LANDIS-II Biological Disturbance Agent v4.1 Extension User Guide

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1 Introduction

This document describes 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 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 user's 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 with respect to internal model calculations. However, the OUTCOME of the extension in terms of the damage inflicted (i.e., locations where cohorts are killed by BDA effects of a given intensity) are still reported as by disturbance severity class (1=least severe, 3 = most severe) to be consistent with the outputs of other LANDIS-II disturbance extensions.

1.2 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, secondary host, and minor host values are user-defined values raging between 0 and 1, and nonhost 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 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.

1.2.1 Site resource modifiers

Site resource modifiers are optional parameters used to adjust SRD to reflect variation in the quality of food resources introduced by site environment (i.e., ecoregion), recent disturbance, and/or climate factors. Ecoregion modifiers (EMs), disturbance modifiers (DMs), and climate modifiers (CMs) generally range between –1 and +1 and will be added to the SRD value of all active sites where host species are present. Note that large negative values (e.g., -99) may be entered to effectively block outbreak activity from occurring under the specified circumstances (e.g., unfavorable climate). EMs are assumed to be constant for the entire simulation, DMs decline linearly with the time since last disturbance, and

CMs are dynamically related to variables coming from either the Climate Library or an input file. DMs are flexibly designed to accommodate a range of disturbance types including wind, fire, harvest, other BDA agents, and BiomassInsects. In the case of harvest, DMs are linked to specific prescriptions. CMs are likewise flexibly designed to accommodate a range of weather or climate variables, months over which the variables apply, and multi-year averaging of variables from the Climate Library. CMs may also be input as a text file to effectively prescribe an outbreak sequence and/or intensity sequence external to the BDA extension. SRD is then modified by EM and the sum of all DMs and CMs:

$$SRD_m = SRD + EM + (DM_{wind} + DM_{fire} + ...) + (CM_1 + CM_2 + …) \quad (1)$$

The user should calibrate the above modifiers to reflect the relative influence of species composition/age structure, the abiotic environment, recent disturbance, and climate. For example, the application of EM 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.

1.3 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).

1.4 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.

1.5 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 ecoregion, past disturbance, and/or climate (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).

1.6 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.

1.6.1 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 of site BDP (EpidemicThresh). Initial epicenters can be selected anywhere in the landscape where sites meet this

criterion. Seed epicenters are selected from outside the outbreak zone defined at time *t–1* and follow the same selection criterion as initial epicenters. Outbreak zone epicenters are selected from inside the outbreak zone defined at time *t–1* and are selected from sites disturbed at that prior time step. Assuming a chronic disturbance regime, where the BDA is enabled every time step, initial epicenters start an outbreak in year 1, outbreak epicenters allow the agent to continue to disturb cells within a given outbreak zone where host still exists, and to spread from that outbreak zone according to the rules defined in section 1.6.2., and seed epicenters enable the outbreak to initiate new disturbance patches beyond the range defined by the agent's dispersal capacity.

The number of initial epicenters is a simple user-defined parameter. The number of seed epicenters are defined by a Michaelis-Menton equation:

$$N = (N_{max} * p)/(Km + p) \qquad\qquad (3)$$

Where N = number of seed epicenters, N_{max} = maximum number of seed epicenters (SeedEpicenterMax), and Km is the Michaelis-Menton constant (SeedEpicenterCoeff), and p is the proportion of active cells in the landscape meeting the threshold criteria (EpicenterThresh). Km in the above equation may be defined in Eq 3 as the proportion of active cells meeting the criteria at which $N = N_{max}/2$, defining the shape of the hyperbolic curve relating epicenter number to the proportion of cells eligible for selection (Figure 2).

