

SORTIE-ND User Manual

Version 7.02

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SORTIE-ND User Manual

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SORTIE-ND License

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Data license

You may use the SORTIE-ND software for any purpose, including the creation of data for publication in a scientific book or journal. One of the primary goals of scientific experiments is replicability of results. Therefore, if you have modified the SORTIE-ND software, you may not publish data from it using the names "SORTIE" or "SORTIE-ND" unless you do one of the following: 1) send a copy of the source code of your changes back to the SORTIE-ND team at the Institute of Ecosystem Studies for inclusion in the standard version or 2) publish enough detail about your changes so that they could be replicated by a reasonably proficient programmer.

This product includes software developed by the Apache Software Foundation (<http://www.apache.org/>).

What's New

Version 7.2

Note: If you have a parameter file from an earlier version, load your file and save it. SORTIE-ND will automatically make any needed adjustments to your parameter file. If there are errors, your file may be too old. Load and save into 6.11, then into 7.2.

New in version 7.2:

- New [parameter editing system](#) that keeps all setup in one place
- Created new versions of the [NCI growth](#), [NCI quadrat growth](#), and [NCI mortality](#) behaviors that allow you to completely customize the multiplicative effects on growth and survival
- New behavior [Density dependent infestation](#) to simulate pest and pathogen outbreaks
- New behavior [Size dependent logistic mortality](#)
- New behavior [Stochastic Double Logistic Temp Dependent Neighborhood Disperse](#)
- New behavior [Climate and Competition Dependent Neighborhood Survival](#)
- New behavior [Seasonal Water Deficit](#)
- New climate variables in the [Plot](#) object: Annual Nitrogen Deposition, Seasonal Precipitation, and Water Deficit
- User-defined distribution and sapling mortality for [Generalized Harvest Regime](#)

[What's New archive](#)

Basic SORTIE modeling concepts

SORTIE is an individual-based forest simulator designed to study neighborhood processes. This means that the trees in the forest are modeled individually, not as averages or spatial aggregates. Each individual has a location in space. SORTIE specializes in modeling the interactions of trees with their nearest neighbors to study local neighborhood dynamics.

SORTIE state data

The basic SORTIE model state is defined by the plot, trees, and grids. The [plot](#) is the underlying location in which the simulation takes place. It has a particular size and shape, and attributes for climate and geographic location. The [trees](#) are the individuals making up the forest on the plot. [Grids](#) hold additional data that varies from place to place, such as soil chemistry or light level at the forest floor. All of these together define the model state at a particular time.

Behaviors

The processes that act to change the model state are called [behaviors](#). Behaviors often correspond to biological processes. They are individually contained units, but often work

together to create a complex, interacting system. For instance, a simulation might consist of three behaviors: a behavior to calculate light levels for trees, one to determine the amount of tree growth as a result of the amount of light, and one to select trees to die if they grow too slowly. Behaviors are placed in a certain order to correctly structure their interactions.

The simulation

Forests tend to operate on annual cycles, and so does SORTIE. The unit of time in SORTIE is the [timestep](#). It represents a set of one or more years. A single timestep consists of each behavior acting once, in their defined order. The process is repeated for the number of timesteps that you set, and that's a single simulation, or run.

The basic structure of the SORTIE system is very simple. Its power lies in its incredible flexibility. Almost every aspect of the model is under direct user control.

The parameter file

When you start the SORTIE software, you are using a tool that helps you to define the state data and behaviors that will make up a simulation. Once you have done this, you have created a [parameter file](#). The parameter file completely defines a run. You can load and run your parameter file any time.

Setting up SORTIE-ND for your site

The major research projects involving SORTIE all began with multi year field studies to gather data and analyze tree life cycle processes in the location being studied. This resulted in SORTIE simulations that reflect as accurately as possible local conditions in the real world.

This means that there is no "standard" setup, and no database of tree species, sites, and parameters to draw from. SORTIE was intended to study real locations, and that tends to mean starting by finding out how trees behave at a study site.

This does not mean that you must start with field studies. Neither does it mean that you have to study real places - SORTIE has also been used for purely theoretical work. What it means is that you will need to gather a lot of information before you start.

Look at the example provided on the [SORTIE website](#), read some of the [SORTIE related publications](#), and begin to build your parameter file. You'll quickly see what information you need.

Plot

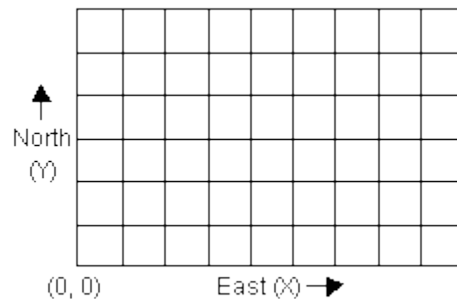
The plot in SORTIE is the simulation of the physical space in which the model runs. It has a size, a climate, and a geographical location.

Plot size

You can think of the plot as a rectangle (although it's not really - more on that later). You tell the plot what its east-west and north-south dimensions are. It's useful to keep your plot size in mind when you are setting up your parameters and viewing your output, since many SORTIE values are per hectare units. The size of your plot also makes a difference in run time - the larger the plot, the longer the run. The absolute minimum size of a plot is 100 meters by 100 meters; 200 meters by 200 meters is a more realistic minimum. It is a careful balance to find a plot size big enough to see the effects you are interested in but not so big that your runs take too long to be practical. Since the length of the run depends on many other factors in addition to plot size, you may need to tweak plot size a bit until you've found a good value.

The SORTIE Coordinate System

SORTIE uses X-Y coordinates, starting at (0, 0), which is at the southwest corner of the plot. Positive Y coordinates increase to the north; positive X coordinates increase to the east. There are no negative plot location values. The coordinate values are in meters.



Plot shape: the torus forest

When you are working with the plot, you think of it as a rectangle. In fact, it is a torus (donut). Each edge connects to the edge on the opposite side. To picture this, imagine a sheet of paper. Roll the sheet of paper into a tube, then bend the tube around so its ends meet. This is what the SORTIE forest looks like. The purpose of this shape is to eliminate edges in the forest. Trees near the "edges" of the plot torus "see" trees on the far "edge" as being right next to them.

The torus shape is what controls the minimum plot size in SORTIE. Some processes in SORTIE require searching a portion of the plot - for instance, to find all the trees in a given circle. If that search took place over too great an area compared to the size of the plot, it would run the risk of searching "around the world." It would work its way around the torus and back to (and past) the place it started, finding the same trees multiple times.

Plot climate and location

The plot also has a climate and a geographical location. Some behaviors use this information but others do not. This information is ignored if it is not needed.

Plot parameters

Parameter name	Description
Number of timesteps	The number of timesteps to run the model. See more on timesteps .
Number of years per timestep	The length of the timestep, in years. It is recommended that this value be a whole number.
Random seed	An integer to use as the seed for SORTIE's random number generator. Zero means that SORTIE chooses its own new seed every time, and repeat runs with the same parameter file will come out different. Any non-zero value triggers one particular sequence of random numbers. In that case, repeat runs with the same parameter file will be the same.
Plot Length in the X (E-W) Direction, in meters	The length of the plot in the east-west direction, in meters.
Plot Length in the Y (N-S) Direction, in meters	The length of the plot in the north-south direction, in meters.
Plot Latitude, in decimal degrees	The plot latitude, expressed in decimal degrees (i.e. 39.10). This information may not be needed in the run, depending on the behaviors that you select; if it is not needed, this value will be ignored.
Mean Annual Precipitation, mm	The mean annual precipitation of the plot, in millimeters. This information may not be needed in the run, depending on the behaviors that you select; if it is not needed, this value will be ignored.
Mean Annual Temperature, degrees C	The mean annual temperature of the plot, in degrees Celsius. This information may not be needed in the run, depending on the behaviors that you select; if it is not needed, this value will be ignored.
Annual Nitrogen	The annual amount of nitrogen deposition in the plot. This information

Deposition	may not be needed in the run, depending on the behaviors that you select; if it is not needed, this value will be ignored.
Seasonal Precipitation	The seasonal precipitation for the plot. This information may not be needed in the run, depending on the behaviors that you select; if it is not needed, this value will be ignored.
Water Deficit	The water deficit for the plot. This information may not be needed in the run, depending on the behaviors that you select; if it is not needed, this value will be ignored.

Timesteps and run length

A run is a single model simulation. It starts at time zero and continues until its defined endpoint is reached. A run is defined by its [parameter file](#). This tells the model how long to run, and what to do during the run.

Timesteps

The basic time unit in the run is the timestep. You set the length and number of the timesteps. Each timestep, the model asks each [behavior](#) to do its work, whatever that work may be. The behaviors are run in the order in which they are listed in the parameter file. (You can see the order using the [Model flow window](#).) The model counts off the timesteps until it has finished the specified number, then cleans up its memory and shuts down.

The length of a timestep is defined in years. Setting a longer timestep means that you can simulate long stretches of time more quickly and with less computer processing time. For example, you could create two parameter files using the same behavior set, each for a run of 100 timesteps. Parameter file A has a timestep length of one year. Parameter file B has a timestep length of five years. Both will take about the same amount of time to run, because each behavior is called upon the same number of times in each run - once per timestep. However, at the end of the run for parameter file A, 100 virtual years will have passed, while for parameter file B, 500 years will have passed. The forests at the end of each of the two runs would probably look quite different.

There is, of course, a tradeoff. When a timestep is more than one year long, behaviors do their best to approximate what happens in those successive years. They can only do that based on the model state at the beginning of the timestep, without knowing how things might change from year to year because of other behaviors. Depending on the simulation, this approximation might create results that are very different from the results that would have come from a single year timestep simulation.

Choosing a timestep length

A one year timestep is the default choice, because it makes sure that SORTIE can model short term interactions directly instead of approximating them. There are two main reasons for choosing a multi-year timestep: shortening processing time for runs that are otherwise unreasonably long, and using parameters that have been estimated for multiple years and cannot easily be rescaled.

That second reason can only apply in rare situations, since most behaviors require parameters scaled to one year, even when a multi-year timestep is being used. Study the documentation for each behavior you want to use. In some cases, behaviors insist on a particular timestep length to ensure proper functioning.

It is difficult to guess how long a parameter file will take to run, so first, try running your parameter file with a one year timestep. If you're happy with how long it took SORTIE to run your parameter file, use one year timesteps.

If you think you might need a multi-year timestep, check the behavior documentation again. Each behavior will describe how it handles timesteps of different lengths. Make sure you think the approach is reasonable. Then, try running two versions of your parameter file, one with one year timesteps and one with multi-year timesteps, with both files modeling the same amount of total time (for instance, 100 one year timesteps and 20 five year timesteps). Make sure you think the difference is reasonable.

What is a tree?

The basic unit of data in the model is the tree. A model tree is a collection of attributes describing one individual. The attributes include location in the [plot](#), species, [life history stage](#), and size. Additional attributes are added as needed for the use of the particular set of [behaviors](#) in a run.

Location and species for a tree never change. [Life history stage](#) transitions are handled automatically as a tree moves through its lifecycle. Tree size and shape are managed according to [allometry](#) settings. Behavior-specific attributes are managed by the appropriate behavior.

You work with these attributes when you select data for [output](#) or work with tree maps when setting up [run initial conditions](#).

How trees are organized - the tree population

Trees are organized by location and size in what is called the tree population. The tree population divides up the plot into 8 m by 8 m grid cells, and tracks the trees in each cell by height.

The tree population is where the list of tree species is defined. It tracks all of the [allometry](#) relationships for each of these species and manages [life history stage](#) transitions and attribute updates for individual trees.

Tree life history stages and transitions

Tree life history stage (also referred to as tree type), along with species, is the basic way to classify trees. When you set up [behaviors](#) for a run, you tell each behavior which trees to act on by species and type. There is support for seven tree life history stages in the model:

- **Seed.**
- **Seedling.** Seedlings are defined as trees less than the height set in the [parameter Max Seedling Height \(meters\)](#) (normally 1.35 meters, thus seedlings have no DBH). Their primary size measurement is the diameter at 10 cm height ($diam_{10}$).
- **Sapling.** Saplings are defined as having a DBH greater than 0 and less than the **Minimum adult DBH** defined in the [tree parameters](#). Seedlings and saplings are sometimes referred to collectively as "juveniles".
- **Adult.** Adults are defined as having a DBH equal to or greater than the **Minimum adult DBH** defined in the [tree parameters](#).
- **Stump.** Stumps are saplings or adults that have been cut by the [Harvest behavior](#).
- **Snag.** Snags are standing dead trees. They can be produced when saplings and adults die due to normal tree [mortality](#) or a [disturbance event](#), such as disease. Only adult trees become snags. See below for more on how trees become snags.
- **Woody debris.** Woody debris comes from fallen snags. Currently, no behavior uses woody debris and this is a placeholder stage only. It is not created at this time.

Tree life history stage transitioning - growth

Seed to seedling. Seeds are modeled only as aggregates, not individuals. Seeds become individual seedlings when they are processed by an [establishment](#) behavior.

Seedling to sapling. When a seedling reaches the maximum seedling height set for its species, it becomes a sapling. The $diam_{10}$ value is converted to a DBH value, which is then used to calculate the rest of the sapling's new dimensions. Since height is re-calculated with a different equation and input parameters, there may be a discontinuity in height values right around the seedling/sapling transition point. If a species uses different allometric relationships for its saplings and adults, another discontinuity may occur at the time of this transition as well. For more on the allometric relationships and how they are calculated, see the [Allometry](#) topic. (The automatic updating of these allometric relationships during the growth phase can be overridden. For more, see the [Growth behaviors](#) topic.)

Sapling to adult. When a sapling's DBH reaches the minimum adult DBH for its species, it becomes an adult.

Tree life history stage transitioning - death

Death also produces tree life history stage transitions. Behaviors can request to a tree population that a tree be killed. How the tree population responds to this request depends on the type of tree, the reason for death, and the type of run.

Mortality reasons

The reasons why a tree is killed are:

- Natural mortality
- Harvest
- Insects
- Fire
- Disease

Check the documentation for your chosen [disturbance behaviors](#) and [mortality behaviors](#) for more information on which codes will apply to your run.

There are life history stages for dead trees, but a run may not be set up to handle them. The tree population takes this into account. It examines the run to see if any behaviors directly deal with stumps and snags. If either is the case, the run is classified as "stump aware" and/or "snag aware".

Here's what happens to a tree to be killed in different situations:

- If a tree is a seedling, it is deleted from memory no matter why it died.
- If a tree is a sapling or adult killed in a harvest, and the run is "stump aware", the tree is converted to a stump.
- Saplings killed for any other reason, or by harvest in a run that is not "stump aware", are deleted from memory.
- If the tree is an adult killed by harvest and the run is not "stump aware", it is deleted from memory.
- If the tree is an adult killed for any reason other than harvest, and the run is "snag aware", the tree is converted to a snag.
- If the tree is an adult killed for any reason other than harvest, and the run is NOT "snag aware", the tree is removed from memory.
- If the tree is already a snag, it is removed from memory.

Stumps exist only for the timestep in which they were created, and then disappear.

You can include information on dead trees in output files. For the purposes of output, dead trees are those which have been removed from memory and are no longer interacting with the model in any way. In this case, a snag is considered alive, although a tree that produced a snag will show up in output mortality records in the timestep in which it died to become a snag. Then the snag would show up again when it was finally removed from the model.

Allometry

The allometry relationships govern a tree's size and shape.

Tree size attributes

- **DBH** (diameter at breast height) is the diameter of a tree trunk in centimeters at 1.35 meters above the ground.
- **Diameter at 10 cm**, or **diam₁₀**, is the diameter of a tree trunk, measured in centimeters, at a height of 10 cm above the ground.
- **Height** is the distance from the ground to the top of the crown, in meters.
- **Crown radius** is the distance from the trunk to the edge of the crown, in meters.
- **Crown depth** is the distance from the top to the bottom of the crown, in meters.

Attributes by life history stage

- **Seedlings:** diam₁₀ and height.
- **Saplings:** diam₁₀, DBH, height, crown radius, and crown depth.
- **Adults and snags:** DBH, height, crown radius, and crown depth.

How size and shape attributes are used

Many behaviors do their work using equations that are functions of tree size in some way. Diameter is by far the most important attribute. Other dimensions may or may not be used in a run, depending on the set of chosen behaviors. How important it is to get the allometric relationships correct depends on how they will be used. Check the documentation of your chosen behaviors. If, for instance, crown shape is not used, it doesn't really matter what relationships you assign.

Trees are not required to conform to their allometric relationships. For instance, growth may cause height and diameter to vary independently of each other.

You choose the relationship used by each life history stage of each species for each attribute. These can be freely mixed-and-matched. Use the [Edit Allometry Functions](#) window to set the allometry functions.

Function	Description
The standard crown depth and radius relationships	Crown dimensions are power functions of tree dimensions.

<u>The Chapman-Richards crown depth and radius relationships</u>	<p>Uses the Chapman-Richards function to calculate crown dimensions.</p>
<u>The non-spatial density dependent crown depth and radius relationships</u>	<p>Uses non-spatial measures of density to calculate crown radius and crown depth.</p>
<u>The NCI crown depth and radius relationships</u>	<p>Calculates crown dimensions as a function of tree size and local crowding.</p>
<u>DBH - diameter at 10 cm relationship</u>	<p>DBH is a linear function of diameter at 10 cm.</p>
<u>The standard diameter-height relationships</u>	<p>Height is a function of DBH or diameter at 10 cm. These are called "standard" because they were the original SORTIE functions.</p>
<u>The linear diameter-height relationship</u>	<p>Height is a linear function of diameter.</p>
<u>The reverse linear diameter-height relationship</u>	<p>Diameter is a linear function of height.</p>
<u>The power diameter-height relationship</u>	<p>Height is a power function of diameter at 10 cm.</p>

The standard crown depth and radius relationships

Parameters

Parameter name	Description
Crown Height Exponent	The exponent in the standard equation for calculating crown depth.
Crown Radius Exponent	The exponent in the standard equation for determining the crown radius.
Slope of Asymptotic Crown Height	Slope of the standard equation for determining crown depth.
Slope of Asymptotic Crown Radius	Slope of the standard equation for determining crown radius.

Crown radius is calculated as:

$$rad = C_1 * DBH^a$$

where:

- *rad* is the crown radius, in meters
- C_1 is the **Slope of Asymptotic Crown Radius** parameter
- a is the **Crown Radius Exponent** parameter
- *DBH* is the tree's DBH, in cm

Crown radius is limited to a maximum of 10 meters.

Crown depth is calculated as

$$ch = C_2 * height^b$$

where

- *ch* is the distance from the top to the bottom of the crown cylinder, in meters
- C_2 is the **Slope of Asymptotic Crown Height** parameter
- *height* is the tree's height in meters
- b is the **Crown Height Exponent** parameter

The Chapman-Richards crown depth and radius relationships

Crown Depth Parameters

Parameter name	Description
Chapman-Richards Asymptotic Crown Height	The asymptotic crown depth (or length), in m, of the Chapman-Richards crown depth equation.
Chapman-Richards Crown Height Intercept	The intercept of the Chapman-Richards crown depth equation. This represents the crown depth, in m, of the smallest possible sapling.
Chapman-Richards Crown Height Shape 1 (b)	The first shape parameter, b, of the Chapman-Richards crown depth equation.
Chapman-Richards Crown Height Shape 2 (c)	The second shape parameter, c, of the Chapman-Richards crown depth equation.

Crown Radius Parameters

Parameter name	Description
Chapman-Richards Asymptotic Crown Radius	The asymptotic crown radius, in m, of the Chapman-Richards crown radius equation.
Chapman-Richards Crown Radius Intercept	The intercept of the Chapman-Richards crown radius equation. This represents the crown radius, in m, of the smallest possible sapling.
Chapman-Richards Crown Radius Shape 1 (b)	The first shape parameter, b, of the Chapman-Richards crown radius equation.
Chapman-Richards Crown Radius Shape 2 (c)	The second shape parameter, c, of the Chapman-Richards crown radius equation.

The Chapman-Richards equation for calculating crown radius is:

$$rad = i + a (1 - e^{-b * DBH})^c$$

where

- *rad* is the crown radius, in meters
- *DBH* is the tree's DBH, in cm
- *i* is the **Chapman-Richards Crown Radius Intercept** parameter, which represents the crown radius of the smallest possible sapling
- *a* is the **Chapman-Richards Asymptotic Crown Radius** parameter
- *b* is the **Chapman-Richards Crown Radius Shape 1 (b)** parameter
- *c* is the **Chapman-Richards Crown Radius Shape 2 (c)** parameter

The Chapman-Richards equation for calculating crown depth is:

$$ch = i + a (1 - e^{-b * H})^c$$

where

- *ch* is the distance from the top to the bottom of the crown cylinder, in meters
- *H* is the tree's height, in m
- *i* is the **Chapman-Richards Crown Height Intercept** parameter, which represents the crown depth of the smallest possible sapling
- *a* is the **Chapman-Richards Asymptotic Crown Height** parameter
- *b* is the **Chapman-Richards Crown Height Shape 1 (b)** parameter
- *c* is the **Chapman-Richards Crown Height Shape 2 (c)** parameter

The non-spatial density dependent crown depth and radius relationships

The density dependent equations for crown radius and crown depth use non-spatial measures of density to influence crown radius and crown depth. Density is measured across the plot as a whole, not locally (thus "non-spatial").

Crown Radius Parameters

Parameter name	Description
Non-Spatial Density Dep. Inst. Crown Height "a"	The "a" term in the instrumental crown depth equation, used to calculate crown radius
Non-Spatial Density Dep. Inst. Crown Height "b"	The "b" term in the instrumental crown depth equation, used to calculate crown radius

Non-Spatial Density Dep. Inst. Crown Height "c"	The "c" term in the instrumental crown depth equation, used to calculate crown radius
Non-Spatial Density Dep. Inst. Crown Height "d"	The "d" term in the instrumental crown depth equation, used to calculate crown radius
Non-Spatial Density Dep. Inst. Crown Height "e"	The "e" term in the instrumental crown depth equation, used to calculate crown radius
Non-Spatial Density Dep. Inst. Crown Height "f"	The "f" term in the instrumental crown depth equation, used to calculate crown radius
Non-Spatial Density Dep. Inst. Crown Height "g"	The "g" term in the instrumental crown depth equation, used to calculate crown radius
Non-Spatial Density Dep. Inst. Crown Height "h"	The "h" term in the instrumental crown depth equation, used to calculate crown radius
Non-Spatial Density Dep. Inst. Crown Height "i"	The "i" term in the instrumental crown depth equation, used to calculate crown radius
Non-Spatial Density Dep. Inst. Crown Height "j"	The "j" term in the instrumental crown depth equation, used to calculate crown radius
Non-Spatial Exp. Density Dep. Crown Radius "D1"	The "D1" term
Non-Spatial Exp. Density Dep. Crown Radius "a"	The "a" term
Non-Spatial Exp. Density Dep. Crown Radius "b"	The "b" term
Non-Spatial Exp. Density Dep. Crown Radius "c"	The "c" term
Non-Spatial Exp.	The "d" term

Density Dep. Crown Radius "d"	
Non-Spatial Exp. Density Dep. Crown Radius "e"	The "e" term
Non-Spatial Exp. Density Dep. Crown Radius "f"	The "f" term

Crown Depth Parameters

Parameter name	Description
Non-Spatial Density Dep. Inst. Crown Radius "a"	The "a" term in the instrumental crown radius equation, used to calculate crown depth
Non-Spatial Density Dep. Inst. Crown Radius "b"	The "b" term in the instrumental crown radius equation, used to calculate crown depth
Non-Spatial Density Dep. Inst. Crown Radius "c"	The "c" term in the instrumental crown radius equation, used to calculate crown depth
Non-Spatial Density Dep. Inst. Crown Radius "d"	The "d" term in the instrumental crown radius equation, used to calculate crown depth
Non-Spatial Density Dep. Inst. Crown Radius "e"	The "e" term in the instrumental crown radius equation, used to calculate crown depth
Non-Spatial Density Dep. Inst. Crown Radius "f"	The "f" term in the instrumental crown radius equation, used to calculate crown depth
Non-Spatial Density Dep. Inst. Crown Radius "g"	The "g" term in the instrumental crown radius equation, used to calculate crown depth
Non-Spatial Density Dep. Inst. Crown Radius "h"	The "h" term in the instrumental crown radius equation, used to calculate crown depth

Non-Spatial Density Dep. Inst. Crown Radius "i"	The "i" term in the instrumental crown radius equation, used to calculate crown depth
Non-Spatial Density Dep. Inst. Crown Radius "j"	The "j" term in the instrumental crown radius equation, used to calculate crown depth
Non-Spatial Log. Density Dep. Crown Height "a"	The "a" term
Non-Spatial Log. Density Dep. Crown Height "b"	The "b" term
Non-Spatial Log. Density Dep. Crown Height "c"	The "c" term
Non-Spatial Log. Density Dep. Crown Height "d"	The "d" term
Non-Spatial Log. Density Dep. Crown Height "e"	The "e" term
Non-Spatial Log. Density Dep. Crown Height "f"	The "f" term
Non-Spatial Log. Density Dep. Crown Height "g"	The "g" term

In addition to the use of density variables, the density dependent equations for crown width uses an estimate of crown depth as a dependent variable (and vice versa). This estimated value of crown width and crown depth (rad_i and ch_i) used in the density dependent equations come from the instrumental variable equations. Calculating the instrumental variables equations avoids "uncoupling" the crown radius - crown depth relationship.

The non-spatial exponential density dependent crown radius function is:

$$rad = DI * DBH^a * Height^b * ch_i^c * STPH^d * BAPH^e * BAL^f$$

where:

- *rad* is the crown radius, in meters
- *D1* is the **Non-Spatial Exp. Density Dep. Crown Radius "D1"** parameter
- *a* is the **Non-Spatial Exp. Density Dep. Crown Radius "a"** parameter
- *b* is the **Non-Spatial Exp. Density Dep. Crown Radius "b"** parameter
- *c* is the **Non-Spatial Exp. Density Dep. Crown Radius "c"** parameter
- *d* is the **Non-Spatial Exp. Density Dep. Crown Radius "d"** parameter
- *e* is the **Non-Spatial Exp. Density Dep. Crown Radius "e"** parameter
- *f* is the **Non-Spatial Exp. Density Dep. Crown Radius "f"** parameter
- *DBH* is the tree's DBH, in cm
- *Height* is the tree height, in meters
- *ch_i* is the instrumental crown depth of the target tree, in meters, calculated using the function below
- *STPH* is number of stems per hectare of adult trees within the entire plot
- *BAPH* is the basal area, in m² per hectare, of adult trees within the entire plot
- *BAL* is the sum of the basal area of all trees taller than the height of the target tree, in m² per hectare

The instrumental equation for calculating *ch_i* is as follows:

$$ch_i = a + b * DBH + c * Height + d * DBH^2 + e * Height^2 + f / DBH + g * STPH + h * BAPH + i * BAL + j * (Height / DBH)$$

where:

- *a* is the **Non-Spatial Density Dep. Inst. Crown Height "a"** parameter
- *b* is the **Non-Spatial Density Dep. Inst. Crown Height "b"** parameter
- *c* is the **Non-Spatial Density Dep. Inst. Crown Height "c"** parameter
- *d* is the **Non-Spatial Density Dep. Inst. Crown Height "d"** parameter
- *e* is the **Non-Spatial Density Dep. Inst. Crown Height "e"** parameter
- *f* is the **Non-Spatial Density Dep. Inst. Crown Height "f"** parameter
- *g* is the **Non-Spatial Density Dep. Inst. Crown Height "g"** parameter
- *h* is the **Non-Spatial Density Dep. Inst. Crown Height "h"** parameter
- *i* is the **Non-Spatial Density Dep. Inst. Crown Height "i"** parameter
- *j* is the **Non-Spatial Density Dep. Inst. Crown Height "j"** parameter
- *DBH* is the tree's DBH, in cm
- *Height* is the tree height, in meters
- *STPH* is number of stems per hectare of adult trees within the entire plot
- *BAPH* is the basal area, in m² per hectare, of adult trees within the entire plot
- *BAL* is the sum of the basal area of all trees taller than the height of the target tree, in m² per hectare

The non-spatial logistic density dependent crown depth function is:

$$ch = \frac{height}{1 + e^{a + b * DBH + c * height + d * rad_i + e * STPH + f * BAPH + g * BAL}}$$

where:

- ch is the crown depth, in meters
- $height$ is the tree's height, in m
- a is the **Non-Spatial Log. Density Dep. Crown Height "a"** parameter
- b is the **Non-Spatial Log. Density Dep. Crown Height "b"** parameter
- c is the **Non-Spatial Log. Density Dep. Crown Height "c"** parameter
- d is the **Non-Spatial Log. Density Dep. Crown Height "d"** parameter
- e is the **Non-Spatial Log. Density Dep. Crown Height "e"** parameter
- f is the **Non-Spatial Log. Density Dep. Crown Height "f"** parameter
- g is the **Non-Spatial Log. Density Dep. Crown Height "g"** parameter
- DBH is the tree's DBH, in cm
- rad_i is the instrumental crown radius of the target tree, in meters, calculated using the function below
- $STPH$ is number of stems per hectare of adult trees within the entire plot
- $BAPH$ is the basal area, in m^2 per hectare, of adult trees within the entire plot
- BAL is the sum of the basal area of all trees taller than the height of the target tree, in m^2 per hectare

The instrumental equation for calculating rad_i is as follows:

$$rad_i = a + b * DBH + c * Height + d * DBH^2 + e * Height^2 + f / DBH + g * STPH + h * BAPH + i * BAL + j * (Height / DBH)$$

where:

- a is the **Non-Spatial Density Dep. Inst. Crown Radius "a"** parameter
- b is the **Non-Spatial Density Dep. Inst. Crown Radius "b"** parameter
- c is the **Non-Spatial Density Dep. Inst. Crown Radius "c"** parameter
- d is the **Non-Spatial Density Dep. Inst. Crown Radius "d"** parameter
- e is the **Non-Spatial Density Dep. Inst. Crown Radius "e"** parameter
- f is the **Non-Spatial Density Dep. Inst. Crown Radius "f"** parameter
- g is the **Non-Spatial Density Dep. Inst. Crown Radius "g"** parameter
- h is the **Non-Spatial Density Dep. Inst. Crown Radius "h"** parameter
- i is the **Non-Spatial Density Dep. Inst. Crown Radius "i"** parameter
- j is the **Non-Spatial Density Dep. Inst. Crown Radius "j"** parameter
- DBH is the DBH of the tree, in cm
- $Height$ is the tree height, in meters
- $STPH$ is number of stems per hectare of adult trees within the entire plot
- $BAPH$ is the basal area, in m^2 per hectare, of adult trees within the entire plot
- BAL is the sum of the basal area of all trees taller than the height of the target tree, in m^2 per hectare

The NCI crown depth and radius relationships

This calculates crown dimensions as a function of tree size and local crowding. The equations are the same for crown depth and crown radius, but they each have separate parameters.

NCI Crown Depth Parameters

Parameter name	Description
NCI Crown Depth - Alpha	NCI function exponent.
NCI Crown Depth - Beta	NCI function exponent.
NCI Crown Depth - Crowding Effect "n"	Crowding effect exponent.
NCI Crown Depth - Gamma	NCI function exponent.
NCI Crown Depth Lambda for Species X Neighbors	The competitive effect of neighbors of species X.
NCI Crown Depth - Max Potential Depth (m)	The maximum possible value for crown depth, in m.
NCI Crown Depth - Max Search Distance for Neighbors (m)	The maximum distance, in m, at which a neighboring tree has competitive effects on a target tree.
NCI Crown Depth - Minimum Neighbor DBH (cm)	The minimum DBH for trees of that species to compete as neighbors. Values are needed for all species.
NCI Crown Depth - Size Effect "d"	Size effect function exponent.

NCI Crown Radius Parameters

Parameter name	Description
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NCI Crown Radius - Alpha	NCI function exponent.
NCI Crown Radius - Beta	NCI function exponent.
NCI Crown Radius - Crowding Effect "n"	Crowding effect exponent.
NCI Crown Radius - Gamma	NCI function exponent.
NCI Crown Radius Lambda for Species X Neighbors	The competitive effect of neighbors of species X.
NCI Crown Radius - Max Potential Radius (m)	The maximum possible value for crown radius, in m.
NCI Crown Radius - Max Search Distance for Neighbors (m)	The maximum distance, in m, at which a neighboring tree has competitive effects on a target tree.
NCI Crown Radius - Minimum Neighbor DBH (cm)	The minimum DBH for trees of that species to compete as neighbors. Values are needed for all species.
NCI Crown Radius - Size Effect "d"	Size effect function exponent.

The crown dimensions are calculated as:

$$CR / CD = [Max CR / Max CD] * Size Effect * Crowding Effect$$

where:

- CR is the crown radius, in m
- CD is the crown depth, in m
- $Max CR$ is the **NCI Crown Radius - Max Potential Radius (m)** parameter
- $Max CD$ is the **NCI Crown Depth - Max Potential Depth (m)** parameter

Size Effect is calculated as:

$$SE = 1 - exp(-d * DBH)$$

where:

- SE is the size effect, between 0 and 1
- d is either the **NCI Crown Depth - Size Effect "d"** parameter or the **NCI Crown Radius - Size Effect "d"** parameter
- DBH is the tree's DBH, in cm

Crowding Effect is calculated as:

$$CE = \exp(-n * NCI)$$

where:

- CE is the crowding effect, between 0 and 1
- n is the **NCI Crown Radius - Crowding Effect "n"** parameter or the **NCI Crown Depth - Crowding Effect "n"** parameter
- NCI is calculated as below

NCI is calculated as:

$$NCI = \sum_{j=1}^S \sum_{k=1}^N \lambda_{jk} \frac{(DBH_{jk})^{\alpha}}{(distance_{jk})^{\beta}} e^{\gamma * DBH_t}$$

where:

- the calculation sums over $j = 1 \dots S$ species and $k = 1 \dots N$ neighbors of each species of at least a DBH of **NCI Crown Radius - Minimum Neighbor DBH** or **NCI Crown Depth - Minimum Neighbor DBH, in cm**, out to a distance of **NCI Crown Radius - Max Search Distance for Neighbors (m)** or **NCI Crown Depth - Max Search Distance for Neighbors (m)**
- α is the **NCI Crown Radius - Alpha** parameter or the **NCI Crown Depth - Alpha** parameter
- β is the **NCI Crown Radius - Beta** parameter or the **NCI Crown Depth - Beta** parameter
- γ is the **NCI Crown Radius - Gamma** parameter or the **NCI Crown Depth - Gamma** parameter
- λ_{jk} is the **NCI Crown Radius Lambda for Species X Neighbors** parameter or the **NCI Crown Depth Lambda for Species X Neighbors** for the target species relative to the kth neighbor's species
- DBH_{jk} is the DBH of the kth neighbor, in cm
- DBH_t is the DBH of the target tree for which to calculate crown dimensions, in cm
- $distance_{jk}$ is distance from target to neighbor, in m

DBH - diameter at 10 cm relationship

Seedlings use the diameter at 10 cm as their primary indicator of size, and have no DBH. Saplings use both DBH and $diam_{10}$. The use of both measurements by saplings helps to maintain continuity between the seedling and adult life history stages. Adults use only DBH.

Parameters

Parameter name	Description
Intercept of DBH to Diameter at 10 cm Relationship	The intercept of the linear relationship between the DBH, in cm, and the diameter at 10 cm height, in cm, in small trees. Used by all species.
Slope of DBH to Diameter at 10 cm Relationship	The slope of the linear relationship between the DBH, in cm, and the diameter at 10 cm height, in cm, in small trees. Used by all species.

DBH and $diam_{10}$ are related as follows:

$$DBH = (diam_{10} * R) + I$$

where

- DBH is the DBH in cm
- $diam_{10}$ is the diameter at 10 cm height, in cm
- R is the **Slope of DBH to Diameter at 10 cm Relationship** parameter
- I is the **Intercept of DBH to Diameter at 10 cm Relationship** parameter

The standard diameter-height relationships

"Standard" is one of the names used to describe a set of allometric functions relating height to diameter. There is one for adults and saplings, and one for seedlings. These are called "standard" because they were the original SORTIE functions and until recently were the only choices.

Parameters

Parameter name	Description
Maximum Tree Height, in meters	The maximum tree height for a species, in meters. No tree, no matter what allometric function it uses, is allowed to get taller than this. Used by all species.
Slope of Asymptotic Height	Exponential decay term in the adult and sapling standard function for DBH and height.
Slope of Height-	The slope of the seedling standard function for diameter at 10 cm and

Diameter at 10 cm
Relationship

height.

The standard sapling and adult DBH - height function is:

$$height = 1.35 + (H_1 - 1.35)(1 - e^{-B*DBH})$$

where:

- *height* is tree height in meters
- H_1 is the **Maximum Tree Height, in m** parameter
- B is the **Slope of Asymptotic Height** parameter
- DBH is tree DBH in cm

In some articles, B (**Slope of Asymptotic Height**) is a published parameter. Other articles instead use H_1 and another parameter, H_2 , which was called the DBH to height relationship. In this case, B can be calculated from published values as $B = H_2/H_1$.

The standard seedling $diam_{10}$ - height function is:

$$height = 0.1 + 30*(1 - e^{(-\alpha * diam_{10})})$$

where:

- *height* is tree height in meters
- α is the **Slope of Height-Diameter at 10 cm Relationship** parameter
- $diam_{10}$ is tree diameter at 10 cm height, in cm

The linear diameter-height relationship

The linear diameter-height relationship is the same for all life history stages, but each stage can use a different set of parameter values.

Parameters

Parameter name	Description
Maximum Tree Height, in meters	The maximum tree height for a species, in meters. No tree, no matter what allometric function it uses, is allowed to get taller than this. Used by all species.
Adult Linear Function Intercept	The intercept of the adult linear function for DBH and height.

Adult Linear Function Slope	The slope of the adult linear function for DBH and height.
Sapling Linear Function Intercept	The intercept of the sapling linear function for DBH and height.
Sapling Linear Function Slope	The intercept of the sapling linear function for DBH and height.
Seedling Linear Function Intercept	The intercept of the seedling linear function for DBH and height.
Seedling Linear Function Slope	The slope of the seedling linear function for DBH and height.

The linear diam - height function is:

$$height = a + b * diam$$

where:

- *height* is tree height, in m
- *a* is the appropriate linear intercept parameter (either **Adult Linear Function Intercept**, **Sapling Linear Function Intercept**, or **Seedling Linear Function Intercept**)
- *b* is the appropriate linear slope parameter (either **Adult Linear Function Slope**, **Sapling Linear Function Slope**, or **Seedling Linear Function Slope**)
- *diam* is DBH (in cm) for saplings and adults, or *diam*₁₀ (in cm) for seedlings

The reverse linear diameter-height relationship

The reverse linear diameter-height relationship is the same for all life history stages, but each stage can use a different set of parameter values. The name comes from the fact that it is almost the same as the linear function, but with height and diameter switched. In other words, in the linear function, height is a linear function of diameter. In the reverse linear function, diameter is a linear function of height.

Parameters

Parameter name	Description
Maximum Tree Height, in meters	The maximum tree height for a species, in meters. No tree, no matter what allometric function it uses, is allowed to get taller than this. Used by all species.

Adult Reverse Linear Function Intercept	The intercept of the adult reverse linear function for DBH and height.
Adult Reverse Linear Function Slope	The slope of the adult reverse linear function for DBH and height.
Sapling Reverse Linear Function Intercept	The intercept of the sapling reverse linear function for DBH and height.
Sapling Reverse Linear Function Slope	The slope of the sapling reverse linear function for DBH and height.
Seedling Reverse Linear Function Intercept	The intercept of the seedling reverse linear function for DBH and height.
Seedling Reverse Linear Function Slope	The slope of the seedling reverse linear function for DBH and height.

The reverse linear diam - height function is:

$$height = (diam - a) / b$$

where:

- *height* is tree height, in m
- *a* is the appropriate reverse linear intercept parameter (either **Adult Reverse Linear Function Intercept**, **Sapling Reverse Linear Function Intercept**, or **Seedling Reverse Linear Function Intercept**)
- *b* is the appropriate reverse linear slope parameter (either **Adult Reverse Linear Function Slope**, **Sapling Reverse Linear Function Slope**, or **Seedling Reverse Linear Function Slope**)
- *diam* is DBH (in cm) for saplings and adults, or *diam*₁₀ (in cm) for seedlings

The power diameter-height relationship

The power diameter-height relationship relates height and diameter with a power function. Since it uses diameter at 10 cm, NOT DBH, it is active for saplings only.

Parameters

Parameter name	Description
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Power Function "a"	The "a" parameter in the power function for the height-diameter relationship.
Power Function Exponent "b"	The exponent, or "b" parameter, in the power function for the height-diameter relationship.

The power diam - height function is:

$$height = a * d_{10}^b$$

where:

- *height* is tree height, in m
- *a* is the **Power Function "a"** parameter
- *b* is the **Power Function Exponent "b"** parameter
- *d₁₀* is diameter at 10 cm (in cm)

Setting up trees: parameters

Here is the complete list of parameters for the tree population and [allometry](#). Not all of them are required.

Tree parameters

Parameters dealing with [tree initial conditions](#) - none of these are required:

- **Initial Densities** The density of trees, in number per hectare, for that size class.
- **Initial Density (#/ha) - Seedling Height Class 1** Number of seedlings per hectare to create in the first seedling height class. The lower bound of this class is 0 cm and the upper bound is the value in the **Seedling Height Class 1 Upper Bound, in cm** parameter.
- **Initial Density (#/ha) - Seedling Height Class 2** Number of seedlings per hectare to create in the second seedling height class. The lower bound of this class is the value in the **Seedling Height Class 1 Upper Bound, in cm** parameter and the upper bound is the value in the **Seedling Height Class 2 Upper Bound, in cm** parameter.
- **Initial Density (#/ha) - Seedling Height Class 3** Number of seedlings per hectare to create in the third seedling height class. The lower bound of this class is the value in the **Seedling Height Class 2 Upper Bound, in cm** parameter and the upper bound is 135 cm (the tallest possible seedling height).
- **Seedling Height Class 1 Upper Bound, in cm** The upper bound of the first seedling height class, in cm, for specifying seedling initial densities. The lower bound of the size class is 0.
- **Seedling Height Class 2 Upper Bound, in cm** The upper bound of the second seedling height class, in cm, for specifying seedling initial densities. The lower bound of the size

class is the **Seedling Height Class 2 Upper Bound, in cm** parameter. There is a third size class, whose lower bound is this parameter's value and whose upper bound is 135 cm.

- **Tree Map To Add As Text** External tree map file to add.

Basic tree population parameters - required:

- **Minimum Adult DBH** The minimum DBH at which trees are considered adults. (See more about tree life history stages [here](#).)
- **Max Seedling Height (meters)** The maximum seedling height, in meters. Trees taller than this height are saplings. (See more about tree life history stages [here](#).)
- **New Seedling Diameter at 10 cm** The average diameter at 10 cm height value for newly created seedlings, when another size is not specified. Actual values are randomized slightly around this value.

In addition to the values listed in the parameter window, the tree population also keeps the list of species and size classes. These can be edited in the [Tree population - edit species list window](#) and [Tree population - edit initial density size classes window](#).

Tree initial conditions

Tree initial conditions are the trees in the SORTIE forest when a simulation begins. The initial conditions are often of vital importance to how a run develops.

There are two ways to add trees at the beginning of the run, and they can be used together or separately. The first is to ask the model to create trees for you according to your chosen species composition and size structure. The second way is to directly list a particular set of trees in a tree map.

Defining initial conditions using species composition and size structure

For saplings and adults, you can set up DBH size classes and enter the desired density in each size class. To set up size classes, use the [Edit size classes window](#). You can define as many size classes as you want. The values that you enter are the upper bounds of each class. Once you have defined all of your size classes, you can enter the desired number of stems per hectare for each species for each class in the [tree parameters](#) which you edit using the [Model settings window](#).

There are two different ways to enter seedling densities. Defining a DBH size class of zero gives you a line for entering stems per hectare of seedlings. These seedlings will be brand new, with sizes approximating the value in the **New Seedling Diameter at 10 cm** [tree parameters](#). If you would like more control over seedling sizes, you can define three height classes densities for each in the tree parameters.

The resulting trees are randomly distributed around the plot. Actual sizes are chosen randomly from a uniform distribution within each size class.

Tree maps

Tree maps are lists of individual trees. You can add one or more maps to your parameter file. The maps can come from detailed output files from other runs, or you can make your own [tab-delimited tree maps](#). The preferred method of incorporating a tree map to a run is to add it directly into a parameter file. However, if the number of trees is very large, it may make the XML file too big to read. In this case, a text tree file's filename can be added to the parameter file instead and SORTIE can read the trees directly from the file.

Choosing how to set up the initial conditions

In most cases, you would define your initial conditions using DBH size classes. They are simple to define and describe. There are cases where you would need a tree map. For example:

- You intend to model a particular real-life plot
- You want to use a mid-run timestep of another simulation as the starting point of a new simulation
- You want a particular spatial pattern of trees instead of a random distribution
- You want to do a set of simulations that all start out exactly the same way

You can mix the two methods as well. If you have a tree map of adults you'd like to use, you can add seedlings and saplings using size classes.

It is important to consider initial conditions for juveniles. It can take awhile for seed dispersal, establishment, and recruitment to create juveniles in a run. You may see strange behavior in your first timesteps if you're missing a whole life cycle stage in your tree population.

Tree data member list

This is a list of the possible data that a tree can have. You can save this data in a [detailed output file](#) by using the [Setup tree save options](#) window.

Not all data is always available. Certain sets of behaviors require additional information about a tree. One of the ways in which behaviors communicate with one another is by defining new pieces of data for trees and then setting and reading values for those data. A piece of data created by a behavior is only attached to those tree species and tree types to which the behavior is applied.

Long name	Short code name	Data type	Description	Created by
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X	X	Float	The coordinate of the tree, in meters, on the X axis in the SORTIE plot .	Tree population - always available
Y	Y	Float	The coordinate of the tree, in meters, on the Y axis in the SORTIE plot .	Tree population - always available
DBH	DBH	Float	The diameter at breast height of a tree, in cm. This does not apply to seedlings.	Tree population - always available
Diameter at 10 cm	Diam10	Float	The tree's diameter at 10 cm height, in cm. This applies only to seedlings and saplings.	Tree population - always available
Height	Height	Float	The tree's height in meters.	Tree population - always available
Crown Radius	Crown Radius	Float	The tree's crown radius in meters. Note that this value is updated only on an as-needed basis. This means that the value may show up as -1, meaning that the tree's crown radius was not requested this time step. Also, this value will almost certainly reflect the tree's size at the beginning of the timestep, when crown dimension calculations are made, rather than the end of the timestep, as with the other tree dimensions. This does not apply to seedlings.	Tree population - always available
Crown Depth	Crown Depth	Float	The tree's crown depth in meters. The same warning applies as with crown radius. This does not apply to seedlings.	Tree population - always available
Age	Age	Integer	The time since death, in years.	Tree

			Only for snags.	population - always available
Why dead	Why dead	Integer	Reason code for why a tree died. Only for snags. Integer of one of the following: 1 = harvest, 2 = natural causes, 3 = disease, 4 = fire, 5 = insects, or 6 = storm	Tree population - always available
Light level	Light	Float	Light level for the tree. This could be GLI, or percent shade (if Sail Light is used).	Any of the light behaviors except the Beer's Law light filter
Growth	Growth	Float	Amount of radial growth per year in mm.	Any of the growth behaviors that increment diameter growth
Light filter respite counter	lf_count	Integer	Number of years of respite for a new seedling from the effects of the light filter.	Beer's law light filter
Rooting height	z	Float	The height, in mm, above ground level at which a seedling is rooted.	Beer's law light filter
Years released	ylr	Integer	The length of the current release period, in years.	The absolute growth behaviors
Years suppressed	yls	Integer	The length of the current suppression period, in years.	The absolute growth behaviors
Dead flag	dead	Integer	A flag for whether a tree has died and why. Integer of one of the following: 0 = not dead, 1 = harvest, 2 = natural causes, 3 = disease, 4 = fire, 5 = insects, or 6 = storm. This is used by the dead tree remover	Any of the mortality behaviors

			behavior to find the trees it should remove.	
Storm Damage Value	stm_dmg	Integer	An integer value with the damage level of a storm and how long it has been damaged. A value of 0 means no damage; a value starting with 1 means medium damage; a value starting with 2 means complete damage. The digits at the end count how many years since the damaging event. For example, a value of 1005 is a tree that received medium damage 5 years ago.	Storm damage applier
Tree Bole Volume	Bole Vol	Float	The volume of a tree, in cubic feet.	Tree bole volume calculator
Tree Volume	Volume	Float	Volume of the tree, in cubic meters.	Tree volume calculator
Tree Biomass	Biomass	Float	Biomass of the tree, in metric tons (Mg).	Dimension analysis
Tree Age	Tree Age	Integer	Age of the tree, in years.	Tree age
Snag Decay Class	SnagDecayClass	Integer	Snag decay class.	Snag Decay Class Dynamics
New Break Height	NewBreakHeight	Float	Snag break height, if the break occurred this timestep. -1 if the snag is unbroken.	Snag Decay Class Dynamics
Snag Old Break Height	SnagOldBreakHeight	Float	Snag break height, if the break occurred in a previous timestep. -1 if the snag is unbroken.	Snag Decay Class Dynamics
Fall	Fall	Boolean	Whether a tree that has died this timestep has fallen (true), or remains standing as a snag (false).	Snag Decay Class Dynamics
Pre-harvest growth	PreHarvGr	Float	Growth prior to the last harvest.	Lagged post harvest

				growth
Last stochastic	autocorr	Float	The previous year's stochastic growth factor.	Michaelis Menton with negative growth - height only
Years Infested	YearsInfested	Integer	The number of years that a tree has been infested with insects or pathogens.	Insect Infestation and Density Dependent Infestation
Density Dependent Resistance Status	DensDepResistanceStatus	Integer	The resistance status of a tree. 1 = resistant; 2 = conditionally susceptible; 3 = susceptible.	Density Dependent Infestation
Vigorous	vigorous	Boolean	Whether a tree is vigorous or not (true or false).	Tree Quality Vigor Classifier
Sawlog	sawlog	Boolean	Whether a tree is sawlog quality or not (true or false).	Tree Quality Vigor Classifier
Tree class	treeclass	Integer	Tree class number, 1-6.	Tree Quality Vigor Classifier

What is a behavior?

Behaviors are the active part of a SORTIE simulation. Nothing in the model is pre-defined, default, or automatic. Everything that happens is done by a behavior, and all behaviors are under user control.

Behaviors fall into two categories. The first category is behaviors that act on trees and roughly correspond to biological and environmental processes. These behaviors calculate how much individual trees grow, select trees that will die, distribute seeds, and perform other similar jobs. The second category is behaviors that perform helper functions for the simulation itself. These behaviors do things like measure and calculate forest metrics and write output.

Each behavior has a clearly defined action. Each behavior in a run performs its action once per timestep in a pre-defined order.

Relationship of behaviors to trees and grids

[Trees](#) and [grids](#) are the [state data](#) of SORTIE. Behaviors act on this data to change it and evolve the model state.

Behaviors are assigned to specific data, and may not act outside this scope.

SORTIE directly manages all the state data needed for a given simulation and automatically ensures the creation of any data that a behavior is assigned to work on. Users can adjust the initial conditions of all state data at the beginning of the simulation.

Choosing behaviors for a run

Setting up behaviors is the most important step in creating a new simulation. To choose which behaviors to include in the run and how to apply them, use the [Model flow window](#).

There are a few general guidelines for choosing a set of behaviors from scratch.

Start with the trees

Behaviors that act on trees are assigned to trees based on species and [life history stage](#) (otherwise referred to as tree type). Move through the tree life cycle for each species and pick behaviors for growth, mortality, and reproduction. There may not be a behavior that does exactly what you want, but with the creative use of [behavior parameters](#), you may be able to achieve the same effect. For instance, there may be a parameter that when assigned a particular value cancels out a function term you don't need, or a set of parameter values that can cause a function to mimic another function shape.

Carefully check the behavior assignments to particular trees. Behaviors often have some rules about how they can be applied, but these tend to be limited in the interests of maximum flexibility. The model doesn't try to second-guess what you are doing beyond making sure the simulation can run as described. Make sure that you applied a complete set of lifecycle behaviors to each species and life history stage.

Check the dependencies

Many behaviors rely on the work of other behaviors. Check the documentation for the set of behaviors you have so far to see if you need to add others. For instance, if you have a behavior that calculates growth as a function of light level, you will need to add a behavior to calculate the light level. Each behavior's documentation will give you all dependency requirements.

Add analysis and output

Forest metrics and output are handled by behaviors just like everything else in SORTIE. Basic metrics like stem density and basal area are handled directly by the output behavior. You can add additional behaviors (called [analysis behaviors](#)) to calculate extra metrics like biomass or tree spatial distribution indexes.

Output is one of a set of behaviors that uses a separate interface for setup - in this case, the [Output setup window](#).

It is generally a good idea to finish setting up a parameter file at this point and to run it. There is generally troubleshooting to be done on the basic lifecycle behaviors and the fewer behaviors that are in a run, the easier it is to identify and fix problems.

Add external events

If you have behaviors you would like to use beyond the basic tree lifecycle, add them at this point. These include things like disturbance events and climate change.

Check behavior order

The [parameter file](#) specifies which behaviors to include in the simulation, and in which order they should be run. Theoretically it is possible to put behaviors in any order, but of course, most simulations constructed that way would not make sense. When you structure a run, the behaviors are placed in functional groups. To prevent nonsensical simulations, you cannot move a behavior outside of its functional group in the overall run order; however, you can re-order behaviors within the functional groups. Sometimes this will have an effect on the overall simulation outcome, and sometimes it won't. Refer to the documentation for individual behaviors and functional groups to learn how run order might affect a behavior.

Setting up behaviors: parameters

Almost all behaviors need values and settings from the user to function. These are called the behavior parameters.

Once you have established the set of behaviors for your run, you will need to provide values for all parameters for those behaviors. To edit the behavior parameters, use the "Edit-> Parameters" menu option. You may want to work with one set of parameters at a time when you are first entering them, because the window will validate your entries before accepting them and it will be easier to troubleshoot one section at a time.

When editing the parameters, if you are not sure what a parameter is or what value you should enter, you can check the parameters page for that behavior functional group. It lists all parameters for all behaviors in that group in alphabetical order with a short description of each, and tells you what behavior they belong to.

Once the parameters are entered, you can view them all at once and save a copy of a text version as a record.

State change behaviors

State change behaviors act on the basic properties of the virtual plot being modeled.

Behavior	Description
Precipitation Climate Change behavior	Changes the value of the Mean Annual Precipitation parameter of the SORTIE plot.
Temperature Climate Change behavior	Changes the value of the Mean Annual Temperature parameter of the SORTIE plot.
Seasonal Water Deficit	Changes the value of the seasonal water deficit parameter of the SORTIE plot.

Precipitation Climate Change

This behavior changes the value of the [Mean Annual Precipitation](#) parameter of the SORTIE plot. This can be used to simulate the effects of climate change. If the run does not have a behavior that uses precipitation, this will have no effect.

Parameters for this behavior

Parameter name	Description
Precipitation Change - B	"B" in the function for varying precipitation through time.
Precipitation Change - C	"C" in the function for varying precipitation through time.
Precipitation Change - Precip Lower Bound	The lower bound for allowed precipitation values.

Precipitation Change - Precip Upper Bound	The upper bound for allowed precipitation values.
Update Seasonal Precipitation Proportionally?	Whether or not to update seasonal precipitation in the same proportion as annual precipitation.

How it works

The value for plot precipitation is a function of time elapsed since the start of the run, as follows:

$$P = P_I + B * t^C$$

where:

- P is the mean annual precipitation, in mm, at time t
- P_I is the mean annual precipitation value at the start of the run, as assigned in the [Plot parameters](#)
- B is the **Precipitation Change - B** parameter
- C is the **Precipitation Change - C** parameter
- t is the time elapsed, in years, since the start of the run

This value is then given to the [Plot](#) object which makes it available to other behaviors in the run.

You can set bounds on the possible precipitation values using the **Precipitation Change - Precip Lower Bound** and **Precipitation Change - Precip Upper Bound** parameters. Values are not allowed to go outside these limits.

If you wish, the other [seasonal precipitation](#) can be updated along with annual precipitation. They are changed in the same proportion that annual precipitation changes. If you want this behavior, set the **Update Seasonal Precipitation Proportionally?** parameter to true.

How to apply it

Add this behavior to the run. You can use it alone or in addition to the [Temperature Climate Change](#) behavior. You do not need to assign this behavior to trees.

Temperature Climate Change

This behavior changes the value of the [Mean Annual Temperature](#) parameter of the SORTIE plot. This can be used to simulate the effects of climate change. If the run does not have a behavior that uses temperature, this will have no effect.

Parameters for this behavior

Parameter name	Description
Temperature Change - B	"B" in the function for varying temperature through time.
Temperature Change - C	"C" in the function for varying temperature through time.
Temperature Change - Temp Lower Bound	The lower bound for allowed temperature values.
Temperature Change - Temp Upper Bound	The upper bound for allowed temperature values.

How it works

The value for plot temperature is a function of time elapsed since the start of the run, as follows:

$$T = T_l + B * t^C$$

where:

- T is the mean annual temperature, in degrees C, at time t
- T_l is the mean annual temperature value at the start of the run, as assigned in the [Plot parameters](#)
- B is the **Temperature Change - B** parameter
- C is the **Temperature Change - C** parameter
- t is the time elapsed, in years, since the start of the run

This value is then given to the [Plot](#) object which makes it available to other behaviors in the run.

You can set bounds on the possible temperature values using the **Temperature Change - Temp Lower Bound** and **Temperature Change - Temp Upper Bound** parameters. Values are not allowed to go outside these limits.

How to apply it

Add this behavior to the run. You can use it alone or in addition to the [Precipitation Climate Change](#) behavior. You do not need to assign this behavior to trees.

Seasonal Water Deficit

This behavior changes the value of the [Seasonal Water Deficit](#) parameter of the SORTIE plot in response to changes in the mean annual temperature and precipitation of the plot. Seasonal water deficit is the difference between potential evapotranspiration in the presence of limitless water and actual evapotranspiration based on available precipitation. As such, it is an index of the degree to which actual supply of moisture fails to meet "demand" for moisture. This assumes that monthly temperature and rainfall patterns do not change along with changes in mean annual temperature and precipitation.

Parameters for this behavior

Parameter name	Description
Available Water Storage in Top 100 cm Soil	Maximum available water storage in the top 100 cm of the soil, in mm.
Proportion of Precipitation in January	Proportion of annual precipitation that falls during the month of January, as a value between 0 and 1.
Proportion of Precipitation in February	Proportion of annual precipitation that falls during the month of February, as a value between 0 and 1.
Proportion of Precipitation in March	Proportion of annual precipitation that falls during the month of March, as a value between 0 and 1.
Proportion of Precipitation in April	Proportion of annual precipitation that falls during the month of April, as a value between 0 and 1.
Proportion of Precipitation in May	Proportion of annual precipitation that falls during the month of May, as a value between 0 and 1.
Proportion of Precipitation in June	Proportion of annual precipitation that falls during the month of June, as a value between 0 and 1.
Proportion of Precipitation in July	Proportion of annual precipitation that falls during the month of July, as a value between 0 and 1.

Proportion of Precipitation in August	Proportion of annual precipitation that falls during the month of August, as a value between 0 and 1.
Proportion of Precipitation in September	Proportion of annual precipitation that falls during the month of September, as a value between 0 and 1.
Proportion of Precipitation in October	Proportion of annual precipitation that falls during the month of October, as a value between 0 and 1.
Proportion of Precipitation in November	Proportion of annual precipitation that falls during the month of November, as a value between 0 and 1.
Proportion of Precipitation in December	Proportion of annual precipitation that falls during the month of December, as a value between 0 and 1.
January Radiation (cal/cm ²)	Global radiation received during the month of January, in cal / cm ² .
February Radiation (cal/cm ²)	Global radiation received during the month of February, in cal / cm ² .
March Radiation (cal/cm ²)	Global radiation received during the month of March, in cal / cm ² .
April Radiation (cal/cm ²)	Global radiation received during the month of April, in cal / cm ² .
May Radiation (cal/cm ²)	Global radiation received during the month of May, in cal / cm ² .
June Radiation (cal/cm ²)	Global radiation received during the month of June, in cal / cm ² .
July Radiation	Global radiation received during the month of July, in cal / cm ² .

(cal/cm ²)	
August Radiation (cal/cm ²)	Global radiation received during the month of August, in cal / cm ² .
September Radiation (cal/cm ²)	Global radiation received during the month of September, in cal / cm ² .
October Radiation (cal/cm ²)	Global radiation received during the month of October, in cal / cm ² .
November Radiation (cal/cm ²)	Global radiation received during the month of November, in cal / cm ² .
December Radiation (cal/cm ²)	Global radiation received during the month of December, in cal / cm ² .
Ratio of January Temp to Annual Temp	January temperature divided by mean annual temperature.
Ratio of February Temp to Annual Temp	February temperature divided by mean annual temperature.
Ratio of March Temp to Annual Temp	March temperature divided by mean annual temperature.
Ratio of April Temp to Annual Temp	April temperature divided by mean annual temperature.
Ratio of May Temp to Annual Temp	May temperature divided by mean annual temperature.
Ratio of June Temp to Annual Temp	June temperature divided by mean annual temperature.
Ratio of July Temp	July temperature divided by mean annual temperature.

to Annual Temp	
Ratio of August Temp to Annual Temp	August temperature divided by mean annual temperature.
Ratio of September Temp to Annual Temp	September temperature divided by mean annual temperature.
Ratio of October Temp to Annual Temp	October temperature divided by mean annual temperature.
Ratio of November Temp to Annual Temp	November temperature divided by mean annual temperature.
Ratio of December Temp to Annual Temp	December temperature divided by mean annual temperature.

How it works

The first step is calculating monthly temperature and precipitation based on the latest values for the plot.

$$T_i = T * RT_i$$

$$P_i = P * RP_i$$

where:

- T_i is temperature, in degrees C, for month i
- P_i is precipitation, in mm, for month i
- P is the mean annual precipitation, in mm
- T is the mean annual temperature, in degrees C
- RT_i is the **Ratio of [month i] Temp to Annual Temp** parameter
- RP_i is the **Proportion of Precipitation in [month i]** parameter

Then PET (monthly potential evapotranspiration) is calculated as:

$$PET_i = 0.013 * (T_i / (T_i + 15)) * (R_s + 50)$$

where:

- PET_i is monthly potential evapotranspiration in mm
- T_i is monthly temperature in degrees C
- R_s is the [month i] **Radiation (cal/cm2)** parameter

If $T_i \leq 0$, then $PET_i = 0$.

In order to calculate actual evapotranspiration, we need monthly soil moisture values. Monthly soil moisture storage is calculated as:

$$sms_i = 0 < sms_{i-1} + precip_i - PET_i < MaxAWS$$

where:

- sms_i is the soil moisture, in mm, for the current month
- sms_{i-1} is the soil moisture, in mm, for the previous month
- $precip_i$ is the monthly precipitation (mm) for the current month
- PET_i is potential evapotranspiration for the current month
- $MaxAWS$ is the **Available Water Storage in Top 100 cm Soil**

It is assumed that the soil is saturated on the last day of the year, so for January, $sms_{i-1} = MaxAWS$.

Monthly actual evapotranspiration (AET) is calculated as:

$$AET_i = sms_i + precip_i$$

if $sms_{i+1} \leq 0$, or

$$AET_i = PET_i$$

if $sms_{i+1} > 0$.

Annual AET is the sum of the monthly AET values, and annual PET is the sum of the monthly PET values; and Seasonal Water Deficit = PET - AET.

This value is then given to the [Plot](#) object which makes it available to other behaviors in the run.

How to apply it

Add this behavior to the run. You do not need to assign this behavior to trees.

Disturbance behaviors

Disturbance behaviors simulate different kinds of forest disruption. These behaviors cause tree damage and death due to a variety of processes.

Behavior	Description
<u>Density Dependent Infestation</u>	Simulates a pathogen outbreak in the plot.
<u>Competition Harvest</u>	Performs harvests in a way that preferentially removes the most competitive individuals in a plot.
<u>Generalized Harvest Regime</u>	The behavior itself decides when harvests will occur and how much to cut based on total plot adult biomass, then chooses trees to cut with the help of a preference algorithm.
<u>Harvest</u>	Implements complex silvicultural treatments.
<u>Harvest interface</u>	Allows SORTIE to work directly with an external harvesting program.
<u>Insect Infestation</u>	Simulates an insect outbreak by choosing and marking infested trees.
<u>Episodic mortality</u>	Allows you to replicate tree-killing events with the same level of control you have when defining Harvest events.
<u>Random browse</u>	Simulates random browsing from herbivores.
<u>Storm disturbance</u>	Simulates the effects of wind damage from storms.
<u>Storm damage applier</u>	Decides which trees are damaged when a storm has occurred and how badly.
<u>Storm damage killer</u>	Kills trees damaged in storms.
<u>Storm direct killer</u>	Kills trees based on storm severity, without an intervening damage step.
<u>Selection harvest</u>	Allows you to specify target basal areas for a tree population as a method of harvest input, instead of designing specific harvest events.
<u>Windstorm</u>	Kills trees due to storm events.

Density Dependent Infestation

This behavior simulates an outbreak of a pest or pathogen in the plot. It chooses and marks affected trees, allowing other behaviors to make use of this information. The number of affected trees is a function of time since infestation began. The infestation has no spatial pattern.

This behavior only chooses trees for infestation. It does not kill them or alter their dynamics in any way. Other behaviors may take advantage of the infestation status of trees.

Parameters for this behavior

Parameter name	Description
Infestation "a"	The value of "a" in the equation for determining the proportion of infested trees.
Infestation "bx"	The value of "bx" in the equation for determining the proportion of infested trees.
Infestation "by"	The value of "by" in the equation for determining the proportion of infested trees.
Infestation Cohort DBH Threshold	The minimum DBH for a tree to be in the larger cohort for infestation. Use 0 if you don't want to divide the trees into cohorts.
Infestation Max Rate	The "max" value in the equation for determining the proportion of infested trees, as a value between 0 and 1.
Infestation Min DBH	The minimum DBH at which a tree can become infested.
First Year of Infestation Relative to Start	The year that an infestation starts, relative to the beginning of the run (it is year 0 before the first timestep begins). A negative value means the infestation started before the run did.
Proportion of Conditionally Susceptible Trees (0-1)	The proportion of the trees in the plot that are to be classed as conditionally susceptible, as a value between 0 and 1.
Proportion of Resistant Trees (0-1)	The proportion of the trees in the plot that are to be classed as resistant, as a value between 0 and 1.

How it works

Trees fall into three categories: resistant, conditionally susceptible, and susceptible. Trees classed as resistant are never infected. Trees classed as conditionally susceptible and susceptible are

treated the same by this behavior but may be treated differently by others. The proportion of trees that are resistant and conditionally susceptible are entered in the **Proportion of Resistant Trees (0-1)** and **Proportion of Conditionally Susceptible Trees (0-1)** parameters, respectively, as a value between 0 and 1. Trees are randomly assigned to these categories according to these proportions and retain their categorization for life. This assignment is recorded in a [tree data member](#) called "Resistance Status".

The proportion of trees of a particular species infested as a function of time is as follows:



where:

- P is the proportion of the eligible tree population infested.
- a is the **Infestation "a"** parameter.
- max is the **Insect Infestation Max Rate** parameter, as a value between 0 and 1. This is the maximum infestation rate that will occur regardless of how long the infestation lasts.
- T is the time, in years, since the start of the infestation.

"b" is calculated as follows:

$$b = bx * BA + by$$

where:

- bx is the **Infestation "bx"** parameter
- by is the **Infestation "by"** parameter
- BA is the proportion of tree basal area in the plot of individuals with DBH above the minimum infestible DBH

BA is the basal area of trees in to which this species applies (above the minimum infestible DBH) divided by total plot basal area. Both resistant and non-resistant trees count towards the basal area of the behavior trees. For total plot basal area, all saplings and adults count.

The proportion of trees infested at time T does not depend on additions to or subtractions from the pool of eligible trees. Each timestep, the number of infested trees of each species is counted and additional trees are randomly selected for new infestation until approximately the right number are infested. If for some reason there are more trees infested than there should be at that time, no additional trees are infested.

Susceptible individuals can be split into two size cohorts, with the cutoff DBH set as the **Infestation Cohort DBH Threshold** parameter. All the individuals above this DBH are infected before any below the cutoff are. (Note that when the value of **Infestation Max Rate** is less than one, it is possible that no individuals below the DBH cutoff will ever be infected.)

When selecting trees for infestation, the location of the trees is not considered. It is assumed that all trees have an equal chance of becoming infested no matter where they are in the plot. This behavior uses a [tree data member](#) called "Years Infested" to track which trees are infested and how long they have been so.

