

# LANDIS-II Biological Disturbance Agent v1.1 Extension User Guide

Brian R. Sturtevant<sup>1</sup>

Eric J. Gustafson<sup>1</sup>

Hong S. He<sup>2</sup>

Robert M. Scheller<sup>3</sup>

<sup>1</sup>USFS North Central Research Station

<sup>2</sup>University of Missouri-Columbia

<sup>3</sup>University of Wisconsin-Madison

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# 1 Introduction

This document describes the **Biological Disturbance Agent** extension for the LANDIS-II model. For information about the model and its core concepts, see the *LANDIS-II Conceptual Model Description*. This version of the BDA 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.

## 1.1 What's new in version 1.1

This document describes the current version (1.1) of the extension. The differences between this version and the previous version (1.0) include:

- Fixed a bug that caused the extension to crash the first timestep it ran.
- Fixed a bug where the extension was not providing information about the site it was disturbing to the cohort module.

## 2 Biological Disturbance Agents

### 2.1 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.

## 2.2 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.

### 2.2.1 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:

$$SRD_m = SRD + LTM + (DM_{wind} + DM_{fire} + ...) \quad (1)$$

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.

## 2.3 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  $SRD_m$  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).

## 2.4 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.

## 2.5 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:

$$BDP = a \cdot \{ [SRD_m + (NRD \cdot NW)] / (1 + NW) \} \cdot (ROS/3) \quad (2)$$

where  $a$  is a user-defined calibration parameter (by default,  $a$  should = 1);  $SRD_m$  = the species and age composition of the site (SRD), optionally modified by land type and/or past disturbance (Equation 1); NRD = the

mean  $SRD_m$  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  $SRD_m$  to exceed 1.0, by definition  $BDP$  cannot exceed 1.0 (i.e., 100% probability of disturbance).  $SRD_m$  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  $BDP < 0.33$  = intensity class 1;  $0.33 < BDP < 0.67$  = intensity class 2;  $BDP > 0.67$  = 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. Cohort mortality follows these rules: intensity class 1 disturbance kills all susceptibility class 1 cohorts, intensity class 2 disturbance kills susceptibility classes 1 and 2, and intensity class 3 disturbance kills susceptibility classes 1-3. Susceptibility class 4 species age cohorts, including all non host species, cannot be disturbed by the BDA. 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).

## 2.6 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.

### 2.6.1 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:

$$Y_i = A_i * \exp(-c_i X_i) \quad (3)$$

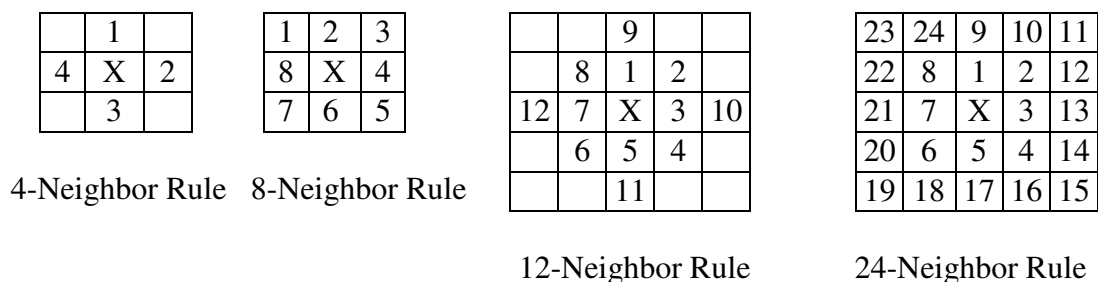
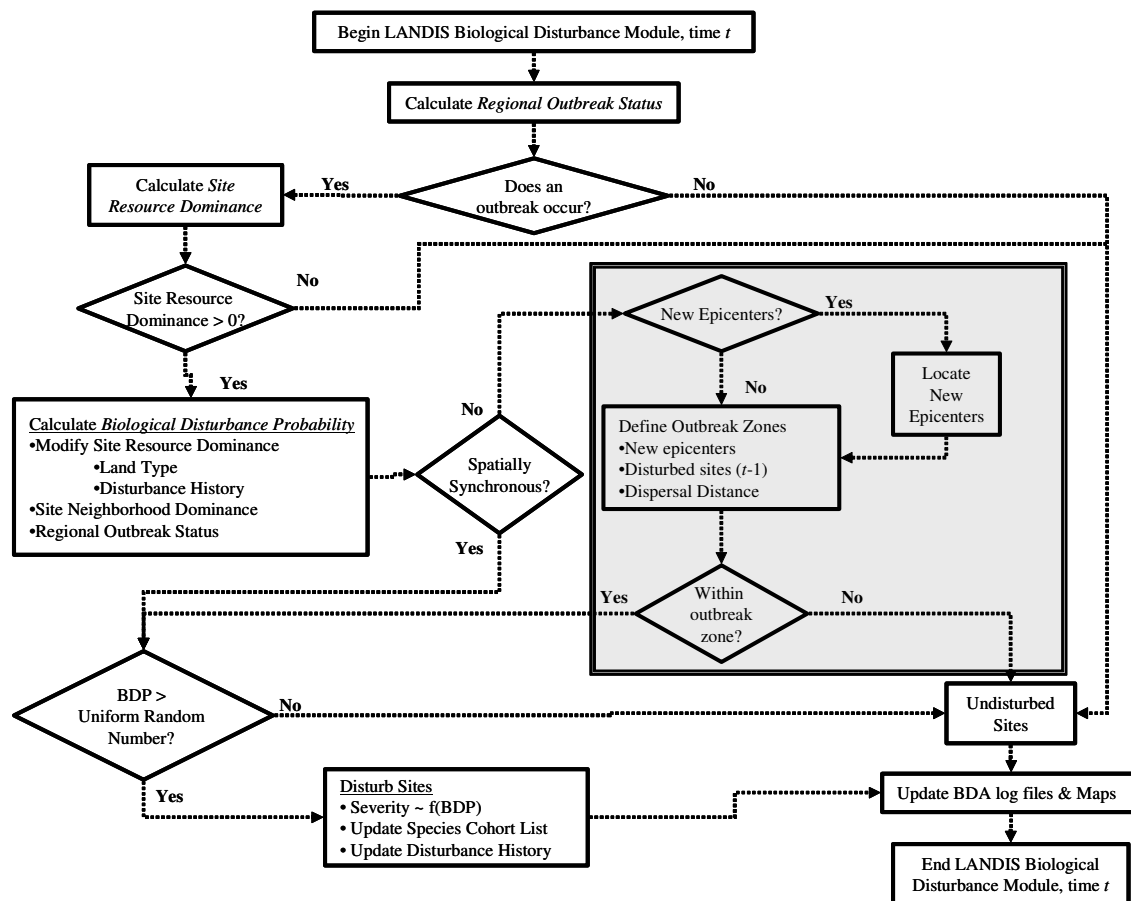
Here,  $A_i$  = the number of qualified potential epicenter sites (i.e., the number of sites either inside or outside the last outbreak zone where  $BDP > \text{the epidemic threshold}$ ),  $X_i$  = the current number of selected epicenters of a given type, and  $Y_i$  = the number of sites that can be checked. Coefficient  $c_i$  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  $c$ .

