# LANDIS-II Climate-Biomass Biological Disturbance Agent v2.4 User Guide

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# 1 Introduction

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

## 1.1 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 was 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" have 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.

## 1.2 Climate-Biomass Alterations

The original BDA extension used random or cyclical patterns to determine regional outbreaks (see below). In this variation of the BDA extension, climatic data determine the beginning and end of outbreaks. In addition, site resource dominance (see below) is determined by tree species and their **biomass**.

## 1.3 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, the age cohorts present on that site, **and their biomass**. The relative resource value of a given species cohort is defined by its host preference class, where preferred host, secondary host, and minor host values are user-defined values raging between 0 and 1, and non-host has a value of 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 cumulative biomass. Species identified as "ignored" do not contribute to the calculation of average resource value; whereas non-host species that are not ignored contribute a value of 0.

### 1.3.1 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 are 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. The application of LTM can easily cause a full step increase or decrease in disturbance intensity relative to that calculated using species composition alone, depending on the intensity class thresholds.

## 1.4 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).

## 1.5 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.

## 1.6 BDA effects

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

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

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 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.

The mortality of individual cohorts is a probabilistic function of the vulnerability probability (VulnProb) of the cohort's susceptibility class and the site 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 product of BDP and VulnProb to determine if a cohort is killed. The separation of mortality probability from the calculation of BDP allows for cohorts that on their own do not have high preference as hosts, but when occurring in conjunction with highly preferred host cohorts can be highly susceptible to mortality due to "spill-over" from the preferred hosts 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).

## 1.7 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.

### 1.7.1 Epicenters

Epicenters are defined as central sites from which a BDA may disperse. There are three types of epicenters. The first type is initial epicenters, which are sites randomly selected at time = 0 to initiate new outbreak zones in the first time step. The second type is seed epicenters, which are 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. The third type is outbreak zone epicenters, which are 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 BDP. 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 > 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*.

### 1.7.2 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.**

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

4-Neighbor Rule

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

8-Neighbor Rule

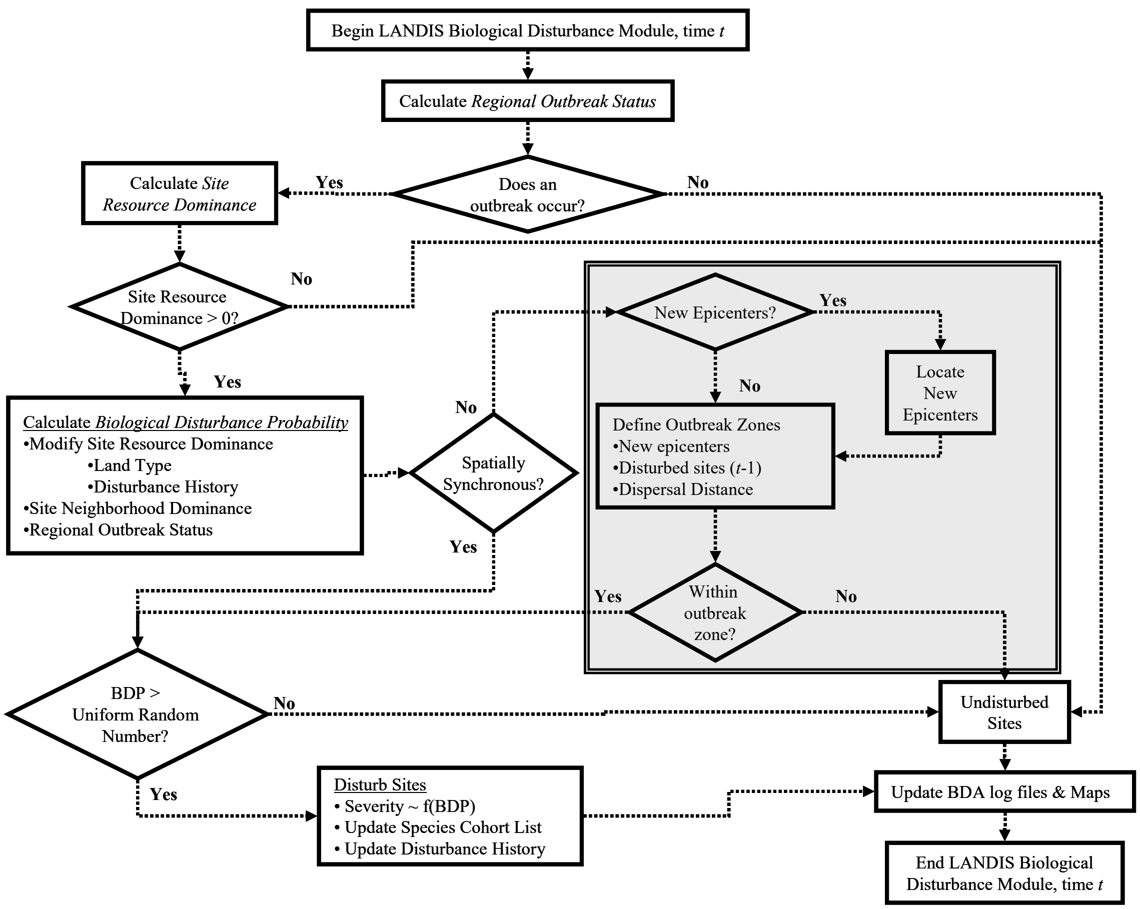
| | | | | |
|---|---|---|---|---|
| | | 9 | | |
| | 8 | 1 | 2 | |
| 12 | 7 | X | 3 | 10 |
| | 6 | 5 | 4 | |
| | | 11 | | |