You choose when an infestation begins with the **First Year of Infestation Relative to Start** parameter. The first year is relative to the start of the run (year 0 is just before the start of timestep 1; at the end of timestep 1, the current year is equal to the number of years per timestep). The infestation start year can be negative, indicating that the infestation is already in progress at the start of the run. In this case, the behavior will calculate the current proportion of infested trees according to the equation above and choose the appropriate number from the initial conditions trees. They will be randomly assigned an infestation time corresponding to the distribution of times expected after that many years of infestation.

Once started, an infestation never ends even if all trees in the infestible pool die. Any new trees of infestible species that enter the plot will be eligible for infestation.

How to apply it

Apply this behavior to saplings and/or adults of any species. All species to which this behavior applies are treated as a common pool for determining things like proportion of basal area.

Competition Harvest

Competition Harvest performs harvests in a way that preferentially removes the most competitive individuals in a plot. It also decides when and how much to harvest based on criteria you give it.

Trees removed by this behavior will have a mortality reason code of "harvest".

Parameters for this behavior

Parameter name	Description
Competition Harvest: Amount of Harvest Per Species (0 - 1)	Trees to harvest can be treated as a common pool where species identity is not a factor in selecting trees for harvest. In this case, all values should be set to 1.0. Otherwise, species can be harvested at a fixed proportion. In this case, set the proportion to harvest for each species as a value between 0 and 1, with all values adding up to 1.
Competition Harvest: Amount to Harvest	Amount to harvest, depending on the harvest type. If this is a fixed interval harvest (the value in Competition Harvest: Harvest Type is set to "Fixed Interval"), this is the basal area of the plot after harvesting, in m ² /ha; if this is a fixed basal area threshold harvest with a fixed amount to cut ("Fixed BA Amt"), this is the amount of basal area to cut, in m ² /ha;

	if this is a fixed basal area threshold harvest with proportion of total to cut ("Fixed BA %"), this is the proportion of the total plot's basal area to cut between 0 and 1.
Competition Harvest: C	The slope of the curve "C" of the competitive effect of a target on a neighbor of each species.
Competition Harvest: D	The steepness of the curve "D" of the competitive effect of a target on a neighbor of each species.
Competition Harvest: DBH Effect of Targets (alpha)	Exponent controlling the effect of a target's DBH on neighbors.
Competition Harvest: Distance Effect of Targets (beta)	Exponent controlling the effect of distance between target and neighbors.
Competition Harvest: Filename for List of Harvested Trees	Optional. If there is a value in this field, the Competition Harvest behavior will write a tab-delimited text file of this name with all the trees cut during the run. In batch runs this will get overwritten and only contain the last run's list.
Competition Harvest: Fixed BA Harvest Threshold (m2/ha)	For fixed basal area threshold harvests (the value in Competition Harvest: Harvest Type is set to either "Fixed BA %" or "Fixed BA Amt"), this is the amount of basal area that the plot must have before a harvest occurs. This value is ignored if the harvest type is "Fixed Interval".
Competition Harvest: Fixed Interval Harvest Interval (yr)	For fixed basal area threshold harvests (the value in Competition Harvest: Harvest Type is set to "Fixed Interval"), this is the number of years between harvests. This value is ignored if the harvest type is "Fixed BA %" or "Fixed BA Amt".
Competition Harvest: Harvest Type	The type of harvest to perform. "Fixed BA %" means that there is a harvest every time the plot reaches a fixed basal area threshold, and the amount cut is a proportion of the total basal area; "Fixed BA Amt" means that there is a harvest every time the plot reaches a fixed basal area threshold, and the amount to cut is a fixed amount of basal area; "Fixed Interval" means that there is a harvest every X years, with the plot being harvested until it is cut back to a certain amount of basal area.
Competition Harvest: Minimum DBH to Harvest	The minimum DBH, in cm, of trees that can be harvested.
Competition	For fixed basal area threshold harvests (the value in Competition

Harvest: Min Years Between Fixed BA Harvests	Harvest: Harvest Type is set to either "Fixed BA %" or "Fixed BA Amt"), this is the minimum number of years that must pass between harvests, even if the plot basal area is over the harvesting threshold. This value is ignored if the harvest type is "Fixed Interval".
Competition Harvest: Maximum DBH to Harvest	The maximum DBH, in cm, of trees that can be harvested.
Competition Harvest: Max Radius of Competitive Effects (m)	The maximum radius in meters at which a target tree of that species competitively affects other trees.
Competition Harvest: Species i Target Lambda	The competitive effect of targets of Species i on neighbors of every other species.
Competition Harvest: Size Sensitivity (gamma)	The effect of a neighbor tree's size on its sensitivity to competition.
Competition Harvest: Target DBH Divisor	The value by which target DBHs are divided when calculating competitive effects. This can be used to make units adjustments.
Gen Harvest Acceptable Deviation From Cut Target	The amount by which it is acceptable to deviate from the harvest target basal area removal without triggering a second harvest pass. Expressed as a proportion of the target basal area, between 0 and 1.

How it works

Competition Harvest performs harvests when specific conditions are met in the plot. The amount harvested is also based on conditions in the plot. There are three ways to specify the timing and amount of harvesting. The desired method is set in the **Competition Harvest: Harvest Type** parameter. The harvest types are:

- *Fixed basal area threshold, cutting a specific amount of basal area.* (Set the harvest type parameter to "Fixed BA Amt".) A harvest occurs whenever the plot's basal area exceeds a certain threshold, set in the **Competition Harvest: Fixed BA Harvest Threshold (m²/ha)** parameter. The same amount of basal area is harvested every time, set in the **Competition Harvest: Amount to Harvest** parameter. To make sure that harvests do not happen too frequently, set a minimum interval between harvests in the **Competition Harvest: Min Years Between Fixed BA Harvests** parameter.
- *Fixed basal area threshold, cutting a proportion of the plot basal area.* (Set the harvest type parameter to "Fixed BA %".) This is the same as the first harvest type, except the

amount to harvest is different. This harvest removes a set proportion of the plot's basal area. Set this proportion (between 0 and 1) in the **Competition Harvest: Amount to Harvest** parameter.

- *Fixed interval, cutting plots back to a basal area threshold.* Harvests occur at a fixed interval, set in the **Competition Harvest: Fixed Interval Harvest Interval (yr)** parameter. The first timestep will have a harvest. Harvests remove trees until the plot reaches a specific amount of basal area, set in the **Competition Harvest: Amount to Harvest** parameter.

Competition Harvest uses these criteria to determine when and how much to cut. Harvests occur over the the entire plot area.

During a harvest, Competition Harvest calculates how much basal area it needs to cut. It can select trees without regard to species, or it can remove trees in a set ratio. Species ratio is set in the **Competition Harvest: Amount of Harvest Per Species (0 - 1)** parameter. If all values are set to 1, this means that species identity is ignored when selecting individuals for harvesting. Otherwise, the species are cut in the proportions entered. The values should add up to one. For example, if Species 1 is set to 0.25 and Species 2 is 0.75, then Competition Harvest will try to make 25% of the basal area removed come from Species 1 individuals and 75% come from Species 2. Of course, there are trade-offs between removing the most competitive individuals and making sure specific species targets are met.

When selecting trees for harvesting, Competition Harvest removes the individuals that have the greatest competitive effects on their neighbors. The neighbors of an individual are all sapling and adult trees within the radius specified in the **Competition Harvest: Max Radius of Competitive Effects (m)** parameter. (Seedlings, snags, and dead trees never count as neighbors.) The competitive effect (COE) of tree *i* on the *N* neighbors surrounding it is:

$$COE = \sum_{j=1}^N \exp \left(-C_j * DBH_j^{\gamma_j} * \lambda_j * \left(\frac{DBH_i^{\alpha_j}}{dist^{\beta_j}} \right)^{D_j} \right)$$

where:

- *C* is the **Competition Harvest: C** parameter for the species of neighbor *j*
- *D* is the **Competition Harvest: D** parameter for the species of neighbor *j*
- *α* is the **Competition Harvest: DBH Effect of Targets (alpha)** parameter for the species of neighbor *j*
- *β* is the **Competition Harvest: Distance Effect of Targets (beta)** parameter for the species of neighbor *j*
- *γ* is the **Competition Harvest: Size Sensitivity (gamma)** parameter for the species of neighbor *j*

- DBH_j is the DBH, in cm, of neighbor j
- λ is the **Competition Harvest: Species i Target Lambda** parameter for the species of neighbor j, where Species i is the target's species
- DBH_i is the DBH, in cm, of target i
- $dist$ is the distance between target and neighbor, in meters

Competition Harvest removes the tree with the highest COE value in the plot, then updates the COE of each tree in the vicinity so that the removed tree is no longer a neighbor. This process is repeated until the harvest cut target has been reached. If removing a tree will cause the harvest to overshoot its cutting target, a random number is compared to the amount of overshoot to determine if the tree will be removed, then harvest ends. If species are to be cut in a certain proportion, then separate cut targets are maintained for each species. If the highest COE individual is of a species whose cut target has been reached, it is not cut and Harvest Competition searches for the highest COE individuals of other species.

Only trees to which you have applied the Competition Harvest behavior are considered for harvesting. You can only apply the behavior to saplings and adults. You can specify a size range to cut using the **Competition Harvest: Minimum DBH to Harvest** and **Competition Harvest: Maximum DBH to Harvest** parameters.

The Competition Harvest behavior stores how much it actually cut each timestep in the [Competition Harvest Results grid](#). Additionally (and optionally), you can give the behavior a filename with the **Competition Harvest: Filename for List of Harvested Trees** parameter. If a filename is present, Competition Harvest will write to this file a list of the individuals harvested each timestep for the entire run. The file is a tab-delimited text file, with a header line, and five columns: X, Y, Species, DBH, and Timestep cut.

How to apply it

Apply this behavior to saplings and/or adults of any species.

Generalized Harvest Regime

This behavior can perform harvest very flexibly, depending on the parameters used. The behavior itself decides when harvests will occur and how much to cut, then chooses trees to cut with the help of a preference algorithm.

Trees removed by this behavior will have a mortality reason code of "harvest".

Parameters for this behavior

Parameter name	Description
Gen Harvest Regime	"A" in the function that calculates cut preference of individual trees.

Cut Preference "A"	
Gen Harvest Regime Cut Preference "B"	"B" in the function that calculates cut preference of individual trees.
Gen Harvest Regime Cut Preference "C"	"C" in the function that calculates cut preference of individual trees.
Gen Harvest Regime Cut Preference "Alpha"	Alpha in the function that calculates cut preference of individual trees.
Gen Harvest Regime Cut Preference "Beta"	Beta in the function that calculates cut preference of individual trees.
Gen Harvest Regime Cut Preference "Beta"	Beta in the function that calculates cut preference of individual trees.
Gen Harvest Regime Cut Preference "Gamma"	Gamma in the function that calculates cut preference of individual trees.
Gen Harvest Regime Cut Preference "Mu"	Mu in the function that calculates cut preference of individual trees.
Gen Harvest Regime Harvest Probability "A"	"A" term in the function that determines the probability that the plot will be harvested this time step.
Gen Harvest Regime Harvest Probability "B"	"B" term in the function that determines the probability that the plot will be harvested this time step.
Gen Harvest Regime Harvest Probability "M"	"M" term in the function that determines the probability that the plot will be harvested this time step.
What should calculations be based on?	Flag for whether calculations should be based on total adult biomass or total adult basal area.
Do sapling mortality as a result of harvest?	Whether or not harvests cause associated sapling mortality.
Gen Harvest Regime Sapling Mortality	"p" in the function to calculate amount of sapling mortality. Ignored if "Do sapling mortality as a result of harvest?" is set to No.

"p"	
Gen Harvest Regime Sapling Mortality "m"	"m" in the function to calculate amount of sapling mortality. Ignored if "Do sapling mortality as a result of harvest?" is set to No.
Gen Harvest Regime Sapling Mortality "n"	"n" in the function to calculate amount of sapling mortality. Ignored if "Do sapling mortality as a result of harvest?" is set to No.
Distribution controlling harvest amount	Whether to use a gamma distribution or a user-defined class-based distribution to determine the amount to harvest.
Gamma Distribution Mean Function "Alpha"	"Alpha" term in the function that determines mean amount of basal area to be removed from the plot. This mean is used in a random draw on a gamma distribution to determine actual target removal. This parameter is ignored if the distribution controlling harvest amount is not set to gamma.
Gamma Distribution Mean Function "Beta"	"Beta" term in the function that determines mean amount of basal area to be removed from the plot. This mean is used in a random draw on a gamma distribution to determine actual target removal. This parameter is ignored if the distribution controlling harvest amount is not set to gamma.
Gamma Distribution Mean Function "Mu"	"Mu" term in the function that determines mean amount of basal area to be removed from the plot. This mean is used in a random draw on a gamma distribution to determine actual target removal. This parameter is ignored if the distribution controlling harvest amount is not set to gamma.
Gamma Distribution Scale Parameter	C Scale parameter for the gamma probability distribution function random draw to determine actual target removal. This parameter is ignored if the distribution controlling harvest amount is not set to gamma.
User Distribution Intensity Class 1 Upper Bound	Upper bound in the first intensity class in the user-defined distribution to determine target harvest removal. This is expressed as a proportion of adult basal area removed between 0 and 1. Lower bound on this class is 0. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 2 Upper Bound	Upper bound in the second intensity class in the user-defined distribution to determine target harvest removal. This is expressed as a proportion of adult basal area removed between 0 and 1. Ignored if the distribution controlling harvest amount is not set to user-defined.

User Distribution Intensity Class 3 Upper Bound	Upper bound in the third intensity class in the user-defined distribution to determine target harvest removal. This is expressed as a proportion of adult basal area removed between 0 and 1. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 4 Upper Bound	Upper bound in the fourth intensity class in the user-defined distribution to determine target harvest removal. This is expressed as a proportion of adult basal area removed between 0 and 1. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 5 Upper Bound	Upper bound in the fifth intensity class in the user-defined distribution to determine target harvest removal. This is expressed as a proportion of adult basal area removed between 0 and 1. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 6 Upper Bound	Upper bound in the sixth intensity class in the user-defined distribution to determine target harvest removal. This is expressed as a proportion of adult basal area removed between 0 and 1. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 7 Upper Bound	Upper bound in the seventh intensity class in the user-defined distribution to determine target harvest removal. This is expressed as a proportion of adult basal area removed between 0 and 1. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 8 Upper Bound	Upper bound in the eighth intensity class in the user-defined distribution to determine target harvest removal. This is expressed as a proportion of adult basal area removed between 0 and 1. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 9 Upper Bound	Upper bound in the ninth intensity class in the user-defined distribution to determine target harvest removal. This is expressed as a proportion of adult basal area removed between 0 and 1. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 1 Probability	The probability that a harvest will remove an amount of adult basal area within the range defined in the first intensity class. This is expressed as a probability between 0 and 1. All class probabilities must add up to 1. Zeroes are allowed. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 2 Probability	The probability that a harvest will remove an amount of adult basal area within the range defined in the second intensity class. This is expressed as a probability between 0 and 1. All class probabilities must add up to 1. Zeroes are allowed. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution	The probability that a harvest will remove an amount of adult basal area

Intensity Class 3 Probability	within the range defined in the third intensity class. This is expressed as a probability between 0 and 1. All class probabilities must add up to 1. Zeroes are allowed. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 4 Probability	The probability that a harvest will remove an amount of adult basal area within the range defined in the fourth intensity class. This is expressed as a probability between 0 and 1. All class probabilities must add up to 1. Zeroes are allowed. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 5 Probability	The probability that a harvest will remove an amount of adult basal area within the range defined in the fifth intensity class. This is expressed as a probability between 0 and 1. All class probabilities must add up to 1. Zeroes are allowed. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 6 Probability	The probability that a harvest will remove an amount of adult basal area within the range defined in the sixth intensity class. This is expressed as a probability between 0 and 1. All class probabilities must add up to 1. Zeroes are allowed. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 7 Probability	The probability that a harvest will remove an amount of adult basal area within the range defined in the seventh intensity class. This is expressed as a probability between 0 and 1. All class probabilities must add up to 1. Zeroes are allowed. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 8 Probability	The probability that a harvest will remove an amount of adult basal area within the range defined in the eighth intensity class. This is expressed as a probability between 0 and 1. All class probabilities must add up to 1. Zeroes are allowed. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 9 Probability	The probability that a harvest will remove an amount of adult basal area within the range defined in the ninth intensity class. This is expressed as a probability between 0 and 1. All class probabilities must add up to 1. Zeroes are allowed. Ignored if the distribution controlling harvest amount is not set to user-defined.
User Distribution Intensity Class 10 Probability	The probability that a harvest will remove an amount of adult basal area within the range defined in the tenth intensity class. This is expressed as a probability between 0 and 1. All class probabilities must add up to 1. Zeroes are allowed. Ignored if the distribution controlling harvest amount is not set to user-defined.

How it works

The behavior calculates many probabilities to decide whether and what to cut. These calculations can be based on either total adult biomass in the plot (Mg/ha), or total adult basal area in the plot (m²/ha). The parameter **What should calculations be based on?** indicates which to use. If biomass is chosen, biomass is calculated using the [Dimension analysis](#) behavior.

Deciding whether a harvest occurs in a timestep

The behavior begins the timestep by deciding whether or not a harvest will occur. The probability of harvest is calculated as follows:

$$P = 1 - ae^{-mBio^b}$$

where:

- P is the probability that the plot will be harvested this time step
- Amt is either the total plot adult biomass (Mg/ha) or the total plot adult basal area (m²/ha)
- a is the **Gen Harvest Regime Harvest Probability "A"** parameter
- m is the **Gen Harvest Regime Harvest Probability "M"** parameter
- b is the **Gen Harvest Regime Harvest Probability "B"** parameter

A random number is compared to this probability to decide whether or not a harvest will occur. The frequency of harvest in previous timesteps is not taken into account.

Deciding the target amount of basal area to remove

Target removal amount is drawn from a probability distribution function. There are two choices: the gamma function, or a user-defined function with ten intensity classes and associated probabilities for each. Choose the function you want with the **Distribution controlling harvest amount** parameter.

If the gamma is used, the mean of the distribution (as percentage of adult basal area to remove between 0 and 100) is calculated as follows:

$$BAR = \alpha e^{-\mu Bio^\beta}$$

where:

- BAR is the mean percent of total plot adult basal area to remove, between 0 and 100
- Amt is either the total plot adult biomass (Mg/ha) or the total plot adult basal area (m²/ha)
- α is the **Gen Harvest Regime Remove Amount "Alpha"** parameter
- β is the **Gen Harvest Regime Remove Amount "Beta"** parameter
- μ is the **Gen Harvest Regime Remove Amount "Mu"** parameter

This mean value is used, along with the **Gen Harvest Regime Gamma Scale Parameter**, in a draw on the [gamma distribution](#) in order to get the actual target removal rate. If a value above 100% is drawn, this value is discarded and the draw is repeated until a value of less than 100% is drawn.

The adult plot biomass or basal area in the equations above is the total for all species. All species must participate in harvest, and only adults are counted and cut.

If the probability distribution function is user-defined, you define ten harvest intensity classes and the probability that the harvest will fall into each of these. Enter the upper bound of each intensity class, as a proportion of total basal area removed, in the **User Distribution Intensity Class X Upper Bound** parameter. The lower bound of the first class is 0. The upper bound of class 10 is 1. Values must increase with each class but classes do not have to be the same size.

For each intensity class, the value in the parameter **User Distribution Intensity Class X Probability** is the probability, between 0 and 1, that a harvest within the range of removal values defined by that class will occur. Zeroes are allowed, and harvests within a class of 0 probability will never occur. All ten class probabilities must add up to 1.

This behavior turns the probabilities for all the classes into a cumulative probability function. A random number drawn on the uniform distribution between 0 and 1 is used against the cumulative probabilities to determine which class the harvest falls into. Then a second uniform random draw on the range of values in that class is used to choose the target proportion of adult basal area to remove.

Deciding which individuals to cut

A preference function determines the probability that an individual will be cut, as follows:

$$P_i = \left[1 - \gamma_i e^{-\beta_i BAR^{\alpha_i}} \right] * \left[e^{-0.5 \left(\frac{DBH - \mu_i}{\sigma} \right)^2} \right]$$

where:

- P_i is the probability that individual i will be cut
- α_i is the **Gen Harvest Regime Cut Preference "Alpha"** parameter for the species of individual i
- β_i is the **Gen Harvest Regime Cut Preference "Beta"** parameter for the species of individual i
- γ_i is the **Gen Harvest Regime Cut Preference "Gamma"** parameter for the species of individual i
- μ_i is the **Gen Harvest Regime Cut Preference "Mu"** parameter for the species of individual i
- BAR is the percent of total adult basal area to remove, between 0 and 100
- DBH is the individual's DBH

The term σ is:

$$\sigma = a + b * BAR^c$$

where:

- a is the **Gen Harvest Regime Cut Preference "A"** parameter
- b is the **Gen Harvest Regime Cut Preference "B"** parameter
- c is the **Gen Harvest Regime Cut Preference "C"** parameter
- BAR is the percent of total adult basal area to remove, between 0 and 100

An individual's probability of removal is compared with a random number to determine if that individual is cut.

The preference function takes into account the target basal area removal rate of the plot. However, the function shape does not necessarily produce a mean removal probability equal to that of the target removal rate, particularly near 0 and 100. If you wish, the behavior can refine the probabilities on a second pass to get closer to the target. You can set a tolerance using the **Gen Harvest Acceptable Deviation From Cut Target** parameter. This is expressed as a proportion of the removal rate, between 0 and 1. So a value of 0.1 allows first-pass acceptable deviation of 10 percent from the target. If the actual removal rate falls outside this limit, the function adjusts all preferences by a correction factor and re-evaluates individual cut decisions. No more than two passes will be made, even if the second pass does not achieve a removal rate within the tolerance. Setting a high tolerance such that a second pass is not often needed eliminates a lot of calculations and will allow a run to be faster.

Saplings can be subjected to an increased mortality rate as a consequence of harvesting. You can turn this on by setting the parameter **Do sapling mortality as a result of harvest?** to "Yes". (Setting it to "No" means there is no effect of harvest on sapling mortality at all.)

The function for the probability of sapling mortality as a result of a harvest event is:



where:

- PCR is the percent of basal area removed in this harvest, between 0 and 100
- p is the **Gen Harvest Regime Sapling Mortality "p"** parameter
- m is the **Gen Harvest Regime Sapling Mortality "m"** parameter
- n is the **Gen Harvest Regime Sapling Mortality "n"** parameter

Saplings are randomly chosen to die at this rate. All species are affected equally. Saplings are killed with a mortality code of "harvest".

How to apply it

Apply this behavior to the adults of all species. If you choose to make calculations based on biomass, you must also apply the [Dimension analysis](#) behavior to the same trees.

Harvest

Trees removed by this behavior will have a mortality reason code of "harvest".

How it works

SORTIE can implement complex silvicultural treatments. Harvest events are defined by species, timestep, amount to remove, type of cut, and area of the plot. You can define as many harvest events as you wish. For information on planting new seedlings, see the [Planting behaviors](#) topic.

There are three types of harvest: gap cut, partial cut, and clear cut. The primary function of entering the harvest type is to control [substrate](#) composition after the harvest occurs. In a partial cut harvest, though, you have more flexibility in choosing which trees are cut. You can define up to four size classes, and specify the amount of trees to remove in one of four ways: as a percentage of total basal area, as an absolute amount of basal area, as a percentage of total tree density, or as an absolute amount of tree density.

The Harvest behavior selects the trees to remove in the same way for all three harvest types. When it is determining which trees to remove, it starts by finding the largest tree in the area of the plot affected by the harvest. It works its way through the trees from largest to smallest, assessing whether to cut each one until it either runs out of trees or reaches its cut target. This process preferentially removes the largest trees in each size range, unless the harvest is a percentage of density cut, in which case all trees in the target size ranges have an equal probability of being cut. If Harvest is cutting a percentage of basal area or an absolute amount of basal area, it will only cut a tree if its basal area will not cause the total to be more than the target. This means that, for basal-area-defined cuts, the Harvest behavior may skip some bigger trees and cut smaller ones in order to more exactly cut its target. Each species is cut separately. So, a request to remove 20% of three species will remove 20% of each of them, no matter what their relative proportions to each other.

Trees can be prioritized for harvest. You can choose a [tree data member](#) and a range of values for that data member. For instance, you could prioritize trees with growth values between 5 and 10. Trees meeting a priority are cut first.

You can set up to three priorities. All trees meeting the first priority are cut first, then all trees meeting the second priority, then all meeting the third, then all other trees. Cutting stops when the target removal amount has been met. DBH ranges are honored. If there is a priority tree outside the cut DBH ranges, it will not be cut under any circumstances. The exception to priority ordering is in the case of a basal area cut target. If a priority tree would cause too much basal area to be removed, a smaller non-priority tree may be cut instead to more precisely reach the target. Priorities may not be applied to percent of density cuts, because these cuts are stochastic in nature so prioritization is meaningless. You can prioritize by the same data member more than

once; for instance, first cut trees with growth between 5 and 10, then with growth between 0 and 5.

Although seedlings are not properly harvested, a harvest can kill them just the same. You can specify the proportion of seedlings that are killed within the harvest area for each species. The seedlings of a species can be killed even if that species is not being harvested. Seedlings in the harvest area are randomly chosen to die based on the mortality rate for their species. They are given "harvest" as a mortality reason.

Trees that are harvested are removed immediately. When light is calculated for that timestep, gaps opened up by the harvest will be visible. If there are behaviors which apply to [stumps](#), a stump is created for each logged tree. Otherwise, the tree completely disappears.

The actual amount of tree harvest may not be exactly what was specified, since the Harvest behavior can't remove part of a tree to get the numbers right. The behavior stores how much it actually cut each timestep in the [Harvest Results grid](#). To optimize the accuracy of the Harvest behavior, use larger cut ranges and high proportions of the plot area to make sure there is a big pool of trees to choose from.

How to apply it

Add the behavior to the run through the [Model Flow window](#). You do not apply it to particular trees at that time. The behavior setup will allow you to design your harvests.

Harvest interface

The harvesting interface allows SORTIE to work directly with another program. SORTIE tells the other program what trees are eligible for harvesting, and the other program replies with its choices. This lets users write code for harvesting without having to modify SORTIE itself.

Warning - this link between SORTIE and another program is inefficient. It may be very slow when there are large numbers of trees. It is for convenience, not speed.

Trees removed by this behavior will have a mortality reason code of "harvest".

How it works

After adding the Harvest Interface behavior to your run, you set it up using the [Harvest Interface window](#). Parameters in this documentation are defined by their names on that screen.

You either create or find a separate program (an executable) that reads a text file of trees, makes decisions about which to kill, then writes those trees to kill to another text file. You tell SORTIE where to find this executable using **Path and filename of the executable** on the [Edit Harvest Interface](#) window.

Each harvest timestep, SORTIE writes a text file with a list of trees eligible for harvest. The trees in the list are those to which the Harvest Interface behavior is applied. You choose which trees those are in **Behavior currently assigned to** on the [Edit Harvest Interface](#) window. Once the file is written, SORTIE then launches your executable. Your executable writes a file in response with the list of trees it wishes SORTIE to kill.

Trees that are cut are treated exactly like those in SORTIE harvest. That is, they disappear completely and do not become snags. See the documentation on [Harvest](#) for more details. The cut details for each timestep are written to the [Harvest Results grid](#). (Warning - if you put both the Harvest and Harvest Interface behavior in the same run, they will overwrite each other's results in the grid.)

Because the process can be slow, you can set harvests to occur less often than every timestep. To do this, use **How often to harvest, in years** on the [Edit Harvest Interface](#) window.

Optionally, you can also add new tree data members that are controlled by the executable. The executable can write a file with a list of trees to update, and the new values for those variables for each tree.

File formats

Each harvesting timestep, SORTIE begins by writing a file of all trees eligible for harvest. You give SORTIE the path and name of that file in **Tree file that SORTIE will write** on the [Edit Harvest Interface](#) window. SORTIE does not care what the filename nor file extension is. The file is tab-delimited text. It has the following format:

Line 1, two columns: Current timestep, total number of timesteps
Line 2, column names, 6+n columns: "X", "Y", "Species", "Type", "Diam", "Height", [...]
Subsequent lines, 6+n columns, one line per tree: X, Y, species number, type number, DBH/diam10, height, [...].

Species is given as a number from 0 to $x - 1$, where x is the number of species. The number counts the species in the order in which they are listed in the parameter file, which is the same as the order they are listed in the [Edit Species](#) window.

Type is given as a number as well. The type numbers are:

1. Seedling
2. Sapling
3. Adult
4. Stump
5. Snag

Stumps are not available for harvesting.

The "Diam" value is diameter at 10 cm if the tree type is seedling, and DBH in all other cases. Both of these values are in cm.

The "Height" value is the height of the tree in meters.

The [...] represents additional columns that you can ask SORTIE to include. You set this up using the **File columns** section of the [Edit Harvest Interface](#) window. You can choose any other [tree data member](#) that applies to all of the kinds of trees to which the harvest interface is applied, including new ones that you add. The list of tree data members depends on the other behaviors in the run. The column header matches the internal SORTIE name of the data member (which is what is displayed to you when you choose new data members). You cannot change the first six default columns.

The executable writes a file in response with the trees that it wishes to harvest (**Tree harvest file that the executable will write** on the [Edit Harvest Interface](#) window). If you have set up new tree data members, the executable also writes a second file with a list of live trees to update (**Tree update file that the executable will write** on the [Edit Harvest Interface](#) window). All trees in both of these files must come from the tree list that SORTIE wrote for that timestep. No tree may appear in both files.

The file format of the user response files is identical to that of the SORTIE file, with the same columns in the same order.

Each harvest timestep, all these files are overwritten.

If there are no trees eligible for harvesting, SORTIE still writes a file with only the first two header lines (no individual tree lines). It expects the executable to do the same if it does not want trees harvested or updated.

Adding new variables

You can request that SORTIE create new data members under the executable's control for the trees to which this behavior applies. Set this up in the **New tree data members to add** section of the [Edit Harvest Interface](#) window. You can create as many as you want. You can give them any name up to 9 characters long. They each hold a float value. The values are uninitialized in newly created trees.

If you want the new data members to be written to the file that SORTIE writes, make sure you put them in the list of file columns.

If new data members have been created, SORTIE expects the executable, each time it is called, to write a file with the list of trees it wishes to update, and the new values for these data members. You can only make changes to the new data members that you create. You cannot change any other attribute of a tree.

The user executable

The user executable launches, runs, and quits once per harvest timestep. SORTIE waits for it to finish before resuming. This means it must do any necessary initialization and setup each harvest timestep.

The executable can be written in any language, and can do anything it wishes. The only two requirements is that it be a standalone executable, and that it produce the file of trees to harvest that SORTIE expects.

The executable should be prepared for the condition that there are no trees in the file SORTIE writes, and should write empty files if it doesn't want any trees harvested or updated.

SORTIE's behavior cannot be guaranteed in the event of a crash in the user executable.

The executable probably has its own input data for setup. If it takes arguments during launch, you can give SORTIE a string to pass to the executable in **Arguments to pass to the executable** on the [Edit Harvest Interface](#) window.

SORTIE provides a convenience feature for those executables that read setup parameters from a file. You may wish to set up a SORTIE batch run where your executable uses different parameters for each run. You can give SORTIE a file of all the parameters for the entire batch in a text file, and for each run, it will separate out that run's parameters and write them to a file for your executable. The parameters for a single run must be on a single line of the entire batch file, and will be written to a one-line file for the individual run. Specify the entire-batch parameters file in **Parameters file for batch run**, and the single-run file in **Single-run parameters file for batch run** on the [Edit Harvest Interface](#) window.

For example, suppose there is an executable that takes three parameters. It reads these parameters from a one-line file named "par.txt", like this:

par1	par2	par3
------	------	------

You can set up a batch of three runs, then set up all the parameters in a single file, like this:

par1_1	par2_1	par3_1
par1_2	par2_2	par3_2
par1_3	par2_3	par3_3

You give SORTIE this file, and tell it to write "par.txt" for each run. The first run in the batch, SORTIE will write the first line to "par.txt"; the second run in the batch, it will write the second line to "par.txt", etc.

Tips:

If you are having trouble with SORTIE not finding your code's output file, try explicitly writing out directories in your code (i.e. "C:\sortie\file.txt" instead of just "file.txt").

How to apply it

It is easiest if you add the harvest interface after the rest of your parameter file is complete, so that you have full access to data members. Open [Edit->Harvest Interface](#) and complete the setup. This adds the harvest interface behavior to your run. To remove it, use the [Model flow window](#).

Insect Infestation

This behavior simulates an insect outbreak. It chooses and marks affected trees, allowing other behaviors to make use of this information. The number of affected trees is a function of time since infestation began. The infestation has no spatial pattern.

This behavior only chooses trees for infestation. It does not kill them or alter their dynamics in any way. Other behaviors may take advantage of the infestation status information of trees.

Parameters for this behavior

Parameter name	Description
Insect Infestation First Timestep	The timestep that an insect infestation begins.
Insect Infestation Initial Rate	The rate of infestation on the first timestep of the outbreak.
Insect Infestation Max Rate	The maximum rate of infestation.
Insect Infestation Min DBH	The minimum DBH of trees that can become infested.
Insect Infestation X0	The time at which 0.5 of the maximum infestation rate occurs.
Insect Infestation Xb	Parameter controlling the steepness of the rise of the infestation rate.

How it works

The proportion of trees of a particular species infested as a function of time is as follows:

$$P = I + \frac{(Max - I)}{1 + \left(\frac{T}{X_0}\right)^{X_b}}$$

where:

- P is the proportion of the eligible tree population infested.
- I is the **Insect Infestation Initial Rate** parameter, as a value between 0 and 1. This is the function intercept, or the infestation rate at the first timestep of infestation.
- Max is the **Insect Infestation Max Rate** parameter, as a value between 0 and 1. This is the maximum infestation rate that will occur regardless of how long the infestation lasts.
- T is the time, in years, since the start of the infestation.
- X_0 is the **Insect Infestation X0** parameter. This is the time at which half of the maximum infestation rate is reached.
- X_b is the **Insect Infestation Xb** parameter. This controls the steepness of the rise of the curve.

You choose when an infestation begins with the **Insect Infestation First Timestep** parameter. The only way that an infestation ends is if there are no more infested trees in the plot.

You can set a minimum DBH of infestation, using the **Insect Infestation Min DBH** parameter.

The proportion of trees infested at time T does not depend on additions to or subtractions from the pool of eligible trees. Each timestep, the number of infested trees of each species is counted and additional trees are randomly selected for new infestation until approximately the right number are infested. If for some reason there are more trees infested than there should be at that time, no additional trees are infested.

When selecting trees for infestation, the location of the trees is not considered. It is assumed that all trees have an equal chance of becoming infested no matter where they are in the plot. This behavior uses a [tree data member](#) called "Years Infested" to track which trees are infested and how long they have been so.

How to apply it

Apply this behavior to saplings and/or adults of any species.

Episodic Mortality

Trees removed by this behavior will have a mortality reason code of "disease".

How it works

The Episodic Mortality behavior allows you to replicate tree-killing events with the same level of control you have when defining Harvest events. A planned mortality episode can simulate disease, an insect outbreak, fire, or the like. The main difference between Harvest and Episodic Mortality is that the Episodic Mortality behavior can create [snags](#), or standing dead trees. A large snag proportion can significantly affect the light and substrate dynamics of a SORTIE run.

Defining a mortality episode is like defining a partial cut harvest. (Mortality episodes have no automatic impact on [substrate](#) dynamics like harvest events do, although the newly dead trees may be a source of harvest input.) You can define up to four size classes, and specify the amount of trees to kill in one of four ways: as a percentage of total basal area, as an absolute amount of basal area, as a percentage of total tree density, or as an absolute amount of tree density.

When the Episodic Mortality behavior is determining which trees to remove, it starts by finding the largest tree in the area of the plot affected by the mortality episode. It works its way through the trees from largest to smallest, assessing whether to kill each one until it either runs out of trees or reaches its cut target. This process preferentially removes the largest trees in each size range, unless the event is defined by a percentage of density, in which case all trees in the target size ranges have an equal probability of being killed. If Episodic Mortality is removing a percentage of basal area or an absolute amount of basal area, it will only kill a tree if its basal area will not cause the total to be more than the target. This means that, for basal-area-defined cuts, the behavior may skip some bigger trees and cut smaller ones in order to more exactly cut its target. Each species is cut separately. So, a request to remove 20% of three species will remove 20% of each of them, no matter what their relative proportions to each other.

Seedlings can also be killed as part of a planned mortality episode. You can specify the proportion of seedlings that are killed within the target area for each species. The seedlings of a species can be killed even if that species is not otherwise participating in the episode. Seedlings in the target area are randomly chosen to die based on the mortality rate for their species. They are given "disease" as a mortality reason.

What happens to dead trees depends on the rest of the run. If there are other behaviors in the run that deal directly with snags or create them, then the run is "snag-aware". In this case, all adult trees killed are turned into snags (saplings never become snags). If the run is not "snag-aware", then the trees are marked as dead. When/if the [dead tree remover behavior](#) runs, the dead trees will be removed at that time. These dead trees are available as input to [Substrate](#).

The actual amount of trees killed may not be exactly what was specified, since the Episodic Mortality behavior can't remove part of a tree to get the numbers right. The behavior stores how much it actually cut each timestep in the [Mortality Episode Results grid](#). To optimize the accuracy of the behavior, use larger kill ranges and high proportions of the plot area to make sure there is a big pool of trees to choose from.

How to apply it

Add the behavior to the run through the [Model Flow window](#). You do not apply it to particular trees at that time. The behavior setup will allow you to design your mortality episodes.

Random browse

This behavior simulates random browsing from herbivores.

Parameters for this behavior

Parameter name	Description
Random Browse - Annual Browse Probability (0-1)	The annual probability, from 0 to 1, of being browsed. This is the mean probability if the probability is being varied each timestep.
Random Browse - Probability PDF	The PDF used to vary the browse probability. "None" means the same probability is always used. "Normal" means that each timestep, for each species, a new probability is drawn from a normal distribution.
Random Browse - Browse Probability Standard Deviation	If the probability is being varied each timestep according to a normal distribution, this is the standard deviation of that distribution. This value is ignored if the probability is not being varied.

How it works

The trees eligible for browsing are those trees to which this behavior is applied. Each species has a probability of browse that is the same for all members of that species. Each timestep, for each eligible tree, a random number is used against its species probability to decide whether the tree is browsed.

The probability of browse for a species can be constant, or it can vary each timestep. If it is constant, the probability of browse is always the value in the **Random Browse - Annual Browse Probability (0-1)** parameter. If the probability is to vary, a new value is drawn from a random distribution, using the value in **Random Browse - Annual Browse Probability (0-1)** parameter as the mean and the value in **Random Browse - Browse Probability Standard Deviation** as the standard deviation. This draw happens once per species per timestep; all individuals of a species always face the same probability of browse in a given timestep.

If the timestep length is more than one year, the annual probability of browse is turned into a timestep probability using $TP = 1 - (1 - AP)^N$, where TP is the timestep probability of browse, AP is the annual probability, and N is the length of a timestep, in years.

Trees that are chosen as browsed are marked as browsed. This behavior does nothing else to them. Other behaviors, such as growth and mortality, may use this information.

How to apply it

Apply this behavior to any species and type of tree.

Storm disturbance

This behavior simulates the effects of wind damage from storms. Its function is to assess whether or not storms have occurred in the current timestep, and if they have, how much damage they have caused. This behavior does not actually cause any trees to be damaged; that is the function of the [Storm damage applier](#) behavior.

Parameters for this behavior

Parameter name	Description
Plot Storm Susceptibility Pattern	How storm damage susceptibility varies across the plot. If "Uniform", then all locations in the plot have an equal susceptibility. If "Mapped", then a map is used to show the way locations in the plot vary in susceptibility.
Return Interval for Severity Storm Class 0 - 0.1	The return interval, in years, of storms of severity 0 - 0.1. Set this to 0 to turn off storms of this severity.
Return Interval for Severity Storm Class 0.1 - 0.2	The return interval, in years, of storms of severity 0.1 - 0.2. Set this to 0 to turn off storms of this severity.
Return Interval for Severity Storm Class 0.2 - 0.3	The return interval, in years, of storms of severity 0.2 - 0.3. Set this to 0 to turn off storms of this severity.
Return Interval for Severity Storm Class 0.3 - 0.4	The return interval, in years, of storms of severity 0.3 - 0.4. Set this to 0 to turn off storms of this severity.
Return Interval for Severity Storm Class 0.4 - 0.5	The return interval, in years, of storms of severity 0.4 - 0.5. Set this to 0 to turn off storms of this severity.
Return Interval for Severity Storm Class 0.5 - 0.6	The return interval, in years, of storms of severity 0.5 - 0.6. Set this to 0 to turn off storms of this severity.
Return Interval for Severity Storm Class 0.6 - 0.7	The return interval, in years, of storms of severity 0.6 - 0.7. Set this to 0 to turn off storms of this severity.
Return Interval for Severity Storm Class 0.7 - 0.8	The return interval, in years, of storms of severity 0.7 - 0.8. Set this to 0 to turn off storms of this severity.

Return Interval for Severity Storm Class 0.8 - 0.9	The return interval, in years, of storms of severity 0.8 - 0.9. Set this to 0 to turn off storms of this severity.
Return Interval for Severity Storm Class 0.9 - 1.0	The return interval, in years, of storms of severity 0.9 - 1.0. Set this to 0 to turn off storms of this severity.
Standard Deviation (lognormal or normal)	If the Storm Damage Application parameter is set to "Stochastic" and the Stochastic Pattern Damage Distribution is set to either "Normal" or "Lognormal", this is the standard deviation used when randomizing storm severity across the plot. This parameter is ignored if the Storm Damage Application parameter is not set to "Stochastic" and the Stochastic Pattern Damage Distribution is not set to either "Normal" or "Lognormal".
Stochastic Pattern Damage Distribution	If the Storm Damage Application parameter is set to "Stochastic", this is the probability distribution function to use for randomizing storm severity across the plot. This parameter is ignored if the Storm Damage Application parameter is not set to "Stochastic".
Storm Damage Application	How storm damage is applied to different locations across the plot. If "Deterministic", the storm's severity is applied equally to all locations. If "Stochastic", the storm's severity is randomized across the plot according to your chosen probability distribution function.
Storm - Storm Cyclicity Sine Curve d	Parameter that controls the cyclicity of storm frequency. For no cyclicity, set this value to 0. This value is part of the sine curve term and controls the sine amplitude.
Storm - Storm Cyclicity Sine Curve f	Parameter that controls the cyclicity of storm frequency. This value is part of the sine curve term and controls the sine frequency.
Storm - Storm Cyclicity Sine Curve g	Parameter that controls the cyclicity of storm frequency. This value is part of the sine curve term and controls where on the sine curve storms start occurring.
Storm - Storm Cyclicity Trend Function Intercept (i)	Parameter that controls the trend of cyclicity of storm frequency. This value is part of the trend term and is the intercept of the function controlling the increase or decrease of overall frequency cycling. For no cyclicity at all, set this term to 1. For no trend in cyclicity, set this term to 0.
Storm - Storm Cyclicity Trend Function Slope (m)	Parameter that controls the trend of cyclicity of storm frequency. This value is part of the trend term and is the slope at which frequency cycling increases or decreases. For no cyclicity, or no trend in cyclicity, set this term to 0.

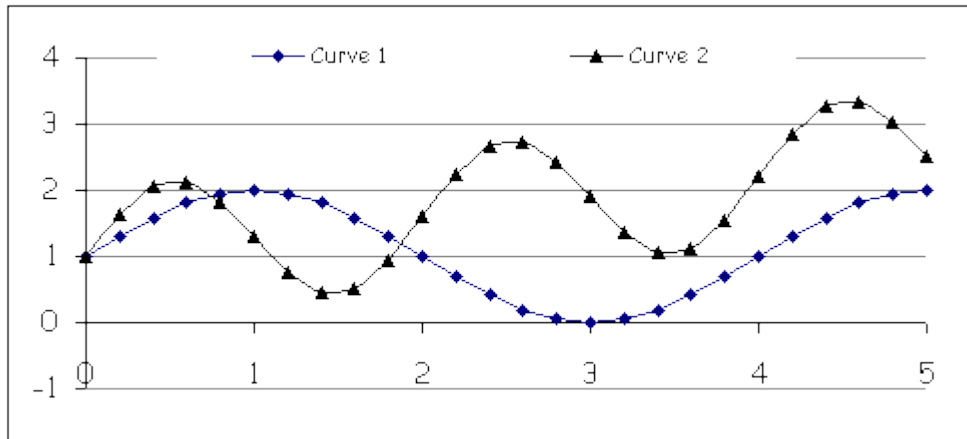
How it works

There are two ways storms can occur: randomly according to a storm regime of your choosing, or scheduled at certain timesteps. Both methods can be used together.

Random storms according to a storm regime

Storm severity is assessed on a scale from 0 (no damage) to 1 (total damage). This interval of storm severity values is subdivided into ten storm severity classes. You assign each storm severity class a return interval. The reciprocal of the return interval gives the annual probability of each type of storm.

The overall frequency of storms can remain constant, or it can change through time. It has been reported in [Goldenburg et al 2001](#) that storm activity in the North Atlantic cycles along with sea surface temperature. This behavior can thus change the storm frequency over time, using either a sinusoidal pattern, a constant linear change, or both together. In the figure below, curve 1 is a basic sine wave. Curve 2 has a sinusoidal pattern plus an upwards trend.



The actual probability of an individual storm that takes place in a storm regime with a cyclical frequency is:

$$P'(F_i) = P(F_i) * ([d * \sin(\pi * (x-g) / (2f))] + [mx + i])$$

Note that the new probability is a baseline probability, $P(F_i)$, multiplied by a value that adjusts the probability according to where the model is at the given time in the frequency cycle. The frequency cycle multiplier is itself made up of two terms added together. The first term is the sine curve cycling, and the second term is the overall trend upwards or downwards.

Terms in the equation:

- $P'(F_i)$ is this timestep's annual probability of a storm of the i th return interval, adjusted according to the frequency cyclicity

- $P(F_i)$ is the baseline probability of a storm of the i th return interval; that is, the reciprocal of the values specified in the **Return Interval for Severity Storm Class X** parameters
- $x = 4 * t / Sr$, where t is the number of years since the run started and Sr is the **Storm - Sea Surface Temperature Cyclicity Period (Years)** parameter
- d is the **Storm - Storm Cyclicity Sine Curve d** parameter, which controls the sine curve's amplitude
- f is the **Storm - Storm Cyclicity Sine Curve f** parameter, which controls the sine curve's frequency
- g is the **Storm - Storm Cyclicity Sine Curve g** parameter, which controls where on the sine curve storms start occurring
- m is the **Storm - Storm Cyclicity Trend Function Slope (m)** parameter
- i is the **Storm - Storm Cyclicity Trend Function Intercept (i)** parameter

To turn off all cyclicity and use constant storm probabilities, set **Storm - Storm Cyclicity Sine Curve d** to 0, **Storm - Storm Cyclicity Trend Function Slope (m)** to 0, and **Storm - Storm Cyclicity Trend Function Intercept (i)** to 1. (The other values are unimportant.) To use only the sine portion with no trend line, set both **Storm - Storm Cyclicity Trend Function Slope (m)** and **Storm - Storm Cyclicity Trend Function Intercept (i)** to 0. To use only the trend portion, set **Storm - Storm Cyclicity Sine Curve d** to 0.

To decide whether storms occur, the behavior compares a random number to the annual probability of each storm severity class. For timesteps that are longer than one year, the behavior repeats the random number test for each year in the timestep. This process is repeated for each storm severity class separately. This means that multiple storms can occur in a single timestep, and if the timestep is longer than one year, there can be multiple storms in the same severity class.

Scheduled storms

You can also schedule storms to occur at certain timesteps. Use the [Edit Scheduled Storms](#) window to do this. You specify the year (NOT the timestep) you want the storm to occur, and a minimum and maximum severity for each. The actual storm severity will be a random number between the maximum and minimum. You can schedule as many as you want, including multiple storms per timestep. If there is also a storm regime present (non-zero values for the return intervals), those storms can also occur. The storm regime storms can also happen between scheduled storms.

If a storm occurs, the behavior calculates the amount of damage that occurs. A storm's damage index (severity) is randomly chosen within the boundaries of its severity class. The damage is stored in a grid called [Storm Damage](#). The final output of the behavior is a map of storm damage (severity) across the plot, as an index between 0 and 1. If multiple storms occur, each storm's severity is recorded separately.

The way storm damage is calculated depends on two things: the pattern of storm susceptibility across the plot (entered in the **Plot Storm Susceptibility Pattern** parameter), and the method of storm damage application (entered in the **Storm Damage Application** parameter). Storm susceptibility is measured on a scale from 0 (not susceptible to damage) to > 1 (highly

susceptible to damage). The pattern of storm susceptibility can be either "Uniform", meaning all locations within the plot have a susceptibility of 1, or "Mapped", meaning that you will provide a map with a susceptibility for each location in a grid called [Storm Susceptibility](#). The method of storm damage application can be either "Deterministic", meaning that each location receives the storm's severity index, or "Stochastic", meaning that the storm's severity index provides a mean around which individual location severities are randomized.

There are two possible probability distribution functions for stochastic damage application: normal and lognormal.

The normal distribution is:

$$p(x)dx = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{x^2}{2\sigma^2}} dx$$

where σ is the function standard deviation. Mean is zero in this equation; the final value is reached by adding the function result to the mean.

The lognormal distribution is:

$$p(x)dx = \frac{1}{x\sqrt{2\pi\sigma^2}} e^{-\left(\frac{\ln(x)-\zeta}{\sigma}\right)^2} dx$$

where ζ is the function mean and σ is the standard deviation.

Combining these two parameters provides four possibilities for the way a storm's damage is applied:

1. *Mapped Deterministic*. The damage index for a location equals the susceptibility of that location multiplied by the storm's severity index.
2. *Mapped Stochastic*. The storm severity for each location is determined by performing a random draw on a probability distribution function, with the overall storm severity providing the function mean. Each location's severity is multiplied by its susceptibility to arrive at the final storm damage index for that location.
3. *Uniform Deterministic*. All plot locations are directly assigned the storm's severity index.
4. *Uniform Stochastic*. The storm damage index for each location is determined by performing a random draw on a probability distribution function, with the overall storm severity providing the function mean.

How to apply it

Add the behavior to the behavior list for your run. A few rules:

- If you set the **Plot Storm Susceptibility Pattern** parameter equal to "Mapped", you must provide a map of plot susceptibility values. You do this by using the [Grid Value Edit Window](#) to enter values 0 or greater for each cell of the grid called [Storm Susceptibility](#).
- If you set the **Storm Damage Application** parameter equal to "Stochastic", you must choose a probability function in the **Stochastic Pattern Damage Distribution**. If you choose "Lognormal" or "Normal", you must provide a function standard deviation in the **Standard Deviation (lognormal or normal)** parameter.
- If you do not also enable the [Storm damage applier](#) behavior, storms may occur but nothing else will happen; trees won't suffer any damage as a result. You can also set all storm return intervals to 0 to turn off storms.

Storm damage applier

The purpose of this behavior is to apply storm damage to individual trees. This behavior decides which trees are damaged when a storm has occurred and how badly. It also keeps track of the time since damage for damaged trees, and after a "healing period" returns them to healthy (undamaged) status.

There are three possible damage categories for a tree: no damage, medium damage, and heavy damage. Other behaviors can use the damage categories to determine what effects the storm damage had on a tree (slow growth, death, etc).

Parameters for this behavior

Parameter name	Description
Minimum DBH for Storm Damage, in cm	The minimum DBH for trees that can be damaged or killed by storms. Trees smaller than this are never damaged no matter what storms occur.
Number of Years Damaged Trees Take to Heal	The number of years it takes a damaged tree to heal. After this time it is considered undamaged.
Storm Damage Intercept (a) for Medium Damage	The storm damage intercept parameter (a) for the equation calculating the probability of medium damage.
Storm Damage Intercept (a) for Heavy Damage	The storm damage intercept parameter (a) for the equation calculating the probability of heavy damage.
Storm DBH Coefficient (d)	The storm DBH coefficient (d) for the equations calculating the probability of damage.
Storm Intensity	The storm intensity coefficient (b) for the equations calculating

Coefficient (b)

probability of damage.

How it works

The behavior [Storm disturbance](#) determines whether a storm has occurred. When it does, an individual tree can either get no damage, medium damage, or heavy damage. The tree's probability of damage in a given damage category is:

$$P(d_i) = \frac{\exp(a_i + b * c * DBH^d)}{1 + \exp(a_i + b * c * DBH^d)}$$

where:

- i is the damage category, either medium or heavy
- a_i is the storm damage intercept for that tree's species for that damage category, either the **Storm Damage Intercept (a) for Medium Damage** parameter or the **Storm Damage Intercept (a) for Heavy Damage** parameter
- b is the **Storm Intensity Coefficient (b)** parameter for that tree's species
- c is the storm's severity at the tree's location, between 0 and 1, as calculated by the [Storm disturbance](#) behavior
- d is the **Storm DBH Coefficient (d)** parameter for that tree's species

This behavior uses a random number to determine what damage category a tree falls in. If the random number is less than the probability for medium damage, the tree is undamaged. If the random number is greater than the probability for medium damage but less than the probability for heavy damage, the tree gets medium damage. If the random number is greater than the probability for heavy damage, the tree gets heavy damage.

If a tree is damaged, a counter is set for time since damage. This behavior checks this counter every timestep. When the amount of time specified in the **Number of Years Damaged Trees Take to Heal** has passed, the tree is considered healed and no longer has a record of storm damage.

If a damaged tree is damaged again in a new storm, it gets the most severe damage category that can apply to it and must go through the maximum healing time again in order to become undamaged.

How to apply it

Apply this behavior to the trees that can receive storm damage. You may not apply this behavior to seedlings. If you wish to use the [Storm damage killer](#) behavior to create snags from storm-killed trees, you must apply this behavior to the snag tree type. Along with this behavior, you must also add the [Storm disturbance](#) behavior.

Storm damage killer

This behavior kills trees damaged in storms. It decides which damaged trees die, and if they become snags, it manages the snag population by causing snag tip-up and removal. This behavior does not decide which trees get damaged in a storm; that is the job of the [Storm damage applier](#) behavior.

Trees removed by this behavior will have a mortality reason code of "storm".

Parameters for this behavior

Parameter name	Description
Minimum DBH for Storm Damage, in cm	The minimum DBH for trees that can be damaged or killed by storms. Trees smaller than this are never damaged no matter what storms occur.
Number of Years Storm-Damaged Snags Last	The number of years snags damaged in storms last before disappearing. If snags are not used in a run, this is not required.
Storm Heavy Damage Survival Prob Intercept (a)	The "a" value in the probability of survival logit function for trees with heavy damage.
Storm Heavy Damage Survival Prob DBH Coeff. (b)	The "b" value in the probability of survival logit function for trees with heavy damage.
Storm Medium Damage Survival Prob Intercept (a)	The "a" value in the probability of survival logit function for trees with medium damage.
Storm Medium Damage Survival Prob DBH Coeff. (b)	The "b" value in the probability of survival logit function for trees with medium damage.
Storm - Prop. Heavy Damage Dead Trees that Tip Up	The proportion of those heavily damaged trees that are killed in the storm that tip up, as a value between 0 and 1. For how a tipped-up tree is treated, see the behavior description.

How it works

Trees that have received medium or heavy damage from the [Storm damage applier](#) behavior have a certain probability of survival. (Undamaged trees, and any trees with a DBH smaller than the

values set in the **Minimum DBH for Storm Damage, in cm** parameter, are ignored.) The probability is:

$$p = \frac{\exp(a_i + b_i * DBH)}{1 + \exp(a_i + b_i * DBH)}$$

where:

- p is the tree's probability of survival, between 0 and 1
- a_i is either the **Storm Medium Damage Survival Prob Intercept (a)** or the **Storm Heavy Damage Survival Prob Intercept (a)** parameter, depending on the tree's damage category
- b is either the **Storm Medium Damage Survival Prob DBH Coeff. (b)** or the **Storm Heavy Damage Survival Prob DBH Coeff. (b)** parameter, depending on the tree's damage category
- DBH is the tree's DBH, in cm

Once the survival probability has been calculated, this behavior uses a random number to determine whether it lives or dies. Damaged trees are only at risk of dying at the time of the storm that damages them; if they survive it, this behavior will not try to kill them again even if they are still damaged. A certain proportion of heavily damaged trees that die create tip-ups. The probability of this is in the parameter **Storm - Prop. Heavy Damage Dead Trees that Tip Up**.

If snags are used in this run, those trees that die in either damage category (except for tip-ups) become snags. A time-since-damage counter is set for each of these snags. After the amount of time specified in the **Number of Years Storm-Damaged Snags Last** has passed, this behavior will remove those snags, "killing" them. They are not available for later processes such as substrate. This behavior will not do anything to any snag that it did not kill. If snags are not used in this run, trees that die have a flag set indicating that they are dead. They are available during the timestep in which they die to substrate and other processes, in exactly the same manner as trees that die due to natural mortality. They will be subject to the same cleanup and removal processes as well.

If a heavily-damaged dead tree tips up, and snags are used in the run, the tip-up becomes a snag that has its "dead" flag set to true. It is available during the timestep in which it dies to substrate and other processes, in exactly the same manner as other snags that die due to natural mortality. It is subject to the same cleanup and removal processes as well. If snags are not used in the run, then tip-ups are treated like all other storm-killed trees.

Saplings that are killed in storms never become snags. They are killed in the manner described above for trees that die in a non-snag run. Existing snags are never at risk for storm damage or mortality, but the behavior must be applied to the snag tree type in order to cause storm-killed adults to become snags.

How to apply it

Apply this behavior to the trees that can be killed in storms. You must also apply the [Storm damage applier](#) behavior to the same trees. You may not apply this behavior to seedlings. If you wish to have storm-killed trees become snags, you must apply this behavior to the snag tree type. This may cause snags to appear due to natural mortality and other causes; you must use other behaviors to manage these snags.

You must also have any kind of [mortality behavior](#) applied to each tree species and life history stage to which this behavior is applied.

Storm direct killer

This behavior kills trees based on storm severity, without an intervening damage step.

Trees removed by this behavior will have a mortality reason code of "storm".

Parameters for this behavior

Parameter name	Description
Storm Direct Killer - a	The "a" value in the probability of mortality logit function.
Storm Direct Killer - b	The "b" value in the probability of mortality logit function.

How it works

When storms occur, trees to which this behavior are applied have the following probability of mortality:

$$p = \frac{\exp(a + b * D)}{1 + \exp(a + b * D)}$$

where:

- p is the tree's probability of mortality, between 0 and 1
- a is the **Storm Direct Killer - a** parameter
- b is the **Storm Direct Killer - b** parameter
- D is the storm damage at the tree's location

Once the mortality probability has been calculated, this behavior uses a random number to determine whether it lives or dies. If more than one storm has occurred in the current timestep, each storm gets a separate, independent chance to kill trees.

Trees that die have a "dead" flag set to true and are treated in the rest of the run like trees that have died due to natural mortality.

How to apply it

Apply this behavior to the trees that can be killed in storms. You must also use the [Storm disturbance](#) behavior and have any kind of [mortality behavior](#) applied to each tree species and life history stage to which this behavior is applied.

Selection harvest

This behavior allows you to specify target basal areas for a tree population as a method of harvest input, instead of designing specific harvest events.

Trees removed by this behavior will have a mortality reason code of "harvest".

Parameters for this behavior

Parameter name	Description
Selection Harvest Cut Range 1 Lower DBH (cm)	The lower bound of the first DBH cut range, in cm.
Selection Harvest Cut Range 1 Upper DBH (cm)	The upper bound of the first DBH cut range, in cm.
Selection Harvest Cut Range 1 Target Basal Area (m ² /ha)	The target basal area, in square meters per hectare, of the first cut range.
Selection Harvest Cut Range 2 Lower DBH (cm)	The lower bound of the second DBH cut range, in cm.
Selection Harvest Cut Range 2 Upper DBH (cm)	The upper bound of the second DBH cut range, in cm.
Selection Harvest Cut Range 2 Target Basal Area (m ² /ha)	The target basal area, in square meters per hectare, of the second cut range.
Selection Harvest Cut Range 3 Lower	The lower bound of the third DBH cut range, in cm.

DBH (cm)	
Selection Harvest Cut Range 3 Upper DBH (cm)	The upper bound of the third DBH cut range, in cm.
Selection Harvest Cut Range 3 Target Basal Area (m ² /ha)	The target basal area, in square meters per hectare, of the third cut range.
Selection Harvest Cut Range 4 Lower DBH (cm)	The lower bound of the fourth DBH cut range, in cm.
Selection Harvest Cut Range 4 Upper DBH (cm)	The upper bound of the fourth DBH cut range, in cm.
Selection Harvest Cut Range 4 Target Basal Area (m ² /ha)	The target basal area, in square meters per hectare, of the fourth cut range.
Selection Harvest Initial Age	The initial age.

How it works

You can specify up to four DBH ranges. You provide the lower and upper DBH bounds of these ranges, and the target amount of basal area for each. Each timestep, this behavior calculates the amount of basal area in each of these ranges. If it is greater than the target, this behavior signals to the Harvest behavior that it should remove enough basal area to bring each range back down to its target basal area. Since Harvest actually does the tree removal, see that behavior's documentation for the method used. If the amount of basal area in any given range is less than the target, no trees are cut in that range.

How to apply it

Add this behavior to your run. Harvest is also needed in the run, and should be placed after Selection Harvest in the behavior order.

Windstorm

Windstorm kills trees due to storm events.

Trees removed by this behavior will have a mortality reason code of "storm".

Parameters for this behavior

Parameter name	Description
Windstorm - DBH Exponent (b)	The "b" value in the equation used to determine the mortality of an individual tree as a result of a storm.
Windstorm - Minimum DBH for Windstorm Mortality	The minimum DBH for trees to be killed in storm events.
Windstorm - Mortality Intercept (a)	The "a" value in the equation used to determine the mortality of an individual tree as a result of a storm.
Windstorm - Sea Surface Temperature Cyclicity Period (Years)	Parameter that controls the cyclicity of storm frequency. This value cannot be 0.
Windstorm - Severity for 1 Year Return Interval Storm	The severity of storms with a 1 year return interval, as a value between 0 (no mortality) and 1 (complete devastation).
Windstorm - Severity for 5 Year Return Interval Storm	The severity of storms with a 5 year return interval, as a value between 0 (no mortality) and 1 (complete devastation).
Windstorm - Severity for 10 Year Return Interval Storm	The severity of storms with a 10 year return interval, as a value between 0 (no mortality) and 1 (complete devastation).
Windstorm - Severity for 20 Year Return Interval Storm	The severity of storms with a 20 year return interval, as a value between 0 (no mortality) and 1 (complete devastation).
Windstorm - Severity for 40 Year Return Interval Storm	The severity of storms with a 40 year return interval, as a value between 0 (no mortality) and 1 (complete devastation).
Windstorm - Severity for 80 Year Return Interval	The severity of storms with a 80 year return interval, as a value between 0 (no mortality) and 1 (complete devastation).

Storm	
Windstorm - Severity for 160 Year Return Interval Storm	The severity of storms with a 160 year return interval, as a value between 0 (no mortality) and 1 (complete devastation).
Windstorm - Severity for 320 Year Return Interval Storm	The severity of storms with a 320 year return interval, as a value between 0 (no mortality) and 1 (complete devastation).
Windstorm - Severity for 640 Year Return Interval Storm	The severity of storms with a 640 year return interval, as a value between 0 (no mortality) and 1 (complete devastation).
Windstorm - Severity for 1280 Year Return Interval Storm	The severity of storms with a 1280 year return interval, as a value between 0 (no mortality) and 1 (complete devastation).
Windstorm - Severity for 2560 Year Return Interval Storm	The severity of storms with a 2560 year return interval, as a value between 0 (no mortality) and 1 (complete devastation).
Windstorm - Storm Cyclicity Sine Curve d	Parameter that controls the cyclicity of storm frequency. For no cyclicity, set this value to 0. This value is part of the sine curve term and controls the sine amplitude.
Windstorm - Storm Cyclicity Sine Curve f	Parameter that controls the cyclicity of storm frequency. This value is part of the sine curve term and controls the sine frequency.
Windstorm - Storm Cyclicity Sine Curve g	Parameter that controls the cyclicity of storm frequency. This value is part of the sine curve term and controls where on the sine curve storms start occurring.
Windstorm - Storm Cyclicity Trend Function Intercept (i)	Parameter that controls the trend of cyclicity of storm frequency. This value is part of the trend term and is the intercept of the function controlling the increase or decrease of overall frequency cycling. For no cyclicity at all, set this term to 1. For no trend in cyclicity, set this term to 0.
Windstorm - Storm Cyclicity Trend Function Slope (m)	Parameter that controls the trend of cyclicity of storm frequency. This value is part of the trend term and is the slope at which frequency cycling increases or decreases. For no cyclicity, or no trend in cyclicity, set this

	term to 0.
Windstorm - Storm Intensity Coefficient (c)	The "c" value in the equation used to determine the mortality of an individual tree as a result of a storm.
Windstorm - Timestep to Start Storms	The first timestep that storms are allowed to occur.

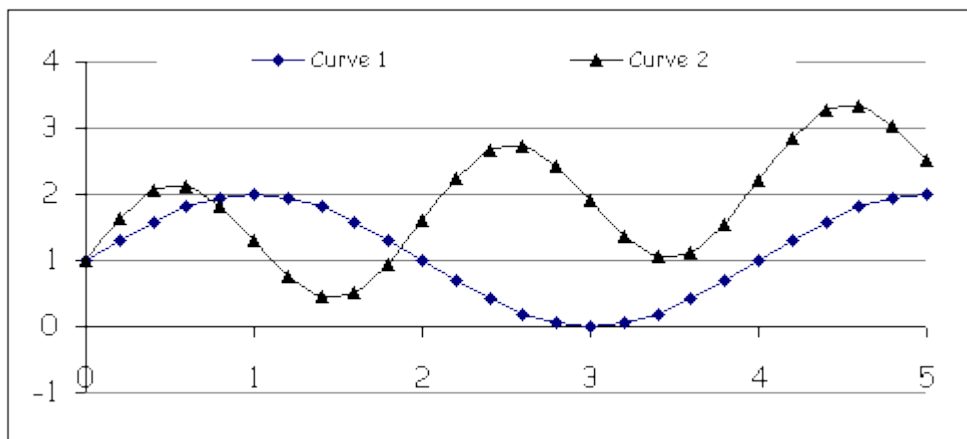
How it works

Using the parameters, you provide a general "shape" of storm intensity. SORTIE then decides which storms occur each timestep, and which trees die as a result.

This behavior defines 11 storm return intervals: 1, 5, 10, 20, 40, 80, 160, 320, 640, 1280, and 2560 years. Each has a set annual probability: for example, an 80-year return interval storm has an annual probability of $1/80$, or 0.0125. For each year of each timestep, for each return interval, SORTIE generates a random number to decide whether a storm of that return interval will occur. This means that there can be multiple storms in a timestep, or no storms at all. In a multi-year timestep, a storm of a given return interval can happen more than once.

You give each return interval a storm severity value, between 0 and 1. These are defined in the **Windstorm - Severity for X Year Return Interval Storm** parameters. A severity of 0 means no tree mortality; a severity of 1 approaches 100% mortality.

The overall frequency of storms can remain constant, or it can change through time. It has been reported in [Goldenburg et al 2001](#) that storm activity in the North Atlantic cycles along with sea surface temperature. This behavior can thus change the storm frequency over time, using either a sinusoidal pattern, a constant linear change, or both together. In the figure below, curve 1 is a basic sine wave. Curve 2 has a sinusoidal pattern plus an upwards trend.



The actual probability of an individual storm that takes place in a storm regime with a cyclical frequency is:

$$P'(F_i) = P(F_i) * ([d * \sin(\pi * (x-g) / (2f))] + [mx + i])$$

Note that the new probability is a baseline probability, $P(F_i)$, multiplied by a value that adjusts the probability according to where the model is at the given time in the frequency cycle. The frequency cycle multiplier is itself made up of two terms added together. The first term is the sine curve cycling, and the second term is the overall trend upwards or downwards.

Terms in the equation:

- $P'(F_i)$ is this timestep's annual probability of a storm of the i th return interval, adjusted according to the frequency cyclicity
- $P(F_i)$ is the baseline probability of a storm of the i th return interval; that is, the inverse of the values specified in the **Windstorm - Severity for X Year Return Interval Storm** parameters
- $x = 4 * t / Sr$, where t is the number of years since storms started and Sr is the **Windstorm - Sea Surface Temperature Cyclicity Period (Years)** parameter
- d is the **Windstorm - Storm Cyclicity Sine Curve d** parameter, which controls the sine curve's amplitude
- f is the **Windstorm - Storm Cyclicity Sine Curve f** parameter, which controls the sine curve's frequency
- g is the **Windstorm - Storm Cyclicity Sine Curve g** parameter, which controls where on the sine curve storms start occurring
- m is the **Windstorm - Storm Cyclicity Trend Function Slope (m)** parameter
- i is the **Windstorm - Storm Cyclicity Trend Function Intercept (i)** parameter

To turn off all cyclicity and use constant storm probabilities, set **Windstorm - Storm Cyclicity Sine Curve d** to 0, **Windstorm - Storm Cyclicity Trend Function Slope (m)** to 0, and **Windstorm - Storm Cyclicity Trend Function Intercept (i)** to 1. (The other values are unimportant.) To use only the sine portion with no trend line, set both **Windstorm - Storm Cyclicity Trend Function Slope (m)** and **Windstorm - Storm Cyclicity Trend Function Intercept (i)** to 0. To use only the trend portion, set **Windstorm - Storm Cyclicity Sine Curve d** to 0.