### 2.6.2 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.****Figure 2.-BDA flow diagram.**

## 2.7 References

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- 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.
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## 2.8 Acknowledgements

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## 3 Input Files

### 3.1 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.

### 3.2 Input File Parameters

#### 3.2.1 Extension title, time step

The first parameter is the title of the input file:

```
LandisData "Base BDA"
```

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

```
Timestep 15
```

#### 3.2.2 Output map names

Two parameters configure the output files. The first parameter, **MapNames**, provides the naming convention for the fire 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 bda/{agentName}-{timestep}.gis
```

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 bda/bda-log.csv
```

#### 3.2.3 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.

### 3.3 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).

#### 3.3.1 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.

*TempType* valid inputs = pulse, variablepulse, and continuous. *TempType* 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  $\mu$  and standard deviation  $\sigma$ , and “RFuniform” for a uniformly distributed random function defined by a minimum interval (*MinI*) and a maximum value (*MaxI*).

The definition of RandomParameter1 depends on the RandomFunction selected:  $\mu$  if using *RFnormal*, or *MinI* if using *RFuniform*.

The definition of RandomParameter2 also depends on the RandomFunction selected:  $\sigma$  if using *RFnormal*, or *MaxI* 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
RandomFunction          RFnormal  << RFnormal or RFuniform
RandomParameter1       25
RandomParameter2       10
MinROS                  0
MaxROS                  3
```

### 3.3.2 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)  $\leq$  *DispersalRate*  $\leq$  (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 time = 0. This is typically used to initiate an outbreak(s) that will spread over the course of the simulation. [Range = 0 – Number of Active Sites]

*SeedEpicenter* determines **if** new epicenters will “seed” new outbreaks outside of current outbreak zones.

*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.

*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.

*InitialCondition* specifies whether an input map is used to define known outbreaks at time = 0.

*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
>>InitialCondition  none   <<map or none
DispersalTemplate    4N     <<MaxRadius, 4N,
                           <<8N, 12N, or 24N
```

### 3.3.3 Neighborhood Resource Dominance parameters

Next are Neighborhood Resource Dominance parameters.

*NeighborhoodFlag* determines whether NRD is used in calculating BDP.

The Neighborhood speed up 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’).

*NeighborhoodRadius* 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:

```
>>----- NRD Inputs -----
NeighborhoodFlag yes    <<yes or no
NeighborhoodSpeedUp none <<none, 2x, 3x, or 4x
NeighborhoodRadius 1000 <<meters
NeighborShape      uniform <<uniform, linear, or gaussian
```

NeighborWeight 10

### 3.3.4 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:

```
EcoregionModifiers
>>Ecoregion Modifier
eco1      0.16
eco26     0.0
eco5      -0.16
```

### 3.3.5 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
```

### 3.3.6 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 six (6) parameters must be provided.

Minor, Secondary, and Primary Host Ages 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.

Susceptibility Class Ages indicate the minimum age at which a species enters a respective tree species cohort 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. Example:

BDASpeciesParameters

>>	Minor	2nd	Major	Susceptibility		
>>Species	Host	Host	Host	Class3	Class2	Class1
>>Name	Age	Age	Age	Age	Age	Age
>>-----						
abiebals	0	20	30	0	20	40
piceglau	0	20	70	30	60	999
picemari	20	60	999	20	60	999

## 4 Output Files

### 4.1 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.

### 4.2 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.