

Epidemiological Disturbance Agent v2.0 LANDIS-II Extension User Guide

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Table of Contents

Contents

Table of Contents.....	1
1 Introduction.....	2
1.1 Major Releases.....	2
1.1.1 Version 2.0 (August 2018).....	2
1.1.2 Version 1.0.....	2
1.2 Minor Releases.....	2
2 Epidemiological Disturbance Agents.....	3
2.1 Overview of EDA.....	3
2.2 Site Host Index.....	4
2.2.1 Site host index modifiers.....	4
2.3 Weather.....	5
2.4 Epidemiological processes.....	6
2.4.1 Dispersal kernel.....	7
2.4.2 Cohorts mortality.....	8
2.5 Future Development.....	9
2.6 References.....	10
2.7 Acknowledgements.....	11
3 Input Files.....	12
3.1 Input File Rules.....	12
3.2 Input File Parameters.....	12
3.2.1 Extension title, time step.....	12
3.2.2 Output map names.....	12
3.2.3 MORT map names (Optional).....	12
3.2.4 Log file.....	13
3.2.5 EDA entries.....	13
3.3 Individual EDA Parameter Files.....	13
3.3.1 Start and end years (Optional).....	13
3.3.2 Climate Input parameters.....	13
3.3.3 Derived Climate Variables.....	14
3.3.4 Weather Index.....	15
3.3.5 Transmission parameters.....	16
3.3.6 Ecoregion Modifiers (Optional).....	17
3.3.7 Disturbance Modifiers (Optional).....	17
3.3.8 Species parameters.....	18
3.3.9 Ignored species (Optional).....	19
4 Output Files.....	20
4.1 EDA Status Map.....	20
4.2 EDA Mortality Map (Optional).....	20
4.3 EDA Log file.....	20

1 Introduction

This document describes the **Epidemiological Disturbance Agent (EDA)** extension ('plug-in') for the LANDIS-II model. Users should read the *LANDIS-II Model User's Guide* and *LANDIS-II Conceptual Model Description* prior to reading this document. The EDA extension generally follows the behavior of the epidemiological model described in Filipe et al. (2012). Because EDA only uses cohort age information, it could work with any succession extension, however it is dependent on the Climate Library. So, it is compatible only with succession extensions that have implemented the Climate Library (e.g., NECN Succession). Partial cohort removal and growth reductions are not possible in the current version.

Important Note: This extension is parallelized to decrease computational time. Speed increases based on the number of cores (CPUs) that you allocate to the model (important if submitting to a cluster) or have on your local computer. Currently the model is given maximum priority, meaning that it takes all computer resources and is reluctant to release them for other purposes (i.e. if you need to do something else consider using another computer for that).

1.1 Major Releases

1.1.1 Version 2.0 (August 2018)

Compatible with Core v7.

1.1.2 Version 1.0

This is the first version released for the EDA extension.

1.2 Minor Releases

No minor releases at this time.

2 Epidemiological Disturbance Agents

2.1 Overview of EDA

Epidemiological disturbances, such as pathogens and disease outbreaks, are critically important agents of forest change that cause tree mortality at scales ranging from individual trees of a single species to entire regions. Despite some similarities with the LANDIS-II Biological Disturbance Agent extension, the EDA extension is specifically designed to simulate asymmetric weather-driven transmission of pathogen infection within a multi-host landscape. Transmission is modeled as a dynamic process on a meta-population comprising N contiguous subpopulations represented by cells (sites) arranged on a lattice. Each cell represents either a forest stand with its own vegetation composition or a patch without vegetation. Tree mortality following pathogen infection influences forest succession, fire, other biological disturbance, or harvesting at landscape scales. Epidemiological disturbances in LANDIS are probabilistic at the cell (site) scale, where each site is assigned a probability of being in one of the following states: **Susceptible** (S), **Infected** (infectious non-symptomatic) (I), **Diseased** (infectious and symptomatic) (D) (Fig. 1).