For each storm that occurs, Windstorm decides what trees will die as a result. A tree's probability of mortality is calculated as follows:

$$p = \frac{\exp(a + c * s * DBH^b)}{1 + \exp(a + c * s * DBH^b)}$$

where:

- p is the tree's probability of mortality

- a is the **Windstorm - Mortality Intercept (a)** parameter
- c is the **Windstorm - Storm Intensity Coefficient (c)** parameter
- b is the **Windstorm - DBH Exponent (b)** parameter
- DBH is the tree's DBH, in cm
- s is the storm's severity, set in the parameter for its return interval

Below severity 0.1, the model becomes unreliable; so in that case, the severity is treated as a straight probability of mortality for all trees. For example, if a storm occurs of severity 0.05, all trees have the same 5% chance of dying. If a storm return interval's severity is set to 0, then that storm never occurs.

It is possible for a storm to occur and kill no trees, especially if it is a very mild storm or the forest has no large trees. Unlike the other SORTIE storm behaviors, there is no damaged-but-alive state. After a windstorm a tree is either dead or in perfect health.

Storm events happen "independently". Every time a storm happens, all eligible trees have a separate chance of mortality. Of course, the storms can never truly be independent. A storm can only kill the trees that another storm hasn't already killed.

Trees killed in a windstorm are treated like trees killed in natural mortality. They will form snags if the run uses snags, and are available for processes such as substrate.

Seedlings and snags are never killed by storms. For adults and saplings, only those trees to which the Windstorms behavior has been applied will be considered for storm mortality; and of those trees, only those trees with a DBH larger than the value in the **Windstorm - Minimum DBH for Windstorm Mortality** parameter can be killed.

You can delay the introduction of windstorms into the run using the **Windstorm - Timestep to Start Storms** parameter. If this value is greater than 0, no storms will occur until that timestep is reached.

Information on what storms occurred during a run is saved in the [Windstorm Results grid](#). This grid lists how many storms occurred each timestep, and the basal area and density killed of each species in that storm.

How to apply it

Add this behavior to your run and apply it to saplings and/or adults of any species. If you wish to get results on storm events, save the [Windstorm Results grid](#) data in a detailed output file. You can then view the contents of this grid as a [table](#) using SORTIE's data visualization system.

Management behaviors

Management behaviors help the process of forest management.

Behavior	Description
Tree Quality Vigor Classifier	Classifies trees according to vigor and stem quality.

Tree Quality Vigor Classifier

The Tree Quality Vigor Classifier assigns trees to a classification system based on vigor and stem quality. This classification can then be used as a criterion in other behaviors.

There are four classes (1, 2, 3, 4) for deciduous species and two classes (5, 6) for conifers. The four classes used for deciduous species result from the combination of two possible vigor states and two stem quality levels. For conifers, only vigor is considered. The two vigor status are "vigorous" and "non-vigorous", where non-vigorous trees are considered at high risk of dying before the next harvest. The quality levels are "with sawlog potential" and "without sawlog potential".

Parameters for this behavior

Parameter name	Description
Quality Vigor Classifier - Prob New Adults Sawlog	Probability that new adult trees will be classed as "sawlog" quality, expressed as a value between 0 and 1. Does not apply to coniferous trees.
Quality Vigor Classifier - Prob New Adults Vigorous	Probability that new adult trees will be classed as "vigorous", expressed as a value between 0 and 1.
Quality Vigor Classifier - Quality Beta 0	β_0 in the quality probability equation. Ignored for conifers.
Quality Vigor Classifier - Quality Beta 1 Class 1	β_{1class} in the quality probability equation for trees with a current tree class of 1. Ignored for conifers.
Quality Vigor Classifier - Quality Beta 1 Class 2	β_{1class} in the quality probability equation for trees with a current tree class of 2. Ignored for conifers.
Quality Vigor Classifier - Quality Beta 1 Class 3	β_{1class} in the quality probability equation for trees with a current tree class of 3. Ignored for conifers.

Beta 1 Class 3	
Quality Vigor Classifier - Quality Beta 1 Class 4	$\beta_{1\text{class}}$ in the quality probability equation for trees with a current tree class of 4. Ignored for conifers.
Quality Vigor Classifier - Quality Beta 2	β_2 in the quality probability equation. Ignored for conifers.
Quality Vigor Classifier - Quality Beta 3	β_3 in the quality probability equation. Ignored for conifers.
Quality Vigor Classifier - Species Type	Whether a species is deciduous or coniferous.
Quality Vigor Classifier - Vigor Beta 0	β_0 in the vigor probability equation.
Quality Vigor Classifier - Vigor Beta 1 Class 1	$\beta_{1\text{class}}$ in the vigor probability equation for trees with a current tree class of 1.
Quality Vigor Classifier - Vigor Beta 1 Class 2	$\beta_{1\text{class}}$ in the vigor probability equation for trees with a current tree class of 2.
Quality Vigor Classifier - Vigor Beta 1 Class 3	$\beta_{1\text{class}}$ in the vigor probability equation for trees with a current tree class of 3.
Quality Vigor Classifier - Vigor Beta 1 Class 4	$\beta_{1\text{class}}$ in the vigor probability equation for trees with a current tree class of 4.
Quality Vigor Classifier - Vigor Beta 1 Class 5	$\beta_{1\text{class}}$ in the vigor probability equation for trees with a current tree class of 5.
Quality Vigor Classifier - Vigor Beta 1 Class 6	$\beta_{1\text{class}}$ in the vigor probability equation for trees with a current tree class of 6.
Quality Vigor Classifier - Vigor Beta 2	β_2 in the vigor probability equation.

Quality Vigor
Classifier - Vigor
Beta 3

β_3 in the vigor probability equation.

How it works

Tree classification is as follows:

Species Type	Vigor	Quality	DBH Range	Class
Deciduous	Vigorous	Sawlog	> 0	1
Deciduous	Vigorous	Not sawlog	> 0	2
Deciduous	Not vigorous	Sawlog	> 23 cm	3
Deciduous	Not vigorous	Sawlog	\leq 23 cm	4
Deciduous	Not vigorous	Not sawlog	> 0	4
Coniferous	Vigorous	NA	> 0	5
Coniferous	Not vigorous	NA	> 0	6

Species are defined as deciduous or coniferous using the **Quality Vigor Classifier - Species Type** parameter.

Trees that do not have vigor and quality designations, such as new adult trees or initial conditions trees that were not specifically assigned these values, are randomly given vigor and quality according to defined probabilities that these trees are vigorous or of sawlog quality. These probabilities are defined, as values between 0 and 1, in the **Quality Vigor Classifier - Prob New Adults Vigorous** and **Quality Vigor Classifier - Prob New Adults Sawlog** parameters. Coniferous species are not assigned a quality value and values entered for those species are ignored.

Vigor and quality for a tree may change through time. The probability of transition between states is a function of previous class and size, and is evaluated for each tree each timestep. The probability of a tree being vigorous in the current timestep is:

$$p = \frac{e^{\beta_x}}{1 + e^{\beta_x}}$$

where:

$$\beta_x = \beta_0 + \beta_{1class} + \beta_2 * DBH + \beta_3 * \ln(DBH)$$

where:

- β_0 is the **Quality Vigor Classifier - Vigor Beta 0** parameter
- β_{1class} is one of the following depending on the current class designation of the tree:
 - **Quality Vigor Classifier - Vigor Beta 1 Class 1**
 - **Quality Vigor Classifier - Vigor Beta 1 Class 2**
 - **Quality Vigor Classifier - Vigor Beta 1 Class 3**
 - **Quality Vigor Classifier - Vigor Beta 1 Class 4**
 - **Quality Vigor Classifier - Vigor Beta 1 Class 5**
 - **Quality Vigor Classifier - Vigor Beta 1 Class 6**
- β_2 is the **Quality Vigor Classifier - Vigor Beta 2** parameter
- β_3 is the **Quality Vigor Classifier - Vigor Beta 3** parameter
- DBH is the tree's DBH in cm

Deciduous trees are further evaluated for tree quality. The probability of a tree being of sawlog quality in the current timestep is:

$$p = \frac{e^{\beta_x}}{1 + e^{\beta_x}}$$

where:

$$\beta_x = \beta_0 + \beta_{1class} + \beta_2 * DBH + \beta_3 * \ln(DBH)$$

where:

- β_0 is the **Quality Vigor Classifier - Quality Beta 0** parameter
- β_{1class} is one of the following depending on the current class designation of the tree:
 - **Quality Vigor Classifier - Quality Beta 1 Class 1**
 - **Quality Vigor Classifier - Quality Beta 1 Class 2**
 - **Quality Vigor Classifier - Quality Beta 1 Class 3**
 - **Quality Vigor Classifier - Quality Beta 1 Class 4**
- β_2 is the **Quality Vigor Classifier - Quality Beta 2** parameter
- β_3 is the **Quality Vigor Classifier - Quality Beta 3** parameter
- DBH is the tree's DBH in cm

Note that since only deciduous trees get a quality designation, there is no need for β_1 parameters for classes 5 and 6, which only apply to conifers.

Once a tree's probability of vigorousness and sawlog quality have been established, random numbers determine the final state. Then class assignment proceeds as above.

This behavior creates three [tree data members](#): "Vigorous", "Sawlog", and "Tree class".

How to apply it

Apply this behavior to adults of any species. It cannot be applied to any other life history stage.

Light behaviors

Light is the key resource for trees in the SORTIE model. Consequently, great care is taken in SORTIE to calculate the amount of light that each tree gets - in fact, these calculations take up more processing time than any other during model runs.

There are two basic light index types used by SORTIE to describe the amount of light a tree receives. The first is the Global Light Index, or GLI. GLI is the percentage of full sun received at a point. The second index is the Sail Light index, which is the proportion of shade seen at a point, from none to total. (The name Sail Light comes from the fact that the shape of shading neighbor tree crowns is approximated by a 2D rectangle, like a sail).

[How light calculations work](#)

Behavior	Description
Average Light behavior	Averages GLI values to produce a set of values with a coarser spatial resolution.
Basal Area Light behavior	Calculates light levels as a function of the basal area of trees in a neighborhood.
Beer's law light filter behavior	Simulates a filter that reduces light according to Beer's Law.
Constant GLI behavior	Assigns a constant GLI value to all trees to which it is assigned.
Gap Light behavior	Shortcuts the light calculation process by considering GLI to be binary: either full light or no light.
GLI light behavior	Calculates a Global Light Index (GLI) value for each individual.
GLI Map Creator behavior	Calculates a GLI value for each cell in a grid to create a light map.
GLI Points File Creator behavior	Calculates GLI values for individual points in the plot.
Quadrat-based GLI	Calculates GLI for grid cells and assigns trees the GLI of their cell.

light behavior	
Sail light behavior	Calculates a Sail Light index value for each individual.
Storm Light behavior	Calculates light levels as a function of number of trees damaged in storms.

Average Light

This behavior averages GLI values to produce a set of values with a coarser spatial resolution.

How it works

This behavior does not actually calculate GLI. It averages the GLI values in the [GLI Map](#) grid, which is created by the [GLI Map Creator](#) behavior.

This behavior creates its own map, called [Average Light](#). The value for each cell in this grid is an average of the cells of GLI Map in the same area. If the size of the cells of Average Light is an exact multiple of the size of the cells of GLI Map, then a straight average is calculated. If the size is not an exact multiple, each Average Light cell value is an average of the values of all the cells of GLI Map that overlap it in area, even if only partially.

Trees to which this behavior are applied get the value of their location in the Average Light grid.

How to apply it

This behavior may be applied to seedlings, saplings, and adults of any species. The [GLI Map Creator](#) behavior must also be used, and must come before Average Light in the run order. Once both behaviors have been added to your run, set up the cell sizes of the two grids the way you want them using the [Grid Setup window](#).

Basal Area Light behavior

This behavior calculates light levels as a function of the basal area of trees in a neighborhood. The light levels are randomized using a lognormal probability distribution. Because of this random element, to ensure some continuity through time, light levels only change when the local neighborhood tree basal area has changed by a certain amount.

Parameters for this behavior

Parameter name	Description
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Basal Area Light - Angiosperm "b" Parameter	The "b" value used to calculate mean GLI from angiosperm basal area.
Basal Area Light - Angiosperm "c" Parameter	The "c" value used to calculate mean GLI from angiosperm basal area.
Basal Area Light - Conifer "b" Parameter	The "b" value used to calculate mean GLI from conifer basal area.
Basal Area Light - Conifer "c" Parameter	The "c" value used to calculate mean GLI from conifer basal area.
Basal Area Light - Lognormal PDF Sigma	Sigma value for the lognormal probability distribution.
Basal Area Light - Mean GLI "a" Parameter	The "a" value used to calculate mean GLI from basal area.
Basal Area Light - Minimum BA Change for New GLI (m2)	The amount by which total basal area (angiosperm plus conifer), in square meters, must change in order to trigger a new GLI calculation in a grid cell.
Basal Area Light - Minimum DBH for Trees	The minimum DBH, in cm, of trees that count towards basal area.
Basal Area Light - Search Radius for Neighbors (m)	The radius, in meters, of the circle that is searched for neighbors.
Basal Area Light - Species Type	Whether each species is a conifer or an angiosperm, for the purposes of light calculations.

How it works

This behavior uses a [grid](#) called [Basal Area Light](#) to manage light levels. Light levels are calculated for each cell in the grid; trees to which this behavior are assigned receive the light level of the cell in which they are located.

The behavior begins by calculating the total basal area and angiosperm basal area in the neighborhood of each Basal Area Light grid cell. The neighborhood is a circle with its center on

the center of the grid cell, and a radius given in the **Basal Area Light - Search Radius for Neighbors (m)** parameter. Whether a neighborhood tree counts as angiosperm or conifer depends on what its species is set to in the **Basal Area Light - Species Type** parameter. Seedlings and snags are never included in these basal area totals. Other trees are only included if their DBH is equal to or greater than the value set in the **Basal Area Light - Minimum DBH for Trees** parameter. Once the basal areas are calculated, the behavior adds them together to create a total basal area, and compares this value to the previous timestep's total basal area. If the value has not changed by more than the amount set in the **Basal Area Light - Minimum BA Change for New GLI (m2)** parameter, no further action is taken. The previous timestep's GLI and basal area values are kept.

For each grid cell in which a new GLI is to be calculated, a mean GLI value is calculated as follows:

$$GLI_m = \frac{a}{1 + \left(\frac{BA_a}{c_a} \right)^{b_a} + \left(\frac{BA_c}{c_c} \right)^{b_c}}$$

where:

- GLI_m is the mean GLI value, as a value between 0 and 100
- a is the **Basal Area Light - Mean GLI "a" Parameter**
- b_a is the **Basal Area Light - Angiosperm "b" Parameter**
- c_a is the **Basal Area Light - Angiosperm "c" Parameter**
- BA_a is the angiosperm basal area for that grid cell, in square meters
- b_c is the **Basal Area Light - Conifer "b" Parameter**
- c_c is the **Basal Area Light - Conifer "c" Parameter**
- BA_c is the conifer basal area for that grid cell, in square meters

This mean GLI is translated into a ζ value for the lognormal random draw as follows:

$$\zeta = \ln(GLI_m) - (\sigma^2/2)$$

where GLI_m is the mean GLI value calculated above, and σ is the **Basal Area Light - Lognormal PDF Sigma** parameter.

This value is then used to produce a random lognormally distributed number, from the following distribution:

$$p(x)dx = \frac{1}{x\sqrt{2\pi\sigma^2}} e^{-\left(\frac{(\ln(x)-\zeta)^2}{2\sigma^2} \right)} dx$$

where ζ is the value calculated above, and σ is the **Basal Area Light - Lognormal PDF Sigma** parameter. This number is the GLI value, between 0 and 100.

Once each Basal Area Light grid cell has gotten a GLI value, trees to which this behavior applies get the value of GLI from the grid cell in which they are located.

How to apply it

This behavior may be applied to seedlings, saplings, and adults of any species.

Beer's law light filter

How it works

This behavior simulates a filter that reduces light according to Beer's Law.

Parameters for this behavior

Parameter name	Description
Height of Light Filter, in m	Height, in meters, at which the Beer's law light filter hangs.
Light Filter Light Transmission Coefficient	Amount of light that is blocked by the light filter.

How it works

Imagine a fog that hangs out on the forest floor and ends abruptly at a certain height. All trees shorter than the top of the fog layer will have their light attenuated but not blocked completely. The closer they get to the top of the fog the more light is let in. The amount of light which actually gets through is calculated according to Beer's Law, where $transmission = e^{-az}$, where a is the **Light Filter Light Transmission Coefficient** parameter and z = thickness of the filter, in meters (which is the distance from the light point to the top of the filter - the **Height of Light Filter, in m** parameter). This filter behavior can be used to, for instance, replicate the effects of an herbaceous layer in reducing light to young seedlings. The height of the filter is randomized slightly each time the thickness of the filter over the light point is calculated to introduce a stochastic element.

Trees can be given a respite from the effects of the filter. This behavior does not set the respite counter but it will respect any values which another behavior has put in.

Trees can be given a rooting height in addition to their normal height. This value is added to their existing height to get their effective height, which is what will be applied when determining the thickness of the filter overhead. Again, this behavior does not set this height but will use it if another behavior sets it.

This behavior DOES NOT ACTUALLY CALCULATE LIGHT LEVELS. Any tree species and types to which this filter is applied must also have one of the other light behaviors assigned to it. This behavior assumes the value is a GLI value; using Sail Light will probably not produce good results.

This behavior only affects tree types and species to which it is applied in the behavior list of the parameter file. It will ignore all other trees, even if they are short enough to be beneath the filter level.

How to apply it

This behavior may be applied to seedlings, saplings, and adults of any species.

Constant GLI

Parameters for this behavior

Parameter name	Description
Constant GLI - Constant GLI Value (0-100)	The GLI value assigned to all trees.

How it works

This assigns a constant GLI value to all trees to which it is assigned. This value is set in the **Constant GLI - Constant GLI Value (0-100)** parameter.

How to apply it

This behavior may be applied to seedlings, saplings, and adults of any species.

Gap Light behavior

This behavior shortcuts the light calculation process by considering GLI to be binary: either full light (100%) or no light (0%). This simulates a simplified version of gap light dynamics.

How it works

This behavior uses a [grid](#) object called [Gap Light](#) to determine the basic position of plot gaps. If a grid cell contains no adult trees, it is considered a gap. If there are any adults of any species, then it is non-gap.

The trees to which this behavior has been applied get their GLI values based on the gap status of the grid cell in which they are located. If the gap status is TRUE, then they receive a GLI value of 100%. If it is FALSE, they receive a value of 0%.

How to apply it

This behavior may be applied to seedlings, saplings, and adults of any species.

GLI light

For more on what GLI is and how it is calculated, see [here](#).

Parameters for this behavior

Parameter name	Description
Height of Fisheye Photo	When a fish-eye photo is simulated for a tree, this positions the photo at either the top of the crown or at mid-crown. Seedlings always get fisheye photos at top-of-crown no matter what this value is.
Minimum Solar Angle for GLI Light, in rad	This is the minimum angle at which sunlight is seen, in radians. Below this value the sky is assumed to be dark due to shading neighbors.
Number of Altitude Sky Divisions for GLI Light Calculations	Number of grid cells into which the sky is divided from horizon to zenith, for the purpose of calculating light direction.
Number of Azimuth Sky Divisions for GLI Light Calculations	Number of grid cells into which the sky is divided around the horizon, for the purpose of calculating light direction.

General light parameters used by this behavior

Parameter name	Description
Beam Fraction of Global Radiation	The fraction of total solar radiation that is direct beam radiation (as opposed to diffuse). Expressed as a value between 0 and 1.

Clear Sky Transmission Coefficient	Used to determine the amount of solar radiation seen at the plot location.
First Day of Growing Season	The first day of the growing season, as a Julian day (number between 1 and 365). Trees only get light during the growing season.
Last Day of Growing Season	The last day of the growing season, as a Julian day (number between 1 and 365). Trees only get light during the growing season.
Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the tree crown for each species. Expressed as a fraction between 0 and 1. A value must be provided for all species, even if they don't all use light.
Snag Age Class 1 Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is less than or equal to "Upper Age (Yrs) of Snag Light Transmission Class 1". Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Snag Age Class 2 Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is greater than "Upper Age (Yrs) of Snag Light Transmission Class 1", but is less than or equal to "Upper Age (Yrs) of Snag Light Transmission Class 2". Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Snag Age Class 3 Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is greater than "Upper Age (Yrs) of Snag Light Transmission Class 2". Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Upper Age (Yrs) of Snag Light Transmission Class 1	The upper age limit, in years, defining the first age class of snag light transmission. Snags with an age less than or equal to this age have a light transmission coefficient matching "Snag Age Class 1 Light Transmission Coefficient". If your run does not work with snags, you can ignore this.
Upper Age (Yrs) of Snag Light Transmission Class 2	The upper age limit, in years, defining the second age class of snag light transmission. Snags with an age greater than the upper limit for size class 1, but less than or equal to this age, have a light transmission coefficient matching "Snag Age Class 2 Light Transmission Coefficient". Snags with an age greater than this value are in age class three. If your run does not work with snags, you can ignore this.

How it works

This behavior calculates a Global Light Index (GLI) value for each individual of each tree type to which it is assigned. GLI values range from 0 (no sun) to 100 (full sun).

How to apply it

This behavior may be applied to seedlings, saplings, and adults of any species.

GLI Map Creator

For more on what GLI is and how it is calculated, see [here](#).

Parameters for this behavior

Parameter name	Description
Height at Which GLI is Calculated for GLI Map, in meters	Height at which GLI is calculated.
Minimum Solar Angle for GLI Map Creator, in rad	This is the minimum angle at which sunlight is seen, in radians. Below this value the sky is assumed to be dark due to shading neighbors.
Number of Altitude Sky Divisions for GLI Map Creator Calculations	Number of grid cells into which the sky is divided from horizon to zenith, for the purpose of calculating light direction.
Number of Azimuth Sky Divisions for GLI Map Creator Calculations	Number of grid cells into which the sky is divided around the horizon, for the purpose of calculating light direction.

General light parameters used by this behavior

Parameter name	Description
Beam Fraction of Global Radiation	The fraction of total solar radiation that is direct beam radiation (as opposed to diffuse). Expressed as a value between 0 and 1.
Clear Sky Transmission Coefficient	Used to determine the amount of solar radiation seen at the plot location.
First Day of	The first day of the growing season, as a Julian day (number between 1

Growing Season	and 365). Trees only get light during the growing season.
Last Day of Growing Season	The last day of the growing season, as a Julian day (number between 1 and 365). Trees only get light during the growing season.
Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the tree crown for each species. Expressed as a fraction between 0 and 1. A value must be provided for all species, even if they don't all use light.
Snag Age Class 1 Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is less than or equal to "Upper Age (Yrs) of Snag Light Transmission Class 1". Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Snag Age Class 2 Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is greater than "Upper Age (Yrs) of Snag Light Transmission Class 1", but is less than or equal to "Upper Age (Yrs) of Snag Light Transmission Class 2". Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Snag Age Class 3 Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is greater than "Upper Age (Yrs) of Snag Light Transmission Class 2". Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Upper Age (Yrs) of Snag Light Transmission Class 1	The upper age limit, in years, defining the first age class of snag light transmission. Snags with an age less than or equal to this age have a light transmission coefficient matching "Snag Age Class 1 Light Transmission Coefficient". If your run does not work with snags, you can ignore this.
Upper Age (Yrs) of Snag Light Transmission Class 2	The upper age limit, in years, defining the second age class of snag light transmission. Snags with an age greater than the upper limit for size class 1, but less than or equal to this age, have a light transmission coefficient matching "Snag Age Class 2 Light Transmission Coefficient". Snags with an age greater than this value are in age class three. If your run does not work with snags, you can ignore this.

How it works

This behavior calculates a GLI value for each cell in a [grid](#) object called [GLI Map](#). The height at which this GLI value is calculated is set by the **Height at Which GLI is Calculated for GLI Map, in meters** parameter. These values are not used by any other behavior. You can save the values in the GLI Map grid into a [detailed output file](#) and view the map data later.

How to apply it

Add the behavior to the run. Be sure to save the GLI Map grid in the detailed output file in order to be able to view the results.

GLI Points File Creator behavior

This behavior calculates GLI values for individual points in the plot.

Parameters for this behavior

Parameter name	Description
GLI Points Input File	The file containing the points for which to calculate GLI. This file will overwrite any existing points. For best results, enter a fully-qualified pathname (i.e. "c:\sortie\my_file.txt").
GLI Points Output File	The file to which results will be written each timestep. Any existing data in this file will be overwritten at the start of the run.
Minimum Solar Angle for GLI Points Creator, in rad	This is the minimum angle at which sunlight is seen, in radians. Below this value the sky is assumed to be dark due to shading neighbors.
Number of Altitude Sky Divisions for GLI Points Creator	Number of grid cells into which the sky is divided from horizon to zenith, for the purpose of calculating light direction.
Number of Azimuth Sky Divisions for GLI Points Creator	Number of grid cells into which the sky is divided around the horizon, for the purpose of calculating light direction.

General light parameters used by this behavior

Parameter name	Description
Beam Fraction of Global Radiation	The fraction of total solar radiation that is direct beam radiation (as opposed to diffuse). Expressed as a value between 0 and 1.
Clear Sky Transmission Coefficient	Used to determine the amount of solar radiation seen at the plot location.
First Day of Growing Season	The first day of the growing season, as a Julian day (number between 1 and 365). Trees only get light during the growing season.

Last Day of Growing Season	The last day of the growing season, as a Julian day (number between 1 and 365). Trees only get light during the growing season.
Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the tree crown for each species. Expressed as a fraction between 0 and 1. A value must be provided for all species, even if they don't all use light.
Snag Age Class 1 Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is less than or equal to "Upper Age (Yrs) of Snag Light Transmission Class 1". Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Snag Age Class 2 Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is greater than "Upper Age (Yrs) of Snag Light Transmission Class 1", but is less than or equal to "Upper Age (Yrs) of Snag Light Transmission Class 2". Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Snag Age Class 3 Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is greater than "Upper Age (Yrs) of Snag Light Transmission Class 2". Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Upper Age (Yrs) of Snag Light Transmission Class 1	The upper age limit, in years, defining the first age class of snag light transmission. Snags with an age less than or equal to this age have a light transmission coefficient matching "Snag Age Class 1 Light Transmission Coefficient". If your run does not work with snags, you can ignore this.
Upper Age (Yrs) of Snag Light Transmission Class 2	The upper age limit, in years, defining the second age class of snag light transmission. Snags with an age greater than the upper limit for size class 1, but less than or equal to this age, have a light transmission coefficient matching "Snag Age Class 2 Light Transmission Coefficient". Snags with an age greater than this value are in age class three. If your run does not work with snags, you can ignore this.

How it works

You provide, as input, a file that contains the list of points for which you would like GLI values. The file is tab-delimited text, and has the following format:

X	Y	Height (m)
12.4	36.5	1.2

128.7	19.5	0.68
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The first row is assumed to be a header row and is ignored. Each subsequent row is a single point for which to calculate GLI. You can include as many as you wish. The first column is the point's X coordinate; the second is the Y coordinate; and the third column is the height above the ground, in meters. Name the file whatever you wish. Put the file name for the points file in the **GLI Points Input File** parameter. It is best to use a fully-qualified path name (i.e. "c:\sortie\my_points.txt"). SORTIE-ND will load the points into the parameter file. If you are working with a parameter file that already contains GLI points because they were saved into it previously, you do not need to enter another file and can leave the **GLI Points Input File** parameter blank.

Each timestep, this behavior calculates GLI at each of the points specified. It then writes the results to another tab-delimited text file. You enter the filename of this file in the **GLI Points Output File** parameter. It should be fully-qualified (i.e. "c:\sortie\points_output.txt") and should have a ".txt" extension. If the file already exists when the SORTIE-ND run begins, the contents will be overwritten. This means that this behavior cannot successfully be used in batch runs where a parameter file will be run multiple times.

How to apply it

This behavior does not need to be applied to trees. It can stand alone as the only light behavior if you wish.

Quadrat-based GLI light

For more on what GLI is and how it is calculated, see [here](#).

Parameters for this behavior

Parameter name	Description
Number of Altitude Sky Divisions for Quadrat Light Calculations	Number of grid cells into which the sky is divided from horizon to zenith, for the purpose of calculating light direction.
Number of Azimuth Sky Divisions for Quadrat Light Calculations	Number of grid cells into which the sky is divided around the horizon, for the purpose of calculating light direction.
Quadrat GLI - Always Calculate All	Whether or not to always calculate a GLI for all cells in the Quadrat GLI grid. If false, GLIs are only calculated when needed by a tree. Set this

GLIs	value to true if you are planning to save and use maps of the Quadrat GLI grid. If not, leaving it to false makes SORTIE run faster.
Height at Which GLI is Calculated for Quadrats, in meters	Height at which GLI is calculated.
Minimum Solar Angle for Quadrat Light, in rad	This is the minimum angle at which sunlight is seen, in radians. Below this value the sky is assumed to be dark due to shading neighbors.

General light parameters used by this behavior

Parameter name	Description
Beam Fraction of Global Radiation	The fraction of total solar radiation that is direct beam radiation (as opposed to diffuse). Expressed as a value between 0 and 1.
Clear Sky Transmission Coefficient	Used to determine the amount of solar radiation seen at the plot location.
First Day of Growing Season	The first day of the growing season, as a Julian day (number between 1 and 365). Trees only get light during the growing season.
Last Day of Growing Season	The last day of the growing season, as a Julian day (number between 1 and 365). Trees only get light during the growing season.
Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the tree crown for each species. Expressed as a fraction between 0 and 1. A value must be provided for all species, even if they don't all use light.
Snag Age Class 1 Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is less than or equal to "Upper Age (Yrs) of Snag Light Transmission Class 1". Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Snag Age Class 2 Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is greater than "Upper Age (Yrs) of Snag Light Transmission Class 1", but is less than or equal to "Upper Age (Yrs) of Snag Light Transmission Class 2". Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Snag Age Class 3 Amount Canopy	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is greater than "Upper Age

Light Transmission (0-1)	(Yrs) of Snag Light Transmission Class 2". Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Upper Age (Yrs) of Snag Light Transmission Class 1	The upper age limit, in years, defining the first age class of snag light transmission. Snags with an age less than or equal to this age have a light transmission coefficient matching "Snag Age Class 1 Light Transmission Coefficient". If your run does not work with snags, you can ignore this.
Upper Age (Yrs) of Snag Light Transmission Class 2	The upper age limit, in years, defining the second age class of snag light transmission. Snags with an age greater than the upper limit for size class 1, but less than or equal to this age, have a light transmission coefficient matching "Snag Age Class 2 Light Transmission Coefficient". Snags with an age greater than this value are in age class three. If your run does not work with snags, you can ignore this.

How it works

This behavior uses a [grid](#) object, called [Quadrat GLI](#), to help it assign GLI values to the trees to which it is assigned. The grid cells are the quadrats, in this case; this is a throwback to old SORTIE terminology. Each grid cell in which there is a tree to which this behavior applies has a GLI value calculated at its center, at a height that the user specifies. All other trees to which this behavior applies that are in that same grid cell get that same GLI value. This behavior saves having to calculate a different GLI value for each tree. GLI values range from 0 (no sun) to 100 (full sun).

For efficiency, this behavior does not calculate the value of a grid cell if there are no trees in that cell. In this case, the light value of the cell is -1. To force it to always calculate all GLIs (useful if you intend to save maps of the Quadrat GLI grid), set the **Quadrat GLI - Always Calculate All GLIs** parameter to true.

How to apply it

This behavior may be applied to seedlings, saplings, and adults of any species.

Sail light

For more on what the Sail Light index is and how it is calculated, see [here](#).

Parameter name	Description
Sail Light Maximum Shading Neighbor Distance, in meters	The radius, in meters, from a tree for which neighbors will be searched who can shade that tree.

Sail Light Minimum Solar Angle, in degrees	The azimuth angle, in degrees, below which it is assumed trees will see no light.
Calculated Crown Depth	When the shape of a tree's shading neighbors is assessed to see how much light each blocks, their crowns can either conform to each neighbor's true crown height or they can be approximated at the full height of the tree.
Height of Fisheye Photo	When a fish-eye photo is simulated for a tree, this positions the photo at either the top of the crown or at mid-crown. Seedlings always get fisheye photos at top-of-crown no matter what this value is.
Beam Fraction of Global Radiation	The fraction of total solar radiation that is direct beam radiation (as opposed to diffuse). Expressed as a value between 0 and 1.
Clear Sky Transmission Coefficient	Used to determine the amount of solar radiation seen at the plot location.
First Day of Growing Season	The first day of the growing season, as a Julian day (number between 1 and 365). Trees only get light during the growing season.
Last Day of Growing Season	The last day of the growing season, as a Julian day (number between 1 and 365). Trees only get light during the growing season.
Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the tree crown for each species. Expressed as a fraction between 0 and 1. A value must be provided for all species, even if they don't all use light.
Snag Age Class 1 Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is less than or equal to "Upper Age (Yrs) of Snag Light Transmission Class 1". Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Snag Age Class 2 Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is greater than "Upper Age (Yrs) of Snag Light Transmission Class 1", but is less than or equal to "Upper Age (Yrs) of Snag Light Transmission Class 2". Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Snag Age Class 3 Amount Canopy Light Transmission (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is greater than "Upper Age (Yrs) of Snag Light Transmission Class 2". Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.

Upper Age (Yrs) of Snag Light Transmission Class 1	The upper age limit, in years, defining the first age class of snag light transmission. Snags with an age less than or equal to this age have a light transmission coefficient matching "Snag Age Class 1 Light Transmission Coefficient". If your run does not work with snags, you can ignore this.
Upper Age (Yrs) of Snag Light Transmission Class 2	The upper age limit, in years, defining the second age class of snag light transmission. Snags with an age greater than the upper limit for size class 1, but less than or equal to this age, have a light transmission coefficient matching "Snag Age Class 2 Light Transmission Coefficient". Snags with an age greater than this value are in age class three. If your run does not work with snags, you can ignore this.

How it works

This behavior calculates a Sail Light index value for each individual of each tree type to which it is assigned. Sail Light values go from 0 (full sun) to 1 (full shade).

How to apply it

This behavior may be applied to seedlings, saplings, and adults of any species.

Storm Light behavior

This behavior calculates light levels as a function of number of trees damaged in [storms](#). Light levels are stored in a grid for later retrieval by other behaviors; this behavior does not directly assign light to trees.

Parameters for this behavior

Parameter name	Description
Storm Light - Intercept of Light Function	Intercept of the function to determine light level.
Storm Light - Max Radius (m) for Damaged Neighbors	The maximum distance, in meters, within which the Storm Light behavior searches for damaged trees.
Storm Light - Max Years Damaged Trees Affect Light	The maximum amount of time, in years, after storm damage that a tree will still be counted in the number of damaged trees.
Storm Light - Max Years Snags Affect	The maximum amount of time, in years, after death that a snag will still be counted in the number of damaged trees.

Light	
Storm Light - Minimum Trees For Full Canopy	The minimum number of adult trees and snags within the value in Storm Light - Max Radius (m) for Damaged Neighbors for the point to be considered under full canopy.
Storm Light - Slope of Light Function	Slope of the function to determine light level.
Storm Light - Standard Deviation	If the value in the Storm Light - Stochasticity parameter is "Normal" or "Lognormal", the standard deviation of the probability distribution function. If stochasticity is "Deterministic", this value is ignored.
Storm Light - Stochasticity	What method to use for randomizing light values, if desired.

How it works

This behavior uses a [grid](#) called [Storm Light](#) to manage light levels. Each timestep, it calculates the light level at the center of each grid cell and places it in the grid.

The light level is calculated as follows:

$$GLA = ((1 - T/M) * 100) + (a + b * N)$$

where:

- *GLA* is the light level, as a value between 0 and 100
- *T* is the number of adult trees and snags within the search radius
- *M* is the **Storm Light - Minimum Trees For Full Canopy** parameter
- *a* is the **Storm Light - Intercept of Light Function** parameter
- *b* is the **Storm Light - Slope of Light Function** parameter
- *N* is the proportion of trees that are dead or were heavily damaged in recent storms

This behavior calculates the light levels at the center of each grid cell by examining the trees within the distance given in the **Storm Light - Max Radius (m) for Damaged Neighbors** parameter.

The first term in the equation, $((1 - T/M) * 100)$, corrects the light level if the point is not under full canopy. All adults and snags, no matter what storm damage, are counted up and assigned to *T*. If $T \geq M$, then the first term is set to 0 and only the second part, $(a + b * N)$, is evaluated. If $T < M$, then the first term adds to the linear portion the proportion of full sun equal to the proportion of trees missing from the full canopy.

For the second, linear term, the behavior counts the number of dead and heavily damaged trees as a proportion of all adults and snags. Trees count as heavily damaged if they are either snags

that were created as a result of a storm killing an adult tree, or live adults with heavy storm damage. All storm damaged trees have a time-since-damage counter; only those eligible trees with a counter value less than or equal to the value in the **Storm Light - Max Years Damaged Trees Affect Light** parameter are counted. Saplings and seedlings never count. All snags count, whether they were created by a tree or another mortality process. Their age as a snag must also be less than the **Storm Light - Max Years Snags Affect Light** parameter.

The GLA value can be used as-is, or it can be used as the mean in a PDF to introduce a stochastic element. You can choose either "Normal" or "Lognormal" in the **Storm Light - Stochasticity** parameter, then supply a standard deviation in the **Storm Light - Standard Deviation** parameter. Using "Deterministic" as the stochasticity causes the GLA to be used as-is.

How to apply it

You do not need to apply this behavior to individual trees. While it is recommended that you also include the [Storm damage applier](#) behavior in your run, this is not required.

Growth behaviors

Growth behaviors change the size of a tree. A tree has two basic size dimensions: diameter and height. A growth behavior can change the tree size dimensions using one of two methods.

In the first method, the behavior calculates an amount of diameter change, and then adds this amount to the tree's diameter. The tree's new height is calculated from the new diameter using the appropriate [allometry equation](#). This is the default method. Behaviors using this method have the tag "diam with auto height" in their name.

In the second method, diameter change and height change are calculated separately by two different behaviors. Behaviors that operate on diameter and height independently must be paired together. Behaviors using this method have the tag "diam only" or "height only" in their names.

When incrementing a tree's diameter with new growth, seedlings and saplings have the amount of growth change applied to their diameter at 10 cm. Adults have the amount applied to their DBH. For more on tree types and their measurements, see the [tree life history stages](#) topic. For more on tree size relationships, including how trees transition between life history stages, see the [allometry](#) topic.

Note: All behaviors convert growth to diameter growth in cm for internal consistency. The equations below reflect this. Some behaviors may take parameters in mm, or for radial growth. Take careful note of your behavior's parameters.

It is important to be careful when using different behaviors for height and diameter growth. The values are not required to conform to the tree's [allometry equation](#). This may create trees whose dimensions are no longer linked with an allometric function. This is not considered a problem, although it may have unintended effects. For instance: if tree seedlings or saplings get separate

diameter and height increments, then their diameters and heights will be "uncoupled." This means that you cannot use one of the size dimensions to predict the other through an allometric equation. Trees with the same diameter will have different heights, and vice versa. If you assign the adults to a behavior that increments diameter and then automatically updates height according to the allometry equations, you are likely to notice strange results for new adult trees. You will lose the variability in height/diameter ratio that was developed. Suddenly, all trees with the same diameter will have the same height again, and vice versa. This means that individuals may suddenly jump in height, or even shrink.

The "Allometric height growth" and "allometric diameter growth" behaviors were developed to help bridge this gap. When used with a behavior that only increments diameter or height, they will preserve height or diameter differences that have developed across individuals in a species.

Behavior	Description
<u>Absolute growth limited to radial increment</u>	Calculates an amount of diameter growth according to the Michaelis-Menton absolute growth equation. Growth is limited to a maximum of a constant radial increment.
<u>Absolute growth limited to basal area increment</u>	Calculates an amount of diameter growth according to the Michaelis-Menton absolute growth equation. Growth is limited to a maximum of a constant basal area increment.
<u>Non-limited absolute growth</u>	Calculates an amount of diameter growth according to the Michaelis-Menton absolute growth equation.
<u>Allometric diameter growth - diam only</u>	If you have a behavior that primarily updates tree height, this behavior updates diameter to ensure even growth.
<u>Allometric height growth</u>	If you have a behavior that primarily updates tree diameter, this behavior updates height to ensure even growth.
<u>Constant basal area growth</u>	Calculates the amount of diameter change from a constant basal area increment.
<u>Browsed relative growth</u>	Simulates herbivory by allowing trees to grow at different rates when browsed versus unbrowsed.
<u>Constant radial growth</u>	Calculates the amount of diameter change from a constant radial increment.
<u>Double resource</u>	Uses a double Michaelis-Menton function to calculate relative growth based on two resources: light and a second resource.

relative growth	
Lagged post harvest growth	Increments growth as a function of DBH and neighboring basal area, and incorporates a lag period after harvesting during which trees acclimate to their post-harvest growing conditions.
Linear growth	Does either diameter or height growth as a linear function of GLI.
Linear bi-level growth	Increments growth according to a simple linear equation, with the possibility of two sets of parameters for each species: one for high-light conditions and one for low-light conditions.
Linear growth w/ exponential shade reduction	Calculates either diameter or height growth as a function of GLI.
Logistic growth	Calculates either diameter or height growth as a logistic function of GLI.
Logistic growth w/ size dependent asymptote	Calculates either diameter or height growth as a function of tree size and GLI.
Lognormal bi-level growth - height only	Increments growth according to a lognormal equation, with the possibility of two sets of parameters for each species: one for high-light conditions and one for low-light conditions.
Lognormal with exponential shade reduction	Calculates either diameter or height growth as a function of tree size and GLI.
Michaelis Menton with negative growth - height only	Uses a modified Michaelis-Menton function to do height growth. You can optionally add autocorrelation and a degree of stochasticity to the growth.
Michaelis Menton with photoinhibition - height only	Uses a modified Michaelis-Menton function to do height growth.
NCI growth	Uses multiple effects, including neighbor competitiveness, to calculate growth rates.

NCI quadrat growth	Uses multiple effects, including neighbor competitiveness, to calculate growth rates. For processing efficiency, growth is calculated for each species on a per grid cell basis.
Power growth - height only	Uses a power function to do height growth.
Puerto Rico semi-stochastic - diam only	Combines a deterministic growth function for small trees with completely stochastic growth for larger trees. It's meant to be used when a species uses a height growth behavior as the primary growth method.
Puerto Rico storm bi-level growth - diam with auto height	Increments growth according to two possible growth equations, one to be used in low-light conditions and the other to be used in high-light conditions. This behavior was originally created for the Puerto Rico model.
Relative growth limited to radial increment	Calculates an amount of diameter growth according to the Michaelis-Menton relative growth equation. Growth is limited to a maximum of a constant radial growth increment.
Relative growth limited to basal area increment	Calculates an amount of diameter growth according to the Michaelis-Menton relative growth equation. Growth is limited to a maximum of the constant basal area growth increment.
Non-limited relative growth	Calculates an amount of diameter growth according to the Michaelis-Menton relative growth equation.
Relative growth - height only	Calculates an amount of height growth according to the Michaelis-Menton relative growth equation.
Stochastic gap growth	Uses a shortcut for simulating gap dynamics with very competitive conditions. This behavior causes rapid growth in high light, with a unique "winner"; low light produces no growth at all.

Absolute growth behaviors

Several behaviors apply an absolute growth version of the Michaelis-Menton function.

Parameters for these behaviors

Parameter name	Description
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Adult Constant Area Growth in sq. cm/yr	The constant amount of basal area by which to increase a tree's basal area. Applies to basal-area-increment-limited behaviors.
Adult Constant Radial Growth in mm/yr	The constant value by which to increase a tree's radius at breast height. Applies to radial-increment-limited-growth behaviors.
Asymptotic Diameter Growth (A)	Asymptote of the Michaelis-Menton growth function at high light - function term A below.
Slope of Growth Response (S)	Slope of the Michaelis-Menton growth function at zero light - function term S below.
Length of Current Release Factor	Controls the magnitude of the effects of release.
Length of Last Suppression Factor	Controls the magnitude of the effects of suppression.
Mortality Threshold for Suppression	Defines the growth rate for suppressed status in terms of tree mortality. The value is expressed as the proportion of trees which die at the growth rate which defines suppressed status, expressed as a fraction between 0 and 1. For instance, if this value is 0.1, the growth rate for suppressed status is one at which 10% of trees die with that growth.
Years Exceeding Threshold Before a Tree is Suppressed	The number of years for which a tree's growth must be below the defined suppression threshold before it is considered to be suppressed.

Absolute growth is calculated with the equation:

$$Y = SF \left(\frac{A * GLI}{A/S + GLI} \right)$$

where

- $Y = \log_{10}(\text{radial growth} + 1)$
- SF is the suppression factor
- A is the **Asymptotic Diameter Growth (A)** parameter
- S is the **Slope of Growth Response (S)** parameter
- GLI is the global light index, calculated by a [light behavior](#)

Amount of diameter growth per timestep is calculated as

$$\text{growth} = (((10^Y - 1) * 2) / 10) * T$$

where T is the number of years per timestep.

The absolute growth behaviors also take into account suppression status. A tree is considered suppressed if its growth rate for the previous timestep falls below a certain threshold. That threshold is the rate of growth at which X% of juveniles die, where X is a user-settable parameter. The threshold is calculated for each species by solving the [BC mortality equation](#) for G (growth), where m is the threshold growth rate.

A tree's suppression state is a multiplicative factor in its growth rate. If a tree is not suppressed, the suppression factor in the growth equation is set to 1 (no effect on growth). If the tree is suppressed, the suppression factor is calculated as follows:

$$SF = e^{((g*YLR) - (d*YLS))}$$

where:

- *SF* is the suppression factor
- *g* is the **Length of Current Release Factor** parameter
- *YLR* is the length of the last (or current) period of release, in years
- *d* is the **Length of Last Suppression Factor** parameter
- *YLS* is the length of the last (or current) period of suppression, in years

Details of this model are published in [Wright et al 2000](#).

Absolute growth limited to radial increment

How it works

This behavior calculates an amount of diameter growth according to the absolute growth equation. Growth is limited to a maximum of the constant radial increment for the species of tree to which it is being applied. The increment is calculated as described in the "Constant radial growth" behavior. Note that the increment parameter specifies **radial** growth; the behavior makes all necessary conversions.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Absolute growth limited to basal area increment

How it works

This behavior calculates an amount of diameter growth according to the absolute growth equation. Growth is limited to a maximum of a constant basal area increment. The amount of diameter increase is calculated by dividing the annual basal area increment of the tree's species by the diameter of the tree. The increment is calculated as described in the "Constant basal area growth" behavior.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Non-limited absolute growth - diam with auto height

How it works

The amount of diameter increase returned by the absolute growth equation is applied to the tree.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Absolute growth behaviors

Several behaviors apply an absolute growth version of the Michaelis-Menton function.

Parameters for these behaviors

Parameter name	Description
Adult Constant Area Growth in sq. cm/yr	The constant amount of basal area by which to increase a tree's basal area. Applies to basal-area-increment-limited behaviors.
Adult Constant Radial Growth in mm/yr	The constant value by which to increase a tree's radius at breast height. Applies to radial-increment-limited-growth behaviors.
Asymptotic Diameter Growth (A)	Asymptote of the Michaelis-Menton growth function at high light - function term A below.
Slope of Growth	Slope of the Michaelis-Menton growth function at zero light - function

Response (S)	term S below.
Length of Current Release Factor	Controls the magnitude of the effects of release.
Length of Last Suppression Factor	Controls the magnitude of the effects of suppression.
Mortality Threshold for Suppression	Defines the growth rate for suppressed status in terms of tree mortality. The value is expressed as the proportion of trees which die at the growth rate which defines suppressed status, expressed as a fraction between 0 and 1. For instance, if this value is 0.1, the growth rate for suppressed status is one at which 10% of trees die with that growth.
Years Exceeding Threshold Before a Tree is Suppressed	The number of years for which a tree's growth must be below the defined suppression threshold before it is considered to be suppressed.

Absolute growth is calculated with the equation:

$$Y = SF \left(\frac{A * GLI}{A/S + GLI} \right)$$

where

- $Y = \log_{10}(\text{radial growth} + 1)$
- SF is the suppression factor
- A is the **Asymptotic Diameter Growth (A)** parameter
- S is the **Slope of Growth Response (S)** parameter
- GLI is the global light index, calculated by a [light behavior](#)

Amount of diameter growth per timestep is calculated as

$$\text{growth} = (((10^Y - 1) * 2) / 10) * T$$

where T is the number of years per timestep.

The absolute growth behaviors also take into account suppression status. A tree is considered suppressed if its growth rate for the previous timestep falls below a certain threshold. That threshold is the rate of growth at which X% of juveniles die, where X is a user-settable parameter. The threshold is calculated for each species by solving the [BC mortality equation](#) for G (growth), where m is the threshold growth rate.

A tree's suppression state is a multiplicative factor in its growth rate. If a tree is not suppressed, the suppression factor in the growth equation is set to 1 (no effect on growth). If the tree is suppressed, the suppression factor is calculated as follows:

$$SF = e^{((g*YLR) - (d*YLS))}$$

where:

- *SF* is the suppression factor
- *g* is the **Length of Current Release Factor** parameter
- *YLR* is the length of the last (or current) period of release, in years
- *d* is the **Length of Last Suppression Factor** parameter
- *YLS* is the length of the last (or current) period of suppression, in years

Details of this model are published in [Wright et al 2000](#).

Absolute growth limited to radial increment

How it works

This behavior calculates an amount of diameter growth according to the absolute growth equation. Growth is limited to a maximum of the constant radial increment for the species of tree to which it is being applied. The increment is calculated as described in the "Constant radial growth" behavior. Note that the increment parameter specifies **radial** growth; the behavior makes all necessary conversions.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Absolute growth limited to basal area increment

How it works

This behavior calculates an amount of diameter growth according to the absolute growth equation. Growth is limited to a maximum of a constant basal area increment. The amount of diameter increase is calculated by dividing the annual basal area increment of the tree's species by the diameter of the tree. The increment is calculated as described in the "Constant basal area growth" behavior.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Non-limited absolute growth - diam with auto height

How it works

The amount of diameter increase returned by the absolute growth equation is applied to the tree.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Absolute growth behaviors

Several behaviors apply an absolute growth version of the Michaelis-Menton function.

Parameters for these behaviors

Parameter name	Description
Adult Constant Area Growth in sq. cm/yr	The constant amount of basal area by which to increase a tree's basal area. Applies to basal-area-increment-limited behaviors.
Adult Constant Radial Growth in mm/yr	The constant value by which to increase a tree's radius at breast height. Applies to radial-increment-limited-growth behaviors.
Asymptotic Diameter Growth (A)	Asymptote of the Michaelis-Menton growth function at high light - function term A below.
Slope of Growth Response (S)	Slope of the Michaelis-Menton growth function at zero light - function term S below.
Length of Current Release Factor	Controls the magnitude of the effects of release.
Length of Last Suppression Factor	Controls the magnitude of the effects of suppression.
Mortality Threshold	Defines the growth rate for suppressed status in terms of tree mortality.

for Suppression	The value is expressed as the proportion of trees which die at the growth rate which defines suppressed status, expressed as a fraction between 0 and 1. For instance, if this value is 0.1, the growth rate for suppressed status is one at which 10% of trees die with that growth.
Years Exceeding Threshold Before a Tree is Suppressed	The number of years for which a tree's growth must be below the defined suppression threshold before it is considered to be suppressed.

Absolute growth is calculated with the equation:

$$Y = SF \left(\frac{A * GLI}{A/S + GLI} \right)$$

where

- $Y = \log_{10}(\text{radial growth} + 1)$
- SF is the suppression factor
- A is the **Asymptotic Diameter Growth (A)** parameter
- S is the **Slope of Growth Response (S)** parameter
- GLI is the global light index, calculated by a [light behavior](#)

Amount of diameter growth per timestep is calculated as

$$\text{growth} = (((10^Y - 1) * 2) / 10) * T$$

where T is the number of years per timestep.

The absolute growth behaviors also take into account suppression status. A tree is considered suppressed if its growth rate for the previous timestep falls below a certain threshold. That threshold is the rate of growth at which $X\%$ of juveniles die, where X is a user-settable parameter. The threshold is calculated for each species by solving the [BC mortality equation](#) for G (growth), where m is the threshold growth rate.

A tree's suppression state is a multiplicative factor in its growth rate. If a tree is not suppressed, the suppression factor in the growth equation is set to 1 (no effect on growth). If the tree is suppressed, the suppression factor is calculated as follows:

$$SF = e^{((g * YLR) - (d * YLS))}$$

where:

- SF is the suppression factor
- g is the **Length of Current Release Factor** parameter

- *YLR* is the length of the last (or current) period of release, in years
- *d* is the **Length of Last Suppression Factor** parameter
- *YLS* is the length of the last (or current) period of suppression, in years

Details of this model are published in [Wright et al 2000](#).

Absolute growth limited to radial increment

How it works

This behavior calculates an amount of diameter growth according to the absolute growth equation. Growth is limited to a maximum of the constant radial increment for the species of tree to which it is being applied. The increment is calculated as described in the "Constant radial growth" behavior. Note that the increment parameter specifies **radial** growth; the behavior makes all necessary conversions.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Absolute growth limited to basal area increment

How it works

This behavior calculates an amount of diameter growth according to the absolute growth equation. Growth is limited to a maximum of a constant basal area increment. The amount of diameter increase is calculated by dividing the annual basal area increment of the tree's species by the diameter of the tree. The increment is calculated as described in the "Constant basal area growth" behavior.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Non-limited absolute growth - diam with auto height

How it works

The amount of diameter increase returned by the absolute growth equation is applied to the tree.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Allometric diameter and height growth

How it works

These behaviors are designed to be secondary growth behaviors. If you have a behavior that primarily updates one tree dimension (diameter or height), one of these behaviors can be used on the other dimension to ensure even growth. These behaviors calculate a growth amount based on the allometry equations. The amount of growth is:

$$Y = f(X_{t+1}) - f(X_t)$$

where Y is the amount of growth calculated by this behavior, $f(X)$ is the [allometry](#) equation relating diameter and height, X_t is the other tree dimension (either height or diameter) before the primary growth is applied, and X_{t+1} is the other tree dimension after primary growth is applied. The allometric diameter growth behavior can be paired with any height-only growth behavior, and the allometric height growth behavior can be paired with any diam-only growth behavior.

How to apply it

These behaviors can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a growth behavior applied that grows the opposite tree dimension.

Allometric diameter and height growth

How it works

These behaviors are designed to be secondary growth behaviors. If you have a behavior that primarily updates one tree dimension (diameter or height), one of these behaviors can be used on the other dimension to ensure even growth. These behaviors calculate a growth amount based on the allometry equations. The amount of growth is:

$$Y = f(X_{t+1}) - f(X_t)$$

where Y is the amount of growth calculated by this behavior, $f(X)$ is the [allometry](#) equation relating diameter and height, X_t is the other tree dimension (either height or diameter) before the primary growth is applied, and X_{t+1} is the other tree dimension after primary growth is applied.

The allometric diameter growth behavior can be paired with any height-only growth behavior, and the allometric height growth behavior can be paired with any diam-only growth behavior.

How to apply it

These behaviors can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a growth behavior applied that grows the opposite tree dimension.

Constant basal area growth

Parameters for these behaviors

Parameter name	Description
Adult Constant Area Growth in sq. cm/yr	The constant amount of basal area by which to increase a tree's basal area.

How it works

The amount of diameter increase is calculated from a constant basal area increment. The increase is calculated as follows:

$$Y = (g / diam) * 100 * T$$

where

- Y is the amount of diameter increase, in cm
- g is the **Adult Constant Area Growth in sq. cm/yr** parameter
- $diam$ is the tree's diameter, in cm
- T is the number of years per timestep

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Browsed relative growth behavior

This behavior simulates herbivory by allowing trees to grow at different rates when browsed versus unbrowsed.

Parameters for this behavior

Parameter name	Description
Asymptotic Diameter Growth (A)	Asymptote of the Michaelis-Menton growth function at high light - function term A below.
Slope of Growth Response (S)	Slope of the Michaelis-Menton growth function at zero light - function term S below.
Relative Michaelis-Menton Growth - Diameter Exponent	The exponent to be used with diameter when calculating relative growth.
Browsed Asymptotic Diameter Growth (A)	Asymptote of the Michaelis-Menton growth function at high light when a plant has been browsed.
Browsed Slope of Growth Response (S)	Slope of the Michaelis-Menton growth function at zero light when a plant has been browsed.
Browsed Diameter Exponent	The diameter exponent for growth when a plant has been browsed.

How it works

Trees grow according to the relative growth version of the Michaelis-Menton function. The same function is used for both browsed and unbrowsed trees, but the parameters are different. The function is:

$$Y = \left[\left[\frac{A * GLI}{A/S + GLI} \right] \right]$$

where:

- Y is the amount of annual relative growth
- A is the **Asymptotic Diameter Growth (A)** or **Browsed Asymptotic Diameter Growth (A)** parameter
- S is the **Slope of Growth Response (S)** or **Browsed Slope of Growth Response (S)** parameter
- GLI is the global light index, calculated by a [light behavior](#)

Growth is compounded over multiple timesteps with the equation:

$$G = ((Y + 1)^T - 1) * diam^X$$

where:

- G is the amount of diameter growth for the timestep, in cm
- $diam$ is the diameter of the tree in cm (at 10 cm height if seedling or sapling, or DBH if adult)
- T is the number of years per timestep
- X is the **Relative Michaelis-Menton Growth - Diameter Exponent** or **Browsed Diameter Exponent** parameter

Whether or not a tree is browsed is determined by the [Random browse](#) behavior.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) and the [Random browse](#) behavior applied. You can use either the diam with auto height or diam only version.

Constant radial growth

Parameters for these behaviors

Parameter name	Description
Adult Constant Radial Growth in mm/yr	The constant value by which to increase a tree's radius at breast height.

How it works

The amount of diameter increase is calculated from the constant radial increment. The increase is calculated as follows:

$$Y = (g_4 / 10) * 2 * T$$

where

- Y is the amount of diameter growth, in cm, to add to the tree
- g_4 is the **Adult Constant Radial Growth in mm/yr** parameter
- T is the number of years per timestep

Note that the increment parameter specifies **radial** growth; the behavior makes all necessary conversions to diameter growth.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Double resource relative growth

This behavior uses a double Michaelis-Menton function to calculate relative growth based on two resources: light and a second resource. The identity of the second resource is unimportant and could be anything, from exchangeable calcium levels to soil moisture.

Parameters for this behavior

Parameter name	Description
Asymptotic Diameter Growth (A)	Asymptote of the Michaelis-Menton growth function at high light - function term A below.
Slope of Growth Response (S)	Slope of the Michaelis-Menton growth function at zero light - function term S below.
Double resource - Influence of Resource (C)	The parameter governing the influence of the second resource on the double-resource Michaelis-Menton equation.

How it works

Relative growth is calculated with the equation:

$$Y = \left(\frac{(A + (C * R)) * GLI}{\frac{(A + (C * R))}{S} + GLI} \right)$$

where:

- Y is the amount of annual relative growth
- A is the **Asymptotic Diameter Growth (A)** parameter
- S is the **Slope of Growth Response (S)** parameter
- C is the **Double resource - Influence of Resource (C)** parameter, in units appropriate to the value of R
- R is the amount of the second resource, in units appropriate to the value of C

- *GLI* is the global light index, calculated by a [light behavior](#)

Growth is compounded over multiple timesteps with the equation:

$$G = ((Y + 1)^T - 1) * diam$$

where:

- *G* is the amount of diameter growth for the timestep, in cm
- *diam* is the diameter of the tree in cm (at 10 cm height if seedling or sapling, or DBH if adult)
- *T* is the number of years per timestep

Note that setting the C parameter in the equation above to 0 eliminates the second resource and makes this equivalent to the "Non-limited relative growth" behavior.

The amount of the second resource is captured in a grid object called [Resource](#). Currently it is up to you to enter a map of the values for this resource grid; for instructions on how to do this, see the [Grid Setup Window](#) topic. This behavior does not in any way alter the values in this grid.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You must also enter a map of second resource values into the [Resource](#) grid. You can use either the diam with auto height or diam only version.

Lagged post harvest growth

This behavior increments growth as a function of DBH and neighboring basal area, and incorporates a lag period after harvesting during which trees acclimate to their post-harvest growing conditions.

Parameters for this behavior

Parameter name	Description
Post Harvest Growth - DBH Growth Effect	The effect of DBH on growth.
Post Harvest Growth - DBH NCI Effect	The effect of DBH on the neighborhood competition index.
Post Harvest Growth	Maximum annual radial growth, in mm.

- Max Growth Constant	
Post Harvest Growth - NCI Constant	A constant adjusting the effects of NCI.
Post Harvest Growth - NCI Distance (m)	The maximum distance at which neighboring trees can have competitive effects.
Post Harvest Growth - Time Since Harvest Rate Param	A parameter controlling the rate at which the actual growth approaches the potential growth after a harvest.

How it works

A tree's *potential* growth is calculated by:

$$PARG = \alpha * \exp(-\delta * DBH) * \exp(-\eta BA * \exp(-\omega * DBH))$$

where:

- *PARG* is potential annual radial growth (mm/y)
- *DBH* is in cm
- *BA* is the basal area (in sq m) of adult trees within the distance given in the **Post Harvest Growth - NCI Distance (m)** parameter
- α is the **Post Harvest Growth - Max Growth Constant** parameter, the maximum radial growth in millimeters per year
- δ is the **Post Harvest Growth - DBH Growth Effect** parameter
- η is the **Post Harvest Growth - NCI Constant** parameter
- ω is the **Post Harvest Growth - DBH NCI Effect** parameter

If no harvest has occurred yet in this run, then the tree's actual growth, *ARG*, equals *PARG*. If a harvest has occurred at some point during this run, then *ARG* is calculated by:

$$ARG = ARG_{pre} + (PARG - ARG_{pre}) * (1 - \exp(-\tau * H * t))$$

where:

- *ARG* is annual radial growth (mm/y) for the current timestep
- ARG_{pre} is annual radial growth for the last timestep prior to harvest
- *H* is the number of timesteps since the last harvest
- *t* is the number of years per timestep
- τ is the **Post Harvest Growth - Time Since Harvest Rate Param** parameter

Annual radial growth *ARG* is used to calculate timestep diameter growth using

$$DG = ARG * t * 2/10$$

where t is the number of years per timestep.

Model forms are based on those in Thorpe et al. 2010.

How to apply it

This behavior can be applied to saplings and adults of any species.

Linear growth

This behavior does either diameter or height growth as a linear function of GLI.

Parameters for this behavior

Parameter name	Description
Simple Linear - Diam Intercept in mm/yr (a)	Intercept of the linear growth function, or growth at no light, in mm/yr, for diameter growth.
Simple Linear - Diam Slope (b)	Slope of the linear growth function, for diameter growth.
Simple Linear - Height Intercept in cm/yr (a)	Intercept of the linear growth function, or growth at no light, in cm/yr, for height growth.
Simple Linear - Height Slope (b)	Slope of the linear growth function, for height growth.

How it works

This behavior calculates an amount of diameter or height growth as:

$$Y = (a + (b * GLI)) * T$$

where

- Y = amount of radial increase, in mm, or amount of height increase, in cm
- a = **Simple Linear - Diam Radial Intercept in mm/yr (a)** parameter (for diameter growth) or the **Simple Linear - Height Intercept in cm/yr (a)** parameter (for height growth)

- b = **Simple Linear - Diam Radial Slope (b)** parameter (for diam growth) or the **Simple Linear - Height Slope (b)** parameter (for height growth)
- GLI = global light index, as a percentage between 0 and 100, calculated by a [light behavior](#)
- T = number of years per timestep

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can choose either a diam with auto height, diam only, or height only version.

Linear bi-level growth

This behavior increments growth according to a simple linear equation, with the possibility of two sets of parameters for each species: one for high-light conditions and one for low-light conditions. This can also be used alone without the light levels.

Parameters for this behavior

Parameter name	Description
Linear Bi-Level - Intercept for High-Light Growth (a)	The intercept of the linear growth function used in high-light conditions.
Linear Bi-Level - Intercept for Low-Light Growth (a)	The intercept of the linear growth function used in low-light conditions.
Linear Bi-Level - Slope for High-Light Growth (b)	The slope of the linear growth function used in high-light conditions.
Linear Bi-Level - Slope for Low-Light Growth (b)	The slope of the linear growth function used in low-light conditions.
Linear Bi-Level - Threshold for High-Light Growth (0 - 100)	The threshold between low-light and high-light parameters, as a value between 0 and 100.

How it works

The equation used by this behavior to increment growth is:

$$Y = (a + b * diam) * T$$

where

- Y = amount of diameter growth in cm
- a = growth intercept; in high-light conditions, this is the **Linear Bi-Level - Intercept for High-Light Growth (a)** parameter; in low-light conditions, this is the **Linear Bi-Level - Intercept for Low-Light Growth (a)** parameter
- b = growth slope; in high-light conditions, this is the **Linear Bi-Level - Slope for High-Light Growth (b)** parameter; in low-light conditions, this is the **Linear Bi-Level - Slope for Low-Light Growth (b)** parameter
- $diam$ = diameter (diameter at 10 cm for seedlings and saplings, DBH for adults)
- T = number of years per timestep

Light levels come from the [Storm Light](#) grid produced by the [Storm Light](#) behavior. The threshold between the use of high-light and low-light parameters is set in the **Linear Bi-Level - Threshold for High-Light Growth (0 - 100)** parameter.

This behavior can also be used without Storm Light. In this case, only the low-light growth parameters are used.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. If you wish to use the light-level parameter switch, also use the [Storm Light](#) behavior. You can use either the diam with auto height or diam only version.

Linear growth w/ exponential shade reduction

This behavior does either diameter or height growth as a function of GLI.

Parameters for this behavior

Parameter name	Description
Shaded Linear - Diam Intercept in mm/yr (a)	Intercept of the size dependent growth potential, in mm/yr, for diameter growth.
Shaded Linear - Diam Shade	Effect of shading, for diameter growth.

Exponent (c)	
Shaded Linear - Diam Slope (b)	Slope of the size dependent annual growth potential, for diameter growth.
Shaded Linear - Height Intercept in cm/yr (a)	Intercept of the size dependent growth potential, in cm/yr, for height growth.
Shaded Linear - Height Shade Exponent (c)	Effect of shading, for height growth.
Shaded Linear - Height Slope (b)	Slope of the size dependent annual growth potential, for height growth.

How it works

This behavior calculates an amount of diameter or height growth as:

$$Y = (a + (b * diam)) * (GLI/100)^c * T$$

where

- Y = amount of diameter increase, in mm; or the amount of height increase, in cm
- a = **Shaded Linear - Diam Intercept in mm/yr (a)** parameter (for diameter growth) or the **Shaded Linear - Height Intercept in cm/yr (a)** parameter (for height growth)
- b = **Shaded Linear - Diam Slope (b)** parameter (for diameter growth) or the **Shaded Linear - Height Slope (b)** parameter (for height growth)
- c = **Shaded Linear - Diam Shade Exponent (c)** parameter (for diameter growth) or the **Shaded Linear - Height Shade Exponent (c)** parameter (for height growth)
- $diam$ = diameter (diameter at 10 cm for seedlings and saplings, DBH for adults)
- GLI = global light index, as a percentage between 0 and 100, calculated by a [light behavior](#)
- T = number of years per timestep

If calculating height growth: In order to find the total amount of height increase for a timestep, the behavior takes as an input the amount of diameter growth increase. Assume that the number of years per timestep is X. The amount of diameter increase is divided by X. Then the logistic growth equation is calculated X times, with the diameter incremented by the amount of diameter increase per timestep each time. The total height increment is the sum of the X individual height increments.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can choose either a diam with auto height, diam only, or height only version.

Logistic growth

This behavior does either diameter or height growth as a function of GLI.

Parameters for this behavior

Parameter name	Description
Logistic - Asymptotic Diam Growth - Full Light in mm/yr (a)	Asymptotic annual growth at full light, in mm/yr, for diameter growth.
Logistic - Diam Shape Param 1 (b)	Shape parameter 1, for diameter growth.
Logistic - Diam Shape Param 2 (c)	Shape parameter 2, for diameter growth.
Logistic - Asymptotic Height Growth - Full Light in cm/yr (a)	Asymptotic annual growth at full light, in cm/yr, for height growth.
Logistic - Height Shape Param 1 (b)	Shape parameter 1, for height growth.
Logistic - Height Shape Param 2 (c)	Shape parameter 2, for height growth.