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.



## 1.8 Major Releases

### 1.8.1 Version 2.4 (October 2021)

First official release; prior versions were only for internal release and testing. Note that Climate-Biomass BDA is derived from version 4.0 of the BDA extension. Detailed information about past releases can be found there.

## 1.9 Minor Releases (this major release)

## 1.10 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.

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.

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Sturtevant, B. R; Miranda, B. R; Shinneman, D. J; Gustafson, E. J; Wolter, P. T. 2012. Comparing modern and presettlement forest dynamics of a subboreal wilderness: Does spruce budworm enhance fire risk? Ecological Applications. 22: 1278-1296.

## 1.11 Acknowledgements

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Service. Valuable contributions to the development of the model and extensions were made by Eric J. Gustafson, and David J. Mladenoff.

# 2 Input Files

## 2.1 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.

## 2.2 Input File Parameters

### 2.2.1 Extension title, time step

The first parameter is the title of the input file:

```
LandisData  "Biomass BDA"
```

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

```
Timestep   15
```

### 2.2.2 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          bda/{agentName}-{timestep}.img
```

### 2.2.3 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       bda/{agentName}-SRD-{timestep}.img
```

### 2.2.4 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       bda/{agentName}-NRD-{timestep}.img
```

### 2.2.5 Biological disturbance probability (BDP) map names (Optional)

The next parameter, **BDPMapNames**, provides the naming convention for the BDA site BDP files. This input is optional, and users who do not want BDP 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:

```
BDPMapNames bda/{agentName}-DBP-{timestep}.img
```

### 2.2.6 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           bda/bda-log.csv
```

### 2.2.7 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.

## 2.3 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:

```
LandisData "BDA Agent"
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 (see Section 2.5). Site Resources Dominance Mode (SRDMode) may be set to either "max" or "mean" (see Section 2.2).

### 2.3.1 Regional Outbreak Status parameters

For the Climate-Biomass BDA, these parameters have been simplified. Currently, only one outbreak pattern is allowed.

*OutbreakPattern represents the type of function used to control the temporal pattern of outbreaks. Options are "CyclicNormal" and "CyclicUniform" and "**Climate**". The first two options represent a cyclic occurrence of outbreak, and differ in the distribution used to estimate time between outbreaks. CyclicNormal uses a normal distribution defined by a mean (Mean) and standard deviation (StDev), and CyclicUniform uses a uniform distribution random function defined by a maximum interval (MaxInterval) and a minimum value (MinInterval).*

*The required input parameters following OutbreakPattern vary depending on the pattern selected. CyclicNormal is followed by Mean and StDev, while CyclicUniform is followed by MaxInterval and MinInterval.*

*TimeSinceLastEpidemic represents the time in years since the last outbreak. When using a StartYear greater than 0, the TimeSinceLastEpidemic parameter is applied relative to the StartYear (see section 3.3.1).*

*VariableName* is invoked if the "Climate" outbreak pattern is selected; it indicates the internal function used to determine whether an outbreak should start or continue. Currently there is only one option: "**CWD+WinterT**". **Alternative formulations can easily be added to the code.** CWD+WinterT describes the climatic triggers required for an outbreak: **Climatic Water Deficit** (CWD) must be below a given threshold and the average January temperature must exceed a given threshold; CWD is calculated internally within the model based on the climate data provided. We chose this initial formulation to capture bark beetle outbreaks in the western USA.

*Threshold1* is minimum requirement for CWD (mm / year).

*Threshold2* is the minimum requirement for WinterT (degrees Celcius).

*OutbreakLag* indicates how long after the conditions defined that an outbreak will begin.

*TimeSinceLastClimate* indicates the necessary lag since the last outbreak began.

*TemporalType* is invoked with either *CyclicNormal* or *CyclicUniform*; valid inputs = *pulse* or *variablepulse*. *TemporalType* determines whether outbreaks are binary (either *MinROS* or *MaxROS* – see definitions below;

*TemporalType* = “pulse”) or if the ROS can range between those values (*TemporalType* = “variable pulse”). For a continuous temporal pattern (every time step at the same outbreak level) choose TemporalType “pulse” and set MaxROS and MinROS to the same value greater than 0.

*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 0 (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.**

### 2.3.2 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) ≤ *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
```