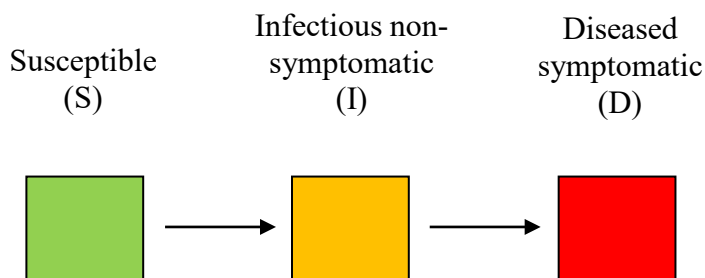


Figure 1. Compartmental structure of the epidemiological model (see equations in Section 2.4)

Probabilities are compared with a uniform random number to determine whether the site becomes infected or, if already infected, to become diseased. Disease causes species- and cohort-specific mortality in the cell. The following sections describe the main assumptions made in the development the EDA extension and the epidemiological model of pathogen transmission in the spatiotemporal landscape defined by host and weather variables. At its core, the spread model implemented in the current version is similar to that in Meentemeyer *et al.* (2011) but with

differences in formulation and detail as it is designed for a different purpose, namely, predicting regional (as opposed to state-wide) natural spread. The chosen modeling framework should accommodate several plant pathosystem types, and more than one EDA may be simulated concurrently to examine their interactions.

More detail on the EDA module and its behavior can be found in Tonini *et al.* (2016).

2.2 Site Host Index

Site host index (SHI) accounts for the spatial distribution of known hosts of the epidemiological agent (pathogen) and is a combined function of tree species composition and the age cohorts present on that site. This approach allows the quantification of susceptibility for each non-infected cell to become infected, and the suitability of each infected cell to produce infectious spores. The relative host index value of a given species cohort is defined by its host competency class, where low, medium, and high competency classes are user-defined using values ranging between 1 and 10, with non-host having a value of 0. The EDA module compares a look-up table with the species cohort list generated by LANDIS to calculate SHI at time t using one of two methods: 1) the host value from the maximum host competency class present, or 2) an average host value of all tree species present, where the host value of each species is represented by the one assigned to oldest cohort. 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. *NOTE: non-sporulating hosts (i.e. hosts that do not contribute to pathogen or disease transmission) should not be included in the host index calculation.*

2.2.1 Site host index modifiers

Site host index modifiers (SHIMs) are optional parameters used to adjust SHI to reflect variation introduced by both site environment (i.e., land type) and recent disturbances. Both land type modifiers (LTMs) and disturbance modifiers (DMs) can range between -1 and +1, and will be added to the SHI value of all affected sites where host species are present ($SHI > 0$). LTMs are assumed to be constant for the entire simulation, while DMs have a defined duration and decline linearly with the time since last disturbance (t_{DST}) as follows:

$$DM_{DST}(t) = DM_{max,DST} * \frac{DM_{duration,DST} - t_{DST}}{DM_{duration,DST}}$$

Disturbances that may affect a given EDA include fire, wind, other EDA agents and insects, as well as harvest prescriptions. SHI is then modified by LTM and the sum of all DMs:

$$SHIM(t) = SHI(t) + LTM + (DM_{wind}(t) + DM_{fire}(t) + \dots)$$

The user should calibrate the above modifiers to reflect the relative influence of species composition/age structure, the abiotic environment, and recent disturbance. SHIM is normalized by its spatial mean over the entire study area, $SHI(t) = \frac{SHIM(t)}{SHIM_{mean}}$, and is incorporated in the epidemiological model by modifying the transmission rate β (see Section 2.3). Moreover, normalization of SHI allows comparison of β against homogeneous landscape conditions (where SHIM = 1) and to interpret β as the rate of secondary infection of typical cells by a single infected typical cell in an uninfected landscape.

2.3 Weather

An *annual weather index*, $w(t)$, is used to account for the effect of weather conditions on the probability of uninfected hosts becoming infected, and infected hosts sporulating and spreading the EDA. Weather predictors (or transformations thereof) should be selected based on their relevance to the chosen EDA. The weather index is multiplied by a baseline transmission rate, β_0 , to produce a time-dependent transmission rate,

$$\beta(t) = w(t)\beta_0$$

where β_0 is defined by the user. The *basic* weather index for year t , $W(t)$, comprises the cumulative effect of N weather predictors (e.g. rainfall alone, or rainfall and temperature) between two months, specified by the user (e.g. April to June), and is calculated as follows:

$$w(t) = \sum_{d \in [month_A(t), \dots, month_B(t)]} X_1 * X_2 * \dots * X_N \quad (1)$$