How it works

The amount of diameter increase is calculated as:

$$Y = \frac{a}{1 + e^{(b - (c * GLI))}} * T$$

where

- Y = amount of diameter increase, in mm, or the amount of height increase, in cm

- a = **Logistic - Asymptotic Diam Growth - Full Light in mm/yr (a)** parameter (for diameter growth) or the **Logistic - Asymptotic Height Growth - Full Light in cm/yr (a)** parameter (for height growth)
- b = **Logistic - Diam Shape Param 1 (b)** parameter (for diameter growth) or the **Logistic - Height Shape Param 1 (b)** parameter (for height growth)
- c = **Logistic - Diam Shape Param 2 (c)** parameter (for diameter growth) or the **Logistic - Height Shape Param 2 (c)** parameter (for height growth)
- GLI = global light index, as a percentage between 0 and 100, calculated by a [light behavior](#)
- T = number of years per timestep

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can choose either a diam with auto height, diam only, or height only version.

Logistic growth w/ size dependent asymptote

This behavior does either diameter or height growth as a function of tree size and GLI.

Parameters for this behavior

Parameter name	Description
Size Dep. Logistic - Diam Intercept (a)	Intercept of the size dependent annual growth potential, for diameter growth.
Size Dep. Logistic - Diam Shape Param 1 (c)	Shape parameter 1 for shade reduction of annual growth, for diameter growth.
Size Dep. Logistic - Diam Shape Param 2 (d)	Shape parameter 2 for shade reduction of annual growth, for diameter growth.
Size Dep. Logistic - Diam Slope (b)	Slope of the size dependent annual growth potential, for diameter growth.
Size Dep. Logistic - Height Intercept (a)	Intercept of the size dependent annual growth potential, for height growth.
Size Dep. Logistic - Height Shape Param 1 (c)	Shape parameter 1 for shade reduction of annual growth, for height growth.

Size Dep. Logistic - Height Shape Param 2 (d)	Shape parameter 2 for shade reduction of annual growth, for height growth.
Size Dep. Logistic - Height Slope (b)	Slope of the size dependent annual growth potential, for height growth.

How it works

This behavior calculates annual diameter or height increases as:

$$Y = \frac{a + (b * diam)}{1 + e^{(c - (d * GLI))}}$$

where

- Y = amount of diameter increase, in mm, or the amount of height increase, in cm
- a = **Size Dep. Logistic - Diam Intercept (a)** parameter (for diameter growth) or the **Size Dep. Logistic - Height Intercept (a)** parameter (for height growth)
- b = **Size Dep. Logistic - Diam Slope (b)** parameter (for diameter growth) or the **Size Dep. Logistic - Height Slope (b)** parameter (for height growth)
- c = **Size Dep. Logistic - Diam Shape Param 1 (c)** parameter (for diameter growth) or the **Size Dep. Logistic - Height Shape Param 1 (c)** parameter (for height growth)
- d = **Size Dep. Logistic - Diam Shape Param 2 (d)** parameter (for diameter growth) or the **Size Dep. Logistic - Height Shape Param 2 (d)** parameter (for height growth)
- GLI = global light index, as a percentage between 0 and 100, calculated by a [light behavior](#)
- $diam$ = diameter (diameter at 10 cm for seedlings and saplings, DBH for adults)

For diameter growth: Assume that the number of years per timestep is X . In order to find the total amount of diameter increase for a timestep, the logistic growth equation is calculated X times, with the diameter incremented by the amount of diameter increase for the previous year. The total diameter increment is the sum of the X individual diameter increments.

For height growth: In order to find the total amount of height increase for a timestep, the behavior takes as an input the amount of diameter growth increase. Assume that the number of years per timestep is X . The amount of diameter increase is divided by X . Then the logistic growth equation is calculated X times, with the diameter incremented by the amount of diameter increase per timestep each time. The total height increment is the sum of the X individual height increments.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can choose either a diam with auto height, diam only, or height only version.

Lognormal bi-level growth - height only

This behavior increments growth according to a lognormal equation, with the possibility of two sets of parameters for each species: one for high-light conditions and one for low-light conditions. This can also be used alone without the light levels.

Parameters for this behavior

Parameter name	Description
Lognormal Bi-Level - Max Growth in High Light (m)	The maximum height growth, in meters, under high-light conditions.
Lognormal Bi-Level - Max Growth in Low Light (m)	The maximum height growth, in meters, under low-light conditions.
Lognormal Bi-Level - X ₀ for High-Light Growth	The X ₀ parameter to use under high-light growth conditions.
Lognormal Bi-Level - X ₀ for Low-Light Growth	The X ₀ parameter to use under low-light growth conditions.
Lognormal Bi-Level - X _b for High-Light Growth	The X _b parameter to use under high-light growth conditions.
Lognormal Bi-Level - X _b for Low-Light Growth	The X _b parameter to use under low-light growth conditions.
Lognormal Bi-Level - Threshold for High-Light Growth (0 - 100)	The light threshold value between high-light and low-light conditions.

How it works

The equation used by this behavior to increment growth is:

$$Y = T * MG * e^{-1/2 \left[\frac{\ln(H/X_0)}{X_b} \right]^2}$$

where

- Y - amount of height growth in m
- MG - maximum growth, in meters; in high-light conditions, this is the **Lognormal Bi-Level - Max Growth in High Light (m)** parameter; in low-light conditions, this is the **Lognormal Bi-Level - Max Growth in Low Light (m)** parameter
- X_0 - in high-light conditions, this is the **Lognormal Bi-Level - X0 for High-Light Growth** parameter; in low-light conditions, this is the **Lognormal Bi-Level - X0 for Low-Light Growth** parameter
- X_b - in high-light conditions, this is the **Lognormal Bi-Level - Xb for High-Light Growth** parameter; in low-light conditions, this is the **Lognormal Bi-Level - Xb for Low-Light Growth** parameter
- H - tree height in meters
- T - number of years per timestep

Light levels come from the [Storm Light](#) grid produced by the [Storm Light](#) behavior. The threshold between the use of high-light and low-light parameters is set in the **Lognormal Bi-Level - Threshold for High-Light Growth (0 - 100)** parameter.

This behavior can also be used without Storm Light. In this case, only the low-light growth parameters are used.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a diam-only growth behavior applied. If you wish to use the light-level parameter switch, also use the [Storm Light](#) behavior.

Lognormal with exponential shade reduction

This behavior does either diameter or height growth as a function of tree size and GLI.

Parameters for this behavior

Parameter name	Description
Lognormal - Diam Effect of Shade (c)	Effect of shade, for diameter growth.

Lognormal - Diam Growth Increment at Diam 36, in mm/yr (a)	Annual growth increment at diameter 36, in mm/yr, for diameter growth.
Lognormal - Diam Shape Parameter (b)	Shape parameter, for diameter growth.
Lognormal - Height Effect of Shade (c)	Effect of shade, for height growth.
Lognormal - Height Growth Increment at Diam 36, in cm/yr (a)	Annual growth increment at diameter 36, in cm/yr, for height growth.
Lognormal - Height Shape Parameter (b)	Shape parameter, for height growth.

How it works

This behavior calculates annual diameter or height increases as:

$$Y = \left(a * e^{-0.5 \left(\frac{\ln(\text{diam} / 36)}{b} \right)^2} \right) * \left(\frac{GLI}{100} \right)^c$$

where

- Y = amount of diameter increase, in mm, or the amount of height increase, in cm
- a = **Lognormal - Diam Growth Increment at Diam 36, in mm/yr (a)** parameter (for diameter growth) or the **Lognormal - Height Growth Increment at Diam 36, in cm/yr (a)** parameter (for height growth)
- b = **Lognormal - Diam Shape Parameter (b)** parameter (for diameter growth) or the **Lognormal - Height Shape Parameter (b)** parameter (for height growth)
- c = **Lognormal - Diam Effect of Shade (c)** parameter (for diameter growth) or the **Lognormal - Height Effect of Shade (c)** parameter (for height growth)
- GLI = global light index, as a percentage between 0 and 100, calculated by a [light behavior](#)
- diam = diameter (diameter at 10 cm for seedlings and saplings, DBH for adults)

For diameter growth: Assume that the number of years per timestep is X . In order to find the total amount of diameter increase for a timestep, the lognormal growth equation is calculated X times, with the diameter incremented by the amount of diameter increase for the previous year. The total diameter increment is the sum of the X individual diameter increments.

For height growth: In order to find the total amount of height increase for a timestep, the behavior takes as an input the amount of diameter growth increase. Assume that the number of years per timestep is X. The amount of diameter increase is divided by X. Then the lognormal growth equation is calculated X times, with the diameter incremented by the amount of diameter increase per timestep each time. The total height increment is the sum of the X individual height increments.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can choose either a diam with auto height, diam only, or height only version.

Michaelis Menton with negative growth - height only

This behavior uses a modified Michaelis-Menton function to do height growth. You can optionally add autocorrelation and a degree of stochasticity to the growth.

Parameters for this behavior

Parameter name	Description
Michaelis-Menton Neg Growth - Alpha	Alpha parameter.
Michaelis-Menton Neg Growth - Beta	Beta parameter. Cannot be equal to zero.
Michaelis-Menton Neg Growth - Gamma	Gamma parameter.
Michaelis-Menton Neg Growth - Phi	Phi parameter.
Michaelis-Menton Neg Growth - Growth Standard Deviation	Standard deviation of growth stochasticity, cm / yr. Use zero if growth should have no stochasticity.
Michaelis-Menton Neg Growth - Autocorrelation Prob (0-1)	Probability of autocorrelation from year to year, as a value from 0 to 1. Use 0 if there should be no autocorrelation.

How it works

The amount of height growth is calculated as:

$$Y = \frac{\alpha GLI}{GLI + \alpha / \beta} H^\varphi - \gamma$$

where:

- Y is the amount of height growth for one year, in cm
- GLI is the light level
- α is the **Michaelis-Menton Neg Growth - Alpha** parameter
- β is the **Michaelis-Menton Neg Growth - Beta** parameter
- γ is the **Michaelis-Menton Neg Growth - Gamma** parameter
- φ is the **Michaelis-Menton Neg Growth - Phi** parameter
- H is the tree's height in cm

Optionally, the value of Y can be randomized by adding to it a stochastic factor SF , which is a random draw on a normal distribution with mean zero and standard deviation set using the **Michaelis-Menton Neg Growth - Growth Standard Deviation** parameter. SF can be positive or negative and is in units of centimeters of height growth. If you do not want to add SF , set the value of this parameter to zero.

If you are using the stochastic factor SF , you can also introduce autocorrelation in the growth stochasticity. Each year, for each tree, a random number is compared to the value in the **Michaelis-Menton Neg Growth - Autocorrelation Prob (0-1)** parameter for that tree's species to determine if the stochastic factor will be autocorrelated for that year. If it is autocorrelated, the previous year's stochastic factor SF is added to Y to determine height growth. If it is not autocorrelated, a new value for SF is drawn. If you do not wish to use autocorrelation, set the value of the autocorrelation parameter to zero. Autocorrelation is ignored if there is no growth stochasticity.

If the timestep is more than one year long, growth is recalculated for each year of the timestep, increasing the height each time. Stochasticity and autocorrelation are also evaluated on a yearly basis.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) and a diameter growth behavior applied.

Michaelis Menton with photoinhibition - height only

This behavior uses a modified Michaelis-Menton function to do height growth.

Parameters for this behavior

Parameter name	Description
Michaelis-Menton with Photoinhibition - Alpha	Alpha parameter.
Michaelis-Menton with Photoinhibition - Beta	Beta parameter. Cannot be equal to zero.
Michaelis-Menton with Photoinhibition - D	D parameter.
Michaelis-Menton with Photoinhibition - Phi	Phi parameter.

How it works

The amount of height growth is calculated as:

$$Y = \left(\frac{\alpha}{1 + \frac{\alpha}{\beta * GLI}} - D * GLI \right) H^\varphi$$

where:

- Y is the amount of height growth for one year, in cm
- GLI is the light level
- α is the **Michaelis-Menton with Photoinhibition - Alpha** parameter
- β is the **Michaelis-Menton with Photoinhibition - Beta** parameter
- D is the **Michaelis-Menton with Photoinhibition - D** parameter
- φ is the **Michaelis-Menton with Photoinhibition - Phi** parameter
- H is the tree's height in cm

If the timestep is more than one year long, growth is recalculated for each year of the timestep, increasing the height each time.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) and a diameter growth behavior applied.

NCI growth

This behavior features a maximum growth rate that is adjusted using a set of factors of your choice. You can choose any combination you wish. In particular, this has several ways to implement the the effects of neighbor competitiveness to influence growth rates ("NCI" stands for neighborhood competition index).

Each species has a maximum potential growth rate that is reduced for individual trees according to the effects you select.

Parameters for this behavior

Parameter name	Description
NCI Maximum Potential Growth, cm/yr	Maximum potential diameter growth for a tree, in cm/yr.
Growth Increment Adjustment PDF	PDF to use to stochastically adjust the growth increment (including "none" for no adjustment).
Std Deviation for Normal or Lognormal Adjustment	Value for standard deviation if the parameter Growth Increment Adjustment PDF is set to "normal" or "lognormal".

How it works

For a tree, the amount of growth is the maximum potential growth times any of a possible set of factors affecting growth:

$$Growth = Max\ Growth * [Size\ Effects] * [Shading\ Effects] * [Crowding\ Effects] * [Damage\ Effects] * [Precipitation\ Effects] * [Temperature\ Effects] * [Nitrogen\ Effects] * [Infection\ Effects]$$

Max Growth is the maximum diameter growth the tree can attain, in cm/yr, entered in the **NCI Maximum Potential Growth, cm/yr** parameter. You can have an effect in each category (or none at all) which acts to reduce the maximum growth rate. Each of these effects is a value between 0 and 1.

Effects choices (note that only those effects that do not depend on a target individual are allowed):

- [Size effects](#)
- [Shading effects](#)
- [Crowding effects](#)
- [Damage effects](#)
- [Precipitation effects](#)
- [Temperature effects](#)
- [Nitrogen effects](#)
- [Infection effects](#)

The amount of growth is in cm/year. For multi-year timesteps, the behavior will calculate total growth with a loop. Each loop iteration will increment diameter for one year. For each year, any effects with diameter as a term are recalculated with the previous year's updated diameter value. (NCI values are constant throughout this loop - for neighbors only the size at the start of the timestep is used.)

The growth increment can be applied as-is, or stochasticity can be added. To introduce stochasticity, set the value of the parameter **Growth Increment Adjustment PDF** to your choice of probability distribution function. The calculated growth increment will be used as the mean value in a random draw on that PDF, with the standard deviation set to the value in the **Std Deviation for Normal or Lognormal Adjustment**. If the value of the resulting draw is negative, the growth increment is set to zero to avoid negative growth.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. (Some effects have limitations on application to juveniles - check individual effects documentation.) You can use either the diam with auto height or diam only version.

NCI quadrat growth

This behavior features a maximum growth rate that is adjusted using a set of factors of your choice. You can choose any combination you wish. In particular, this has several ways to implement the effects of neighbor competitiveness to influence growth rates ("NCI" stands for neighborhood competition index). For processing efficiency, growth is calculated for each species on a per grid cell basis.

Parameters for this behavior

Parameter name	Description
NCI Maximum Potential Growth,	Maximum potential diameter growth for a tree, in cm/yr.

cm/yr	
Growth Increment Adjustment PDF	PDF to use to stochastically adjust the growth increment (including "none" for no adjustment).
Std Deviation for Normal or Lognormal Adjustment	Value for standard deviation if the parameter Growth Increment Adjustment PDF is set to "normal" or "lognormal".

How it works

This behavior tracks growth using the [NCI Quadrat Growth](#) grid. Each tree gets the growth rate calculated for the grid cell in which it is found. You can set the grid cell size to set the balance between neighborhood composition resolution (smaller grid cells) and processing time (larger grid cells).

For a given species in a given grid cell, the amount of diameter growth per year is calculated as:

$$Growth = Max\ Growth * [Crowding\ Effects] * [Precipitation\ Effects] * [Temperature\ Effects] * [Nitrogen\ Effects] * [Infection\ Effects]$$

Max Growth is the maximum diameter growth the tree can attain, in cm/yr, entered in the **NCI Maximum Potential Growth, cm/yr** parameter. You can have an effect in each category (or none at all) which acts to reduce the maximum growth rate. Each of these effects is a value between 0 and 1.

Effects choices:

- [Crowding effects](#)
- [Precipitation effects](#)
- [Temperature effects](#)
- [Nitrogen effects](#)
- [Infection effects](#)

The amount of growth is in cm/year. For multi-year timesteps, the annual growth rate is multiplied by the number of years per timestep.

The growth increment can be applied as-is, or stochasticity can be added. To introduce stochasticity, set the value of the parameter **Growth Increment Adjustment PDF** to your choice of probability distribution function. The calculated growth increment will be used as the mean value in a random draw on that PDF, with the standard deviation set to the value in the **Std Deviation for Normal or Lognormal Adjustment**. If the value of the resulting draw is negative, the growth increment is set to zero to avoid negative growth.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. You can use either the diam with auto height or diam only version.

Power growth - height only

This behavior uses a power function to do height growth.

Parameters for this behavior

Parameter name	Description
Power Height Growth - n	The coefficient in the power function for height growth.
Power Height Growth - Exp	The exponent in the power function for height growth.

How it works

The amount of height growth is calculated as:

$$Y = n H^{\varphi}$$

where:

- Y is the amount of height growth for one year, in cm
- n is the **Power Height Growth - n** parameter
- φ is the **Power Height Growth - Exp** parameter
- H is the tree's height in cm

If the timestep is more than one year long, growth is recalculated for each year of the timestep, increasing the height each time.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a diameter growth behavior applied.

Puerto Rico semi-stochastic - diam only

This behavior combines a deterministic growth function for small trees with completely stochastic growth for larger trees. It's meant to be used when a species uses a height growth behavior as the primary growth method.

Parameters for this behavior

Parameter name	Description
PR - "a" Parameter for Deterministic Growth	"a" parameter used to calculate deterministic growth when a tree is below the stochastic height threshold.
PR - "b" Parameter for Deterministic Growth	"b" parameter used to calculate deterministic growth when a tree is below the stochastic height threshold.
PR - Height Threshold for Stochastic Growth (m)	The tree height threshold, in meters, between deterministic and stochastic growth.
PR - Mean DBH (cm) for Stochastic Growth	The mean for DBH values, in cm, when a tree uses stochastic growth. This is the mean of the DBH value, NOT the amount of growth.
PR - DBH Standard Deviation for Stochastic Growth	Standard deviation for DBH values when a tree uses stochastic growth. This is the standard deviation of the DBH value, NOT the amount of growth.

How it works

The divide between the two growth functions is defined in the **PR - Height Threshold for Stochastic Growth (m)** parameter. Trees shorter than this use the following function:

$$Y = (A * \exp(-B * Height)) - Diam$$

where:

- Y = diameter growth for the timestep, in cm
- a = **PR - "a" Parameter for Deterministic Growth** parameter
- b = **PR - "b" Parameter for Deterministic Growth** parameter
- $Height$ = tree height in cm AFTER height growth in the current timestep
- $diam$ = diameter of the tree at which to apply growth (before growth), in cm

Above the height cutoff, trees are assigned random diameters drawn from a normal distribution. The normal distribution is defined by the **PR - Mean DBH (cm) for Stochastic Growth** and **PR**

- **DBH Standard Deviation for Stochastic Growth** parameters, and represents the distribution of DBH values, NOT growth values. The amount of growth for a tree is $Y = D' - D$, where Y is the amount of growth, D' is the new diameter chosen from the normal distribution, and D is the previous diameter. This means that growth can be negative. The effect is to create a tree population with normally-distributed diameters, where any individual tree may jump from place to place within the distribution.

How to apply it

This function can be applied to seedlings, saplings, or adults of any species. Any tree using this behavior must also use a height-only growth behavior.

Puerto Rico storm bi-level growth - diam with auto height

Puerto Rico storm bi-level growth - diam with auto height

This behavior increments growth according to two possible growth equations, one to be used in low-light conditions and the other to be used in high-light conditions. This behavior was originally created for the Puerto Rico model.

Parameters for this behavior

Parameter name	Description
PR Storm Bi-Level - Threshold for High-Light Growth (0 - 100)	The threshold between low-light and high-light equations, as a value between 0 and 100.
PR Storm Bi-Level - High-Light "a"	The "a" value in the high-light growth function.
PR Storm Bi-Level - High-Light "b"	The "b" value in the high-light growth function.
PR Storm Bi-Level - Intercept for Low-Light Growth (a)	The intercept of the linear growth function used in low-light conditions.
PR Storm Bi-Level - Slope for Low-Light Growth (b)	The slope of the linear growth function used in high-light conditions.

How it works

Light levels come from the [Storm Light](#) grid produced by the [Storm Light](#) behavior. The threshold between the use of the high-light and low-light functions is set in the **PR Storm Bi-Level - Threshold for High-Light Growth (0 - 100)** parameter.

The function used in low-light conditions is:

$$Y = (a + b * diam) * T$$

where

- Y = amount of diameter growth in cm
- a = **PR Storm Bi-Level - Intercept for Low-Light Growth (a)** parameter
- b = **PR Storm Bi-Level - Slope for Low-Light Growth (b)** parameter
- $diam$ = diameter (diameter at 10 cm for seedlings and saplings, DBH for adults)
- T = number of years per timestep

The function used in high-light conditions is:

$$H = T * a * diam * e^{(-b * N)}$$

where

- H = amount of **height** growth, in cm
- a = **PR Storm Bi-Level - High-Light "a"** parameter
- b = **PR Storm Bi-Level - High-Light "b"** parameter
- $diam$ = diameter (diameter at 10 cm for seedlings and saplings, DBH for adults)
- N = number of years since the last storm, from the [Storm Damage](#) grid produced by the [Storm disturbance](#) behavior
- T = number of years per timestep

H is expressed in centimeters of height growth. This is transformed into a number of cm of diameter growth, which is what this behavior passes along. This means that during tree life history stage transitions, the height the tree ends up with is not guaranteed to match the height calculated by the high-light growth function.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. You must also use the [Storm disturbance](#) and [Storm Light](#) behaviors.

Relative growth behaviors

Several behaviors apply a relative growth version of the Michaelis-Menton function.

Parameters for these behaviors

Parameter name	Description
Adult Constant Area Growth in sq. cm/yr	The constant amount of basal area by which to increase a tree's basal area. Applies to basal-area-increment-limited behaviors.
Adult Constant Radial Growth in mm/yr	The constant value by which to increase a tree's radius at breast height. Applies to radial-increment-limited-growth behaviors.
Asymptotic Diameter Growth (A)	Asymptote of the Michaelis-Menton growth function at high light - function term A below; for diameter growth.
Asymptotic Height Growth (A)	Asymptote of the Michaelis-Menton growth function at high light - function term A; for height growth.
Slope of Growth Response (S)	Slope of the Michaelis-Menton growth function at zero light - function term S below.
Relative Michaelis-Menton Growth - Diameter Exponent	The exponent to be used with diameter when calculating relative growth.

Relative growth is calculated with the equation:

$$Y = \left[\left(\frac{A * GLI}{A/S + GLI} \right) \right]$$

where:

- Y is the amount of annual relative growth
- A is the **Asymptotic Diameter Growth (A)** or **Asymptotic Height Growth (A)** parameter
- S is the **Slope of Growth Response (S)** or **Slope of Height Growth Response (S)** parameter
- GLI is the global light index, calculated by a [light behavior](#)

Diameter growth is compounded over multiple timesteps with the equation:

$$G = ((Y + 1)^T - 1) * diam^X$$

where:

- G is the amount of diameter growth for the timestep, in cm

- *diam* is the diameter of the tree in cm (at 10 cm height if seedling or sapling, or DBH if adult)
- *T* is the number of years per timestep
- *X* is the **Relative Michaelis-Menton Growth - Diameter Exponent** parameter

Relative height growth is calculated slightly differently. The details are discussed in the section for the [Relative growth - height only](#) behavior below. Relative growth is discussed in [Pacala et al 1996](#).

Relative growth limited to radial increment

How it works

This behavior calculates an amount of diameter growth according to the relative growth equation. Growth is limited to a maximum of the constant radial growth increment for the species of tree to which it is being applied. The increment is calculated as described in the "Constant radial growth" behavior. Note that the increment parameter specifies **radial** growth; the behavior makes all necessary conversions.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the *diam* with auto height or *diam* only version.

Relative growth limited to basal area increment

How it works

This behavior calculates an amount of diameter growth according to the relative growth equation. Growth is limited to a maximum of a constant basal area increment. The amount of diameter increase is calculated by dividing the annual basal area increment of the tree's species by the diameter of the tree. The increment is calculated as described in the "Constant basal area growth" behavior.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the *diam* with auto height or *diam* only version.

Non-limited relative growth

How it works

The amount of increase returned by the relative growth equation is applied to the tree.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied.

Relative growth - height only

This behavior uses the Michaelis-Menton function to do height growth.

How it works

After the Michaelis-Menton function is used to calculate Y as described in the section above, the amount of height growth is calculated as:

$$G = Y * Height^X$$

where:

- G is the amount of height growth for one year, in cm
- $Height$ is the height of the tree in cm
- X is the **Relative Michaelis-Menton Growth - Height Exponent** parameter

If the timestep is more than one year long, growth is recalculated for each year of the timestep, increasing the height each time.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) and a diameter growth behavior applied.

Relative growth behaviors

Several behaviors apply a relative growth version of the Michaelis-Menton function.

Parameters for these behaviors

Parameter name	Description
Adult Constant Area Growth in sq. cm/yr	The constant amount of basal area by which to increase a tree's basal area. Applies to basal-area-increment-limited behaviors.

Adult Constant Radial Growth in mm/yr	The constant value by which to increase a tree's radius at breast height. Applies to radial-increment-limited-growth behaviors.
Asymptotic Diameter Growth (A)	Asymptote of the Michaelis-Menton growth function at high light - function term A below; for diameter growth.
Asymptotic Height Growth (A)	Asymptote of the Michaelis-Menton growth function at high light - function term A; for height growth.
Slope of Growth Response (S)	Slope of the Michaelis-Menton growth function at zero light - function term S below.
Relative Michaelis-Menton Growth - Diameter Exponent	The exponent to be used with diameter when calculating relative growth.

Relative growth is calculated with the equation:

$$Y = \left[\left(\frac{A * GLI}{A/S + GLI} \right) \right]$$

where:

- Y is the amount of annual relative growth
- A is the **Asymptotic Diameter Growth (A)** or **Asymptotic Height Growth (A)** parameter
- S is the **Slope of Growth Response (S)** or **Slope of Height Growth Response (S)** parameter
- GLI is the global light index, calculated by a [light behavior](#)

Diameter growth is compounded over multiple timesteps with the equation:

$$G = ((Y + 1)^T - 1) * diam^X$$

where:

- G is the amount of diameter growth for the timestep, in cm
- $diam$ is the diameter of the tree in cm (at 10 cm height if seedling or sapling, or DBH if adult)
- T is the number of years per timestep
- X is the **Relative Michaelis-Menton Growth - Diameter Exponent** parameter

Relative height growth is calculated slightly differently. The details are discussed in the section for the [Relative growth - height only](#) behavior below. Relative growth is discussed in [Pacala et al 1996](#).

Relative growth limited to radial increment

How it works

This behavior calculates an amount of diameter growth according to the relative growth equation. Growth is limited to a maximum of the constant radial growth increment for the species of tree to which it is being applied. The increment is calculated as described in the "Constant radial growth" behavior. Note that the increment parameter specifies **radial** growth; the behavior makes all necessary conversions.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Relative growth limited to basal area increment

How it works

This behavior calculates an amount of diameter growth according to the relative growth equation. Growth is limited to a maximum of a constant basal area increment. The amount of diameter increase is calculated by dividing the annual basal area increment of the tree's species by the diameter of the tree. The increment is calculated as described in the "Constant basal area growth" behavior.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Non-limited relative growth

How it works

The amount of increase returned by the relative growth equation is applied to the tree.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied.

Relative growth - height only

This behavior uses the Michaelis-Menton function to do height growth.

How it works

After the Michaelis-Menton function is used to calculate Y as described in the section above, the amount of height growth is calculated as:

$$G = Y * Height^X$$

where:

- G is the amount of height growth for one year, in cm
- $Height$ is the height of the tree in cm
- X is the **Relative Michaelis-Menton Growth - Height Exponent** parameter

If the timestep is more than one year long, growth is recalculated for each year of the timestep, increasing the height each time.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) and a diameter growth behavior applied.

Relative growth behaviors

Several behaviors apply a relative growth version of the Michaelis-Menton function.

Parameters for these behaviors

Parameter name	Description
Adult Constant Area Growth in sq. cm/yr	The constant amount of basal area by which to increase a tree's basal area. Applies to basal-area-increment-limited behaviors.
Adult Constant Radial Growth in mm/yr	The constant value by which to increase a tree's radius at breast height. Applies to radial-increment-limited-growth behaviors.

Asymptotic Diameter Growth (A)	Asymptote of the Michaelis-Menton growth function at high light - function term A below; for diameter growth.
Asymptotic Height Growth (A)	Asymptote of the Michaelis-Menton growth function at high light - function term A; for height growth.
Slope of Growth Response (S)	Slope of the Michaelis-Menton growth function at zero light - function term S below.
Relative Michaelis-Menton Growth - Diameter Exponent	The exponent to be used with diameter when calculating relative growth.

Relative growth is calculated with the equation:

$$Y = \left[\left(\frac{A * GLI}{A/S + GLI} \right) \right]$$

where:

- Y is the amount of annual relative growth
- A is the **Asymptotic Diameter Growth (A)** or **Asymptotic Height Growth (A)** parameter
- S is the **Slope of Growth Response (S)** or **Slope of Height Growth Response (S)** parameter
- GLI is the global light index, calculated by a [light behavior](#)

Diameter growth is compounded over multiple timesteps with the equation:

$$G = ((Y + 1)^T - 1) * diam^X$$

where:

- G is the amount of diameter growth for the timestep, in cm
- diam is the diameter of the tree in cm (at 10 cm height if seedling or sapling, or DBH if adult)
- T is the number of years per timestep
- X is the **Relative Michaelis-Menton Growth - Diameter Exponent** parameter

Relative height growth is calculated slightly differently. The details are discussed in the section for the [Relative growth - height only](#) behavior below. Relative growth is discussed in [Pacala et al 1996](#).

Relative growth limited to radial increment

How it works

This behavior calculates an amount of diameter growth according to the relative growth equation. Growth is limited to a maximum of the constant radial growth increment for the species of tree to which it is being applied. The increment is calculated as described in the "Constant radial growth" behavior. Note that the increment parameter specifies **radial** growth; the behavior makes all necessary conversions.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Relative growth limited to basal area increment

How it works

This behavior calculates an amount of diameter growth according to the relative growth equation. Growth is limited to a maximum of a constant basal area increment. The amount of diameter increase is calculated by dividing the annual basal area increment of the tree's species by the diameter of the tree. The increment is calculated as described in the "Constant basal area growth" behavior.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Non-limited relative growth

How it works

The amount of increase returned by the relative growth equation is applied to the tree.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied.

Relative growth - height only

This behavior uses the Michaelis-Menton function to do height growth.

How it works

After the Michaelis-Menton function is used to calculate Y as described in the section above, the amount of height growth is calculated as:

$$G = Y * Height^X$$

where:

- G is the amount of height growth for one year, in cm
- $Height$ is the height of the tree in cm
- X is the **Relative Michaelis-Menton Growth - Height Exponent** parameter

If the timestep is more than one year long, growth is recalculated for each year of the timestep, increasing the height each time.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) and a diameter growth behavior applied.

Relative growth behaviors

Several behaviors apply a relative growth version of the Michaelis-Menton function.

Parameters for these behaviors

Parameter name	Description
Adult Constant Area Growth in sq. cm/yr	The constant amount of basal area by which to increase a tree's basal area. Applies to basal-area-increment-limited behaviors.
Adult Constant Radial Growth in mm/yr	The constant value by which to increase a tree's radius at breast height. Applies to radial-increment-limited-growth behaviors.
Asymptotic Diameter Growth (A)	Asymptote of the Michaelis-Menton growth function at high light - function term A below; for diameter growth.
Asymptotic Height Growth (A)	Asymptote of the Michaelis-Menton growth function at high light - function term A; for height growth.
Slope of Growth	Slope of the Michaelis-Menton growth function at zero light - function

Response (S)	term S below.
Relative Michaelis-Menton Growth - Diameter Exponent	The exponent to be used with diameter when calculating relative growth.

Relative growth is calculated with the equation:

$$Y = \left[\left(\frac{A * GLI}{A/S + GLI} \right) \right]$$

where:

- Y is the amount of annual relative growth
- A is the **Asymptotic Diameter Growth (A)** or **Asymptotic Height Growth (A)** parameter
- S is the **Slope of Growth Response (S)** or **Slope of Height Growth Response (S)** parameter
- GLI is the global light index, calculated by a [light behavior](#)

Diameter growth is compounded over multiple timesteps with the equation:

$$G = ((Y + 1)^T - 1) * diam^X$$

where:

- G is the amount of diameter growth for the timestep, in cm
- $diam$ is the diameter of the tree in cm (at 10 cm height if seedling or sapling, or DBH if adult)
- T is the number of years per timestep
- X is the **Relative Michaelis-Menton Growth - Diameter Exponent** parameter

Relative height growth is calculated slightly differently. The details are discussed in the section for the [Relative growth - height only](#) behavior below. Relative growth is discussed in [Pacala et al 1996](#).

Relative growth limited to radial increment

How it works

This behavior calculates an amount of diameter growth according to the relative growth equation. Growth is limited to a maximum of the constant radial growth increment for the species of tree to which it is being applied. The increment is calculated as described in the

"Constant radial growth" behavior. Note that the increment parameter specifies **radial** growth; the behavior makes all necessary conversions.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Relative growth limited to basal area increment

How it works

This behavior calculates an amount of diameter growth according to the relative growth equation. Growth is limited to a maximum of a constant basal area increment. The amount of diameter increase is calculated by dividing the annual basal area increment of the tree's species by the diameter of the tree. The increment is calculated as described in the "Constant basal area growth" behavior.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied. You can use either the diam with auto height or diam only version.

Non-limited relative growth

How it works

The amount of increase returned by the relative growth equation is applied to the tree.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) applied.

Relative growth - height only

This behavior uses the Michaelis-Menton function to do height growth.

How it works

After the Michaelis-Menton function is used to calculate Y as described in the section above, the amount of height growth is calculated as:

$$G = Y * Height^X$$

where:

- G is the amount of height growth for one year, in cm
- $Height$ is the height of the tree in cm
- X is the **Relative Michaelis-Menton Growth - Height Exponent** parameter

If the timestep is more than one year long, growth is recalculated for each year of the timestep, increasing the height each time.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [light behavior](#) and a diameter growth behavior applied.

Stochastic Gap Growth

This behavior uses a shortcut for simulating gap dynamics with very competitive conditions. This behavior causes rapid growth in high light, with a unique "winner"; low light produces no growth at all.

How it works

This behavior simulates high growth in gap conditions. It relies on the [Gap Light](#) grid created by the [Gap Light](#) behavior to tell it where the gaps are. In this grid, each cell is either in gap (with 100% GLI) or not in gap (with 0% GLI). If a cell is in gap, a tree in that cell is randomly chosen out of all the trees to which the behavior applies to be promoted directly to adult tree status (even if it is a seedling). This tree represents the "winner". All other trees in the cell do not grow. In cells that are not in gap, no trees grow.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have the [Gap Light behavior](#) applied.

Mortality behaviors

The mortality behaviors cause tree death due to natural life cycle causes and competition. Tree death due to disturbance is covered by other behaviors.

Mortality behaviors do not actually remove dead trees from memory. They set a flag which marks trees as dead. This is because some other behaviors, such as the [Substrate](#) group, have

specific interest in dead trees. Dead trees are eventually removed from memory by the [Dead tree remover](#) behavior. You may notice this behavior in your behavior list. It is included automatically. It is important to include this behavior in your run to avoid incorrect results in behaviors that use dead trees and unacceptably slow model run times.

Behavior	Description
Aggregated Mortality	Kills trees randomly to match a predetermined mortality rate, clumping together the deaths in both time and space.
BC Mortality	Kills trees as a function of growth rate.
Browsed Stochastic Mortality	Simulates the effects of herbivory by allowing different background mortality rates for browsed and unbrowsed trees.
Climate and Competition Dependent Neighborhood Survival	Assesses tree survival as a function of mean annual temperature, water deficit, and neighbor adult basal area. For efficiency, it calculates survival rates for cells in a grid and assigns trees the survival probability of the grid cell in which they are found.
Competition Mortality	Kills trees as a function of growth. Uses the results of the NCI growth behavior.
Density Self-Thinning Mortality	Calculates the probability of mortality of an individual juvenile tree as a function of the density and mean diameter of the neighborhood trees.
Exponential Growth and Resource-Based Mortality	Calculates probability of mortality as a function of growth and some second resource.
GMF Mortality	Kills trees as a function of growth rate.
Gompertz Density Self Thinning	Calculates the probability of mortality of an individual tree as a function of the density of conspecific neighborhood trees.
Growth and Resource-Based Mortality	Calculates probability of survival as a function of growth and some second resource.
Height-GLI	Calculates the probability of mortality using a Weibull function of tree height

Weibull Mortality with Browse	and GLI (light level). It can also simulate the effects of herbivory by using different parameters for browsed and unbrowsed trees.
Insect Infestation Mortality	Causes mortality in trees that are infested with insects.
Logistic Bi-Level Mortality	Calculates the probability of survival according to a logistic equation, with the possibility of two sets of parameters for each species: one for high-light conditions and one for low-light conditions.
NCI Mortality	Uses multiple effects, including neighbor competitiveness, to calculate mortality rates.
Post Harvest Skidding Mortality	Simulates an increase in mortality after harvesting attributable to skidding damage or other effects.
Self Thinning	Uses a pseudo-density dependent function designed to increase the death rate in dense uniform-age stands.
Senescence	Provides for an uptick in mortality rates among large adult trees.
Size Dependent Logistic Mortality	Mortality rates are a logistic function of tree size.
Stochastic Bi-Level Mortality - Storm Light	Applies a constant rate of mortality to trees, with different rates for high-light and low-light conditions. This works with the Storm Light behavior.
Stochastic Bi-Level Mortality - GLI	Applies a constant rate of mortality to trees, with different rates for high-light and low-light conditions. This works with the GLI behavior.
Stochastic Mortality	Produces background mortality by randomly choosing trees to die according to a specified rate.
Suppression Duration Mortality	Evaluates mortality as a function of tree age. This is particularly useful for simulating suppression in seedlings.
Temperature dependent neighborhood	Assesses tree survival as a function of mean annual temperature and neighbor adult basal area. For efficiency, it calculates survival rates for cells in a grid and assigns trees the survival probability of the grid cell in which they are found.

survival	
Weibull Snag Mortality	Controls snag fall according to a Weibull function of snag age.

Aggregated Mortality

Aggregated Mortality is similar to the [Stochastic Mortality](#) behavior in that it kills trees randomly to match a predetermined mortality rate. However, Aggregated Mortality clumps together the deaths in both time and space.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Aggregated Mortality Annual Kill Amount (0-1)	The annual mortality rate for a mortality episode, as a proportion between 0 and 1.
Aggregated Mortality Clump Size	Whether the size of a clump of trees to kill is deterministic or chosen from a negative binomial probability distribution.
Aggregated Mortality Clumping Parameter	If the size of tree clumps to kill is drawn from a negative binomial probability distribution, this is the clumping parameter for the distribution. This is not required if a deterministic clump size is used.
Aggregated Mortality Number of Trees To Aggregate	Determines the size of the clumps of trees killed. If the clump size is deterministic, all clumps will be this size. If the size is to be drawn from a negative binomial probability distribution, then this is the mean clump size.
Aggregated Mortality Return Interval (years)	The return interval for mortality episodes.

How it works

Mortality occurs in discrete episodes, which have an average return interval. For any timestep, the probability that a mortality episode will occur is T/RI , where T is the number of years per timestep and RI is the **Aggregated Mortality Return Interval (years)** parameter. Each timestep, this behavior uses a random number to decide if a mortality episode occurs. Between mortality episodes, this behavior does not kill any trees.

If a mortality episode occurs, this behavior kills some of the total pool of trees to which it has been applied. The base annual mortality rate proportion is given in the **Aggregated Mortality Annual Kill Amount (0-1)** parameter. Since the parameter gives an annual rate, the actual mortality rate is $1-(1-AD)^T$, where AD is the annual amount to kill and T is the number of years per timestep.

During a mortality episode, this behavior kills the trees in discrete clumps. The behavior uses a random number with each tree in its pool of eligible trees to decide if that tree dies. If it dies, the behavior also kills the trees closest to it. Only trees to which this behavior has been applied are killed; other neighbors are left alone. The size of these clumps of dead trees can either be deterministic or drawn from a negative binomial probability distribution. This option is set in the **Aggregated Mortality Clump Size** parameter. If the size is deterministic, the size of all clumps is given in the **Aggregated Mortality Number of Trees To Aggregate** parameter. If the size is from a negative binomial distribution, that parameter gives the mean, u , for the function

$$P(x | u, k) = \frac{\Gamma(x + k)}{\Gamma(k) x!} \left(\frac{u}{u + k} \right)^x \left(1 + \frac{u}{k} \right)^{-k}$$

where k , the clumping parameter, is the **Aggregated Mortality Clumping Parameter** parameter.

If the **Aggregated Mortality Return Interval (years)** and **Aggregated Mortality Number of Trees To Aggregate** parameters are both set to 1, then this behavior functions exactly like the [Stochastic Mortality](#) behavior.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Only those trees to which this behavior has been applied will be killed. This behavior can be combined with other mortality behaviors, but for best results, it should be the first one to occur.

BC mortality

BC mortality is a growth-based mortality behavior.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Light-Dependent Mortality	Light-dependent mortality.

Mortality at Zero Growth

Mortality rate at zero growth.

How it works

The BC mortality model evaluates the following function to determine the probability of a tree's mortality:

$$m = 1 - \exp(-(T * m_1) * \exp(-m_2 * G))$$

where:

- m is the probability of mortality
- T is the number of years per timestep
- m_1 is the **Mortality at Zero Growth** parameter
- m_2 is the **Light-Dependent Mortality** parameter
- G is amount of radial growth, in mm/yr, added to the tree's diameter during T

BC mortality is described in [Kobe and Coates 1997](#).

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [growth behavior](#) applied.

Browsed Stochastic Mortality

This simulates the effects of herbivory by allowing different background mortality rates for browsed and unbrowsed trees.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Background Mortality Rate	The proportion of trees that die each year, as a value between 0 and 1.
Browsed Background Mortality Rate	The proportion of browsed trees that die each year, as a value between 0 and 1.

How it works

Whether or not a tree is browsed is determined by the [Random browse](#) behavior. For each tree, if it has not been browsed, that species's **Background Mortality Rate** parameter is used; if it has been browsed, the species's **Browsed Background Mortality Rate** parameter is used. A random number is compared to the appropriate rate to decide if the tree dies.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have the [Random browse](#) behavior applied.

Climate and Competition Dependent Neighborhood Survival

This behavior assesses tree survival as a function of mean annual temperature, water deficit, and neighbor adult basal area. For efficiency, it calculates survival rates for cells in a grid and assigns trees the survival probability of the grid cell in which they are found.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Climate Comp Dep Neighborhood Surv - A	A in the survival function.
Climate Comp Dep Neighborhood Surv - B	B in the survival function.
Climate Comp Dep Neighborhood Surv - C	C in the survival function.
Climate Comp Dep Neighborhood Surv - D	D in the survival function.
Climate Comp Dep Neighborhood Surv - M	M in the survival function.

M	
Climate Comp Dep Neighborhood Surv - N	N in the survival function.
Climate Comp Dep Neighborhood Surv - Neigh Search Radius (m)	Maximum radius to search for crowding neighbors, in meters.

How it works

This behavior uses the [Climate Comp Dep Neighborhood Survival](#) grid to keep track of survival rates. The annual probability of survival for a given species and given grid cell is calculated as:



where:

- *Surv* is the annual probability of survival
- *A* is the **Climate Comp Dep Neighborhood Surv - A** parameter
- *B* is the **Climate Comp Dep Neighborhood Surv - B** parameter
- *M* is the **Climate Comp Dep Neighborhood Surv - M** parameter
- *N* is the **Climate Comp Dep Neighborhood Surv - N** parameter
- *C* is the **Climate Comp Dep Neighborhood Surv - C** parameter
- *D* is the **Climate Comp Dep Neighborhood Surv - D** parameter
- *T* is the mean annual temperature in degrees Celsius as entered in the [Plot](#)
- *T* is the water deficit as entered in the [Plot](#)
- *BAT* is the adult total basal area in the neighborhood, in square meters

BAT is the basal area of all adults within the distance from the center of the grid cell set in the **Temp Dependent Neighborhood Surv - Neigh Search Radius (m)** parameter.

The probability of survival is for a single year. For multi-year timesteps, the timestep survival probability is the annual probability raised to the power of the number of years per timestep.

Trees receive the survival probability calculated for the grid cell in which they are found. A random number is used to determine whether a tree lives or dies.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species.

Competition Mortality

Competition mortality is a growth-based mortality behavior. It uses the results of the [NCI growth](#) behavior.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Competition Mortality Shape Parameter (Z)	Determines the shape of the mortality function.
Competition Mortality Maximum Parameter (max)	The maximum relative increment of growth subject to mortality.

How it works

NCI growth in SORTIE is calculated in the following way:

$$Growth = Max\ Growth * Size\ Effect * Shading\ Effect * Crowding\ Effect * Damage\ Effect$$

Max Growth is the maximum diameter growth the tree can attain, in cm/yr, entered in the **NCI Maximum Potential Growth, cm/yr** parameter. *Size Effect*, *Shading Effect*, *Crowding Effect*, and *Damage Effect* are all factors which act to reduce the maximum growth rate and will vary depending on the conditions a tree is in. Each of these effects is a value between 0 and 1.

In the Competition mortality behavior, the following measure is used as predictor variable for probability of mortality:

$$Relative\ increment = Growth / PG$$

The *relative increment* is the ratio between the growth for an individual tree and the maximum growth possible for that tree. The *Growth* is the tree's growth for the previous timestep. *PG* is calculated as follows:

$$PG = Max\ Growth * SE$$

where Max Growth is the NCI growth parameter **NCI Maximum Potential Growth, cm/yr**, and *SE* is the Size Effect. Size Effect is calculated as follows:

$$SE = e^{-0.5 \left[\frac{\ln(DBH/X_0)}{X_b} \right]^2}$$

where:

- *DBH* is of the target tree, in cm
- X_0 is the **NCI Size Effect Mode, in cm (X0)** NCI growth parameter
- X_b is the **NCI Size Effect Variance, in cm (Xb)** NCI growth parameter

Once the *relative increment* for an individual tree has been calculated, the probability of mortality for that individual is calculated in the following way:

$$Prob = Z^{relative\ increment / max}$$

where:

- *Prob* is the probability of mortality
- Z is the **Competition Mortality Shape Parameter (Z)** parameter
- *max* is the **Competition Mortality Maximum Parameter (max)** parameter, which indicates the maximum *relative increment* subject to mortality
-

All trees with a *relative increment* greater than or equal to *max* will live.

How to apply it

This behavior can be applied to saplings and adults of any species. It cannot be applied to seedlings. Any tree species/type combination to which it is applied must also have NCI growth. **This behavior can only be applied with a one year timestep.**

Density Self-Thinning Mortality

This behavior calculates the probability of mortality of an individual juvenile tree as a function of the density and mean diameter of the neighborhood trees. Only neighborhood seedlings and saplings are taken into account in this behavior.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
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Density Self-Thinning Asymptote (A)	The asymptote of the density self-thinning function.
Density Self-Thinning Density Effect (S)	The parameter controlling the density effect of the density self-thinning function.
Density Self-Thinning Diameter Effect (C)	The parameter controlling the effect of neighbor mean diameter of the density self-thinning function.
Density Self-Thinning Minimum Density for Mortality (#/ha)	The minimum density of neighbors, in stems/ha, for density self-thinning mortality. A tree with a lower density of neighbors than this value will not die.
Density Self-Thinning Neighborhood Radius, in m	The maximum radius, in m, within which to search for neighbors to calculate neighbor density for density self-thinning.

How it works

The probability of mortality is calculated with a double Michaelis-Menton function:

$$P_m = \left(\frac{(A + (C \times diam_m)) \times density}{\frac{(A + (C \times diam_m))}{S} + density} \right)$$

where:

- P_m is the probability of mortality for an individual tree
- $density$ is the density of neighboring seedlings and saplings, in stems/ha, within a radius defined in the **Density Self-Thinning Neighborhood Radius, in m** parameter
- $diam_m$ is the mean diameter of neighbors, measured 10 cm above root collar in cm
- A is the **Density Self-Thinning Asymptote (A)** parameter
- C is the **Density Self-Thinning Diameter Effect (C)** parameter
- S is the **Density Self-Thinning Density Effect (S)** parameter

If the value of $density$ is less than the value in the **Density Self-Thinning Minimum Density for Mortality (#/ha)** parameter, the tree does not die.

How to apply it

This behavior can be applied to seedlings and saplings of any species. It cannot be applied to adults. **This behavior can only be applied with a one year timestep.**

Exponential Growth and Resource-Based Mortality

This behavior calculates probability of mortality as a function of growth and some second resource. The identity of the second resource is unimportant and could be anything, from exchangeable calcium levels to soil moisture.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Exponential Growth-Resource - a	The mortality at zero growth scaled as a function of the resource.
Exponential Growth-Resource - b	The light-dependent mortality parameter.
Exponential Growth-Resource - c	The resource-dependent mortality parameter.
Exponential Growth-Resource - d	Function term d.

How it works

The probability of mortality for a tree is calculated with the following equation:

$$Prob = (d + a * R) * \exp(- (b + c * R) * G)$$

where:

- *Prob* is the annual probability of mortality, as a value between 0 and 1
- *R* is the amount of the second resource
- *G* is the amount of radial growth, in mm/yr
- *a* is the **Exponential Growth-Resource - a** parameter - the mortality at zero growth scaled as a function of the resource *R*
- *b* is the **Exponential Growth-Resource - b** parameter - the light dependent mortality
- *c* is the **Exponential Growth-Resource - c** parameter - the resource dependent mortality
- *d* is the **Exponential Growth-Resource - d** parameter

The amount of the second resource is captured in a grid object called [Resource](#). Currently it is up to you to enter a map of the values for this resource grid; for instructions on how to do this, see the [Grid Setup Window](#) topic. This behavior does not in any way alter the values in this grid.

The mortality probability as calculated above is an annual probability. For multi-year timesteps, the timestep probability is $1 - (1 - AP)^X$, where AP is the annual probability and X is the number of years per timestep. Once a tree's timestep survival probability has been calculated, it is compared to a random number to determine whether the tree lives or dies.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [growth behavior](#) applied. You must also enter a map of second resource values into the [Resource](#) grid.

GMF mortality

GMF mortality is a growth-based mortality behavior.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Light-Dependent Mortality	Light-dependent mortality.
Mortality at Zero Growth	Mortality rate at zero growth.

How it works

The GMF mortality model evaluates the following function to determine the probability of a tree's mortality:

$$m = m_1 * e^{-m_2 G}$$

where:

- m is the probability of mortality
- m_1 is the **Mortality at Zero Growth** parameter, for mortality over 2.5 years (see Kobe et al 1995)
- m_2 is the **Light-Dependent Mortality** parameter, for mortality over 2.5 years (see Kobe et al 1995)

- G is amount of radial growth, in mm/yr, added to the tree's diameter this timestep

The GMF mortality equation is for a 5 year timestep. The mortality parameters are for a 2.5 year probability of mortality. To calculate the 5 year probability of mortality, SORTIE uses $p' = 1 - (1 - p)^2$. Once the probability of mortality is calculated for a tree, SORTIE generates a random number to which to compare it to determine whether the tree will live or die.

This model was originally described in [Kobe et al 1995](#).

How to apply it

The GMF mortality function assumes a timestep length of five years, so that must be your [timestep length](#) in order to use this behavior. This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [growth behavior](#) applied.

Gompertz Density Self Thinning Mortality

This behavior calculates the probability of mortality of an individual tree as a function of the density of conspecific neighborhood trees.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Gompertz Density Self Thinning - G	G in the function for probability of mortality.
Gompertz Density Self Thinning - H	H in the function for probability of mortality.
Gompertz Density Self Thinning - I	I in the function for probability of mortality.
Gompertz Density Self Thinning - Min Neighbor Height (m)	Minimum height for conspecific neighbors to be counted towards density.
Gompertz Density Self Thinning - Neighbor Search Radius (m)	Radius for which to search for conspecific neighbors.

How it works

The density of conspecific neighbors is the number of stems per square meter of trees above the height set in the **Conspecific Tree Minimum Neighbor Height (m)** parameter, within the radius from the target tree's location set in the **Conspecific Tree Search Radius (m)** parameter.

The probability of mortality is calculated as follows:

$$P_m = G * \exp(-\exp(H - I * Den))$$

where:

- P_m is the probability of mortality for an individual tree
- Den is the density of conspecific neighbor trees, stems/m²
- G is the **Gompertz Density Self Thinning - G** parameter
- H is the **Gompertz Density Self Thinning - H** parameter
- I is the **Gompertz Density Self Thinning - I** parameter

How to apply it

This behavior can be applied to trees of any species.

Growth and Resource-Based Mortality

This behavior calculates probability of survival as a function of growth and some second resource. The identity of the second resource is unimportant and could be anything, from exchangeable calcium levels to soil moisture.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Growth/Resource - Scaling Factor (rho)	Scaling factor to reduce survival at the mode of the survival probability function.
Growth/Resource - Function Mode (mu)	Determines the mode of the function along a gradient of the resource R (the mode is the optimal niche of a species).
Growth/Resource - Survival Increase with Growth (delta)	Specifies the increase in survival caused by amount of growth.
Growth/Resource -	Affects the shape of the survival probability distribution in low-growth

Low-Growth
Survival Parameter
(sigma)

conditions.

How it works

The probability of survival for a tree is calculated with the following equation:

$$Pr ob = \rho * e^{\left(\frac{-(R-\mu)^2}{2((\delta G)+\sigma)^2} \right)}$$

where:

- *Prob* is the annual probability of survival, as a value between 0 and 1
- *R* is the amount of the second resource
- *G* is the amount of radial growth, in mm/yr
- ρ is the **Growth/Resource - Scaling Factor (rho)** parameter, which is a scaling factor to reduce survival at the mode of the survival probability function
- μ is the **Growth/Resource - Function Mode (mu)** parameter, which determines the mode of the function along a gradient of the resource *R* (this corresponds to the optimal niche of a species, meaning where it is the top competitor, the absolute winner of competition)
- δ is the **Growth/Resource - Survival Increase with Growth (delta)** parameter, which specifies the increase in survival caused by amount of growth
- σ is the **Growth/Resource - Low-Growth Survival Parameter (sigma)** parameter, which affects the shape of the survival probability distribution in low-growth conditions

The amount of the second resource is captured in a grid object called [Resource](#). Currently it is up to you to enter a map of the values for this resource grid; for instructions on how to do this, see the [Grid Setup Window](#) topic. This behavior does not in any way alter the values in this grid.

The survival probability as calculated above is an annual probability. For multi-year timesteps, the timestep probability is AP^X , where *AP* is the annual probability and *X* is the number of years per timestep. Once a tree's timestep survival probability has been calculated, it is compared to a random number to determine whether the tree lives or dies.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. Any tree species/type combination to which it is applied must also have a [growth behavior](#) applied. You must also enter a map of second resource values into the [Resource](#) grid.

Height-GLI Weibull Mortality with Browse

This behavior calculates the probability of mortality using a Weibull function of tree height and GLI (light level). It can also simulate the effects of herbivory by using different parameters for browsed and unbrowsed trees.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Height-GLI Weibull - a	The "a" parameter in the Weibull function for calculating annual mortality.
Height-GLI Weibull - b	The "b" parameter in the Weibull function for calculating annual mortality.
Height-GLI Weibull - c	The "c" parameter in the Weibull function for calculating annual mortality.
Height-GLI Weibull - d	The "d" parameter in the Weibull function for calculating annual mortality.
Height-GLI Weibull - Max Mortality (0 - 1)	The maximum mortality probability for a species, expressed as a proportion between 0 and 1.
Height-GLI Weibull - Browsed a	The "a" parameter in the Weibull function for calculating annual mortality for a browsed tree.
Height-GLI Weibull - Browsed b	The "b" parameter in the Weibull function for calculating annual mortality for a browsed tree.
Height-GLI Weibull - Browsed c	The "c" parameter in the Weibull function for calculating annual mortality for a browsed tree.
Height-GLI Weibull - Browsed d	The "d" parameter in the Weibull function for calculating annual mortality for a browsed tree.
Height-GLI Weibull - Browsed Max Mortality (0 - 1)	The maximum mortality probability for a browsed tree, expressed as a proportion between 0 and 1.

How it works

The same function is used to calculate the probability of mortality for both browsed and unbrowsed trees, but the parameters are different. The function is:

$$p = M_{max} * \exp(-a * H^b - c * GLI^d)$$

where

- p - annual probability of mortality
- M_{max} - the **Height-GLI Weibull - Max Mortality (0 - 1)** or **Height-GLI Weibull - Browsed Max Mortality (0 - 1)** parameter
- a - the **Height-GLI Weibull - a** or **Height-GLI Weibull - Browsed a** parameter
- b - the **Height-GLI Weibull - b** or **Height-GLI Weibull - Browsed b** parameter
- c - the **Height-GLI Weibull - c** or **Height-GLI Weibull - Browsed c** parameter
- d - the **Height-GLI Weibull - d** or **Height-GLI Weibull - Browsed d** parameter
- H - tree height in meters
- GLI - light level, between 0 and 100% of full sun

If the timestep length is not one year, the actual probability of mortality for the timestep is calculated as $p' = 1 - (1 - p)^T$, where p is the annual probability of mortality, p' is the timestep probability of mortality, and T is the number of years per timestep. Once the mortality probability for the timestep is known for a tree, then a random number is compared to this probability to determine if the tree lives or dies.

Light levels can come from any of the [light behaviors](#) that directly assign a tree its light level. It is expected that this is a GLI value, from 0 to 100% of full sun.

Whether or not a tree is browsed is determined by the [Random browse](#) behavior. If the Random browse behavior does not apply to a tree, or is not present in the run, the unbrowsed parameters are always used. The other parameters can be ignored.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. You must also use a [light behavior](#). If you wish to include the effects of herbivory, also include the [Random browse](#) behavior in the run.

Insect Infestation Mortality

This behavior causes mortality in trees that are infested with insects, as determined by the [Insect Infestation](#) behavior.

Trees killed by this behavior will have a mortality reason code of "insect".

Parameters for this behavior

Parameter name	Description
Insect Mortality - Intercept	The mortality rate, between 0 and 1, at the first timestep of infestation.

Insect Mortality - Max Mortality Rate (0-1)	Maximum mortality rate, between 0 and 1.
Insect Mortality - X0	The time at which 0.5 of the maximum mortality rate occurs.
Insect Mortality - Xb	Parameter controlling the steepness of the rise of the mortality rate.

How it works

The mortality rate of trees as a function of time infested is as follows:

$$P = I + \frac{(Max - I)}{1 + \left(\frac{T}{X_0}\right)^{X_b}}$$

where:

- P is the mortality rate, between 0 and 1.
- I is the **Insect Mortality - Intercept** parameter, as a value between 0 and 1. This is the function intercept, or the mortality rate at the first timestep of infestation.
- Max is the **Insect Mortality - Max Mortality Rate (0-1)** parameter, as a value between 0 and 1. This is the maximum mortality rate that will occur regardless of how long a tree has been infested.
- T is the time, in years, that an individual has been infested.
- X_0 is the **Insect Mortality - X0** parameter. This is the time at which half of the maximum mortality rate is reached.
- X_b is the **Insect Mortality - Xb** parameter. This controls the steepness of the rise of the curve.

Once the mortality rate for an infested individual has been determined, a random number determines whether it will live or die.

The [Insect Infestation](#) behavior decides which trees become infested, and tracks the amount of time each individual has been infested.

How to apply it

Apply this behavior to saplings and/or adults of any species. Any tree to which this behavior is applied must also have the [Insect Infestation](#) behavior applied.

Logistic bi-level mortality

This behavior calculates the probability of survival according to a logistic equation, with the possibility of two sets of parameters for each species: one for high-light conditions and one for low-light conditions. This can also be used alone without the light levels.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Logistic Bi-Level - Low-Light "a"	The "a" parameter used in low-light conditions.
Logistic Bi-Level - Low-Light "b"	The "b" parameter used in low-light conditions.
Logistic Bi-Level - High-Light "a"	The "a" parameter used in high-light conditions.
Logistic Bi-Level - High-Light "b"	The "b" parameter used in high-light conditions.
Logistic Bi-Level - High-Light Mortality Threshold (0-100)	The threshold between low-light and high-light parameters, as a value between 0 and 100.

How it works

The equation used by this behavior to calculate survival probability is:

$$p = \frac{\exp(a + b * D)}{1 + \exp(a + b * D)}$$

where

- p - annual probability of survival
- a - in high-light conditions, this is the **Logistic Bi-Level - High-Light "a"** parameter; in low-light conditions, this is the **Logistic Bi-Level - Low-Light "a"** parameter
- b - in high-light conditions, this is the **Logistic Bi-Level - High-Light "b"** parameter; in low-light conditions, this is the **Logistic Bi-Level - Low-Light "b"** parameter
- D - tree diam, in cm; $diam_{10}$ for seedlings, DBH for others

If the timestep length is not one year, the actual probability of survival for the timestep is calculated as $p' = p^T$, where p is the annual probability of survival, p' is the timestep probability

of survival, and T is the number of years per timestep. Once the survival probability for the timestep is known for a tree, then a random number is compared to this probability to determine if the tree lives or dies.

Light levels come from the [Storm Light](#) grid produced by the [Storm Light](#) behavior. The threshold between the use of high-light and low-light parameters is set in the **Logistic Bi-Level - High-Light Mortality Threshold (0-100)** parameter.

This behavior can also be used without Storm Light. In this case, only the low-light mortality parameters are used.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. If you wish to use the light-level parameter switch, also use the [Storm Light](#) behavior.

NCI mortality

This behavior features a maximum survival rate that is adjusted using a set of factors of your choice. You can choose any combination you wish. In particular, this has several ways to implement the effects of neighbor competitiveness to influence survival rates ("NCI" stands for neighborhood competition index).

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
NCI Max Survival Probability (0-1)	The maximum probability of survival, as a value between 0 and 1.
NCI Parameter Period (years)	If your parameters are for a period other than one year, the length of time (in years) of that period.

How it works

For a tree, the annual probability of survival is the maximum survival probability times any of a possible set of factors affecting survival:

$$\text{Prob. Survival} = \text{Max Survival} * [\text{Size Effects}] * [\text{Shading Effects}] * [\text{Crowding Effects}] * [\text{Damage Effects}] * [\text{Precipitation Effects}] * [\text{Temperature Effects}] * [\text{Nitrogen Effects}] * [\text{Infection Effects}]$$

Max Survival is the **NCI Max Survival Probability (0-1)** parameter. You can have an effect in each category (or none at all) which acts to reduce the maximum survival rate. Each of these effects is a value between 0 and 1.

Parameters are not always analyzed on an annual basis. If this is the case, use the **NCI Parameter Period (years)** parameter to specify the length of time in years that your parameters are based on. This behavior will adjust each tree's survival probability to an appropriate timestep length.

Effects choices:

- [Size effects](#)
- [Shading effects](#)
- [Crowding effects](#)
- [Precipitation effects](#)
- [Temperature effects](#)
- [Nitrogen effects](#)
- [Infection effects](#)

The survival probability as calculated above is an annual probability. For multi-year timesteps, the timestep probability is AP^X , where AP is the annual probability and X is the number of years per timestep. Once a tree's timestep survival probability has been calculated, it is compared to a random number to determine whether the tree lives or dies.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. (Some effects have limitations on application to juveniles - check individual effects documentation.)

Post Harvest Skidding Mortality

This mortality behavior simulates an increase in mortality after harvesting attributable to skidding damage or other effects. The increase in mortality tapers off through time. DBH and neighborhood basal area can also affect mortality in this behavior.

Model forms are based on those in Thorpe et al. 2010.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Post Harvest Skid	Maximum distance, in m, for neighbors to have a competitive effect.

Mort - Crowding Effect Radius	
Post Harvest Skid Mort - Pre-Harvest Background Mort Rate	Annual mortality rate, 0-1, if no harvest has occurred this run.
Post Harvest Skid Mort - Snag Recruitment Background Prob	Annual postharvest risk of standing death after harvest effects have completely tapered off.
Post Harvest Skid Mort - Snag Recruitment Basic Prob	Basic probability of standing death after harvest.
Post Harvest Skid Mort - Snag Recruitment Crowding Effect	The effect of neighborhood basal area on standing death probability.
Post Harvest Skid Mort - Snag Recruitment Rate Param	Determines how quickly the effects of harvesting on standing death probability taper off.
Post Harvest Skid Mort - Snag Recruitment Skidding Effect	Effect of harvest intensity on postharvest probability of standing death.
Post Harvest Skid Mort - Windthrow Background Prob	Annual postharvest risk of windthrow after harvest effects have completely tapered off.
Post Harvest Skid Mort - Windthrow Crowding Effect	The effect of neighborhood basal area on windthrow probability.
Post Harvest Skid Mort - Windthrow Harvest Basic Prob	Basic annual probability for windthrow after a harvest.

Post Harvest Skid Mort - Windthrow Harvest Rate Param	Determines how quickly the effects of harvesting on windthrow probability taper off.
Post Harvest Skid Mort - Windthrow Intensity Effect	Intensity effect parameter used for determining risk of windthrow.
Post Harvest Skid Mort - Windthrow Size Effect	Size effect term when determining risk of windthrow.

How it works

If no harvest has occurred yet in this run, the probability of dying in a timestep is:

$$Prob = 1 - (1 - \beta)^t$$

where:

- *Prob* is the probability of dying before the end of the timestep
- β is the **Post Harvest Skid Mort - Pre-Harvest Background Mort Rate** parameter
- *t* is the number of years per timestep

If a harvest has occurred in the tree's cell during the run, the probability of mortality is:

$$Prob = 1 - \prod_{i=1}^t (1 - W_i - S_i)$$

multiplying over years $i = 1 \dots t$ (number of years per timestep);

$$W_i = (\rho_w + \delta_w * DBH + \kappa_w * m - \eta_w * BA) * \exp(-\tau_w * (H * t + i)) + \omega$$

where:

- W_i is the annual post-harvest risk of windthrow
- ρ_w is the **Post Harvest Skid Mort - Windthrow Harvest Basic Prob** parameter
- δ_w is the **Post Harvest Skid Mort - Windthrow Size Effect** parameter
- *DBH* is the tree's DBH in cm
- κ_w is the **Post Harvest Skid Mort - Windthrow Intensity Effect** parameter
- *m* is the harvest intensity from the tree's "HarvInten" data member, from the HARP external harvesting program (available for download from the SORTIE web site)
- η_w is the **Post Harvest Skid Mort - Windthrow Crowding Effect** parameter

- BA is the neighborhood basal area, in sq m per ha, within a radius set by the **Post Harvest Skid Mort - Crowding Effect Radius** parameter
- τ_w is the **Post Harvest Skid Mort - Windthrow Harvest Rate Param** parameter
- H is the number of timesteps since the last harvest in this tree's grid cell
- t is the number of years per timestep
- ω is the **Post Harvest Skid Mort - Windthrow Background Prob** parameter

and

$$S_i = (\rho_s + \kappa_s * m + \varphi_s * BA) * \exp(-\tau_s * (H * t + i)) + \zeta$$

where:

- S_i is the annual postharvest risk of standing death
- ρ_s is the **Post Harvest Skid Mort - Snag Recruitment Basic Prob** parameter
- κ_s is the **Post Harvest Skid Mort - Snag Recruitment Skidding Effect** parameter
- m is the harvest intensity from the tree's "HarvInten" data member, from the HARP external harvesting program (available for download from the SORTIE web site)
- φ_s is the **Post Harvest Skid Mort - Snag Recruitment Crowding Effect** parameter
- BA is the neighborhood basal area, in sq m per ha, within a radius set by the **Post Harvest Skid Mort - Crowding Effect Radius** parameter
- τ_s is the **Post Harvest Skid Mort - Snag Recruitment Rate Param** parameter
- H is the number of timesteps since the last harvest in this tree's grid cell
- t is the number of years per timestep
- ζ is the **Post Harvest Skid Mort - Snag Recruitment Background Prob** parameter

How to apply it

This behavior can be applied to saplings and adults of any species. In order for the harvest intensity term to have an effect, the float data member "HarvInten" must be registered for all species/type combos to which this behavior is applied, by using the HARP external harvesting program along with the [Harvest Interface](#).

Self thinning

Self-thinning is a behavior that uses a pseudo-density dependent function designed to increase the death rate in dense uniform-age stands. You specify a maximum DBH at which to apply it - above this DBH a tree will not die.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
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Self-Thinning Intercept	Intercept of the self-thinning linear function.
Self-Thinning Slope	Slope of the self-thinning linear function.
Maximum DBH for Self-Thinning	Maximum DBH at which self-thinning applies. Above this value, no mortality occurs.

