SORTIE-ND User Manual

Version 6.06

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SORTIE-ND User Manual

What's New

Version 6.06 released March 31, 2006

Note: If you have a parameter file from an earlier version, and you are using behaviors that have been updated in version 6.05, load your file and save it. SORTIE-ND will automatically make any needed adjustments to your parameter file.

New in version 6.06:

- New allometry equation for saplings - the [power diameter-height relationship](#)
- Updated allometry equation - the [DBH - diameter at 10 cm relationship](#) now has an intercept term
- New seed survival behavior - [Storm Light Dependent Seed Survival](#), which works with the light levels produced by the [Storm Light](#) behavior
- New mortality behavior - [Stochastic Bi-Level Mortality](#), which uses two different mortality rates in high and low light
- New disturbance behavior - [Windstorm](#), which follows a given storm regime to produce storms and kill trees as a result

- New growth behavior - Basal Area NCI Growth, which calculates tree growth as a function of neighborhood basal area
- New light behavior - Basal Area Light, which calculates light levels as a function of neighborhood basal area of angiosperms and conifers
- New disturbance behavior - Storm Killer - that kills trees damaged in storms. This behavior takes over and expands a function previously performed by the Storm Damage Applier behavior
- New analysis behavior - Tree Age, which tracks tree ages
- New mortality behavior - Height-GLI Weibull Mortality, which calculates tree mortality as a function of tree height and light levels
- New growth behavior - Puerto Rico Storm Bi-Level Growth, which uses two functions to calculate growth before and after storms
- New analysis behavior - Merchantable Timber Value, which calculates the value of merchantable timber in a plot
- New analysis behavior - Carbon Value, which calculates the amount of carbon in a plot and its value
- Stand and Stock output tables now display species-specific values as well as plot total values
- The Storm Light behavior has an updated equation for light calculation
- The main window is now equipped with scroll bars, to allow you to use more space when viewing charts and graphs
- The Tree Setup window is now capable of changing the name of a species
- The Density Dependent Seed Survival behavior's survival area has been standardized to per square meter
- The Relative Michaelis-Menton growth behaviors now have an additional exponent on diameter
- The Substrate behavior uses a new equation for decayed log decay
- Developers: The C++ model code has been ported to the GCC compiler set and the Eclipse development environment

Version 6.05 released August 3, 2005

Note: If you have a parameter file from an earlier version, and you are using behaviors that have been updated in version 6.04, load your file and save it. SORTIE-ND will automatically make any needed adjustments to your parameter file.
New in version 6.05:

- The Substrate behavior has been rewritten to combine all current substrate models into one behavior
- New establishment behavior - Establishment with Microtopography - that allows seedlings to have a rooting height above the ground
- Two new allometry equations for crown shape - the Chapman-Richards function
- The stock and stand tables for detailed output now have a mean DBH column
- The equation for mean annual increment in the stock table has changed
- Bug fix - seedlings that use either the GLI light or Sail light behaviors automatically use a top-of-crown fisheye photo point

- Changes have been made to the [Parameters window](#) to make parameter editing easier
- Changes have been made to [output table](#) formatting to make them easier to read

Version 6.04 released May 16, 2005

Note: If you have a parameter file from an earlier version, and you are using behaviors that have been updated in version 6.04, load your file and save it. SORTIE-ND will automatically make any needed adjustments to your parameter file.
New in version 6.04:

- You can now choose the appropriate [allometry](#) equation for each species for each life history stage
- You can now set the height boundary between seedlings and saplings for [trees](#)
- The [establishment behaviors](#) have been restructured, allowing you to mix and match seed survival effects
- The [Storm damage applier](#) behavior can create tip-ups from storm-killed trees
- New harvest behavior - [Selection harvest](#) - that allows SORTIE-ND to decide when to perform harvests based on target basal area levels
- New behavior - [GLI Points File Creator](#) - which calculates GLI at certain specific points
- New light behavior - [Storm Light behavior](#) - that uses storm damage as a proxy for finding light levels
- New growth behavior - [Puerto Rico semi-stochastic growth](#)
- New growth behavior - [Linear bi-level growth](#) - that can grow trees with two sets of parameters based on light level
- New growth behavior - [Lognormal bi-level growth](#) - that can grow trees with two sets of parameters based on light level
- New mortality behavior - [Logistic Bi-Level Mortality](#) - that can use two sets of parameters based on light level
- [NCI growth](#) and [NCI Mortality](#) now each have a flag for whether or not to include snags in NCI calculations
- Refinement of [substrate](#) dynamics for snags, allowing them to tip-up at different rates from live trees

Version 6.03 released April 6, 2005

New in version 6.03:

- New function form for the [NCI Mortality](#) behavior
- New mortality behavior which calculates mortality as a function of neighbor density - the [Density Self-Thinning Mortality](#) behavior
- New format for [tab-delimited tree maps](#), which can be prepared in any spreadsheet program and added to SORTIE-ND
- New [data visualization chart type](#) - histograms for grid values

- New behavior for calculating tree volume - the [Tree bole volume calculator](#) behavior
- Updated [Substrate behavior documentation](#)
- New behavior for calculating tree biomass - the [Dimension analysis](#) behavior
- New feature for running [batches](#)
- NCI behaviors ([NCI Mortality](#) and [NCI growth](#)) now have a parameter for minimum DBH of crowding neighbors
- The [Storm damage applier](#) behavior now can kill trees immediately as a result of storm damage
- Changes to the [File menu](#) options

Version 6.02 released March 10, 2005

New in version 6.02:

- New [tree data members](#) for Light level and Diameter Growth
- New behavior for creating GLI maps - [Gap Light](#) behavior.
- New line graphs in [data visualization](#) for relative volume and absolute volume.
- Seedling initial density can now be controlled by three [height classes](#).
- New growth-based mortality behavior - [Competition Mortality](#).
- New mortality as a function of growth and a second resource - [Growth and Resource-Based Mortality](#).
- New function form for the [NCI growth](#) behaviors.
- New growth functions using a double Michaelis-Menton function of light and a second resource - [Double resource relative growth](#).
- New light behavior which simplifies GLI calculations for extremely competitive gap dynamics - [Gap Light behavior](#).
- New growth behavior for simulating extremely competitive gap dynamics - [Stochastic gap growth](#).
- Snag size classes for the [Weibull snag mortality](#) behavior are now species-specific.

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Getting started with SORTIE

In this document:
[How does SORTIE work?](#)
[How do I start working with SORTIE?](#)

How does SORTIE work?

It is important when starting with SORTIE to understand a little bit about how SORTIE works. SORTIE is a program designed to simulate the life cycles of individual trees and

assess the impacts of various external events on them. SORTIE does this by creating individual virtual trees and allowing certain processes chosen by the user to act on these trees. These processes are called behaviors and usually correspond to biological processes. 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. The behaviors have a certain order in which they act. When all of the behaviors have acted once, that's a single timestep. The process is repeated for the number of timesteps that you set, and that's a single simulation, or run.

Different species have different requirements, of course, and trees undergo different processes at various points within their life cycle. Behaviors can be applied to very specific tree subsets and you can use different versions of a similar behavior to get the effects you wish to achieve.

How do I start working with SORTIE?

First, you may want to familiarize yourself with the various parts of the simulation engine. Read about trees, behaviors, and grids (a kind of data structure). Read a little about how a run progresses. Then, you should read about parameter files, which is the way that you input your settings into SORTIE.

Once you've done that, you are ready to start building a parameter file. To create a file from scratch, read the topic creating a parameter file from scratch. Once you have a parameter file, you can read about advanced additions to it in the topic adding to a parameter file.

Once you have a parameter file, you simply load it using the File menu, then choose "Model->Run". That's all there is to it! Wait for the simulation to end, then look at your output files using the model's data visualization capabilities.

Getting started - users of previous versions of SORTIE

If you have used SORTIE before, you're in luck. You can probably start doing runs right away. The early versions of SORTIE-ND were designed to be backwards compatible; your old files should load and run. Newer versions of SORTIE-ND can then use the files created by the earlier versions.

Before you do a run, you may want to familiarize yourself with what's new. First, read about behaviors. They replace submodels. When before you might choose the "BC juvenile growth" submodel, for instance, now you will choose a growth behavior. All submodels from the old model have been translated to behaviors in the new model. They

may have been slightly generalized and given different names, but when you read the documentation on the individual behaviors you should be able to find the ones you want.

Then, read about the new parameter files. Read about your output options with the topics on summary output files and detailed output files.

You can load an old parameter file into SORTIE-ND up to version 6.04. Download and install a version, and load your old parameter file using the File menu. You can then save it in a new format. This file will then be readable by newer versions of SORTIE-ND. If you need help, each version of SORTIE-ND has its own user manual that will guide you through.

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Run setup and progression

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.

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. The model counts off the timesteps until it has finished the specified number, then cleans up its memory and shuts down.

Run parameters

- **Number of timesteps** The number of timesteps for which to run the model.
- **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

In this document:
The SORTIE coordinate system
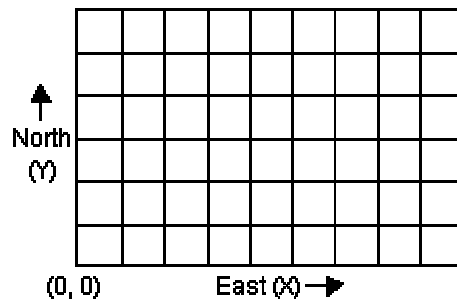The Torus Forest
Plot parameters

The plot in SORTIE is the simulation of the physical space in which the model runs. 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. **IMPORTANT:** The new coordinates are different from the older versions of SORTIE, in which the axes were switched. When the new version converts older files, the coordinate conversions are made automatically.

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 parameters

- **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 degrees and partial degrees (i.e. 39.10).

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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. In this document:

[Setting up the tree population](#)
[Setting up the behavior list](#)
[Setting parameter values](#)
[Other options](#)

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 [Tree setup window](#). At a minimum, you must create a list of tree species. If you want to define the initial conditions of your tree population using densities in size classes, and you know what you want your size classes to be, you can set them up at this point. Otherwise, you can always come back to this window by choosing "Edit->Tree setup".

Setting up the behavior list

After your tree population is defined, 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->Parameters", which will open the Parameters window. You may want to only display and edit one category of parameter at a time, since all values in the parameter window must be valid before you can save your changes.

Other options

Once you have completed the three steps above, you have created a basic parameter file. For more options on adding to a parameter file, see the topic Adding to a parameter file.

Adding to a parameter file

This topic covers the additions you can make to a parameter file. For more on how to create a basic parameter file from scratch, see the topic Creating a parameter file. Otherwise, you can start with an existing parameter file and modify it.

A basic parameter file has the tree population list of species defined, the run behaviors list assembled, and the parameters entered. Once that's complete, here's some extra additions you might make.

Output
Tree maps
Grid setup
Replicating a point in another run

Output

A basic parameter file creates no output by default. You can perform a run with it but you will not be able to see any of the results, since SORTIE-ND's data visualization can only occur on run output. 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.

Tree maps

You can set up an initial tree population using density values in size classes using the Parameters window. You can also input a known list of trees in a tree map using the "File->Open file" command. There are two kinds of tree maps: those from detailed output files, and those you create directly in tab-delimited text. For more on entering the maps from a detailed output file (the most likely source), see the detailed output file topic. For

more on the tab-delimited tree map file format, see the [tab-delimited tree map](#) topic. You can combine these methods of defining tree initial conditions or use any one alone.

Grid setup

You can manipulate the settings for [grids](#) to further optimize your run. For many grids, you can set the sizes of the grid cells using the [Grid setup window](#). When you have a group of related behaviors sharing a group of related grids, you can assign them the same grid cell size or even multiples of a size to ensure efficient data transfer between them with fewer approximations.

You can also add [grid maps](#) to set the initial conditions for some grids using the ["File->Open file"](#) command. For more on entering the maps from a detailed output file (the most likely source), see the [detailed output file](#) topic. You can also use the [Grid layer setup](#) window to directly edit the values of grid maps.

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 (the most likely source), see the [detailed output file](#) topic.

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Output in SORTIE

By default, no output occurs during a SORTIE run. You set up output files and choose what data should be saved in them in order to perform data analysis.

There are two kinds of output files, [summary output files](#) and [detailed output files](#). Summary output files save high-level data for a run, like population density and basal area. Detailed output files save more detailed data - in fact, as much detail as you want to have; they are very flexible.

To set up output, choose ["Edit->Output options"](#). Once you have produced output files, you can ask SORTIE to display charts and graphs using the [data visualization features](#). You can also use certain kinds of output as initial conditions in subsequent runs.

Output strategies in SORTIE

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. You can see a list of chart types and what they require here. 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 will might 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.

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 output as initial conditions, see the detailed output files topic.)

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.

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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 Tree setup 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 and data files in SORTIE-ND. You can open parameter files this way, and then add map files or detailed output files to the run. You can load files that may not be complete or valid for a run. To check a file, you can save it, or open the Parameters window and then click OK to trigger a file validation.

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 is incorrect. 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.

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.

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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 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"`). This ensures that the model will be able to find the file when it comes time to run the batch. Of course, it also means that you should have your parameter files in the right locations before preparing your batch file, for greatest ease.

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.

Save batch file. Once the batch list is the way you want it, use this button to write the file.

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Edit menu

Parameters. Use this option to edit parameter values for the run. The parameters needing values changes depending on the [behaviors](#) for the run. For more details on this option, see the [Parameters window](#) topic. For details on individual parameters, see the behavior to which they belong.

Episodic events. Use this option to edit planned episodic events, such as silvicultural treatments and episodic mortality. For more details on this option, see the [Edit Episodic Events Window](#) topic.

Tree setup. Use this option to edit the basics of the tree population. For more details on this option, see the Tree setup window topic.

Grid layer setup. Use this option to edit the basics 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.
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Tree setup window

This window is reached from the menu option "Edit->Tree Setup" in the main SORTIE-ND window. It allows you to control some basic aspects of the tree population.

Edit list of species. The top of the window is devoted to editing the species list. The box just below this label is the list of current species. You can add and remove species from this list. To add a species, type its name in the box labeled "New species", and click the button marked "Add". To remove a species, select a species in the list and click the button marked "Remove". To change the name of a species, select it, type the new name in the box, and click the button "Rename".

Edit initial densities size classes... This button allows you to edit the size classes for tree population initial density by opening the Edit size classes window. Size classes help you to define the initial conditions for the tree population. Size classes are not required if you do not want to define your initial tree population this way.

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, even if you click "Cancel" for the window.

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 probably transform them yourself into a tab-delimited map file that SORTIE-ND can accept; see the Tab-delimited tree map topic.
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Edit size classes window

This window is reached from the Tree setup window. It allows you to edit the size classes for the tree population. Size classes help you define an initial tree population for your run. When you have size classes set up, you can specify an initial density of trees in each size class in the Parameters 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".

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. It has the following options:

Choosing a grid to work with
Cell length in X (E-W) direction, in m
Cell length in Y (N-S) direction, in m
Apply cell size changes
View/edit/save grid values...
Clear grid map

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.

15-Sep-2004 02:45 PM

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. (You load grid maps using the "File->Open

file" command. For more on entering the maps from a detailed output file (the most likely source), see the [detailed output file](#) 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. If there is a cursor blinking in a cell when you click "OK", the value for that cell might not save. Whenever you're done entering data, it's a good idea to click outside the last cell so that this won't happen.

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.

16-Sep-2004 10:04 AM

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 is 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". In this window:
[Adding new behaviors](#)
[Changing behavior order - the "Up" and "Down" buttons](#)

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". In this window:
[Adding new behaviors](#)
[Removing behaviors](#)
[Apply to (species) (type)](#)
[Apply to all (type)](#)

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. 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.

Parameters window

This window is reached using the menu option "Edit->Parameters" from the main SORTIE window. It allows you to edit the parameter values for your run. In this window:
Choose which parameters to display
Editing values
Saving the values to a file for review
Error messages when you click "OK"

Choose which parameters to display

This is a small window that appears before the main window to allow you to choose what you want to see displayed. There may not be parameters for all choices that you see on the list. Choose any subset of parameters to display, or choose "All" to see everything.

Editing values

The main parameter display window shows you your chosen parameter groups. Only those parameters that are applicable to the [behaviors](#) that are currently active in the run are shown. To edit a value, double-click its cell. You can copy and paste back and forth from Excel, and within the parameter 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 the values to a file for review

You can save the parameter window you are currently viewing as a tab-delimited text file for your own reference. Choose "File->Save window as file". You can then open the file you have saved in any spreadsheet or text editor program. The file that you save cannot be used as input to SORTIE.

Error messages when you click "OK"

When you click "OK" in the parameter window, the data in the window is checked to make sure it is complete and valid. If there is a problem, you are given an error message and the opportunity to correct the problem. You are not allowed to save invalid data changes. For more on what an individual piece of data is and what limitations may be placed on it, consult the individual behavior documentation (find it by looking at the header that the piece of data is under).

16-Nov-2004 06:47 AM

Edit Episodic Events Window

This window is reached using the menu option "Edit->Episodic events" from the main window. This window allows you to set up silvicultural treatments and planned mortality episodes.

In this document:
[Window layout](#)
[Displaying current episodic events](#)
[Creating new episodic events](#)
[Editing existing episodic events](#)
[Deleting existing episodic events](#)
[Episodic events edit windows](#)

Window layout

The purpose of the main window is to display episodic events which have already been defined, and to provide the starting point for creating new episodic events or editing existing ones. On the left is a panel with three tabs labeled "Harvests", "Plantings", and

"Mortality Episodes". (For more on harvests and planned mortality episodes, see the Disturbance Behaviors topic. For more on Plantings, see the Planting Behaviors topic.) On the right is a map of the plot. On this map is displayed the plot grid cells to which a episodic event is applied. In addition, if there has been a tree map defined, existing trees are also displayed. The color key for these trees is at the far right.

Note to users of previous versions of SORTIE: In the past, trees would be displayed on the harvest plot if they had been either created by tree map or by size class initial densities. This was because, since the interface and the core model were completely integrated, the initial density data had already been used to create the initial population of trees. Now the interface and the core model are separated; there are no trees produced from initial density data until the core model executes when "Model->Run" is chosen from the main model window.

If you need to know the initial tree population and distribution in order to create your episodic events, use a tree map. If you want to create a tree map with a random distribution of trees from size class data, do the following:

1. Load your parameter file without episodic event information.
2. Enter the appropriate size classes using "Edit->Tree Setup", and the appropriate initial density information using "Edit->Parameters".
3. In the parameters, set the length of the run to be 1 timestep.
4. Using "Edit->Output Options", create a detailed output file with the X, Y, and DBH of the saplings and adults of each species.
5. Save the parameter file under a different name.
6. Choose "Model->Run" from the main SORTIE window, or run one timestep. This causes the model to be run. A tree map of the initial density data you entered is then created.
7. Load your original parameter file again.
8. Use the instructions in the detailed output files topic to get the detailed output timestep file for timestep 0 and add it to the parameter file.
9. Proceed to enter your episodic events.

Displaying current episodic events

To display existing episodic events, choose the tab of the type of episodic event you would like to see. The episodic events are numbered in the order that they were entered. You will see the currently displayed episodic event and what its number is of the total (for example, "Showing harvest 3 of 5"). Use the backward and forward buttons to move back and forth through the current episodic events. On the left, you will see information about the episodic event. On the map to the right, the current episodic event cells are displayed in color. Untreated plot cells are white.