Figure 1. - Michaelis-Menton function defining Seed Epicenter numbers as a function of the proportion of active cells where site BDP ≥ EpidemicThresh.
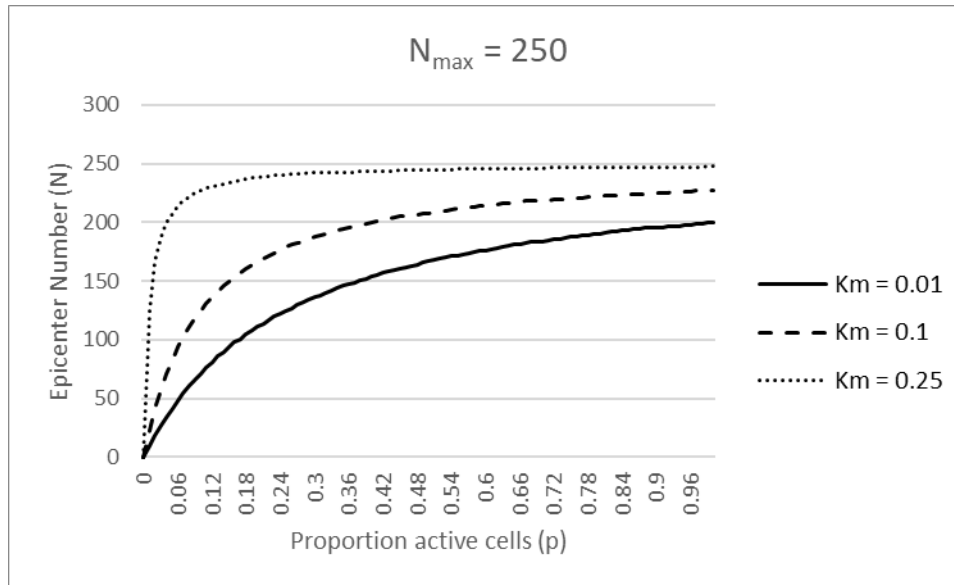
Potential cells eligible as outbreak epicenters are defined by the intensity class of cells disturbed in the outbreak at time t-1, where logical OutbreakEpicenterThresh values are integers 1-3. The number of outbreak epicenters is defined as a simple proportion of eligible cells (OutbreakEpicenterCoeff).

1.6.2. 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 2).

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 2.-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
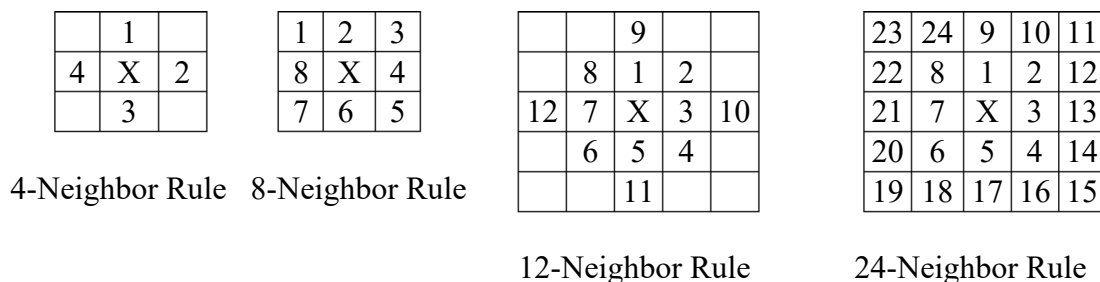
Figure 3.-BDA flow diagram.
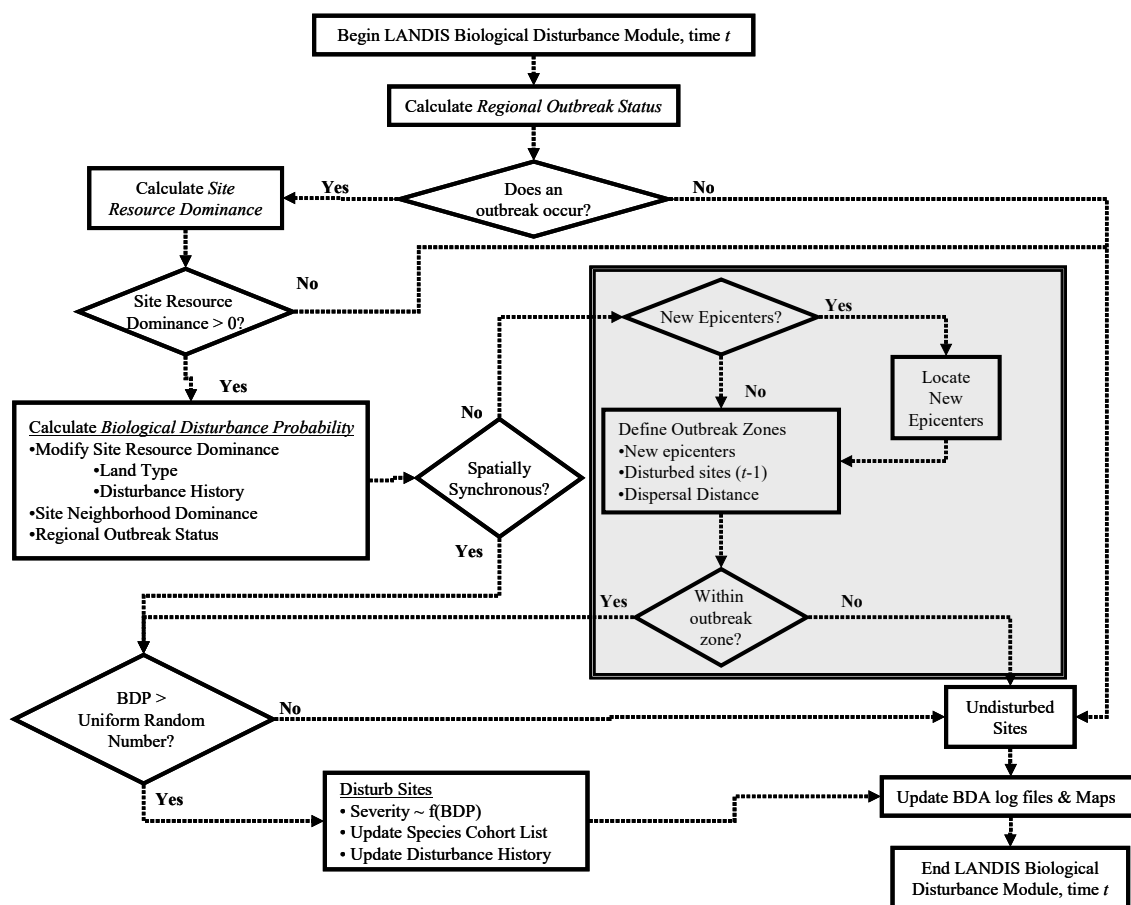
1.7 Major Releases