How it works

Self-thinning uses a simple linear function of probability of mortality as a function of DBH, assuming the tree is below the maximum DBH at which to apply self-thinning. After evaluating this function for a tree, it uses a random number to determine whether the tree dies.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species.

Senescence

Senescence mortality provides for an uptick in mortality rates. It is meant to slightly increase the death rate among large adult trees.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Senescence Mortality Alpha	Controls the senescence mortality rate.
Senescence Mortality Beta	Controls the senescence mortality rate.
DBH at Onset of Senescence, in cm	DBH at which senescence takes effect.
DBH of Maximum Senescence Mortality Rate, as an integer in cm	The DBH at which maximum mortality occurs. Trees with a DBH greater than this value experience no further increase in the mortality rate.

How it works

All trees to which senescence is applied are evaluated for senescence mortality. In practice, trees below the onset of senescence DBH very rarely die. The probability of death rises with DBH until the DBH of maximum senescence rate is reached, at which point it levels off.

To assess whether a tree will die due to senescence, the following function is evaluated:

$$m_s = \frac{e^{(\alpha + \beta(DBH - DBH_s))}}{1 + e^{(\alpha + \beta(DBH - DBH_s))}}$$

where:

- m_s is the probability of mortality
- α (**Senescence Mortality Alpha** parameter) and β (**Senescence Mortality Beta** parameter) control the magnitude of the uptick
- DBH is the tree's DBH, in cm
- DBH_s is the **DBH at Onset of Senescence, in cm** parameter

The probability is compared to a random number to determine whether the individual tree will die.

How to apply it

Senescence may be applied to saplings and adults of any species. It cannot be applied to seedlings.

Size Dependent Logistic Mortality

Size Dependent Logistic Mortality applies a mortality function that is a logistic function of tree size. Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Max Mortality (0-1)	Maximum mortality rate, as a value between 0 and 1.
X0	Logistic function X_0 parameter.
Xb	Logistic function X_b parameter.

How it works

For each tree to which this behavior is applied, the following function is evaluated:



where:

- p is the probability of mortality
- X_0 is the **X0** parameter, representing the inflection point of the curve
- X_b is the **Xb** parameter
- *diam* is d_{10} for seedlings, and DBH for all other trees, in cm

The probability is compared to a random number to determine whether the individual tree will die.

How to apply it

This behavior may be applied to seedlings, saplings, and adults of any species.

Stochastic Bi-Level Mortality

This behavior applies a constant rate of mortality to trees, with different rates for high-light and low-light conditions. There are two versions, designed to work with different behaviors that calculate light levels (Stochastic Bi-Level Mortality - Storm Light and Stochastic bi-level mortality - GLI)

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Stochastic Bi-Level - High-Light Mortality Probability (0-1)	The annual probability of mortality under high-light conditions, as a proportion between 0 and 1.
Stochastic Bi-Level - High-Light Mortality Threshold	The threshold between low-light and high-light mortality rates, as a value between 0 and 100.
Stochastic Bi-Level - Low-Light Mortality Probability (0-1)	The annual probability of mortality under low-light conditions, as a proportion between 0 and 1.

How it works

In the version of the behavior called Stochastic Bi-Level Mortality - Storm Light, light levels come from the [Storm Light](#) grid produced by the [Storm Light](#) behavior. In the version called Stochastic Bi-Level Mortality - GLI, light levels come from any [light behavior](#) that can be applied directly to trees.

The threshold between the use of high-light and low-light parameters is set in the **Stochastic Bi-Level - High-Light Mortality Threshold** parameter. The units depend on which index of light is being used. Check the documentation on your chosen light behavior carefully.

For each tree, a random number is compared to that species's probability of mortality to determine if it dies. If light levels qualify as high light, the probability of mortality is the value in the **Stochastic Bi-Level - High-Light Mortality Probability (0-1)** parameter; if the light levels are low, the probability of mortality is the value in the **Stochastic Bi-Level - Low-Light Mortality Probability (0-1)** parameter.

If the timestep length is not one year, the probability of mortality is adjusted from an annual mortality probability to a timestep probability.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. If you have chosen the version marked "Storm Light", you must also use the [Storm Light](#) behavior. If you have chosen the version marked "GLI", you must assign a [light behavior](#) to all trees to which you assign this mortality.

Stochastic Bi-Level Mortality

This behavior applies a constant rate of mortality to trees, with different rates for high-light and low-light conditions. There are two versions, designed to work with different behaviors that calculate light levels (Stochastic Bi-Level Mortality - Storm Light and Stochastic bi-level mortality - GLI)

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Stochastic Bi-Level - High-Light Mortality Probability (0-1)	The annual probability of mortality under high-light conditions, as a proportion between 0 and 1.
Stochastic Bi-Level - High-Light Mortality Threshold	The threshold between low-light and high-light mortality rates, as a value between 0 and 100.

Stochastic Bi-Level -
Low-Light Mortality
Probability (0-1)

The annual probability of mortality under low-light conditions, as a proportion between 0 and 1.

How it works

In the version of the behavior called Stochastic Bi-Level Mortality - Storm Light, light levels come from the [Storm Light](#) grid produced by the [Storm Light](#) behavior. In the version called Stochastic Bi-Level Mortality - GLI, light levels come from any [light behavior](#) that can be applied directly to trees.

The threshold between the use of high-light and low-light parameters is set in the **Stochastic Bi-Level - High-Light Mortality Threshold** parameter. The units depend on which index of light is being used. Check the documentation on your chosen light behavior carefully.

For each tree, a random number is compared to that species's probability of mortality to determine if it dies. If light levels qualify as high light, the probability of mortality is the value in the **Stochastic Bi-Level - High-Light Mortality Probability (0-1)** parameter; if the light levels are low, the probability of mortality is the value in the **Stochastic Bi-Level - Low-Light Mortality Probability (0-1)** parameter.

If the timestep length is not one year, the probability of mortality is adjusted from an annual mortality probability to a timestep probability.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. If you have chosen the version marked "Storm Light", you must also use the [Storm Light](#) behavior. If you have chosen the version marked "GLI", you must assign a [light behavior](#) to all trees to which you assign this mortality.

Stochastic mortality

This behavior produces a background mortality rate. Individuals within the pool of trees to which this behavior applies are randomly selected to die.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Background	The proportion of trees that die each year, as a value between 0 and 1.

Mortality Rate

How it works

For each tree, a random number is compared to that species's **Background Mortality Rate** parameter to determine if it falls in the pool of trees that die.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species.

Suppression Duration Mortality

This behavior evaluates mortality as a function of tree age. This is particularly useful for simulating suppression in seedlings.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Suppression Duration Mortality - Max Mortality Rate (0-1)	The maximum mortality rate for suppressed trees.
Suppression Duration Mortality - X0	X0 in the suppression mortality function. This is the age at which half of the maximum mortality rate is reached.
Suppression Duration Mortality - Xb	Xb in the suppression mortality function.

How it works

A tree's probability of mortality is:

$$p = \frac{Max}{1 + \left(\frac{Age}{X_0}\right)^{X_b}}$$

where:

- p is the probability of mortality
- Max is the **Suppression Duration Mortality - Max Mortality Rate (0-1)** parameter
- X_0 is the **Suppression Duration Mortality - X0** parameter
- X_b is the **Suppression Duration Mortality - Xb** parameter
- Age is the tree's age, in years

The value for X_0 is the age at which half of the maximum mortality rate is reached. Tree age is tracked using the [Tree Age Calculator](#) behavior. Initial conditions trees get a mortality of zero because their age is unreliable.

How to apply it

This behavior can be applied to trees of any species. Trees must also have the [Tree Age Calculator](#) behavior applied.

Temperature dependent neighborhood survival

This behavior assesses tree survival as a function of mean annual temperature and neighbor adult basal area. For efficiency, it calculates survival rates for cells in a grid and assigns trees the survival probability of the grid cell in which they are found.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Temp Dependent Neighborhood Surv - A	A in the survival function.
Temp Dependent Neighborhood Surv - B	B in the survival function.
Temp Dependent Neighborhood Surv - M	M in the survival function.
Temp Dependent Neighborhood Surv - N	N in the survival function.

N	
Temp Dependent Neighborhood Surv - Neigh Search Radius (m)	Maximum radius to search for crowding neighbors, in meters.

How it works

This behavior uses the [Temperature Dependent Neighborhood Survival](#) grid to keep track of survival rates. The annual probability of survival for a given species and given grid cell is calculated as:

$$Surv = e^{-A*BAT^B} * e^{-0.5\left[\frac{T-M}{N}\right]^2}$$

where:

- *Surv* is the annual probability of survival
- *A* is the **Temp Dependent Neighborhood Surv - A** parameter
- *B* is the **Temp Dependent Neighborhood Surv - B** parameter
- *M* is the **Temp Dependent Neighborhood Surv - M** parameter
- *N* is the **Temp Dependent Neighborhood Surv - N** parameter
- *T* is the mean annual temperature in degrees Celsius as entered in the [Plot](#)
- *BAT* is the adult total basal area in the neighborhood, in square meters

BAT is the basal area of all adults within the distance from the center of the grid cell set in the **Temp Dependent Neighborhood Surv - Neigh Search Radius (m)** parameter.

The probability of survival is for a single year. For multi-year timesteps, the timestep survival probability is the annual probability raised to the power of the number of years per timestep.

Trees receive the survival probability calculated for the grid cell in which they are found. A random number is used to determine whether a tree lives or dies.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species.

Weibull snag mortality behavior

This behavior controls [snag](#) fall. Snags are standing dead trees. Obviously, they can't die again, so the word "mortality" is a bit of a misnomer. We call the behavior a mortality behavior because it functionally fits in this behavior class.

Snags that are "killed" by this behavior are considered to have fallen over. If [Substrate behaviors](#) are enabled, then these fallen trees are available to become new fresh log substrate. Any that are not picked up by substrate will be dealt with by the [Dead tree remover](#) behavior.

Trees killed by this behavior will have a mortality reason code of "natural".

Parameters for this behavior

Parameter name	Description
Weibull Annual "a" Parameter for Snag Size Class 1 Mortality	Weibull annual "a" parameter for those trees whose DBH is less than or equal to the value in "Upper DBH of snag size class 1".
Weibull Annual "a" Parameter for Snag Size Class 2 Mortality	Weibull annual "a" parameter for those trees whose DBH is greater than the value in "Upper DBH of snag size class 1" but less than or equal to the value in "Upper DBH of snag size class 2".
Weibull Annual "a" Parameter for Snag Size Class 3 Mortality	Weibull annual "a" parameter for those trees whose DBH is greater than the value in "Upper DBH of snag size class 2".
Weibull Annual "b" Parameter for Snag Size Class 1 Mortality	Weibull annual "b" parameter for those trees whose DBH is less than or equal to the value in "Upper DBH of snag size class 1".
Weibull Annual "b" Parameter for Snag Size Class 2 Mortality	Weibull annual "b" parameter for those trees whose DBH is greater than the value in "Upper DBH of snag size class 1" but less than or equal to the value in "Upper DBH of snag size class 2".
Weibull Annual "b" Parameter for Snag Size Class 3 Mortality	Weibull annual "b" parameter for those trees whose DBH is greater than the value in "Upper DBH of snag size class 2".
Weibull Upper DBH of Snag Size Class 1	The upper DBH value of trees in size class 1.
Weibull Upper DBH of Snag Size Class 2	The upper DBH value of trees in size class 2. Trees with a value greater than this are considered to be in size class 3.

How it works

The behavior uses a Weibull function to determine the number of snags of a certain age left standing at a given time. The equation is:

$$S = e^{-(a \cdot T)^b}$$

where:

- S is proportion of snags still standing, between 0 and 1
- a and b are Weibull parameters (**Weibull Annual "a" Parameter for Snag Size Class X Mortality parameter** and **Weibull Annual "b" Parameter for Snag Size Class X Mortality parameter**)
- T is the snag age in years

Different sizes of snags fall at different rates. This behavior allows you to define three snag size classes and enter different "a" and "b" parameters for each.

A random number is used against this equation for a given tree to determine if it falls in the current timestep.

How to apply it

This behavior can be applied to snags of any species.

Substrate behaviors

Substrate is what seedlings germinate in - soil, rock, and the organic layers on top. The quality of the substrate can make a big difference in a seedling's ability to survive and establish. The substrate composition in any one place is constantly shifting and changing as new substrate is added to the forest floor and as existing substrate decays. These behaviors keep track of the substrate conditions at different locations through time.

Behavior	Description
Substrate behavior	Keeps track of six kinds of substrate: forest floor litter, forest floor moss, scarified soil, tip-up mounds, decayed logs, and fresh logs.
Detailed Substrate behavior	This behavior is a modification of the Substrate behavior that primarily incorporates greater detail in tracking log cover.

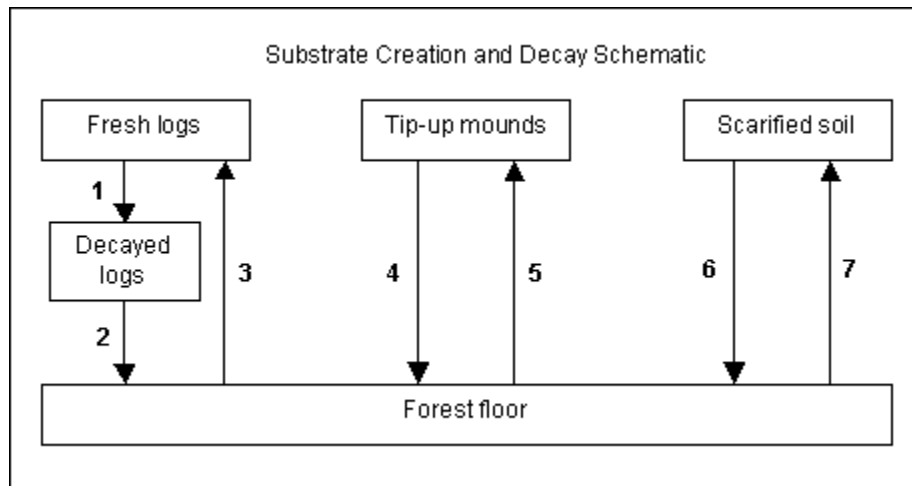
Substrate

This behavior keeps track of six kinds of substrate: forest floor litter, forest floor moss, scarified soil, tip-up mounds, decayed logs, and fresh logs. Forest floor litter and forest floor moss form a common pool in fixed relative proportion to each other. These six substrates form a cycle. Fresh logs decay into decayed logs. Decayed logs, scarified soil, and tip-up mounds decay into forest floor litter and moss. (If no new substrate were created, eventually the whole forest would be uniformly covered in forest floor substrate.) The creation of new substrate decreases the amount of forest floor litter and moss and starts the process over again.

There are two ways in which new substrate is added: harvest treatments and tree fall. Each kind of harvest treatment (partial cut, gap cut, and clear cut) has its own substrate signature, which you set in the parameters. The existing substrate proportions after a harvest are erased and replaced with this signature.

The other type of substrate change event, tree fall, allows SORTIE to account for small-scale dynamics by allowing some dead trees to fall and create tip-up mounds. When a live tree dies, there is a certain probability that the tree will fall at death to create new fresh log substrate. Snags marked as "dead" always contribute new fresh log substrate. For both dead snags and live trees, there is a certain probability that the tree will expose an area of tip-up mounds substrate. Any new substrate created this way is added in to the existing substrate, but does not completely replace it like harvest does.

Substrate relationships

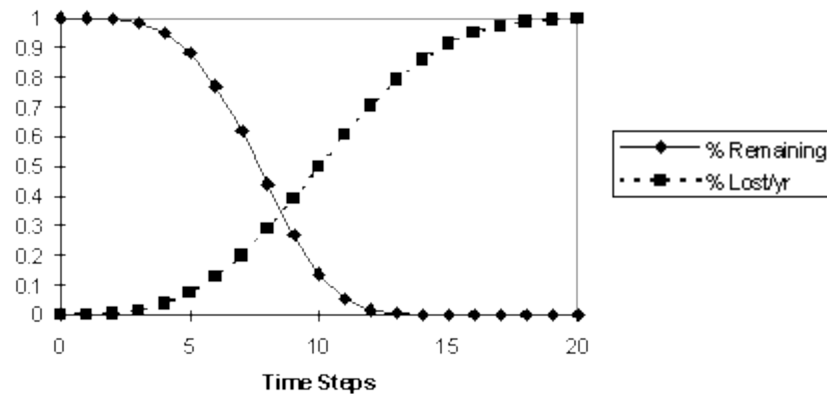


Relationships 1, 2, 4, and 6 represent the decay of the different substrates as a function of substrate age according to the equation

$$y = e^{\alpha * t^{\beta}}$$

where t is time in years. Graphed, this equation looks like this:

Hypothetical Substrate Loss Function



In this diagram, there are two kinds of substrate, A and B. A decays into B according to the equation above. The amount of A and B together sum to 1 for this diagram. The curve for "% Remaining" is the amount of A. The curve for "% Lost/yr" is the amount of B. When $\beta > 1$, the rate of loss/time step increases over time (giving an initial lag period when there is little loss of the substrate). When $\beta < 1$ the substrate disappears most rapidly immediately after substrate creation (less likely). $\beta = 1$ gives a constant % loss per time step (i.e. exponential decline). (In this example, $\alpha = 0.0002$ and $\beta = 4$.)

Relationship 3 governs the amount of fresh logs created each time step as a result of tree mortality. For the purposes of adding new substrate, fallen logs are assumed to be cone-shaped. Since they land on their sides, the area of the cone is approximated to a triangle. Thus, each new fresh log contributes the following amount of new fresh log area:

$$FL = (DBH * h)/2$$

where:

- FL is new fresh log area, in square meters
- DBH is the DBH of the fallen tree, in m
- h is the height of the fallen tree, in m

A dead adult or sapling as a certain probability of contributing fresh log substrate; this probability is specified in the **Proportion of Dead that Fall** parameter. Snags always add fresh log substrate upon their "death".

How new fresh log area is distributed depends on the value in the **Use Directional Tree Fall** parameter. If false, a dead tree contributes all of its fresh log area into the grid cell where it was rooted. In other words, it doesn't fall over so much as vertically collapse. If true, a trees is allowed to fall in a random direction. The amount of new fresh log area is distributed over the grid cells that the log overlays.

Relationship 5 governs the amount of newly exposed tip-up mounds created by fallen dead trees. For each fallen tree, the amount of new tip-up mounds area is calculated as

$$OA = \pi * (r * F)^2$$

where

- OA is the new tip-up mounds area in square meters
- r is the tree trunk radius in meters
- F is the **Uprooted Tree Radius Increase Factor for Root Rip-Out** parameter, which accounts for the effects of root disturbance

A tree contributes all of its new tip-up mounds area to the grid cell where it was rooted. Saplings never create tip-up mounds. Fallen adults create new tip-ups with the probability specified in the **Proportion of Fallen that Uproot** parameter; snags contribute at the probability in **Proportion of Fallen that Uproot**.

Relationship 7 results from harvests only. Scarified soil creation results from the use of machinery and skidding during a harvest.

Parameters for this behavior

Parameter name	Description
Clear Cut Proportion of Decayed Logs	The proportion of substrate that is decayed logs in areas that had a clear cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Clear Cut Proportion of Fresh Logs	The proportion of substrate that is fresh logs in areas that had a clear cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Clear Cut Proportion of Scarified Soil	The proportion of substrate that is scarified soil in areas that had a clear cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Clear Cut Proportion of Tip-Up Mounds	The proportion of substrate that is tip-up mounds substrate in areas that had a clear cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Decayed Log Annual Decay Alpha	The α exponent in the decay equation $y = e^{\alpha * t^\beta}$, as applied to decayed logs. Note that this is annual decay.
Decayed Log Annual Decay Beta	The β exponent in the decay equation $y = e^{\alpha * t^\beta}$, as applied to decayed

	logs. Note that this is annual decay.
Fresh Log Annual Decay Alpha	The α exponent in the decay equation $y = e^{\alpha * t^\beta}$, as applied to fresh logs. Note that this is annual decay.
Fresh Log Annual Decay Beta	The β exponent in the decay equation $y = e^{\alpha * t^\beta}$, as applied to fresh logs. Note that this is annual decay.
Gap Cut Proportion of Decayed Logs	The proportion of substrate that is decayed logs in areas that had a gap cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Gap Cut Proportion of Fresh Logs	The proportion of substrate that is fresh logs in areas that had a gap cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Gap Cut Proportion of Scarified Soil	The proportion of substrate that is scarified soil in areas that had a gap cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Gap Cut Proportion of Tip-Up Mounds	The proportion of substrate that is tip-up mounds substrate in areas that had a gap cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Clear Cut Proportion of Scarified Soil	The proportion of substrate that is scarified soil in areas that had a clear cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Clear Cut Proportion of Tip-Up Mounds	The proportion of substrate that is tip-up mounds substrate in areas that had a clear cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Decayed Log Annual Decay Alpha	The α exponent in the decay equation $y = e^{\alpha * t^\beta}$, as applied to decayed logs. Note that this is annual decay.
Decayed Log Annual Decay Beta	The β exponent in the decay equation $y = e^{\alpha * t^\beta}$, as applied to decayed logs. Note that this is annual decay.
Fresh Log Annual Decay Alpha	The α exponent in the decay equation $y = e^{\alpha * t^\beta}$, as applied to fresh logs. Note that this is annual decay.
Fresh Log Annual Decay Beta	The β exponent in the decay equation $y = e^{\alpha * t^\beta}$, as applied to fresh logs. Note that this is annual decay.

Gap Cut Proportion of Decayed Logs	The proportion of substrate that is decayed logs in areas that had a gap cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Gap Cut Proportion of Fresh Logs	The proportion of substrate that is fresh logs in areas that had a gap cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Gap Cut Proportion of Scarified Soil	The proportion of substrate that is scarified soil in areas that had a gap cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Gap Cut Proportion of Tip-Up Mounds	The proportion of substrate that is tip-up mounds substrate in areas that had a gap cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Initial Conditions Proportion of Decayed Logs	The proportion of plot substrate that is decayed logs when the run starts, as a value between 0 and 1. If a map of substrate values is included in the parameter file (see Grid initial conditions for information on how to do this), then the map values will be used for the initial conditions and this number will be ignored.
Initial Conditions Proportion of Fresh Logs	The proportion of plot substrate that is fresh logs when the run starts, as a value between 0 and 1. If a map of substrate values is included in the parameter file (see Grid initial conditions for information on how to do this), then the map values will be used for the initial conditions and this number will be ignored.
Initial Conditions Proportion of Scarified Soil	The proportion of plot substrate that is scarified soil when the run starts, as a value between 0 and 1. If a map of substrate values is included in the parameter file (see Grid initial conditions for information on how to do this), then the map values will be used for the initial conditions and this number will be ignored.
Initial Conditions Proportion of Tip-Up Mounds	The proportion of plot substrate that is tip-up mounds substrate when the run starts, as a value between 0 and 1. If a map of substrate values is included in the parameter file (see Grid initial conditions for information on how to do this), then the map values will be used for the initial conditions and this number will be ignored.
Maximum Number of Years that Decay Occurs	The number of years that a substrate disturbance event has effect before it is deleted - the lifetime of a substrate cohort.
Partial Cut Proportion of Decayed Logs	The proportion of substrate that is decayed logs in areas that had a partial cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.

Partial Cut Proportion of Fresh Logs	The proportion of substrate that is fresh logs in areas that had a partial cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Partial Cut Proportion of Scarified Soil	The proportion of substrate that is scarified soil in areas that had a partial cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Partial Cut Proportion of Tip-Up Mounds	The proportion of substrate that is tip-up mounds substrate in areas that had a partial cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Partial Cut Proportion of Scarified Soil	The proportion of substrate that is scarified soil in areas that had a partial cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Partial Cut Proportion of Tip-Up Mounds	The proportion of substrate that is tip-up mounds substrate in areas that had a partial cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Proportion of Dead that Fall	The proportion of the total number of newly dead trees that fall each year, as a value between 0 and 1. This does not apply to snags.
Proportion of Fallen that Uproot	The proportion of fallen trees that uproot to create new tip-up mound substrate, as a value between 0 and 1.
Proportion of Forest Floor Litter/Moss Pool that is Moss	The fixed proportion of the forest floor litter/moss pool that is moss. Expressed as a value between 0 and 1.
Proportion of Snags that Uproot	The proportion of "dead" snags that uproot to create new tip-up mound substrate, as a value between 0 and 1. Not required if snags are not used in the run.
Proportion of Fallen that Uproot	The proportion of fallen trees that uproot to create new tip-up mound substrate, as a value between 0 and 1.
Proportion of Forest Floor Litter/Moss Pool that is Moss	The fixed proportion of the forest floor litter/moss pool that is moss. Expressed as a value between 0 and 1.
Proportion of Snags that Uproot	The proportion of "dead" snags that uproot to create new tip-up mound substrate, as a value between 0 and 1. Not required if snags are not used in the run.
Scarified Soil Annual Decay Alpha	The α exponent in the decay equation $y = e^{-\alpha * t^\beta}$, as applied to scarified soil. Note that this is annual decay.

Scarified Soil Annual Decay Beta	The β exponent in the decay equation $y = e^{-\alpha * t^\beta}$, as applied to scarified soil. Note that this is annual decay.
Tip-Up Mounds Annual Decay Alpha	The α exponent in the decay equation $y = e^{-\alpha * t^\beta}$, as applied to tip-up mounds substrate. Note that this is annual decay.
Tip-Up Mounds Annual Decay Beta	The β exponent in the decay equation $y = e^{-\alpha * t^\beta}$, as applied to tip-up mounds substrate. Note that this is annual decay.
Uprooted Tree Radius Increase Factor for Root Rip- Out	The amount by which to multiply the tree's radius when calculating the size of the new tip-up mounds soil exposed by fallen trees (see equation below). This is meant to allow for the effects of roots.
Use Directional Tree Fall	If true, dead trees fall in a random direction and possibly contribute new fresh log across several Substrate grid cells. If false, dead trees collapse vertically and contribute all their fresh log area to the cell in which they are rooted.

How it works

The relative proportions of each kind of substrate are tracked in the [Substrate grid](#). You can change this grid's cell resolution. Within each cell, the grid keeps track of each substrate's area as a proportion of the total area.

Each timestep, Substrate looks for harvest events and tree death. It finds harvest events by looking in the [Harvest grid](#); it finds dead trees by looking for the flag set by the [Mortality behaviors](#). Harvest events completely replace existing substrate with their substrate signatures. Each dead tree "rolls the dice" with a random number to determine if it falls, and, if it falls, if it exposes tip-up mounds substrate. All the new substrate created by harvest and tree fall is then totaled up.

When there is new substrate in a grid cell, Substrate reduces the other substrate amounts in the cell to make way for the amount of new substrate. Then Substrate creates a record of the substrate change, called a "cohort." The substrates in a cohort decay as the cohort ages. Cohorts have a set lifetime of a certain number of years, which you set in the parameters. After this they are deleted. This means that the effects of a substrate change event linger, with decreasing intensity, for a number of years after the event occurs.

The final proportions of scarified soil, tip-up mounds, and fresh logs are found by adding up the decayed values in the cohorts. The final proportion of decayed logs is found by adding up the amount by which fresh logs have decayed in each cohort. The final proportion of the moss/litter

pool is whatever grid cell area is left over. The pool is further split into moss and litter by using the fixed proportion of each in the pool.

How to apply it

Apply Substrate to all trees which can create substrate by becoming fallen logs. This generally means that it should be applied to saplings and adults of all species. Substrate cannot be applied to seedlings. Any tree species/type combination to which it is applied must also have a [mortality behavior](#) applied.

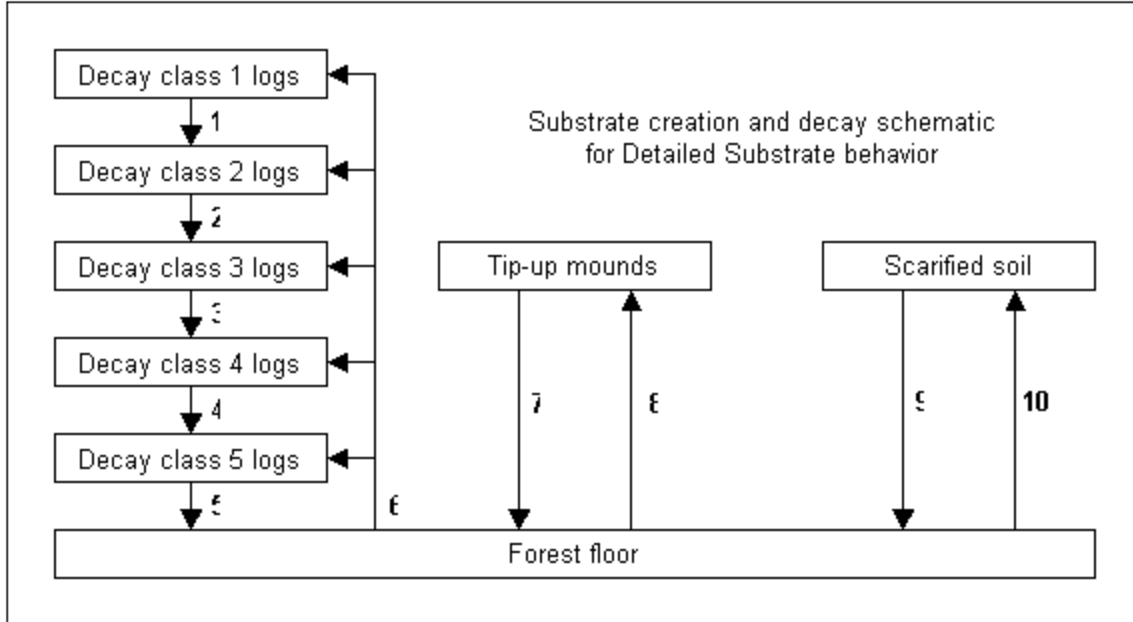
Detailed Substrate

This behavior is a modification of the Substrate behavior that primarily incorporates greater detail in tracking log cover. In Detailed Substrate, the pool for logs is divided into up to 3 species groups, 2 size classes, and 5 decay classes, whereas the Substrate behavior has 1 species/size class and 2 decay classes for logs. Also, unlike Substrate, Detailed Substrate is designed to work with [snag dynamics](#) behaviors that assign data members representing fall or break heights of trees and snags. This way, the processes of tree (and snag) breakage and fall are separated from their input into the log substrate pool. There is also a change from Substrate to the way harvesting adds new substrate, and values for log volume are calculated in addition to projected area (cover).

Like Substrate, Detailed Substrate keeps track of the relative cover of forest floor litter, moss, scarified soil, tip-up mounds, and logs each timestep. Unless explained otherwise, the manner in which Detailed Substrate calculates and tracks these components is the same as for the Substrate behavior.

Detailed Substrate divides logs into species groups, size classes, and decay classes. Logs in each combination of species group, size class, and decay class can have different initial proportions, proportions after harvest, and decay parameters from all other types of logs. Each species to which this behavior is assigned belongs to one species group (assigned with the **Species Group** parameter). As saplings, adults, and snags enter the substrate pool, they are added to the logs for the appropriate species group. Log substrate belongs to one of two size classes defined by diameter. The threshold diameter separating the two size classes is defined by the **Boundary Between Log Diam Classes (cm)** parameter. When a sapling, adult, or snag enters the substrate pool, the area input to each size class is calculated separately. The species group and size class to which log substrate is added do not change over time.

Log substrate is also divided into 5 decay classes. Over time, decay class 1 logs decay into decay class 2 logs, then decay class 3 logs, then decay class 4 logs, then decay class 5 logs, then forest floor litter and moss. The relationship among these states, as well as tip-up mounds and scarified soil, is depicted in the figure below.



Like in Substrate, decay among the log decay classes and for tip-up mounds and scarified soil (relationships 1-5, 7, and 9), is a function of substrate age according to the equation:

$$y = e^{\alpha * t^{\beta}}$$

where t is time in years since the last decay transition. Decay calculations for the 5 log decay classes are performed on an annual basis so it is possible to advance by more than one decay class in a single multi-year timestep. At the end of each timestep, the age of all logs is rounded to the nearest multiple of the timestep duration. This is necessary to keep memory requirements manageable.

Log substrate is created by the processes of tree fall and breakage along the bole (relationship 6). Detailed Substrate looks at flags set by [mortality](#) and [snag dynamics](#) behaviors to determine whether a sapling, adult tree, or snag has either fallen or broken to a certain height in the current timestep. If so, it adds the appropriate area to the log substrate pool. Like in Substrate, tree boles are modeled as cones. The projected horizontal area is therefore a triangle if the top of the tree is included, or a trapezoid if only considering the lower section of a tree. New log substrate does not need to enter in decay class 1: the **Prop. Live Trees Entering Decay Class X (0-1)** and **Prop. Snags Entering Decay Class X (0-1)** parameters determine the probability of entering the substrate pool in each of the 5 decay classes for both snags and dead saplings/adults.

Detailed Substrate allows new substrate proportions to be specified following clear cut, gap, and partial harvesting. If the total proportion of substrate after harvesting specified by parameters is

less than 1, the remainder will be distributed in proportion to pre-harvest substrate values. In comparison, remaining substrate after harvest is assigned to moss and litter pools in the Substrate behavior. This change is designed to allow legacy substrates, such as logs and tip-up mounds, to persist after a harvest event.

In addition to tracking log area, Detailed Substrate also stores the volume of each type of log substrate in each grid cell. For new inputs, log volume is calculated as:

$$LV = 1/3 * \pi * (DBH / 2)^2 * h$$

where:

- *LV* is new log volume, in m³
- *DBH* is the DBH of the fallen tree, in m
- *h* is the height of the fallen tree, in m

For initial volume and volume added after harvest:

$$LV = 1/3 * \pi * 100 * PLA * (MDBH / 2)$$

where:

- *LV* is initial log volume or volume added after harvest, in m³/ha
- *PLA* is the proportional log area in the grid cell, from 0 to 1
- *MDBH* is the mean DBH of logs of that type (either initial or added by harvest). These are set with parameters. A reasonable default is values of 0.5 and 1.5 of the diameter boundary are used for small and large size classes, respectively

Log volume differs from log area proportions in that it does not have an upper bound. Each time new substrate is added, existing log substrate proportions are reduced so that the total of all substrate proportions is still less than or equal to 1. However, new inputs from tree fall and breakage do not reduce existing log volume (that is, logs can be on top of each other and still contribute to volume but not area). The volume of logs is reduced after harvesting when scarified soil is added (that is, log volume is destroyed in the area that is scarified). Log volume also decreases as pieces decay from decay class 5 to forest floor litter and moss.

Parameters for this behavior

Parameter name	Description
Boundary Between Log Diam Classes (cm)	DBH boundary between the "small" and "large" log size classes, in cm.
Clear Cut Large Logs Mean Diameter	After a clear cut harvest, the mean diameter of logs in the "large" size class, in cm. This is not required if the Harvest behavior is not used.

(cm)	
Clear Cut Small Logs Mean Diameter (cm)	After a clear cut harvest, the mean diameter of logs in the "small" size class, in cm. This is not required if the Harvest behavior is not used.
Clear Cut Proportion of Scarified Soil	The proportion of substrate that is scarified soil in areas that had a clear cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Clear Cut Proportion of Tip-Up Mounds	The proportion of substrate that is tip-up mounds substrate in areas that had a clear cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Gap Cut Small Logs Mean Diameter (cm)	After a gap cut harvest, the mean diameter of logs in the "small" size class, in cm. This is not required if the Harvest behavior is not used.
Gap Cut Large Logs Mean Diameter (cm)	After a gap cut harvest, the mean diameter of logs in the "large" size class, in cm. This is not required if the Harvest behavior is not used.
Gap Cut Proportion of Scarified Soil	The proportion of substrate that is scarified soil in areas that had a gap cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Gap Cut Proportion of Tip-Up Mounds	The proportion of substrate that is tip-up mounds substrate in areas that had a gap cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Clear Cut Proportion of Scarified Soil	The proportion of substrate that is scarified soil in areas that had a clear cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Clear Cut Proportion of Tip-Up Mounds	The proportion of substrate that is tip-up mounds substrate in areas that had a clear cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Gap Cut Small Logs Mean Diameter (cm)	After a gap cut harvest, the mean diameter of logs in the "small" size class, in cm. This is not required if the Harvest behavior is not used.
Gap Cut Large Logs Mean Diameter (cm)	After a gap cut harvest, the mean diameter of logs in the "large" size class, in cm. This is not required if the Harvest behavior is not used.
Gap Cut Proportion of Scarified Soil	The proportion of substrate that is scarified soil in areas that had a gap cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.
Gap Cut Proportion of Tip-Up Mounds	The proportion of substrate that is tip-up mounds substrate in areas that had a gap cut harvest event, as a value between 0 and 1. This is not required if the Harvest behavior is not used.

Initial Conditions Proportion of Scarified Soil	The proportion of plot substrate that is scarified soil when the run starts, as a value between 0 and 1. If a map of substrate values is included in the parameter file (see Grid initial conditions for information on how to do this), then the map values will be used for the initial conditions and this number will be ignored.
Initial Conditions Proportion of Tip-Up Mounds	The proportion of plot substrate that is tip-up mounds substrate when the run starts, as a value between 0 and 1. If a map of substrate values is included in the parameter file (see Grid initial conditions for information on how to do this), then the map values will be used for the initial conditions and this number will be ignored.
Initial Large Logs Mean Diameter (cm)	For initial conditions, the mean diameter of logs in the "large" size class, in cm.
Initial Small Logs Mean Diameter (cm)	For initial conditions, the mean diameter of logs in the "small" size class, in cm.
Maximum Number of Years that Decay Occurs	The number of years that a substrate disturbance event has effect before it is deleted - the lifetime of a substrate cohort.
Partial Cut Large Logs Mean Diameter (cm)	After a partial cut harvest, the mean diameter of logs in the "large" size class, in cm. This is not required if the Harvest behavior is not used.
Partial Cut Small Logs Mean Diameter (cm)	After a partial cut harvest, the mean diameter of logs in the "small" size class, in cm. This is not required if the Harvest behavior is not used.
Prop. Live Trees Entering Decay Class X (0-1)	The proportion of live trees entering each of the five decay classes. The proportion for all five classes together must add up to 1.
Prop. Snags Entering Decay Class X (0-1)	The proportion of snags entering each of the five decay classes. The proportion for all five classes together must add up to 1.
Scarified Soil Annual Decay Alpha	The α exponent in the decay equation $y = e^{\alpha * t^{\beta}}$, as applied to scarified soil. Note that this is annual decay.
Scarified Soil Annual Decay Beta	The β exponent in the decay equation $y = e^{\alpha * t^{\beta}}$, as applied to scarified soil. Note that this is annual decay.
Species Group	Which species group (1-3) each species is assigned to.
Species Group X Large Class Y Clear	After a clear cut harvest, the proportion of substrate area that is large logs of species group X, decay class Y. All clear cut values added together

Cut Log (0-1)	must be less than or equal to 1. This is not required if the Harvest behavior is not used.
Species Group X Small Class Y Clear Cut Log (0-1)	After a clear cut harvest, the proportion of substrate area that is small logs of species group X, decay class Y. All clear cut values added together must be less than or equal to 1. This is not required if the Harvest behavior is not used.
Species Group X Large Class Y Gap Cut Log (0-1)	After a gap cut harvest, the proportion of substrate area that is large logs of species group X, decay class Y. All gap cut values added together must be less than or equal to 1. This is not required if the Harvest behavior is not used.
Species Group X Small Class Y Gap Cut Log (0-1)	After a gap cut harvest, the proportion of substrate area that is small logs of species group X, decay class Y. All gap cut values added together must be less than or equal to 1. This is not required if the Harvest behavior is not used.
Species Group X Large Class Y Initial Log Prop (0-1)	For the initial conditions, the proportion of substrate area that is large logs of species group X, decay class Y. All initial conditions values added together must be less than or equal to 1.
Species Group X Small Class Y Initial Log Prop (0-1)	For the initial conditions, the proportion of substrate area that is small logs of species group X, decay class Y. All initial conditions values added together must be less than or equal to 1.
Species Group X Large Class Y Log Decay Alpha	The α exponent in the decay equation, as applied to large logs of species group X, decay class Y. This value must be a negative number.
Species Group X Small Class Y Log Decay Alpha	The α exponent in the decay equation, as applied to small logs of species group X, decay class Y. This value must be a negative number.
Species Group X Large Class Y Log Decay Beta	The β exponent in the decay equation, as applied to large logs of species group X, decay class Y.
Species Group X Small Class Y Log Decay Beta	The β exponent in the decay equation, as applied to small logs of species group X, decay class Y.
Species Group X Large Class Y Partial Cut Log (0-1)	After a partial cut harvest, the proportion of substrate area that is large logs of species group X, decay class Y. All partial cut values added together must be less than or equal to 1. This is not required if the Harvest behavior is not used.
Species Group X	After a partial cut harvest, the proportion of substrate area that is small

Small Class Y Partial Cut Log (0-1)	logs of species group X, decay class Y. All partial cut values added together must be less than or equal to 1. This is not required if the Harvest behavior is not used.
Tip-Up Mounds Annual Decay Alpha	The α exponent in the decay equation $y = e^{-\alpha * t^\beta}$, as applied to tip-up mounds substrate. Note that this is annual decay.
Tip-Up Mounds Annual Decay Beta	The β exponent in the decay equation $y = e^{-\alpha * t^\beta}$, as applied to tip-up mounds substrate. Note that this is annual decay.
Uprooted Tree Radius Increase Factor for Root Rip-Out	The amount by which to multiply the tree's radius when calculating the size of the new tip-up mounds soil exposed by fallen trees (see equation below). This is meant to allow for the effects of roots.
Use Directional Tree Fall	If true, dead trees fall in a random direction and possibly contribute new fresh log across several Substrate grid cells. If false, dead trees collapse vertically and contribute all their fresh log area to the cell in which they are rooted.

How it works

The relative proportions of each kind of substrate are tracked in the [Detailed Substrate](#) grid. Within each cell, the grid keeps track of each substrate's area as a proportion of the total area, as well as volume for each type of log substrate in m³/ha. The behavior also summarizes and copies values into the [Substrate](#) grid for compatibility with other behaviors that use that grid.

Each timestep, Detailed Substrate looks for harvest events and new tree inputs. It finds harvest events by looking in the Harvest grid. Harvest events add new scarified soil, tip-up, and log substrate. The behavior finds fallen and broken trees by looking for the flags set by [mortality](#) and [snag dynamics](#) behaviors. Each fallen and broken tree (or snag) "rolls the dice" with a random number to determine the log decay class it will enter as substrate. Fallen adult trees and snags also use a random number to determine whether they expose tip-up mound substrate. All the new substrate created by harvest and tree inputs is then totaled up. When there is new substrate in a grid cell, Detailed Substrate reduces the other substrate amounts in the cell to make way for the amount of new substrate.

All existing substrates are decayed each timestep as they age. After they reach their maximum lifespan, which is set by parameters, they are deleted. The final proportions of scarified soil, tip-up, and logs are found by adding up the values representing each substrate age. The final proportion of the moss/litter pool is whatever grid cell area is left over. The pool is further split into moss and litter by using fixed proportions of each in the pool, as specified by the **Proportion of Forest Floor Litter/Moss Pool that is Moss** parameter.

How to apply it

Apply Detailed Substrate to all trees which can create substrate by becoming fallen logs. This generally means that it should be applied to adults and snags of all species. Substrate cannot be applied to seedlings or saplings. Any tree species/type combination to which it is applied must also have a mortality and snag dynamics behavior applied.

Epiphytic establishment behaviors

Epiphytic establishment behaviors allow seeds to germinate epiphytically.

Behavior	Description
Tree Fern Establishment behavior	Simulates the establishment of seedlings epiphytically on tree ferns.

Tree Fern Establishment

This behavior was developed to simulate the establishment of seedlings epiphytically on tree ferns. Rather than tracking individual seedlings that germinate and grow on a tree fern during its life, this assumes that upon a tree fern's death, there is a possibility that a seedling will establish in that spot. For the purposes of this behavior, multiple species can serve as possible epiphytic substrates, but only one species will establish upon them.

Note: this behavior is applied to the epiphytic substrate trees (species and life history stage), not the establishing species.

Parameters for this behavior

Because the [Tree Fern Establishment](#) behavior makes light calculations, a set of light parameters is included in its parameter list. These are used in exactly the same way as the light behavior parameters. However, the values are independent of those which may be used for other light behaviors. If updates are made to the light parameters of an existing parameter file, they must be updated in both places.

Parameter name	Description
Tree Fern Establishment Species of New Seedlings	The species of seedlings which are establishing epiphytically on the substrate species.

Tree Fern Establishment Seedling Prob "a"	The variable a in the function used to calculate the probability of the establishment of a seedling on a dead substrate tree.
Tree Fern Establishment Seedling Prob "b"	The variable b in the function used to calculate the probability of the establishment of a seedling on a dead substrate tree.
Tree Fern Establishment Seedling Prob "c"	The variable c in the function used to calculate the probability of the establishment of a seedling on a dead substrate tree.
Tree Fern Establishment Seedling Height "m"	The intercept in the linear function for seedling rooting height.
Tree Fern Establishment Seedling Height "n"	The slope in the linear function for seedling rooting height.

How it works

There can be multiple species of epiphytic substrate trees, but only one establishing species. The establishing species is specified using **Tree Fern Establishment Species of New Seedlings** parameter.

When an individual of one of the epiphytic substrate tree species (that is, a tree fern) dies, there is a certain probability that one of its presumed epiphytic seedlings will root in its location. This probability is:

$$P = 1 - (1 / (1 + \exp(a + b * Height + c * GLI)))$$

where

- P is the probability of a seedling rooting in that location
- $Height$ is the height of the dead substrate tree, in m
- GLI is the light level (0 - 100) taken at the trunk of the substrate tree, halfway between the ground and the bottom of the crown
- a is the **Tree Fern Establishment Seedling Prob "a"** parameter
- b is the **Tree Fern Establishment Seedling Prob "b"** parameter
- c is the **Tree Fern Establishment Seedling Prob "c"** parameter

The GLI is calculated from the forest as it is at the tree's death; this may be different from any GLI value calculated at the beginning of the timestep, since growth will have occurred. The substrate tree itself is not yet a snag (if snags are used in the run), so it will cast shade as a living tree would.

SORTIE uses a random number to decide whether a new seedling will root based on this probability. If a seedling does root, its height is:

$$HS = m + n * Height$$

where

- *HS* is the seedling height, in cm
- *Height* is the height of the dead substrate tree, in m
- *m* is the **Tree Fern Establishment Seedling Height "m"** parameter
- *n* is the **Tree Fern Establishment Seedling Height "n"** parameter

The seedling's location is exactly the same as that of the dead substrate tree. Its diameter is calculated from its height using the appropriate allometric function. It is not forced to be a seedling; if its height is tall enough to become a sapling, this is allowed. This behavior does nothing further to the dead substrate tree. It is subject to substrate dynamics, snag formation, or any other post-mortality process being used in the run, just like any other dead tree.

How to apply it

This behavior can be applied to saplings and adults of any species. The species to which it is applied are the **substrate** species, not the establishing species. It should be executed after mortality and before dead tree remover behaviors have been applied in each timestep.

Mortality utility behaviors

This type of behavior performs cleanup by removing dead trees from memory at the appropriate time. This function is very important - if it did not occur, then the model would slow exponentially as memory filled up and those behaviors that look at recently dead trees would start getting strange results.

Behavior	Description
Dead tree remover	Removes dead trees from memory.

Snag dynamics behaviors

Snag dynamics behaviors increase control over snag fall and decay.

Behavior	Description
Snag Decay Class	Controls transitions among snag decay classes and snag falls. There are two fall models: one that applies to trees that die in the current time step (and may fall

[Dynamics behavior](#)

without become a snag), and one that applies to pre-existing snags.

Snag Decay Class Dynamics

This behavior controls transitions among snag decay classes and snag falls. There are two fall models, one that applies to trees that die in the current time step (and may fall without become a snag), and one that applies to pre-existing snags. Fall probability is a function of tree size, decay class, neighborhood basal area, and recent harvest activity. Trees and snags that do not fall are run through a snag decay class transition matrix.

Model forms are based on those in [Vanderwel et al. 2006](#).

Parameters for this behavior

Parameter name	Description
Snag Decay Class Dynamics Snag Fall Alpha	Snag fall alpha parameter.
Snag Decay Class Dynamics Snag Fall Beta	Snag fall beta parameter.
Snag Decay Class Dynamics Snag Fall Eta	Snag fall eta parameter.
Snag Decay Class Dynamics Snag Fall Gamma 2	Snag fall gamma 2 parameter.
Snag Decay Class Dynamics Snag Fall Gamma 3	Snag fall gamma 3 parameter.
Snag Decay Class Dynamics Snag Fall Gamma 4	Snag fall gamma 4 parameter.
Snag Decay Class Dynamics Snag Fall Gamma 5	Snag fall gamma 5 parameter.
Snag Decay Class	Snag fall kappa parameter.

Dynamics Snag Fall Kappa	
Snag Decay Class Dynamics Snag Fall Zeta	Snag fall zeta parameter.
Snag Decay Class Dynamics Tree Fall Alpha	Tree fall alpha parameter.
Snag Decay Class Dynamics Tree Fall Beta	Tree fall beta parameter.
Snag Decay Class Dynamics Tree Fall Delta	Tree fall delta parameter.
Snag Decay Class Dynamics Tree Fall Iota	Tree fall iota parameter.
Snag Decay Class Dynamics Tree Fall Lambda	Tree fall lambda parameter.
Snag Decay Class Dynamics Tree Fall Theta	Tree fall theta parameter.
Snag Decay Class Dynamics Live To Class 1 Prob (0-1)	Probability of a snag that did not fall moving from live (killed this timestep) to decay class 1.
Snag Decay Class Dynamics Live To Class 2 Prob (0-1)	Probability of a snag that did not fall moving from live (killed this timestep) to decay class 2.
Snag Decay Class Dynamics Live To Class 3 Prob (0-1)	Probability of a snag that did not fall moving from live (killed this timestep) to decay class 3.
Snag Decay Class Dynamics Live To Class 4 Prob (0-1)	Probability of a snag that did not fall moving from live (killed this timestep) to decay class 4.
Snag Decay Class Dynamics Live To	Probability of a snag that did not fall moving from live (killed this timestep) to decay class 5.

Class 5 Prob (0-1)	
Snag Decay Class Dynamics Class 1 To Class 1 Prob (0-1)	Probability of a snag that did not fall remaining in decay class 1.
Snag Decay Class Dynamics Class 1 To Class 2 Prob (0-1)	Probability of a snag that did not fall moving from decay class 1 to decay class 2.
Snag Decay Class Dynamics Class 1 To Class 3 Prob (0-1)	Probability of a snag that did not fall moving from decay class 1 to decay class 3.
Snag Decay Class Dynamics Class 1 To Class 4 Prob (0-1)	Probability of a snag that did not fall moving from decay class 1 to decay class 4.
Snag Decay Class Dynamics Class 1 To Class 5 Prob (0-1)	Probability of a snag that did not fall moving from decay class 1 to decay class 5.
Snag Decay Class Dynamics Class 2 To Class 2 Prob (0-1)	Probability of a snag that did not fall remaining in decay class 2.
Snag Decay Class Dynamics Class 2 To Class 3 Prob (0-1)	Probability of a snag that did not fall moving from decay class 2 to decay class 3.
Snag Decay Class Dynamics Class 2 To Class 4 Prob (0-1)	Probability of a snag that did not fall moving from decay class 2 to decay class 4.
Snag Decay Class Dynamics Class 2 To Class 5 Prob (0-1)	Probability of a snag that did not fall moving from decay class 2 to decay class 5.
Snag Decay Class Dynamics Class 3 To Class 3 Prob (0-1)	Probability of a snag that did not fall remaining in decay class 3.
Snag Decay Class Dynamics Class 3 To Class 4 Prob (0-1)	Probability of a snag that did not fall moving from decay class 3 to decay class 4.
Snag Decay Class Dynamics Class 3 To Class 5 Prob (0-1)	Probability of a snag that did not fall moving from decay class 3 to decay class 5.

Snag Decay Class Dynamics Class 4 To Class 4 Prob (0-1)	Probability of a snag that did not fall remaining in decay class 4.
Snag Decay Class Dynamics Class 4 To Class 5 Prob (0-1)	Probability of a snag that did not fall moving from decay class 4 to decay class 5.
Snag Decay Class Dynamics Class 5 To Class 5 Prob (0-1)	Probability of a snag that did not fall remaining in decay class 5. This value is always 1.
Snag Decay Class Dynamics Maximum Snag Break Height	Maximum height at which snags break. The actual height is a random draw between this value and the minimum.
Snag Decay Class Dynamics Minimum Snag Break Height	Minimum height at which snags break. The actual height is a random draw between this value and the maximum.

How it works

Trees that died in the current timestep have a certain probability of falling before the end of the current timestep. (Note that trees that die in a mortality episode do NOT count as trees that died in the current timestep, but as existing snags.) The behavior represents the probability of falling before the end of the timestep as:

$$\Pr(\text{fall}) = \frac{e^{f(x)}}{1 + e^{f(x)}}$$

$$f(x) = \alpha + \beta_{spp} + \delta DBH + \theta BA + \iota H + \lambda (DBH * H)$$

where:

- $\Pr(\text{fall})$ is the probability of the tree falling
- α is the **Snag Decay Class Dynamics Tree Fall Alpha** parameter
- β_{spp} is the **Snag Decay Class Dynamics Tree Fall Beta** parameter for the tree's species
- DBH is the DBH in cm
- δ is the **Snag Decay Class Dynamics Tree Fall Delta** parameter
- θ is the **Snag Decay Class Dynamics Tree Fall Theta** parameter
- BA is the basal area (m²/ha) of live trees in the current tree's cell of the [Snag Decay Class Dynamics Basal Area](#) grid
- ι is the **Snag Decay Class Dynamics Tree Fall Iota** parameter
- H is whether (1) or not (0) a harvest occurred this timestep
- λ is the **Snag Decay Class Dynamics Tree Fall Lambda** parameter

For snags that were created in a previous timestep, the behavior represents the probability of falling during the timestep as:

$$\Pr(\text{fall}) = \frac{e^{f(x)}}{1 + e^{f(x)}}$$

$$f(x) = \alpha + \beta_{spp} + \gamma_{dc} + \zeta \ln(DBH) + \eta \ln(DBH)^2 + \kappa BA_H$$

where:

- $\Pr(\text{fall})$ is the probability of the snag falling
- α is the **Snag Decay Class Dynamics Snag Fall Alpha** parameter
- β_{spp} is the **Snag Decay Class Dynamics Snag Fall Beta** parameter for the tree's species
- γ_{dc} is the **Snag Decay Class Dynamics Snag Fall Gamma X** parameter, where X is the snag's decay class
- DBH is the DBH in cm
- ζ is the **Snag Decay Class Dynamics Snag Fall Zeta** parameter
- η is the **Snag Decay Class Dynamics Snag Fall Eta** parameter
- κ is the **Snag Decay Class Dynamics Snag Fall Kappa** parameter
- BA_H is the basal area (m²/ha) of harvested trees in the current snag's cell of the [Snag Decay Class Dynamics Basal Area](#) grid

If a tree or snag does not fall, its condition at the end of the timestep will be represented by a snag decay class. Decay class 1 is the least decayed condition and decay class 5 is the most decayed. Parameters should be entered to specify the probability of going from a live tree or one of five decay classes to each of the higher decay classes over a five year timestep, given that the snag is still standing. The transition probabilities for each initial condition must sum to 1.

For all models, parameter values should correspond to the probability of fall for a five-year timestep. The behavior will re-scale the probability of fall for other timestep lengths if necessary.

Basal area amounts are tracked in the [Snag Decay Class Dynamics Basal Area](#) grid. Each timestep, the amount of basal area, in square meters per hectare, is totaled across all species for live trees (live adults and adults that died in the current timestep) and harvested trees. The size of the grid cells is approximately 400 square meters. A tree's neighborhood basal area is the value in the grid cell where the tree is located.

How to apply it

This behavior can be applied to adults and snags of any species. It should be executed after mortality and dead tree remover behaviors have been applied in each timestep.

Disperse behaviors

Disperse behaviors create and distribute tree seeds around the plot. Dispersal is the first step in seedling recruitment.

Seed totals for different species are stored in the [Dispersed Seeds grid](#). Each of the disperse behaviors adds seeds to this grid. The [Establishment behaviors](#) decide which seeds in the grid turn into new seedlings.

For these behaviors, "parent trees" refers to trees over the minimum reproductive DBH for a species. These are the only trees which can contribute new seeds to the plot.

While there is support in the model for seeds to act as individuals (see [Tree life history stages](#)), these seeds are not individuals but merely numbers in a grid. You could not, for instance, create a list of individual seed positions.

Seed randomization

The numbers of seeds added by the disperse behaviors can be randomized. You choose how randomization will be applied. If the seed distribution is deterministic, no randomization is done. Otherwise, you can choose a probability distribution function and the number of seeds is treated as the mean of that function. You may need to supply additional parameters, depending on the probability distribution function you choose. This randomization applies to the seeds from all disperse behaviors that you have chosen.

There are four choices for probability distribution functions: the normal, the lognormal, the Poisson, and the negative binomial. The forms for these functions can be found [here](#).

Behavior	Description
Non-spatial disperse behavior	Scatters seeds uniformly across the plot. Non-spatial disperse has two components: basal-area-dependent seed rain and non-density-dependent (bath) seed rain, the two of which are independent and can be used together or separately.
Masting non-spatial disperse behavior	Adds stochasticity to basic seed rain by simulating masting and basic inter - year variation in seed production.
Spatial disperse behaviors	General information on the spatial disperse algorithm
Non-gap spatial disperse behavior	Disperses seeds in a spatial way, ignoring forest cover.

Gap spatial disperse behavior	Gap spatial disperse takes forest cover into account when determining the number and placement of seeds.
Masting spatial disperse behavior	Variant of the Non-gap spatial disperse behavior that adds masting and more stochasticity in seed production.
Stochastic Double Logistic Temp Dependent Neighborhood Disperse behavior	Calculates seed density based on a double-logistic function of annual mean temperature and basal area of neighborhood adults.
Temperature dependent neighborhood disperse behavior	Calculates seed density based on annual mean temperature and the basal area of neighborhood adults.

Non-spatial disperse

The "non-spatial" in non-spatial disperse refers to the fact that this behavior ignores the location of parent trees and scatters seeds uniformly across the plot. Non-spatial disperse has two components: basal-area-dependent seed rain and non-density-dependent (bath) seed rain, the two of which are independent and can be used together or separately. For basal-area-dependent seed rain, the number of seeds added is in direct proportion to the amount of basal area of parent trees of a given species. Bath seed rain adds a constant number of seeds each timestep, even if there are no parent trees of that species in the plot.

Parameters for this behavior

Parameter name	Description
Intercept of Mean Non-Spatial Seed Rain, seeds/m ² /yr	The intercept of the non-spatial seed rain function. This is the bath seed rain term. Set this value to zero to turn off bath non-spatial seed rain.
Slope Mean Non-Spatial Seed Rain, seeds/m ² /ha of BA/yr	The slope of the non-spatial seed rain function. This is the basal-area-dependent seed rain term. Set this value to zero to turn off basal-area-dependent non-spatial seed rain.

Minimum DBH for Reproduction, in cm	The minimum DBH at which a tree can reproduce. This value does not have to match the Minimum adult DBH .
Seed Distribution	<p>The distribution method to be applied to seeds (randomization). The forms for these functions can be found here. Choices are:</p> <ul style="list-style-type: none"> • Deterministic - no randomization. • Poisson - use the number of seeds as the mean in a Poisson probability distribution function. • Normal - use the number of seeds as the mean in a normal probability distribution function. You must then supply a standard deviation for the function. • Lognormal - use the number of seeds as the mean in a lognormal probability distribution function. You must then supply a standard deviation for the function. • Negative binomial - use the number of seeds as the mean in a negative binomial probability distribution function. You must then supply a clumping parameter.
Seed Dist. Clumping Parameter (Neg. Binomial)	If you have chosen the negative binomial probability distribution function for "Seed distribution", this is the clumping parameter of the function, in seeds per m ² . If you have not chosen that PDFs, then this parameter is not required.
Seed Dist. Std. Deviation (Normal or Lognormal)	If you have chosen the normal or lognormal probability distribution functions for "Seed distribution", this is the standard deviation of the function, in seeds per m ² . If you have not chosen these PDFs, then this parameter is not required.

How it works

Non-spatial disperse calculates how many seeds to distribute as:

$$\lambda = \mu * BA + \kappa$$

where:

- λ is the mean number of seeds per m²
- μ is the **Slope Mean Non-Spatial Seed Rain, seeds/m2/ha of BA/yr** parameter
- BA is the basal area of the parent species in m²
- κ is the **Intercept of Mean Non-Spatial Seed Rain, seeds/m2/yr** parameter

From this, the number of seeds per grid cell of the [Dispersed Seeds](#) grid is calculated, and then that number is added to each grid cell.

In the equation above, μ is the basal-area-dependent seed rain term. Setting this value to zero turns off density-dependent seed rain. κ is the bath seed rain term. Setting this value to zero turns off bath seed rain.

How to apply it

Apply this behavior to adults of the species you wish to use non-spatial disperse.

Masting non-spatial disperse behavior

This behavior adds stochasticity to basic seed rain by simulating masting and basic inter - year variation in seed production.

Parameters for this behavior

Parameter name	Description
Mast NS Disperse - Binomial P (Mast Chance)	"p" value for the binomial distribution used to randomly decide whether to mast each timestep.
Mast NS Disperse - Masting Group	Species in the same group always mast together. If all the group numbers are different, then each species masts separately. The actual numbers do not matter, just whether species have identical numbers.
Mast NS Disperse - Mast Inv. Gauss. Mu	Mu parameter for the inverse Gaussian distribution for choosing seeds in masting conditions. Values are only required for those species using this distribution when masting.
Mast NS Disperse - Mast Inv. Gauss. Lambda	Lambda parameter for the inverse Gaussian distribution for choosing seeds in masting conditions. Values are only required for those species using this distribution when masting.
Mast NS Disperse - Non-Mast Inv. Gauss. Mu	Mu parameter for the inverse Gaussian distribution for choosing seeds in non-masting conditions. Values are only required for those species using this distribution when not masting.
Mast NS Disperse - Non-Mast Inv. Gauss. Lambda	Lambda parameter for the inverse Gaussian distribution for choosing seeds in non-masting conditions. Values are only required for those species using this distribution when not masting.
Mast NS Disperse - Mast Normal Mean	Mean parameter for the normal distribution for choosing seeds in masting conditions. Values are only required for those species using this distribution when masting.
Mast NS Disperse -	Standard deviation parameter for the normal distribution for choosing

Mast Normal Standard Deviation	seeds in masting conditions. Values are only required for those species using this distribution when masting.
Mast NS Disperse - Non-Mast Normal Mean	Mean parameter for the normal distribution for choosing seeds in non-masting conditions. Values are only required for those species using this distribution when not masting.
Mast NS Disperse - Non-Mast Normal Standard Deviation	Standard deviation parameter for the normal distribution for choosing seeds in non-masting conditions. Values are only required for those species using this distribution when not masting.
Mast NS Disperse - PDF Masting Conditions	Which probability distribution to use to choose number of seeds during masting events.
Mast NS Disperse - PDF Non-Masting Conditions	Which probability distribution to use to choose number of seeds when not masting.
Minimum DBH for Reproduction, in cm	The minimum DBH at which a tree can reproduce. This value does not have to match the Minimum adult DBH .
Seed Distribution	<p>The distribution method to be applied to seeds (randomization). The forms for these functions can be found here. Choices are:</p> <ul style="list-style-type: none"> • Deterministic - no randomization. • Poisson - use the number of seeds as the mean in a Poisson probability distribution function. • Normal - use the number of seeds as the mean in a normal probability distribution function. You must then supply a standard deviation for the function. • Lognormal - use the number of seeds as the mean in a lognormal probability distribution function. You must then supply a standard deviation for the function. • Negative binomial - use the number of seeds as the mean in a negative binomial probability distribution function. You must then supply a clumping parameter.
Seed Dist. Clumping Parameter (Neg. Binomial)	If you have chosen the negative binomial probability distribution function for "Seed distribution", this is the clumping parameter of the function, in seeds per m ² . If you have not chosen that PDFs, then this parameter is not required.
Seed Dist. Std. Deviation (Normal or Lognormal)	If you have chosen the normal or lognormal probability distribution functions for "Seed distribution", this is the standard deviation of the function, in seeds per m ² . If you have not chosen these PDFs, then this parameter is not required.

How it works

Deciding when to mast. Each timestep, each species may mast or not. Mast is determined by making a random draw from a binomial distribution, with the "p" value for the distribution set using the **Mast NS Disperse - Binomial P (Mast Chance)** parameter. Masting decisions are made completely independently for each species (except in the case of masting groups; more on those later).

The number of seeds, in seeds per square meter, is then drawn from a second probability distribution. The distribution choices are normal and inverse Gaussian. A species can use different distributions for mast and non-mast timesteps. You choose the distributions using the **Mast NS Disperse - PDF Masting Conditions** and **Mast NS Disperse - PDF Non-Masting Conditions** parameters. You then set up the values for the different distributions using the appropriate parameters. You do not need to set values for distributions that a species does not use.

Once the number of seeds per square meter has been established for a species, that quantity of seed is distributed evenly across the plot. The presence or absence of parent trees of that species makes no difference to the number of seeds.

To simulate synchrony in masting, species can be collected into masting groups. The decision to mast or not to mast using the binomial distribution is performed once for each group, using the first species in the group's "p" value. The number of seeds per square meter is established as for a single species; but those seeds are divided amongst the group's species according to the relative basal area of adults of each species in the plot. If there are no trees of any of the group's species, the seeds are divided equally amongst the species.

How to apply it

Apply this behavior to adults of the species you wish to use.

Spatial disperse behaviors

Spatial disperse behaviors rely on the location and size of parent trees to determine the number and placement of seeds. The placement of the seeds is controlled by a probability distribution function. You can choose between the Weibull and lognormal functions.

The Weibull function is as follows:

$$R_i = \frac{STR}{n} \sum_{k=1}^T \left(\frac{DBH_k}{30} \right)^\beta e^{-\Gamma m_{ik}^\theta}$$

where,

$$n = \int_0^{\infty} e^{-Dm_{ik}^{\theta}} dm_{ik}$$

and where:

- R_i is the density (#/m²) of seedlings at a given point i
- STR , the "standardized total recruits", is the number of seedling recruits produced by a 30 cm DBH parent tree (the **Weibull Canopy Annual STR** or **Weibull Gap Annual STR** parameters)
- DBH_k is the DBH in cm of the $k = 1 \dots T$ parent trees within a specified radius of location i
- D is a species-specific dispersal parameter (the **Weibull Canopy Dispersal** or **Weibull Gap Dispersal** parameters)
- m_{ik} is the distance (in meters) from point i to the k th parent tree
- θ and β are disperse parameters (the **Weibull Canopy Theta** or **Weibull Gap Theta** and **Weibull Gap Beta** or **Weibull Canopy Beta** parameters)

The lognormal function is as follows:

$$R_i = \frac{STR}{n} \sum_{k=1}^T \left(\frac{DBH_k}{30} \right)^{\beta} e^{-0.5 \left(\frac{\ln(m_{ik}/X_0)}{X_b} \right)^2}$$

where,

$$n = \int_0^{\infty} e^{-0.5 \left(\frac{\ln(m_{ik}/X_0)}{X_b} \right)^2} dm_{ik}$$

and where:

- R_i is the density (#/m²) of seedlings at a given point i
- STR , the "standardized total recruits", is the number of seedling recruits produced by a 30 cm DBH parent tree (the **Lognormal Canopy Annual STR** or **Lognormal Gap Annual STR** parameters)
- DBH_k is the DBH in cm of the $k = 1 \dots T$ parent trees within a specified radius of location i
- m_{ik} is the distance (in meters) from point i to the k th parent tree
- X_0 is the mean of the function (the **Lognormal Canopy X_0** or **Lognormal Gap X_0** parameters)
- X_b is the standard deviation of the function (the **Lognormal Canopy X_b** or **Lognormal Gap X_b** parameters)
- β is a disperse parameter (the **Lognormal Canopy Beta** or **Lognormal Gap Beta** parameters)

The maximum distance that seeds are allowed to disperse is the length of the grid in the longest direction, up to a maximum of 1000 meters. Because of the torus shape of the plot, a seed deposited at the very limit of the distance could end up back underneath the parent tree. For this reason, if you are using a very flat dispersal kernel, you may wish to consider a non-spatial disperse method.

The normalizer (Equation 3 of [Ribbens et al 1994](#)) serves two functions. It reduces parameter correlation between *STR* and the dispersion parameter (*D*); and scales the distance-dependent dispersion term so that *STR* is in meaningful units - i.e. the total # of seedlings produced in the entire seedling shadow of a 30 cm DBH parent tree.

Non-gap spatial disperse

Non-gap spatial disperse is called "non-gap" to distinguish it from "gap" disperse. The "non-gap" means that forest cover is ignored.