For more on what displayed information means, see the topics on episodic event entry, below.

Creating new episodic events

Choose the tab of the type of episodic event you would like to create. Then click "New". A new window will come up where you can enter the episodic event. For more on how to enter the episodic event, see the topics on episodic event entry, below.

Editing existing episodic events

Choose the tab of the type of episodic event you would like to edit. Use the backward and forward buttons to navigate through the episodic events and display the one you want to edit. Then click "Edit". A new window will come up displaying the episodic event. Edit it as you wish. For more, see the topics on episodic event entry, below.

Deleting existing episodic events

Choose the tab of the type of episodic event you would like to delete. Use the backward and forward buttons to navigate through the episodic events and display the one you want to delete. Then click "Delete".

Episodic events edit windows

For more on how to enter episodic events, see the individual episodic event edit topics.
[Edit Harvest](#)
[Edit Mortality Episode](#)
[Edit Planting](#)
[Edit planting diameter at 10 cm](#)
04-Jun-2004 02:30 PM

Edit Harvest Window

This window is reached from the [Edit Episodic Events Window](#) by clicking on the "Harvest" tab and selecting "New" or "Edit".

This window is where you create a new harvest event or edit an existing one. Along the left portion of the window, you enter data about the harvest. On the map in the center, you select the area of the plot to which to apply your harvest. If a tree map has been entered, those trees are displayed on the map and the species key is to the right. (For more on tree maps and episodic events, see the [Edit Episodic Events Window](#) topic.)

In this document:
[Entering data about the harvest](#)
[Choosing the area to which to apply the harvest](#)

Entering data about the harvest

Timestep. Enter the timestep in which you wish the harvest to occur. You can create more than one harvest per timestep.

Species applied to. Put a checkbox next to each species to which this harvest is to apply. If a species is not checked, no trees of that species will be cut. You can cut the same species more than once in a timestep, but if the cut areas of the two harvests overlap, there is no attempt to consolidate them and you may not get the results you expect.

Cut type. Select the type of cut you are performing. The cut type makes no difference to the way that trees are selected for harvest. Its main effect is to change the substrate composition of the plot. If you want to select multiple size classes for cutting, select "Partial cut".

Cut amount type. This only applies if you have selected "Partial cut" under "Cut type". Enter how you intend to specify the amount to cut in each size class you want to cut. The same cut amount type applies to all size classes.

- *% of density.* You intend to specify cut amounts as a percentage of total density to remove, from 0 to 100. The trees removed will be randomly distributed between the minimum and maximum diameters in the size class. For small tree populations, the amount actually removed may not be exactly what was entered.
- **Amt. density (#/ha).** You intend to specify cut amounts as a number of trees per hectare to remove. SORTIE will calculate the actual number of trees to remove by multiplying this number by the area to which the harvest is applied. The trees are removed in size order, starting with the tallest in the size class, until the target number has been reached or there are no more trees in that size class.
- *% of basal area.* You intend to specify cut amounts as a percentage of total basal area to remove, from 0 to 100. SORTIE will add up the basal area in the size class in the cut area and take the percentage in order to figure out how much to cut. SORTIE will work its way down the trees in the cut area in size order, removing each one that brings the amount of basal area removed closer to the target amount without going over. If the size class range and the cut area are both large, the amount of basal area removed is likely to be very close to the target.
- **Amt. basal area (m^2/ha).** You intend to specify cut amounts as an amount of basal area to remove, in square meters per hectare. SORTIE will calculate the actual amount of basal area to remove by multiplying the cut amount by the area to which the harvest is applied. SORTIE will work its way down the trees in the cut area in size order, removing each one that brings the amount of basal area removed closer to the target amount without going over. If the size class range and the cut area are both large, the amount of basal area removed is likely to be very close to the target.

Diameter Range(s) to cut. Enter the size class ranges you are cutting. You must enter at least one, but in order to enter more than one, you must specify "Partial cut" under "Cut type". For each size class, enter the minimum and maximum DBH, and the amount to cut

in that range. The units of amount to cut will depend on what you have entered in "Cut amount type". Cut ranges may not overlap.

Choosing the area to which to apply the harvest

To specify the plot area to which to apply the harvest, select the appropriate cells on the map. Cells are each 8 meters by 8 meters. Selected cells will show up in color, and unselected cells will be white. You can click and drag to mark out an area, or click on individual cells. Clicking or dragging on selected (colored) cells causes them to become unselected (white).

07-Dec-2004 10:27 AM

Edit Mortality Episode Window

This window is reached from the [Edit Episodic Events Window](#) by clicking on the "Mortality Episodes" tab and selecting "New" or "Edit".

This window is where you create a new planned mortality episode or edit an existing one. Along the left portion of the window, you enter data about the planned mortality episode. On the map in the center, you select the area of the plot to which to apply your planned mortality episode. If a tree map has been entered, those trees are displayed on the map and the species key is to the right. (For more on tree maps and episodic events, see the [Edit Episodic Events Window](#) topic.)

In this document:
[Entering data about the planned mortality episode](#)
[Choosing the area to which to apply the planned mortality episode](#)

Entering data about the planned mortality episode

Timestep. Enter the timestep in which you wish the planned mortality episode to occur. You can create more than one planned mortality episode per timestep.

Species applied to. Put a checkbox next to each species to which this planned mortality episode is to apply. If a species is not checked, no trees of that species will be killed. You can kill trees of the same species more than once in a timestep, but if the areas of the two planned mortality episodes overlap, there is no attempt to consolidate them and you may not get the results you expect.

Amount of mortality type. Enter how you intend to specify the amount of trees to kill in each size class to which the planned mortality episode applies. The same amount type applies to all size classes.

- ***% of density.*** You intend to specify kill amounts as a percentage of total density, from 0 to 100. The trees killed will be randomly distributed between the minimum and maximum diameters in the size class. For small tree populations, the amount actually killed may not be exactly what was entered.
- **Amt. density (#/ha).** You intend to specify kill amounts as a number of trees per hectare. SORTIE will calculate the actual number of trees to kill by multiplying this number by the area to which the planned mortality episode is applied. The trees are removed in size order, starting with the tallest in the size class, until the target number has been reached or there are no more trees in that size class.
- ***% of basal area.*** You intend to specify kill amounts as a percentage of total basal area, from 0 to 100. SORTIE will add up the basal area in the size class in the cut area and take the percentage in order to figure out how much to kill. SORTIE will work its way down the trees in the disturbed area in size order, killing each one that brings the amount of basal area killed closer to the target amount without going over. If the size class range and the disturbed area are both large, the amount of basal area killed is likely to be very close to the target.
- **Amt. basal area (m^2/ha).** You intend to specify kill amounts as an amount of basal area, in square meters per hectare. SORTIE will calculate the actual amount of basal area to kill by multiplying this number by the area to which the planned mortality episode is applied. SORTIE will work its way down the trees in the disturbed area in size order, killing each one that brings the amount of basal area killed closer to the target amount without going over. If the size class range and the disturbed area are both large, the amount of basal area killed is likely to be very close to the target.

Diameter Range(s) to kill. Enter the size class ranges you are killing. You must enter at least one. For each size class, enter the minimum and maximum DBH, and the amount to kill in that range. The units of amount to kill will depend on what you have entered in "Amount of mortality type". Kill ranges may not overlap.

Choosing the area to which to apply the planned mortality episode

To specify the plot area to which to apply the planned mortality episode, select the appropriate cells on the map. Cells are each 8 meters by 8 meters. Selected cells will show up in color, and unselected cells will be white. You can click and drag to mark out an area, or click on individual cells. Clicking or dragging on selected (colored) cells causes them to become unselected (white).

07-Dec-2004 10:55 AM

Edit Planting Window

This window is reached from the [Edit Episodic Events Window](#) by clicking on the "Plantings" tab and selecting "New" or "Edit".

This window is where you create a new planting event or edit an existing one. Along the left portion of the window, you enter data about the planting. On the map in the center, you select the area of the plot to which to apply your planting. If a tree map has been entered, those trees are displayed on the map and the species key is to the right. (For more on tree maps and episodic events, see the Edit Episodic Events Window topic.)

In this document:
Entering data about the planting
Choosing the area to which to apply the planting

Entering data about the planting

Timestep. Enter the timestep in which you wish the planting to occur. You can create more than one planting per timestep.

Percentage of each species. For each species, enter the percentage of total trees planted that should be of that species, as a value between 0 and 100. Enter zero in order to not plant a species. Values should add up to 100. When SORTIE plants a seedling, it compares a random number to these values to determine its species. This ensures a random distribution of species in the planted population, but it also means that, if the number of seedlings to plant is small, the actual percentages of each species planted may not exactly match the entered values.

Plant spacing. Select the seedling spacing. If you select "Gridded", the seedlings are placed at a fixed distance from each other. If you select "Random", the seedlings are randomly scattered around the plant area.

 # total trees/ha. You enter this value if the "Plant spacing" is set to "Random". This is the total number of seedlings to plant, as a value per hectare. SORTIE determines the actual number to plant by multiplying this value by the planting area.

Spacing (m). You enter this value if the "Plant spacing" is set to "Gridded". This is the distance, in meters, between newly planted seedlings in an 8 meter by 8 meter plot grid cell. If this distance is larger than 4, only one seedling per grid cell will be planted.

Choosing the area to which to apply the planting

To specify the plot area to which to apply the planting, select the appropriate cells on the map. Cells are each 8 meters by 8 meters. Selected cells will show up in color, and unselected cells will be white. You can click and drag to mark out an area, or click on individual cells. Clicking or dragging on selected (colored) cells causes them to become unselected (white).

07-Dec-2004 10:26 AM

Edit diameter at 10 cm

This window is reached through the Edit Episodic Events Window by clicking on the "Plantings" tab and clicking the button marked "Edit initial diameter at 10 cm."

When planting seedlings (see more on the planting behavior or the Edit Planting Window), you can allow their size to default to the value in the "New seedling diameter at 10 cm" parameter of the tree population, or you can specify values for each species. All plantings for a run share the same set of values.

For each species, enter the diameter at 10 cm value for newly planted seedlings of that species. Actual values will be slightly randomized around these values.

07-Dec-2004 10:55 AM

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 more on output in SORTIE, including a guide on what to save, see the Output in SORTIE topic. For a list of data visualization options and what you need to save to use them, see the Data Visualization topic.

Save Summary Output File (.out)

This button opens the Summary output file setup window for saving short, or 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.

25-Jan-2005 12:50 PM

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. What you save for output depends on what data you want to be

available to you after the run. For a list of data visualization options and what you need to save to use them, see the Data Visualization 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.

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 using the data visualization tools. 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.

This option takes effect right away and cannot be canceled.

Clear everything. Erases all detailed output settings. This option takes effect right away and cannot be canceled.

Trees. Sets options for saving 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.

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Setup tree save options window

For more on the different tree types, see the trees topic. For more on the data available to save, see the tree data member list 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. What you save for output depends on what data you want to be available to you after the run. For a list of data visualization options and what you need to save to use them, see the Data Visualization topic.

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.

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".

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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. What you save for output depends on what data you want to be available to you after the run. For a list of data visualization options and what you need to save to use them, see the Data Visualization 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".

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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. Only one of these files may be saved per run. What you save for output depends on what data you want to be available to you after the run. For a list of data visualization options and what you need to save to use them, see the Data Visualization topic.

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 trees. For the definition of seedling, sapling, adult, and snag, see the trees topic.

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.

Edit Subplots Window

You reach this window by clicking the "Set up subplots..." button on the [Summary output file setup 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. Say you 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.

Displaying additional information

Subplots are often used to analyze the effects of specific episodic events such as silvicultural treatments. (To input episodic events, use the [Edit Episodic Events Window](#).) To help you with this, the subplots window will display episodic events for you on the map. You can display harvest, planned mortality episodies, 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.

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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.

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Help menu

Contents. Accesses the SORTIE help.

Trees

In this document:
Tree background
Tree life history stage transitioning - growth and death
Tree parameters

The basic unit of data in the model is the tree. Each tree is a discrete individual with a location in space and attributes which describe its size and shape. More information about how tree size is measured and how different aspects of tree shape are calculated can be found in the Allometry topic. In addition, a tree may carry data added to it by Behaviors to help simulate different processes.

Tree life history stages

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.** The seed life history stage is currently not used by any behavior, but is available if there is a need to model seeds as individuals.
- **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.
- **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. Stumps exist only for the timestep in which they were created, and then disappear.
- **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 it is not actually created.

Tree life history stage transitioning - growth and death

Trees transition between life history stages as they grow. When a seedling reaches the maximum 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.)

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. The reasons why a tree is killed are natural causes, harvest, insects, fire, and disease (there may not be behaviors set up to create tree death for all of these reasons).

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.

Tree organization

Trees are organized by location and size in what is called the tree population. The tree population indexes trees into 8 m by 8 m areas, lined up by height. The population acts as a librarian for [behaviors](#) that wish to find certain sets of trees upon which to act.

Tree population initial conditions

When setting up a simulation, a key part is to define the initial tree population. 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 by describing a particular pattern of densities by species and size range (size class). You define size classes in the Tree setup window, and enter densities in the [Parameters window](#). The second way is to directly list a particular set of trees in a [tree map](#) within the parameter file.

Tree parameters

- **Initial Densities** The density of trees, in number per hectare, for that size class. Trees are randomly placed within the chosen size range, which starts at the value of the size class beneath (or 0 if there is none) and ends at the value for the current size class. The aim is for an even distribution. You can also set up a size class for seedlings. Seedlings set up this way are given a slightly randomized value of

"New seedling diameter at 10 cm", below. You can further specify seedling initial densities using the seedling height class parameters. You can set up size classes in the [Tree setup window](#).

- **Initial Density (#/ha) - Seedling Height Class 1** Number of seedlings per hectare to create in the first seedling height class (not required). 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 (not required). 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 (not required). 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).
- **Minimum Adult DBH** The minimum DBH at which trees are considered adults. (See more about tree life history stages, above.)
- **Max Seedling Height (meters)** The maximum seedling height, in meters. Trees taller than this height are saplings. (See more about tree life history stages, above.)
- **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.
- **Seedling Height Class 1 Upper Bound, in cm** The upper bound of the first seedling height class, in cm, for specifying seedling initial densities (not required). 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 (not required). 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.

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 setup window](#).

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Allometry

In this document:
[Allometry parameters](#)
[The "standard" crown height and width relationships](#)
[The "Chapman-Richards" crown height and width relationships](#)

Allometry is the relationships between various aspects of a tree's size and shape. A tree may use different relationships for different [life history stages](#).

You can choose the relationship used by each life history stage of each species. These can be freely mixed-and-matched.

Definitions: **DBH** (diameter at breast height) is the diameter of a tree trunk at 1.35 meters above the ground. **Diameter at 10 cm**, or **$diam_{10}$**, is the diameter of a tree trunk 10 cm above the ground.

In general, crowns are modeled as cylinders, with a radius and a height. Specific behaviors may make different assumptions but if so they should be clearly stated in that behavior's documentation.

Seedlings in SORTIE-ND do not have crowns. Saplings and adults (and, in some cases, snags) all use the same relationships to describe crown shape.

Allometry parameters

- **Adult Crown Height-Height Function** The allometric relationship used to relate tree height (in m) and height (or length) of the crown (in m) for adult trees. Each of the choices is described in detail below.
- **Adult Crown Radius-Diameter Function** The allometric relationship used to relate DBH (in cm) and crown radius (in m) for adult trees. Each of the choices is described in detail below.
- **Adult Height-Diameter Function** The allometric relationship used to relate DBH and height for adult trees. Each of the choices is described in detail below.
- **Adult Linear Function Intercept** The intercept of the [adult linear function](#) for DBH and height. Any species not using that function can omit this value.
- **Adult Linear Function Slope** The slope of the [adult linear function](#) for DBH and height. Any species not using that function can omit this value.
- **Adult Reverse Linear Function Intercept** The intercept of the [adult reverse linear function](#) for DBH and height. Any species not using that function can omit this value.
- **Adult Reverse Linear Function Slope** The slope of the [adult reverse linear function](#) for DBH and height. Any species not using that function can omit this value.
- **Chapman-Richards Asymptotic Crown Height** The asymptotic crown height (or length), in m, of the Chapman-Richards crown height equation. Any species not using that function can omit this value.

- **Chapman-Richards Asymptotic Crown Radius** The asymptotic crown radius, in m, of the Chapman-Richards crown radius equation. Any species not using that function can omit this value.
- **Chapman-Richards Crown Height Intercept** The intercept of the Chapman-Richards crown height equation. This represents the crown height, in m, of the smallest possible sapling. Any species not using that function can omit this value.
- **Chapman-Richards Crown Height Shape 1 (b)** The first shape parameter, b, of the Chapman-Richards crown height equation. Any species not using that function can omit this value.
- **Chapman-Richards Crown Height Shape 2 (c)** The second shape parameter, c, of the Chapman-Richards crown height equation. Any species not using that function can omit this value.
- **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. Any species not using that function can omit this value.
- **Chapman-Richards Crown Radius Shape 1 (b)** The first shape parameter, b, of the Chapman-Richards crown radius equation. Any species not using that function can omit this value.
- **Chapman-Richards Crown Radius Shape 2 (c)** The second shape parameter, c, of the Chapman-Richards crown radius equation. Any species not using that function can omit this value.
- **Crown Height Exponent** The exponent in the [standard equation](#) for calculating crown height. Any species not using that function can omit this value.
- **Crown Radius Exponent** The exponent in the [standard equation](#) for determining the crown radius. Any species not using that function can omit this value.
- **Intercept of DBH to Diameter at 10 cm Relationship** The intercept of the linear relationsip between the DBH, in cm, and the diameter at 10 cm height, in cm, in small trees. Used by all species.
- **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.
- **Power Function "a"** The "a" parameter in the [power function](#) for the height-diameter relationship. Any species not using that function can omit this value.
- **Power Function Exponent "b"** The exponent, or "b" parameter, in the [power function](#) for the height-diameter relationship. Any species not using that function can omit this value.
- **Sapling Crown Height-Height Function** The allometric relationship used to relate tree height (in m) and height (or length) of the crown (in m) for saplings. Each of the choices is described in detail below.
- **Sapling Crown Radius-Diameter Function** The allometric relationship used to relate DBH (in cm) and crown radius (in m) for saplings. Each of the choices is described in detail below.
- **Sapling Height-Diameter Function** The allometric relationship used to relate DBH and height for saplings. Each of the choices is described in detail below.
- **Sapling Linear Function Intercept** The intercept of the [sapling linear function](#) for DBH and height. Any species not using that function can omit this value.