where X_1, \dots, X_N represent the weather predictors and the cumulative sum runs over days d included between two user-defined months ($month_A$ and $month_B$) for the current year t . If necessary, weather predictors in (1) can be replaced by derived (e.g., aggregated, or transformed) versions. As an example, a predictor can be aggregated (summed or averaged) over N consecutive days of a week or month (e.g., cumulative precipitation). Transformed predictors are expressed by a function, $f(X)$. In the current

version of the module, only a polynomial transformation is available for the user, defined as:

$$f(X) = A + B * \exp(C * [\ln(\frac{X}{D}) / E]^F)$$

where A, B, C, D, E, F are constants specified by the user. As an example, such a transformation can reflect changes in rate of pathogen sporulation at increasing temperature values. The *actual* weather index, $w(t)$, is normalized by the mean W_{mean} over the available time series of historical weather predictors: $w(t) = W(t) / W_{mean}$. This normalization follows the same spirit as that for the host index: it is such that β_0 can be interpreted as the annual transmission rate under average (or under constant) weather conditions. The weather index built this way is annually varying but spatially-uniform across the whole study area.

2.4 Epidemiological processes

The epidemiological model shares features with spatially-structured metapopulation models and relies on a few important assumptions:

- 1) Only the presence/absence of infection in each cell is accounted for. This simplification ignores a transient effect (occurrence, spread and intensification) within the same cell, assuming that an effective level of inoculum is reached *rapidly* (but still below the maximum sporulating capacity of the cell). Improving this approximation would require a much larger computational effort in the parameter estimation procedure described in Filipe *et al.* (2012).
- 2) Infected cells immediately become infectious, which is particularly true for an EDA with a small latent period across its host range.
- 3) Infected sites remain infectious for an undetermined long period, hence no species can recover from infection throughout the simulation.

Every time step t , a susceptible cell (site) i can become *cryptically infected* subject to a force of infection $\Lambda_i(t)$ and, once infected, it can become diseased at rate r_D . Despite potentially containing dead hosts, *symptomatically infected* (diseased) cells have the same transmission rate, i.e. are as infectious as cryptically infected cells. The probabilities that cell i is in each of the possible states (**Susceptible**, **Infected**, **Diseased**), $P_{i,S}$, $P_{i,I}$, and $P_{i,D}$, respectively, are governed by a system of differential equations:

$$\frac{\Delta P_{i,S}}{\Delta t} = - \Lambda_i(t) P_{i,S}$$

$$\frac{\Delta P_{i,I}}{\Delta t} = \Lambda(t)P_{i,S} - r_D P_{i,I}$$

The initial conditions for each cell, at the estimated time of onset of the outbreak, are $P_{i,S} = 1$, $P_{i,I} = 0$, $P_{i,D} = 0$, except at the cell estimated to be the location of the first infection, where $P_{i,S} = 0$, $P_{i,I} = 1$, $P_{i,D} = 0$. The force of infection, $\Lambda_i(t)$, is given by:

$$\Lambda(t) = \beta(t) \sum_{j \neq i} SHIM_j(t) * SHIM_i(t) * P_{j,I+D|i,S} * K(d_{ij})$$

where $\beta(t) = \beta_0 w(t)$ is the transmission rate, with $w(t)$ the annual index of weather fluctuation about a N-year average (see Section 2.3) and β_0 the baseline rate; $K(d_{ij})$ is a dispersal kernel (see Section 2.4.1) for a given distance d between target and source cells; $P_{j,I+D|i,S}$ is the conditional probability that source cell j is infectious (either cryptic or symptomatic infection) given that target cell i is susceptible. To first order of approximation, we assume that $P_{j,I+D|i,S} \approx P_{j,I} + P_{j,D}$, which we expect to be a reasonable approximation to the infection pattern, especially when dispersal is not too localized.

2.4.1 Dispersal kernel

The dispersal kernel used in the EDA is derived from, and shares code with, the seed dispersal kernel described by Lichti et al. (in prep). The probability that EDA disperse a distance d from the source was expressed by two main functional forms, often used in the literature: a power-law and a negative exponential. Their generic form can be defined as follows.

$$K_{PowerLa}(d) = d^{-\alpha}$$

$$K_{NegExp}(d) = e^{-d/\alpha}$$

EDA produced in a source cell can only be deposited in a cell different from the source, i.e. transmission in force of infection is conditional on EDA being dispersed outside the source cell. The rationale for this choice is that infection processes within a cell are not tracked (no transient effect). In addition, the kernel must integrate to 1 within a chosen 2D spatial neighborhood window (excluding the source cell). The 2D window accounts for all possible ways through which the target cell can become infected by a given source cell. A user-defined maximum radial distance is used to limit EDA dispersal within a chosen neighborhood size. For cases where only local, short-distance dispersal events are considered, this parameter becomes essential to reduce computational burden. Similarly to the seed dispersal routines currently

implemented in all LANDIS-II succession modules, only isotropic dispersal (no wind-assisted directional spread) was considered for this version of the EDA module.