Parameters for this behavior

Parameter name	Description
Beta for Stumps	The β value for stumps. Stumps use the same probability distribution function as the live members of their species. Only required if a behavior is being applied to stumps.
Canopy Function Used	The probability distribution function to be used to distribute seeds in canopy conditions. For the behaviors Non-gap spatial disperse and Masting spatial disperse, these PDFs are always the ones used.
Lognormal Canopy Annual STR	The annual <i>STR</i> value (Standardized Total Recruits, or all seeds produced by a 30 cm DBH tree in one year) for the lognormal function under canopy conditions (see equation below). This is only required if the canopy probability distribution function is lognormal.
Lognormal Canopy Beta	The β for the lognormal function under canopy conditions (see equation below). This is only required if the canopy probability distribution function is lognormal.
Lognormal Canopy X_0	The mean of the lognormal function under canopy conditions, or under non-masting conditions in the case of Masting spatial disperse (see equation below). This is only required if the canopy probability distribution function is lognormal.
Lognormal Canopy X_b	The standard deviation of the lognormal function under canopy conditions, or under non-masting conditions in the case of Masting

	spatial disperse (see equation below). This is only required if the canopy probability distribution function is lognormal.
Minimum DBH for Reproduction, in cm	The minimum DBH at which a tree can reproduce. This value does not have to match the Minimum adult DBH .
Seed Distribution	<p>The distribution method to be applied to seeds (randomization). The forms for these functions can be found here. Choices are:</p> <ul style="list-style-type: none"> • Deterministic - no randomization. • Poisson - use the number of seeds as the mean in a Poisson probability distribution function. • Normal - use the number of seeds as the mean in a normal probability distribution function. You must then supply a standard deviation for the function. • Lognormal - use the number of seeds as the mean in a lognormal probability distribution function. You must then supply a standard deviation for the function. • Negative binomial - use the number of seeds as the mean in a negative binomial probability distribution function. You must then supply a clumping parameter.
Seed Dist. Clumping Parameter (Neg. Binomial)	If you have chosen the negative binomial probability distribution function for "Seed distribution", this is the clumping parameter of the function, in seeds per m ² . If you have not chosen that PDFs, then this parameter is not required.
Seed Dist. Std. Deviation (Normal or Lognormal)	If you have chosen the normal or lognormal probability distribution functions for "Seed distribution", this is the standard deviation of the function, in seeds per m ² . If you have not chosen these PDFs, then this parameter is not required.
STR for Stumps	The annual STR value (Standardized Total Recruits, or all seeds produced by a 30 cm DBH tree in one year) for stumps. Stumps use the same probability distribution function as the live members of their species. Only required if a behavior is being applied to stumps.
Weibull Canopy Annual STR	The annual STR value (Standardized Total Recruits, or all seeds produced by a 30 cm DBH tree in one year) for the Weibull function under canopy conditions (see equation below). This is only required if the canopy probability distribution function is Weibull.
Weibull Canopy Beta	The β for the Weibull function under canopy conditions (see equation below). This is only required if the canopy probability distribution function is Weibull.
Weibull Canopy	The dispersal value for the Weibull function under canopy conditions, or

Dispersal	under non-masting conditions in the case of Masting spatial disperse (see equation below). This is only required if the canopy probability distribution function is Weibull.
Weibull Canopy Theta	The θ for the Weibull function under canopy conditions, or under non-masting conditions in the case of Masting spatial disperse (see equation below). This is only required if the canopy probability distribution function is Weibull.

How it works

For each tree greater than reproductive age, the number of seeds produced is calculated as

$$seeds = STR * (DBH/30)^\beta$$

These seeds are cast in random azimuth directions from the tree, and at random distances that conform to the chosen probability distribution function (see more about spatial disperse behavior seed distribution [here](#)).

How to apply it

Apply this behavior to all trees of at least the minimum reproductive age for your chosen species. If the minimum reproductive age is less than the [Minimum adult DBH](#), be sure to apply this behavior to saplings as well as adults. In the parameters, choose the appropriate probability distribution function for each species under "Canopy function used".

This behavior can be used to simulate the suckering of stumps. Apply this behavior to tree type "[stump](#)" of your chosen species. Stumps reproduce like other parent trees. They use the same probability distribution function and parameters as live members of their species, but they get their own β and STR values so that they can produce different numbers of seeds.

Gap spatial disperse

Gap spatial disperse takes forest cover into account when determining the number and placement of seeds. The two possible forest covers are gap and closed canopy. A "gap" is defined as a cell in the [Dispersed Seeds](#) grid with no more adults than the value of the "Maximum adults allowed in gap cell" parameter, above.

Parameters for this behavior

Parameter name	Description
Beta for Stumps	The β value for stumps. Stumps use the same probability distribution function as the live members of their species. Only required if a behavior

	is being applied to stumps.
Canopy Function Used	The probability distribution function to be used to distribute seeds in canopy conditions. For the behaviors Non-gap spatial disperse and Masting spatial disperse, these PDFs are always the ones used.
Gap Function Used	The probability distribution function to be used to distribute seeds in gap conditions.
Lognormal Canopy Annual STR	The annual STR value (Standardized Total Recruits, or all seeds produced by a 30 cm DBH tree in one year) for the lognormal function under canopy conditions (see equation below). This is only required if the canopy probability distribution function is lognormal.
Lognormal Canopy Beta	The β for the lognormal function under canopy conditions (see equation below). This is only required if the canopy probability distribution function is lognormal.
Lognormal Canopy X_0	The mean of the lognormal function under canopy conditions, or under non-masting conditions in the case of Masting spatial disperse (see equation below). This is only required if the canopy probability distribution function is lognormal.
Lognormal Canopy X_b	The standard deviation of the lognormal function under canopy conditions, or under non-masting conditions in the case of Masting spatial disperse (see equation below). This is only required if the canopy probability distribution function is lognormal.
Lognormal Gap Annual STR	The annual STR value (Standardized Total Recruits, or all seeds produced by a 30 cm DBH tree in one year) for the lognormal function under gap conditions (see equation below). This is only required if the gap probability distribution function is lognormal.
Lognormal Gap Beta	The β for the lognormal function under gap conditions (see equation below). This is only required if the gap probability distribution function is lognormal.
Lognormal Gap X_0	The mean of the lognormal function under gap conditions (see equation below). This is only required if the gap probability distribution function is lognormal.
Lognormal Gap X_b	The standard deviation of the lognormal function under gap conditions (see equation below). This is only required if the gap probability distribution function is lognormal.
Maximum Parent Trees Allowed in Gap Cell	Maximum number of trees above the minimum DBH for reproduction that are allowed in a grid cell for that cell to still have gap status (as opposed to closed canopy).

Seed Distribution	<p>The distribution method to be applied to seeds (randomization). The forms for these functions can be found here. Choices are:</p> <ul style="list-style-type: none"> • Deterministic - no randomization. • Poisson - use the number of seeds as the mean in a Poisson probability distribution function. • Normal - use the number of seeds as the mean in a normal probability distribution function. You must then supply a standard deviation for the function. • Lognormal - use the number of seeds as the mean in a lognormal probability distribution function. You must then supply a standard deviation for the function. • Negative binomial - use the number of seeds as the mean in a negative binomial probability distribution function. You must then supply a clumping parameter.
Seed Dist. Clumping Parameter (Neg. Binomial)	<p>If you have chosen the negative binomial probability distribution function for "Seed distribution", this is the clumping parameter of the function, in seeds per m². If you have not chosen that PDFs, then this parameter is not required.</p>
Seed Dist. Std. Deviation (Normal or Lognormal)	<p>If you have chosen the normal or lognormal probability distribution functions for "Seed distribution", this is the standard deviation of the function, in seeds per m². If you have not chosen these PDFs, then this parameter is not required.</p>
STR for Stumps	<p>The annual STR value (Standardized Total Recruits, or all seeds produced by a 30 cm DBH tree in one year) for stumps. Stumps use the same probability distribution function as the live members of their species. Only required if a behavior is being applied to stumps.</p>
Weibull Canopy Annual STR	<p>The annual STR value (Standardized Total Recruits, or all seeds produced by a 30 cm DBH tree in one year) for the Weibull function under canopy conditions (see equation below). This is only required if the canopy probability distribution function is Weibull.</p>
Weibull Canopy Beta	<p>The β for the Weibull function under canopy conditions (see equation below). This is only required if the canopy probability distribution function is Weibull.</p>
Weibull Canopy Dispersal	<p>The dispersal value for the Weibull function under canopy conditions, or under non-masting conditions in the case of Masting spatial disperse (see equation below). This is only required if the canopy probability distribution function is Weibull.</p>
Weibull Canopy	<p>The θ for the Weibull function under canopy conditions, or under non-</p>

Theta	masting conditions in the case of Masting spatial disperse (see equation below). This is only required if the canopy probability distribution function is Weibull.
Weibull Gap Annual STR	The annual STR value (Standardized Total Recruits, or all seeds produced by a 30 cm DBH tree in one year) for the Weibull function under gap conditions (see equation below). This is only required if the gap probability distribution function is Weibull.
Weibull Gap Beta	The β value for the Weibull function under gap conditions (see equation below). This is only required if the gap probability distribution function is Weibull.
Weibull Gap Dispersal	The dispersal value for the Weibull function under gap conditions (see equation below). This is only required if the gap probability distribution function is Weibull.
Weibull Gap Theta	The θ value for the Weibull function under gap conditions (see equation below). This is only required if the gap probability distribution function is Weibull.

How it works

The behavior starts each timestep by updating the forest cover of each cell (gap or canopy). It counts all trees above the minimum DBH for reproduction in each cell and compares that number to the Maximum parent trees allowed in gap cell parameter. The behavior will count trees of all species to determine gap status. However, if it finds a tree of a species that is not one of the ones this behavior is assigned to, it will use the tree's minimum adult DBH parameter instead of the minimum DBH for reproduction.

For each tree greater than the reproductive age, the number of seeds produced is calculated as

$$seeds = STR * (DBH/30)^\beta$$

using the higher of gap or canopy *STR* along with its matching β .

Each seed is given a random azimuth angle. It is then given a random distance that conforms to the probability distribution function of the current forest cover of the parent (see more about spatial disperse behavior seed distribution [here](#)). Once the seed has an azimuth and a distance, the function determines which grid cell it should drop in.

Once the seed has a target grid cell, that cell's cover is checked. Then the seed's survival is evaluated. If the seed is in the cover type with the higher STR, it automatically survives. Otherwise, a random number is compared to the ratio of the lower STR to the higher STR to determine if it survives.

If the seed survives, it may need to be repositioned. If both parent and seed are under closed canopy, the seed is dropped where it is. If the parent is in gap and seedling is in canopy, a new distance is calculated as though the parent was also in canopy. The shortest of the two distances is used to determine where the seed lands. If the seed lands in a gap cell, the behavior "walks out" the line of the seed's path from parent to target landing cell, checking each intermediate grid cell's cover along the way. If any of the grid cells in the line are under canopy cover, the seed drops in the first canopy cell it reaches.

How to apply it

Apply this behavior to all trees of at least the minimum reproductive age for your chosen species. If the minimum reproductive age is less than the [Minimum adult DBH](#), be sure to apply this behavior to saplings as well as adults. In the parameters, choose the appropriate probability distribution function for each species for each forest cover type.

This behavior can be used to simulate the suckering of stumps. Apply this behavior to tree type "[stump](#)" of your chosen species. Stumps reproduce like other parent trees, except they always assume they are in a gap. They use the same probability distribution function and parameters as live members of their species, but they get their own β and STR values so that they can produce different numbers of seeds.

Masting spatial disperse behavior

This behavior is a variant of the [Non-gap spatial disperse](#) behavior that adds masting and more stochasticity in seed production.

Parameters for this behavior

Parameter name	Description
Canopy Function Used	The probability distribution function to be used to distribute seeds in canopy conditions. For the behaviors Non-gap spatial disperse and Masting spatial disperse, these PDFs are always the ones used.
Lognormal Canopy X_0	The mean of the lognormal function under canopy conditions, or under non-masting conditions in the case of Masting spatial disperse (see equation below). This is only required if the canopy probability distribution function is lognormal.
Lognormal Canopy X_b	The standard deviation of the lognormal function under canopy conditions, or under non-masting conditions in the case of Masting spatial disperse (see equation below). This is only required if the canopy probability distribution function is lognormal.
Masting Disperse -	The β value under masting conditions.

Masting Beta	
Masting Disperse - Masting CDF "a"	The "a" value in the cumulative density function that is used to decide when masting events occur.
Masting Disperse - Masting CDF "b"	The "b" value in the cumulative density function that is used to decide when masting events occur.
Masting Disperse - Masting Group	Species in the same group always mast together. If all the group numbers are different, then each species masts separately. The actual numbers do not matter, just whether species have identical numbers.
Masting Disperse - Masting Lognormal X_0	The mean of the lognormal function under masting conditions. This is only required for a species if the canopy probability distribution function for that species is lognormal.
Masting Disperse - Masting Lognormal X_b	The standard deviation of the lognormal function under masting conditions. This is only required for a species if the canopy probability distribution function for that species is lognormal.
Masting Disperse - Masting STR Mean	The mean annual STR value under masting conditions. If the Masting Disperse - STR Draw PDF is Deterministic, then this is the STR value used.
Masting Disperse - Masting STR Standard Deviation	The standard deviation of the STR value under masting conditions. If the Masting Disperse - STR Draw PDF is Deterministic, then this value is not used.
Masting Disperse - Mast Proportion Participating (0-1)	The proportion of all adults for a species that participate in disperse during a masting timestep, as a value between 0 and 1.
Masting Disperse - Non-Masting Beta	The β value under non-masting conditions.
Masting Disperse - Non-Masting STR Mean	The mean annual STR value under non-masting conditions. If the Masting Disperse - STR Draw PDF is Deterministic, then this is the STR value used.
Masting Disperse - Non-Masting STR Standard Deviation	The standard deviation of the STR value under non-masting conditions. If the Masting Disperse - STR Draw PDF is Deterministic, then this value is not used.
Masting Disperse - Non-Mast Proportion Participating (0-1)	The proportion of all adults for a species that participate in disperse during a non-masting timestep, as a value between 0 and 1.
Masting Disperse - Masting Weibull	The dispersal value for the weibull function under masting conditions. This is only required for a species if the canopy probability distribution

Dispersal	function for that species is weibull.
Masting Disperse - Masting Weibull Theta	The θ for the weibull function under masting conditions. This is only required for a species if the canopy probability distribution function for that species is weibull.
Masting Disperse - Stochastic STR Draw Frequency	If the STR value is stochastic, this determines whether a new value is generated once per species per timestep or once per tree per timestep. If the Masting Disperse - STR Draw PDF is Deterministic, then this value is not used.
Masting Disperse - STR Draw PDF	Whether the STR value should be deterministic, or generated each timestep using a normal or lognormal distribution.
Minimum DBH for Reproduction, in cm	The minimum DBH at which a tree can reproduce. This value does not have to match the Minimum adult DBH .
Seed Distribution	<p>The distribution method to be applied to seeds (randomization). The forms for these functions can be found here. Choices are:</p> <ul style="list-style-type: none"> • Deterministic - no randomization. • Poisson - use the number of seeds as the mean in a Poisson probability distribution function. • Normal - use the number of seeds as the mean in a normal probability distribution function. You must then supply a standard deviation for the function. • Lognormal - use the number of seeds as the mean in a lognormal probability distribution function. You must then supply a standard deviation for the function. • Negative binomial - use the number of seeds as the mean in a negative binomial probability distribution function. You must then supply a clumping parameter.
Seed Dist. Clumping Parameter (Neg. Binomial)	If you have chosen the negative binomial probability distribution function for "Seed distribution", this is the clumping parameter of the function, in seeds per m^2 . If you have not chosen that PDFs, then this parameter is not required.
Seed Dist. Std. Deviation (Normal or Lognormal)	If you have chosen the normal or lognormal probability distribution functions for "Seed distribution", this is the standard deviation of the function, in seeds per m^2 . If you have not chosen these PDFs, then this parameter is not required.
Weibull Canopy Dispersal	The dispersal value for the Weibull function under canopy conditions, or under non-masting conditions in the case of Masting spatial disperse (see equation below). This is only required if the canopy probability distribution function is Weibull.

Weibull Canopy
Theta

The θ for the Weibull function under canopy conditions, or under non-masting conditions in the case of Masting spatial disperse (see equation below). This is only required if the canopy probability distribution function is Weibull.

How it works

Deciding when to mast. For each timestep, the probability of masting for each species is calculated from the following cumulative distribution function:

$$y = \frac{1}{1 + \left(\frac{X}{a}\right)^b}$$

where:

- y is the probability of masting
- X is the number of years since last mast
- a is the **Masting Disperse - Masting CDF "a"** parameter
- b is the **Masting Disperse - Masting CDF "b"** parameter

When the run starts, it is assumed a masting last event took place in timestep -1. A random number is used to determine whether a mast occurs in the current timestep. Disperse happens the same way in mast and non-mast timesteps, but the parameters used are different.

Species may be organized into groups to create synchrony in masting. The **Masting Disperse - Masting Group** parameter allows you to assign group numbers to species. The actual value of the group number is not important. It only matters if more than one species has the same number. If one species in a group masts, all species in that group do. Each group's mast decision is made separately, so sometimes more than one group may mast at a time. If all species have a different group number, then they all mast independently of one another.

Which trees disperse. Of the group of trees eligible to disperse (those with DBHs above the value in the **Minimum DBH for Reproduction, in cm** parameter), some can be randomly selected to participate in disperse. The proportion dispersing is set in **Masting Disperse - Mast Proportion Participating (0-1)** for mast timesteps, and **Masting Disperse - Non-Mast Proportion Participating (0-1)** for non-mast timesteps. The group of trees participating is chosen again each timestep. No adjustment is made to the number of seeds produced per tree. Fewer trees participating in disperse means fewer total seeds will be produced.

STR stochasticity. The STR value may be randomized each timestep. Use the **Masting Disperse - STR Draw PDF** parameter to choose from a normal or lognormal probability distribution. You can then set the mean and standard deviations for each species, which are

different in masting and non-masting timesteps. You can also leave the STR value deterministic, in which case the mean STR value is used directly.

If you choose to use a stochastic STR, the STR value can be generated once per species per timestep, or once per tree per timestep. If the value is generated once per species, all individuals of that species use the same STR value that timestep.

Once the behavior has decided whether masting occurs, and what the STR values are, then disperse proceeds exactly as described in the [Non-gap spatial disperse](#) behavior.

How to apply it

Apply this behavior to all trees of at least the minimum reproductive age for your chosen species. If the minimum reproductive age is less than the [Minimum adult DBH](#), be sure to apply this behavior to saplings as well as adults.

Stochastic Double Logistic Temp Dependent Neighborhood Disperse behavior

This behavior calculates seed density based on annual mean temperature and the basal area of neighborhood adults.

Parameters for this behavior

Parameter name	Description
Minimum DBH for Reproduction, in cm	The minimum DBH at which a tree can reproduce. This value does not have to match the Minimum adult DBH .
Colonization PA	PA in the function determining probability of colonization.
Colonization PB	PB in the function determining probability of colonization.
Colonization PM	PM in the function determining probability of colonization.
Cumulative Colonization Probability Period (years)	The period over which the probability of colonization is cumulative.
Fecundity Temperature Effect A1	A ₁ in the temperature effect portion of fecundity. Ignored if "Use Temperature-Dependent Fecundity?" is set to false.
Fecundity	B ₁ in the temperature effect portion of fecundity. Ignored if "Use

Temperature Effect Bl	Temperature-Dependent Fecundity?" is set to false.
Fecundity Temperature Effect Cl	C _l in the temperature effect portion of fecundity. Ignored if "Use Temperature-Dependent Fecundity?" is set to false.
Fecundity Temperature Effect Ah	A _h in the temperature effect portion of fecundity. Ignored if "Use Temperature-Dependent Fecundity?" is set to false.
Fecundity Temperature Effect Bh	B _h in the temperature effect portion of fecundity. Ignored if "Use Temperature-Dependent Fecundity?" is set to false.
Fecundity Temperature Effect Ch	C _h in the temperature effect portion of fecundity. Ignored if "Use Temperature-Dependent Fecundity?" is set to false.
Max Search Distance for Conspecific Adults (m)	The maximum distance to search for conspecific adults when determining number of seeds.
Original Analysis Plot Size (m ²)	The size of the seedling plots in the original parameter analysis, in square meters. This is used to scale the per-grid-cell seed values.
Presence Threshold in Absence of Adults (0-1)	Threshold value, between 0 and 1, of the presence test function above which a species will be allowed to disperse in the absence of parents. 0 always includes a species, 1 always excludes it.
Seeds RA	RA in the final seed calculation.
Seeds RB	RB in the final seed calculation.
Use Temperature-Dependent Fecundity?	Whether or not to use the temperature effect portion of fecundity. If this is false, fecundity = RB.

How it works

The mean number of seeds in each cell of the [Dispersed Seeds](#) grid is calculated as:

$$Seeds = RA + fec * BAC$$

where:

- *Seeds* is the mean number of seeds in the cell
- *RA* is the **Seeds RA** parameter

- BAC is the total basal area of neighborhood conspecific adults in square meters within a radius of **Max Search Distance for Conspecific Adults (m)**
- fec is a fecundity term (more below)

The mean seed value, above, is used as the mean on a Poisson random draw. The final seed number assigned to the grid is:

$$Final\ seeds = seeds * (CA/OA) * Y$$

where:

- $seeds$ is the result of the Poisson draw
- CA is the area of the grid cell, in square meters
- OA is the **Original Analysis Plot Size (m2)** parameter
- Y is the number of years per timestep

Note that this behavior works on a per-grid-cell basis, rather than calculating seed densities on a per-square-meter basis. This is because the Poisson function is influenced by seed grid cell size. You can use the **Original Analysis Plot Size (m2)** parameter to scale results to original analysis plot size, but for best results, the seed grid cell size should be set to the same or slightly larger than the original analysis seed plot size.

"fec" is a per capita seedling production (fecundity) term. It is a function of temperature and is calculated as:



where:

- RB is the **Seeds RB** parameter
- T is the annual mean temperature, in **degrees Kelvin**, calculated from the value in degrees C in the [Plot](#)
- a_l is the **Fecundity Temperature Effect Al** parameter
- b_l is the **Fecundity Temperature Effect Bl** parameter
- c_l is the **Fecundity Temperature Effect Cl** parameter
- a_h is the **Fecundity Temperature Effect Ah** parameter
- b_h is the **Fecundity Temperature Effect Bh** parameter
- c_h is the **Fecundity Temperature Effect Ch** parameter

The temperature-dependent portion of fecundity is optional. If the parameter **Use Temperature-Dependent Fecundity?** is set to false, then $fec = RB$.

Colonization

Note that the RA parameter in the mean seeds equation is an intercept, potentially allowing bath rain of seeds for species for which there are no parents present. To manage this, the behavior uses a colonization test. The **cumulative** probability of colonization is:



where:

- PC_c is the cumulative probability of colonization
- pa is the **Colonization PA** parameter
- pb is the **Colonization PB** parameter
- pm is the **Colonization PM** parameter
- T is the annual mean temperature, in degrees Celsius, as entered for the [Plot](#)

PC_c is the cumulative probability of colonization over an arbitrary time period T . PC_c is used to calculate the annualized probability of colonization as:

$$PC_a = 1 - [(1 - PC_c)^{(1/T)}]$$

where:

- PC_a is the annualized probability of colonization
- T is the **Cumulative Colonization Probability Period (years)** parameter

The behavior compares PC_a to a random number to determine whether this species is allowed to colonize this timestep. If so, it disperses as described above.

How to apply it

Apply this behavior to adults of the species you wish to use.

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Temperature dependent neighborhood disperse behavior

This behavior calculates seed density based on annual mean temperature and the basal area of neighborhood adults.

Parameters for this behavior

Parameter name	Description
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Minimum DBH for Reproduction, in cm	The minimum DBH at which a tree can reproduce. This value does not have to match the Minimum adult DBH .
Seed Distribution	<p>The distribution method to be applied to seeds (randomization). The forms for these functions can be found here. Choices are:</p> <ul style="list-style-type: none"> • Deterministic - no randomization. • Poisson - use the number of seeds as the mean in a Poisson probability distribution function. • Normal - use the number of seeds as the mean in a normal probability distribution function. You must then supply a standard deviation for the function. • Lognormal - use the number of seeds as the mean in a lognormal probability distribution function. You must then supply a standard deviation for the function. • Negative binomial - use the number of seeds as the mean in a negative binomial probability distribution function. You must then supply a clumping parameter.
Seed Dist. Clumping Parameter (Neg. Binomial)	If you have chosen the negative binomial probability distribution function for "Seed distribution", this is the clumping parameter of the function, in seeds per m ² . If you have not chosen that PDFs, then this parameter is not required.
Seed Dist. Std. Deviation (Normal or Lognormal)	If you have chosen the normal or lognormal probability distribution functions for "Seed distribution", this is the standard deviation of the function, in seeds per m ² . If you have not chosen these PDFs, then this parameter is not required.
Temp Dep Neigh Disperse - A	A in the seed density calculation.
Temp Dep Neigh Disperse - B	B in the seed density calculation.
Temp Dep Neigh Disperse - M	M in the seed density calculation.
Temp Dep Neigh Disperse - N	N in the seed density calculation.
Temp Dep Neigh Disperse - Max Distance for Conspecific Adults (m)	The maximum distance to search for conspecific adults.

Temp Dep Neigh Disperse - Presence B	B in the presence test calculation.
Temp Dep Neigh Disperse - Presence M	M in the presence test calculation.
Temp Dep Neigh Disperse - Presence Threshold (0-1)	Threshold value, between 0 and 1, of the presence test function above which a species will be allowed to disperse in the absence of parents. 0 always includes a species, 1 always excludes it.

How it works

This behavior examines the neighborhood of each grid cell of the [Dispersed Seeds](#) grid to determine how many seeds to place in that cell. Expected seed density in a cell for a particular species is calculated as:

$$Seeds = A + fec * BAC$$

where:

- *Seeds* is number of seeds per square meter
- *A* is the **Temp Dep Neigh Disperse - A** parameter
- *BAC* is the total basal area of neighborhood conspecific adults in square meters
- *fec* is a fecundity term

"fec" is a per capita seedling production (fecundity) term. It is a function of temperature and is calculated as:

$$fec = B * e^{-0.5 \left[\frac{T-M}{N} \right]^2}$$

where:

- *B* is the **Temp Dep Neigh Disperse - B** parameter
- *M* is the **Temp Dep Neigh Disperse - M** parameter
- *N* is the **Temp Dep Neigh Disperse - N** parameter
- *T* is the annual mean temperature, in degrees Celsius, as entered for the [Plot](#)

BAC is the basal area of all conspecific adult trees found within a given radius of the grid cell center. The radius is set using the **Temp Dep Neigh Disperse - Max Distance for Conspecific Adults (m)** parameter.

Note that the A parameter is an intercept, potentially allowing bath rain of seeds for species for which there are no parents present. To manage this, the behavior uses a "presence test", which is the normalized probability of finding a species on a plot as a function of temperature:

$$P = e^{-0.5\left(\frac{T-M}{B}\right)^2}$$

where:

- P is the normalized presence probability
- B is the **Temp Dep Neigh Disperse - Presence B** parameter, which controls the width of the peak
- M is the **Temp Dep Neigh Disperse - Presence M** parameter, which is the function mean, or the temperature (in degrees Celsius) at which the probability of finding the species equals 1
- T is the annual mean temperature, in degrees Celsius, as entered for the [Plot](#)

You control the acceptable threshold for the presence test using the **Temp Dep Neigh Disperse - Presence Threshold (0-1)** parameter. If the value of the presence test function is above this value, the species is allowed to disperse in the absence of adults in the plot. A threshold value of 0 always allows the species to disperse; a value of 1 always excludes it. Note that if there are adults of that species in the plot, the species disperses, no matter what the presence test says.

Once the number of seeds per square meter for a species has been calculated, it is multiplied by the grid cell area and number of years per timestep to determine the final number of seeds to add to the grid cell.

How to apply it

Apply this behavior to adults of the species you wish to use.

Seed predation behaviors

Seed predation occurs after [seed dispersal](#) has occurred and serves to reduce the number of seeds by simulating seed consumption by predators.

Behavior	Description
Functional response seed predation behavior	Simulates functional response seed predation, where the number of predators is a function of the amount of food that has been consumed.
Neighborhood seed	Simulates seed predation as a function of tree neighborhood and masting events.

predation behavior	
Functional response seed predation behavior (linked)	Works together with the Neighborhood seed predation behavior (linked) behavior to model seed predation.
Neighborhood seed predation behavior (linked)	Works together with the Functional response seed predation behavior (linked) behavior to model seed predation.

Functional response seed predation

This behavior simulates functional response seed predation, where the number of predators is a function of the amount of food that has been consumed. Since seed predator life cycles are often very short, this behavior runs as a mini-model within the context of the larger simulation. It simulates weekly timesteps of seed fall, seed consumption, and predator response for as much of the year as the user desires. The mini-model simulates a single year, which starts at the beginning of seed fall. It is possible to define two seasons during the year with different parameters for seed consumption. All species are assumed to drop seeds at the same time, at a constant rate. You set the number of weeks that seedfall should occur. Once seedfall is over, there are no new additions to the predator food pool. There is then an optional period of germination in which the food pool of seeds is further reduced by some proportion of those remaining seeds germinating into seedlings (seedlings cannot be eaten). Once the model has finished running, the leftover seeds that were not consumed by predators, or those seeds that escaped through germination, are available as input to the [Establishment behaviors](#).

Parameters for this behavior

Parameter name	Description
Func Resp - Demographic Efficiency, Season 1	The seed predator population demographic efficiency for season 1.
Func Resp - Demographic Efficiency, Season 2	The seed predator population demographic efficiency for season 2.
Func Resp - Density Dependent Coeff,	The coefficient describing the effect that density-dependent factors have on the predator population instantaneous rate of change, in season 1.

Season 1	
Func Resp - Density Dependent Coeff, Season 2	The coefficient describing the effect that density-dependent factors have on the predator population instantaneous rate of change, in season 2.
Func Resp - Foraging Efficiency	The predator population foraging efficiency for each seed species.
Func Resp - Keep Predator Densities Between Timesteps	If true, this means that the final predator density at the end of the behavior mini-model run is the initial density for the next mini-model run. If false, every time the behavior mini-model runs, it is re-initialized with the value of the "Predator initial density - num/sq m" parameter.
Func Resp - Max Decline Rate, Season 1, predators/week	The maximum rate of decline in the predator population in the absence of any food, in predators per week, for season 1.
Func Resp - Max Decline Rate, Season 2, predators/week	The maximum rate of decline in the predator population in the absence of any food, in predators per week, for season 2.
Func Resp - Max Intake Rate - seeds per predator per day	The maximum number of seeds of each species that can be eaten by one predator in one day.
Func Resp - Number of Weeks in Which Seedfall Occurs	The number of weeks at the beginning of the behavior mini-model run that seedfall occurs.
Func Resp - Predator Initial Density - num/sq m	The initial density of the predator population, in numbers per m ² . This will be used the first time this behavior is run. Whether this density is used for subsequent behavior mini-model runs depends on the value of the "Keep Predator Densities Between Timesteps" parameter.
Func Resp - Proportion of Seeds Germinating Each Week	During the period that germination occurs, this is the fraction of the seed pool that is removed due to seed germination. Expressed as a value between 0 and 1.
Func Resp - Seed Predation Output Filename, If Desired	The filename where the mini-model will store its intermediate results for later analysis, if desired. This value is not required.
Func Resp - Week Germination Begins	The week during the behavior mini-model run that germination begins to occur. If you do not want germination to occur, set this value greater than or equal to the "Weeks to run seed predation model (1 - 52)" parameter. This value must be between 0 and 52.

Func Resp - Week Season 2 Begins	The week that the second season begins, if desired.
Func Resp - Weeks to Run Seed Predation Model (1 - 52)	The number of weeks (timesteps) to run the behavior's mini-model. This number must be between 1 and 52.

How it works

The behavior's mini-model begins with the number of seeds of each species to which it is applied that are available in each cell of the [Dispersed Seeds](#) grid. Each cell gets its own run of the mini-model. The pool of seeds in one cell for all species to which this behavior applies is treated as a single food pool for one year's time (even if the model [timestep length](#) is greater than one year). For all the species to which this behavior is applied, the seeds are assumed to be equally available; however, each species can have its own parameters for actual consumption rate. The initial number of predators is calculated from the **Predator initial density - num/sq m** parameter or, if the mini-model has run before and the **Preserve predator densities between SORTIE timesteps** parameter is set to true, from the final density of the last mini-model run.

The behavior mini-model run begins at the part of the year in which seedfall occurs. The number of seeds in the seed rain is the total seed pool, which is evenly divided over the user-defined seed rain length. The predator population has as a food source the number of seeds added during the current week's rain (if the rain is going on) plus any leftover seeds from previous weeks which have not been consumed. Beginning at a certain week in the spring, the number of seeds available to the mice is further reduced by a certain percentage each week to simulate germination. Once germination begins, it continues until the predator model finishes running. In order to correctly calculate mouse consumption and ensure that the seeds which germinate are actually available later, the behavior keeps track of the seeds actually consumed; it is this number which is subtracted from total seeds at the end.

Seed offtake for each week is calculated as

$$O = \sum (IR_s * N)$$

where

- O is offtake (total number of seeds consumed)
- IR_s is per capita seed offtake for each species
- N is the number of predators

Per capita seed offtake for a single seed species is

$$IR_s = c_s(1 - e^{-(S*D)}) * p_s$$

where

- c_s is the **Func Resp - Max Intake Rate - seeds per predator per day** parameter for that seed species
- S is the number of seeds per predator per day
- D is the **Func Resp - Foraging Efficiency** parameter
- p_s is the proportion of the total seed pool made up by that species

Predator response to food availability can be different for two seasons in the year. The dividing line between the seasons is given with the **Func Resp - Week Season 2 Begins** parameter. If you want a uniform response with no seasonal differences, you can set this value to 1 or 52, or set the predator response parameters to be the same for both seasons.

The number of predators in each cell's population is calculated as

$$N_t = N_{t-1} * e^{r_{t-1}}$$

where

- N_t is number of predators for the current timestep
- N_{t-1} is number of predators in the previous timestep
- r_{t-1} is instantaneous rate of change in predator abundance for the previous timestep

The instantaneous rate of change per week, r , is calculated as

$$r = (a + d * \Sigma (IR_s) + g*N) / 12$$

where

- a is the **Func Resp - Max Decline Rate, Season 1 (or 2), predators/week** parameter
- d is the **Func Resp - Demographic Efficiency, Season 1 (or 2)** parameter
- g is the **Func Resp - Density Dependent Coeff, Season 1 (or 2)** parameter
- N is number of predators per hectare

How to apply it

This behavior may be applied to seeds of any species. Any species to which it is applied must also have a [Disperse behavior](#) applied as well.

Neighborhood seed predation

This simulates seed predation as a function of tree neighborhood and masting events. The same equations are used to calculate the amount of seed eaten, but there are different parameters for masting and non-masting timesteps. Masting events can be determined in one of two ways: by seed levels rising above a threshold that you set, or by masting having occurred as defined by one of the masting disperse behaviors.

Parameters for this behavior

Parameter name	Description
Neighborhood Predation - Counts For Masting?	Determines which species are included when totaling up seed numbers to determine whether or not masting has occurred.
Neighborhood Predation - Mast Event Decision Method	Determines how masting is decided. If this is set to "Seed threshold", then masting events occur when seed levels are above a set threshold. If this is set to "Ask disperse", then masting has occurred if any of the applicable species masted as determined by the masting disperse behaviors.
Neighborhood Predation - Masting "p0"	The "p ₀ " term in the seed offtake equation under masting conditions.
Neighborhood Predation - Species i Masting "pn"	The "p _n " term for species i in the seed offtake equation under masting conditions.
Neighborhood Predation - Masting Seed Density, #/m ² /yr	The density of edible seed that indicates masting has occurred.
Neighborhood Predation - Minimum Neighbor DBH (cm)	The minimum DBH of trees to be included when calculating the basal area composition of the neighborhood.
Neighborhood Predation - Neighbor Search Radius (m)	The radius to search for trees when calculating the basal area composition of the neighborhood.
Neighborhood Predation - Non-Masting "p0"	The "p ₀ " term in the seed offtake equation under non-masting conditions.
Neighborhood Predation - Species i Non-Masting "pn"	The "p _n " term for species i in the seed offtake equation under non-masting conditions.

How it works

Masting timesteps are those with a heavy density of edible seeds. The first step in a given time step is deciding whether or not masting is occurring. There are two methods available for making the masting decision. You set your chosen method using the **Neighborhood Predation - Mast Event Decision Method** parameter.

If the event decision method is set to "Seed threshold", masting events occur whenever seed density rises above a certain threshold. You set the threshold for this density in the **Neighborhood Predation - Masting Seed Density, #/m²/yr** parameter. You then set which species are included in the mast count with the **Neighborhood Predation - Counts For Masting?** parameter. (Species which do not count towards masting may still be predated.) The seed density is set as an annual average so the density will be calculated the same way for different-length timesteps. If the total plotwide average annual seed density is greater than this value, the timestep is treated as a masting timestep. Only those seeds of species to which this behavior applies are considered in the density.

If the event decision method is set to "Ask disperse", masting events occur whenever any of the species to which this behavior applies masts according to either the [Masting non-spatial disperse behavior](#) or the [Masting spatial disperse behavior](#). You can use either of these behaviors, both of them, or neither (in which case masting never occurs). If any species to which this behavior is applied has masted with either behavior, then this is a masting time step.

If there are no adult trees in the plot, then masting does not occur according to either method.

The seeds in each grid cell of the [Dispersed Seeds](#) grid are treated separately for predation, according to their local neighborhood composition. The relative basal area of each species is calculated, from the total basal area of individuals within **Neighborhood Predation - Neighbor Search Radius (m)** meters of the grid cell center that have a DBH greater than **Neighborhood Predation - Minimum Neighbor DBH (cm)**. The amount of seed eaten for each species is calculated as:

$$Y = \frac{e^{(p_0+X)}}{1 + e^{(p_0+X)}}$$

where Y is the proportion of that species' seed that is eaten, and p_0 is either the **Neighborhood Predation - Masting "p0"** or the **Neighborhood Predation - Non-Masting "p0"** parameter for that species. X is calculated as follows:

$$X = \sum_{n=1}^N p_n RBA_n$$

where p_n is either the **Neighborhood Predation - Species i Masting "pn"** or the **Neighborhood Predation - Species i Non-Masting "pn"** of species n , and RBA_n is the relative basal are of species n .

The eaten seeds are removed from the [Dispersed Seeds](#) grid.

In order to make results more verifiable, Neighborhood Seed Predation produces a grid called [Neighborhood Seed Predation](#). This grid stores the pre predation seed rain and amount of seeds eaten for each cell in the [Dispersed Seeds](#) grid. This grid has no effect on calculations but can be saved in the output file for review.

How to apply it

This behavior may be applied to seeds of any species. Any species to which it is applied must also have a [Disperse behavior](#) applied as well.

Functional response seed predation (linked)

Parameters for this behavior

Parameter name	Description
Func Resp - Demographic Efficiency, Season 1	The seed predator population demographic efficiency for season 1.
Func Resp - Demographic Efficiency, Season 2	The seed predator population demographic efficiency for season 2.
Func Resp - Density Dependent Coeff, Season 1	The coefficient describing the effect that density-dependent factors have on the predator population instantaneous rate of change, in season 1.
Func Resp - Density Dependent Coeff, Season 2	The coefficient describing the effect that density-dependent factors have on the predator population instantaneous rate of change, in season 2.
Func Resp - Foraging Efficiency	The predator population foraging efficiency for each seed species.
Func Resp - Keep Predator Densities Between Timesteps	If true, this means that the final predator density at the end of the behavior mini-model run is the initial density for the next mini-model run. If false, every time the behavior mini-model runs, it is re-initialized with the value of the "Predator initial density - num/sq m" parameter.
Func Resp - Max Decline Rate, Season 1, predators/week	The maximum rate of decline in the predator population in the absence of any food, in predators per week, for season 1.

Func Resp - Max Decline Rate, Season 2, predators/week	The maximum rate of decline in the predator population in the absence of any food, in predators per week, for season 2.
Func Resp - Max Intake Rate - seeds per predator per day	The maximum number of seeds of each species that can be eaten by one predator in one day.
Func Resp - Number of Weeks in Which Seedfall Occurs	The number of weeks at the beginning of the behavior mini-model run that seedfall occurs.
Func Resp - Predator Initial Density - num/sq m	The initial density of the predator population, in numbers per m ² . This will be used the first time this behavior is run. Whether this density is used for subsequent behavior mini-model runs depends on the value of the "Keep Predator Densities Between Timesteps" parameter.
Func Resp - Proportion of Seeds Germinating Each Week	During the period that germination occurs, this is the fraction of the seed pool that is removed due to seed germination. Expressed as a value between 0 and 1.
Func Resp - Seed Predation Output Filename, If Desired	The filename where the mini-model will store its intermediate results for later analysis, if desired. This value is not required.
Func Resp - Week Germination Begins	The week during the behavior mini-model run that germination begins to occur. If you do not want germination to occur, set this value greater than or equal to the "Weeks to run seed predation model (1 - 52)" parameter. This value must be between 0 and 52.
Func Resp - Week Season 2 Begins	The week that the second season begins, if desired.
Func Resp - Weeks to Run Seed Predation Model (1 - 52)	The number of weeks (timesteps) to run the behavior's mini-model. This number must be between 1 and 52.

How it works

This behavior is used together with the [Neighborhood seed predation behavior \(linked\)](#) behavior. The two behaviors work together to model seed predation.

This behavior performs the functional response model in almost exactly the same way as the [Functional response seed predation](#) behavior. However, instead of removing the eaten seeds, it calculates a whole-plot offtake rate for the group of species to which it has been applied. This

rate is always for the plot as a whole, not for individual cells of the seed grid. This offtake rate is then available for use by the [Neighborhood seed predation behavior \(linked\)](#) behavior, and no further action is taken.

This behavior can be used in the same run with the non-linked version of this behavior. The two sets of species are kept completely separate, and there are two separate sets of parameters.

How to apply it

This behavior may be applied to seeds of any species. Any species to which it is applied must also have a [Disperse behavior](#) applied as well. Presumably, the [Neighborhood seed predation behavior \(linked\)](#) behavior will be applied to the same set of species, and should be placed after this behavior in the ordered list of model behaviors.

Neighborhood seed predation (linked)

Parameters for this behavior

Parameter name	Description
Neighborhood Predation - "p0"	The "p0" term in the seed offtake equation when in linked mode.
Neighborhood Predation - Species i "pn"	The "pn" term for species i in the seed offtake equation when in linked mode.
Neighborhood Predation - Minimum Neighbor DBH (cm)	The minimum DBH of trees to be included when calculating the basal area composition of the neighborhood, when in linked mode.
Neighborhood Predation - Neighbor Search Radius (m)	The radius to search for trees when calculating the basal area composition of the neighborhood, when in linked mode.

How it works

This behavior is used together with the [Functional response seed predation behavior \(linked\)](#) behavior. The two behaviors work together to model seed predation.

The actual amount of seed eaten is calculated by the [Functional response seed predation behavior \(linked\)](#) behavior. This behavior then distributes the offtake according to neighborhood composition.

The behavior begins by calculating the Y values for each grid cell as in the non-linked version (masting is ignored - there is only one set of parameters). Then the Y values are adjusted so that their mean is equal to the amount of whole-plot offtake Z as calculated by the [Functional response seed predation behavior \(linked\)](#). The adjustments are made as follows:

1. Calculate $\text{logit}(Z)$
2. Calculate the $\text{logit}(Y)$ s and subtract the minimum value from each (as well as the $\text{logit}(Z)$) so they will all be positive
3. Average the $\text{logit}(Y)$ s
4. Divide $\text{logit}(Z)$ by average $\text{logit}(Y)$ to get a correction factor
5. Multiply each $\text{logit}(Y)$ by the correction factor
6. Add back the same minimum value formerly subtracted
7. Back transform $\text{logit}(Y)$ to Y and use when removing seeds

Then the seeds are removed according to the adjusted Y values.

This behavior can be used in the same run with the non-linked version of this behavior. The two sets of species are kept completely separate, and there are two separate sets of parameters.

This behavior may be applied to seeds of any species. Any species to which it is applied must also have a [Disperse behavior](#) applied, as well as the [Functional response seed predation behavior \(linked\)](#). This behavior should be placed after that behavior in the ordered list of model behaviors.

In order to make results more verifiable, Neighborhood Seed Predation produces a grid called [Neighborhood Seed Predation](#). This grid stores the pre predation seed rain and amount of seeds eaten for each cell in the [Dispersed Seeds](#) grid. This grid has no effect on calculations but can be saved in the output file for review.

Establishment behaviors

Establishment behaviors assess seed survival and create new seedlings from seeds. Establishment behaviors do not create or distribute the seeds. The [Disperse behaviors](#) perform that function.

The seed survival behaviors act to reduce the number of seeds based on various environmental effects. They can be used alone or in combination. Once they have completed their work, the number of surviving seeds can be turned into seedlings by either the [Seed Establishment](#) or [Establishment with Microtopography](#) behaviors.

Behavior	Description
Conspecific Tree Density Dependent Seed Survival	Assesses seed survival as a function of the local density of conspecific trees.

Density Dependent Seed Survival	Assesses seed survival as a function of the local density of conspecific seeds.
Establishment with Microtopography	Simulates microtopography in the plot and assigns new seedlings a rooting height as a function of the type of substrate on which they land.
Light Dependent Seed Survival	Assesses seed survival as a function of the Global Light Index (GLI) of the location in which a seed lands.
Proportional Seed Survival	Reduces the number of seeds by a set amount.
Seed Establishment	Converts seeds into seedlings.
Storm Light Dependent Seed Survival	This behavior assesses seed survival as a function of the light level of the location in which a seed lands.
Substrate Based Seed Survival With Microtopography	This behavior assesses seed survival based on substrate conditions, allowing for site microtopography to influence seed survival.
Substrate Dependent Seed Survival No Gap Status	This behavior assesses seed survival as a function of the substrate composition of the grid cells in which seeds land.
Substrate Dependent Seed Survival With Gap Status	This behavior assesses seed survival as a function of both the substrate composition of the grid cells in which seeds land and the cells' forest cover (gap or canopy).

Conspecific Tree Density Dependent Seed Survival

This behavior assesses seed survival as a function of the local density of conspecific trees. This behavior is very similar to [Density Dependent Seed Survival](#).

Parameters for this behavior

Parameter name	Description
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Conspecific Tree Minimum Neighbor Height (m)	The minimum height, in meters, of conspecific neighbors to include in local density calculations.
Conspecific Tree Search Radius (m)	The radius, in meters, to search for conspecific neighbors to include in local density calculations.
Slope of Density Dependence	The slope of the density dependence function for determining how many seedlings establish per square meter (c in the equations below).
Steepness of Density Dependence	The steepness of the density dependence function for determining how many seedlings establish per square meter (δ in the equations below).

How it works

This behavior takes the seeds that have been dispersed to each grid cell of the [Dispersed Seeds grid](#) and calculates how many will survive. The survival probability is a function of the density of conspecific neighbors.

The density of conspecific neighbors is the number of stems per square meter of trees above the height set in the **Conspecific Tree Minimum Neighbor Height (m)** parameter, within the radius set in the **Conspecific Tree Search Radius (m)** parameter.

The number of seeds that survives is calculated as

$$R_{sp} = S_{sp} * \exp(-c * Den_{sp}^{\delta})$$

where:

- R_{sp} is the number of surviving seeds of a given species in the seed grid cell
- S_{sp} is the original number of seeds of that species in that grid cell
- Den_{sp} is the density of conspecific neighbors (number per square meter) of that species in that grid cell
- c is the **Slope of Density Dependence** parameter
- δ is the **Steepness of Density Dependence** parameter

Once the number of surviving seeds has been determined, the behavior assigns that number back to the Dispersed Seeds grid cell.

How to apply it

Apply this behavior to seeds of your desired species. Any species to which it is applied must also have any [disperse behavior](#) applied.

Density Dependent Seed Survival

This behavior assesses seed survival as a function of the local density of conspecific seeds.

Parameters for this behavior

Parameter name	Description
Slope of Density Dependence	The slope of the density dependence function for determining how many seedlings establish per square meter (c in the equations below).
Steepness of Density Dependence	The steepness of the density dependence function for determining how many seedlings establish per square meter (δ in the equations below).

How it works

This behavior takes the seeds that have been dispersed to each grid cell of the [Dispersed Seeds grid](#) and calculates how many will survive. The number of seeds that survives is calculated as

$$R_{sp} = S_{sp} * \exp(-c * Den_{sp}^{\delta})$$

where:

- R_{sp} is the number of surviving seeds of a given species in the seed grid cell
- S_{sp} is the original number of seeds of that species in that grid cell
- Den_{sp} is the density of seeds (number per square meter) of that species in that grid cell
- c is the **Slope of Density Dependence** parameter
- δ is the **Steepness of Density Dependence** parameter

Once the number of surviving seeds has been determined, the behavior assigns that number back to the Dispersed Seeds grid cell. If there is only one seed in a grid cell, it always survives.

How to apply it

Apply this behavior to seeds of your desired species. Any species to which it is applied must also have any [disperse behavior](#) applied.

Establishment with Microtopography

This behavior germinates seeds into seedlings. It simulates microtopography in the plot and assigns new seedlings a rooting height as a function of the type of substrate on which they land (from the [Substrate behavior](#)). This behavior is designed to work with both the Substrate and the

[Beer's law light filter](#) behaviors to simulate shading by ferns. The rooting height that seedlings get influences the amount of light they receive. Seeds that land on fresh logs, in addition, are eligible for a respite from the Beer's law light filter behavior.

Parameters for this behavior

Parameter name	Description
Mean Height of Fresh Log Substrate, in m	The mean height of fresh log substrate, in meters.
Mean Height of Mounds, in m	The mean height of mounded areas, in meters.
# Years Respite from Fern Shading for Seeds on Fresh Logs	The maximum number of years that seeds can get respite from fern shading, as implemented by the Beer's law light filter behavior .
Proportion of Plot Area that is Mound	Proportion of the plot area that is mound area, between 0 and 1.
Standard Deviation of Fresh Log Substrate Height, in m	The standard deviation of height of fresh log substrate, in meters.
Standard Deviation of Mound Height, in m	The standard deviation of the height of mounded areas, in meters.

How it works

Each timestep, the behavior starts by getting the substrate proportions for each cell of the [Dispersed Seeds grid](#). The six substrate types are further divided into mound and non-mound types of each according to the **Proportion of Ground Area that is Mound** parameter. The relative proportions of the different kinds of substrate are thus the same on mound and non-mound areas.

The seeds in the Dispersed Seeds grid cell are then divided up among the substrate types in that cell according to their proportions relative to each other (so if 60% of the cell area is mound forest floor moss, that's the substrate type that 60% of the seeds land on). A seedling is created from each seed. Seedlings are randomly placed within their seed grid cell area and have a slightly randomized value of [New seedling diameter at 10 cm](#).

Each seedling then gets a rooting height according to the substrate type upon which it has germinated. If it has germinated on fresh logs, its rooting height is a random number drawn from

a normal distribution controlled by the **Mean Height of Fresh Log Substrate, in m** and **Standard Deviation of Fresh Log Substrate Height, in m** parameters (no distinction is made between mound and non-mound fresh logs). If it's on a mound substrate, its rooting height is a random number drawn from a normal distribution controlled by the **Mean Height of Mounds, in m** and **Standard Deviation of Mound Height, in m** parameters. If it's on a non-mound substrate, its rooting height is zero.

If a seedling germinates on fresh log, it has the chance of getting a respite from the effects of the [Beer's law light filter](#) behavior, which it expects to simulate fern shading. Fallen logs crash through the fern layer, and it takes a while for the ferns to grow back over the top of the log. This length of time is the maximum possible respite length, and is set in the **# Years Respite from Fern Shading for Seeds on Fresh Logs** parameter. [Substrate](#) keeps track of the age of its fresh log cohorts, so that it is possible to randomly assign the seedling to a fresh log of a specific age, given the relative proportions of various-aged fresh log cohorts. The age of the log is subtracted from the maximum respite length, and this value is assigned to the seedling. Thus a log that fell this timestep would give a seedling the maximum respite, whereas a much older log may not give any respite at all.

How to apply it

Apply this behavior to seeds of your desired species. Any species to which it is applied must also satisfy the following requirements:

- A disperse behavior must be applied
- The [Substrate](#) behavior must be applied
- The [Beer's Law light filter](#) behavior must be applied

Light Dependent Seed Survival

This behavior assesses seed survival as a function of the Global Light Index (GLI) of the location in which a seed lands. Light level calculations can take into account the change in light blocking by snags and trees with storm damage, if desired.

Parameters for this behavior

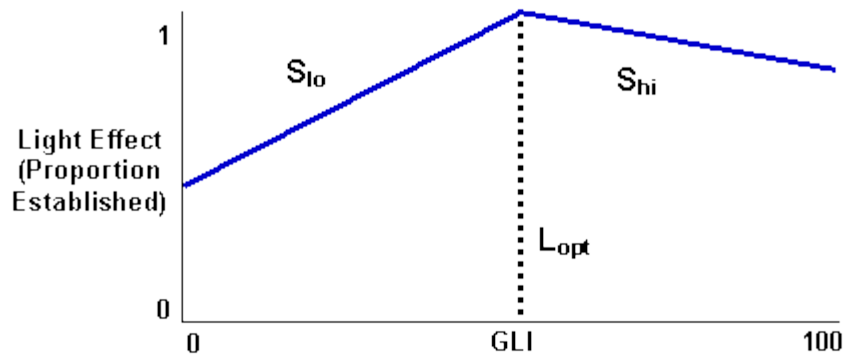
Parameter name	Description
Beam Fraction of Global Radiation	The fraction of total solar radiation that is direct beam radiation (as opposed to diffuse). Expressed as a value between 0 and 1. See more on GLI calculations .
Clear Sky Transmission Coefficient	Used to determine the amount of solar radiation seen at the plot location. See more on GLI calculations .

First Day of Growing Season for GLI Light Calculations	The first day of the growing season, as a Julian day (number between 1 and 365). Seeds only get light during the growing season. See more on GLI calculations .
GLI of Optimum Establishment, 0-100	The GLI value of optimum survival for seeds, as a value between 0 and 100.
Height in m At Which to Calculate GLI	The height, in meters, at which to calculate GLI at the center of each grid cell.
Last Day of Growing Season for GLI Light Calculations	The last day of the growing season, as a Julian day (number between 1 and 365). Seeds only get light during the growing season. See more on GLI calculations .
Light Extinction Coeff of Complete Damage Trees (0-1)	The fraction of light transmitted by the crowns of trees with complete Storm damage . Not required if storms are not used. Expressed as a value between 0 and 1. If storms are used, a value must be supplied for every species. See more on GLI calculations .
Light Extinction Coeff of Medium Damage Trees (0-1)	The fraction of light transmitted by the crowns of trees with medium Storm damage . Not required if storms are not used. Expressed as a value between 0 and 1. If storms are used, a value must be supplied for every species. See more on GLI calculations .
Light Extinction Coeff of Undamaged Trees (0-1)	The fraction of light transmitted by the crowns of regular live trees (and if storms are being used, trees with no Storm damage). Expressed as a value between 0 and 1. A value must be supplied for every species. See more on GLI calculations .
Minimum Solar Angle for GLI Calculations, in rad	This is the minimum angle at which sunlight is seen, in radians. Below this value the sky is assumed to be dark due to shading neighbors. See more on GLI calculations .
Number of Altitude Sky Divisions for GLI Light Calculations	Number of grid cells into which the sky is divided from horizon to zenith, for the purpose of calculating light direction. See more on GLI calculations .
Number of Azimuth Sky Divisions for GLI Light Calculations	Number of grid cells into which the sky is divided around the horizon, for the purpose of calculating light direction. See more on GLI calculations .
Slope of Dropoff Above the Optimum	The slope of the line describing the drop off in seedling survival as a function of GLI above the optimum GLI.

GLI	
Slope of Dropoff Below Optimum GLI	The slope of the line describing the dropoff in seedling survival as a function of GLI below the optimum GLI.
Snag Age Class 1 Light Extinction Coefficient (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is less than or equal to Upper age (yrs) of snag light extinction class 1 . Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Snag Age Class 2 Light Extinction Coefficient (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is greater than Upper age (yrs) of snag light extinction class 1 , but is less than or equal to Upper age (yrs) of snag light extinction class 2 . Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Snag Age Class 3 Light Extinction Coefficient (0-1)	Fraction of light transmitted through the snag tree crown for each species. Applies to those snags whose age is greater than Upper age (yrs) of snag light extinction class 2 . Expressed as a fraction between 0 and 1. If your run does not work with snags, you can ignore this. Otherwise, a value must be provided for all species.
Upper Age (Yrs) of Snag Light Extinction Class 1	The upper age limit, in years, defining the first age class of snag light extinction. Snags with an age less than or equal to this age have a light extinction coefficient matching Snag age class 1 light extinction coefficient . If your run does not work with snags, you can ignore this.
Upper Age (Yrs) of Snag Light Extinction Class 2	The upper age limit, in years, defining the second age class of snag light extinction. Snags with an age greater than the upper limit for size class 1, but less than or equal to this age, have a light extinction coefficient matching Snag age class 2 light extinction coefficient . Snags with an age greater than this value are in age class three. If your run does not work with snags, you can ignore this.

How it works

The effects of light levels on seed survival is graphed as:



To assess the effects of light level on the number of seeds that survive, this behavior calculates the GLI at the center of each grid cell in the [Dispersed Seeds grid](#) at the height specified in the **Height in m At Which to Calculate GLI** parameter (value is in meters). The calculation proceeds exactly as described in the [Light Behaviors](#). In order to perform these GLI calculations, this behavior requires its own copy of the key GLI setup parameters.

If you wish to use [storms](#) in your run, this behavior can take into account the fact that storm-damaged trees may have different light extinction coefficients. These light extinction coefficients are specified in the **Light Extinction Coeff of Complete Damage Trees (0-1)** and **Light Extinction Coeff of Medium Damage Trees (0-1)** parameters.

Once GLI has been calculated, the proportion of seeds that survive for a given species is calculated as:

- If $GLI < GLI_{opt}$, $LE = 1 - (S_{lo}(GLI_{opt} - GLI))$
- If $GLI = GLI_{opt}$, $LE = 1$
- If $GLI > GLI_{opt}$, $LE = 1 - (S_{hi}(GLI - GLI_{opt}))$

where

- GLI is the GLI at the center of the [Dispersed Seeds](#) grid cell at the height in the **Height in m At Which to Calculate GLI** parameter
- GLI_{opt} is the **GLI of Optimum Establishment, 0-100** parameter
- S_{lo} is the **Slope of Dropoff Below Optimum GLI** parameter
- S_{hi} is the **Slope of Dropoff Above the Optimum GLI** parameter

Once the proportion of seeds that survive at the given GLI has been calculated, this value is multiplied by the number of seeds to reduce them by the proper amount. The new reduced number of seeds is put back in the Dispersed Seeds grid.

How to apply it

Apply this behavior to seeds of your desired species. Any species to which it is applied must also have a [Disperse behavior](#) applied. Storm damage is optional.

Proportional Seed Survival

This behavior reduces the number of seeds by a set amount.

Parameters for this behavior

Parameter name	Description
Proportion Germinating Between 0 and 1	The proportion of seeds of a species that survive germination, as a value between 0 and 1.

How it works

In each cell of the [Dispersed Seeds grid](#), this multiplies the number of seeds present by the **Proportion Germinating Between 0 and 1** parameter, reducing the total number available. The new number of seeds is placed back in the Dispersed Seeds grid.

How to apply it

Apply this behavior to seeds of any species. Any species to which this is applied must have a [Disperse behavior](#) applied as well.

Seed Establishment

This behavior converts seeds into seedlings.

How it works

This behavior goes through each grid cell in the [Dispersed Seeds grid](#) and, for each species to which this behavior applies, converts each seed into a seedling. The seedlings are randomly placed within the grid cell area and have a slightly randomized value of [New seedling diameter at 10 cm](#).

How to apply it

Apply this behavior to seeds of any species. A species to which this is applied must also have a [Disperse behavior](#) applied.

Storm Light Dependent Seed Survival

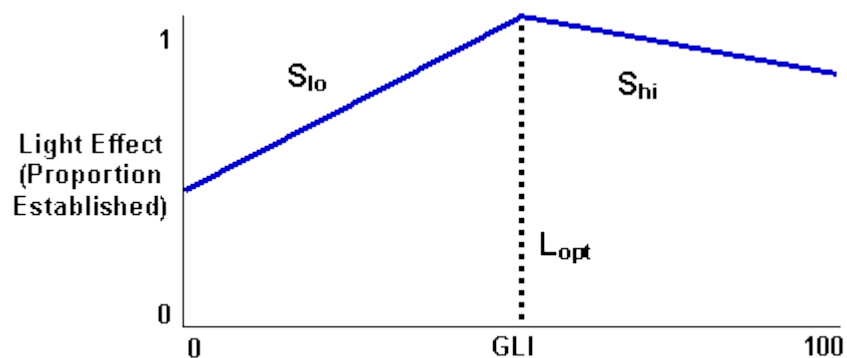
This behavior assesses seed survival as a function of the light level of the location in which a seed lands. Light level calculations are performed by the [Storm Light](#) behavior. (This behavior is exactly like Light Dependent Seed Survival except for the method of light level calculation.)

Parameters for this behavior

Parameter name	Description
GLI of Optimum Establishment, 0-100	The GLI value of optimum survival for seeds, as a value between 0 and 100.
Slope of Dropoff Above the Optimum GLI	The slope of the line describing the drop off in seedling survival as a function of GLI above the optimum GLI.
Slope of Dropoff Below Optimum GLI	The slope of the line describing the dropoff in seedling survival as a function of GLI below the optimum GLI.

How it works

The effects of light levels on seed survival is graphed as:



To assess the effects of light level on the number of seeds that survive, this behavior retrieves the light level from the [Storm Light](#) grid that corresponds to the point in the center of each [Dispersed Seeds](#) grid cell.

The proportion of seeds that survive for a given species is calculated as:

- If $GLI < GLI_{opt}$, $LE = 1 - (S_{lo}(GLI_{opt} - GLI))$
- If $GLI = GLI_{opt}$, $LE = 1$
- If $GLI > GLI_{opt}$, $LE = 1 - (S_{hi}(GLI - GLI_{opt}))$

where

- GLI is the light level at the center of the [Dispersed Seeds](#) grid cell

- GLI_{opt} is the **GLI of Optimum Establishment, 0-100** parameter
- S_{lo} is the **Slope of Dropoff Below Optimum GLI** parameter
- S_{hi} is the **Slope of Dropoff Above the Optimum GLI** parameter

Once the proportion of seeds that survive at the given light level has been calculated, this value is multiplied by the number of seeds to reduce them by the proper amount. The new reduced number of seeds is put back in the Dispersed Seeds grid.

How to apply it

Apply this behavior to seeds of your desired species. Any species to which it is applied must also have a [Disperse behavior](#) and the [Storm Light](#) behavior applied.

Substrate Based Seed Survival With Microtopography

This behavior assesses seed survival based on substrate conditions, allowing for site microtopography to influence seed survival. In this scenario, the plot is divided into small-scale mounds. The portion of the plot that is slightly elevated is "mound". The portion of the plot between the mounds, at lower elevation, is "ground". The size of the mounds and their height is not important.

Parameters for this behavior

Parameter name	Description
Fraction Seeds Germinating on Ground Decayed Logs	The proportion of those seeds that land on decayed logs ground substrate that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Ground Forest Floor Litter	The proportion of those seeds that land on forest floor litter ground substrate that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Ground Forest Floor Moss	The proportion of those seeds that land on forest floor moss ground substrate that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Ground Fresh Logs	The proportion of those seeds that land on fresh logs ground substrate that survive to become seedlings. Expressed as a value between 0 and 1.

Fraction Seeds Germinating on Ground Scarified Soil	The proportion of those seeds that land on scarified soil ground substrate that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Ground Tip-Up	The proportion of those seeds that land on tip-up ground substrate that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Mound Decayed Logs	The proportion of those seeds that land on decayed logs mound substrate that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Mound Forest Floor Litter	The proportion of those seeds that land on forest floor litter mound substrate that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Mound Forest Floor Moss	The proportion of those seeds that land on forest floor moss mound substrate that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Mound Fresh Logs	The proportion of those seeds that land on fresh logs mound substrate that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Mound Scarified Soil	The proportion of those seeds that land on scarified soil mound substrate that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Mound Tip-Up	The proportion of those seeds that land on tip-up mound substrate that survive to become seedlings. Expressed as a value between 0 and 1.
Proportion of Plot Area that is Mound	The proportion of plot area that is mound area, as opposed to ground area. Expressed as a value between 0 and 1.

How it works

The area of the plot that is "mound" and the area that is "ground" are in fixed relative proportion to each other. This fixed proportion is entered in the **Proportion of Plot Area that is Mound** parameter. Each grid cell in the [Substrate grid](#) has been divided by the Substrate behavior into six substrate types; each of those types is further divided into "mound" and "ground" according to the fixed proportion, making twelve total substrate types. For example, if 20% of a grid cell's area is forest floor litter, and 60% of the plot area is mound, then the area of the grid cell that is

forest floor litter mound substrate is 12% and the area of grid cell that is forest floor litter ground substrate is 8%.

The behavior takes the substrate composition of each grid cell in the [Substrate grid](#), calculates the amount of the twelve substrate types, and converts it into a single number for each species, called the substrate favorability index. The favorability index is the sum of the proportions of each substrate multiplied by the proportion of seeds that germinate on that substrate. This index represents the proportion of total seeds of that species that are expected to survive in that area of the plot. This index is stored in the grid [Substrate Favorability](#).

The behavior then goes through each grid cell in the [Dispersed Seeds grid](#) and assesses the survival for the seeds of those species to which it applies. This behavior starts by giving each seed a random temporary location within the Dispersed Seeds grid cell. Then, it retrieves the substrate favorability at that point from the Substrate Favorability grid. It then compares a random number to the substrate favorability to determine whether the seed lives. This method ensures that we can assess substrate favorabilities correctly when the Dispersed Seeds and Substrate grids have different grid cell resolutions.

Once this process is complete, the number of surviving seeds for each species is assigned back to the Dispersed Seeds grid.

How to apply it

This behavior may be applied to seeds of any species. A species to which this is applied must also have a [Disperse behavior](#) applied. Also, the [Substrate behavior](#) must be used in the run.

Substrate Dependent Seed Survival No Gap Status

This behavior assesses seed survival based on substrate conditions.

Parameters for this behavior

Parameter name	Description
Fraction Seeds Germinating on Canopy Decayed Logs	The proportion of those seeds that land on decayed logs under canopy conditions that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Canopy Fresh Logs	The proportion of those seeds that land on fresh logs under canopy conditions that survive to become seedlings. Expressed as a value between 0 and 1.

Fraction Seeds Germinating on Canopy Forest Floor Litter	The proportion of those seeds that land on forest floor litter under canopy conditions that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Canopy Forest Floor Moss	The proportion of those seeds that land on forest floor moss under canopy conditions that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Canopy Scarified Soil	The proportion of those seeds that land on scarified soil under canopy conditions that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Canopy Tip-Up	The proportion of those seeds that land on tip-up mounds substrate under canopy conditions that survive to become seedlings. Expressed as a value between 0 and 1.

How it works

The behavior takes the substrate composition of each grid cell in the [Substrate grid](#) and converts it into a single number for each species, called the substrate favorability index. The favorability index is the sum of the proportions of each substrate multiplied by the proportion of seeds that germinate on that substrate. This index represents the proportion of total seeds of that species that are expected to survive in that area of the plot. This index is stored in the grid [Substrate Favorability](#). (In the parameters list, the proportions used are the canopy proportions.)

The behavior then goes through each grid cell in the [Dispersed Seeds grid](#) and assesses the survival for the seeds of those species to which it applies. This behavior starts by giving each seed a random temporary location within the Dispersed Seeds grid cell. Then, it retrieves the substrate favorability at that point from the Substrate Favorability grid. It then compares a random number to the substrate favorability to determine whether the seed lives. This method ensures that we can assess substrate favorabilities correctly when the Dispersed Seeds and Substrate grids have different grid cell resolutions.

Once this process is complete, the number of surviving seeds for each species is assigned back to the Dispersed Seeds grid.

How to apply it

This behavior may be applied to seeds of any species. A species to which this is applied must also have a [Disperse behavior](#) applied. Also, the [Substrate behavior](#) must be used in the run.

Substrate Dependent Seed Survival With Gap Status

This behavior assesses seed survival as a function of both the substrate composition of the grid cells in which seeds land and the cells' forest cover (gap or canopy). This behavior allows for different germination favorability for substrates under the two forest covers.