- **Sapling Linear Function Slope** The intercept of the [sapling linear function](#) for DBH and height. Any species not using that function can omit this value.
- **Sapling Reverse Linear Function Intercept** The intercept of the [sapling reverse linear function](#) for DBH and height. Any species not using that function can omit this value.
- **Sapling Reverse Linear Function Slope** The slope of the [sapling reverse linear function](#) for DBH and height. Any species not using that function can omit this value.
- **Seedling Height-Diameter Function** The allometric relationship used to relate diameter at 10 cm and height for seedlings. Each of the choices is described in detail below.
- **Seedling Linear Function Intercept** The intercept of the [seedling linear function](#) for DBH and height. Any species not using that function can omit this value.
- **Seedling Linear Function Slope** The slope of the [seedling linear function](#) for DBH and height. Any species not using that function can omit this value.
- **Seedling Reverse Linear Function Intercept** The intercept of the [seedling reverse linear function](#) for DBH and height. Any species not using that function can omit this value.
- **Seedling Reverse Linear Function Slope** The slope of the [seedling reverse linear function](#) for DBH and height. Any species not using that function can omit this value.
- **Slope of Asymptotic Crown Height** Slope of the [standard equation](#) for determining crown height. Any species not using that function can omit this value.
- **Slope of Asymptotic Crown Radius** Slope of the [standard equation](#) for determining crown radius. Any species not using that function can omit this value.
- **Slope of Asymptotic Height** Exponential decay term in the adult and sapling [standard function](#) for DBH and height. Any species not using that function can omit this value.
- **Slope of DBH to Diameter at 10 cm Relationship** The slope of the linear relationsip between the DBH, in cm, and the diameter at 10 cm height, in cm, in small trees. Used by all species.
- **Slope of Height-Diameter at 10 cm Relationship** The slope of the seedling [standard function](#) for diameter at 10 cm and height. Any species not using that function can omit this value.

The "standard" crown height and width relationships

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 height 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 height and width relationships

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 height 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 height 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

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.

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.

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.

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.

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.

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
- d_{10} is diameter at 10 cm (in cm)

Last updated: 25-Jan-2006 03:17 PM

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.

Data that is always present

Some data are fundamental to a tree and are always available for saving. They are:

- **X.** The coordinate of the tree, in meters, on the X axis in the SORTIE plot.
- **Y.** The coordinate of the tree, in meters, on the Y axis in the SORTIE plot.
- **DBH.** The diameter at breast height of a tree, in cm. This does not apply to seedlings.
- **Diameter at 10 cm (diam10).** The tree's diameter at 10 cm height, in cm. This applies only to seedlings and saplings.
- **Height.** The tree's height in meters.
- **Age.** The time since death, in years. Only for snags.

Behavior-specific data

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.

- **Light level.** Light level for the tree. This could be GLI, or percent shade (if Sail Light is used). This is created by any of the light behaviors except the Beer's Law light filter.
- **Diameter growth.** Amount of diameter growth per year in mm. This is created by any of the growth behaviors that increment diameter growth.

- **Light filter respite counter (lf_count).** Created by the [Beer's law light filter](#) behavior. It contains the years of respite for a new seedling from the effects of the light filter.
- **Rooting height (z).** The height, in mm, above ground level at which a seedling is rooted. Created by the [Beer's law light filter](#) behavior.
- **Years released (ylr).** The length of the current release period, in years. Created by the [absolute growth](#) behaviors.
- **Years suppressed (yls).** The length of the current suppression period, in years. Created by the [absolute growth](#) behaviors.
- **Dead flag (dead).** A boolean flag for whether a tree has died. Created by any of the [mortality](#) behaviors. This is used by the [dead tree remover](#) behavior to find the trees it should remove.
- **Tree Bole Volume.** The volume of a tree, in cubic feet. Created by the [Tree bole volume calculator](#) behavior.
- **Tree Volume.** Volume of the tree, in cubic meters. Created by the [Tree volume calculator](#) behavior.
- **Tree Biomass.** Biomass of the tree, in metric tons (Mg). Created by the [Dimension analysis](#) behavior.
- **Tree Age.** Age of the tree, in years. Created by the [Tree age](#) behavior.

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Behaviors

In this document:
[Defining the scope of a behavior's actions](#)
[Behavior order and dependencies](#)
[Behavior data](#)
[Links to individual behavior documentation](#)

Behaviors perform all the action when a simulation is running. Each behavior represents a step in the overall simulation. It retrieves data, manipulates it, and stores the result. Usually, a behavior roughly corresponds to a biological process, such as tree growth. When you define a simulation, the most important step is to choose which behaviors will run, to what data they will apply, and in what order they will run.

Defining the scope of a behavior's actions

Behaviors act on data to achieve a result. The data in the model is [trees](#) and [grids](#). For those behaviors that act on trees, you must tell them what trees to act on. For instance, if you had a behavior which applied a Michaelis-Menton growth function to trees, you may tell it to act on saplings of species 1, 2, and 3; adults of those species may have a different growth behavior applied to them. The [individual behavior documentation](#) tells you how each behavior can be applied.

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 or warn you against things that don't make sense. Therefore, it is important to carefully check the behavior setup yourself before starting a run. Common mistakes include applying two different behaviors of the same type to the same set of trees, and failing to provide a complete set of behaviors to a particular type of tree. These types of situations make "computer" sense, and a simulation can be run when they occur. However, they do not make scientific sense and unexpected results may occur.

To choose which behaviors to include in the run and how to apply them, use the Model flow window.

Behavior order and dependencies

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 to learn how run order might affect a behavior.

Behaviors work on data in sequence. Some behaviors require that a specific step has been taken before they can do their job. This means that, in order to use some behaviors, you must also use certain other behaviors. The individual behavior documentation will tell you about its requirements.

To change the order in which behaviors act, use the Model flow window.

Behavior data

Behaviors help define trees and grids based on the work they need to do. They will create a grid if they need one, or they may attach a new piece of data to the trees to which they are applied. Other behaviors rely on the presence of the grids and tree data members in order to read the results of previous behaviors and make their own calculations. For specifics on these data and what behaviors create them, see the list of grids that can be created and list of tree data members that can be added. To view this data, save a detailed output file.

Usually, a behavior also needs settings and inputs from you to do its job. This data is included in the parameter file. To edit settings for behaviors, use the Parameters window. If a behavior does not have all of the data it requires, you will receive an error message.

Links to individual behavior documentation

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Disturbance behaviors

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

In this document:
[Disturbance parameters](#)
[Harvest](#)
[Planned episodic mortality](#)
[Storm disturbance](#)
[Storm damage applier](#)
[Storm killer](#)
[Selection harvest](#)
[Windstorm](#)

Disturbance parameters

Note: the [Harvest](#) and [Planned episodic mortality](#) behaviors do not have their parameters entered through the [Parameters Window](#). Set up these behaviors using the [Edit Episodic Events Window](#).

- **Clumping Parameter (neg. binomial)** If the **Storm Damage Application** parameter is set to "Stochastic" and the **Stochastic Pattern Damage Distribution** is set to "Negative Binomial", this is the clumping parameter 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 "Negative Binomial". Used by the [Storm disturbance](#) behavior.
- **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. Used by the [Storm damage applier](#) and [Storm killer](#) behaviors.

- **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. Used by the [Storm damage applier](#) behavior.
- **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. Used by the [Storm killer](#) behavior.
- **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. Used by the [Storm disturbance](#) behavior.
- **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. Used by the [Storm disturbance](#) behavior.
- **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. Used by the [Storm disturbance](#) behavior.
- **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. Used by the [Storm disturbance](#) behavior.
- **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. Used by the [Storm disturbance](#) behavior.
- **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. Used by the [Storm disturbance](#) behavior.
- **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. Used by the [Storm disturbance](#) behavior.
- **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. Used by the [Storm disturbance](#) behavior.
- **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. Used by the [Storm disturbance](#) behavior.
- **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. Used by the [Storm disturbance](#) behavior.
- **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. Used by the [Storm disturbance](#) behavior.
- **Selection Harvest Cut Range 1 Lower DBH (cm)** The lower bound of the first DBH cut range, in cm. Used by the [Selection harvest](#) behavior.
- **Selection Harvest Cut Range 1 Upper DBH (cm)** The upper bound of the first DBH cut range, in cm. Used by the [Selection harvest](#) behavior.

- **Selection Harvest Cut Range 1 Target Basal Area (m2/ha)** The target basal area, in square meters per hectare, of the first cut range. Used by the [Selection harvest](#) behavior.
- **Selection Harvest Cut Range 2 Lower DBH (cm)** The lower bound of the second DBH cut range, in cm. Used by the [Selection harvest](#) behavior.
- **Selection Harvest Cut Range 2 Upper DBH (cm)** The upper bound of the second DBH cut range, in cm. Used by the [Selection harvest](#) behavior.
- **Selection Harvest Cut Range 2 Target Basal Area (m2/ha)** The target basal area, in square meters per hectare, of the second cut range. Used by the [Selection harvest](#) behavior.
- **Selection Harvest Cut Range 3 Lower DBH (cm)** The lower bound of the third DBH cut range, in cm. Used by the [Selection harvest](#) behavior.
- **Selection Harvest Cut Range 3 Upper DBH (cm)** The upper bound of the third DBH cut range, in cm. Used by the [Selection harvest](#) behavior.
- **Selection Harvest Cut Range 3 Target Basal Area (m2/ha)** The target basal area, in square meters per hectare, of the third cut range. Used by the [Selection harvest](#) behavior.
- **Selection Harvest Cut Range 4 Lower DBH (cm)** The lower bound of the fourth DBH cut range, in cm. Used by the [Selection harvest](#) behavior.
- **Selection Harvest Cut Range 4 Upper DBH (cm)** The upper bound of the fourth DBH cut range, in cm. Used by the [Selection harvest](#) behavior.
- **Selection Harvest Cut Range 4 Target Basal Area (m2/ha)** The target basal area, in square meters per hectare, of the fourth cut range. Used by the [Selection harvest](#) behavior.
- **Selection Harvest Initial Age** The initial age. Used by the [Selection harvest](#) behavior.
- **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". Used by the [Storm disturbance](#) behavior.
- **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". Used by the [Storm disturbance](#) behavior.
- **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. Used by the [Storm disturbance](#) behavior.
- **Storm Damage Intercept (a) for Medium Damage** The storm damage intercept parameter (a) for the equation calculating the probability of medium damage. Used by the [Storm damage applier](#) behavior.

- **Storm Damage Intercept (a) for Heavy Damage** The storm damage intercept parameter (a) for the equation calculating the probability of heavy damage. Used by the Storm damage applier behavior.
- **Storm DBH Coefficient (d)** The storm DBH coefficient (d) for the equations calculating the probability of damage. Used by the Storm damage applier behavior.
- **Storm Heavy Damage Survival Prob Intercept (a)** The "a" value in the probability of survival logit function for trees with heavy damage. Used by the Storm killer behavior.
- **Storm Heavy Damage Survival Prob DBH Coeff. (b)** The "b" value in the probability of survival logit function for trees with heavy damage. Used by the Storm killer behavior.
- **Storm Intensity Coefficient (b)** The storm intensity coefficient (b) for the equations calculating probability of damage. Used by the Storm damage applier behavior.
- **Storm Medium Damage Survival Prob Intercept (a)** The "a" value in the probability of survival logit function for trees with medium damage. Used by the Storm killer behavior.
- **Storm Medium Damage Survival Prob DBH Coeff. (b)** The "b" value in the probability of survival logit function for trees with medium damage. Used by the Storm killer behavior.
- **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. Used by the Storm killer behavior.
- **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. Used by the Windstorm behavior.
- **Windstorm - Minimum DBH for Windstorm Mortality** The minimum DBH for trees to be killed in storm events. Used by the Windstorm behavior.
- **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. Used by the Windstorm behavior.
- **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). Used by the Windstorm behavior.
- **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). Used by the Windstorm behavior.
- **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). Used by the Windstorm behavior.
- **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). Used by the Windstorm behavior.

- **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). Used by the [Windstorm](#) behavior.
- **Windstorm - Severity for 80 Year Return Interval Storm** The severity of storms with a 80 year return interval, as a value between 0 (no mortality) and 1 (complete devastation). Used by the [Windstorm](#) behavior.
- **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). Used by the [Windstorm](#) behavior.
- **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). Used by the [Windstorm](#) behavior.
- **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). Used by the [Windstorm](#) behavior.
- **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). Used by the [Windstorm](#) behavior.
- **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). Used by the [Windstorm](#) behavior.
- **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. Used by the [Windstorm](#) behavior.
- **Windstorm - Timestep to Start Storms** The first timestep that storms are allowed to occur. Used by the [Windstorm](#) behavior.

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. Trees of any size except seedlings can be cut.

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 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

There are two ways to add Harvest events to a SORTIE run. To define a new harvest, use the [Edit Episodic Events Window](#). If you are a user of a previous version of SORTIE and have a harvest regime file you would like to use, there are instructions for adding it to your run in the [Adding to a parameter file](#) topic.

Episodic Mortality

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. Trees of any size except seedlings can be cut.

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.

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

To define planned mortality episodes, use the Edit Episodic Events Window.

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.

How it works

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.

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.

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, the damage is additive, up to a maximum value of 1 (total damage).

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 three possible probability distribution functions for stochastic damage application: normal, lognormal, and negative binomial.

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:

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

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

The negative binomial distribution is:

$$P\{x \mid u,k\} = \frac{\Gamma(x+k)}{\Gamma(k)x!}\left(\frac{u}{u+k}\right)^{x}\left(1+\frac{u}{k}\right)^{-k}$$

where u is the function mean and k is the clumping parameter. This is Equation 3.103 from Hilborn and Mangel.

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 choose "Negative Binomial", you must provide a function clumping value in the **Clumping Parameter (neg. binomial)** 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).

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:

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

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 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 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.

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.

Selection harvest

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

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. It is similar to the other storm behaviors, with a few key differences. For those long-time users of SORTIE, this is the same as the Windstorm submodel in the pre-6 versions of SORTIE.

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.

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.

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Light behaviors

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Light is the key resource for trees in the SORTIE model. A tree's growth, and therefore its probability of mortality and reproductive ability, is a function of the amount of light it receives. 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

In order to calculate the amount of light a tree gets, SORTIE simulates taking a fisheye photograph over each tree to determine which parts of the sky are blocked by taller trees nearby. SORTIE determines how much light comes from different parts of the sky and takes this into account, so shading neighbors in different directions will have different impacts on the total amount of light a tree gets.

The fisheye photo can be taken at one of two positions - either at the top of the crown or at mid-crown. The major difference between the two is that when the photograph is taken at mid-crown, trees near the same height as the target tree will be included in the shading effects. This can make a big difference in even-age stands.

Sky Simulation

At the beginning of a run, if light behaviors are being used, the amount of light coming from each part of the sky for the plot's location is calculated. The sun's position in the sky is tracked throughout the growing season. Diffuse radiation, assumed to be isotropic (coming equally from all directions), is then added to the direct beam radiation. Below the minimum solar angle, it is assumed that no light comes from those portions of the sky because of the density of the surrounding forest. (It is wise not to set this angle too low - otherwise SORTIE must look very far away for shading neighbors.)

To determine the amount of sun coming from each portion of the sky, the sky is first divided into a hemispheric grid. For GLI calculations, the grid cells are equal-area segments of a user-settable resolution. For Sail Light calculations, the sky is divided into one-degree-sized grid cells. For each day in the growing season, the times of sunrise and sunset are calculated, and then the sun's position in the sky grid is tracked at 5-minute intervals throughout the day. (The equations are below.) At each solar position, the amount of direct beam radiation received from the sun at that position is calculated, taking into account atmospheric effects. Each sky segment keeps track of the total amount of direct beam radiation coming from it for the duration of the growing season.

The total amount of light in the sky is the amount of direct beam radiation plus the amount of diffuse radiation. Once the total amount of direct beam radiation is known, the amount of diffuse radiation is calculated accordingly and added equally to all portions of the sky. Each sky segment is then relativized to hold the percentage of total light coming from that segment.

Determining a tree's light index

For each timestep, SORTIE calculates the amount of light each tree receives by simulating a fisheye photograph. To "take" the photo, the model looks at the hemisphere of sky around and above a tree and determines which portions of it are blocked by neighboring trees. It then totals up how much light is left to reach the tree.

Only tree crowns block light in the model. Trunks do not shade. Because seedlings are modeled as sticks with no crowns, they don't shade either.

The first step in creating the simulated fisheye photo is to determine how far from the tree to search for shading neighbors. For GLI, this is done by comparing the height of the fisheye photo to the maximum possible tree height and determining how far away a tree of this height could be and still have its crown appear in the sky above the minimum solar angle. All trees within this search radius that are taller than the height of the fisheye photo (and thus can be "seen" by it) are added into the "photo." For Sail Light, the search distance is specified by the user.

To add a shading neighbor to the photo, the light behavior determines the amount and location of sky covered by its crown. In a GLI calculation, neighbor crowns are approximated as cylinders. In a Sail Light calculation, neighbor crowns are approximated as 2-D rectangles with a width equal to their crown diameter and a height equal to their crown height (or, as an added simplification, the behavior can assume the crowns of shading neighbors extend all the way to the ground).

The amount of radiation received from the portion of the sky blocked by the shading neighbor is multiplied by the light transmission coefficient for the neighbor's species. The effects of multiple neighbors blocking the same patch of sky are multiplicative.

Once all shading neighbors have been added to the fisheye photo, the amount of light that can still be seen from each region of the sky is totaled up into the appropriate index.

Sky Simulation Equations

All equations are from Iqbal, 1983.

At a given (solar) time, the sun's zenith angle is calculated by:
$$cos\ \theta = sin\ \delta\ sin\varphi + cos\ \delta\ cos\ \varphi\ cos\ \omega$$

and its azimuth angle is calculated by:

$$cos\ \psi = (sin\ \alpha\ sin\ \varphi - sin\ \delta)/cos\ \alpha\ cos\ \varphi$$

where:

- θ = angle from zenith, in degrees
- δ = solar declination, in degrees
- φ = **Plot Latitude, in decimal degrees** parameter (from Plot)
- α = the solar altitude (angle from horizon), in degrees
- ω = the hour angle (solar time).

Azimuth here is south zero, east positive.

Solar declination is calculated by

$$\delta = 0.006918 - 0.399912\ cos\ \Gamma + 0.070257\ sin\ \Gamma - 0.006758\ cos\ 2\Gamma + 0.000907\ sin\ 2\Gamma - 0.002697\ cos\ 3\Gamma + 0.00148\ sin\ 3\Gamma$$

where δ = solar declination in radians and Γ is the day angle, in radians.

The day angle is calculated by $\Gamma = 2\pi(d - 1)/365$ where Γ is the day angle in radians and d is the Julian day number (day of the year between 1 and 365).

So, once we finally have the azimuth and altitude angles for the sun's position in the sky, we can calculate the amount of direct beam radiation coming from it and add it to the appropriate grid cell. The direct beam radiation equation is

$$I = E_0 * \tau^m * cos(\theta)$$

where

- I is the beam radiation
- E_0 is the earth's eccentricity
- τ is the **Clear Sky Transmission Coefficient** parameter
- m is the optical mass of the atmosphere
- θ is the zenith angle of the sun.

Eccentricity is calculated by

$$E_0 = 1.000110 + 0.034221\ cos\ \Gamma + 0.001280\ sin\ \Gamma + 0.000719\ cos\ 2\Gamma + 0.000077\ sin\ 2\Gamma$$

where Γ is the day angle (equation above).

Optical mass of the atmosphere is calculated by

$$m = sec(\theta)$$

where θ is the zenith angle of the sun. SORTIE uses a numerical approximation method instead of the *sec* to correct at low altitudes.