NOTE: Version 4.1 (and later versions) is no longer backwards compatible with the individual BDA input files used for Version 4.0 and earlier, due to changes in the dispersal algorithm that changed some variable names (See Section 1.8 below).

- If using BDA input files from prior versions that do NOT actually use the dispersal inputs (i.e., Dispersal set to "no"), replacing the old Dispersal Inputs with those from the example file, and resetting the Dispersal to "no" will allow you to reuse the old file.

- If using BDA input files from prior versions that DO use the dispersal inputs (i.e., Dispersal set to "yes"), see the revised section in the User Guide for details on how to properly set up the new dispersal algorithms, using the example file as a template.

IMPORTANT: If you had a previous version of Base BDA installed:

- The previous version of the Base BDA extension should be uninstalled before installing the current version. This should be done using the Windows 'Add or remove programs' tool. The uninstallation should remove the file C:\Program Files\LANDIS-II-v7\extensions\Landis.Extension.BaseBDA-v4.dll. If that file is not removed during uninstallation, it can be deleted manually prior to installing the new version.

- Previous versions of the extension installed example files in the following location: C:\Program Files\LANDIS-II-v7\examples\Base BDA. The new version does not include example files packaged with the installer, and will not overwrite the examples provided by an earlier version. Uninstalling the older version using the Windows uninstaller should remove the example files. To get an updated set of example files compatible with v4.1, follow the 'Example Files' download link on the extension webpage (https://landis-ii-foundation.github.io/Extension-Base-BDA/), and save to a file location with appropriate user permission to modify and write files.

1.7.1 Version 4.0 (March 2019)

Compatible with Core v7.0.

Minor bug fix to allow event log file to write to location and file name specified in the input file.

1.7.2 Version 3.0 (October 2015)

This matches the version described and applied in Sturtevant et al. 2012. The major modifications from the previous version (2.0) of the BDA extension are listed here.

- Metadata Library incorporated allowing interoperability with visualization tools.

- Bug fix to Neighborhood Resources Dominance (NRD): The NRD calculation had an error in logic that required neighborhood cells to have Site Resource Dominance (SRD) > 0 to be included in the neighborhood averaging. When non-host species are meant to decrease the susceptibility (host value = 0), sites that contain only those non-hosts should be included in the NRD calculation.

- New user inputs now define the Biological Disturbance Probability (BDP) thresholds to reach the different intensity classes (1-3). These were previously hard-coded to be 0.33, 0.66, and 1.0.

- 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.

- **Stochastic mortality**: If a site is disturbed (based on biological disturbance probability [BDP], described in 2.5 below) the mortality of individual cohorts is now a probabilistic function of the mortality probability (*MortProb*) 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. This feature can be used to account for the advanced regeneration strategy of certain species, where small, young cohorts exist under the main canopy and are able to survive an insect/disease outbreak, but older cohorts are highly susceptible.