Parameters for this behavior

Parameter name	Description
Fraction Seeds Germinating on Canopy Decayed Logs	The proportion of those seeds that land on decayed logs under canopy conditions that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Canopy Fresh Logs	The proportion of those seeds that land on fresh logs under canopy conditions that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Canopy Forest Floor Litter	The proportion of those seeds that land on forest floor litter under canopy conditions that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Canopy Forest Floor Moss	The proportion of those seeds that land on forest floor moss under canopy conditions that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Canopy Scarified Soil	The proportion of those seeds that land on scarified soil under canopy conditions that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Canopy Tip-Up	The proportion of those seeds that land on tip-up mounds substrate under canopy conditions that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Gap Decayed Logs	The proportion of those seeds that land on decayed logs under gap conditions that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Gap Fresh Logs	The proportion of those seeds that land on fresh logs under gap conditions that survive to become seedlings. Expressed as a value between 0 and 1.

Fresh Logs	between 0 and 1.
Fraction Seeds Germinating on Gap Forest Floor Litter	The proportion of those seeds that land on forest floor litter under gap conditions that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Gap Forest Floor Moss	The proportion of those seeds that land on forest floor moss under gap conditions that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Gap Scarified Soil	The proportion of those seeds that land on scarified soil under gap conditions that survive to become seedlings. Expressed as a value between 0 and 1.
Fraction Seeds Germinating on Gap Tip-Up	The proportion of those seeds that land on tip-up mounds substrate under gap conditions that survive to become seedlings. Expressed as a value between 0 and 1.

How it works

The behavior takes the substrate composition of each grid cell in the [Substrate grid](#) and converts it into a single number for each species, called the substrate favorability index. The favorability index is the sum of the proportions of each substrate multiplied by the proportion of seeds that germinate on that substrate under that cell's cover (canopy or gap). This index represents the proportion of total seeds of that species that are expected to survive in that area of the plot. This index is stored in the grid [Substrate Favorability](#).

The behavior then goes through each grid cell in the [Dispersed Seeds grid](#) and assesses the survival for the seeds of those species to which it applies. This behavior starts by giving each seed a random temporary location within the Dispersed Seeds grid cell. Then, it retrieves the substrate favorability at that point from the Substrate Favorability grid. It then compares a random number to the substrate favorability to determine whether the seed lives. This method ensures that we can assess substrate favorabilities correctly when the Dispersed Seeds and Substrate grids have different grid cell resolutions.

Once this process is complete, the number of surviving seeds for each species is assigned back to the Dispersed Seeds grid.

How to apply it

This behavior may be applied to seeds of any species. A species to which this is applied must also have the [Gap spatial disperse behavior](#) applied. Also, the [Substrate behavior](#) must be used in the run.

Planting behaviors

Planting

Planting directly creates new seedlings. When you create a new planting, you specify the timestep in which to plant, the species to plant and the relative amount of each, whether new seedling spacing is gridded or random, how many seedlings to plant and how far apart (if gridded), and the area of the plot to plant. You can create as many plantings as you like.

How it works

Planting keeps track of planting events to perform in a private [grid](#). Each timestep that there is a planting, the behavior begins by determining whether the planting is gridded or random.

If the planting is random, the total number of seedlings to plant is calculated by multiplying the total seedling density by the area to plant. Then that number of seedlings is scattered randomly around the plant area. If the planting is gridded, each grid cell in the plant area is planted individually. In each cell is placed the number of seedlings that can fit at the specified spacing. Since each 8 meter by 8 meter grid cell is planted individually, large spacing distances may result in a very low number of seedlings being planted; at a 6 meter spacing, for instance, only one seedling per cell would be planted. For best results, the distance between seedlings should divide evenly into 8 meters.

Each seedling's species is determined by comparing a random number to the relative abundance of each species. This means that the species distribution may not be exactly what was specified, but the larger the number of seedlings the more accurate the species distribution will be.

The plant behavior outputs what it did each timestep into the [Planting Results](#) grid. If you wish to review the results of the grid, save it in a [detailed output file](#).

How to apply it

Add the behavior to the run through the [Model Flow window](#). You do not apply it to particular trees at that time. The behavior setup will allow you to design your plantings.

Analysis behaviors

Analysis behaviors are those whose only purpose is to prepare data for output. They do not change model state, such as growing trees or updating grid values. They assemble, calculate, or analyze data for the user.

Behavior	Description
Carbon Value	Calculates the amount of carbon per species and its value.
Dimension	Calculates the biomass of trees based on DBH. This approach comes from

Analysis	Jenkins et al, 2004.
Foliar Chemistry	Calculates chemistry components as a function of DBH.
Merchantable Timber Value	Calculates the value of merchantable timber.
Partitioned DBH Biomass	Calculates biomass as a linear function of DBH, partitioned into leaf, branch, and bole biomass.
Partitioned Height Biomass	Calculates biomass as a linear function of tree height, partitioned into leaf and bole biomass.
Ripley's K Calculator	Calculates the Ripley's K function for all trees in the plot as well as for the members of each species.
Relative Neighborhood Density Calculator	Calculates the relative neighborhood density index (Ω) as described in Condit et al 2000.
State Reporter	Reports the values of state variables.
Storm Killed Partitioned DBH Biomass	Calculates biomass of trees killed in storms as a linear function of DBH, partitioned into leaf, branch, and bole biomass.
Storm Killed Partitioned Height Biomass	Calculates biomass of trees killed in storms as a linear function of tree height, partitioned into leaf and bole biomass.
Tree Bole Volume calculator	Calculates merchantable tree volume.
Tree Age	Calculates tree age.
Tree Volume Calculator	Calculates the volume of tree trunks to find both merchantable volume and total volume.

Carbon Value

This behavior calculates the amount of carbon per species and its value.

Parameters for this behavior

Parameter name	Description
Carbon Value - Carbon Amount of Biomass (0-100%)	The percentage of biomass that is carbon, as a value between 0 and 100.
Carbon Value - Price Per Metric Ton Carbon	The price per metric ton of carbon. The currency is unimportant.

How it works

This behavior relies on the [Dimension Analysis](#) behavior to calculate each tree's biomass in metric tons. It then multiplies this value by the **Carbon Value - Carbon Amount of Biomass (0-100%)** parameter to find each tree's amount of carbon in metric tons. This behavior finds the total amount of carbon in each species, and then multiplies it by the **Carbon Value - Price Per Metric Ton Carbon** to find each species' carbon value.

Both the amount of carbon, in metric tons, for each species and the value of that carbon are saved in a grid called [Carbon Value](#). You can save these values in a detailed output file for analysis.

How to apply it

Apply this behavior to saplings, adults, or snags of any species. These trees must also use the [Dimension Analysis](#) behavior. *This behavior does not automatically create output.* Once you have added this behavior to your run, the [Detailed output setup window](#) for trees will have a tree data member called "Mg Carbon", which has each tree's amount of carbon in metric tons. Also, the [Detailed output grid setup window](#) will list the [Carbon Value grid](#). You can then view the contents of this grid as a [table](#) using SORTIE's data visualization system.

Dimension Analysis

This behavior calculates the biomass of trees based on DBH. This approach comes from [Jenkins et al, 2004](#).

Parameters for this behavior

Parameter name	Description
Dimension Analysis	The units of biomass that the chosen biomass equation is expected to

Biomass Units	produce, based on the parameters entered. SORTIE-ND will use this to convert the biomass value to metric tons (Mg).
Dimension Analysis Correction Factor	The correction factor needed by some biomass equations that calculate $\ln(\text{biomass})$, $\log_{10}(\text{biomass})$, or $\log_{100}(\text{biomass})$. This value is ignored if the value for the Dimension Analysis: Use Correction Factor? parameter for this species is false.
Dimension Analysis DBH Units	The units of DBH that are appropriate to the biomass equation coefficients being entered. SORTIE-ND will convert a tree's DBH to these units before calculating biomass.
Dimension Analysis Equation ID	The biomass equation ID to use when calculating biomass for a particular species.
Dimension Analysis Parameter (a)	The value for a in a biomass equation. The appropriate value and units for this parameter depend on the values entered in the Dimension Analysis Equation ID , Dimension Analysis DBH Units , and Dimension Analysis Biomass Units parameters.
Dimension Analysis Parameter (b)	The value for b in a biomass equation. The appropriate value and units for this parameter depend on the values entered in the Dimension Analysis Equation ID , Dimension Analysis DBH Units , and Dimension Analysis Biomass Units parameters.
Dimension Analysis Parameter (c)	The value for c in a biomass equation. Whether this parameter is used, and the appropriate value and units for this parameter, depend on the values entered in the Dimension Analysis Equation ID , Dimension Analysis DBH Units , and Dimension Analysis Biomass Units parameters.
Dimension Analysis Parameter (d)	The value for d in a biomass equation. Whether this parameter is used, and the appropriate value and units for this parameter, depend on the values entered in the Dimension Analysis Equation ID , Dimension Analysis DBH Units , and Dimension Analysis Biomass Units parameters.
Dimension Analysis Parameter (e)	The value for e in a biomass equation. Whether this parameter is used, and the appropriate value and units for this parameter, depend on the values entered in the Dimension Analysis Equation ID , Dimension Analysis DBH Units , and Dimension Analysis Biomass Units parameters.
Dimension Analysis: Use Correction Factor?	Whether or not the chosen biomass equation requires a correction factor to be multiplied by the result.

How it works

The paper above outlines 9 different biomass equations in Table 6, as follows:

ID	Equation
1	$\log_{10} \text{biomass} = a + b * (\log_{10}(\text{dia}^c))$
2	$\ln \text{biomass} = a + b * \text{dia} + c * (\ln(\text{dia}^d))$
3	$\ln \text{biomass} = a + b * \ln(\text{dia}) + c * (d + (e * \ln(\text{dia})))$
4	$\text{biomass} = a + b * \text{dia} + c * (\text{dia}^d)$
5	$\text{biomass} = a + (b * \text{dia}) + c * (\text{dia}^2) + d * (\text{dia}^3)$
6	$\text{biomass} = a * (\exp(b + (c * \ln(\text{dia})) + (d * \text{dia})))$
7	$\text{biomass} = a + ((b * (\text{dia}^c)) / ((\text{dia}^c) + d))$
8	$\log_{100} \text{biomass} = a + (b * \log_{10}(\text{dia}))$
9	$\ln \text{biomass} = \ln(a) + (b * \ln(\text{dia}))$

In all equations, *dia* is DBH. You choose the equation ID that you wish to use for each species.

There are many different published parameters using the equation forms above, which use a range of different units. Thus, you specify what units *dia* (that is, DBH) is in, and what units of biomass the equation is expected to produce. The possible DBH units are millimeters (mm), centimeters (cm), and inches (in); the possible biomass units are grams (g), kilograms (kg), and pounds (lb). This behavior handles all unit conversions so that biomass is appropriately calculated. The final biomass values are reported in metric tons (Mg).

For those equations that calculate log10, log100, or ln biomass, some papers specify a correction factor to remove bias that may be introduced when biomass is calculated. If you wish, you may use such a correction factor. Set the value of the **Dimension Analysis: Use Correction Factor?** parameter to "true", then specify the appropriate correction factor in the **Dimension Analysis Correction Factor** parameter. This value is multiplied by the final biomass value.

How to apply it

Apply this behavior to saplings, adults, or snags of any species. *This behavior does not automatically create output.* Once you have added this behavior to your run, the [Detailed output setup window](#) for trees will have a tree data member called "Tree Biomass". Add this to your detailed output file to output biomass in metric tons (Mg). You can then view charts and graphs with the resulting volume data using data visualization on your detailed output file.

Foliar Chemistry

This behavior calculates chemistry components as a function of DBH. The components calculated are N, P, specific leaf area (SLA), percent acid detergent fiber, percent acid detergent cellulose, percent acid detergent lignin, percent condensed tannins, and total phenolics.

Parameters for this behavior

Parameter name	Description
Foliar Chemistry - Cellulose Concentration	The proportion of foliar dry weight (0-1) that is acid detergent cellulose.
Foliar Chemistry - Fiber Concentration	The proportion of foliar dry weight (0-1) that is acid detergent fiber.
Foliar Chemistry - Foliar Weight (a)	The "a" parameter in the equation for foliar dry weight.
Foliar Chemistry - Foliar Weight (b)	The "b" parameter in the equation for foliar dry weight.
Foliar Chemistry - Lignin Concentration	The proportion of foliar dry weight (0-1) that is acid detergent lignin.
Foliar Chemistry - N Concentration	The proportion of foliar dry weight (0-1) that is N.
Foliar Chemistry - P Concentration	The proportion of foliar dry weight (0-1) that is P.
Foliar Chemistry - Phenolics Concentration	The proportion of foliar dry weight (0-1) that is phenolics.
Foliar Chemistry - SLA Concentration	The proportion of foliar dry weight (0-1) that is specific leaf area.
Foliar Chemistry - Tannins Concentration	The proportion of foliar dry weight (0-1) that is tannins.

How it works

For each tree, the foliar dry weight is calculated as:

$$F = a * DBH^b$$

where

- F = foliar dry weight in kg
- a = the **Foliar Chemistry - Foliar Weight (a)** parameter
- b = the **Foliar Chemistry - Foliar Weight (b)** parameter
- DBH = tree's DBH in cm

For each component, the amount is the tree's foliar dry weight multiplied by the parameter for that component's concentration.

The weight of each component, in metric tons, is summed for each species and saved in a grid called [Foliar Chemistry](#). You can save these values in a detailed output file for analysis. You of course can skip any of the components by entering 0's for their concentration parameter values.

How to apply it

Apply this behavior to saplings, adults, or snags of any species. *This behavior does not automatically create output.* Once you have added this behavior to your run, the [Detailed output grid setup window](#) will list the [Foliar Chemistry](#) grid. You can then view the contents of this grid as a [table](#) using SORTIE's data visualization system.

Merchantable Timber Value

This behavior calculates the value of merchantable timber.

Parameters for this behavior

Parameter name	Description
Merchantable Timber Value Form Class	The form class of the species. Valid values are 78, 79, 80, 81, 84, and 85.
Merchantable Timber Value Price / 1000 Board Feet	The price per thousand board feet for each species. The currency used doesn't matter.

How it works

The value for each tree is calculated by finding out its volume in board feet, and multiplying that by the price for its species. The price is held in the **Merchantable Timber Value Price / 1000 Board Feet** parameter. The currency used doesn't matter. The tree's final value is placed in a tree data member called "Merchantable Value". The total value for each species is saved in a grid called [Merchantable Timber Value](#). You can save these values in a detailed output file for analysis.

The volume of merchantable timber in a tree depends on its size and form class. These control how many 16-foot logs there are in a tree, and how many board feet of timber (assuming 0.25-inch thickness) those logs can create. The form class is entered in the **Merchantable Timber Value Form Class** parameter.

The behavior begins by finding out how many 16-foot logs the tree can provide in its bole. The base of the bole is the top of the cut stump; the top of the bole is the merchantable height. This behavior defines the merchantable height as the height at which the trunk diameter inside the bark tapers to 60% of DBH. The behavior tries fitting in as many 16-foot logs as possible before the 60% taper occurs. The amount of taper at the top of the first 16-foot log is established by the tree's form class. A species's form class is the percentage of DBH to which the bole has tapered at the top of the first 16-foot log.

Then the behavior determines how many more logs the tree contains. The amount of taper at the top of the first 16-foot log is subtracted from the DBH, to see how much taper is left before the 60% merchantable-height diameter is reached. There is no formula that establishes clearly how many logs will fit; the behavior uses a trial-and-error approach taken from [Messavage and Girard, 1956](#). This paper includes the table below for upper-log taper for trees of various DBH and bole heights. The behavior uses this table to determine the maximum number of logs it can fit into the taper available.

Trees below 10 inches of DBH contain no merchantable timber and have a value of zero. Trees greater than 40 inches of DBH are treated like 40-inch trees.

Once the behavior figures out how many 16-foot logs a tree contains, it uses another set of tables, based on form class, to determine how many board-feet of timber the tree contains. These tables are also from [Messavage and Girard, 1956](#), and are shown below.

Average upper-log taper (inches) in 16-foot logs

DBH (in)	2-log tree		3-log tree		4-log tree			5-log tree				6-log tree				
	2d log	3d log	2d log	3d log	2d log	3d log	4th log	2d log	3d log	4th log	5th log	2d log	3d log	4th log	5th log	6th log
10	1.4	1.2	1.4	---	---	---	---	---	---	---	---	---	---	---	---	---
12	1.6	1.3	1.5	1.1	1.4	1.9	---	---	---	---	---	---	---	---	---	---
14	1.7	1.4	1.6	1.2	1.5	2	---	---	---	---	---	---	---	---	---	---
16	1.9	1.5	1.7	1.2	1.6	2.1	---	---	---	---	---	---	---	---	---	---
18	2	1.6	1.8	1.3	1.7	2.2	---	---	---	---	---	---	---	---	---	---
20	2.1	1.7	1.9	1.4	1.8	2.4	1.1	1.6	2.2	2.9	---	---	---	---	---	---
22	2.2	1.8	2	1.4	2	2.5	1.1	1.7	2.3	2.9	---	---	---	---	---	---

24	2.3	1.8	2.2	1.5	2.2	2.6	1.1	1.8	2.4	3.1	---	---	---	---	---
26	2.4	1.9	2.3	1.5	2.3	2.7	1.1	1.9	2.5	3.2	---	---	---	---	---
28	2.5	1.9	2.5	1.6	2.4	2.8	1.2	1.9	2.6	3.3	0.9	1.4	2.1	3.2	4.4
30	2.6	2	2.6	1.7	2.5	3	1.2	2	2.7	3.5	0.9	1.4	2.1	3.2	4.5
32	2.7	2	2.7	1.7	2.5	3.1	1.2	2.1	2.9	3.7	1	1.4	2.1	3.2	4.6
34	2.8	2.1	2.7	1.8	2.5	3.3	1.3	2.1	3	3.8	1	1.4	2.2	3.3	4.7
36	2.8	2.1	2.8	1.8	2.6	3.4	1.3	2.2	3	3.9	1.1	1.5	2.2	3.3	4.9
38	2.9	2.1	2.8	1.9	2.6	3.4	1.3	2.2	3.1	3.9	1.1	1.5	2.3	3.4	5.1
40	2.9	2.2	2.8	1.9	2.7	3.4	1.4	2.3	3.2	4	1.2	1.5	2.4	3.5	5.3

**Volume (board feet) by number of usable 16 foot logs
Form Class 78:**

DBH (inches)	1 log	2 logs	3 logs	4 logs	5 logs	6 logs
10	36	59	73	---	---	---
11	46	76	96	---	---	---
12	56	92	120	137	---	---
13	67	112	147	168	---	---
14	78	132	174	200	---	---
15	92	156	208	242	---	---
16	106	180	241	285	---	---
17	121	206	278	330	---	---
18	136	233	314	374	---	---
19	154	264	358	427	---	---
20	171	296	401	480	542	---
21	191	332	450	542	616	---
22	211	368	500	603	691	---
23	231	404	552	663	714	---
24	251	441	605	723	782	---
25	275	484	665	800	865	---
26	299	528	725	877	1,021	---

27	323	572	788	952	1,111	---
28	347	616	850	1,027	1,201	1,358
29	375	667	920	1,112	1,308	1,488
30	403	718	991	1,198	1,415	1,619
31	432	772	1,070	1,299	1,526	1,754
32	462	826	1,149	1,400	1,637	1,888
33	492	880	1,226	1,495	1,750	2,026
34	521	934	1,304	1,590	1,864	2,163
35	555	998	1,394	1,702	2,000	2,312
36	589	1,063	1,485	1,814	2,135	2,461
37	622	1,124	1,578	1,926	2,272	2,616
38	656	1,186	1,670	2,038	2,410	2,771
39	694	1,258	1,769	2,166	2,552	2,937
40	731	1,329	1,868	2,294	2,693	3,103

Form Class 79:

DBH (inches)	1 log	2 logs	3 logs	4 logs	5 logs	6 logs
10	38	61	77	---	---	---
11	48	78	100	---	---	---
12	58	96	124	141	---	---
13	70	117	153	176	---	---
14	82	138	182	211	---	---
15	95	160	214	252	---	---
16	108	183	246	292	---	---
17	124	212	286	340	---	---
18	140	240	325	388	---	---
19	158	272	370	442	---	---
20	176	305	414	496	561	---
21	196	342	464	558	636	---
22	216	378	514	621	710	---

23	238	418	571	687	792	---
24	260	458	628	753	875	---
25	282	499	685	826	960	---
26	305	540	742	899	1,046	---
27	331	588	810	980	1,144	---
28	357	635	877	1,061	1,242	1,404
29	385	686	948	1,148	1,350	1,537
30	413	737	1,020	1,235	1,458	1,670
31	444	792	1,100	1,338	1,572	1,808
32	474	848	1,181	1,440	1,685	1,945
33	506	907	1,265	1,544	1,808	2,094
34	538	966	1,349	1,647	1,932	2,244
35	570	1,026	1,435	1,754	2,000	2,384
36	602	1,087	1,521	1,860	2,189	2,525
37	638	1,154	1,620	1,980	2,338	2,694
38	674	1,220	1,720	2,101	2,488	2,862
39	712	1,292	1,822	2,232	2,632	3,031
40	750	1,365	1,923	2,362	2,775	3,200

Form Class 80:

DBH (inches)	1 log	2 logs	3 logs	4 logs	5 logs	6 logs
10	39	63	80	---	---	---
11	49	80	104	---	---	---
12	59	98	127	146	---	---
13	71	120	156	181	---	---
14	83	141	186	216	---	---
15	98	166	221	260	---	---
16	112	190	256	305	---	---
17	128	219	296	354	---	---
18	144	248	336	402	---	---

19	162	281	382	457	---	---
20	181	314	427	512	580	---
21	201	350	478	575	656	---
22	221	387	528	638	732	---
23	244	428	586	706	816	---
24	266	469	644	773	899	---
25	290	514	706	852	992	---
26	315	558	767	931	1,086	---
27	341	606	836	1,014	1,185	---
28	367	654	904	1,096	1,284	1,453
29	396	706	977	1,184	1,394	1,588
30	424	758	1,050	1,272	1,503	1,723
31	454	814	1,132	1,376	1,618	1,862
32	485	870	1,213	1,480	1,733	2,001
33	518	930	1,298	1,586	1,858	2,152
34	550	989	1,383	1,691	1,984	2,304
35	585	1,055	1,477	1,806	2,124	2,458
36	620	1,121	1,571	1,922	2,264	2,612
37	656	1,188	1,672	2,044	2,416	2,783
38	693	1,256	1,772	2,167	2,568	2,954
39	732	1,330	1,874	2,300	2,714	3,127
40	770	1,403	1,977	2,432	2,860	3,300

Form Class 81:

DBH (inches)	1 log	2 logs	3 logs	4 logs	5 logs	6 logs
10	40	65	82	---	---	---
11	50	82	106	---	---	---
12	60	100	130	150	---	---
13	72	122	160	186	---	---
14	85	144	190	221	---	---

15	100	170	228	268	---	---
16	115	197	265	316	---	---
17	132	226	306	366	---	---
18	148	256	346	415	---	---
19	166	290	392	471	---	---
20	185	323	439	527	598	---
21	206	360	492	592	676	---
22	227	398	544	656	754	---
23	250	439	602	724	838	---
24	272	480	659	791	923	---
25	298	528	726	877	1,024	---
26	324	575	793	963	1,124	---
27	351	624	863	1,047	1,226	---
28	378	674	933	1,131	1,327	1,502
29	406	726	1,006	1,220	1,438	1,640
30	435	779	1,080	1,310	1,549	1,777
31	466	836	1,162	1,416	1,666	1,918
32	497	892	1,245	1,522	1,784	2,059
33	530	953	1,332	1,628	1,910	2,214
34	563	1,014	1,419	1,734	2,037	2,368
35	600	1,084	1,518	1,859	2,188	2,534
36	637	1,154	1,618	1,984	2,338	2,700
37	674	1,223	1,721	2,109	2,494	2,874
38	712	1,292	1,824	2,234	2,649	3,049
39	751	1,366	1,928	2,368	2,796	3,224
40	790	1,441	2,032	2,502	2,944	3,399

Form Class 84:

DBH (inches)	1 log	2 logs	3 logs	4 logs	5 logs	6 logs
10	43	71	91	---	---	---

11	54	91	118	---	---	---
12	66	111	145	168	---	---
13	80	135	178	208	---	---
14	93	159	212	248	---	---
15	108	185	249	295	---	---
16	123	211	286	342	---	---
17	142	244	332	398	---	---
18	160	277	377	453	---	---
19	180	314	428	524	---	---
20	200	351	479	576	657	---
21	223	392	537	649	744	---
22	246	434	595	722	830	---
23	271	480	660	798	925	---
24	296	525	724	873	1,020	---
25	322	572	790	958	1,118	---
26	347	619	855	1,042	1,217	---
27	376	673	932	1,136	1,331	---
28	406	727	1,010	1,230	1,445	1,636
29	438	786	1,092	1,330	1,569	1,790
30	470	844	1,173	1,429	1,693	1,943
31	504	907	1,265	1,546	1,823	2,101
32	538	970	1,357	1,664	1,953	2,259
33	574	1,037	1,453	1,782	2,096	2,431
34	611	1,104	1,549	1,901	2,240	2,603
35	647	1,173	1,648	2,023	2,387	2,766
36	683	1,242	1,746	2,145	2,534	2,929
37	724	1,318	1,859	2,284	2,706	3,123
38	765	1,393	1,972	2,422	2,877	3,317
39	808	1,476	2,088	2,570	3,042	3,512

40	851	1,558	2,203	2,719	3,208	3,706
----	-----	-------	-------	-------	-------	-------

Form Class 85:

DBH (inches)	1 log	2 logs	3 logs	4 logs	5 logs	6 logs
10	45	74	94	---	---	---
11	56	94	122	---	---	---
12	68	114	150	173	---	---
13	82	138	184	214	---	---
14	95	163	217	254	---	---
15	111	191	257	304	---	---
16	127	219	297	355	---	---
17	146	252	342	412	---	---
18	164	285	388	468	---	---
19	184	322	440	531	---	---
20	205	360	492	594	678	---
21	228	402	550	667	765	---
22	251	444	609	740	852	---
23	276	490	675	818	950	---
24	302	537	741	895	1,047	---
25	330	588	812	986	1,153	---
26	357	638	882	1,076	1,259	---
27	387	693	961	1,172	1,374	---
28	417	745	1,040	1,267	1,490	1,689
29	448	807	1,122	1,368	1,616	1,844
30	481	866	1,205	1,469	1,741	1,999
31	516	930	1,298	1,588	1,874	2,160
32	550	993	1,391	1,706	2,006	2,321
33	587	1,061	1,488	1,827	2,150	2,495
34	624	1,129	1,586	1,948	2,294	2,669
35	663	1,204	1,692	2,080	2,454	2,846

36	702	1,278	1,797	2,212	2,614	3,022
37	744	1,355	1,912	2,352	2,788	3,219
38	785	1,432	2,027	2,493	2,962	3,416
39	828	1,515	2,144	2,644	3,130	3,614
40	872	1,598	2,260	2,795	3,298	3,813

How to apply it

Apply this behavior to saplings, adults, or snags of any species. *This behavior does not automatically create output.* Once you have added this behavior to your run, the [Detailed output setup window](#) for trees will have a tree data member called "Merchantable Value". Add this to your detailed output file to output volume in cubic feet. You can also use the [Detailed output grid setup window](#) to save the data members in the [Merchantable Timber Value grid](#), which contains the total value for each species. You can then view the contents of this grid as a [table](#) using SORTIE's data visualization system.

Partitioned DBH Biomass

This behavior calculates biomass as a linear function of DBH, partitioned into leaf, branch, and bole biomass.

Parameters for this behavior

Parameter name	Description
Partitioned DBH Biomass - Bole Slope (a)	The slope in the linear biomass equation for boles.
Partitioned DBH Biomass - Bole Intercept (b)	The intercept in the linear biomass equation for boles.
Partitioned DBH Biomass - Branch Slope (a)	The slope in the linear biomass equation for branches.
Partitioned DBH Biomass - Branch Intercept (b)	The intercept in the linear biomass equation for branches.
Partitioned DBH	The slope in the linear biomass equation for leaves.

Biomass - Leaf Slope (a)	
Partitioned DBH Biomass - Leaf Intercept (b)	The intercept in the linear biomass equation for leaves.

How it works

The mass of all components is calculated using the same equation, but using different parameters. The equation is:

$$Bio_i = a_i * DBH + b_i$$

where

- Bio_i = biomass in kg dry weight of the component in question
- a_i = the "a" parameter for the component
- b_i = the "b" parameter for the component
- DBH = tree's DBH in cm

The amount of each type of biomass, in metric tons, for each species is saved in a grid called [Partitioned Biomass](#). You can save these values in a detailed output file for analysis. You of course can skip any of the components by entering 0's for their parameter values.

How to apply it

Apply this behavior to saplings, adults, or snags of any species. *This behavior does not automatically create output.* Once you have added this behavior to your run, the [Detailed output grid setup window](#) will list the [Partitioned Biomass](#) grid. You can then view the contents of this grid as a [table](#) using SORTIE's data visualization system.

Partitioned Height Biomass

This behavior calculates biomass as a linear function of tree height, partitioned into leaf and bole biomass.

Parameters for this behavior

Parameter name	Description
Partitioned Height Biomass - Leaf Slope (a)	The slope in the linear biomass equation for leaves.

Partitioned Height Biomass - Leaf Intercept (b)	The intercept in the linear biomass equation for leaves.
Partitioned Height Biomass - Bole Slope (a)	The slope in the linear biomass equation for boles.
Partitioned Height Biomass - Bole Intercept (b)	The intercept in the linear biomass equation for boles.

How it works

The biomass of leaves and boles is calculated using the same equation, but using different parameters. The equation is:

$$Bio_i = a_i * Height + b_i$$

where

- Bio_i = biomass in kg dry weight of either leaves, branches, or the bole
- a_i = either the **Partitioned Height Biomass - Leaf Slope (a)** or **Partitioned Height Biomass - Bole Slope (a)** parameters
- b_i = either the **Partitioned Height Biomass - Leaf Intercept (b)** or **Partitioned Height Biomass - Bole Intercept (b)** parameters
- $Height$ = tree's height in meters

The amount of each type of biomass, in metric tons, for each species is saved in a grid called [Partitioned Biomass](#). You can save these values in a detailed output file for analysis.

How to apply it

Apply this behavior to saplings, adults, or snags of any species. *This behavior does not automatically create output.* Once you have added this behavior to your run, the [Detailed output grid setup window](#) will list the [Partitioned Biomass](#) grid. You can then view the contents of this grid as a [table](#) using SORTIE's data visualization system.

Ripley's K Calculator

This behavior calculates the Ripley's K function for all trees in the plot as well as for the members of each species.

Parameters for this behavior

Parameter name	Description
Ripley's K - Maximum Distance (m)	The maximum distance out to which to calculate K values.
Ripley's K - Distance Increment (m)	The distance increments at which K will be calculated. Smaller increments mean a smoother curve but also more processing time.

How it works

The Ripley's K function is a measure of the way trees are spatially distributed across the plot. K values are calculated repeatedly for a succession of distances out to a maximum, giving a curve. The Ripley's K statistic for a given distance t is calculated as:

$$\hat{K}(t) = \frac{AX}{n^2}$$

where:

- $K(t)$ is the K value at distance t
- A is the plot area in square meters
- X is the number of pairs of trees in the plot less than t meters apart
- n is the total number of trees in the plot

The size of the distance increment is given in the **Ripley's K - Distance Increment (m)** parameter. The maximum distance out to which to calculate K is given in the **Ripley's K - Maximum Distance (m)** parameter. Most Ripley's K formulas come with a term for edge correction, which is not needed in SORTIE-ND as the plot has no edges. (See [the SORTIE-ND Plot](#) topic for more on the plot's shape.)

Only saplings and adult trees are included in K calculations.

The K values are calculated for all trees in the plot as well as for individual species. In the case of an individual species, X is the number of pairs of trees of that species, and n is the total number of trees of that species.

The resulting K values are stored in the [Ripley's K](#) grid.

How to apply it

Add this behavior to your run. There is no need to apply it to specific tree species or types. Indeed, any such specifications will be ignored. *This behavior does not automatically create output.* Once you have added this behavior to your run, the [Detailed output grid setup window](#)

will list the [Ripley's K](#) grid. Save all the data members of this grid. You can then view the K values as a [line graph](#) and use the graph to save the K values as a text file.

Relative Neighborhood Density Calculator

Parameters for this behavior

Parameter name	Description
Relative Neighborhood Density - Maximum Distance (m)	The maximum distance out to which to calculate Relative Neighborhood Density Index (Ω) values.
Relative Neighborhood Density - Distance Increment (m)	The distance increments at which the Relative Neighborhood Density Index (Ω) will be calculated. Smaller increments mean a smoother curve but also more processing time.

This behavior calculates the relative neighborhood density index (Ω) as described in Condit et al 2000. Ω is a measure of the aggregation of a species. It is the average density of conspecific neighbors at a certain distance divided by the overall density of trees in the plot. A perfectly random distribution of individuals for a species would result in $\Omega = 1$. $\Omega > 1$ at short distances indicates species aggregation. $\Omega < 1$ at short distances indicates spacing among individuals.

How it works

Ω values are calculated for each species for a succession of distances out to a maximum. For each tree, the conspecific neighbors are counted in a ring described by the radii x to Δx . This value is divided by the area of the ring to get the density of neighbors at that distance. This density is averaged over all trees of each species. This average density of neighbors at a given distance is then relativized by dividing by the density of that species across the plot.

$$\Omega = \frac{\sum N_x / T * A_x}{den}$$

where:

- Ω is the relative neighborhood density at distance x to Δx for a species
- N_x is the total number of conspecific neighbors for that species found between x and Δx
- T is the total number of saplings and adults of that species in the plot
- A_x is the area of the ring $x + \Delta x$

- *den* is the total plot density for trees of that species

The size of the distance increment, x , is given in the **Relative Neighborhood Density - Distance Increment (m)** parameter. The maximum distance out to which to calculate Ω is given in the **Relative Neighborhood Density - Maximum Distance (m)** parameter.

Only saplings and adult trees are included in Ω calculations.

The resulting Ω values are stored in the [Relative Neighborhood Density](#) grid.

How to apply it

Add this behavior to your run. There is no need to apply it to specific tree species or types. Indeed, any such specifications will be ignored. *This behavior does not automatically create output.* Once you have added this behavior to your run, the [Detailed output grid setup window](#) will list the [Relative Neighborhood Density](#) grid. Save all the data members of this grid. You can then view the Ω values as a [line graph](#) and use the graph to save the Ω values as a text file.

State Reporter

This behavior reports the values of state variables.

How it works

Each timestep, this behavior retrieves the values of various variables capturing the current base state of SORTIE and stores them in the grid [State Variables](#). Currently the only state variables captured are for climate.

How to apply it

Add this behavior to your run. *This behavior does not automatically create output.* Once you have added this behavior to your run, the [Detailed output grid setup window](#) will list the [State Variables](#) grid. You can then view the contents of this grid as a [table](#) using SORTIE's data visualization system.

Storm Killed Partitioned DBH Biomass

This behavior calculates biomass of trees killed in storms as a linear function of DBH, partitioned into leaf, branch, and bole biomass.

Parameters for this behavior

Parameter name	Description
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Partitioned DBH Biomass - Bole Slope (a)	The slope in the linear biomass equation for boles.
Partitioned DBH Biomass - Bole Intercept (b)	The intercept in the linear biomass equation for boles.
Partitioned DBH Biomass - Branch Slope (a)	The slope in the linear biomass equation for branches.
Partitioned DBH Biomass - Branch Intercept (b)	The intercept in the linear biomass equation for branches.
Partitioned DBH Biomass - Leaf Slope (a)	The slope in the linear biomass equation for leaves.
Partitioned DBH Biomass - Leaf Intercept (b)	The intercept in the linear biomass equation for leaves.

How it works

Biomass is calculated in exactly the same way and using the same parameters as for the [Partitioned DBH Biomass](#) behavior, except it only calculates the biomass of those trees killed by the [Storm damage killer](#) behavior.

How to apply it

Apply this behavior to saplings, adults, or snags of any species. *This behavior does not automatically create output.* Once you have added this behavior to your run, the [Detailed output grid setup window](#) will list the [Storm Killed Partitioned Biomass](#) grid. You can then view the contents of this grid as a [table](#) using SORTIE's data visualization system.

Storm Killed Partitioned Height Biomass

This behavior calculates biomass of trees killed in storms as a linear function of tree height, partitioned into leaf and bole biomass.

Parameters for this behavior

Parameter name	Description
----------------	-------------

Partitioned Height Biomass - Leaf Slope (a)	The slope in the linear biomass equation for leaves.
Partitioned Height Biomass - Leaf Intercept (b)	The intercept in the linear biomass equation for leaves.
Partitioned Height Biomass - Bole Slope (a)	The slope in the linear biomass equation for boles.
Partitioned Height Biomass - Bole Intercept (b)	The intercept in the linear biomass equation for boles.

How it works

Biomass is calculated in exactly the same way and using the same parameters as for the [Partitioned Height Biomass](#) behavior, except it only calculates the biomass of those trees killed by the [Storm damage killer](#) behavior.

How to apply it

Apply this behavior to saplings, adults, or snags of any species. *This behavior does not automatically create output.* Once you have added this behavior to your run, the [Detailed output grid setup window](#) will list the [Storm Killed Partitioned Biomass](#) grid. You can then view the contents of this grid as a [table](#) using SORTIE's data visualization system.

Tree Bole Volume Calculator

This behavior calculates merchantable tree volume. Make sure to distinguish between this behavior and the other tree volume behavior.

Parameters for this behavior

Parameter name	Description
Bole Volume Form Class, 60% - 100%	Calculates the amount of taper to the top of the first 16-foot log in a tree. This is the diameter at the top of that log, as a percentage of DBH between 60 and 100.
Bole Volume Parameter (b0)	The b_0 parameter for the bole volume equation.

Bole Volume Parameter (b1)	The <i>b1</i> parameter for the bole volume equation.
Bole Volume Parameter (b2)	The <i>b2</i> parameter for the bole volume equation.
Bole Volume Parameter (b3)	The <i>b3</i> parameter for the bole volume equation.
Bole Volume Parameter (b4)	The <i>b4</i> parameter for the bole volume equation.
Bole Volume Parameter (b5)	The <i>b5</i> parameter for the bole volume equation.

How it works

Tree volume is calculated as follows:

$$V = b0 + (b1 * DBH^{b2}) + (b3 * DBH^{b4} * Height^{b5})$$

where:

- *V* = gross volume in cubic feet
- *Height* = bole length in feet, as a multiple of 16 (for usable 16-foot logs)
- *DBH* = DBH in inches
- *b0* - *b5* are the following parameters: **Bole Volume Parameter (b0)**, **Bole Volume Parameter (b1)**, **Bole Volume Parameter (b2)**, **Bole Volume Parameter (b3)**, **Bole Volume Parameter (b4)**, and **Bole Volume Parameter (b5)**

The bole length is the number of 16-foot logs the tree can provide, in feet (i.e. 3 logs = bole length of 48 feet). The base of the bole is the top of the cut stump; the top of the bole is the merchantable height. This behavior defines the merchantable height as the height at which the trunk diameter inside the bark tapers to 60% of DBH.

To determine at what bole length the merchantable height occurs, the behavior tries fitting in as many 16-foot logs as possible before the 60% taper occurs. The amount of taper at the top of the first 16-foot log is established by the form classes. A species's form class is the percentage of DBH to which the bole has tapered at the top of the first 16-foot log. This value is entered as the **Bole Volume Form Class, 60% - 100%** parameter.

Then the behavior determines how many more logs the tree contains. The amount of taper at the top of the first 16-foot log is subtracted from the DBH, to see how much taper is left before the 60% merchantable-height diameter is reached. There is no formula that establishes clearly how many logs will fit; the behavior uses a trial-and-error approach taken from [Messavage and](#)

[Girard, 1956](#). This paper includes the table below for upper-log taper for trees of various DBH and bole heights. The behavior uses this table to determine the maximum number of logs it can fit into the taper available.

Trees below 10 inches of DBH have no volume. Trees greater than 40 inches of DBH are treated like 40-inch trees.

DBH (in)	2-log tree		3-log tree		4-log tree			5-log tree				6-log tree				
	2d log	3d log	2d log	3d log	2d log	3d log	4th log	2d log	3d log	4th log	5th log	2d log	3d log	4th log	5th log	6th log
10	1.4	1.2	1.4	---	---	---	---	---	---	---	---	---	---	---	---	---
12	1.6	1.3	1.5	1.1	1.4	1.9	---	---	---	---	---	---	---	---	---	---
14	1.7	1.4	1.6	1.2	1.5	2	---	---	---	---	---	---	---	---	---	---
16	1.9	1.5	1.7	1.2	1.6	2.1	---	---	---	---	---	---	---	---	---	---
18	2	1.6	1.8	1.3	1.7	2.2	---	---	---	---	---	---	---	---	---	---
20	2.1	1.7	1.9	1.4	1.8	2.4	1.1	1.6	2.2	2.9	---	---	---	---	---	---
22	2.2	1.8	2	1.4	2	2.5	1.1	1.7	2.3	2.9	---	---	---	---	---	---
24	2.3	1.8	2.2	1.5	2.2	2.6	1.1	1.8	2.4	3.1	---	---	---	---	---	---
26	2.4	1.9	2.3	1.5	2.3	2.7	1.1	1.9	2.5	3.2	---	---	---	---	---	---
28	2.5	1.9	2.5	1.6	2.4	2.8	1.2	1.9	2.6	3.3	0.9	1.4	2.1	3.2	4.4	---
30	2.6	2	2.6	1.7	2.5	3	1.2	2	2.7	3.5	0.9	1.4	2.1	3.2	4.5	---
32	2.7	2	2.7	1.7	2.5	3.1	1.2	2.1	2.9	3.7	1	1.4	2.1	3.2	4.6	---
34	2.8	2.1	2.7	1.8	2.5	3.3	1.3	2.1	3	3.8	1	1.4	2.2	3.3	4.7	---
36	2.8	2.1	2.8	1.8	2.6	3.4	1.3	2.2	3	3.9	1.1	1.5	2.2	3.3	4.9	---
38	2.9	2.1	2.8	1.9	2.6	3.4	1.3	2.2	3.1	3.9	1.1	1.5	2.3	3.4	5.1	---
40	2.9	2.2	2.8	1.9	2.7	3.4	1.4	2.3	3.2	4	1.2	1.5	2.4	3.5	5.3	---

How to apply it

Apply this behavior to saplings, adults, or snags of any species. *This behavior does not automatically create output.* Once you have added this behavior to your run, the [Detailed output setup window](#) for trees will have a tree data member called "Tree Bole Volume". Add this to your detailed output file to output volume in cubic feet. You can then view charts and graphs with the resulting volume data using data visualization on your detailed output file.

Tree Age

This behavior calculates tree age.

How it works

The age of a tree, in years, is kept in a tree data member called "Tree Age" and updated each timestep. If this behavior is after the establishment behaviors, new seedlings will have an age equal to one timestep on the timestep they are created.

Some trees can be created at the beginning of a run, either in a tree map or to provide a specified initial tree density. These trees are given an age of 10000, so they can be easily distinguished from trees created during a run. If a tree map is provided and the trees are specifically given an age in the map, that age is kept and they are not re-assigned an age of 10000.

This behavior may not be applied to snags, since they have a different age counter.

How to apply it

Apply this behavior to the trees for which you want to track age. You can then save the "Tree Age" data in a detailed output file for analysis.

Tree Volume Calculator

This behavior calculates the volume of tree trunks. It can be used to find both merchantable volume and total volume. Make sure to distinguish between this behavior and the other tree volume behavior.

Parameters for this behavior

Parameter name	Description
Taper Equation Initial Multiplier (a0)	The a_0 parameter in the taper equation below.
Taper Equation DBH Exponent (a1)	The a_1 parameter in the taper equation below.
Taper Equation Height Exponent (a2)	The a_2 parameter in the taper equation below.
Taper Equation X Exponent 1 (b1)	The b_1 parameter in the taper equation below.

Taper Equation X Exponent 2 (b2)	The b_2 parameter in the taper equation below.
Taper Equation X Exponent 3 (b3)	The b_3 parameter in the taper equation below.
Taper Equation X Exponent 4 (b4)	The b_4 parameter in the taper equation below.
Taper Equation X Exponent 5 (b5)	The b_5 parameter in the taper equation below.
Taper Equation X Exponent 6 (b6)	The b_6 parameter in the taper equation below.
Diameter-Outside-Bark Constant (a1)	The a_1 parameter in the equation for calculating tree diameter outside bark, below.
Diameter-Outside-Bark First Degree Parameter (a2)	The a_2 parameter in the equation for calculating tree diameter outside bark, below.
Diameter-Outside-Bark Second Degree Parameter (a3)	The a_3 parameter in the equation for calculating tree diameter outside bark, below.
Height to Begin Calculating Trunk Volume, in cm	The height at which volume calculations begin. For merchantable volume calculations, this can be thought of as the stump height. The height is height off the ground in cm.
Minimum Trunk Diameter for Volume Calculations, in cm	The trunk diameter (inside the bark) at which volume calculations end. For merchantable volume calculations, this is the minimum usable trunk diameter. The diameter is in cm.
Trunk Segment Length for Volume Calculations, in m	The length, in m, of segments into which the tree trunk is divided for volume calculations. A smaller value means a greater degree of accuracy; a larger value means a faster processing time.

How it works

Tree volume is estimated by dividing the trunk into segments, and calculating the volume of each segment. You control where the trunk starts and stops, and the length of segments used.

Trunks start at the value in the **Height to Begin Calculating Trunk Volume, in cm** parameter. To calculate merchantable volume, set this to the average stump height. To calculate total volume, set this to zero. Trunks end when their diameter inside the tree bark becomes smaller than the volume in the **Minimum Trunk Diameter for Volume Calculations, in cm** parameter.

For merchantable volume, set this to the minimum usable diameter. For total volume, set this to zero.

Trunks are divided into segments for volume calculations. The length of these segments is set in the **Trunk Segment Length for Volume Calculations, in m** parameter. Setting this to a smaller value increases the accuracy of the calculations. Setting this to a larger value increases the speed at which the calculations are made. The total tree's volume is the sum of the volumes of each of the segments. Any segments whose beginning or ending diameter is less than the value in the **Minimum Trunk Diameter for Volume Calculations, in cm** parameter are not included in the volume total.

The volume of a tree trunk segment is found as follows:

$$V = ((A_1 + A_2) / 2) * l$$

where:

- A_1 is the cross-sectional area at the bottom of the trunk segment, in square meters
- A_2 is the cross-sectional area at the top of the trunk segment, in square meters
- V is the volume of the trunk segment, in cubic meters
- l is the length of the trunk segment (value in the **Trunk Segment Length for Volume Calculations, in m** parameter)

The cross-sectional area of a tree trunk at a particular point above the ground (such as at the beginning or end of a trunk segment) is calculated as:

$$A = \pi(d / 2)^2$$

where A is the cross-sectional area, in square meters, and d is the diameter of the tree inside the bark at that height, in meters.

To find the diameter of the tree trunk inside the bark at a particular height above the ground, the taper equation is used. (This equation comes from Kozak (2004) Forest Chronicle 80: 507 - 515; it's the "2002 model"). The equation is:

$$d_i = a_0 D^{a_1} H^{a_2} X_i^{b_1 z_i^4 + b_2 [1 / e^{D/H}] + b_3 X_i^{0.1} + b_4 [1 / D] + b_5 H^{Q_i} + b_6 X_i}$$

where:

- $X_i = (1 - (h_i / H)^{1/3}) / (1 - p^{1/3})$
- $Q_i = 1 - (h_i / H)^{1/3}$
- $p = 1.3 / H$
- $z_i = h_i / H$ (proportional height above the ground)

- D is the outside bark diameter, in cm, at breast height (1.35 m) (equation below)
- H is the total tree height (m)
- h_i is the height from the ground (m) at which to calculate the diameter inside the bark
- d_i is the inside bark diameter at h_i height from ground (cm)
- a_0 is the **Taper Equation Initial Multiplier (a0)** parameter
- a_1 is the **Taper Equation DBH Exponent (a1)** parameter
- a_2 is the **Taper Equation Height Exponent (a2)** parameter
- b_1 is the **Taper Equation X Exponent 1 (b1)** parameter
- b_2 is the **Taper Equation X Exponent 2 (b2)** parameter
- b_3 is the **Taper Equation X Exponent 3 (b3)** parameter
- b_4 is the **Taper Equation X Exponent 4 (b4)** parameter
- b_5 is the **Taper Equation X Exponent 5 (b5)** parameter
- b_6 is the **Taper Equation X Exponent 6 (b6)** parameter

SORTIE-ND considers its DBH parameter to be diameter without bark. To find the diameter outside the bark, the equation is:

$$D = a_1 + a_2DBH + a_3DBH^2$$

where:

- D is the diameter outside the bark, in cm
- DBH is the diameter inside the bark, in cm (SORTIE's DBH)
- a_1 is the **Diameter-Outside-Bark Constant (a1)** parameter
- a_2 is the **Diameter-Outside-Bark First Degree Parameter (a2)** parameter
- a_3 is the **Diameter-Outside-Bark Second Degree Parameter (a3)** parameter

Important note. The math in this behavior is particularly susceptible to producing extreme numbers if the parameters are not chosen very carefully. These extreme numbers (incredibly large or small numbers) will crash SORTIE if they happen, and cannot be guarded against ahead of time. Be very careful when selecting parameters, and test your parameters to ensure they produce sensible results for a wide range of tree sizes. If you have problems with SORTIE crashing, try verifying that this behavior is the problem by removing it from the run and trying again. If you can verify that this behavior is the problem, carefully re-examine your parameters.

How to apply it

Apply this behavior to saplings, adults, or snags of any species. *This behavior does not automatically create output.* Once you have added this behavior to your run, the [Detailed output setup window](#) for trees will have a tree data member called "Tree Volume". Add this to your detailed output file to output volume in cubic meters. You can then view charts and graphs with the resulting volume data using data visualization on your detailed output file.

What is a grid?

A grid is a structure for holding model data that varies across space. It contains cells, organized by row and column, that cover the entire plot. Grids are part of the [state data](#) of SORTIE.

Examples of grids are soil fertility (substrate), storm damage susceptibility maps, and number of seeds dispersed.

A single grid can be set up to hold more than one value per cell. In addition, packets of information called packages can be attached to individual cells to add to the amount of information a grid can carry. There is no limit to the number of packages that can be attached to a cell. An example of data which might come in packages is a grid holding data on harvest events, with each package representing a discrete harvest.

How grids are created and used

Which grids are used for a run depends entirely on which [behaviors](#) are used. All grids are created automatically by a behavior. A grid that is not needed in a run will not be created.

Behaviors use grids for three primary reasons:

- To map spatial variation in some aspect of the plot (as with a storm damage susceptibility map)
- To pass information from behavior to behavior (as with a substrate map which is updated by one behavior and used by another to determine likelihood of seed establishment)
- To report something for output (number of trees harvested, amount of biomass)

Grid cell size

Grids are always exactly the same size as the [plot](#). Grids have an X and a Y axis, which match the orientation and size of the plot's axes. Grids are divided along the X and Y axes separately, so that each cell within the grid is a rectangle. If the chosen grid cell sizes do not divide evenly into the X and Y plot lengths, the length of the cells in the last rows in each direction will be the remainder value. Grids can carry more than one value per cell. Grid cell size applies to all values in the grid. The amount of memory and processing time required for a grid is proportional to the number of total values it holds, which is the number of values per cell multiplied by the number of cells.

For most grids, you can define the size of the cells by using the [Grid setup window](#). You do not have to choose the size of a grid's cells; all grids have default values. If you choose to adjust a grid's cell size, you should pick the largest possible value that adequately captures the resolution of the process being modeled, to minimize the model's memory requirements and maximize the speed required to update it. If you have a set of behaviors that work together and you are defining cell sizes for multiple grids, picking even multiples of a number for different grids (such as 2, 4, 8...) will help maximize the efficiency of data transfer between them.

Setting up grid initial conditions

In addition to setting a grid's [cell size](#), you can also set its initial values. As with trees, setting the initial values of a grid can have an impact on the outcome of a run.

For many grids setting the initial values in the grid cells is not required, or in some cases, even allowed: for instance, a grid that is used to report on plot biomass will not accept input. The documentation for the behavior that creates the grid will guide you as to whether you can or need to provide initial values.

If setting the initial values for a grid is optional, you choose to set them generally because you want to reproduce conditions from another run.

There are two ways to add grid initial conditions to a parameter file: the first is the [Grid setup](#) window. This allows you to work with grid values directly in a spreadsheet-like format. The other way is to [add a grid map from a detailed output file](#).

Grid list

Complete list of all grids:

[Average
Light grid](#)

[Basal Area
Light grid](#)

[Carbon Value
grid](#)

[Climate
Comp Dep
Neighborhood
Survival grid](#)

[Competition
Harvest
Results grid](#)

[Detailed
Substrate grid](#)

[Detailed
Substrate
calcs grid](#)

[Dispersed
Seeds grid](#)

[Foliar
Chemistry
grid](#)

[Gap Light
grid](#)

[GLI Map grid](#)

[Harvest
Master Cuts
grid](#)

[Harvest
Results grid](#)

[Merchantable
Timber Value
grid](#)

[Mortality
Episode
Master Cuts
grid](#)

[Mortality
Episode
Results grid](#)

[NCI Quadrat
Growth grid](#)

[Neighborhood
Seed
Predation grid](#)

[Partitioned
Biomass grid](#)

[Planting
Results grid](#)

[Quadrat GLI
grid](#)

[Relative](#)

[Neighborhood
Density grid](#)

[Resource grid](#)

[Ripley's K
grid](#)

[Seed
Predators grid](#)

[Snag Decay
Class
Dynamics
Basal Area
grid](#)

[State
Variables grid](#)

[Storm
Damage grid](#)

[Storm Killed
Partitioned
Biomass grid](#)

[Storm Light
grid](#)

[Storm
Susceptibility
grid](#)

[Substrate grid](#)

[Substrate
calcs grid](#)

[Substrate
Favorability
grid](#)

[Temperature
Dependent
Neighborhood
Survival grid](#)

[Windstorm](#)

[Results grid](#)

[Years Since Last Harvest grid](#)

Average Light Grid

Average Light

This grid is created by the [Average Light](#) behavior. It contains the averages of the values of the [GLI Map](#) grid. It is important to set the cell sizes of the two grids exactly as you want them. The default grid cell resolution is set to 8 m X 8 m.

Data in the grid

Data member name	Description
GLI	Average GLI value

Basal Area Light Grid

This grid is created by the [Basal Area Light](#) behavior. Each grid cell holds tree basal area data and a light level. The grid cell resolution defaults to 8 m X 8 m. You can set whatever new resolution you wish.

Data in the grid

Data member name	Description
Light	The light level as calculated by the Basal Area Light behavior
Conifer Basal Area	The basal area, in square meters, of conifers that count towards the light calculation
Angiosperm Basal Area	The basal area, in square meters, of angiosperms that count towards the light calculation

Carbon Value Grid

This grid is created by the [Carbon Value behavior](#). It holds the amount of carbon and the value of that carbon for each species. This grid has one cell for the whole plot. It will ignore any changes you make to the resolution. If this grid's data is saved in a detailed output file, you can view the contents of this grid as a [table](#) using SORTIE's data visualization system.

Data in the grid

Data member name	Description
Mg of Carbon for Species X	The amount of carbon in the plot for Species X, in metric tons
Carbon Value for Species X	The value of the carbon for Species X

Climate Comp Dep Neighborhood Survival Grid

This grid is created by the [Climate and Competition Dependent Neighborhood Survival](#) behavior. It holds the timestep survival rate for each species in each grid cell.

Data in the grid

Data member name	Description
Survival for Species X	The survival rate for Species X for that cell. The rate is per timestep, not annual. Note that the value may be -1 if there were no trees of Species X in the grid cell for that timestep.
Neighbor basal area	The adult neighbor basal area, in square meters

Competition Harvest Results Grid

This grid is created by the [Competition Harvest behavior](#). This is where data on competition harvest results is stored. The data is stored raw - no conversion to per-hectare amounts.

The default grid cell resolution is set to one grid cell for the entire plot. You can set whatever new resolution you wish.

Data in the grid

Data member name	Description
Cut Density, species x	Number of trees cut in the current timestep for the given species
Cut Basal Area, species x	Total basal area cut in the current timestep for the given species

DetailedSubstrate Grid

This grid is created by the [Detailed Substrate behavior](#). The grid holds the relative proportions of the various substrate types. If the [Harvest behavior](#) is present for the run, then this grid's resolution must match the Harvest Results grid. Otherwise, it defaults to a cell resolution of 8 m X 8 m, which you can change. This grid holds [packages](#) with a different data structure from the main grid to track Substrate cohorts.

Data in the grid

Data member name	Description
Proportion of scarified soil	The proportion of the grid cell area that is scarified soil
Proportion of forest floor	The proportion of the grid cell area that is forest floor
Proportion of tip-up mounds	The proportion of the grid cell area that is tip-up mounds
Total Log	Total logs, expressed as a proportion between 0 and 1. The sum of all log proportions
Total Log Volume	Total log volume, in m ³ per ha. The sum of all log volumes
Prop Sp Group X Small Decay Y	Species group X, decay class Y small logs, as a proportion between 0 and 1
Prop Sp Group X Large Decay Y	Species group X, decay class Y large logs, as a proportion between 0 and 1
Vol Sp Group X Small Decay Y	Species group X, decay class Y small log volume in m ³ per ha
Vol Sp Group X Large Decay Y	Species group X, decay class Y large log volume in m ³ per ha

Packages:

Data member name	Description
Substrate cohort age	The age of the substrate cohort, in timesteps

Substrate cohort new scarified soil substrate	The proportion of cell area that is scarified soil added in this cohort
Substrate cohort new tip-up mounds substrate	The proportion of cell area that is tip-up mounds substrate added in this cohort

Detailed Substrate calcs Grid

This grid is called "detailedsubstratecalcs" and is created by the [Detailed Substrate behavior](#). This grid is used for intermediate calculations when calculating the values in the Detailed Substrate grid. The grid cell resolution must match Detailed Substrate's.

Data in the grid

Data member name	Description
Amount of new tip-up mounds	New tip-up mounds area by grid cell, in square meters
New Log Area Sp Group X Small Decay Y	Area of new small logs added this timestep for species group X, decay class Y, in square meters
New Log Area Sp Group X Large Decay Y	Area of new large logs added this timestep for species group X, decay class Y, in square meters
Prop Sp Group X Small Decay Y Timestep Z	Fresh small logs added Z timesteps ago for species group X, decay class Y, as a proportion of grid cell area
Prop Sp Group X Large Decay Y Timestep Z	Fresh large logs added Z timesteps ago for species group X, decay class Y, as a proportion of grid cell area

Dispersed Seeds Grid

This grid is created by the [Disperse behaviors](#). It holds the number of seeds of each species that have been created by dispersal. This grid defaults to a cell resolution of 8 m X 8 m, which you can change.

Data in the grid

Data member name	Description
Number of seeds for Species X	The number of seeds in each grid cell belonging to Species X

Gap status	Whether the cell is in gap (true) or under closed canopy (false). Only used if there are behaviors which use forest cover.
Adult tree count	The count of adult trees, for determining gap status. Only used if there are behaviors which use forest cover.

Foliar Chemistry Grid

This grid is created by the [Foliar Chemistry](#) behavior. This is where the amount of different foliar chemistry components is stored. All data is stored raw, no conversion to per-hectare amounts.

The grid cell resolution is set to 8 m X 8 m. You can change this to whatever you wish.

Data in the grid

Data member name	Description
Kg N for [species X]	Amount of N for species X, in kg
Kg P for [species X]	Amount of P for species X, in kg
Kg SLA for [species X]	Amount of SLA for species X, in kg
Kg Lignin for [species X]	Amount of lignin for species X, in kg
Kg Fiber for [species X]	Amount of fiber for species X, in kg
Kg Cellulose for [species X]	Amount of cellulose for species X, in kg
Kg Tannins for [species X]	Amount of tannins for species X, in kg
Kg Phenolics for [species X]	Amount of phenolics for species X, in kg

Gap Light Grid

This grid is created by the [Gap Light](#) behavior. Each grid cell holds the cell's gap status, either TRUE or FALSE. The grid cell resolution defaults to 8 m X 8 m. You can set whatever new resolution you wish.

Data in the grid

Data member name	Description
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Is Gap

Whether (TRUE) or not (FALSE) that grid cell has gap status

GLI Map Grid

This grid is created by the [GLI Map Creator](#) behavior. The grid holds a GLI value in each cell. The grid cell resolution defaults to 8 m X 8 m. You can set whatever new resolution you wish.

Data in the grid

Data member name	Description
GLI	GLI value, as a percentage of full sun between 0 and 100

Harvest Master Cuts Grid

This grid is created by the [Harvest behavior](#). This is where directions to SORTIE for harvests for the run are stored. The actual name of the grid is "harvestmastercuts".

The only thing you may change in this grid is the grid cell resolution. You may set it to anything you wish. You can change it with either the [Grid Setup](#) window (accessible only if harvest events have already been created) or with the [Edit Harvest Window](#).

Data in the grid

There is no user accessible data in the grid.

Harvest Results Grid

This grid is created by the [Harvest behavior](#). This is where data on harvest results is stored. The data is stored raw - no conversion to per-hectare amounts.

The grid cell resolution is always set to match the [Harvest Master Cuts](#) grid. Any changes you make to the grid cell resolution will be ignored.

Data in the grid

Data member name	Description
Harvest Type	Type of harvest that occurred in the current timestep, or -1 if none has occurred

Cut Density, species x, cut range y	Number of trees cut in the current timestep for the given species and cut range
Cut Basal Area, species x, cut range y	Total basal area cut in the current timestep for the given species and cut range
Cut Seedlings, species x	Seedlings killed as part of a harvest event in the current timestep for the given species

Merchantable Timber Value Grid

This grid is created by the [Merchantable Timber Value behavior](#). It holds the merchantable timber value for each species. This grid has one cell for the whole plot. It will ignore any changes you make to the resolution. If this grid's data is saved in a detailed output file, you can view the contents of this grid as a [table](#) using SORTIE's data visualization system.

Data in the grid

Data member name	Description
Value for Species X	The merchantable timber value for Species X

Mortality Episode Master Cuts Grid

This grid is created by the [Episodic Mortality behavior](#). This is where directions to SORTIE for planned mortality episodes for the run are stored. The actual name of the grid is "mortepisodemastercuts".

The only thing you may change in this grid is the grid cell resolution. You may set it to anything you wish. You can change it with either the [Grid Setup](#) window (accessible only if planned mortality episode events have already been created) or with the [Edit Mortality Episode Window](#).

Data in the grid

There is no user accessible data in the grid.

Mortality Episode Results Grid

This grid is created by the [Episodic Mortality behavior](#). This is where data on planned mortality episode results is stored. The data is stored raw - no conversion to per-hectare amounts.

The grid cell resolution is always set to match the [Mortality Episode Master Cuts](#) grid. Any changes you make to the grid cell resolution will be ignored.

Data in the grid

Data member name	Description
Cut Density, species x, cut range y	Number of trees killed in the current timestep for the given species and cut range
Cut Basal Area, species x, cut range y	Total basal area killed in the current timestep for the given species and cut range
Cut Seedlings, species x	Seedlings killed as part of a planned mortality episode in the current timestep for the given species

NCI Quadrat Growth Grid

This grid is created by one of the [NCI quadrat growth](#) behaviors. It holds the growth rate for each species. Set this grid to the resolution you desire for neighborhood growth calculations. This grid may not be set up with initial values.

Data in the grid

Data member name	Description
Growth for Species X	The amount of diameter growth for the timestep for all trees of that species in the grid cell.

Neighborhood Seed Predation Grid

This grid is created by the [Neighborhood Seed Predation](#) and [Neighborhood Seed Predation \(linked\)](#) behaviors. This grid stores the seed rain before predation and the amount of seeds eaten. The grid resolution must match the [Dispersed Seeds grid](#). All data is stored raw, no conversion to per hectare amounts.

Data in the grid

Data member name	Description
Pre-predation	Number of seeds of species x in the grid cell before predation. Note that if a

seeds for species x	species is not subject to seed predation, its value may show up here as zero despite having seeds present. Its seeds are not missing, just ignored.
Proportion seeds eaten for species x	Proportion of the seeds of species x eaten this timestep, as a value between 0 and 1.

Partitioned Biomass Grid

This grid is created by the [Partitioned DBH Biomass](#) and [Partitioned Palm Biomass](#) behaviors. This is where the amount of biomass is stored, partitioned into leaf, bole, and branch (if applicable) biomass. All data is stored raw, no conversion to per-hectare amounts.

The grid cell resolution is set to 8 m X 8 m. You can change this to whatever you wish. The grid is shared by the two behaviors mentioned above, so changing it for one changes it for both.

Data in the grid

Data member name	Description
Mg Leaf Biomass for [species X]	Amount of leaf biomass for species X, in Mg
Mg Bole Biomass for [species X]	Amount of bole biomass for species X, in Mg
Mg Branch Biomass for [species X]	Amount of branch biomass for species X, in Mg
Mg Leaf Palm Biomass for [species X]	Amount of palm leaf biomass for species X, in Mg
Mg Bole Palm Biomass for [species X]	Amount of palm bole biomass for species X, in Mg

Planting Results Grid

This grid is created by the [Planting behavior](#). This is where data on planting results is stored. The data is stored raw - no conversion to per-hectare amounts.

The grid cell resolution is set to 8 m X 8 m. You cannot change the grid cell resolution for this grid.

Data in the grid

Data member name	Description
Planted Species X	Number of trees of Species X cut in the current timestep

Quadrat GLI Grid

This grid is created by the [Quadrat-based GLI Light](#) behavior. The grid holds a GLI value in each cell ("quadrat" being a term previously used in SORTIE to describe small grid cells). The grid cell resolution defaults to 2 m X 2 m. You can set whatever new resolution you wish.

Data in the grid

Data member name	Description
GLI	GLI value, or -1 if there were no trees to which to assign a GLI value in that grid cell

Relative Neighborhood Density Grid

This grid holds values for the Relative Neighborhood Density (Ω) statistic as calculated by the [Relative Neighborhood Density Calculator](#) behavior. The grid holds an Ω value for each distance increment for each species. This can be a great many values. The grid cell resolution is always set to one cell covering the entire plot. You cannot change this.

Data in the grid

Data member name	Description
Max Distance	Maximum distance to which to calculate Ω , in meters. Including this in the output is not necessary but will improve the SORTIE graphing capability.
Distance Inc	How often to calculate Ω , in meters. Including this in the output is not necessary but will improve the SORTIE graphing capability.
Species X Dist Y Omega Value	The Ω value for Species X at the Yth distance increment. This is not necessarily the distance in meters.

Resource Grid

This grid holds values for a second growth resource for use by the [Double resource relative growth](#) and [Growth and Resource-Based Mortality](#) behaviors. The actual identity of the resource is unknown and unimportant. The grid holds a value for resource level in each cell and it is assumed that the units scale appropriately to the parameters for the growth behavior. The grid cell resolution defaults to 8 m X 8 m. You can set whatever new resolution you wish.

Data in the grid

Data member name	Description
Resource	Resource amount, in whatever units are appropriate

Ripley's K Grid

This grid holds values for the Ripley's K statistic as calculated by the [Ripley's K Calculator](#) behavior. The grid holds a K value for each distance increment for each species. This can be a great many values. The grid cell resolution is always set to one cell covering the entire plot. You cannot change this.

Data in the grid

Data member name	Description
Max Distance	Maximum distance to which to calculate K, in meters. Including this in the output is not necessary but will improve the SORTIE graphing capability.
Distance Inc	How often to calculate K, in meters. Including this in the output is not necessary but will improve the SORTIE graphing capability.
All Species Dist Y K Value	The K value for all plot trees at the Yth distance increment. This is not necessarily the distance in meters.
Species X Dist Y K Value	The K value for Species X at the Yth distance increment. This is not necessarily the distance in meters.

Seed Predators Grid

This grid is created by the [Functional response seed predation](#) behavior. It holds the number of seed predators in each seed grid at the end of the predation model run. This grid's resolution must match that of [Dispersed Seeds](#).

Data in the grid

Data member name	Description
Number Predators	The number of predators in each grid cell.

Snag Decay Class Dynamics Basal Area Grid

This grid is created by the [Snag Decay Class Dynamics](#) behavior. It holds the amount of basal area for live and cut trees. Maps and grid resolution changes for this grid are not honored.

Data in the grid

Data member name	Description
Live BA Per Ha	The amount of basal area, in square meters per hectare, of live adults.
Cut BA Per Ha	The amount of basal area, in square meters per hectare, of trees harvested this timestep.

State Variables Grid

This grid is created by the [State Reporter](#) behavior. There is one grid cell for the entire plot, which holds state variables.

Data in the grid

Data member name	Description
Temperature C	The plot mean annual temperature, as stored in the Plot .
Precipitation mm	The plot mean annual temperature, as stored in the Plot .
Water Deficit	The plot seasonal water deficit, as stored in the Plot .
Seasonal Precipitation	The plot seasonal precipitation, as stored in the Plot .

