDA are assumed constant for the length of the simulation, and are defined by a suite of temporal disturbance functions that define the landscape scale intensity of the BDA at a given time step, termed Regional Outbreak Status (ROS). ROS units are integer classes ranging from 0 (no outbreak) to 3 (intense outbreak). The time to the next outbreak is calculated following each outbreak event using either a uniform or a normal random function.

The magnitude of simulated regional outbreak severities is controlled by the MinROS and MaxROS parameters. MinROS defines the “background” outbreak activity that will occur in each time step. Outbreak type (“TempType” in the BDA parameter file) determines whether outbreaks are binary (either MinROS or MaxROS; TempType = “pulse”) or if the ROS can range between those values (TempType = “variable pulse”). For the variable pulse outbreak type, the ROS value is randomly selected for each outbreak event from the range between MinROS+1 and MaxROS.

## BDA effects

Both the probability that a site is disturbed by a given BDA and the intensity of that disturbance are controlled by *biological disturbance probability (BDP)*. BDP is defined by the following equation:

BDP = *a* ·{[SRDm + (NRD\*NW)]/(1+NW)} · (ROS/3) (2)

where *a* is a user-defined calibration parameter (by default, *a* should = 1); SRDm = the species and age composition of the site (SRD), optionally modified by land type and/or past disturbance (Equation 1); NRD = the mean SRDm of sites within the neighborhood surrounding a site; NW = Neighborhood Weight, a parameter designed to define the relative importance between site and neighborhood resources; and ROS = Regional Outbreak Status.

Sites are selected for disturbance by comparing BDP with a uniform random number ranging from 0-1. Note that while equation 1 allows SRDm to exceed 1.0, by definition BDP cannot exceed 1.0 (i.e., 100% probability of disturbance). SRDm values exceeding 1.0 can therefore only further enhance the probability of disturbance if additional variables such as neighborhoods or temporal disturbance functions are applied. Once a site is disturbed, the disturbance intensity class is calculated for the site to determine which species cohorts die, based on their tolerance class. Disturbance intensity is a direct function of BDP, where the user can define the thresholds between classes. The user inputs Class2\_SV and Class3\_SV set these values, such that BDP < Class2\_SV = intensity class 1; Class2\_SV < BDP < Class3\_SV = intensity class 2; BDP > Class3\_SV = intensity class 3 disturbance. Unlike fire or wind disturbance, there is no predefined function that estimates susceptibility class as a function of species tolerance class. Instead, susceptibility class is defined directly by a lookup table similar to that used for host preference class.

In this modified extension, the mortality of individual cohorts is a probabilistic function of the vulnerability probability (VulnProb) of the corresponding susceptibility class for the cohort and the BDP. The user defines which species and ages fall into each susceptibility class (1-3), and the probability of cohort mortality for each class. The same random number used to select sites for disturbance (above) is compared to the site BDP \* cohort VulnProb to determine if a cohort is killed. The exception to this rule is that all cohorts of ‘abiebals’ greater than BFAgeCutoff are killed. Cohorts of ‘abiebals’ less than or equal to BFAgeCutoff, follow the same rules as other species cohorts.

If no other BDA options are simulated, the BDA module finishes by updating species cohort lists, updating the time since last biological disturbance, outputting a map of BDA disturbance events, and updating the BDA log (Figure 2).

## BDA dispersal

Some epidemics occur at spatial scales smaller than the typical simulation area of LANDIS. Accounting for BDA dispersal and spread will be necessary for these cases. The BDA dispersal procedure defines smaller spatial zones within the modeled landscape where insect disturbance may occur within a given time step. Within these restricted spatial zones, the BDA operates exactly the same as if the outbreak were synchronous. Note that the dispersal procedures for the BDA module are still under development.

### Epicenters

Epicenters are defined as central sites from which a BDA may disperse. There are three types of epicenters: 1) initial epicenters–sites randomly selected at time = 0 to initiate new outbreak zones in the first time step; 2) seed epicenters–sites randomly selected at each time step an outbreak occurs to initiate new outbreak zones outside the outbreak zone defined at time *t–1* during the simulation; and 3) outbreak zone epicenters–sites randomly selected from within the last outbreak zone (i.e., time = t-1) to continue the spread of an outbreak in consecutive time steps. The BDA module will randomly select epicenters from a subset of sites that are above user-specified threshold site vulnerability. Initial epicenters can be selected anywhere in the landscape where sites meet this criterion; seed and outbreak zone epicenters are selected from outside and inside (respectively) the outbreak zone defined at time *t–1*.