2.4.2 Cohorts mortality

Within each diseased cell, the mortality of individual cohorts is a probabilistic function of the mortality probability (MortProb) of the cohort's vulnerability class. The user defines which species and ages fall into each vulnerability class (low-high), and the probability of cohort mortality for each class. Probabilities are compared with a uniform random number to determine whether an entire age-cohort dies (i.e. is removed) or not. Dead cohorts are subsequently removed as part of the LANDIS-II succession component. If no other EDA options are simulated, the module finishes by updating species cohort lists, updating the time since last disturbance, outputting maps of cell states (1 = Susceptible, 2 = Infected, 3 = Diseased) and per-cell cohort mortality, as well as updating the EDA log file (Figure 2).

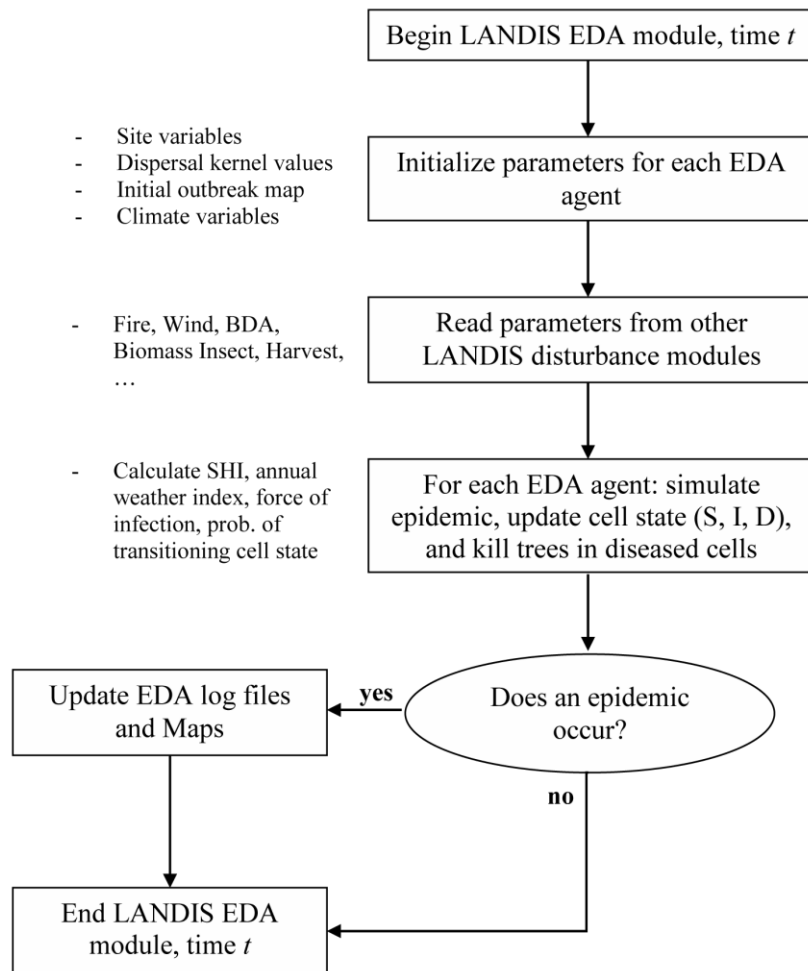


Figure 2. EDA flow diagram.

2.5 Future Development

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

- Climate Variables** – Climate variables are currently limited to those available through the Climate Library. Users may want to use different climate/weather variables which could be read in from a separate file, or added to the Climate Library.
- Site Host Index** – Species host value is determined by the oldest age class present. A better approach would be to use all age classes

present, weighted by their above-ground biomass. Note, this would change compatibility with succession extensions to only those that carry biomass as a cohort attribute.