This process is repeated for each day in the growing season. The growing season starts with the **First Day of Growing Season** parameter and ends with the **Last Day of Growing Season** parameter.

Snags in light calculations

Snags are standing dead trees (more in the [trees](#) topic). They can block light like live trees do. For SORTIE purposes, snag crowns are frozen in the shape they had when the tree died, but they transmit more and more light as they lose branches. SORTIE tracks a snag's age in order to replicate this decay. You define three snag age classes and a light transmission coefficient for each. For as long as a snag stands, it will block the light of neighboring trees, but to a lesser degree through time.

You don't have to include snags in light calculations. If you do not have any behaviors in your run that either create snags or directly work with them, then your run is classified as "snag-unaware" and snags will not be created. In this case, the snag parameters are not required. However, if your run is "snag-aware" and snags may be created, you must supply the snag light transmission parameters.

Light parameters

- **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. Used by all behaviors making GLI or Sail Light calculations. See equations above for more on how this is used.
- **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. Used only by the [Sail light](#) behavior.
- **Clear Sky Transmission Coefficient** Used to determine the amount of solar radiation seen at the plot location. Applies to all behaviors making GLI or Sail Light calculations. See equations above for more on how this is used.
- **Basal Area Light - Angiosperm "b" Parameter** The "b" value used to calculate mean GLI from angiosperm basal area. Used by the [Basal Area Light](#) behavior.
- **Basal Area Light - Angiosperm "c" Parameter** The "c" value used to calculate mean GLI from angiosperm basal area. Used by the [Basal Area Light](#) behavior.
- **Basal Area Light - Conifer "b" Parameter** The "b" value used to calculate mean GLI from conifer basal area. Used by the [Basal Area Light](#) behavior.
- **Basal Area Light - Conifer "c" Parameter** The "c" value used to calculate mean GLI from conifer basal area. Used by the [Basal Area Light](#) behavior.
- **Basal Area Light - Lognormal PDF Sigma** Sigma value for the lognormal probability distribution. Used by the [Basal Area Light](#) behavior.

- **Basal Area Light - Mean GLI "a" Parameter** The "a" value used to calculate mean GLI from basal area. Used by the [Basal Area Light](#) behavior.
- **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. Used by the [Basal Area Light](#) behavior.
- **Basal Area Light - Minimum DBH for Trees** The minimum DBH, in cm, of trees that count towards basal area. Used by the [Basal Area Light](#) behavior.
- **Basal Area Light - Species Type** Whether each species is a conifer or an angiosperm, for the purposes of light calculations. Used by the [Basal Area Light](#) behavior.
- **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. Used by all behaviors making GLI or Sail light calculations.
- **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"). File format is below. Used by the [GLI Points File Creator](#) behavior.
- **GLI Points Output File** The file to which the [GLI Points File Creator](#) behavior will write its results each timestep. Any existing data in this file will be overwritten at the start of the run.
- **Height at Which GLI is Calculated for GLI Map, in meters** Height at which the [GLI Map Creator behavior](#) calculates GLI.
- **Height at Which GLI is Calculated for Quadrats, in meters** Height at which the [Quadrat-based GLI light behavior](#) calculates GLI.
- **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. Applies to all behaviors making GLI or Sail light calculations. Seedlings always get fisheye photos at top-of-crown no matter what this value is.
- **Height of Light Filter, in m** Height, in meters, at which the Beer's law light filter hangs. Only applies to the [Beer's law light filter](#) behavior.
- **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. Used by all behaviors making GLI or Sail light calculations.
- **Light Transmission Coefficient (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.
- **Light Filter Light Transmission Coefficient** Amount of light that is blocked by the light filter. Only applies to the [Beer's law light filter](#) behavior.
- **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. This value applies to the [GLI light](#) behavior.
- **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. This value applies to the [GLI Map Creator](#) behavior.

- **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. This value applies to the GLI Points File Creator behavior.
- **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. This value applies to the Quadrat-based GLI light behavior, if the value should be different from the value being used by the GLI light behavior.
- **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. Used by the GLI light behavior, as well as the Quadrat-based light behavior if a different value is not specified for it.
- **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. Used by the GLI Map Creator behavior. If the GLI light behavior is also used, this value is not required.
- **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. Used by the GLI Points File Creator behavior. If the GLI light behavior is also used, this value is not required.
- **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. Used by the Quadrat-based light behavior. If the GLI light behavior is also used, this value is not required.
- **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. Used by the GLI light behavior, as well as the Quadrat-based light and GLI Map Creator behaviors if different values are not specified for them.
- **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. Used by the GLI Map Creator behavior. If the GLI light behavior is also used, this value is not required.
- **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. Used by the GLI Points File Creator behavior. If the GLI light behavior is also used, this value is not required.
- **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. Used by the Quadrat-based light behavior. If the GLI light behavior is also used, this value is not required.
- **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. Used only in the Sail Light behavior.

- **Sail Light Minimum Solar Angle, in degrees** The azimuth angle, in degrees, below which it is assumed trees will see no light. Used only by the Sail Light behavior.
- **Snag Age Class 1 Light Transmission 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 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. Used by all behaviors making GLI or Sail Light calculations.
- **Snag Age Class 2 Light Transmission 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 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. Used by all behaviors making GLI or Sail Light calculations.
- **Snag Age Class 3 Light Transmission 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 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. Used by all behaviors making GLI or Sail Light calculations.
- **Storm Light - Intercept of Light Function** Intercept of the function to determine light level. Used by the Storm Light behavior.
- **Storm Light - Max Radius (m) for Damaged Neighbors** The maximum distance, in meters, within which the Storm Light behavior searches for damaged trees. Used by the Storm Light behavior.
- **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. Used by the Storm Light behavior.
- **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. Used by the Storm Light behavior.
- **Storm Light - Slope of Light Function** Slope of the function to determine light level. Used by the Storm Light behavior.
- **Storm Light - Std. Dev. or Clump Parameter** If the value in the **Storm Light - Stochasticity** parameter is "Normal" or "Lognormal", the standard deviation of the probability distribution function; if the value is "Negative Binomial", the clumping parameter for the PDF; if "Deterministic", this value is ignored. Used by the Storm Light behavior.
- **Storm Light - Stochasticity** What method to use for randomizing light values, if desired. Used by the Storm Light behavior.
- **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. Used by all behaviors making GLI or Sail Light calculations.

- **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. Used by all behaviors making GLI or Sail Light calculations.

Quadrat-based GLI light

For more on what GLI is and how it is calculated, see above.

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).

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 above.

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.

Sail light

For more on what the Sail Light index is and how it is calculated, see above.

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.

Constant full GLI

How it works

This assigns a GLI value of full sun (100%) to all trees to which it is assigned.

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.

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.

GLI Map Creator

For more on what GLI is and how it is calculated, see above.

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

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.

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.

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 number of trees 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 >= 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 number of heavily damaged trees, N, is counted. 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. Snags that were created because a tree was killed by a process other than a storm are not counted.

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.

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.

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. **NOTE**: The parameters for this behavior are dependent on the size of the cells in the Basal Area Light grid. Changing the size of the cells without changing the parameters may give different results.

The behavior begins by calculating the total basal area and angiosperm basal area in each of the Basal Area Light grid cells. Whether a species counts as angiosperm or conifer is set 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:

$$GLI_m = \frac{a}{1 + \left(BA_a \middle/ c_a \right)^{ba} + \left(BA_c \middle/ c_c \right)^{ba}}$$

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.

GLI Points File Creator behavior

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

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

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.

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Growth behaviors

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How growth is applied

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

In the first method, the behavior calculates an amount of diameter increase, 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 way that growth has been applied in all previous versions of SORTIE, and is the method you should choose if you are in doubt about which one you want. Behaviors using this method have the tag "diam with auto height" in their name.

In the second method, the behavior calculates an amount of diameter increase, and then adds this amount to the tree's diameter. The height is not allowed to change. The rationale behind this is that tree diameter and height are not always strictly coupled by the allometry equations; sometimes, diameter and height should be allowed to vary independently. If you use a growth behavior of this type, it is required that you pair it with a separate behavior incrementing height. Behaviors using this method have the tag "diam only" in their name.

In the third method, the behavior calculates an amount of height increase, and then adds this amount to the tree's height. The diameter is not allowed to change. The rationale is the same as that for the second method. If you use a growth behavior of this type, it is required that you pair it with a separate behavior incrementing diameter. Behaviors using this method have the tag "height only" in their name.

Growth behaviors using the second and third method must work together in pairs. Behaviors using the first method work alone. If you pair a behavior using method one with a behavior using method three, the height-incrementing behavior will be ignored.

When incrementing a tree's diameter with new growth, seedlings and saplings have the amount of growth increase 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 trees 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 mixing different growth methods for different life history stages of a tree species. 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. Say that you do not have data on separate diameter and height growth for adults, so 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 incrementer" behavior was developed to help bridge this gap. When used with a behavior that only increments diameter, it will preserve height differences that have developed across individuals in a species.

Growth parameters

- **Adult Constant Area Growth in sq. cm/yr** The constant amount of basal area by which to increase a tree's basal area. Used in basal-area-increment-limited behaviors and constant basal area growth behaviors.
- **Adult Constant Radial Growth in mm/yr** The constant value by which to increase a tree's radius at breast height. Used in radial-increment-limited-growth behaviors and constant radial increment behaviors.
- **Asymptotic Diameter Growth (A)** Asymptote of the Michaelis-Menton growth function at high light in absolute and relative growth behaviors - A in the equations below. Used in absolute and relative growth behaviors.
- **Double resource - Influence of Resource (C)** The parameter governing the influence of the second resource on the double-resource Michaelis-Menton equation. Used by the [Double resource relative growth - diam with auto height](#) and [Double resource relative growth - diam only](#) behaviors.
- **Include Snags in NCI Calculations** Whether or not to include snags when finding competitive neighbors for NCI. Used in the [NCI growth behavior - diam with auto height](#) and [NCI growth behavior - diam only](#) behaviors.
- **Length of Current Release Factor** Controls the magnitude of the effects of release. Used in absolute growth behaviors.
- **Length of Last Suppression Factor** Controls the magnitude of the effects of suppression. Used in absolute growth behaviors.
- **Linear Bi-Level - Intercept for High-Light Growth (a)** The intercept of the linear growth function used in high-light conditions. Used in the [Linear bi-level growth - diam with auto height](#) and [Linear bi-level growth - diam only](#) behaviors.
- **Linear Bi-Level - Intercept for Low-Light Growth (a)** The intercept of the linear growth function used in low-light conditions. Used in the [Linear bi-level growth - diam with auto height](#) and [Linear bi-level growth - diam only](#) behaviors.
- **Linear Bi-Level - Slope for High-Light Growth (b)** The slope of the linear growth function used in high-light conditions. Used in the [Linear bi-level growth - diam with auto height](#) and [Linear bi-level growth - diam only](#) behaviors.
- **Linear Bi-Level - Slope for Low-Light Growth (b)** The slope of the linear growth function used in low-light conditions. Used in the [Linear bi-level growth - diam with auto height](#) and [Linear bi-level growth - diam only](#) behaviors.
- **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. Used in the [Linear bi-level growth - diam with auto height](#) and [Linear bi-level growth - diam only](#) behaviors.
- **Logistic - Asymptotic Diam Growth - Full Light in mm/yr (a)** Asymptotic annual growth at full light, in mm/yr. Used by the [Logistic growth - diam with auto height](#) and [Logistic growth - diam only](#) behaviors.
- **Logistic - Asymptotic Height Growth - Full Light in cm/yr (a)** Asymptotic annual growth at full light, in cm/yr. Used by the [Logistic growth - height only](#) behavior.
- **Logistic - Diam Shape Param 1 (b)** Shape parameter 1. Used by the [Logistic growth - diam with auto height](#) and [Logistic growth - diam only](#) behaviors.
- **Logistic - Diam Shape Param 2 (c)** Shape parameter 2. Used by the [Logistic growth - diam with auto height](#) and [Logistic growth - diam only](#) behaviors.

- **Logistic - Height Shape Param 1 (b)** Shape parameter 1. Used by the [Logistic growth - height only](#) behavior.
- **Logistic - Height Shape Param 2 (c)** Shape parameter 2. Used by the [Logistic growth - height only](#) behavior.
- **Lognormal Bi-Level - Max Growth in High Light (m)** The maximum height growth, in meters, under high-light conditions. Used by the [Lognormal bi-level growth - height only](#) behavior.
- **Lognormal Bi-Level - Max Growth in Low Light (m)** The maximum height growth, in meters, under low-light conditions. Used by the [Lognormal bi-level growth - height only](#) behavior.
- **Lognormal Bi-Level - X0 for High-Light Growth** The X_0 parameter to use under high-light growth conditions. Used by the [Lognormal bi-level growth - height only](#) behavior.
- **Lognormal Bi-Level - X0 for Low-Light Growth** The X_0 parameter to use under low-light growth conditions. Used by the [Lognormal bi-level growth - height only](#) behavior.
- **Lognormal Bi-Level - Xb for High-Light Growth** The X_b parameter to use under high-light growth conditions. Used by the [Lognormal bi-level growth - height only](#) behavior.
- **Lognormal Bi-Level - Xb for Low-Light Growth** The X_b parameter to use under low-light growth conditions. Used by the [Lognormal bi-level growth - height only](#) behavior.
- **Lognormal Bi-Level - Threshold for High-Light Growth (0 - 100)** Used by the [Lognormal bi-level growth - height only](#) behavior.
- **Lognormal - Diam Effect of Shade (c)** Effect of shade. Used by the [Lognormal with exponential shade reduction - diam with auto height](#) and [Lognormal with exponential shade reduction - diam only](#) behaviors.
- **Lognormal - Diam Growth Increment at Diam 36, in mm/yr (a)** Annual growth increment at diameter 36, in mm/yr. Used by the [Lognormal with exponential shade reduction - diam with auto height](#) and [Lognormal with exponential shade reduction - diam only](#) behaviors.
- **Lognormal - Diam Shape Parameter (b)** Shape parameter. Used by the [Lognormal with exponential shade reduction - diam with auto height](#) and [Lognormal with exponential shade reduction - diam only](#) behaviors.
- **Lognormal - Height Effect of Shade (c)** Effect of shade. Used by the [Lognormal with exponential shade reduction - height only](#) behavior.
- **Lognormal - Height Growth Increment at Diam 36, in cm/yr (a)** Annual growth increment at diameter 36, in cm/yr. Used by the [Lognormal with exponential shade reduction - height only](#) behavior.
- **Lognormal - Height Shape Parameter (b)** Shape parameter. Used by the [Lognormal with exponential shade reduction - height only](#) behavior.
- **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. Used in absolute growth behaviors.

- **NCI Alpha** NCI function exponent. Used in the [NCI growth behavior - diam with auto height](#) and [NCI growth behavior - diam only](#) behaviors.
- **NCI Beta** NCI function exponent. Used in the [NCI growth behavior - diam with auto height](#) and [NCI growth behavior - diam only](#) behaviors.
- **NCI Crowding Effect Slope (C)** The slope of the curve for the crowding effect equation. Used in the [NCI growth behavior - diam with auto height](#) and [NCI growth behavior - diam only](#) behaviors.
- **NCI Crowding Effect Steepness (D)** The steepness of the curve for the crowding effect equation. Used in the [NCI growth behavior - diam with auto height](#) and [NCI growth behavior - diam only](#) behaviors.
- **NCI Damage Effect - Complete Storm Damage (0-1)** The fraction by which a tree's growth rate is reduced when it has sustained complete storm damage. Set this to 1 if you are not including storms in your run. Used in the [NCI growth behavior - diam with auto height](#) and [NCI growth behavior - diam only](#) behaviors.
- **NCI Damage Effect - Medium Storm Damage (0-1)** The fraction by which a tree's growth rate is reduced when it has sustained medium storm damage. Set this to 1 if you are not including storms in your run. Used in the [NCI growth behavior - diam with auto height](#) and [NCI growth behavior - diam only](#) behaviors.
- **Species i NCI lambda neighbors** The competitive effect of neighbors of species i on the target tree species's growth, between 0 and 1. Used in the [NCI growth behavior - diam with auto height](#) and [NCI growth behavior - diam only](#) behaviors.
- **NCI Maximum Crowding Distance, in meters** The maximum distance, in m, at which a neighboring tree has competitive effects on a target tree. Used in the [NCI growth behavior - diam with auto height](#) and [NCI growth behavior - diam only](#) behaviors.
- **NCI Maximum Potential Growth, cm/yr** Maximum potential diameter growth for a tree, in cm/yr. Used in the [NCI growth behavior - diam with auto height](#) and [NCI growth behavior - diam only](#) behaviors.
- **NCI Minimum Neighbor DBH, in cm** The minimum DBH for trees of that species to compete as neighbors. Used for all species, not just those using NCI growth. Used in the [NCI growth behavior - diam with auto height](#) and [NCI growth behavior - diam only](#) behaviors.
- **NCI DBH Divisor (q)** The value by which neighbor DBHs are divided when calculating NCI. Set this value to something greater than 1 if necessary to decrease the competitive effects of neighbors. Used in the [NCI growth behavior - diam with auto height](#) and [NCI growth behavior - diam only](#) behaviors.
- **NCI Neighbor Storm Damage (eta) - Complete (0-1)** The fraction to which a neighbor's competitive effect is reduced when the neighbor has sustained complete storm damage. Set this to 1 if you are not including storms in your run. Used in the [NCI growth behavior - diam with auto height](#) and [NCI growth behavior - diam only](#) behaviors.
- **NCI Neighbor Storm Damage (eta) - Medium (0-1)** The fraction to which a neighbor's competitive effect is reduced when the neighbor has sustained medium storm damage. Set this to 1 if you are not including storms in your run. Used in

the NCI growth behavior - diam with auto height and NCI growth behavior - diam only behaviors.

- **NCI Shading Effect Coefficient (m)** The coefficient in the shading effect equation. Set this value to 0 if you do not wish to use shading. Used in the NCI growth behavior - diam with auto height and NCI growth behavior - diam only behaviors.
- **NCI Shading Effect Exponent (n)** The exponent in the shading effect equation. If you set the **NCI Shading Effect Coefficient (m)** parameter to 0, this value is ignored. Used in the NCI growth behavior - diam with auto height and NCI growth behavior - diam only behaviors.
- **NCI Size Effect Mode, in cm (X0)** The mode of the size effect curve. Used in the NCI growth behavior - diam with auto height and NCI growth behavior - diam only behaviors.
- **NCI Size Effect Variance, in cm (Xb)** The variance of the size effect curve. Used in the NCI growth behavior - diam with auto height and NCI growth behavior - diam only behaviors.
- **NCI Size Sensitivity to NCI (gamma)** The sensitivity of a tree's growth rate to its DBH. Set this to 0 to remove the DBH term altogether. Used in the NCI growth behavior - diam with auto height and NCI growth behavior - diam only behaviors. behaviors.
- **PR - "a" Parameter for Deterministic Growth** "a" parameter used to calculate deterministic growth when a tree is below the stochastic height threshold. Used in the Puerto Rico semi-stochastic - diam only behavior.
- **PR - "b" Parameter for Deterministic Growth** "b" parameter used to calculate deterministic growth when a tree is below the stochastic height threshold. Used in the Puerto Rico semi-stochastic - diam only behavior.
- **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. Used in the Puerto Rico semi-stochastic - diam only behavior.
- **PR - Height Threshold for Stochastic Growth (m)** The tree height threshold, in meters, between deterministic and stochastic growth. Used in the Puerto Rico semi-stochastic - diam only behavior.
- **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. Used in the Puerto Rico semi-stochastic - diam only behavior.
- **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. Used in the Puerto Rico storm bi-level growth - diam with auto height behavior.
- **PR Storm Bi-Level - High-Light "a"** The "a" value in the high-light growth function. Used in the Puerto Rico storm bi-level growth - diam with auto height behavior.
- **PR Storm Bi-Level - High-Light "b"** The "b" value in the high-light growth function. Used in the Puerto Rico storm bi-level growth - diam with auto height behavior.