The number of initial epicenters is a simple user-defined parameter. The following negative exponential equation determines how many new epicenters will be generated both inside and outside existing outbreak zones:

*Yi* = *Ai*\*exp (- *ciXi*) (3)

Here, *Ai* = the number of qualified potential epicenter sites (i.e., the number of sites either inside or outside the last outbreak zone where BDP > the *epidemic threshold*), *Xi* = the current number of selected epicenters of a given type, and *Yi* = the number of sites that can be checked. Coefficient *ci* is a user-defined parameter that controls statistically how many new epicenters may be generated for either seed epicenter or outbreak zone epicenter type. The number of epicenters will decrease with increasing *c*.

### Spatial outbreak zones

Outbreak zones are defined using dispersal routines that spread from an epicenter to a circular boundary with a radius defined by the annual dispersal distance of a BDA, multiplied by the number of years in a time step (i.e., 10). An outbreak zone either automatically expands to this maximum limit (termed “regular dispersal”) or occurs as a percolation process through a binary landscape, where it may only spread through sites containing host tree species. Ability to spread over nonhost cells is defined by a user-defined neighborhood rule (*sensu* Gardner 1999). Available structuring elements include 4, 8, 12, and 24 nearest neighbors (Figure 1).

The dispersal routines will attempt to spread each epicenter to its maximum dispersal distance using the neighborhood rule defined by the user. An outbreak zone from a given epicenter with may overlap one created from a nearby epicenter. The cumulative area of all zones created during the time step defines the spatial extent over which the BDA may disturb sites during that time step.

**Figure 1.-Available structuring elements.**

|  |  |  |
| --- | --- | --- |
| 1 | 2 | 3 |
| 8 | X | 4 |
| 7 | 6 | 5 |

8-Neighbor Rule

|  |  |  |
| --- | --- | --- |
|  | 1 |  |
| 4 | X | 2 |
|  | 3 |  |

4-Neighbor Rule

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | 9 |  |  |
|  | 8 | 1 | 2 |  |
| 12 | 7 | X | 3 | 10 |
|  | 6 | 5 | 4 |  |
|  |  | 11 |  |  |

12-Neighbor Rule

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| 23 | 24 | 9 | 10 | 11 |
| 22 | 8 | 1 | 2 | 12 |
| 21 | 7 | X | 3 | 13 |
| 20 | 6 | 5 | 4 | 14 |
| 19 | 18 | 17 | 16 | 15 |

24-Neighbor Rule

Figure 2.-BDA flow diagram.



## References

Cappuccino, N.; Lavertu, D.; Bergeron, Y.; Regniere, J. 1998. Spruce budworm impact, abundance and parasitism rate in a patchy landscape. Oecologia. 114: 236-242.

Gardner, R. H. 1999. RULE: map generation and spatial analysis program. In: Landscape ecological analysis: issues and applications. New York, NY: Springer-Verlag: 280-303.

Radeloff, V.C.; Mladenoff, D.J.; Boyce, M.S. 2000. The changing relation of landscape patterns and jack pine budworm populations during an outbreak. Oikos. 90: 417-430.

Scheller, R.M., Domingo, J.B., 2005a. LANDIS-II Core Model Description. University of Wisconsin-Madison, Madison, WI, USA.

Scheller, R.M., Domingo, J.B., 2005b. LANDIS-II Model v5.0 ­– User Guide. University of Wisconsin-Madison, Madison, WI, USA.

Sturtevant, B. R.; Gustafson, E. J.; Li, W., and He, H. S. Modeling biological disturbances in LANDIS: A module description and demonstration using spruce budworm. Ecological Modelling. 2004.

## Acknowledgements

Funding for the development of LANDIS-II has been provided by the North Central Research Station (Rhinelander, Wisconsin) of the U.S. Forest Service. Valuable contributions to the development of the model and extensions were made by Eric J. Gustafson, and David J. Mladenoff.

# Input Files

## Input File Rules

The input rules for the Biological Disturbance Agent (BDA) extension are identical to those of the LANDIS-II Core Model. Please see the LANDIS-II Core User’s Guide for further instruction.