Storm Damage Grid

This grid is created by the [Storm disturbance](#) behavior. Each grid cell holds a storm damage index between 0 and 1. The grid resolution default is 8 m X 8 m. You can change this to whatever you wish, but if you are also using the grid [Storm Susceptibility](#), the resolutions must match.

Data in the grid

Data member	Description
-------------	-------------

name	
Damage Index	The mean storm damage index for all storms occurring in the past timestep, from 0 (no damage) to 1 (total damage)
Time Since Last Storm	The number of years since the last storm occurred in this cell. The last storm is any storm at all of any strength.

Packages:

Data member name	Description
Single Storm Damage Index	Storm damage index for a single storm event

Storm Killed Partitioned Biomass Grid

This grid is created by the [Storm Killed Partitioned DBH Biomass](#) and [Storm Killed Partitioned Palm Biomass](#) behaviors. This is where the amount of biomass is stored, partitioned into leaf, bole, and branch (if applicable) biomass. All data is stored raw, no conversion to per-hectare amounts.

The grid cell resolution is set to 8 m X 8 m. You can change this to whatever you wish. The grid is shared by the two behaviors mentioned above, so changing it for one changes it for both.

Data in the grid

Data member name	Description
Mg Leaf Biomass for [species X]	Amount of storm-killed leaf biomass for species X, in Mg
Mg Bole Biomass for [species X]	Amount of storm-killed bole biomass for species X, in Mg
Mg Branch Biomass for [species X]	Amount of storm-killed branch biomass for species X, in Mg
Mg Leaf Palm Biomass for [species X]	Amount of storm-killed palm leaf biomass for species X, in Mg
Mg Bole Palm Biomass for [species X]	Amount of storm-killed palm bole biomass for species X, in Mg

Storm Light Grid

This grid is created by the [Storm Light](#) behavior. Each grid cell holds a light level value. The grid cell resolution defaults to 8 m X 8 m. You can set whatever new resolution you wish.

Data in the grid

Data member name	Description
Light	The light level as calculated by the Storm Light behavior

Storm Susceptibility Grid

This grid is created by the [Storm disturbance](#) behavior. Each grid cell holds a storm susceptibility index between 0 and 1. The grid resolution default is 8 m X 8 m. You can change this to whatever you wish, but if you are also using the grid [Storm Damage](#), the resolutions must match.

Data in the grid

Data member name	Description
Susceptibility	A storm damage susceptibility for each cell, from 0 (not susceptible to damage) to >1 (very susceptible to damage)

Substrate Grid

This grid is created by the [Substrate behavior](#). The grid holds the relative proportions of the various substrate types. If the [Harvest behavior](#) is present for the run, then this grid's resolution must match the Harvest Results grid. Otherwise, it defaults to a cell resolution of 8 m X 8 m, which you can change. This grid holds [packages](#) with a different data structure from the main grid to track Substrate cohorts.

Data in the grid

Data member name	Description
Proportion of scarified soil	The proportion of the grid cell area that is scarified soil
Proportion of forest floor	The proportion of the grid cell area that is forest floor
Proportion of tip-up mounds	The proportion of the grid cell area that is tip-up mounds
Proportion of fresh logs	The proportion of the grid cell area that is fresh logs
Proportion of decayed logs	The proportion of the grid cell area that is decayed logs

Packages:

Data member name	Description
Substrate cohort age	The age of the substrate cohort, in timesteps
Substrate cohort new scarified soil substrate	The proportion of cell area that is scarified soil added in this cohort
Substrate cohort new tip-up mounds substrate	The proportion of cell area that is tip-up mounds substrate added in this cohort
Substrate cohort new fresh logs	The proportion of cell area that is fresh logs added in this cohort

Substrate calcs Grid

This grid is called "substratecalcs" and is created by the [Substrate behavior](#). This grid is used for intermediate calculations when calculating the values in the Substrate grid. The grid cell resolution must match [Substrate's](#).

Data in the grid

Data member name	Description
Amount of new tip-up mounds	New tip-up mounds area by grid cell, in square meters
Fresh logs X timesteps ago	Fresh logs added X timesteps ago up to the value in the Substrate parameter "Maximum number of years that decay occurs" (converted to timesteps), as a proportion of grid cell area

Substrate favorability Grid

This grid is created by either the [Substrate Dependent Seed Survival No Gap Status](#) or the [Substrate Dependent Seed Survival With Gap Status](#) behavior. It holds the proportion of seeds expected to germinate on the substrate composite of the grid cell. The cell resolution must match the "Substrate" grid, above.

Data in the grid

Data member name	Description
Favorability Index - Species	The proportion of seeds of Species X expected to germinate in

X

that cell

Temperature Dependent Neighborhood Survival Grid

This grid is created by the [Temperature dependent neighborhood survival](#) behavior. It holds the timestep survival rate for each species in each grid cell.

Data in the grid

Data member name	Description
Survival for Species X	The survival rate for Species X for that cell. The rate is per timestep, not annual. Note that the value may be -1 if there were no trees of Species X in the grid cell for that timestep.
Neighbor basal area	The adult neighbor basal area, in square meters

Windstorm Results Grid

This grid is created by the [Windstorm behavior](#). It holds information on what windstorms happened during each timestep. This grid has one cell for the whole plot. It will ignore any changes you make to the resolution.

The data is held in grid packages. There is one package for each storm event. No package means no storms. If this grid's data is saved in a detailed output file, you can view the contents of this grid as a [table](#) using SORTIE's data visualization system.

Data in the grid

There is one of these for each storm event.

Data member name	Description
Storm Severity	The severity of the storm that occurred, between 0 and 1
Basal Area Dead For Species X	The basal area killed in this storm for Species X
Density Dead For Species X	The number of stems killed in this storm for Species X

Years Since Last Harvest Grid

This grid is created by the [Lagged post harvest growth](#) and [Post Harvest Skidding Mortality](#) behaviors. Each grid cell holds the time since a harvest last occurred in that cell. The grid cell resolution defaults to 8 m X 8 m. You can set whatever new resolution you wish.

Data in the grid

Data member name	Description
Time	Time since last harvest
LastUpdated	The timestep the grid was last updated

Creating a parameter file

This topic covers creating a [parameter file](#) from scratch. To make a basic parameter file, you need to define the tree population, choose the list of behaviors that will run, and enter parameter values for your file. You can save your work at any point in the process and come back to it later.

Setting up the tree population

You can use the [File menu](#) and choose the option "New parameter file" for a short wizard that will get you started. First you will see the [Edit species list window](#). Enter a list of tree species. You can always come back to this window to edit the list later by choosing "Edit->Tree setup".

Setting up the behavior list

After you have entered a species list, the wizard will take you to the [Edit simulation flow window](#) so you can set up the list of behaviors for your run. You can approach this from either the tree perspective by setting up the list of behaviors for each tree type, or from the behavior perspective by starting with a list of behaviors and assigning each to specific groups of trees. See the link above for detailed instructions on choosing behaviors. Again, you can always come back to this window to make changes by choosing the menu option "Edit->Model flow". At this point the new parameter file wizard ends.

Setting parameter values

You must complete the steps above before you can edit parameters, because it is the tree population and the list of behaviors that defines what parameters are needed. Once those steps are complete, you can enter your parameter values by choosing the menu option "Edit->Model Settings", which will open the [Model settings window](#).

Output

A basic parameter file creates no output by default. (You can perform a run with it but there will be no results.) There are two kinds of output files: [summary output files](#) and [detailed output files](#). You can set up either or both of these using the [Edit->Output options](#) menu command from the main SORTIE-ND window.

Initial conditions

Set initial conditions for [trees](#) and [grids](#) to define the [model state](#) at the beginning of the run. Initial conditions can have a big effect on run outcome.

Replicating a point in another run

You can replicate a point in another run in your parameter file in order to have it as the starting point in a new run. You might do this to create a "branch point" where you determine what might have happened if the parameters in the first run had been a little different, or perhaps you did a run solely to create mature-forest initial conditions for a new run. The first run should have saved a [detailed output file](#) with as much data as possible. The new parameter file should be compatible with the first - it should have a common species set and most of the same behaviors. You can then load the data from any timestep of the previous run as initial conditions in the current parameter file. For more on entering the maps from a detailed output file, see the [Using output as input to a new run](#) topic.

Types of output files

There are two kinds of output files, [summary output files](#) and [detailed output files](#). You can save either or both kinds of files for a run.

Summary output files save high-level plot-wide density and basal area information for a run. This data is stored in a text format that is small and easy to open and read.

Detailed output files save information on individual grades and trees. They are very flexible. You can save as much or as little detail as you like. You cannot directly open and read these files, but you can use SORTIE to graph and chart the data and produce a wide variety of text output from the files.

Output strategies

Choosing what output to save is a bit of an art form. Save too much data, and your files will be too large and very slow to process. Save too little, and you won't have the data you need after your run. Here are some strategies to help you decide what to save.

What you save depends on what you want to look at. Each chart that SORTIE can display requires a specific set of information. There are several output types: [line graphs](#), [histograms](#), [tree maps](#), [grid maps](#), and [tables](#). Also be aware that, for overall data, the [summary output file](#) is a better choice than the detailed output file. It loads much faster and contains raw data in a format you can use outside of SORTIE without any kind of conversion. If you want to look at changes in tree basal area and density through time, save a summary output file and use it to look at these charts.

When you are first setting up new runs, you are likely to be testing your parameters to make sure they are all right. You will probably be doing several short runs until you are confident that you have chosen the correct behaviors and entered your parameters correctly. At this point you might want to save a lot of data and run for small numbers of timesteps so you can examine all aspects of a run to make sure it is progressing the way you want. Create a detailed output file, and have it save at least X, Y, and diameter information for all trees; save grids for things such as substrate conditions and dispersed seeds so you can look at maps; and save a summary output file so you can quickly examine line graphs and tables of basal area and density through time. Do short runs and examine output until you are confident that your parameter file is set up correctly.

When you are doing a set of research runs, OR you are doing long runs, save the bare minimum of data that you require in order to make your output files as small as possible and to make working with them quicker and easier. If all you care about is plotwide amounts of basal area and density, use a summary file only. If you want that plus a DBH distribution, save only DBH for saplings and adults. If you want to keep tabs on a type of data but you don't need a lot of detail, consider saving this data less often than every timestep. Use a summary file to get plotwide information instead of a detailed output file where possible.

When you are interested in spatial variation, such as when you are working with harvest treatments, you might wish to get statistics on just one area within the plot. You can create [subplots](#) in either summary output or detailed output files. This is also helpful if you have an extremely large plot but you want a lot of detail. In that case, the detailed output file can become too large to work with. A representative subplot may give you the information you need.

To study an interesting effect that you wish to be able to reproduce, you may want to save a detailed output file that you can use as initial conditions in a subsequent run. In this case, you would use the "Save everything" button in the [Setup detailed output file window](#). This file is likely to be extremely large, but can be very useful. As an example: you find that around timestep 15, the curve of sapling density curves up sharply in a very unexpected way. You want to be able to experiment with the growth parameters at timestep 15 to see if you can find what conditions that curve is sensitive to. You could "Save everything" for a run of 20 or so timesteps. You could create a parameter file with new growth parameters, find the timestep in the previous run where the interesting curve shape started, then use that timestep as initial conditions to your new run. For your new run, you would save less data. (For more information on using detailed output as initial conditions, see the [Using output as input to a new run](#) topic.)

Tree output

You can save both high level plot wide tree information and data on individual trees.

Dead trees and live trees in output

You can collect output information on both living trees and trees that died, for both types of output files. This allows you to view various charts and examine statistics for the trees that died each timestep. Dead trees are only recorded in the timestep in which they died. If a tree dies and creates a snag, it will show up twice: once when it creates the snag, and once when the snag is removed from the model. The snag itself is considered "alive" because it is still interacting with the model.

Dead trees are classed by mortality reason code. When you choose what data to save for output, if you save dead trees, you select which mortality codes you would like data for. If you do not save information for a particular mortality reason, it will not show up in the output even though there may be trees that died for that reason. All mortality reasons are always listed, although a particular run may not kill trees for that reason. Check the documentation for your chosen [disturbance behaviors](#) and [mortality behaviors](#) for more information on which codes will apply to your run.

Grid output

Grid data can only be saved in a [detailed output file](#). If a grid stores multiple types of data, you can choose which ones you want to save. For the chosen pieces of data, the output file contains the value for each cell.

Saved grid data can be viewed as a map or a histogram or can be used as initial conditions input for a new run.

Subplots in output

Sometimes you might want to track a portion of the plot separately from the rest of it. You can do this by defining subplots when you set up your output files. You can save separate subplots in both the detailed and summary output files. Subplot data is included in the summary output file. SORTIE produces a detailed output file for the whole plot, and one for each subplot you define.

You can save up to five subplots. The subplots do not have to be continuous in area.

The same data is saved both for subplots and the plot as a whole. Only tree data can be "subplotted". If grid data is saved, the whole grid will always be saved. It is easy to work with only a portion of a grid's data by, for example, printing out the grid using the [Grid Setup window](#).

To create subplots, click the button that says "Set up subplots..." on the output file windows. This will open the [Edit subplots window](#).

If you load a summary output file that contains subplot data for viewing charts and graphs in SORTIE, you will automatically be given separate chart viewing options for the whole plot plus each subplot. To view subplot charts and graphs for detailed output, you can open the detailed output subplot files separately.

Setting up output

You should set up output last, after you have completed your parameter file. What data you will have available to save will depend on how you have chosen to set up your run.

To set up output, choose ["Edit->Output options"](#) from the main SORTIE window. This will lead you to windows that allow you to choose what you want to save for both summary and detailed output files. Your options will depend on the setup of the run.

If you are working with a parameter file that was created on a different computer or by someone else, remember to check the file path and name of the output files. You may need to change the path to one that exists on the computer on which you intend to run the parameter file.

Using output as input to a new run

The tree and grid map data from detailed output files may be used as initial conditions for a new parameter file. This is useful when you want to generate starting conditions for future runs that start with a stable forest structure, or when you want to troubleshoot a run by recreating certain conditions.

Here are the requirements for a detailed output map file to be loaded with a parameter file different from its original file:

- The parameter file must have the same species as the parameter file used to create the detailed output file.
- The [Plot](#) dimensions must be the same.
- Each map that you want to use must make sense as a complete dataset. For instance, you cannot do a run with a tree map in which you have saved the X coordinates of trees but not the Y coordinates.
- If any behavior-specific data was saved for trees, those same behaviors must be enabled for the current run. (For more, see the [tree data member list](#) topic.)

The detailed output file can be used to completely save the state of the model. If your detailed output file saves everything, you could start a new analysis using any timestep of a previous analysis as the starting point. In order to save a complete detailed output file, use the "Save Everything" button on the [Setup detailed output file window](#).

To load a detailed output file as initial conditions, first load the parameter file. Then, using "File->Open File", choose the detailed output file. A window will open showing the sub-files within

the detailed output file, one per timestep. Double-click the timestep you want to load. You can either replace existing data or add to it. If you choose to add data, if an existing tree map is loaded, those trees will be combined with the new tree map. Grid values will be overwritten either way. If you don't want to use all the maps, you can erase those for individual grids and trees using the Edit menu options [Grid layer setup](#) and [Manage tree maps](#).

Loading and displaying data from an output file

SORTIE can display data from both kinds of output files, [summary files](#) and [detailed output files](#). SORTIE analyzes the contents of files that it is given and lets you know what it is capable of displaying from that data.

Load an output file by choosing the menu option "File->Open output file". Choose the file you want to view, either a summary output file with a ".out" extension, or a detailed output file with a ".gz.tar" extension. The file name will appear at the top of the main SORTIE window in the list that says "Open output files". You can have as many files open as you wish.

To display a chart, choose a file in the list marked "Open output files" at the top of the main SORTIE window. SORTIE will analyze the contents of the file and show you what it can display in the list marked "Chart choices for this file". The chart choices are broken apart by type. There may not be a choice for every type of chart. Choose the chart you want to display and click the "Draw Chart" button. The chart will appear in the main SORTIE window. You can open as many charts as you wish. A legend also opens for each file that applies to all its chart windows.

The main SORTIE window acts as a desktop for the chart windows displayed. They can be minimized, maximized, moved, and resized within the window. You can close them using the X button in the top right. You will notice that the legends have check boxes next to each species name, along with a color box. Unchecking the box next to a species removes it from all of that file's charts. Clicking on the color next to the species name lets you choose a new color for that species.

The charts themselves can also be modified by right-clicking on them. You can reset axis ranges and zoom in and out. You can save the graph as a separate image file in PNG format by choosing "Save As", and you can also send the graph to a printer.

The legends for detailed output files have an extra set of controls marked "Timestep" at the bottom. Use the arrows to step back and forth through the timesteps. As you step through and watch a chart, pay attention to axis ranges. The data visualizer is meant to analyze each dataset it charts and optimize the chart accordingly. It does not attempt to keep the view consistent.

The data visualizer can only show you what you have saved from the run. If you do not save any data for a particular species in a detailed output file, for instance, that species won't show up in any charts you open, even if there were many individuals of that species in the run. If your data

does not look the way you expect it to, start by carefully examining your output settings to make sure you actually saved everything you meant to.

Have patience when working with detailed output files. When you move through timesteps, change charts, and open new charts, the data visualizer often must go back and sift through the detailed output file for the data it needs. With large files and long runs this can be very time consuming. If you have an idea of the charts you want to work with, it will be faster if you only save the data needed to create those charts.

Extracting chart data into text format

You can save the raw data used to make any chart to a tab-delimited text file, suitable for viewing in spreadsheet and word processing programs. Use the "File->Save" menu option that appears on all charts, or press Ctrl-S. You can take this raw data to reproduce and adjust the chart in other graphing applications. If you have saved a [summary output file](#), be aware that this file already contains all its data in a tab-delimited text format; you can open this file directly if you wish.

For most charts opened from a detailed output file, you can save the chart data for either just the timestep you are currently viewing, or for the whole run at once. In most cases, saving for the whole run places the data for each timestep in a single file.

You can extract the same chart data from many detailed output files at once using the [Batch Extract Detailed Output Files](#) tool. This tool produces the same results as saving text data for all time steps on each chart.

Batch extract detailed output files tool

This tool allows you to extract chart data for multiple detailed output files at once. The extracted data is a text version of the chart's data for all time steps. For more on extracting text data, see [Extracting chart data into text format](#).

This tool uses a wizard format to set up batch extraction. You reach this tool from the "Tools" menu from the main SORTIE window.

Step 1: Choose detailed output files to extract from.

In the first window of the wizard, you choose which output files to extract from. These files do not have to be in the same directory, nor do they have to be from the same run. Use the file chooser on the left to select files, then use the "Add files to batch" to add them to the batch list. If you change your mind, select files on the batch list on the right, then use the "Remove files from batch" button. Once you have your list of batch files, click "Next".

The wizard will examine your list of detailed output files to determine what data are available for extraction. This may take awhile for a very long list of files. Once the analysis step is done, the wizard will take you to step 2.

Step 2: Choose extraction options.

The next window in the wizard offers you the available list of charts to extract data for, by chart type. This is the same set of options that would be offered if you were using data visualization interactively as usual. The options listed is the set of options available in all of the files in your batch. Some files may be missing some of the options. You can still choose any option; that option will be skipped for any files that do not support it.

When you choose an option, you will be prompted for a file name root. This root will be used along with the detailed output file name to give the final name for each data file. The directory that you specify is where all of the charts of this type will go. You can put each chart in a different directory if you wish. You can put any file extension on the end of the root, or no extension at all. Whatever extension you give will be added to each file name.

In addition to the file name root, you may be prompted for other options required by the chart you have chosen.

You cannot create two different instances of the same chart, even if you intend to use different options. You can set up subsequent batch processes for each different set of options desired.

Click "Finish" to launch the batch extraction. You'll get a progress bar telling you the amount of work completed.

Viewing output data while a run is still in progress

You can view the output from a run as it progresses. SORTIE will keep a set of open charts updated with the results of the latest timestep. Here's how to use this feature:

1. Load your parameter file. Make sure you have the output files set up the way you want.
2. Start the run so SORTIE has some output to display. A simple way to do this is to click the "Run one timestep" button (the one on the main window with two right-facing triangles). When SORTIE has completed the timestep, the message bar at the bottom of the window will display a message indicating that the run has paused. You can also run the model using "Model->Run" from the main menu or the Run button (with the single right-facing arrow); you can pause the run at any point to start viewing data.
3. Once the run is paused, click the "View run output" button. SORTIE will load the output files from the current run and analyze them to determine what charts you can view. (SORTIE will not force you to first pause the run, but it is highly recommended. This

ensures that the model is not trying to write new output to the files at the same time as it is trying to open them to be read.)

4. Open the charts you wish to view (see [Displaying the data from a file](#). If a chart you want is not listed for any output file, it means that the data it requires is not being saved. You must stop the run, change your output options, and start a new run.
5. Start the model running again. As the model completes each timestep, it will update any open charts (while it does this, you may see a message that the model is paused at the bottom of the screen; this is normal). You can open new charts or close existing ones at any point in the run (again, pausing is recommended before opening new charts).

Note: While displaying a current run's output is a useful feature, it is not the most efficient way to do a run. If you do not actually need to keep tabs on a run's progress, or if you are satisfied with the way a current run is going, allow it to run without open charts. The run will execute much faster. If you currently have charts open for a run, you can use the menu command "File->Close run output file" to close each of the run's output files. Once all output files are closed, the run will switch back to the more efficient mode.

Line graphs

You can produce several kinds of line graphs. Four kinds of line graphs: absolute density, relative density, absolute basal area, and relative basal area, can be produced from either summary output files or detailed output files. If you know you want to look at these graphs, you should save a summary output file. The graphing performance will be significantly better. Another set of line graphs, absolute volume and relative volume, can be created via the detailed output file.

If you are saving a summary output file and have defined subplot areas, the line graphs will also be available for each subplot in addition to the whole plot. Subplots are not available in detailed output files.

In order to view basal area and density graphs from a summary output file, save data for each kind of graph you want to see in the [Summary output setup window](#). To view these graphs from a detailed output file, save the "DBH" tree data member for saplings, adults, or snags, or the "Diam 10" tree data member for seedlings. For more on how to save these tree data members, see the [Setup tree save options window](#).

To view volume graphs, in the detailed output file, save the [Tree Volume](#) tree data member for your chosen tree types. To access this tree member, you must add the [Tree volume calculator](#) behavior to your run.

A line graph may also be created for the contents of a few grids.

Histograms

SORTIE can produce a histogram for most tree and grid values in a detailed output file. It will offer to display any value it finds, which can sometimes lead to a crowded histogram display list.

Tree-based histograms display the number of trees per hectare for each species that fall into each of several value groupings for a piece of data. For instance, a height histogram that divided height into one meter increments would show how many trees of each species were from 0 - 1 meters in height, from 1 - 2 meters in height, etc.

Grid-based histograms display the number of grid cells that fall into the groupings. Grids that hold species specific data will also have a histogram option for displaying all species together.

The visualizer attempts to optimize the histogram for the data it is displaying. You can further customize the display of the histogram to suit your data. You have your choice of logarithmic or linear Y axis. You can also redivide the data by specifying the number of bins into which the data is divided, and the size of each bin.

The visualizer defaults to recalculating the bin size for each timestep in order to best display the data, so keep an eye on the bin size as you step through the timesteps. If you change the bin size or number of bins, the visualizer will preserve your changes.

Tree map

A tree map is available when you have saved the X, Y, and either the DBH or crown radius of trees in a detailed output file. The tree map does not display seedlings.

XY DBH Tree Map

This map displays a circle for each tree that corresponds to the size of its DBH. The color matches the species in the legend.

The **DBH Scale Factor** controls the size of the circles being displayed. The size of the tree circles is this value is multiplied by the DBHs. When the value is 1, the circles are approximately life size in relation to each other. Use this value to adjust the display for exceptionally large or small trees; but if the value is not one, remember that the display will not accurately show how close together trees are.

The **Minimum DBH to display** setting controls the smallest trees shown on the map. This value is in meters.

Crown Radius Tree Map

This map displays a circle for each tree that corresponds to the size of its crown radius. The circles are true to size with respect to the plot and each other. The color matches the species in the legend.

The **Minimum Crown Radius to Display** setting controls the smallest trees shown on the map. This value is in meters.

Click the "Update Map" button after you have adjusted either display setting.

Clicking and dragging on the tree map zooms in. Once you have zoomed, you can restore the original scale by clicking the button marked "Restore Original View". If you are zoomed, you can scroll around the map in each of the four directions by clicking the arrow buttons surrounding the map.

Grid maps

Maps are available for almost any kind of grid value. The values are shown in grayscale. Maps of boolean values (true/false) will be displayed as black (false) and white (true); any other kind of numerical value allows you to adjust the grayscale for best viewing with the controls to the left of the map.

- **Min brightness** - the darkest color that shows up on the map, as a value between 0 and 255. This defaults to pure black (value of 0).
- **Min value** - the minimum grid value where the grayscale starts. Any grid values below this value will show up the min brightness color. This defaults to the smallest value for the map.
- **Knee brightness** - the color that corresponds to the knee value, as a value between 0 and 255. The knee brightness defaults to gray halfway between black and white.
- **Knee value** - the grid value corresponding to the knee brightness color. This defaults to halfway between the minimum and maximum grid values. If the map does not show a lot of contrast, this may be because the values are not evenly distributed between the minimum and the maximum grid values. If the map is too dark, set the knee value lower; if it's too light, set it higher.
- **Max brightness** - the lightest color that shows up on the map, as a value between 0 and 255. This defaults to pure white (value of 255).
- **Max value** - the maximum grid value where the grayscale ends. Any grid values above this value will show up the max brightness color. This defaults to the largest value for the map.

The color lightness increases linearly with map value from the minimum to the knee, and linearly again from the knee to the maximum.

Once you have adjusted your display values, click the "Update" button. Updating can be slow. If you can't see a difference, try minimizing and then restoring the chart window; this guarantees that it has refreshed.

Tables

There are several different kinds of tables available in SORTIE. The only thing they have in common is their format.

Plot tables

An overview table is available for both summary output files and detailed output files. This table shows basal area and density information for each tree life history stage. In the case of a summary output file, only the data that you saved in the [summary output file setup window](#) are shown. For a detailed output file, data is shown for each tree species and life history stage for which you have saved at least DBH (or diameter at 10 cm for seedlings). If you know you want to look at this table type, you should save a summary output file. The graphing performance will be significantly better.

Stand tables

When you save DBH data (and optionally, height), you can also view stand tables. These show density or basal area data broken out by DBH size classes that you define. When you first choose a stand table, you will be given a window where you set the size classes and some other display controls. When you click "Display", the table is generated. Since the table displays all timesteps at once, the initial data compilation step can be time consuming.

In addition to density (displayed in stems per hectare) or basal area (displayed in square meters per hectare) by size class, the table also displays the mean DBH for trees which contributed to the table (meaning those which fell outside the size classes would not be included), and, if you have saved height, the average of the 10 tallest trees in the plot (not just the 10 tallest trees that have provided data to the table).

You can choose to include or not live trees and snags. You can also display one species at a time.

Only those trees for which data has been saved can be included. If you omit a species or life history stage, it will not show up in the table.

Stock table

When you save DBH and tree volume (from the [Tree volume calculator](#)), you can view a stock table with tree volume broken out by DBH size classes that you define. In addition, the stock table displays the Mean Annual Increment (MAI), which is calculated as $MAI = \text{Volume}(T) / (\text{number of years per timestep} * T)$ for a given timestep T, and the volume per year for each timestep (for those trees that contributed to the table); and if you have saved height data, the average of the 10 tallest trees in the plot (not just the 10 tallest trees who have provided data to the table).

Grid tables

There are specialized tables for the following grids:

- [Harvest Results](#)
- [Mortality Episode Results](#)
- [Carbon Value](#)
- [Merchantable Timber Value](#)
- [Windstorm Results](#)
- [Partitioned Biomass](#)
- [Storm Killed Partitioned Biomass](#)
- [Storm Damage](#)
- [Foliar Chemistry](#)

If you wish to view these tables, set up your detailed output file to save all the data from your chosen grids.

Timestep tree writer

This is not really a table as such. This tool will write out all tree data saved for a given timestep to a tab-delimited text file.

Starting and managing a run

A run is a single model simulation. It starts at time zero and continues until its defined endpoint is reached. A run is defined by its [parameter file](#). This tells the model how long to run, and what to do during the run.

Starting a run

You begin by [creating](#) or opening a parameter file using the "File->Open file" menu option. Then you choose "Model->Run" from the menu, or click the "Run" button. A file must be complete and all data in it valid if the run is to succeed, so the file will be validated before the run occurs. You will get an error message if there is something wrong with the parameter file. If you have made changes to the parameter file, you'll be prompted to save the file. If you choose not to save the file, a temporary file will be written so the run can proceed.

Checking the progress of a run

At the bottom of the SORTIE window, there is a message bar that will keep you updated on the number of timesteps completed. If you would like to know what is happening in the run, you can [open output files while the run is still in progress](#).

Interrupting and restarting a run

You can pause or stop a run that is in progress. Either use the buttons or the menu options in the "Run" menu. When either option is chosen, SORTIE will finish the current timestep before stopping or pausing. This ensures that output files will be complete and valid. Closing the SORTIE window will force a quit, but the output may be unrecoverable in that case.

The difference between pausing and stopping is that a paused run can be restarted using the run command, but a stopped run cannot.

Batch runs

SORTIE-ND can do simulations one at a time, or in groups. A group of simulations is a batch run. A batch run consists of simulations performed on one or more parameter files, with each parameter file running one or more times.

Setting up a batch run

A batch run is defined using a batch file. You work with batch files using the [Batch file setup](#) window. A batch file is an XML file which lists a set of parameter files to run, and the number of times to run each file.

Before you begin a batch run, prepare all of your parameter files. Save them all to an appropriate place. If you are saving output in your parameter files, make sure that the directory(ies) that the output will be written to already exist. It doesn't matter where you put your parameter files, or where you write your output; but if you move parameter files around, SORTIE-ND may not be able to find them when it runs your batch.

Once all of your parameter files are ready, create and save your batch file.

Batch runs and output

Parameter files being run in batches can write output files. If you are running a parameter file more than once, SORTIE-ND will automatically rename each run's output files so that they will be numbered sequentially. For instance, if your parameter file saves a file called `my_out.out`, and you use a batch to run the file three times, you will get the following output files:

`my_out_1.out`, `my_out_2.out`, and `my_out_3.out`.

Running a batch

Once you have created a batch file, you can run it by choosing "Model->Run Batch...". This allows you to select the batch file you have created. Once you have selected it, SORTIE-ND will begin running your batch. You do not have to have a parameter file of any kind loaded into SORTIE-ND to begin a batch run. If you have a parameter file currently loaded, it will have no effect on the batch run.

You cannot view output during a batch run, like you can with a single run. This is because of the difficulty SORTIE-ND would have in managing the many possible output files. You also cannot pause a batch run, only stop it. However, if you do stop a batch run, any output that was created before you stopped it will still be present and available.

If a simulation within a batch fails for some reason, SORTIE-ND will attempt to skip that simulation and complete the others specified in the file.

The parameter file

What is a parameter file?

A parameter file is a document containing all the data that the model needs to perform a simulation. It is in the XML data format and is written in plain text. Parameter files have a .xml extension.

Contents of a parameter file

At the least, the parameter file must specify the [length of the run](#), describe the [plot](#), define the tree species and their attributes, list the [behaviors](#) in the order in which they will run, and provide whatever [parameters](#) the behaviors need.

In addition, parameter files can define initial conditions for [trees](#) and [grids](#) using parameters or [maps from detailed output files](#).

Editing a parameter file

The SORTIE-ND model interface gives you all the tools you need to create and modify your parameter files. Since they are in plain text, you can look at them in other programs, but modifying them directly is not recommended.

For detailed instructions on creating a new parameter file from scratch, see the [Creating a parameter file](#) topic. To edit existing parameter files, you can use the different choices in the [Edit menu](#).

Validating a parameter file

In order to run, a parameter file must be complete and all data in it valid. As you edit a parameter file, the part that you are editing will be validated as part of the edit process. The complete file is validated every time you save it. You can save a file that does not pass validation, but you cannot run it.

Making a human-readable copy of the parameter file

The parameter file is in the XML data format and is not easily readable by humans. SORTIE will create tab-delimited text versions of data that you can open in any text editor or spreadsheet program. To save your parameter values, use the command File->Save parameter file as text. To save grid map values, use the [Edit->Grid layer setup](#) window. Files you save in this way are for your reference only. They cannot be used as input.

Detailed output files

The model saves its detailed output in a detailed output file. A simulation's detailed output file is in fact a collection of individual files packaged together. Within the detailed output package are two types of files: a copy of the parameter file originally used to perform the run, and individual timestep files, which hold the saved data for each timestep. All the files are written in plain text in the XML data format.

Contents of a detailed output file

Detailed output timestep files are collections of map files that you set up using the [Edit->Output setup window](#). They are identified by having "_x" added to the filename, where "x" is the timestep number. The parameter file copy is given the detailed output package's filename. Each file produced is then compressed using the GZIP program, and all the files for a single run are put into an archive file using the TAR program. The detailed output output for a single run is one file with a ".gz.tar" extension.

For example: if the parameter file "testpar.xml" was used to run 5 timesteps, with a detailed output file to be saved named "my detailed output", at the end of the run there would be a file named "my detailed output.gz.tar". This TAR archive would contain the following files:

- "my detailed output.gz" - a copy of the "testpar.xml" parameter file
- "my detailed output_0.gz" - the data saved after setup occurred, before the model started running. These are the initial conditions.
- "my detailed output_1.gz" - the data saved after the first timestep had run
- "my detailed output_2.gz" - the data saved after the second timestep had run
- "my detailed output_3.gz" - the data saved after the third timestep had run
- "my detailed output_4.gz" - the data saved after the fourth timestep had run
- "my detailed output_5.gz" - the data saved after the fifth timestep had run

The ".gz" extension indicates that these files are compressed. If uncompressed, the ".gz" extension would be replaced with ".xml".

Detailed output files are very flexible and can contain any subset of the model's underlying tree and grid data. You pick each individual piece of data that you wish to save, and the frequency with which you wish to save it. The data can be saved at any interval from every timestep to only at the first and last timesteps, and each piece of data has its own save frequency. You can use this to cut down on detailed output file size. Data you are less interested in can be saved less frequently.

You can also save data separately for just a portion of the plot by defining [subplots](#).

Viewing the data in a detailed output file

The data visualization capabilities of the model interface allow you to see your data graphically. If you want the data raw to do your own analysis, you can save the contents of individual maps within the detailed output files as tab-delimited text. The easiest way to write tree data is to use the [Timestep tree writer tool](#) listed in the "Tables" options after a detailed output file has been loaded for data visualization. Grid map data can be written from any grid map display.

Detailed output files as input to other runs

The maps in a detailed output timestep file can be used as initial conditions on a subsequent run, provided that they are compatible with the parameter file being used. See the [Using output as input to a new run](#) topic.

Copying and renaming detailed output files

Because of their structure, detailed output files cannot be renamed like ordinary files. If you change the file name, the file will be broken. Use the [Copy detailed output file](#) tool in the [Tools menu](#) to safely make a copy of the file with a new name. (You can safely copy and move detailed output files to different file locations as long as the name stays the same.)

Summary output files

The summary output file contains basic plotwide summary data for each timestep in the run. You choose what data you want SORTIE to save using ["Edit->Output options"](#).

You can use the summary output file to save data for both live and dead trees. The dead tree data for a given timestep is only for trees that died in that timestep. The dead trees are coded by [mortality reason](#). You choose which mortality reasons you want to see data for. Not all mortality reasons are available for every run. Check the documentation for your chosen [disturbance behaviors](#) and [mortality behaviors](#) for more information on which codes will apply to your run.

Your choices for what to save are:

- Adult tree relative basal area (Adult Rel BA)
- Adult tree absolute basal area (Adult Abs BA)
- Adult tree relative density (Adult Rel Den)
- Adult tree absolute density (Adult Abs Den)
- Sapling relative basal area (Sapl Rel BA)
- Sapling absolute basal area (Sapl Abs BA)
- Sapling relative density (Sapl Rel Den)
- Sapling absolute density (Sapl Abs Den)

- Seedling absolute density (Sdl Abs Den)
- Snag tree relative basal area (Snag Rel BA)
- Snag tree absolute basal area (Snag Abs BA)
- Snag tree relative density (Snag Rel Den)
- Snag tree absolute density (Snag Abs Den)

Basal area is in square meters per hectare, and density is in numbers per hectare. Relative values are in proportions. Each data type is calculated separately for each species, and absolute data types also include a total across species. For a definition of the different tree types, see the [Tree life history stages](#) topic.

You can define [subplots](#) within the plot to track separately.

Output files are saved as tab-delimited text files with a ".out" extension. You can open them in almost any spreadsheet or word processing program. There is a column for each species for each data type. Each timestep is one row. If you have defined subplots, there is a row for each subplot for each timestep.

You can view graphs of summary output files using SORTIE's data visualization functions. See the [Loading and displaying data from an output file](#) topic.

Tab-delimited tree maps

You can use tab-delimited tree maps to create your own tree map data. You can save files of this type in many programs, particularly spreadsheet programs like Microsoft Excel. You can use these maps to create [tree initial conditions](#).

Files must be in plain text with a ".txt" extension.

Tree map format

Here is an example of a tree map:

X	Y	Species	Type	Diam	Height
10.34	62.1	Maple	Seedling	0.24	0
9.33838	88.9771	Beech	Sapling	4.567	0
5.73746	5.16968	Hemlock	Adult	15.887	15.3
127.039	146.606	Beech	Snag	35.41	28.7
122.571	14.06372	Oak	Sapling	2.91	0
9.31396	50.0366	Maple	Adult	23.554	14.82

The first six columns are required, and must be in that order.

The first row is column headers.

Each subsequent row is the data for one tree. Trees can appear in any order. There is no limit to the number of trees.

The first two columns are the X and Y coordinates of the tree. In the SORTIE-ND coordinate system, the origin is at the southwest corner of the plot. X increases to the east; Y to the north. There are no negative numbers. If there are trees outside the plot boundaries, you are warned of this; if you elect to continue loading the file, those trees are discarded.

The third column is species. The species names must match those that appear in the parameter file, including case, EXCEPT that spaces in the species name must be replaced with underscores. For instance, if the species name is Red Maple, in the file the species is Red_Maple. SORTIE-ND will reject a tree map with an unrecognized species name. To find out what the species names are for your parameter file, use the [Edit species list window](#) to view the list.

The fourth column is tree life history stage. Possible values are "Seedling", "Sapling", "Adult", and "Snag". (Case is unimportant.)

The fifth column is tree diameter in cm. If the life history stage is "Seedling", this value is the diameter at 10 cm height. For all other types, this is DBH. If the diameter value and the life history stage do not match, diameter takes precedence. For instance: if the parameter file specifies that the minimum adult DBH is 10 cm, and the tree map contains a tree designated as a "sapling" with a diameter of 15 cm, then SORTIE-ND will create an adult with a DBH of 15.

The sixth column is tree height in meters. If this value is set to 0, SORTIE-ND will use the allometry equations to calculate tree height. If this value is non-zero, then this height is assigned to the tree, even if the allometric equations would produce a different result. This feature is useful if you intend to use [growth behaviors](#) that separately increment diameter and height for your trees. When in doubt, use 0.

Adding extra data to the tree map

You can add additional data to the tree map beyond the first six columns. You can add extra columns for any item in the [Tree data member list](#). Put the short code name in the column header. There must be a value for each tree for each column, but if that data piece does not apply to that tree, it will be ignored. Even data that will be ignored must be of the proper type - don't use a value such as "NA" in a column of integers, for example.

Using tree maps

Tree maps can be loaded into SORTIE-ND only if there is a parameter file loaded as well. The data in the tree map is expected to match the parameter file: all species in the tree map must be present in the parameter file, and height values must not exceed the maximum height limits.

The the

Once you have prepared a tree map file according to the format below, and once you have loaded a compatible parameter file, use the "File->Open file" command to load your tab-delimited tree map file. If you save your parameter file after this point, the tree map will be included in it. To work with the tree map trees further, including removing them, use the [Manage tree maps window](#).

SORTIE-ND will not alter your tab-delimited tree map file.

Converting pre-6.0 SORTIE tree map files

If you have a tree map file from before SORTIE 6.0, you can simply copy and paste the columns with the following exception: The old version of SORTIE has reversed coordinate axes. So paste the old "X" values into the new "Y" column, and vice versa.

Last updated:

File menu

New parameter file. Use this option to be led through the first steps of creating a new parameter file from scratch. You start with the [Edit species list window](#), then move to the [Edit simulation flow window](#). Once you have completed these steps, you can save your new file and then enter parameters for it. For more on creating a new parameter file, see [Creating a parameter file](#).

New batch file. Use this option to create a new batch file. You can read more about batch runs [here](#). This option opens the [batch file setup](#) window.

Open file. Use this option to open parameter, batch, and data files in SORTIE-ND. You can open [parameter files](#) this way, and then use this option again to add data from [detailed output files](#) to the run.

Save parameter file. Use this option to save a parameter file. You have to specify the filename each time. The filename of the file currently loaded is visible in the bottom left corner of the main SORTIE window. You can save a parameter file, even if it is not complete or valid. If this is the case, you will get a warning message that tells you of the file's problem and asks you if you want to continue with the save. Clicking yes will save the file.

Save parameter file as text. Use this option to save the run values as a tab-delimited text file. You can't use this file as a parameter file but it provides a way to review and archive your settings.

Set working directory. Choosing this option allows you to give SORTIE a directory you wish to work in. Then all windows for working with files will automatically open to this directory.

Open run output. Use this option to use the data visualization functions to graphically view the output of a run. You can open either [short output files](#) or [detailed output files](#) this way.

Exit. Quit SORTIE.

Batch file setup window

This window is reached from the menu option "File->New batch file" in the main SORTIE-ND window, or by opening a batch file using "File->Open file". It allows you to set up a new batch file. For more information on batch runs, see the [batch runs](#) topic.

Batch files define a set of runs that you want SORTIE-ND to do at one time. The batch file can list multiple different parameter files, and can run each file more than once.

Working with a batch file does not in any way affect any parameter files you may also be working on. You can work with batch files without having a parameter file loaded. However, all the parameter files you want to include in your batch file should be complete before you begin.

Batch file name. This is the path and file name of the batch file you are working with.

Add a new parameter file. This section adds a new parameter file to the batch.

Parameter file name. The path and file name to the parameter file(s) to add. You should make this a fully qualified name (i.e. "C:\my files\parameter file 1.xml" rather than "parameter file 1.xml"). (Using the "Browse" button causes this to happen automatically, and you can select multiple files this way.) This ensures that the model will be able to find the file when it comes time to run the batch. You are allowed to enter parameter file names and paths which do not exist on the current computer, to allow you to prepare batch files to run on other machines. Double check that all of your files are in the correct place before you begin to run your batch.

Number of times to run this file. The number of times to run this parameter file during the batch.

Add new parameter file. This button adds a parameter file and a number of times to run to the batch list.

Current parameter files in this batch: This displays the current parameter files in the batch list, along with the number of times each should be run.

Remove. Use this button to remove one or more parameter files from the batch list.

Once the batch list is the way you want it, click OK to write the file.

Edit menu

The options in this menu for editing parameter files.

Model settings. Use this option to edit behavior options, including parameter values, for the run. The settings available here depend on the [behaviors](#) for the run. For more details on this option, see the [Model Settings window](#) topic. For details on individual parameters, see the behavior to which they belong.

Tree population - set allometry functions window. Use this option to set the [allometry functions](#) for tree species and life history stage. For more details on this option, see the [Edit allometry functions window](#) topic.

Tree population - edit species list window. Use this option to add, rename, or remove tree species. For more details on this option, see the [Edit species list window](#) topic.

Tree population - edit initial density size classes window. Use this to change the size classes for [tree initial densities](#). For more details on this option, see the [Edit size classes window](#) topic.

Tree population - manage tree maps window. Use this to add and remove tree maps for [tree initial conditions](#). For more details on this option, see the [Manage tree maps window](#) topic.

Grid layer setup. Use this option to edit the attributes of the currently loaded grids. For more details on this option, see the [Grid setup window](#) topic.

Model flow. Use this option to edit the list of [behaviors](#), their order in the run, and the trees to which they are assigned. For more details on this option, see the [Edit simulation window](#) topic.

Output options. Use this option to set up output for a run. By default, no output is saved. This controls both [short output files](#) and [detailed output files](#). For more details on this option, see the [Output setup window](#) topic.

Model settings window

This window is reached using the menu option "Edit->Model Settings" from the main SORTIE window. It allows you to edit the parameter values for your run.

The options you are given depend on what behaviors have been selected for the [model flow](#). Options for the plot and tree populations are always available.

Each behavior has its own setup button. By default, this opens a window for entering parameter values. For those behaviors that need specialized setup, this button will open the appropriate window.

Edit species list window

This window is reached from the menu option "Edit->Tree Population->Edit species list" in the main SORTIE-ND window. It allows you to the species list of the [tree population](#).

The box under the heading "Edit list of species" contains the list of current species. Changes you make are not final until you click "OK". If you edit the species list beyond just renaming species, you will lose any currently loaded tree map and grid map data.

Add To add a new species, type its name in the box labeled "New species", and click the button marked "Add".

Rename To change the name of a species, first select it in the species list. Then type the new name in the box marked "New species:", and click "Rename".

Copy... This lets you make one species a copy of another species. It opens a window where you can select a species and one or more species to make a copy of that species. If you want to make a new species that is a copy of an existing species, first create the new species using the "Add" button, then use the copy button to select the species it should be a copy of.

Any existing behavior settings and parameters for a species that becomes a copy of another species are removed, and replaced by settings and parameters identical to the species being copied. If the species that becomes a copy was the only species assigned to a behavior, that behavior is removed from the run.

Up and Down This lets you change the order of species in the list. Select one or more species and click the buttons to move them.

Remove To remove a species, select a species in the list and click the button marked "Remove".

Edit size classes window

This window is reached from the menu option "Edit->Tree Population->Edit initial density size classes" in the main SORTIE-ND window. It allows you to edit the size classes for the [tree population](#). Size classes help you define [tree initial conditions](#) for your run. When you have size classes set up, you can specify an initial density of trees in each size class in the [Model settings window](#). You can have as many size classes as you want. The upper DBH bound of a size class is its number. The lower bound of the size class is the size class below it, or zero if there is no lower class. This means you may need one extra class in order to define a lower bound for your smallest class if you want its lower bound to be greater than zero.

The list of currently defined size classes is in the list at the left of the window. To add a new size class, type in its upper DBH bound in the box and click "Add". To remove an existing class, select it in the list to the left and click "Remove". To define a size class for seedlings, add a size class with an upper limit of "0".

Manage tree maps

This window is reached from the menu option "Edit->Tree Population->Manage tree maps" in the main SORTIE-ND window. This allows you to manage tree maps as an addition to the tree population.

Add tree map. This lets you load a [tab-delimited tree map](#) file and add it to your current parameter file. These trees will add to any tree maps already loaded. You will be given the option of adding the file to the parameter file, or keeping it separate. The first method is almost always preferred. However, sometimes a very large map file will make the parameter file too big for SORTIE to read. In this case, the text file can be kept as a separate file and only its filename can be added. SORTIE-ND will then read the file directly when the run begins.

Remove tree map trees. If there is a tree map loaded, then the button marked "Remove tree map trees" is enabled. If you want to remove all currently loaded tree map trees, click this button. This action cannot be undone.

Write tree map to text file. If there is a tree map loaded, then the button marked "Write tree map to text file" is enabled. Click this button to write the contents of the currently loaded tree map to a tab-delimited text file, which you can open in a spreadsheet or text editor. Files created this way are only for your own use. SORTIE-ND cannot accept them as run input. However, you can transform them yourself into a tab-delimited map file that SORTIE-ND can accept; see the [Tab-delimited tree map](#) topic.

Grid Setup Window

This window is reached using the main SORTIE window menu option "Edit->Grid layer setup". It allows you to work with [grids](#) for your run. [More on setting up grid initial conditions.](#)

Choosing a grid to work with

The first step is to choose the grid you would like to work with. The active grids appear in the drop-down list that shows the option "---Please select grid---" when the window is first displayed. The grids that appear in that list depends on the list of [behaviors](#) for this run (editable using the [Edit simulation flow](#) window). If none of the behaviors with which a grid is associated are enabled, then the grid won't show up in the list. When you are finished with a grid, you can choose another from this list.

Cell length in X (E-W) direction, in m

Displays and sets the size of the grid in the X (E-W) direction, in meters. Some grids do not allow you to change their cell size (consult the documentation for [individual grids](#) for any limitations or recommendations). You can enter any number that you wish, between 0 and the length of the [plot](#) in the X direction. The number does not have to be an integer. Once you have entered your desired value, you must click "Update this grid" to save your changes.

Cell length in Y (N-S) direction, in m

Displays and sets the size of the grid in the Y (N-S) direction, in meters. Some grids do not allow you to change their cell size (consult the documentation for [individual grids](#) for any limitations or recommendations). You can enter any number that you wish, between 0 and the length of the [plot](#) in the Y direction. The number does not have to be an integer. Once you have entered your desired value, you must click "Update this grid" to save your changes.

Apply cell size changes

Use this button to update the current grid with any changes you have made to the cell size. If you do not click this button, your changes will be lost. You must click this button for each grid you wish to update.

View/edit/save grid values...

Use this button to open the [Grid Value Edit](#) window. This window allows you to view and change values for grid maps and write them out to tab-delimited text files.

Clear grid map

If there is a map loaded for this grid, then the button marked "Clear grid map" is enabled. If you want to remove a currently loaded map, click this button. This erases all map values for the current grid. This action cannot be undone, even if you click "Cancel" for the window.

Grid Value Edit Window

This window allows you to directly work with the data in the grid maps for a single [grid](#). You can look at the values for maps loaded from a parameter or detailed output file, make changes to existing maps, or enter new values to use as initial conditions. You reach this window from the [Grid Setup](#) window.

When you open this window, you will notice that it is composed of one or more tables. There is one table for each grid data member (see the [individual grid documentation](#) for what each grid data member represents). If a table is completely blank, that means that there is currently no map loaded for this grid, or at least for that data member. If there is a map loaded, you will see values in the tables. (For more on entering the maps from a detailed output file, see the [Using output as input to a new run](#) topic.)

Editing map values

To edit a value, double-click its cell. You can copy and paste back and forth from Excel, and within the window itself. You can use the menu commands on the parameter window "Edit->Copy" and "Edit->Paste", or the keyboard shortcuts Ctrl-C for copy and Ctrl-V for paste.

Saving grid map as text

The window can be saved as tab-delimited text for your own review in a spreadsheet or text editor program. Choose "File->Save window as file". Each value for each data member in the map is saved separately, and there will be a heading for it, even if there were no values in the map. For an explanation of the values that were saved, consult the documentation for [individual grids](#).

Saving the window view to a file is not the same as saving the values in SORTIE. You still need to click "OK" to save any changes you've made. The tab-delimited text file is just for your review. It cannot be used as input to SORTIE directly, although you could copy and paste values from it.

Model flow window

This window is reached using the main SORTIE window menu option "Edit->Model flow". It allows you to choose the [behaviors](#) for a run, put them in a particular order, and assign them to trees. The current behaviors and their tree assignments are displayed in a hierarchical structure. You can view the data in three structures ordered by different hierarchies so that you can quickly find the information you want. Clicking on different parts of the structure bring up windows to edit those options.

You will find that there are multiple ways to find, view, and edit the same information. Once you have experience with this window, you may use different methods to edit behaviors depending on the nature of the edit you need to do.

This window has the following options:
View by behavior

View by data - species first
View by data - type first

View by behavior

This button changes the view to a hierarchical structure that shows behaviors at the top level. Each behavior for the current run is listed in order. Expanding the tree under a behavior shows the grids and trees to which it applies. Clicking on the name of any behavior brings up the [Current run behaviors window](#), where you can edit the list of behaviors, their order, and to what trees they apply. Clicking on any grid name brings up the [Grid setup window](#), where you can set options for grids. Expanding trees shows you the tree types to which the behavior is assigned, first by tree type and then by species. Clicking on a species name brings up the [tree behavior window](#), which you can use to set up the behaviors applied to the chosen tree type and species combination.

View by data - species first

This button changes the view to a hierarchical structure that shows grids and trees at the top level. In the tree structure portions, species is shown at a higher level and tree type (life history stage) is shown beneath. Expanding a tree or grid branching shows what behaviors, in order, apply. Clicking on any grid name brings up the [Grid setup window](#), where you can set options for grids. Clicking on a tree type below a species name brings up the [tree behavior window](#), which you can use to set up the behaviors applied to the chosen tree type and species combination. Clicking on the name of any behavior brings up the [Current run behaviors window](#), where you can edit the list of behaviors, their order, and to what trees they apply.

View by data - type first

This button changes the view to a hierarchical structure that shows grids and trees at the top level. In the tree structure portions, tree type (life history stage) is shown at a higher level and species is shown beneath. Expanding a tree or grid branching shows what behaviors, in order, apply. Clicking on any grid name brings up the [Grid setup window](#), where you can set options for grids. Clicking on a tree species name below a tree type brings up the [tree behavior window](#), which you can use to set up the behaviors applied to the chosen tree type and species combination. Clicking on the name of any behavior brings up the [Current run behaviors window](#), where you can edit the list of behaviors, their order, and to what trees they apply.

Current run behaviors window

This window is reached through the [Edit simulation flow](#) window. It edits the set of [behaviors](#) for a run, the order they are in, and the trees to which they apply (if it is appropriate for them to apply to trees). The current list of behaviors, in order, appears in the box labeled "Current behavior order".

Adding new behaviors

The left-hand side of the window is devoted to choosing new behaviors for this run. Begin by choosing an overall behavior grouping using the drop-down list that shows "---Please select a behavior group" when the window is first opened. When you have chosen a group, a list of individual behaviors for that grouping shows in the box underneath. Select the one you wish to add, then click the button marked ">>" to add it to the list. It automatically places itself with other behaviors in its group, or in the correct place between other groups if it is the first of its group. (Behavior groups are separated by dashed lines.) At this time, you must add new behaviors one at a time. It is possible to select multiple individual behaviors, but the ">>" button will apply to only the first one selected. If you have chosen a behavior that is already on the list, nothing happens.

Certain special behaviors cannot be added this way. If you try to add them, you will see a message saying "---Use this behavior's own dialog". This means that it has options that can be set up through a window accessible from the main SORTIE menu. You can, however, remove these special behaviors from the run from this dialog.

Changing behavior order - the "Up" and "Down" buttons

You can change the behavior order within the overall behavior groupings. Behavior groups are separated by dashed lines. To change a behavior's position in the list, select it in the list labeled "Current behavior order", then click "Up" or "Down" to move it. You cannot move it past a dashed line. This ensures behavior orders that make sense.

Removing behaviors - the "Remove" button

To remove a behavior from the run, select it in the list labeled "Current behavior order" and click the button marked "Remove".

Changing behavior assignments - the "Modify assigned data" button

This button changes the trees to which a behavior applies, if the behavior is of a kind applied to trees (and most are). Select a behavior in the list labeled "Current behavior order" and then click the "Modify assigned data" button. This brings up the [Tree assignments window](#), to allow you to modify the assignments.

Tree behavior edit window

This window is reached through the [Edit simulation flow](#) window. It edits the list of [behaviors](#) for a given tree combination of species and type (life history stage). The combination being edited is displayed in the top of the window. The current list of behaviors, in order, appears in the box labeled "Assigned behaviors".

Adding new behaviors

The left-hand side of the window is devoted to choosing new behaviors to apply to this tree type/species combination. Begin by choosing an overall behavior grouping using the drop-down list that shows "---Please select a behavior group" when the window is first opened. When you have chosen a group, a list of individual behaviors for that grouping shows in the box underneath. Select the one you wish to add, then click the button marked ">>" to add it to the list. It automatically inserts itself in the correct place in the behavior list, based on the order of the master behavior list. (Use the [Current run behaviors](#) window to edit the order of the behaviors in a run.) At this time, you must add new behaviors one at a time. It is possible to select multiple individual behaviors, but the ">>" button will apply to only the first one selected. If you have chosen a behavior that is already on the list, nothing happens.

Not all behaviors can be assigned to all species/type combinations. If you have made an invalid choice, you will see an error message when you click an "Apply to..." button, and you will be given the opportunity to change it. See the documentation for individual behaviors for information on how they can be applied.

Certain special behaviors cannot be added using this window. If you try to add them, you will see a message saying "---Use this behavior's own dialog". This means that it has options that can be set up through a window accessible from the main SORTIE menu.

Removing behaviors

To remove a behavior from the list assigned to this species/type combination, select it in the list labeled "Assigned behaviors" and click the button marked "Remove". This does not affect the behavior's assignment to any other trees.

Apply to (species) (type)

There is a button marked "Apply to (species) (type)" to apply your changes to the tree type/species combination (for instance, "Apply to Species 1 Saplings"). Behaviors you have added to the list are applied to that species/type combination. Behaviors you have removed have that species/type combination deleted from their list. If a tree-dependent behavior no longer applies to anything as a result of your choice, it is removed from the run. If you have made an invalid behavior assignment, you will receive an error message and be given the opportunity to correct your choices.

Apply to all (type)

There is a button marked "Apply to (type)" to apply your changes to all species of the specified tree type. All existing behavior applications for any species of the specified type are deleted and replaced with the behavior choices listed. If a tree-dependent behavior no longer applies to anything as a result of your choice, it is removed from the run. If you have made an invalid

behavior assignment, you will receive an error message and be given the opportunity to correct your choices.

Tree assignments window

This window is reached from the [Current run behaviors window](#) or from the [Edit harvest interface window](#). It modifies the [trees](#) to which a [behavior](#) is applied.

The current list of tree species/type combinations is shown on the right-hand side of the window. The left-hand side allows you to choose a new species/type combination. Choose the appropriate combination where it says "--Please choose a species" and "--Please choose a tree type". Then click the button marked ">>" to add your choice to the list.

You can remove a choice by selecting it in the list on the right, then clicking the "Remove" button.

Not all behaviors can be assigned to all species/type combinations. If you have made an invalid choice, you will see an error message when you click the "OK" button, and you will be given the opportunity to change it. See the documentation for individual behaviors for information on how they can be applied.

Output setup window

This window is reached using the "Edit->Output options" choice on the menu of the main SORTIE window. It is a gateway to managing the output options for a run. What you save for output depends on what data you want to be available to you after the run. For a guide on how to set up output, see the [Output strategies](#) topic.

Save Summary Output File (.out)

This button opens the [Summary output file setup window](#) for saving [summary output files](#). As a quick check, the text just below this button will tell you if there are currently summary output file save settings.

Save Detailed Output File

This button opens the [Setup detailed output file window](#) for saving [detailed output files](#). As a quick check, the text just below this button will tell you if there are currently detailed output file save settings.

Setup detailed output file window

This window is reached from the [Output setup window](#). It is the first step in setting up a [detailed output file](#). For a guide on how to set up output, see the [Output strategies](#) topic.

Output file name. Enter your output file name here. You can use the "Browse" button to help you enter a path. If you don't use a path your file may be hard to find. Detailed output files end up with a ".gz.tar" extension. It is very important that your output file name not have the same name as your parameter file.

Save everything. This saves all possible data. The resulting detailed output file will probably be quite large. This option is handy when you are still tweaking your parameter file. You can save everything, run for a few timesteps, and review the data. This option is also a good one when you wish to have the complete state of the model at every timestep, perhaps to use as input to new runs.

Clear everything. Erases all detailed output settings.

Live Trees. Sets options for saving living trees by opening the [Setup tree save options window](#). The text just below this button will tell you if there are currently any tree save settings. You are not required to save tree data.

Grid data layers. Sets options for saving [grids](#) by opening the [Setup grid save options window](#). The text just below this button will tell you if there are currently any grid save settings. You are not required to save grid data.

Dead Trees. Sets options for saving each timestep's dead trees by opening the [Setup tree save options window](#). The text just below this button will tell you if there are currently any tree save settings. Click for more on [saving live vs. dead trees](#). You are not required to save tree data.

Set up subplots... Sets up subplots for tree data by opening the [Edit subplots window](#). [Subplots](#) are regions within the plot as a whole that will have data saved separately. You can find more information in the [detailed output file](#) topic. You are not required to create subplots.

Setup tree save options window

Click for more on the different [tree life history stages](#), [tree data members](#), and [saving live vs. dead trees](#). For a guide on how to set up output, see the [Output strategies](#) topic.

This window is reached from the [Setup detailed output file window](#). It allows you to choose options for tree data for a [detailed output file](#).

There are four tabs at the top of the window, one each for seedlings, saplings, adults, and snags. For each of these tree types, you choose each piece of data that you want to save, and how often

you want to save it. Some of the data always apply and will always be available. Other types of data only exist when certain [behaviors](#) that need them have been chosen for the current run. Each piece of data may not be available for all species. The window will sort out and ignore any invalid combination.

You can work through the process below as many times as you like until you have your settings the way you want them.

Select one or more species. Begin here by choosing the species of the data you want to save. You can Ctrl + click to select multiple species at once.

For each tree save. For the species that you have selected, click on what you want to save for each tree of that species. You can Ctrl + click to select multiple data at once.

Select one or more death reasons. If you are selecting save options for dead trees, this is a list of possible mortality reasons. Only trees that died for selected mortality reasons will be saved. Your run may not support all of the reasons listed. Check the documentation for your chosen [disturbance behaviors](#) and [mortality behaviors](#) for more information on which mortality codes will apply to your run.

Save every X timesteps. Choose how often, in timesteps, you want to save the data. The number 1 saves every timestep. The number 0 saves only the first and last timesteps. Any other number X saves data every X timesteps.

Add. Use the Add button once you have chosen your data and how often you wish to save it.

What's being saved. This is a list of all of the save settings that are currently set up for this tree type. If it is not displayed here, it won't be saved.

Remove. If you would like to erase a setting, select it in the "What's being saved" box and click "Remove".

Set up grid save options

This window is reached from the [Setup detailed output file window](#). It allows you to choose options for [grid](#) data for a [detailed output file](#). Each grid has different data associated with it, so you must choose them separately. You choose each piece of data you want to save, and how often you want to save it. You can work through the process below as many times as you like until you have your settings the way you want them. For a guide on how to set up output, see the [Output strategies](#) topic.

Select a grid. Choose one of the current run's active grids from this drop-down list. The grids that appear in that list depends on the list of [behaviors](#) for this run (editable using the [Edit](#)

[simulation flow](#) window). If none of the behaviors with which a grid is associated are enabled, then the grid won't show up in the list.

Save every X timesteps. Choose how often, in timesteps, you want to save this grid's data. The number 1 saves every timestep. The number 0 saves only the first and last timesteps. Any other number X saves data every X timesteps.

For this grid save. Choose the data to save for this grid. Ctrl + click to select multiple items. For an explanation of what each grid's data is, see the [individual grid documentation](#).

Add. Use the Add button once you have chosen your data and how often you wish to save it.

What's being saved. This is a list of all of the save settings that are currently set up for all grids.

Remove. If you would like to erase a setting, select it in the "What's being saved" box and click "Remove".

Summary output file setup window

This window is reached from the [Output setup window](#). It allows you to set options for a [summary output file](#).

Output File Name. Enter your output file name here, or choose the "Browse" button to navigate to a path. If you do not enter a path, the file may be hard to find after the run. The extension that will be added, if you haven't added it already, is ".out".

Set up subplots.... Opens the [Edit Subplots](#) window.

The other options allow you to choose saving options for different types (life history stages) of both living and dead trees. Click here for more on [saving live vs. dead trees](#). For the definition of seedling, sapling, adult, and snag, and the difference between living and dead trees, see the [tree life history stages](#) topic. If you choose information for dead trees, you must select which mortality reasons you are interested in. If you do not save information for a particular mortality reason, it will not show up in the output even though there may be trees that died for that reason. All mortality reasons are always listed, although a particular run may not kill trees for that reason. Check the documentation for your chosen [disturbance behaviors](#) and [mortality behaviors](#) for more information on which codes will apply to your run.

Save absolute density. Saves the density of trees of each species of that type, in number per hectare.

Save relative density. Saves the density of trees of each species of that type, as a proportion of total tree density for that type.

Save absolute basal area. Saves the amount of basal area of trees of each species of that type, in square meters per hectare.

Save relative basal area. Saves the amount of basal area of trees of each species of that type, as a proportion of total tree basal area for that type.

Select all. Selects all check marks for both live and dead trees.

Select all. Selects all check marks for both live and dead trees.

Edit Subplots Window

You reach this window by clicking the "Set up subplots..." button on either the [Summary output file setup window](#) or the [Setup detailed output file window](#). This window allows you to define [subplots](#) for output. Subplots are subareas of the plot for which statistics will be tracked separately. They can be as small as a single plot grid cell or as large as the entire plot. They do not have to be continuous in area - you could define several separate patches and put them together in a single subplot. You can define up to five separate subplots. Subplots can overlap.

In the center of the window is a map displaying the subplots. At the right is the legend for any tree map trees which may exist. Along the left panel of the window, you will see a space for the names of five subplots. The colored squares indicate in what color that subplot will show up on the map in the center of the window. At the bottom left are some controls for displaying additional useful information that may help you in defining your subplots.

Defining a subplot

Begin by clicking the radio button for the subplot you want to define (for instance, "Subplot # 1"). Type a name for this subplot. Then choose the squares on the map which define the subplot's area. You can click single squares, or click and drag to select a rectangle. You can unselect a square by clicking it again. The selected cells will show up in the current subplot's color. Everything you click on the map is assumed to apply to the subplot that is currently selected, until you select a new one.

If two subplots overlap, only one of the subplot's colors will show up (the one with the greater number). The hidden subplot still exists; it is okay for subplots to overlap. However, the entire map is still active even for a subplot that is partly covered up. For example, you might select a subplot and then click cells that are covered by a subplot with a higher number. Your clicks are still selecting and de-selecting cells for the subplot with the lower number, but you won't be able to see your selections because the subplot with the higher number is covering them up. To avoid mistakes, you should completely finish each subplot before creating a new one, especially if their areas will overlap. If you need to make changes to a partially hidden subplot, you might want to erase the higher subplot areas and then put them back in when you're done.

If you are setting up both summary and detailed output, and you want to use the same subplots for both, there is a button to copy subplots already defined for the other file type to the current file type.

Subplot grid cell size

You can change the size of the cells used to define subplots with the "Change subplot cell size" button. Harvests, mortality episodes, and planting events will display correctly even if their cell sizes are different; but the location of the edges may be an approximation in this case.

Displaying additional information

Subplots are often used to analyze the effects of specific episodic events such as silvicultural treatments. To help you with this, the subplots window will display episodic events for you on the map. You can display [harvest](#), [planned mortality episodes](#), and [planting](#) events. You scroll through the events in the same order in which they were created in the edit windows. The button colors match the colors in which the events will display on the map. Note that subplots will cover up episodic events that have the same area, and episodic events may cover each other as well. If you are having trouble seeing an episodic event, use the buttons to set all the other episodic events to display the event number 0.

Model menu

Run. Runs the model with the currently loaded parameter file. A file must be complete and all data in it valid if the run is to succeed, so the file will be validated before the run occurs. You will get an error message if there is something wrong with the parameter file. If there are unsaved changes to the current file, a temporary file is written so that the model runs with those changes included. Keep an eye on the status bar at the bottom of the SORTIE screen. It will display the status messages from the running model.

Run Batch... Allows you to select a batch file and then run the batch. You can read more about batch runs [here](#). You create batch setup files using the [batch file setup](#) window. You can run batch files without having a parameter file loaded.

Pause. If there is a run in progress, you can pause it with this option. You can resume the run by choosing "Run" again. This does not apply to batch runs. They cannot be paused, only stopped.

Stop run. If there is a run in progress, this will stop it.

Tools menu

Copy Detailed Output File. Opens the [Copy detailed output file window](#) which can create a copy of a detailed output file with a new name. Detailed output files cannot be renamed like other files. This tool will safely make a copy.

Batch Extract Detailed Output Files. Opens the [Batch Extract Detailed Output Files](#) window, which will allow you to extract from many output files at once.

Help menu

Contents. Accesses the SORTIE help.

Math and functional forms

Randomness in SORTIE-ND

SORTIE uses the Mersenne Twister algorithm to generate random numbers. You can supply a seed to the random number generator in the [Plot parameters](#). Supplying a seed with a value other than 0 causes the random number generator to produce the same sequence of values each time, which would cause two runs of the same parameter file to come out identically. Setting the seed value to zero causes SORTIE to choose its own random seed based on the current machine time.

Probability distribution functions

An important part of SORTIE's functionality is simulating stochasticity in natural processes. In order to do this, many behaviors use a random draw on a probability distribution function to make decisions.

The normal distribution is:



where σ is the function standard deviation. Mean is zero.

The lognormal distribution is:



where λ is the function mean and σ is the standard deviation.

The Poisson distribution is:



where λ is the function mean.

The negative binomial distribution is:



where u is the function mean and k is the clumping parameter. This is Equation 3.103 from [Hilborn and Mangel](#).

The gamma distribution is:



where a is the shape parameter and s is the scale parameter. The function mean is $a*s$.

Further reading

A reference list, along with many reprints, is available at www.sortie-nd.org.

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