- **PR Storm Bi-Level - Intercept for Low-Light Growth (a)** The intercept of the linear growth function used in low-light conditions. Used in the [Puerto Rico storm bi-level growth - diam with auto height](#) behavior.
- **PR Storm Bi-Level - Slope for Low-Light Growth (b)** The slope of the linear growth function used in high-light conditions. Used in the [Puerto Rico storm bi-level growth - diam with auto height](#) behavior.
- **Relative Michaelis-Menton Growth - Diameter Exponent** The exponent to be used with diameter when calculating relative growth. Used in the [Relative growth](#) behaviors.
- **Shaded Linear - Diam Intercept in mm/yr (a)** Intercept of the size dependent growth potential, in mm/yr. Used by the [Linear growth w/ exponential shade reduction - diam with auto height](#) and [Linear growth w/ exponential shade reduction - diam only](#) behaviors.
- **Shaded Linear - Diam Shade Exponent (c)** Effect of shading. Used by the [Linear growth w/ exponential shade reduction - diam with auto height](#) and [Linear growth w/ exponential shade reduction - diam only](#) behaviors.
- **Shaded Linear - Diam Slope (b)** Slope of the size dependent annual growth potential. Used by the [Linear growth w/ exponential shade reduction - diam with auto height](#) and [Linear growth w/ exponential shade reduction - diam only](#) behaviors.
- **Shaded Linear - Height Intercept in cm/yr (a)** Intercept of the size dependent growth potential, in cm/yr. Used by the [Linear growth w/ exponential shade reduction - height only](#) behavior.
- **Shaded Linear - Height Shade Exponent (c)** Effect of shading. Used by the [Linear growth w/ exponential shade reduction - height only](#) behavior.
- **Shaded Linear - Height Slope (b)** Slope of the size dependent annual growth potential. Used by the [Linear growth w/ exponential shade reduction - height only](#) behavior.
- **Simple Linear - Diam Intercept in mm/yr (a)** Intercept of the linear growth function, or growth at no light, in mm/yr. Used by the [Linear growth - diam with auto height](#) and [Linear growth - diam only](#) behaviors.
- **Simple Linear - Diam Slope (b)** Slope of the linear growth function. Used by the [Linear growth - diam with auto height](#) and [Linear growth - diam only](#) behaviors.
- **Simple Linear - Height Intercept in cm/yr (a)** Intercept of the linear growth function, or growth at no light, in cm/yr. Used by the [Linear growth - height only](#) behavior.
- **Simple Linear - Height Slope (b)** Slope of the linear growth function. Used by the [Linear growth - height only](#) behavior.
- **Size Dep. Logistic - Diam Intercept (a)** Intercept of the size dependent annual growth potential. Used by the [Logistic growth w/ size dependent asymptote - diam only](#) and [Logistic growth w/ size dependent asymptote - diam with auto height](#) behaviors.
- **Size Dep. Logistic - Diam Shape Param 1 (c)** Shape parameter 1 for shade reduction of annual growth. Used by the [Logistic growth w/ size dependent asymptote - diam only](#) and [Logistic growth w/ size dependent asymptote - diam with auto height](#) behaviors.

- **Size Dep. Logistic - Diam Shape Param 2 (d)** Shape parameter 2 for shade reduction of annual growth. Used by the [Logistic growth w/ size dependent asymptote - height only](#) and [Logistic growth w/ size dependent asymptote - diam with auto height](#) behaviors.
- **Size Dep. Logistic - Diam Slope (b)** Slope of the size dependent annual growth potential. Used by the [Logistic growth w/ size dependent asymptote - diam only](#) and [Logistic growth w/ size dependent asymptote - diam with auto height](#) behaviors.
- **Size Dep. Logistic - Height Intercept (a)** Intercept of the size dependent annual growth potential. Used by the [Logistic growth w/ size dependent asymptote - height only](#) behavior.
- **Size Dep. Logistic - Height Shape Param 1 (c)** Shape parameter 1 for shade reduction of annual growth. Used by the [Logistic growth w/ size dependent asymptote - height only](#) behavior.
- **Size Dep. Logistic - Height Shape Param 2 (d)** Shape parameter 2 for shade reduction of annual growth. Used by the [Logistic growth w/ size dependent asymptote - height only](#) behavior.
- **Size Dep. Logistic - Height Slope (b)** Slope of the size dependent annual growth potential. Used by the [Logistic growth w/ size dependent asymptote - height only](#) behavior.
- **Slope of Growth Response (S)** Slope of the Michaelis-Menton growth function at zero light for relative and absolute growth behaviors - S in the equations below. Used in absolute and growth behaviors.
- **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. Used in absolute growth behaviors.

Relative growth behaviors

Several behaviors apply a relative growth version of the Michaelis-Menton function. 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)** parameter
- *S* is the **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** parameter

Relative growth is discussed in [Pacala et al 1996](#).

Relative growth limited to radial increment - diam with auto height

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. Tree height is allowed to update automatically according to the allometry equations. 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.

Relative growth limited to radial increment - diam only

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](#) and a height-incrementing growth behavior applied.

Relative growth limited to basal area increment - diam with auto height

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. Tree height is allowed to update automatically according to the allometry equations.

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 limited to basal area increment - diam only

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](#) and a height-incrementing growth behavior applied.

Unlimited relative growth - diam with auto height

How it works

The amount of increase returned by the relative growth equation is applied to the tree. Tree height is allowed to update automatically according to the allometry equations.

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.

Unlimited relative growth - diam only

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](#) and a height-incrementing growth behavior applied.

Double resource relative growth - diam with auto height

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. 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 "Unlimited relative growth" behavior.

How it works

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.

Once growth has been calculated and applied to the tree's diameter, tree height is allowed to update automatically according to the allometry equations.

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.

Double resource relative growth - diam only

How it works

This behavior calculates growth exactly like the "Double resource relative growth - diam with auto height" behavior. Height is updated separately using another 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 a height-incrementing growth behavior applied. You must also enter a map of second resource values into the Resource grid.

Absolute growth behaviors

Several behaviors apply an absolute growth version of the Michaelis-Menton function. Absolute growth is calculated with the equation:

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

where

- Y = log10(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
$$growth = (((10^Y - 1) * 2)/10) * T$$

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 - diam with auto height

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. Tree height is allowed to update automatically according to the allometry equations. 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.

Absolute growth limited to radial increment - diam only

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](#) and a height-incrementing growth behavior applied.

Absolute growth limited to basal area increment - diam with auto height

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. Tree height is allowed to update automatically according to the allometry equations.

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.

Absolute growth limited to basal area increment - diam only

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 and a height-incrementing growth behavior applied.

Unlimited 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. Tree height is allowed to update automatically according to the allometry equations.

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.

Unlimited absolute growth - diam only

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 and a height-incrementing growth behavior applied.

Constant basal area growth - diam with auto height

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

Tree height is allowed to update automatically according to the allometry equations.

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.

Constant basal area growth - diam only

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](#) and a height-incrementing growth behavior applied.

Constant radial growth - diam with auto 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

Tree height is allowed to update automatically according to the allometry equations. 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.

Constant radial growth - diam only

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. /p>

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 height-incrementing growth behavior applied.

NCI growth - diam with auto height

This behavior uses the effects of neighbor competitiveness to influence growth rates ("NCI" stands for neighborhood competition index). A tree's maximum potential growth rate is reduced due to competitiveness and several other possible factors. You can use certain parameter values to turn these influences on and off to reflect the conditions appropriate for your run.

How it works

For a tree, the amount of growth per year is calculated as:

*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.

Size Effect is calculated as:

$$SE = e^{-\frac{1}{2}\left[\frac{\ln\left(DBH/X_0\right)}{X_b}\right]^2}$$

where:

- *DBH* is of the target tree, in cm
- X_0 is the **NCI Size Effect Mode, in cm (X0)** parameter
- X_b is the **NCI Size Effect Variance, in cm (Xb)**

Shading Effect is calculated as:

$$ShE = e^{-m*S^n}$$

where:

- *m* is the **NCI Shading Effect Coefficient (m)** parameter
- *n* is the **NCI Shading Effect Exponent (n)** parameter
- *S* is the amount of shade cast by neighbors, from 0 (no shade) to 1 (full shade). This value should come from the Sail light behavior.

This effect is not required. To omit the Shading Effect, set the **NCI Shading Effect Coefficient (m)** parameter to 0.

Crowding Effect is calculated as:

$$CE = e^{-C*DBH^{\gamma}*NCI^{D}}$$

where:

- *C* is the **NCI Crowding Effect Slope (C)** parameter
- *DBH* is of the target tree, in cm
- *γ* is the **NCI Size Sensitivity to NCI (gamma)** parameter for the target tree's species
- *D* is the **NCI Crowding Effect Steepness (D)** parameter
- *NCI* is this tree's NCI value (equation below)

The *NCI* value sums up the competitive effect of all neighbors with a DBH at least that of the **NCI Minimum Neighbor DBH, in cm** parameter, out to a maximum distance set in the **NCI Max Radius of Crowding Neighbors, in m** parameter. The competitiveness of a neighbor increases with the neighbor's size and decreases with distance and storm damage to the neighbor (optional). The neighbor's species also matters; the effect depends on the relationship between the target species and the neighbor species. Seedlings never compete. You set whether or not snags compete in the **Include Snags in NCI Calculations** parameter.

NCI is calculated as:

$$NCI_i = \sum_{j=1}^{S} \sum_{k=1}^{N} \eta_k \lambda_{ik} \frac{\left(DBH_{jk} \middle/ q \right)^{\alpha}}{(distance_{ik})^{\beta}}$$

where:

- the calculation sums over *j = 1...S* species and *k = 1...N* neighbors of each species of at least a DBH of **NCI Minimum Neighbor DBH, in cm**, out to a distance of **NCI Max Radius of Crowding Neighbors, in m**
- η_k is the storm damage parameter of the kth neighbor, depending on the damage status (optional). If the neighbor is undamaged, the value is 1. If the neighbor has medium damage, the value is the **NCI Neighbor Storm Damage (eta) - Medium (0-1)** parameter for the neighbor species. If the neighbor has complete damage, the value is the **NCI Neighbor Storm Damage (eta) - Complete (0-1)** parameter for the neighbor species. To omit the storm damage term, set all values for the above two parameters to 1.
- *α* is the **NCI Alpha** parameter for the target tree's species
- *β* is the **NCI Beta** parameter for the target tree's species
- DBH_{jk} is the DBH of the kth neighbor, in cm
- *q* is the **NCI DBH Divisor (q)** parameter. Set this to a value greater than 1 to rescale the competitive effects of neighbors

- λ_{ik} is the **Species j NCI Lambda** parameter for the target species relative to the kth neighbor's species
- *distance$_{ik}$* is distance from target to neighbor, in m

The value of *Damage Effect* is optional. If you elect not to use storms in your run, set all values in the **NCI Damage Effect - Medium Storm Damage (0-1)** and **NCI Damage Effect - Complete Storm Damage (0-1)** parameters to 1. If you are using storms, then the value of *Damage Effect* depends on the tree's damage category. If the tree is undamaged, *Damage Effect* equals 1. If the tree has medium storm damage, the value is the **NCI Damage Effect - Medium Storm Damage (0-1)** parameter. If the tree has complete storm damage, the value is the **NCI Damage Effect - Complete Storm Damage (0-1)** parameter.

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 DBH for one year. For each year, any portion of the growth equation with DBH as a term is recalculated with the previous year's updated DBH value.

The final total growth amount is added to the tree's DBH. Height is calculated according to the appropriate allometric equation.

How to apply it

This behavior can be applied to saplings and adults of any species. It cannot be applied to seedlings.

If the *Shading Effect* term is activated in the growth equation, then the trees to which this behavior is applied must also have a [light behavior](#) applied - the Sail light behavior is the one designed to work with the NCI behavior. The use of any other light behavior is at your own risk.

If any storm damage parameters are set to anything other than 1, it is recommended (but not required) that you have the [Storm damage applier](#) behavior applied.

NCI growth - diam only

This behavior works exactly like the "NCI growth - diam with auto height" behavior to calculate an amount of diameter increase.

How to apply it

This behavior can be applied to saplings and adults of any species. It cannot be applied to seedlings.

If the *Shading Effect* term is activated in the growth equation, then the trees to which this behavior is applied must also have a [light behavior](#) applied - the Sail light behavior is the

one designed to work with the NCI behavior. The use of any other light behavior is at your own risk.

If any storm damage parameters are set to anything other than 1, it is recommended (but not required) that you have the [Storm damage applier](#) behavior applied.

Basal area NCI growth - diam with auto height

This behavior uses the effects of neighbor competitiveness to influence growth rates ("NCI" stands for neighborhood competition index). In this case, the NCI is based on the basal area of neighboring trees. A tree's maximum potential growth rate is reduced due to competitiveness and several other possible factors.

How it works

For a tree, the amount of growth per year is calculated as:

*Growth = Max Growth * Size Effect * Crowding 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* and *Crowding Effect* are 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.

Size Effect is calculated as:

$$SE = e^{-\frac{1}{2}\left[\frac{\ln\left(DBH/X_0\right)}{X_b}\right]^2}$$

where:

- *DBH* is of the target tree, in cm
- X_0 is the **NCI Size Effect Mode, in cm (X0)** parameter
- X_b is the **NCI Size Effect Variance, in cm (Xb)**

Crowding Effect is calculated as:

$$CE = exp(-C * (DBH^{\gamma} * BA_n / 1000)^D)$$

where:

- *C* is the **NCI Crowding Effect Slope (C)** parameter
- *DBH* is of the target tree, in cm

- γ is the **NCI Size Sensitivity to NCI (gamma)** parameter for the target tree's species
- D is the **NCI Crowding Effect Steepness (D)** parameter
- BA_n is the sum of the basal areas, in square cm, of trees with a DBH larger than the target tree's DBH

When calculating BA_n, this behavior uses neighbors of all species out to the distance set in the **NCI Max Radius of Crowding Neighbors, in m** parameter. The neighbors must have a DBH larger than the target tree's DBH, and larger than the values set in the **NCI Minimum Neighbor DBH, in cm** parameter. Seedlings and snags never contribute to BA_n.

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 DBH for one year. For each year, any portion of the growth equation with DBH as a term is recalculated with the previous year's updated DBH value.

The final total growth amount is added to the tree's DBH. Height is calculated according to the appropriate allometric equation.

How to apply it

This behavior can be applied to saplings and adults of any species. It cannot be applied to seedlings.

Basal area NCI growth - diam only

This behavior works exactly like the "Basal area NCI growth - diam with auto height" behavior to calculate an amount of diameter increase.

How to apply it

This behavior can be applied to saplings and adults of any species. It cannot be applied to seedlings.

Allometric height incrementer

How it works

This behavior calculates an amount of height growth. The amount of height increase is the difference between the results of the allometry equation for the diameter before and after the growth increment is applied. It can be paired with any behavior that increments diameter only.

This behavior takes as inputs the diameters of a tree before and after its amount of diameter growth increase has been applied (by whatever behavior has calculated this amount of increase). It then uses the diameter-height allometry equation appropriate to the tree type to calculate a height for each diameter. The amount of height increase is the difference between these heights.

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-only growth behavior applied.

Linear growth - height only

How it works

This behavior calculates an amount of height growth as:

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

where

- Y = amount of height increase, in cm
- a = **Simple Linear - Height Intercept in mm/yr (a)** parameter
- b = **Simple Linear - Height Slope (b)** parameter
- 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 and a diameter-only growth behavior applied.

Linear growth - diam with auto height

How it works

This behavior calculates an amount of diameter growth as:

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

where

- Y = amount of diameter increase, in mm
- a = **Simple Linear - Diam Intercept in mm/yr (a)** parameter
- b = **Simple Linear - Diam Slope (b)** parameter

- *GLI* = global light index, as a percentage between 0 and 100, calculated by a [light behavior](#)
- *T* = number of years per timestep

After applying the amount of diameter increase, tree height is allowed to update automatically according to the [allometry](#) equations.

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.

Linear growth - diam only

How it works

This behavior calculates an amount of diameter growth as:
$$Y = (a + (b * GLI)) * T$$
where

- *Y* = amount of diameter increase, in mm
- *a* = **Simple Linear - Diam Intercept in mm/yr (a)** parameter
- *b* = **Simple Linear - Diam Slope (b)** parameter
- *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](#) and a height-only growth behavior applied.

Linear growth w/ exponential shade reduction - height only

How it works

This behavior calculates an amount of height growth as:
$$Y = (a + (b * diam)) * (GLI/100)^c * T$$
where

- *Y* = amount of height increase, in cm
- *a* = **Shaded Linear - Height Intercept in cm/yr (a)** parameter

- b = **Shaded Linear - Height Slope (b)** parameter
- c = **Shaded Linear - Height Shade Exponent (c)** parameter
- $diam$ = 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

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 and a diameter-only growth behavior applied.

Linear growth w/ exponential shade reduction - diam with auto height

How it works

This behavior calculates an amount of diameter growth as:
$$Y = (a + (b * diam)) * (GLI/100)^c * T$$
where

- Y = amount of diameter increase, in mm
- a = **Shaded Linear - Diam Intercept in mm/yr (a)** parameter
- b = **Shaded Linear - Diam Slope (b)** parameter
- c = **Shaded Linear - Diam Shade Exponent (c)** parameter
- $diam$ = 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

After applying the amount of diameter increase, tree height is allowed to update automatically according to the allometry equations.

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.

Linear growth w/ exponential shade reduction - diam only

How it works

This behavior calculates an amount of diameter growth as:

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

where

- Y = amount of diameter increase, in mm
- a = **Shaded Linear - Diam Intercept in mm/yr (a)** parameter
- b = **Shaded Linear - Diam Slope (b)** parameter
- c = **Shaded Linear - Diam Shade Exponent (c)** parameter
- *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 <u>light behavior</u>
- 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 <u>light behavior</u> and a height-only growth behavior applied.

Logistic growth - height only

How it works

The amount of height increase is calculated as:

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

where

- Y = amount of height increase, in cm
- a = **Logistic - Asymptotic Height Growth - Full Light in cm/yr (a)**
- b = **Logistic - Height Shape Param 1 (b)** parameter
- c = **Logistic - Height Shape Param 2 (c)** parameter
- *GLI* = global light index, as a percentage between 0 and 100, calculated by a <u>light behavior</u>
- 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 and a diameter-only growth behavior applied.