## Input File Parameters

### Extension title, time step

The first parameter is the title of the input file:

LandisData “Budworm BDA”

The second parameter is the time step in years. For example:

Timestep 15

### Output map names

Several parameters configure the output files. The first parameter, **MapNames**, provides the naming convention for the BDA severity files. The variables {timestep} and {agentName} are provided. **The user must indicate if the output should be placed in a sub-directory. Also, the user must indicate the file extension.** For example:

MapNames budworm/{agentName}-{timestep}.img

### SRD map names (Optional)

The next parameter, **SRDMapNames**, provides the naming convention for the BDA site resource dominance files. This input is optional, and users who do not want SRD output maps should exclude the entire line of input (including the parameter name). The variables {timestep} and {agentName} are provided. **The user must indicate if the output should be placed in a sub-directory. Also, the user must indicate the file extension.** For example:

SRDMapNames budworm/{agentName}-SRD-{timestep}.img

### NRD map names (Optional)

The next parameter, **NRDMapNames**, provides the naming convention for the BDA neighborhood resource dominance files. This input is optional, and users who do not want NRD output maps should exclude the entire line of input (including the parameter name). The variables {timestep} and {agentName} are provided. **The user must indicate if the output should be placed in a sub-directory. Also, the user must indicate the file extension.** For example:

NRDMapNames budworm/{agentName}-NRD-{timestep}.img

### Vulnerability map names (Optional)

The next parameter, **VulnMapNames**, provides the naming convention for the BDA vulnerability files. This input is optional, and users who do not want vulnerability output maps should exclude the entire line of input (including the parameter name). The variables {timestep} and {agentName} are provided. **The user must indicate if the output should be placed in a sub-directory. Also, the user must indicate the file extension.** For example:

VulnMapNames budworm/{agentName}-Vuln-{timestep}.img

### Log file

The next parameter, **LogFile**, indicates the file name and sub-directory for the single log output file. The text file will be in comma delimited format. There is one output file for all agents. Example:

LogFile budworm/bda-log.csv

### BDA entries

Following is a table of BDA entries. Example:

BDAInputFiles budworm.txt

beetle.dat

Each BDA simulated must have a corresponding BDA parameter file. The file names for each are defined here.

## Individual BDA Parameter Files

Each BDA entry requires a separate suite of parameters, contained within the text file indicated above. The following inputs are required:

AgentName budworm

BDPCalibrator 1

SRDMode mean

BDA name will define the name of the disturbance output. BDP Calibrator represents the “*a*” parameter of equation 2. Site Resources Dominance Mode (SRDMode) may be set to either “max” or “mean” (see Section 1.2).

### Regional Outbreak Status parameters

Next are the temporal parameters that control the landscape scale intensity of the BDA at a given time step, termed Regional Outbreak Status (ROS). ROS units are integer classes ranging from 0 (no outbreak) to 3 (intense outbreak).

*TimeSinceLastEpidemic* represents the time in years since the last outbreak.

*TemporalType* valid inputs = pulse or variablepulse. TemporalType determines whether outbreaks are binary (either MinROS or MaxROS – see definitions below; TempType = “pulse”) or if the ROS can range between those values (TempType = “variable pulse”). **Continuous temporal types are still under development and currently not operational.**

*RandomFunction* represents the type of function used to control the pattern of outbreaks. Options are “RFnormal” for a normally distributed random function defined by a mean *μ* and standard deviation *σ*, and “RFuniform” for a uniformly distributed random function defined by a maximum interval (*MaxI*) and a minimum value (*MinI*).

The definition of RandomParameter1 depends on the RandomFunction selected: *μ* if using *RFnormal*, or *MaxI* if using *RFuniform*.

The definition of RandomParameter2 also depends on the RandomFunction selected: *σ* if using *RFnormal*, or *MinI* if using *RFuniform*.

*MaxROS* = Maximum Outbreak Status; defines the maximum intensity of a regional outbreak. Parameter value must be an integer value between 1 (light outbreak) and 3 (intense outbreak).

*MinROS* = Minimum Outbreak Status; defines the “background” outbreak activity that will occur in each time step. Parameter value must be an integer value between 1 (no outbreak) and 3 (intense outbreak). It can equal MaxROS, but cannot exceed it. **If MinROS is greater than zero, epidemics will occur at every BDA time step.**

Example:

>>-------- Regional Outbreak Inputs -------------

TimeSinceLastEpidemic 20 << years

TemporalType pulse << pulse or variablepulse

RandomFuncton RFnormal << RFnormal or RFuniform

RandomParameter1 25

RandomParameter2 10

MinROS 0

MaxROS 3

### Dispersal Parameters

*Dispersal* determines whether dispersal is used. Options are ‘no’ (synchronous) or ‘yes’ (asynchronous; dispersal turned on).