- Host species can now be flagged as contributing to a specialty dead fuel class, which allows the dead cohorts of these species to be considered by fuel extensions that account for disturbance-related fuels. For example, the Dynamic Fire and Fuel System (DFFS) extension uses the presence of dead conifers to specify certain insect-kill fuel types.

- Each BDA agent can have a specified start and end year. Outbreaks for the agent are constrained to occur only between the start and end years.

- Disturbance modifiers can now how different impacts based on the severity of wind and fire disturbances, and can also be applied to specific harvest prescriptions, biomass insects mortality or defoliation, and other BDA agents.

1.7.3 Version 2.0 (June 2012)

Compatible with Core v6.0.

1.7.4 Version 1.3

The differences between this version and the previous version (1.2) include:

- Fixed a bug that caused intervals between epidemics to be 1 timestep too long.

- Replaced the normal distribution random number generator with Trochuetz.Random which provides greater concurrence between input and output mean and standard deviation.

- Adjusted calculation of time to next epidemic to remove bias caused by rounding off intervals to the next full timestep.

- Improved performance by removing unnecessary memory usage.

- Added optional input to list species that should be ignored in the calculation of site resource dominance.

- Added option to output site resource dominance and neighborhood resource dominance maps.

1.8 Minor Releases

1.8.1 Version 4.1 (January 2024)

- Add climate modifiers that work from input climate file or climate library variables; implements threshold value, aggregation across months, and lag years

- Replace SeedEpicenter numbers with Michaelis-Menton equation.

- Make OutbreakEpicenters meet severity threshold (OutbreakEpicenterThresh), and can spread from previous year even if not in the same BDA timestep.

- OutbreakEpicenters not required to be vulnerable.

- Change OutbreakEpicenterCoeff to be simple multiplier of eligible outbreak epicenters (inside last outbreak)

- If no vulnerable sites, reset as if ROS == 0 (but ROS is not actually changed)

- Enable dark, light, yes no for CFSConifer (for use with Dynamic Fuels v3.0.2)

- Track CohortsKilled by all, CFS conifer, dark, light (for use with Dynamic Fuels v3.0.2)

- Add DisturbedFuel registered site variable (for use with Dynamic Fuels v3.0.2)

- Assign DarkDisturbed and LightDisturbed conditions (for use with Dynamic Fuels v3.0.2)

1.8.2 Version 4.0.1 (May 2019)

Allow users to input 0 for the standard deviation of the CyclicNormal outbreak pattern (see 2.3.2). When StDev is 0, the "random" time between cycles will allows be equal to the Mean (not really random).

1.8.3 Version 3.0.1 (June 2017)

Standardized and updated example files.

1.8.4 Version 2.0.3

Fixed bug that caused an error when multiple disturbance agents disturbed the same site in the same timestep. (Epidemic.cs)

Added registered site variable BDA.TimeOfNext to enable interaction with other extensions. (SiteVars.cs, PlugIn.cs)

1.8.5 Version 2.0.2

Fixed bug in initial time since last outbreak, which was causing time to be double-counted in determining when the first outbreak occurs. (PlugIn.cs)

1.8.6 Version 2.0.1

Fixed bug in shuffle of neighborhood site list. (SiteResources.cs, PlugIn.cs)

1.8.7 Version 1.2

Fixed a bug that prevented the no-dispersal from working correctly (see section 3.3.2).

1.8.8 Version 1.1

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.

1.9 Future Development

This section describes components of the extension that the authors have identified would benefit from future development efforts.

- Site Resource Dominance – Species host value is determined by the oldest age class present. Not all biological disturbances would base SRD on the age of the oldest cohort.

- A biomass version of the BDA that enables both biomass values to affect SRD calculation and partial disturbance of cohorts is in progress.

1.10 References

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1.11 Acknowledgements

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  "Base 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 severityfiles. 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:

```
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 Start and end years (Optional)

The first and last simulation years during which the agent can have an outbreak can be specified. *StartYear* indicates the first year when an outbreak can occur, and *EndYear* defines the last year when an outbreak can occur. These parameters are optional and if excluded all simulation years are possible outbreak years for the agent. When using a *StartYear* greater than 0, the *TimeSinceLastEpidemic* parameter is applied relative to the *StartYear*. For example, if *StartYear* is 50 and *TimeSinceLastEpidemic* is 20, the time of the next outbreak will be calculated as if the last outbreak occurred in year 30 (i.e., 50 - 20).

2.3.2 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).

OutbreakPattern represents the type of function used to control the temporal pattern of outbreaks. Options are "CyclicNormal" and "CyclicUniform". Both 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).

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"). 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.**

Examples:

```
>>-------- Regional Outbreak Inputs -------------
OutbreakPattern   CyclicNormal  << CyclicNormal or
CyclicUniform
Mean              25
StDev             10
TimeSinceLastEpidemic   20    << years
TemporalType      pulse        << pulse or variablepulse
MinROS            0
MaxROS            3


-- OR --

OutbreakPattern   CyclicUniform  << CyclicNormal or
CyclicUniform
MaxInterval       25
MinInterval       10
TimeSinceLastEpidemic   10        << years
TemporalType      variablepulse << pulse or variablepulse
MinROS            0
MaxROS            3
```

Note: The order and names of these parameters have changed from previous versions (<3.0).

2.3.3 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 (initial or seed) 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 proportion of eligible cells disturbed in the outbreak at time t-1 that can serve as points of spread both within and beyond the boundary of the time t-1 outbreak zone. Logical values are integers 1-3.

SeedEpicenter determines **if** new epicenters will "seed" new outbreaks outside of current outbreak zones. Options are 'no' or 'yes'.

SeedEpicenterMax is the "N_{max}*"* parameter in Equation 3.

SeedEpicenterCoeff is the "Km" 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.

Example:

```
>>-------- Dispersal Inputs --------------------
Dispersal              yes    <<yes or no
DispersalRate          1500   <<meters/year
EpidemicThresh         0.7
InitialEpicenterNum    5
OutbreakEpicenterCoeff 0.9
OutbreakEpicenterThresh  1
SeedEpicenter          yes    << yes or no
SeedEpicenterMax       250
SeedEpicenterCoeff     0.1
```

2.3.4 DispersalTemplate   8N   <<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]

Example:

```
>>-------- 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
```

2.3.5 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
```

2.3.6 Ecoregion Modifiers (Optional)

Next, a table of Ecoregion Modifiers is provided. 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
```

2.3.7 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 designate 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
```

2.3.8 Climate Modifiers (Optional)

The optional Climate Modifier table is denoted by the keyword "ClimateModifiers". On the lines immediately below the keyword should be a table consisting of 7 columns representing Variable Name, Source, Threshold, Months, Aggregation, LagYears, and Modifier effect.

The first column is the *Variable Name* which must match a climate variable provided by the *Source*. Variable names from a CSV file can be anything. Variables from the climate library include all of the monthly variables: BuildUpIndex, CO2, DayLength, DroughtCode, DuffMoistureCode, FineFuelMoistureCode, FWI, GDD, MaxRH, MaxTemp, MinRH, NDeposition, NightLength, Ozone, PAR, PET, Precip, RH, ShortWaveRadiation, SpecificHumidity, SPEI, temp, VarPpt, VarTemp, VPD, WindDirection, WindSpeed.

The second column is the *Source*, which should be either "Library" to use the climate library, or the path and filename of a separate CSV file that lists climate variables. A climate CSV file must be formatted with columns representing Year and Month (representing model simulation year starting from 0), and additional columns of climate variables.

The third column is a *Threshold* value that determines over what range of values the climate modifier applies. This entry can be formatted using comparative functions (>,<,=,>=, <=) with a numerical value.

The fourth column is *Months*, which determines which months are used in any aggregation of the climate values. The BDA extension does not directly work with monthly climate values, but must calculate a single value for each year during which it runs. It will use the value calculated using the *Aggregation* method across the range of *Months* defined here.

The fifth column is the *Aggregation* method, used to combine monthly values into an annual value. The current options include "Sum" or "Average", which calculates a total of the monthly values or the mean of the monthly values, respectively.

The sixth column is the *LagYears*, which defines the number of years prior to the current model year to use to calculate the value for the current year. For example, a value of 1 for *LagYears* would use the monthly values from the immediately previous year and the current year in the calculation. A value of 2 would include two previous years and the current year.

The seventh column is the *Modifier* effect, which defines how the climate condition being true (i.e., crosses the *Threshold*) impacts the calculated site resource dominance (see 1.2.1). The modifier effect can be negative

(reduces value of the site) or positive (increases value of the site). A large negative value (e.g., -99) can be used to effectively prevent disturbance when climate conditions are unfavorable for an outbreak.

Example:

ClimateModifiers

>> Var	Source	Threshold	Months	Aggregation	LagYears	Modifier
SPEI	Library	>-0.5	5-7	Average	1	-99.0
temp	Library	<28	8	Average	0	-99.0

2.3.9 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
```

2.3.10 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.