- **Infection** – Transient effects are currently ignored, i.e. an infected cell does not support partial infection of cohorts. A better approach would account for differential levels of infection within a site. Cells immediately become infectious, which may not fit an EDA with a longer latent period across its host range. Finally, recovery from infection is not considered. This assumption may not work for an EDA with empirical evidence for a shorter infectious period.
- **Mortality** – Diseased sites are probabilistically challenged by mortality events. In this version, the entire age cohort of a species is exposed to mortality events. A better approach would account for partial removal of species cohorts. Note, this would change compatibility with succession extensions to only those that carry biomass as a cohort attribute.
- **Dispersal** – Dispersal is currently only isotropic. EDA are often passively dispersed by wind, hence including a directional component may help improve adequate representation of real dispersal patterns.
- **Epidemiological process** – The epidemiological model shares features with spatially-structured metapopulation models. A different modeling framework could consider the amount of an EDA produced at each site (e.g. spores), and disperse them similarly to the recently developed seed dispersal routines, as opposed to using differential equations and force of infection to drive the spread.
- **Management/control strategies** – Differently from Filipe *et al.* (2012), the EDA module does not implement any control strategies. One can try to use the LANDIS-II harvest module to account for the effect of management on EDA spread. However, future versions could include an EDA-specific control component within the same module.

2.6 References

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dispersal: sudden oak death in northern Californian forests. PLoS Comput. Biol. 8(1): e1002328. doi:10.1371/journal.pcbi.1002328

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2.7 Acknowledgements

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3 Input Files

3.1 Input File Rules

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

3.2 Input File Parameters

3.2.1 Extension title, time step

The first parameter is the title of the input file:

```
LandisData    "Base EDA"
```

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

```
Timestep      1
```

3.2.2 Output map names

Several parameters configure the output files. The first parameter, **MapNames**, provides the naming convention for the EDA infection status (1 = Susceptible, 2 = Infected, 3 = Diseased) files. The variables {timestep} and {agentName} must appear in the file name, and are automatically assigned by LANDIS-II based on the agent-specific parameter file. **The user must indicate if the output should be placed in a sub-directory. In addition, the user must indicate the file extension.** For example:

```
MapNames      eda/{agentName}-{timestep}.img
```

3.2.3 MORT map names (Optional)

The next parameter, **MORTMapNames**, provides the naming convention for the EDA cohort mortality files. This input is optional, and users who do not want mortality output maps should exclude the entire line of input (including the parameter name). The variables {timestep} and {agentName} must appear in the file name, and are automatically assigned by LANDIS-II based on the agent-specific parameter file. **The user must indicate if the output should be placed in a sub-directory. In addition, the user must indicate the file extension.** For example:

```
MORTMapNames  eda/{agentName}-MORT-{timestep}.img
```

3.2.4 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          eda/eda-log.csv
```

3.2.5 EDA entries

Following is a table of EDA entries. Example:

```
EDAInputFiles    P_ramorum.txt
                  heterobasidion.dat
```

Each EDA simulated must have a corresponding EDA parameter file. The file names for each are defined here. The first parameter file name should appear on the same line as the keyword ‘EDAInputFiles’, and any additional parameter files should be listed on subsequent lines.

3.3 Individual EDA Parameter Files

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

```
AgentName        ramorum
SHIMode          mean
>>StartYear     50
>>EndYear       100
```

AgentName will define the name used to identify the specific agent in all disturbance outputs. Site Host Index Mode (SHIMode) may be set to either “max” or “mean” (see Section 2.2).

3.3.1 Start and end years (Optional)

The first and last simulation years during which the agent spreads can be specified. *StartYear* indicates the year of initial EDA outbreak, 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.

3.3.2 Climate Input parameters

Next are the climate input parameters that control the weather component of the epidemiological model (see Section 2.3). Following the keyword ‘ClimateVariables’ the user lists what climate variables to read from either

the LANDIS-II climate library (see online documentation) or from an external local file, and whether to apply a transformation to it or not (i.e., none).

Example:

```
ClimateVariables
>> Var Name Source      ClimateVar Transform
>> -----
    temp      Library    DailyTemp    none
```

The first column in this table defines the variable name for internal use. The second column defines the source for the climate data. This must be “Library” to use the internal climate library (this version does not allow use of other climate sources). The third column defines the variable name in the source file (either climate library or external file). The variable name must match a variable in the climate data provided by the source. The fourth column defines any transformation to be applied to the raw climate values. Options are ‘none’ for no transformation, ‘log10’ for a logarithmic (base 10) transformation, ‘log’ for a natural logarithm transformation.

3.3.3 Derived Climate Variables

Next, all climate variables that need to be derived (i.e., aggregated) from their raw form should be specified after the keyword ‘DerivedClimateVariables’.

Example:

```
DerivedClimateVariables
>> Var Name      Source      ClimateVar  Function Time  Count
    -----
    Precip5DSum  Library    DailyPrecip  Sum    Day    5
    TempIndex    Formula    None          None   Day    1
```

The first columns are the same as those listed above, defining the internal variable name, the source and the variable name from the source. An additional source option is available in this table, ‘Formula’. The polynomial function defined below is used to calculate values for variables with the source of ‘Formula’, using other climate variables. The fourth column (Function) defines what type of aggregation to apply, e.g. ‘Mean’ or ‘Sum’, to the raw variable. Time and Count specify what temporal unit (e.g. ‘Day’) and how many units to use for aggregation. Currently, the

model only supports aggregation by Day. To effectively use a weekly aggregation, use a Count of 7, and for monthly use a Count of 30.

If source is set to “Formula”, the user must set all parameters for a pre-defined polynomial functional transform (see Section 2.3). Example:

```
TempIndex      << a + b * exp(c[ln(Variable / d) / e] ^ f)
>> Parameter  Value
>> -----
Variable      temp
a              108.6
b              904.8
c              -0.5
d              15.87
e              0.2422
f              2
```

In this table, the value for ‘Variable’ must match the name of one of the ClimateVariables or DerivedClimateVariables.

3.3.4 Weather Index

The weather predictors (derived, transformed or raw) that go into the formula for computing the annual weather index need to be listed by the user following the keyword ‘WeatherIndexVariables’. Example:

```
WeatherIndexVariables << Var1 * Var2*...
Precip5DSum
TempIndex
```

The weather index will be the product of the listed variables.

The *basic* annual weather index for year t , can comprise the cumulative effect of the selected weather predictors across multiple months.

Following the keyword ‘AnnualWeatherIndex’, the user must specify a numerical index (1-12) for the start and end months (make sure the first number is lower than the second one), as well as a cumulative function (e.g. ‘Sum’, ‘Mean’) to use over the chosen temporal window.

Example:

```
AnnualWeatherIndex
>>Months  Function
>>-----
3 to 6    Sum
```


3.3.5 Transmission parameters

Next are the transmission parameters that control the landscape spread of EDA at a given time step.

Examples:

```
>>----- Transmission Input -----
TransmissionRate  1.8
AcquisitionRate    0.4
InitialEpidemMap   initEpidem1.img
DispersalType      STATIC
DispersalKernel    PowerLaw
DispersalMaxDist   1000
AlphaCoef          3.55
```

TransmissionRate represents the annual transmission rate under average (or under constant) weather conditions. This parameter corresponds to β_0 and is used to produce a time-dependent transmission rate (see Section 2.3).

AcquisitionRate represents the annual rate at which an infected site becomes diseased. This parameter corresponds to r_D (see Section 2.4).

InitialEpidemMap specifies the map name (must have file extension) of presence/absence (1/0) of the initial EDA outbreak. Note that an outbreak can only spread from existing outbreaks. EDA infections cannot independently become established on the landscape.

DispersalType must be: 'STATIC'. STATIC implies that dispersal will be isotropic. A DYNAMIC option using directional wind-based dispersal is planned for future versions. **NOTE: only STATIC is available to the user in this module version (1.0).**

DispersalKernel represents the functional form for the dispersal kernel (see Section 2.4.1) and can be equal to 'PowerLaw' or 'NegExp'.

DispersalMaxDist represents the maximum radial distance used to define the size of a 2D spatial neighborhood dispersal window. Any site falling inside the neighborhood can be a potential source of infection for a given site.

AlphaCoef represents the coefficient found in the formulas defining the functional forms for the dispersal kernels (see Section 2.4.1).

3.3.6 Ecoregion Modifiers (Optional)

Next, an optional 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 (no modification).** The ecoregion name is listed, followed by the modifier value (-10.0 – 10.0). Example:

```
>>Ecoregion Modifiers
eco1      0.16
eco26     0.0
eco5      -0.16
```

The ecoregion names must match those listed in the ecoregion text file reference in the main scenario file.

3.3.7 Disturbance Modifiers (Optional)

Next, an optional table of Disturbance Modifiers is provided following the keyword ‘DisturbanceModifiers’. Disturbance Modifiers need not be listed and need not be listed in any order. The default is NO EFFECT (modifier = 0). For each disturbance that may modify the EDA (e.g., Wind, Fire, Harvest, Biomass Insects, BDA, EDA), three parameters are required: the modifier value (between -10.0 and 10.0) for the first time step following the disturbance, the duration of the modifying effect (in years), and the Disturbance Type. Note that the disturbance modifier value represents the influence of a specific disturbance type on site host index, 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, EDA or Biomass Insects can be applied by using “Wind”, “Fire”, “Harvest”, “BDA”, “EDA” or “BiomassInsects” for the Disturbance Type. Modifiers that apply to specific severity levels for wind, fire, and BDA 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, as well as other EDA 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		
>>SHI Modifier	Duration	Disturbance Type
0.33	20	WindSeverity5 AspenClearcut
-0.25	20	Fire MaxAgeClearcut
0.50	5	BiomassInsectsDefol50

3.3.8 Species parameters

Next, following the keyword 'EDASpeciesParameters', a table of species parameters for the EDA 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 15 parameters must be provided. Species names in the first column must match names provided in the species input file referenced by the main scenario file.

Host Index Class Ages indicate the minimum age at which a species enters the respective host index value class (Low, Medium, and High). These classes are used to calculate Site Host Index (SHI). A value greater than the tree species longevity (e.g., 999) indicates that the species never reaches the indicated class.

Score values for each host index value class (Low, Medium, and High) define the SHI values for cohorts in that class. The Score values must range between 1-3 for the Low class, 4-6 for Medium class, and 7-10 for High class.

Vulnerability Class Ages indicate the minimum age at which a species enters a respective Vulnerability Class (Low, Medium, and High). These classes determine which age cohorts are subject to mortality if a site is diseased. 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 the Low vulnerability class are immune to mortality by disease. This feature can be used to allow young cohorts representing advanced regeneration to survive the disturbance.

MortProb values for each Vulnerability Class define the probability of mortality for cohorts in that class when disturbance occurs. This makes the killing of cohorts probabilistic once a site becomes diseased based on the vulnerability class of each cohort. The MortProb values must range between 0 and 1.

CFS Conifer 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 fuel types (note this particular fuel is designed for dead spruce and fir from spruce budworm, but may be applicable to certain EDA's as well). Parameter options are 'yes' or 'no'. Species that are not listed default to 'no'.

Mortality Plot specifies whether a species should be accounted for when creating mortality maps by EDA. This way, the user can decide whether to plot cohort mortality for one or more species killed by the disease.

Example:

```
EDASpeciesParameters
>>
>>Species  ||  ----- Host Index -----  ||  ----- Vulnerability -----  ||
>>Name      Age Score Age Score Age Score || Age MortProb Age MortProb Age MortProb || CFS Mortality
>>          (1-3)   (4-6)   (7-10) ||
Umbecali    5     3    15     6    40    10   999    0     999    0     999    0     no    no
Lithdens    5     2    20     4    60     7     5    0.14   15    0.25   30    0.3    yes   yes
Sequemp     50    3    999    4    999    7     999    0     999    0     999    0     no    no
```

3.3.9 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 host index. These species should be those that do not affect the host index value either positively or negatively. Non-host species that do not appear in this list are assumed to provide a 0 score for the host index value, reducing its site average value. If a species appears in both the *EDASpeciesParameters* 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
Abiebrac
Abiegran
Alnurhom
```

4 Output Files

4.1 EDA Status Map

The map of each cell's state is labeled 1 for susceptible, 2 for infected, and 3 for diseased. A map is produced for each EDA time step.

4.2 EDA Mortality Map (Optional)

The map of cohort mortality caused by EDA is labeled with values ranging from 0 to the number of cohorts killed in each site. Only cohorts of species that are flagged "yes" in the Mortality Plot field of the EDA Species Parameter table are considered. A map is produced for each EDA time step.

4.3 EDA Log file

The event log is a text file that contains information about every event over the course of the scenario: year, agent name, number of infected sites, number of diseased sites, number of damaged sites (with mortality regardless of species that have been flagged as "yes"), total cohorts killed, total cohorts killed among the species flagged as "yes" in the EDA Species Parameter table.