LANDIS-II Budworm BDA v1.0 Extension User Guide

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1 Introduction

This document describes the **Budworm BDA** 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.

1.1 Modifications to Budworm BDA

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

1.1.1 User-defined suitability class thresholds

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

1.1.2 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.

1.1.3 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.

1.1.4 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.

1.1.5 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.

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. 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.

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:

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

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:

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

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.

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).

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:

$$Y_i = A_i * \exp(- c_i X_i) \tag{3}$$

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.

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.

	1	
4	X	2
	3	

1	2	3
8	X	4
7	6	5

4-Neighbor Rule   8-Neighbor Rule

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

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

12-Neighbor Rule   24-Neighbor Rule
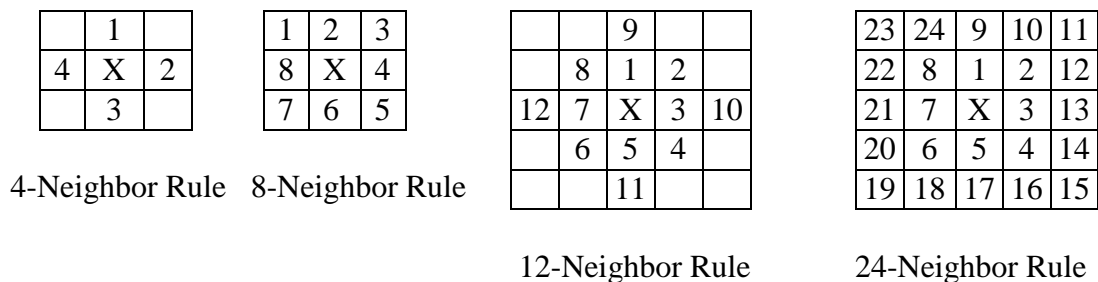
Figure 2.-BDA flow diagram.
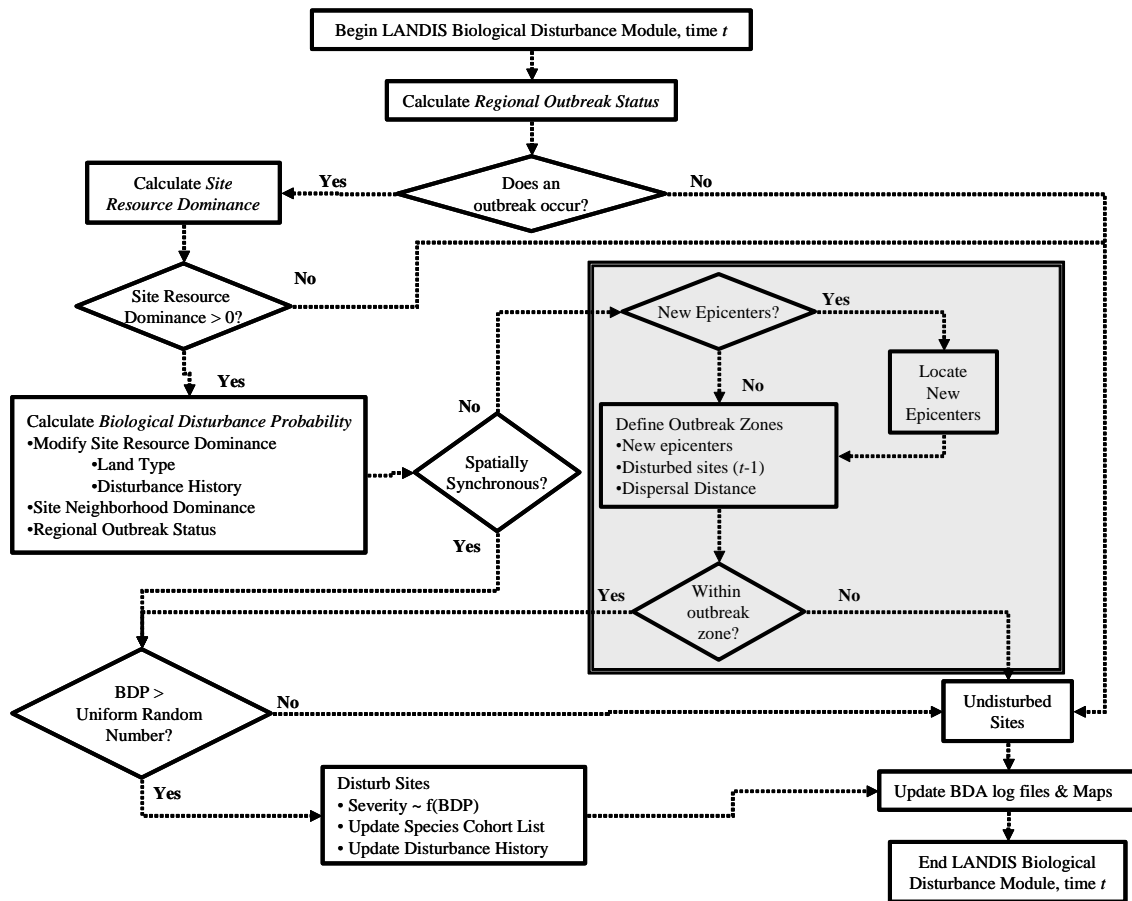
2.7 References

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2.8 Acknowledgements

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  "Budworm BDA"
```

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

```
Timestep    15
```

3.2.2 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            budworm/{agentName}-{timestep}.img
```

3.2.3 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         budworm/{agentName}-SRD-{timestep}.img
```

3.2.4 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        budworm/{agentName}-NRD-{timestep}.img
```

3.2.5 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
```

3.2.6 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            budworm/bda-log.csv
```

3.2.7 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.

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.

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
```

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* $\geq$ (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
```

3.3.3 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
```

3.3.4 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
```

3.3.5 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
```

3.3.6 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
```

3.3.7 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. 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
```

3.3.8 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
```

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 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.

4.3 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.

4.4 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.

4.5 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.