*DispersalRate* defines the annual rate of dispersal in meters per year. The minimum logical value is a function of cell size, whereas the maximum logical value is a function of the map extent, i.e., (cell size / time step) ≤ *DispersalRate* ≥ (max map extent / time step).

*EpidemicThresh* defines the minimum BDP (0-1) required for an Epicenter to be selected.

*InitialEpicenterNum* defines the number of epicenters that will be selected at the time of the first outbreak. This is typically used to initiate an outbreak(s) that will spread over the course of the simulation. [Range = 1 – Number of Active Sites]

*OutbreakEpicenterCoeff* is the “c” parameter corresponding with Equation 3 for epicenters that will start from within the outbreak zone that occurred at time = t-1.

*SeedEpicenter* determines **if** new epicenters will “seed” new outbreaks outside of current outbreak zones. Options are ‘no’ or ‘yes’.

*SeedEpicenterCoeff* is the “c” parameter corresponding with Equation 3 for new epicenters that will start outside of the outbreak zone defined at time = t-1.

*DispersalTemplate* defines the structuring element (i.e., the neighborhood rule) controlling the percolation of the BDA from an epicenter to its dispersal radius defined by DispersalRate×TimeStep. Options are: ‘MaxRadius’ or regular dispersal (i.e., disperse to maximum radius); ‘4N’ = 4-neighbor structuring element; ‘8N’ = 8-neighbor structuring element; ‘12N’ =12-neighbor structuring element; ‘24N’ =24-neighbor structuring element.

Examples:

>>-------- Dispersal Inputs ----------------------

Dispersal yes <<yes or no

DispersalRate 100 <<meters/year

EpidemicThresh 0.3

InitialEpicenterNum 5

OutbreakEpicenterCoeff 0.01

SeedEpicenter yes <<yes or no

SeedEpicenterCoeff 20

DispersalTemplate 4N <<MaxRadius, 4N,

<<8N, 12N, or 24N

### Neighborhood Resource Dominance parameters

Next are Neighborhood Resource Dominance parameters.

*NeighborhoodFlag* determines whether NRD is used in calculating BDP. Options are ‘no’ or ‘yes’.

The *NeighborSpeedUp* flag determines whether the BDA module will use every cell in a neighborhood to calculate Neighborhood Resource Dominance (‘no’), or use the subsampling procedure to calculate NRD (‘yes’).

*NeighborRadius* defines the radius of the neighborhood influence in meters. Logically this variable should not be larger than the extent of the map, but neighborhoods should be at least an order of magnitude smaller than the map extent to avoid excessive edge effects.

*NeighborShape* defines the radial function used to calculate NRD. Valid entries are: uniform, linear, or Gaussian.

*NeighborWeight* (NW) defines the importance of NRD relative to SRD when calculating BDP. [Range: 0.01 - 100]

Examples:

>>-------- Neighborhood Resource Inputs-----------------

NeighborFlag yes <<yes or no

NeighborSpeedUp none <<none, 2x, 3x, or 4x

NeighborRadius 1000 <<meters

NeighborShape uniform <<uniform, linear, or gaussian

NeighborWeight 10

### Budworm Model Inputs

The next section contains parameters added specifically for the Budworm BDA extension.

*Class2\_SV* defines the vulnerability threshold to reach severity class 2. If vulnerability is > 0 and < Class2\_SV, then severity is class 1.

*Class3\_SV* defines the vulnerability threshold to reach severity class 3. If vulnerability is >= Class3\_SV, then severity is class 3.

*BFAgeCutoff* defines the age below which balsam fir cohorts are not killed by a budworm outbreak. This parameter can be set to 0 to allow all cohorts of balsam fir to be killed. For this exception to be applied, the species name for balsam fir must be ‘abiebals’ in the species input file.

Examples:

>>------- Budworm Model Inputs --------

Class2\_SV 0.25

Class3\_SV 0.50

BFAgeCutoff 10

### Ecoregion Modifiers

Next, a table of Land Type Modifiers is provided. Land types (or Ecoregions) need not be listed and need not be listed in order. **The default value is 0.0.** The ecoregion number is listed, followed by the modifier value (-1.0 – 1.0). Example:

>>Ecoregion Modifiers

eco1 0.16

eco26 0.0

eco5 -0.16

### Disturbance Modifiers

Next, a table of Disturbance Modifiers is provided. Disturbance Modifiers need not be listed and need not be listed in any order. The default is NO EFFECT. For each disturbance that may modify the BDA (e.g., Wind, Fire, Harvest, or another BDA), three parameters are required: Disturbance Type, the duration of the modifying effect (in years), and the modifier value (between –1.0 to 1.0) for the first time step following the disturbance. Note that the disturbance modifier value represents the influence of a specific disturbance type on site resource dominance, and is assumed to decline linearly with time since that disturbance for the duration of the modifying effect. Example:

DisturbanceModifiers

>>Type Duration Value

Wind 20 0.33

Fire 10 0.65

### Species parameters

Next, a table of species parameters for the BDA agent. Species need not be listed and may appear in any order. If a species is excluded, the species is never a host. If a species is listed, all 13 parameters must be provided.

Minor, Secondary, and Major *Host Age* indicate the minimum age at which a species enters the respective Host Preference Class. These classes are used to calculate Site Resource Dominance (SRD). A value greater than the tree species longevity (e.g., 999) indicates that the species never reaches the indicated class.

*SRDProb* values for each Host Preference Class (Minor, Secondary, Major) define the SRD values for cohorts in that class. The SRDProb values must range between 0 and 1. The original BDA extension used hard-coded values of 0.33, 0.66, and 1.0 for these values.

*Susceptibility Class Ages* indicate the minimum age at which a species enters a respective Susceptibility Class. These classes determine the age class thresholds of biological disturbance probability (BDP) required to kill a species cohort if a site is disturbed. A value greater than the tree species longevity (e.g., 999) indicates that the species never reaches the indicated class. Cohorts younger than the minimum age for susceptibility class 3 are assigned a susceptibility class of 4, and are immune to the BDA.

*VulnProb* values for each Susceptibility Class (3, 2, 1) define the BDP values for cohorts in that class. This change from the original BDA extension makes the killing of cohorts probabilistic based on the site vulnerability and the susceptibility class of each cohort. The VulnProb values must range between 0 and 1.

*CFSConifer* specifies whether a species is a conifer species with respect to the Canadian Fire and Fuel System. The Dynamic Fire and Fuels System extensions allow conifers killed by the Budworm BDA extension to modify the fuel classes and utilize the budworm-kill specific fuel types in the system. Options are ‘yes’ or ‘no’. Species that are not listed default to ‘no’.

Example:

BDASpeciesParameters

>> | Susceptibility |

>>Species MinorHost 2ndHost MajorHost | Class3 Class2 Class1 | CFS

>>Name Age SRDProb Age SRDProb Age SRDProb | Age VulnProb Age VulnProb Age VulnProb | Conifer?

>> -------------------------------------------------------------------------------------------------

abiebals 0 0.25 20 0.5 40 1.0 0 0 20 0.5 50 1.0 yes

piceglau 0 0.25 20 0.5 40 1.0 0 0 20 0.15 50 0.42 yes

picemari 0 0.25 20 0.5 40 1.0 0 0 20 0 50 0 yes

### Ignored species (Optional)

The keyword IgnoredSpecies, followed by a list of species (each species on a separate line), define the species that should not be included in calculations of site resource dominance. These species should be those that do not affect the resource value to the disturbance agent either positively or negatively. Nonhost species that do not appear in this list are assumed to provide a 0 resource value, which, when averaged with host resource values, reduces the overall resource value. If a species appears in both the BDASpeciesParameters table and the IgnoredSpecies list, the IgnoredSpecies list will override the other parameters for the species, and it will be ignored in calculations of site resource dominance. Example:

IgnoredSpecies

pinuresi

pinustro

# Output Files

## BDA Severity Map

The map of BDA severity is labeled 0 for non-active sites, 1 for active and not disturbed sites, [BDA severity + 1] for all disturbed sites. A map is produced for each BDA time step.

## BDA Site Resource Dominance (SRD) Map (Optional)

The map of BDA SRD is labeled with the SRD value ranging from 0 to 100. A map is produced for each BDA time step.

## BDA Neighborhood Resource Dominance (NRD) Map (Optional)

The map of BDA NRD is labeled with the NRD value ranging from 0 to 100. A map is produced for each BDA time step.

## BDA Site Vulnerability Map (Optional)

The map of BDA site vulnerability is labeled with the vulnerability value ranging from 0 to 100. A map is produced for each BDA time step.

## BDA Log file

The event log is a text file that contains information about every event over the course of the scenario: year, initiation cell coordinates, total event size (number of sites), number of damaged sites, number of cohorts killed total, mean BDA severity across all sites.