Logistic growth - diam with auto height

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
- a = **Logistic - Asymptotic Diam Growth - Full Light in mm/yr (a)** parameter
- b = **Logistic - Diam Shape Param 1 (b)** parameter
- c = **Logistic - Diam Shape Param 2 (c)** parameter
- GLI = global light index, as a percentage between 0 and 100, calculated by a light behavior
- T = number of years per timestep

After applying the amount of diameter increase, tree height is allowed to update automatically according to the allometry equations.

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.

Logistic growth - diam only

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
- a = **Logistic - Asymptotic Diam Growth - Full Light in mm/yr (a)** parameter
- b = **Logistic - Diam Shape Param 1 (b)** parameter
- c = **Logistic - Diam Shape Param 2 (c)** parameter
- 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 <u>light behavior</u> and a height-only growth behavior applied.

Logistic growth w/ size dependent asymptote - height only

How it works

This behavior calculates annual height increases as:

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

where

- *Y* = amount of height increase, in cm
- *a* = **Size Dep. Logistic - Height Intercept (a)** parameter
- *b* = **Size Dep. Logistic - Height Slope (b)** parameter
- *c* = **Size Dep. Logistic - Height Shape Param 1 (c)** parameter
- *d* = **Size Dep. Logistic - Height Shape Param 2 (d)** parameter
- *GLI* = global light index, as a percentage between 0 and 100, calculated by a <u>light behavior</u>
- *diam* = diameter (diameter at 10 cm for seedlings and saplings, DBH for adults)

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 <u>light behavior</u> and a diameter-only growth behavior applied.

Logistic growth w/ size dependent asymptote - diam with auto height

How it works

This behavior calculates annual diameter increases as:

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

where

- Y = amount of diameter increase, in mm
- a = **Size Dep. Logistic - Diam Intercept (a)** parameter
- b = **Size Dep. Logistic - Diam Slope (b)** parameter
- c = **Size Dep. Logistic - Diam Shape Param 1 (c)** parameter
- d = **Size Dep. Logistic - Diam Shape Param 2 (d)** parameter
- 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)

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. After applying the amount of diameter increase, tree height is allowed to update automatically according to the allometry equations.

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.

Logistic growth w/ size dependent asymptote - diam only

How it works

This behavior calculates annual diameter increases as:

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

where

- Y = amount of diameter increase, in mm
- a = **Size Dep. Logistic - Diam Intercept (a)** parameter
- b = **Size Dep. Logistic - Diam Slope (b)** parameter
- c = **Size Dep. Logistic - Diam Shape Param 1 (c)** parameter
- d = **Size Dep. Logistic - Diam Shape Param 2 (d)** parameter

- *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)

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.

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 height-only growth behavior applied.

Lognormal with exponential shade reduction - height only

How it works

This behavior calculates annual height increases as:

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

where

- *Y* = amount of height increase, in cm
- *a* = **Lognormal - Height Growth Increment at Diam 36, in cm/yr (a)** parameter
- *b* = **Lognormal - Height Shape Parameter (b)** parameter
- *c* = **Lognormal - Height Effect of Shade (c)** parameter
- *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)

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](#) and a diameter-only growth behavior applied.

Lognormal with exponential shade reduction - diam with auto height

How it works

This behavior calculates annual height increases as:

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

where

- Y = amount of height increase, in cm
- a = **Lognormal - Diam Growth Increment at Diam 36, in mm/yr (a)** parameter
- b = **Lognormal - Diam Shape Parameter (b)** parameter
- c = **Lognormal - Diam Effect of Shade (c)** parameter
- 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)

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. After applying the amount of diameter increase, tree height is allowed to update automatically according to the [allometry](#) equations.

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.

Lognormal with exponential shade reduction - diam only

How it works

This behavior calculates annual height increases as:

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

where

- *Y* = amount of height increase, in cm
- *a* = **Lognormal - Diam Growth Increment at Diam 36, in mm/yr (a)** parameter
- *b* = **Lognormal - Diam Shape Parameter (b)** parameter
- *c* = **Lognormal - Diam Effect of Shade (c)** parameter
- *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)

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.

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 height-only 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.

Linear bi-level growth - diam with auto height

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.

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.

Linear bi-level growth - diam only

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.

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. Any tree species/type combination to which it is applied must also have a height-only growth behavior applied. If you wish to use the light-level parameter switch, also use the Storm Light behavior.

Lognormal bi-level growth - height only

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.

How it works

The equation used by this behavior to increment growth is:

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

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.

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.

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

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.

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.

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Mortality behaviors

In this document:

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. 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.

Mortality parameters

- **Adult Background Mortality Rate** The proportion of trees that die each year, as a value between 0 and 1. Used by the [Adult stochastic mortality](#) behavior.
- **Adult Self-Thinning Intercept** Intercept of the adult self-thinning linear function. Used by the [Adult self-thinning](#) behavior.
- **Adult Self-Thinning Slope** Slope of the adult self-thinning linear function. Used by the [Adult self-thinning](#) behavior.
- **Competition Mortality Maximum Parameter (max)** The maximum relative increment of growth subject to mortality. Used by the [Competition Mortality](#) behavior.
- **Competition Mortality Shape Parameter (Z)** Determines the shape of the mortality function. Used by the [Competition Mortality](#) behavior.
- **DBH at Onset of Senescence, in cm** DBH at which senescence takes effect. Used by the [Senescence](#) behavior.
- **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. Used by the [Senescence](#) behavior.
- **Density Self-Thinning Asymptote (A)** The asymptote of the density self-thinning function. Used by the [Density Self-Thinning Mortality](#) behavior.
- **Density Self-Thinning Density Effect (S)** The parameter controlling the density effect of the density self-thinning function. Used by the [Density Self-Thinning Mortality](#) behavior.
- **Density Self-Thinning Diameter Effect (C)** The parameter controlling the effect of neighbor mean diameter of the density self-thinning function. Used by the [Density Self-Thinning Mortality](#) behavior.
- **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. Used by the Density Self-Thinning Mortality behavior.

- **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. Used by the Density Self-Thinning Mortality behavior.
- **Growth/Resource - Scaling Factor (rho)** Scaling factor to reduce survival at the mode of the survival probability function. Used by the Growth and Resource-Based Mortality behavior.
- **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). Used by the Growth and Resource-Based Mortality behavior.
- **Growth/Resource - Survival Increase with Growth (delta)** Specifies the increase in survival caused by amount of growth. Used by the Growth and Resource-Based Mortality behavior.
- **Growth/Resource - Low-Growth Survival Parameter (sigma)** Affects the shape of the survival probability distribution in low-growth conditions. Used by the Growth and Resource-Based Mortality behavior.
- **Height-GLI Weibull - a** The "a" parameter in the Weibull function for calculating annual mortality. Used by the Height-GLI Weibull Mortality behavior.
- **Height-GLI Weibull - b** The "b" parameter in the Weibull function for calculating annual mortality. Used by the Height-GLI Weibull Mortality behavior.
- **Height-GLI Weibull - c** The "c" parameter in the Weibull function for calculating annual mortality. Used by the Height-GLI Weibull Mortality behavior.
- **Height-GLI Weibull - d** The "d" parameter in the Weibull function for calculating annual mortality. Used by the Height-GLI Weibull Mortality behavior.
- **Height-GLI Weibull - Max Mortality (0 - 1)** The maximum mortality probability for a species, expressed as a proportion between 0 and 1. Used by the Height-GLI Weibull Mortality behavior.
- **Include Snags in NCI Calculations** Whether or not to include snags when finding competitive neighbors for NCI. Used in the NCI mortality behavior.
- **Juvenile Background Mortality Rate** The proportion of trees that die each year, as a value between 0 and 1. Used by the Juvenile stochastic mortality behavior.
- **Juvenile Self-Thinning Intercept** Intercept of the juvenile self-thinning linear function. Used by the Juvenile self-thinning behavior.
- **Juvenile Self-Thinning Slope** Slope of the juvenile self-thinning linear function. Used by the Juvenile self-thinning behavior.
- **Light-Dependent Mortality** Light-dependent mortality. Used by the GMF mortality and BC morality behaviors.
- **Logistic Bi-Level - Low-Light "a"** The "a" parameter used in low-light conditions. Used by the Logistic Bi-Level Mortality behavior.
- **Logistic Bi-Level - Low-Light "b"** The "b" parameter used in low-light conditions. Used by the Logistic Bi-Level Mortality behavior.
- **Logistic Bi-Level - High-Light "a"** The "a" parameter used in high-light conditions. Used by the Logistic Bi-Level Mortality behavior.
- **Logistic Bi-Level - High-Light "b"** The "b" parameter used in high-light conditions. Used by the Logistic Bi-Level Mortality behavior.

- **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. Used by the Logistic Bi-Level Mortality behavior.
- **Maximum DBH for Adult Self-Thinning** Maximum DBH at which adult self-thinning applies. Above this value, no mortality occurs. Used by the Adult self-thinning behavior.
- **Mortality at Zero Growth** Mortality rate at zero growth. Used by the GMF mortality and BC morality behaviors.
- **NCI Crowding Effect Slope (C)** The slope of the curve for neighbor effects. Used in the NCI mortality behavior.
- **NCI Crowding Effect Steepness (D)** The steepness of the curve for neighbor effects. Used in the NCI mortality behavior.
- **NCI Max Radius of Crowding Neighbors, in m** The maximum distance from a target tree at which neighbors can have a competitive effect. Used in the NCI mortality behavior.
- **NCI Max Survival Probability (0-1)** The maximum annual probability of survival, as a value between 0 and 1. Used in the NCI mortality behavior.
- **NCI Minimum Neighbor DBH, in cm** The minimum DBH for trees of that species to compete as neighbors. Used for all neighbor species, not just those using NCI mortality. Used in the NCI mortality behavior.
- **NCI Neighbor DBH Effect (alpha)** The effect of the DBH of a neighbor tree on its competitiveness for a target species. Used in the NCI mortality behavior.
- **NCI Neighbor Distance Effect (beta)** The effect of the distance of a neighbor tree on its competitiveness for a target species. Used in the NCI mortality behavior.
- **NCI Neighbor Storm Damage (eta) - Complete (0-1)** The fraction to which a neighbor's competitive effect is reduced when the neighbor has sustained complete storm damage. Used in the NCI mortality behavior.
- **NCI Neighbor Storm Damage (eta) - Medium (0-1)** The fraction to which a neighbor's competitive effect is reduced when the neighbor has sustained medium storm damage. Used in the NCI mortality behavior.
- **NCI Shading Effect Coefficient (m)** The coefficient in the shading effect equation. Set this value to 0 if you do not wish to use shading. Used in the NCI mortality behavior.
- **NCI Shading Effect Exponent (n)** The exponent in the shading effect equation. If you set the **NCI Shading Effect Coefficient (m)** parameter to 0, this value is ignored. Used in the NCI mortality behavior.
- **NCI Size Effect Mode, in cm** The mode of the size effect curve. Used in the NCI mortality behavior.
- **NCI Size Effect Variance, in cm** The variance of the size effect curve. Used in the NCI mortality behavior.
- **NCI Size Sensitivity to NCI (gamma)** The sensitivity of a tree's survival probability to its DBH. Used in the NCI mortality behavior.
- **NCI Storm Effect - Complete Damage (0-1)** The fraction by which a tree's survival probability is reduced when it has sustained complete storm damage. Used in the NCI mortality behavior.

- **NCI Storm Effect - Medium Damage (0-1)** The fraction by which a tree's survival probability is reduced when it has sustained medium storm damage. Used in the NCI mortality behavior.
- **Species i NCI Lambda** The scale of the competitive effect of a neighbor tree's species on the target tree's species. Used in the NCI mortality behavior.
- **Senescence Mortality Alpha** Controls the senescence mortality rate. Used by the Senescence behavior.
- **Senescence Mortality Beta** Controls the senescence mortality rate. Used by the Senescence behavior.
- **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. Used by the Stochastic Bi-Level Mortality behavior.
- **Stochastic Bi-Level - High-Light Mortality Threshold (0-100)** The threshold between low-light and high-light mortality rates, as a value between 0 and 100. Used by the Stochastic Bi-Level Mortality behavior.
- **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. Used by the Stochastic Bi-Level Mortality behavior.
- **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". Used by the Weibull snag mortality behavior.
- **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". Used by the Weibull snag mortality behavior.
- **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". Used by the Weibull snag mortality behavior.
- **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". Used by the Weibull snag mortality behavior.
- **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". Used by the Weibull snag mortality behavior.
- **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". Used by the Weibull snag mortality behavior.
- **Weibull Upper DBH of Snag Size Class 1** The upper DBH value of trees in size class 1. Used by the Weibull snag mortality behavior.
- **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. Used by the Weibull snag mortality behavior.

GMF mortality

GMF mortality is a growth-based mortality behavior.

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
- m_2 is the **Light-Dependent Mortality** parameter
- G is amount of radial growth, in mm/yr, added to the tree's diameter this timestep

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.

BC mortality

BC mortality is a growth-based mortality behavior.

How it works

The BC mortality model evaluates the following function to determine the probability of a tree's mortality:

$$m = 1 - e^{-(T*m_1)e^{-m_2 G}}$$

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.

Adult 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. There is nothing in this behavior which makes it specifically for adult trees - the name is to match the old SORTIE conventions.

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.

Juvenile 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. Unlike adult self-thinning, there is no upper DBH limit applied. There is nothing in this behavior which makes it specifically for juvenile trees - the name is to match the old SORTIE conventions.

How it works

Self-thinning uses a simple linear function of probability of mortality as a function of DBH. 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.

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.

Adult 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. There is nothing about this behavior which makes it only applicable to adults. The name conforms to old SORTIE

standards and allows it to be distinguished from the Juvenile stochastic mortality behavior, so that two different rates can be applied to two different groups of trees.

How it works

For each tree, a random number is compared to that species's **Adult 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.

Juvenile 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. There is nothing about this behavior which makes it only applicable to juveniles. The name conforms to old SORTIE standards and allows it to be distinguished from the Adult stochastic mortality behavior, so that two different rates can be applied to two different groups of trees.

How it works

For each tree, a random number is compared to that species's **Juvenile 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.

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.

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:

$$S = e^{-(a*T)^b}$$

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.

NCI mortality

This behavior uses the effects of neighbor competitiveness to influence tree survival ("NCI" stands for neighborhood competition index). A tree's maximum potential probability of survival is reduced due to competitiveness and several other possible factors. You can use certain parameter values to turn these influences on and off to reflect the conditions appropriate for your run.

How it works

For a tree, the annual probability of survival is calculated as:

*Prob. Survival = Max Survival * Storm Effect * Size Effect * Crowding Effect*

Max Survival is the **NCI Max Survival Probability (0-1)** parameter. *Storm Effect*, *Size Effect*, and *Crowding Effect* are all factors which act to reduce the maximum survival probability and will vary depending on the conditions a tree is in. All values are bounded between 0 and 1.

Size Effect is calculated as:

$$SE = e^{-\frac{1}{2}\left[\frac{\ln\left(DBH/X_0\right)}{X_b}\right]^2}$$

where:

- *DBH* is of the target tree, in cm
- X_0 is the **NCI Size Effect Mode, in cm** parameter
- X_b is the **NCI Size Effect Variance, in cm**

Shading Effect is calculated as:

$$ShE = e^{-m*S^n}$$

where:

- *m* is the **NCI Shading Effect Coefficient (m)** parameter
- *n* is the **NCI Shading Effect Exponent (n)** parameter
- *S* is the amount of shade cast by neighbors, from 0 (no shade) to 1 (full shade). This value should come from the Sail light behavior.

This effect is not required. To omit the Shading Effect, set the **NCI Shading Effect Coefficient (m)** parameter to 0.

Crowding Effect is calculated as:

$$CE = e^{-C*DBH^{\gamma}*NCI^{D}}$$

where:

- *C* is the **NCI Crowding Effect Slope (C)** parameter
- *D* is the **NCI Crowding Effect Steepness (D)** parameter
- *DBH* is of the target tree, in cm
- *γ* is the **NCI Size Sensitivity to NCI (gamma)** parameter for the target tree's species
- *NCI* is this tree's NCI value (equation below)

The *NCI* value sums up the competitive effect of all neighbors with a DBH at least that of the **NCI Minimum Neighbor DBH, in cm** parameter, out to a maximum distance set in the **NCI Max Radius of Crowding Neighbors, in m** parameter. The competitiveness of a neighbor increases with the neighbor's size and decreases with distance and storm damage to the neighbor (optional). The neighbor's species also matters; the effect depends on the relationship between the target species and the neighbor species. Seedlings never compete. You set whether or not snags compete in the **Include Snags in NCI Calculations** parameter.

NCI is calculated as:

$$NCI_i = \sum_{j=1}^{S} \sum_{k=1}^{N} \eta_k \lambda_{ik} \frac{\left(DBH_{jk}/q\right)^{\alpha}}{\left(distance_{ik}\right)^{\beta}}$$

where:

- the calculation sums over $j = 1...S$ species and $k = 1...N$ neighbors of each species of at least a DBH of **NCI Minimum Neighbor DBH, in cm**, out to a distance of **NCI Max Radius of Crowding Neighbors, in m**
- η_k is the storm damage parameter of the kth neighbor, depending on the damage status (optional). If the neighbor is undamaged, the value is 1. If the neighbor has medium damage, the value is the **NCI Neighbor Storm Damage (eta) - Medium (0-1)** parameter for the neighbor species. If the neighbor has complete damage, the value is the **NCI Neighbor Storm Damage (eta) - Complete (0-1)** parameter for the neighbor species. To omit the storm damage term, set all values for the above two parameters to 1.
- α is the **NCI Alpha** parameter for the target tree's species
- β is the **NCI Beta** parameter for the target tree's species
- DBH_{jk} is the DBH of the kth neighbor, in cm
- q is the **NCI DBH Divisor (q)** parameter. Set this to a value greater than 1 to rescale the competitive effects of neighbors
- λ_{ik} is the **Species j NCI Lambda** parameter for the target species relative to the kth neighbor's species
- $distance_{ik}$ is distance from target to neighbor, in m

The value of *Damage Effect* is optional. If you elect not to use storms in your run, set all values in the **NCI Damage Effect - Medium Storm Damage (0-1)** and **NCI Damage Effect - Complete Storm Damage (0-1)** parameters to 1. If you are using storms, then the value of *Damage Effect* depends on the tree's damage category. If the tree is undamaged, *Damage Effect* equals 1. If the tree has medium storm damage, the value is the **NCI Damage Effect - Medium Storm Damage (0-1)** parameter. If the tree has complete storm damage, the value is the **NCI Damage Effect - Complete Storm Damage (0-1)** parameter.

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 saplings and adults of any species. It cannot be applied to seedlings.

If the *Shading Effect* term is activated in the growth equation, then the trees to which this behavior is applied must also have a light behavior applied - the Sail light behavior is the

one designed to work with the NCI behavior. The use of any other light behavior is at your own risk.

If any storm damage parameters are set to anything other than 1, it is recommended (but not required) that you have the Storm damage applier behavior applied.

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.

How it works

The probability of survival for a tree is calculated with the following equation:

$$Prob = \rho * e^{\left(\frac{-(R-\mu)^2}{2((\delta G)+\sigma)^2}\right)}$$

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.