### 2.3.3 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
```

### 2.3.4 Intensity Class Thresholds

*IntensityClass2_BDP* defines the BDP threshold to reach intensity class 2. If BDP is > 0 and < IntensityClass2_BDP, then intensity is class 1. That is, the BDP threshold for intensity class 1 is always 0.

*IntensityClass3_BDP* defines the BDP threshold to reach intensity class 3. If BDP is >= IntensityClass3_BDP, then intensity is class 3.

Example:

```
>>-- Intensity Class Thresholds --
IntensityClass2_BDP 0.25
IntensityClass3_BDP 0.50
```

### 2.3.5 Ecoregion Modifiers (Optional)

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
```

### 2.3.6 Disturbance Modifiers (Optional)

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, Biomass Insects, BDA), three parameters are required: the modifier value (between –1.0 to 1.0) for the first time step following the disturbance, the duration of the modifying effect (in years), and Disturbance Type. 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. Multiple disturbance types (separated by white space) can be listed in each line. Modifiers that apply to all sites disturbed (cohorts killed) by wind, fire, harvest, BDA or Biomass Insects can be applied by using "Wind", "Fire", "Harvest", "BDA" or "BiomassInsects" for the Disturbance Type. Modifiers that apply to specific severity levels for wind and fire can be applied by adding "Severity" and the numeric value (1-5). For example, WindSeverity4 would designate modifiers to apply to all sites disturbed by wind with severity class 4. Specific harvest prescriptions can be targeted for modifiers by specifying the name of the prescription under Disturbance Type. The prescription names must exactly match names used in the harvest input files. Specific BDA agents can be targeted for modifiers by specifying the agent name under Disturbance Type. Modifiers that apply to specific defoliation levels for biomass insects can be applied by adding "Defol" and the minimum percent defoliation. For example, BiomassInsectsDefol50 would designation modifiers to apply to all sites with defoliation at or above 50%. Example:

```
DisturbanceModifiers
>>SRD Modifier    Duration    Disturbance Type
  0.33            20          WindSeverity5 AspenClearcut
 -0.25            20          Fire MaxAgeClearcut
  0.50             5          BiomassInsectsDefol50
```

### 2.3.7 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. All previous versions (<3.0) of the 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 cohorts subject to mortality 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. This feature can be used to allow young cohorts representing advanced regeneration to survive the disturbance.

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

*SpecialDeadFuel* specifies whether a species contributes to a specialty dead fuel class for use with fuel extensions that account for disturbance-related fuels. This feature is used to track the number of dead cohorts of these species for each site, which can be used by other extensions. For example, the Dynamic Fire and Fuel System (DFFS) extension uses the presence of dead conifers to specify certain insect-kill fuel types. Paremter options are ‘yes’ or ‘no’. Species that are not listed default to ‘no’.

Example:

```
BDASpeciesParameters
>>                                                   | Susceptibility                               | Special
```

```
>>Species  MinorHost    2ndHost      MajorHost   | Class3        Class2        Class1        | Dead
>>Name     Age SRDProb  Age SRDProb  Age SRDProb | Age MortProb  Age MortProb  Age MortProb  | Fuel?
>> ----------------------------------------------------------------------------------------------------
abiebals    0   0.25     20  0.5       40  1.0      11  1.0        20  1.0        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
```

### 2.3.8 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
```

# 3 Output Files

## 3.1 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.

## 3.2 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.

## 3.3 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.

## 3.4 BDA Biological Disturbance Probability (BDP) Map (Optional)

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

## 3.5 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.