Competition Mortality

Competition mortality is a growth-based mortality behavior. It uses the results of the NCI growth behavior.

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:

$$SE = e^{-\frac{1}{2}\left[\frac{\ln\left(DBH/X_0\right)}{X_b}\right]^2}$$

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.

How it works

The probability of mortality is calculated with a double Michaelis-Menton function:

$$Pm = \left(\frac{(A + (C \times diam_m)) \times density}{\frac{(A + (C \times diam_m))}{S} + density} \right)$$

where:

- *Pm* 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.**

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.

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.

Stochastic bi-level mortality

This behavior applies a constant rate of mortality to trees, with different rates for high-light and low-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 high-light and low-light parameters is set in the **Stochastic Bi-Level - High-Light Mortality Threshold (0-100)** parameter.

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. You must also use the [Storm Light](#) behavior.

Height-GLI Weibull Mortality

This behavior calculates the probability of mortality using a Weibull function of tree height and GLI (light level).

How it works

The equation used by this behavior to calculate mortality probability 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)** parameter
- a - the **Height-GLI Weibull - a** parameter
- b - the **Height-GLI Weibull - b** parameter
- c - the **Height-GLI Weibull - c** parameter
- d - the **Height-GLI Weibull - 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.

How to apply it

This behavior can be applied to seedlings, saplings, and adults of any species. You must also use a [light behavior](#).

Last updated: 26-Jan-2006 03:17 PM

Substrate behaviors

In this document:

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.

Substrate parameters

- **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.
- **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 [Adding to a parameter file](#) 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 [Adding to a parameter file](#) 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 [Adding to a parameter file](#) 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 [Adding to a parameter file](#) 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.
- **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.
- **Scarified Soil Annual Decay Alpha** The α exponent in the decay equation $y = e^{\alpha * f^{\beta}}$, as applied to scarified soil. Note that this is **annual** decay.
- **Scarified Soil Annual Decay Beta** The β exponent in the decay equation $y = e^{\alpha * f^{\beta}}$, as applied to scarified soil. Note that this is **annual** decay.
- **Tip-Up Mounds Annual Decay Alpha** The α exponent in the decay equation $y = e^{\alpha * f^{\beta}}$, 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 $y = e^{\alpha * f^{\beta}}$, 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.

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

Substrate Creation and Decay Schematic
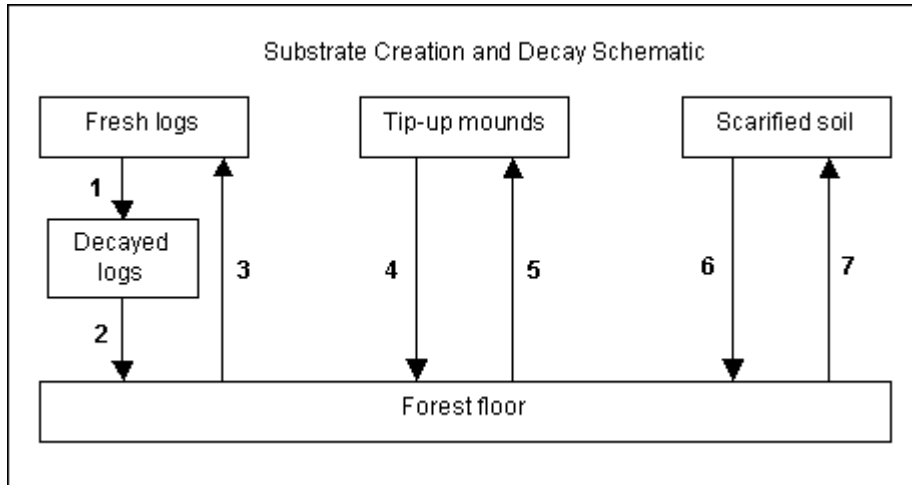
Relationships 1, 2, 4, and 6 represent the decay of the different substrates as a function of substrate age according to the equation

$$y = e^{\alpha * t^{\beta}}$$

where t is time in years. Graphed, this equation looks like this:

Hypothetical Substrate Loss Function
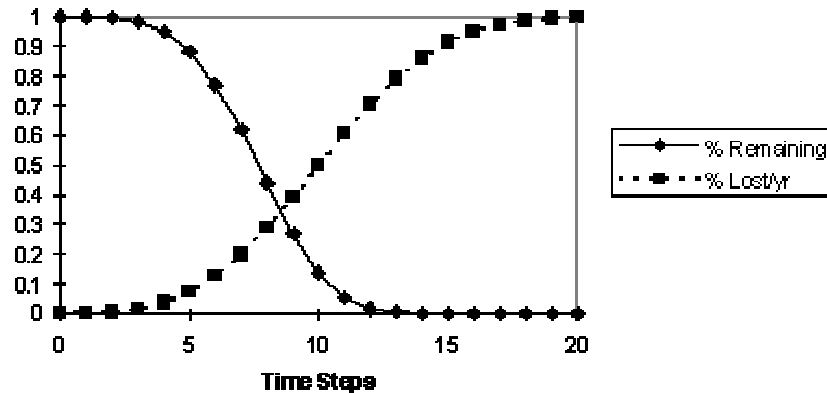
In this diagram, there are two kinds of substrate, A and B. A decays into B according to the equation above. The amount of A and B together sum to 1 for this diagram. The curve for "% Remaining" is the amount of A. The curve for "% Lost/yr" is the amount of B. When $\beta > 1$, the rate of loss/time 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.

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.

Last updated: 03-Aug-2005 09:42 AM

Dead tree remover 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. Currently, there is only one.

Dead tree remover

How it works

This behavior looks for the death flag as set by the mortality behaviors. For each tree that it finds with that flag, it sends a request to the tree population to "kill" the tree. The reason passed to the tree population for the death of the tree is natural death.

How to apply it

This behavior should be applied to all tree species and tree types. All trees to which this behavior is applied must also have a light behavior applied. This is a signal to this behavior that the trees are going to have their data set up in the expected way.

24-Jun-2004 12:38 PM

Disperse behaviors

In this document:
Seed randomization
Disperse parameters
Non-spatial disperse behavior
Spatial disperse behaviors
--Non-gap spatial disperse behavior
--Gap spatial disperse behavior
--Anisotropic spatial disperse behavior

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. You can change this grid's cell resolution. 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 Trees), 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 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.

The lognormal distribution is:

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

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

The Poisson distribution is:

$$f(x,\lambda) = \frac{\lambda^x e^{-\lambda}}{x!}$$

where λ is the function mean.

The negative binomial distribution is:

$$P\{x\,|\,u,k\} = \frac{\Gamma(x+k)}{\Gamma(k)x!} \left(\frac{u}{u+k}\right)^x \left(1+\frac{u}{k}\right)^{-k}$$

where u is the function mean and k is the clumping parameter. This is Equation 3.103 from [Hilborn and Mangel](#).

Disperse parameters

- **Amplitude of Anisotropic Effect** The amplitude of the anisotropic effect (how strongly the distances differ in the maximum and minimum directions). Used by the [Anisotropic spatial disperse](#) behavior.

- **Azimuth Direction of Max Dispersal Distance, in rad** The azimuth direction in radians (north zero, east positive) of the maximum dispersal distance. Used by the Anisotropic spatial disperse behavior.
- **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. Used by the Gap spatial disperse and Non-gap spatial disperse behaviors.
- **Canopy Function Used** The probability distribution function to be used to distribute seeds in canopy conditions. For the behaviors Non-gap spatial disperse and Anisotropic disperse, these PDFs are always the ones used. Used by the Non-gap spatial disperse, Gap spatial disperse, and Anisotropic spatial disperse behaviors.
- **Gap Function Used** The probability distribution function to be used to distribute seeds in gap conditions. Used by the Gap spatial disperse behavior.
- **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. Used by the Non-spatial disperse behavior.
- **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. Used by the Gap spatial disperse, Non-gap spatial disperse, and Anisotropic spatial disperse behaviors. (In the case of the last two, the canopy probability distribution function is the only one used for a species.)
- **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. Used by the Gap spatial disperse, Non-gap spatial disperse, and Anisotropic spatial disperse behaviors. (In the case of the last two, the canopy probability distribution function is the only one used for a species.)
- **Lognormal Canopy X$_0$** The mean of the lognormal function under canopy conditions (see equation below). This is only required if the canopy probability distribution function is lognormal. Used by the Gap spatial disperse, Non-gap spatial disperse, and Anisotropic spatial disperse behaviors. (In the case of the last two, the canopy probability distribution function is the only one used for a species.)
- **Lognormal Canopy X$_b$** The variance of the lognormal function under canopy conditions (see equation below). This is only required if the canopy probability distribution function is lognormal. Used by the Gap spatial disperse, Non-gap spatial disperse, and Anisotropic spatial disperse behaviors. (In the case of the last two, the canopy probability distribution function is the only one used for a species.)
- **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. Used by the [Gap spatial disperse](#) behavior.

- **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. Used by the [Gap spatial disperse](#) behavior.
- **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. Used by the [Gap spatial disperse](#) behavior.
- **Lognormal Gap X_b** The variance of the lognormal function under gap conditions (see equation below). This is only required if the gap probability distribution function is lognormal. Used by the [Gap spatial disperse](#) behavior.
- **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). Used by the [Gap spatial disperse](#) behavior.
- **Maximum Search Distance for Neighbor Parents, in m**

  The maximum distance that the Anisotropic disperse behavior will look for neighbor parents from a particular point. Used by the [Anisotropic spatial disperse](#) behavior.

- **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](#). Used by all disperse behaviors.
- **Seed Distribution** The distribution method to be applied to seeds (randomization). Used by all disperse behaviors. Choices are:
    - Deterministic - no randomization.
    - Poisson - use the number of seeds as the mean in a Poisson probability distribution function. See the equation above.
    - 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. See the equation above.
    - 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. See the equation above.
    - Negative binomial - use the number of seeds as the mean in a negative binomial probability distribution function. You must then supply a clumping parameter. See the equation above.
- **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. Used by all disperse behaviors.
- **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. Used by all disperse behaviors.

- **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. Used by the [Non-spatial disperse](#) behavior.
- **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. Used by the [Non-gap spatial disperse](#), [Gap spatial disperse](#) behaviors.
- **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. Used by the [Gap spatial disperse](#), [Non-gap spatial disperse](#), and [Anisotropic spatial disperse](#) behaviors. (In the case of the last two, the canopy probability distribution function is the only one used for a species.)
- **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. Used by the [Gap spatial disperse](#), [Non-gap spatial disperse](#), and [Anisotropic spatial disperse](#) behaviors. (In the case of the last two, the canopy probability distribution function is the only one used for a species.)
- **Weibull Canopy Dispersal** The dispersal value for the Weibull function under canopy conditions (see equation below). This is only required if the canopy probability distribution function is Weibull. Used by the [Gap spatial disperse](#), [Non-gap spatial disperse](#), and [Anisotropic spatial disperse](#) behaviors. (In the case of the last two, the canopy probability distribution function is the only one used for a species.)
- **Weibull Canopy Theta** The θ for the Weibull function under canopy conditions (see equation below). This is only required if the canopy probability distribution function is Weibull. Used by the [Gap spatial disperse](#), [Non-gap spatial disperse](#), and [Anisotropic spatial disperse](#) behaviors. (In the case of the last two, the canopy probability distribution function is the only one used for a species.)
- **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. Used by the [Gap spatial disperse](#) behavior.
- **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. Used by the [Gap spatial disperse](#) behavior.
- **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. Used by the [Gap spatial disperse](#) behavior.
- **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. Used by the [Gap spatial disperse](#) behavior.

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.

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 m^2
- 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 m^2
- 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 undergo non-spatial disperse.

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:

$$R_i = \frac{STR}{n} \sum_{k=1}^{T} \left(\frac{DBH_k}{30} \right)^{\beta} e^{-Dm_{ik}^{\theta}}$$

where,

$$n = \int_0^\infty e^{-Dm_{ik}^\theta}$$

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 $k = 1...T$ 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 kth 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,

$$n = \int_0^\infty e^{-0.5\left(\frac{ln(m_{ik}/X_0)}{X_b}\right)^2}$$

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 $k = 1...T$ parent trees within a specified radius of location i
- m_{ik} is the distance (in meters) from point i to the kth 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 variance 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 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.

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.

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.

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. 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.

Anisotropic spatial disperse

Anisotropic spatial disperse allows for a directionality in the seed probability distribution function. Seeds are still evenly distributed at all azimuth angles around a parent tree, but the distance varies with azimuth direction. This behavior can simulate things like prevailing wind direction.

IMPORTANT: This behavior does not yet yield good results and needs tweaking. It is recommended that you NOT use it.

How it works

Extra parameters are added to the Weibull and lognormal probability distribution functions to allow for anisotropy. For Weibull:

$$R_i = \frac{STR}{n} \sum_{k=1}^{T} \left(\frac{DBH_k}{30} \right)^{\beta} e^{\left((D - (\mu \cos(\varphi - \delta)))^* m_{ik}^{\theta} \right)}$$

where

$$n = \int_0^{\infty} e^{(D - (\mu \cos(\varphi - \delta)))^* m_{ik}^{\theta}}$$

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…T parent trees within a specified radius of location i
- *D* is a species-specific dispersion parameter (the **Weibull Canopy Dispersal** or **Weibull Gap Dispersal** parameters)
- m_{ik} is the distance (in meters) from point i to the kth 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)
- μ is the amplitude of the anisotropic effect (the **Amplitude of Anisotropic Effect** parameter)
- φ is the azimuth angle of maximum dispersal distance (the **Azimuth Direction of Max Dispersal Distance, in rad** parameter)
- δ is the azimuth angle from the kth parent tree to point i

For lognormal:

$$R_i = \frac{STR}{n} \sum_{k=1}^{T} \left(\frac{DBH_k}{30} \right)^{\beta} e^{\left[-0.5 \left(\frac{ln\left(\frac{m_{ik}}{X_0 - (\mu \cos(\varphi - \delta))} \right)}{X_b} \right)' \right]}$$

where

$$n = \int_0^{\infty} e^{\left[-0.5 \left(\frac{ln\left(\frac{m_{ik}}{X_0 - (\mu \cos(\varphi - \delta))} \right)}{X_b} \right)' \right]}$$

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 $k = 1...T$ parent trees within a specified radius of location i
- m_{ik} is the distance (in meters) from point i to the kth 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 variance of the function (the **Lognormal Canopy X_b** or **Lognormal Gap X_b** parameters)
- μ is the amplitude of the anisotropic effect (the **Amplitude of Anisotropic Effect** parameter)
- φ is the azimuth angle of maximum dispersal distance (the **Azimuth Direction of Max Dispersal Distance, in rad** parameter)
- δ is the azimuth angle from the kth parent tree to point i

As an example, the lognormal function produces the following graph:
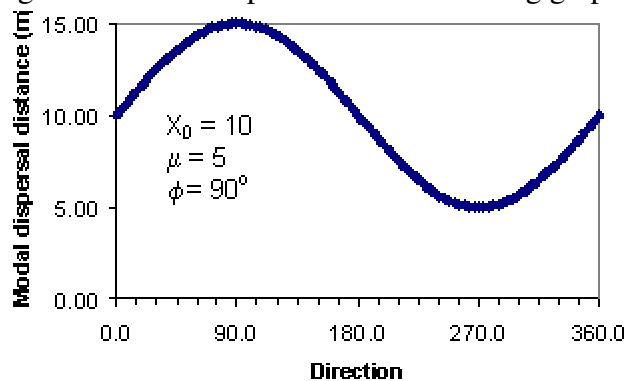
For each grid cell in the [Dispersed Seeds grid](), all neighbor parent trees within a certain radius are found and the appropriate function above is applied to calculate the seed density at that point. That number of seeds is added to the grid cell.

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 cannot be applied to stumps.

Last updated: 22-Aug-2004 08:36 PM

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. Only one predator population can be modeled.

Seed predation parameters

- **Density-Dependent Coefficient** The coefficient describing the effect that density-dependent factors have on the predator population instantaneous rate of change. See equation below.
- **Foraging Efficiency** The predator population foraging efficiency. See equation below.
- **Max Decline Rate in Absence of Food, predators/week** The maximum rate of decline in the predator population in the absence of any food, in predators per week.
- **Max Intake Rate - seeds per predator per day** The maximum number of seeds that can be eaten by one predator in one day.
- **Number of Weeks in Which Seedfall Occurs** The number of weeks at the beginning of the behavior mini-model run that seedfall occurs. The number of seeds that fall is evenly distributed over that number of weeks.
- **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 "Preserve predator densities between SORTIE timesteps" parameter.
- **Predator Population Demographic Efficiency** The seed predator population demographic efficiency. See equation below.

- **Preserve Predator Densies Between SORTIE 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.
- **Proportion of Seeds Removed Each Week During Germination Period** During the period that germination occurs, this is the fraction of the seed pool that is removed due to those seeds having germinated. Expressed as a value between 0 and 1.
- **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.
- **Week During Predation Model Run Germination Begins** The week (timestep) 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.
- **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.

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. 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](#).

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 eaten with equal enthusiasm; the proportions of each type are captured before predation, and any leftover seeds are redistributed according to those proportions. 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
$$O = IR_s * N$$

where

- O is offtake (total number of seeds consumed)
- IR_s is per capita seed offtake
- N is the number of predators

Per capita seed offtake is
$$IR_s = c_s(1 - e^{-(S*D)})$$

where

- c_s is the **Max Intake Rate - seeds per predator per day** parameter
- S is the number of seeds per predator per day
- D is the **Foraging Efficiency** parameter

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, r, is calculated as
$$r = a + d(IR_s) + g(N)$$

where

- *a* is the **Max Decline Rate in Absence of Food, predators/week** parameter
- *d* is the **Predator Population Demographic Efficiency** parameter
- *g* is the **Density-Dependent Coefficient** parameter
- *N* is number of predators

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.

15-Aug-2004 10:11 PM

Establishment behaviors

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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.

Establishment parameters

- **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 [Light Behaviors](#) for more on GLI calculations. Used by the [Light Dependent Seed Survival](#) behavior.

- **Clear Sky Transmission Coefficient** Used to determine the amount of solar radiation seen at the plot location. See [Light Behaviors](#) for more on GLI calculations. Used by the [Light Dependent Seed Survival](#) behavior.
- **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 [Light Behaviors](#) for more on GLI calculations. Used by the [Light Dependent Seed Survival](#) behavior.
- **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. Used by the [Substrate Dependent Seed Survival No Gap Status](#) and [Substrate Dependent Seed Survival With Gap Status](#) behaviors.
- **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. Used by the [Substrate Dependent Seed Survival No Gap Status](#) and [Substrate Dependent Seed Survival With Gap Status](#) behaviors.
- **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. Used by the [Substrate Dependent Seed Survival No Gap Status](#) and [Substrate Dependent Seed Survival With Gap Status](#) behaviors.
- **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. Used by the [Substrate Dependent Seed Survival No Gap Status](#) and [Substrate Dependent Seed Survival With Gap Status](#) behaviors.
- **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. Used by the [Substrate Dependent Seed Survival No Gap Status](#) and [Substrate Dependent Seed Survival With Gap Status](#) behaviors.
- **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. Used by the [Substrate Dependent Seed Survival No Gap Status](#) and [Substrate Dependent Seed Survival With Gap Status](#) behaviors.
- **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. Used by the [Substrate Dependent Seed Survival With Gap Status](#) behavior.
- **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. Used by the [Substrate Dependent Seed Survival With Gap Status](#) behavior.

- **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. Used by the [Substrate Dependent Seed Survival With Gap Status](#) behavior.
- **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. Used by the [Substrate Dependent Seed Survival With Gap Status](#) behavior.
- **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. Used by the [Substrate Dependent Seed Survival With Gap Status](#) behavior.
- **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. Used by the [Substrate Dependent Seed Survival With Gap Status](#) behavior.
- **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. Used by the [Substrate Based Seed Survival With Microtopography](#) behavior.
- **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. Used by the [Substrate Based Seed Survival With Microtopography](#) behavior.
- **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. Used by the [Substrate Based Seed Survival With Microtopography](#) behavior.
- **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. Used by the [Substrate Based Seed Survival With Microtopography](#) behavior.
- **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. Used by the [Substrate Based Seed Survival With Microtopography](#) behavior.
- **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. Used by the [Substrate Based Seed Survival With Microtopography](#) behavior.
- **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. Used by the [Substrate Based Seed Survival With Microtopography](#) behavior.
- **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. Used by the [Substrate Based Seed Survival With Microtopography](#) behavior.

- **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. Used by the [Substrate Based Seed Survival With Microtopography](#) behavior.
- **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. Used by the [Substrate Based Seed Survival With Microtopography](#) behavior.
- **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. Used by the [Substrate Based Seed Survival With Microtopography](#) behavior.
- **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. Used by the [Substrate Based Seed Survival With Microtopography](#) behavior.
- **GLI of Optimum Establishment, 0-100** The GLI value of optimum survival for seeds, as a value between 0 and 100. Used by the [Light Dependent Seed Survival](#) behavior.
- **Height in m At Which to Calculate GLI** The height, in meters, at which to calculate GLI at the center of each grid cell. Used by [Light Dependent Seed Survival](#) behavior.
- **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 [Light Behaviors](#) for more on GLI calculations. Used by the [Light Dependent Seed Survival](#) behavior.
- **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 [Light Behaviors](#) for more on GLI calculations. Used by the [Light Dependent Seed Survival](#) behavior.
- **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 [Light Behaviors](#) for more on GLI calculations. Used by the [Light Dependent Seed Survival](#) behavior.
- **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 [Light Behaviors](#) for more on GLI calculations. Used by the [Light Dependent Seed Survival](#) behavior.
- **Mean Height of Fresh Log Substrate, in m** The mean height of fresh log substrate, in meters. Used by the [Establishment with Microtopography](#) behavior.

- **Mean Height of Mounds, in m** The mean height of mounded areas, in meters. Used by the [Establishment with Microtopography](#) behavior.
- **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 [Light Behaviors](#) for more on GLI calculations. Used by the [Light Dependent Seed Survival](#) behavior.
- **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 [Light Behaviors](#) for more on GLI calculations. Used by the [Light Dependent Seed Survival](#) behavior.
- **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 [Light Behaviors](#) for more on GLI calculations. Used by the [Light Dependent Seed Survival](#) behavior.
- **# 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](#). Used by the [Establishment with Microtopography](#) behavior.
- **Proportion Germinating Between 0 and 1** The proportion of seeds of a species that survive germination, as a value between 0 and 1. Used by the [Proportional Seed Survival](#) behavior.
- **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. Used by the [Substrate Based Seed Survival With Microtopography](#) behavior.
- **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). Used by the [Density Dependent Seed Survival](#) behavior.
- **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. Used by the [Light Dependent Seed Survival](#) behavior.
- **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. Used by the [Light Dependent Seed Survival](#) behavior.
- **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). Used by the [Density Dependent Seed Survival](#) behavior.
- **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. Used by the [Light Dependent Seed Survival](#) behavior.
- **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. Used by the [Light Dependent Seed Survival](#) behavior.

- **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. Used by the [Light Dependent Seed Survival](#) behavior.
- **Standard Deviation of Fresh Log Substrate Height, in m** The standard deviation of height of fresh log substrate, in meters. Used by the [Establishment with Microtopography](#) behavior.
- **Standard Deviation of Mound Height, in m** The standard deviation of the height of mounded areas, in meters. Used by the [Establishment with Microtopography](#) behavior.
- **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. Used by the [Light Dependent Seed Survival](#) behavior.
- **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. Used by the [Light Dependent Seed Survival](#) behavior.

Substrate Dependent Seed Survival No Gap Status

This behavior assesses seed survival based on substrate conditions.

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, above, 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.

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.

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.

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.

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.

The effects of light levels on seed survival is graphed as:
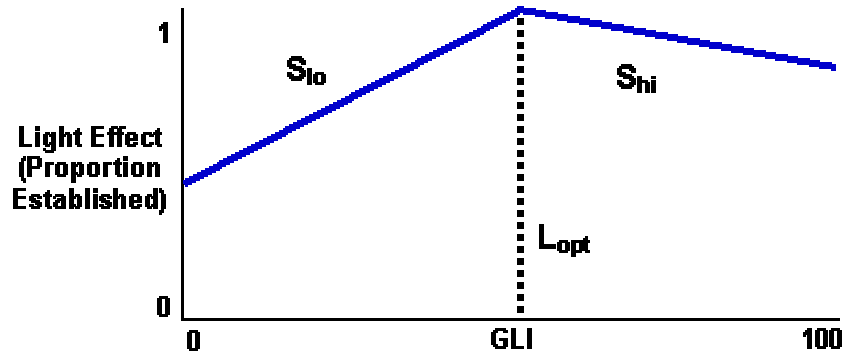
How it works

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.

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.)

The effects of light levels on seed survival is graphed as:
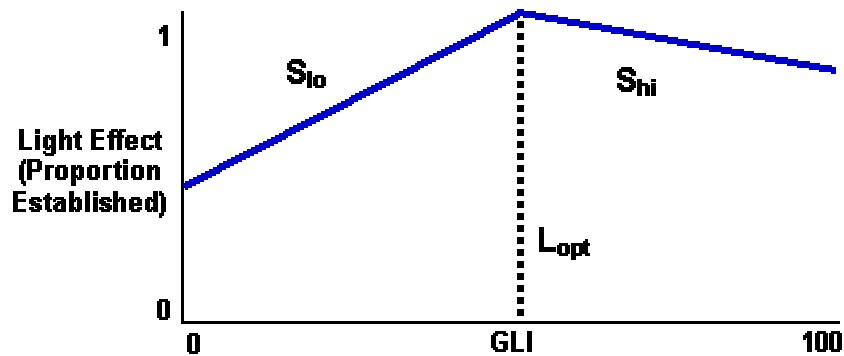
How it works

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.

Density Dependent Seed Survival

This behavior assesses seed survival as a function of the local density of conspecific seeds.

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 become 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.

Proportional Seed Survival

This behavior reduces the number of seeds by a set amount.

How it works

In each cell of the [Dispersed Seeds grid](), this multiples 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.

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.

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

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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

You can apply planting in one of two ways. You can create new planting treatments using the Edit Episodic Events Window by choosing the "Edit->Episodic events" option from the main SORTIE window. If you have existing harvest regime files with planting data from previous versions of SORTIE, you can input them into your run as well. For instructions on how to do this, see the Adding to a parameter file topic.
25-Jan-2005 01:01 PM

Analysis behaviors

In this document:
Analysis parameters
Tree Volume Calculator behavior

[Dimension Analysis behavior](#)
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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.

Analysis parameters

- **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. Used by the [Tree Bole Volume Calculator](#) behavior.
- **Bole Volume Parameter (b0)** The *b0* parameter for the bole volume equation. Used by the [Tree Bole Volume Calculator](#) behavior.
- **Bole Volume Parameter (b1)** The *b1* parameter for the bole volume equation. Used by the [Tree Bole Volume Calculator](#) behavior.
- **Bole Volume Parameter (b2)** The *b2* parameter for the bole volume equation. Used by the [Tree Bole Volume Calculator](#) behavior.
- **Bole Volume Parameter (b3)** The *b3* parameter for the bole volume equation. Used by the [Tree Bole Volume Calculator](#) behavior.
- **Bole Volume Parameter (b4)** The *b4* parameter for the bole volume equation. Used by the [Tree Bole Volume Calculator](#) behavior.
- **Bole Volume Parameter (b5)** The *b5* parameter for the bole volume equation. Used by the [Tree Bole Volume Calculator](#) behavior.
- **Carbon Value - Carbon Amount of Biomass (0-100%)** The percentage of biomass that is carbon, as a value between 0 and 100. Used by the [Carbon Value](#) behavior.
- **Carbon Value - Price Per Metric Ton Carbon** The price per metric ton of carbon. The currency is unimportant. Used by the [Carbon Value](#) behavior.
- **Dimension Analysis Biomass Units** The units of biomass that the chosen biomass equation is expected to produce, based on the parameters entered. SORTIE-ND will use this to convert the biomass value to metric tons (Mg). Used by the [Dimension Analysis](#) behavior.
- **Dimension Analysis Correction Factor** The correction factor needed by some biomass equations that calculate ln(biomass), $\log_{10}$(biomass), or $\log_{100}$(biomass). This value is ignored if the value for the **Dimension Analysis: Use Correction Factor?** parameter for this species is false. Used by the [Dimension Analysis](#) behavior.
- **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. Used by the [Dimension Analysis](#) behavior.

- **Dimension Analysis Equation ID** The biomass equation ID to use when calculating biomass for a particular species. Used by the [Dimension Analysis](#) behavior.
- **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. Used by the [Dimension Analysis](#) behavior.
- **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. Used by the [Dimension Analysis](#) behavior.
- **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. Used by the [Dimension Analysis](#) behavior.
- **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. Used by the [Dimension Analysis](#) behavior.
- **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. Used by the [Dimension Analysis](#) behavior.
- **Dimension Analysis: Use Correction Factor?** Whether or not the chosen biomass equation requires a correction factor to be multiplied by the result. Used by the [Dimension Analysis](#) behavior.
- **Merchantable Timber Value Form Class** The form class of the species. Valid values are 78, 79, 80, 81, 84, and 85. Used by the [Merchantable Timber Value behavior](#) behavior.
- **Merchantable Timber Value Price / 1000 Board Feet** The price per thousand board feet for each species. The currency used doesn't matter. Used by the [Merchantable Timber Value behavior](#) behavior.
- **Taper Equation Initial Multiplier (a0)** The a_0 parameter in the taper equation below. Used by the [Tree Volume Calculator](#) behavior.
- **Taper Equation DBH Exponent (a1)** The a_1 parameter in the taper equation below. Used by the [Tree Volume Calculator](#) behavior.
- **Taper Equation Height Exponent (a2)** The a_2 parameter in the taper equation below. Used by the [Tree Volume Calculator](#) behavior.
- **Taper Equation X Exponent 1 (b1)** The b_1 parameter in the taper equation below. Used by the [Tree Volume Calculator](#) behavior.

- **Taper Equation X Exponent 2 (b2)** The b_2 parameter in the taper equation below. Used by the [Tree Volume Calculator](#) behavior.
- **Taper Equation X Exponent 3 (b3)** The b_3 parameter in the taper equation below. Used by the [Tree Volume Calculator](#) behavior.
- **Taper Equation X Exponent 4 (b4)** The b_4 parameter in the taper equation below. Used by the [Tree Volume Calculator](#) behavior.
- **Taper Equation X Exponent 5 (b5)** The b_5 parameter in the taper equation below. Used by the [Tree Volume Calculator](#) behavior.
- **Taper Equation X Exponent 6 (b6)** The b_6 parameter in the taper equation below. Used by the [Tree Volume Calculator](#) behavior.
- **Diameter-Outside-Bark Constant (a1)** The a_1 parameter in the equation for calculating tree diameter outside bark, below. Used by the [Tree Volume Calculator](#) behavior.
- **Diameter-Outside-Bark First Degree Parameter (a2)** The a_2 parameter in the equation for calculating tree diameter outside bark, below. Used by the [Tree Volume Calculator](#) behavior.
- **Diameter-Outside-Bark Second Degree Parameter (a3)** The a_3 parameter in the equation for calculating tree diameter outside bark, below. Used by the [Tree Volume Calculator](#) behavior.
- **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.

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.

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:

$$D = a_1 + a_2 DBH + a_3 DBH^2$$

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, and enter parameters in the Parameter edit window. *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.

Dimension Analysis

This behavior calculates the biomass of trees based on DBH. This approach comes from [Jenkins et al, 2004](#).

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, and enter parameters in the Parameter edit window. *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.

Tree Bole Volume Calculator

This behavior calculates merchantable tree volume. Make sure to distinguish between this behavior and the other tree volume behavior.

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	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, and enter parameters in the Parameter edit window. *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.

Merchantable Timber Value

This behavior calculates the value of merchantable timber.

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	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

DBH	1 log	2 logs	3 logs	4 logs	5 logs	6 logs
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, and enter parameters in the Parameter edit window. *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.

Carbon Value

This behavior calculates the amount of carbon per species and its value.

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 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.

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Grids

In this document:
Defining grid cell size
Viewing and using grid maps

A grid is a structure for holding model data that varies across space. You can picture a grid by thinking of a spreadsheet. Each cell in the spreadsheet holds a distinct value which is identified by location coordinates (row and column numbers). Behaviors use grids to store data and to share it between behaviors.

Defining 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. Each cell within the grid is a rectangle with a separate X and Y size. 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, and usually do, carry more than one value per cell. Grid cell size applies to all values in the grid. The amount of memory required for a grid cell 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 in the X and Y directions by using the Grid setup window. You do not have to choose the size of a grid's cells; all grids have default values. However, there are times when it makes sense to adjust these values. When choosing a 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 its speed. 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.

Viewing and using grid maps

During the simulation, the model can write out a grid map (the data in a grid) into a detailed output file. You can choose what you would like saved from a grid by using the Output setup window.

Things you can do with grid maps:

- Look at graphical representations of grid maps. To do this, use the model's data visualization capabilities.

- Use them as initial conditions. Since grid values help represent the internal "state" of the model, you can add grid maps to a parameter file for use as initial conditions on another run. For more information, see [Adding to a parameter file](#).
- Look at the values, edit them, and print them out. To do this, use the [Grid setup](#) window.

25-Jan-2005 01:02 PM

Grid list

In this document:
[Basal Area Light grid](#)
[Carbon Value grid](#)
[Dispersed Seeds grid](#)
[Gap Light grid](#)
[GLI Map grid](#)
[Harvest Results grid](#)
[Merchantable Timber Value grid](#)
[Mortality Episode Results grid](#)
[Planting Results grid](#)
[Quadrat GLI grid](#)
[Resource grid](#)
[Seed Predators grid](#)
[Storm Damage grid](#)
[Storm Light grid](#)
[Storm Susceptibility grid](#)
[Substrate calcs grid](#)
[Substrate Favorability grid](#)
[Substrate grid](#)
[Windstorm Results grid](#)

For more on what grids are, see [Grids](#).

Harvest Results

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 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

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

Mortality Episode Results

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 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
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

Storm Damage

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 name	Description
Damage Index	A storm damage index for all storms occurring in the past timestep, from 0 (no damage) to 1 (total damage)
Time Since Last	The number of years since the last storm occurred in this cell. The last

Storm	storm is any storm at all of any strength.

Storm Susceptibility

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)

Quadrat GLI

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

Gap Light

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

Is Gap	Whether (TRUE) or not (FALSE) that grid cell has gap status

Storm Light

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

Basal Area Light

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

GLI Map

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

Resource

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

Substrate

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

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

Dispersed Seeds

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.

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.

Substrate favorability

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 X	The proportion of seeds of Species X expected to germinate in that cell

Planting Results

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

Harvest Type	Type of harvest that occurred in the current timestep - -1 if none has occurred
Planted Species X	Number of trees of Species X cut in the current timestep

Merchantable Timber Value

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

Carbon Value

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

Windstorm Results

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

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The parameter file

In this document:
What is a parameter file?
Contents of a parameter file
Editing a parameter file
Validating a parameter file
Making a human-readable copy of 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

A parameter file is as long as it needs to be, depending on how you want to set up your run. At the least, the parameter file must specify the length of the run (see Run Setup), describe the plot, define the tree species and their attributes, list the behaviors in the order in which they will run, and provide whatever data the behaviors need.

In addition, parameter files can contain very detailed initial conditions in the form of maps of tree and grid data. This data is normally produced in detailed output files. For more on how to add this data to a parameter file, see Adding to a parameter file.

Editing a parameter file

The SORTIE-ND model interface is designed to give you all the tools you need to create and modify your parameter files. You are welcome to view and modify the new parameter files directly, if you wish. They can be opened in any text editor. Be warned, however, that with the XML data format, this is an extremely daunting task and you will never actually need to do it.

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 (Tree Setup to set up the basics of the tree population, Grid Layer Setup to configure grids, Model flow to specify the behaviors to use and in what order, Parameters to provide parameter values, and Output options to set up reporting.

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. It is certainly possible, however, to be working with a parameter file that has a problem of some sort, especially if you started with an existing parameter file instead of from scratch. The file will be validated before you run it, but if you want to do a double-check beforehand, you can either save it from the File menu or view all its parameters in the Parameters window and then click OK. These methods may not catch every problem, but they will catch most of them.

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. The model can make you tab-delimited text versions of your data that you can open in any text editor or spreadsheet program. Unfortunately, there is currently no support for outputting all data at once. If your parameter file contains both parameters and maps, you must convert them separately.

To save your parameter values, use the Edit->Parameters window. 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.

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Detailed output files

In this document:
What is a detailed output file?
Contents of a detailed output file

For more on output, including a guide on what to save, see the topic [Output in SORTIE](#).

What is a detailed output file?

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.

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. Using the example above, here's how you would use a spreadsheet to read map data from timestep three of the "my detailed output.gz.tar" detailed output file:

1. To give context to the map data, you must load the original parameter file using [File->Open file](#). Form the run above, either "testpar.xml" could be used, or its copy in the detailed output file, "my detailed output.xml". If you choose the file "my detailed output.gz.tar" from "File->Open file", you can choose the file "my detailed output.xml" within it.
2. Load the individual timestep file using [File->Open file](#) and choosing "my detailed output.gz.tar". You will be able to choose the individual timestep file within it.
3. Use the [Grid layer setup](#) option or the [Tree setup](#) in the Edit menu to save the files as tab-delimited text. You can then open it from your spreadsheet application or a text editor.

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. 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. (You don't have to use all the maps in the file - more on this later.)
- 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 as described above. 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 Tree setup.

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Summary output files

For more on output, including a guide on what to save, see the topic Output in SORTIE.

The summary output file contains basic summary data for each timestep in the run. It is exactly like it was in previous versions of SORTIE. You choose what data you want SORTIE to save using "Edit->Output options". The choices 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 Trees topic.

You can define areas within the plot to track separately. These are called subplots. These subplots do not have to be continuous, and you can define more than one. In order to define subplots, use the Edit Subplot window. The output options you choose for the main window will apply to the subplots too. You cannot define separate options for them.

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.

Detailed output map files

In this document:
[What are maps?](#)
[Maps as output](#)
[Maps as input](#)
[Creating your own map analyses](#)

What are maps?

Maps are files listing individual values for [trees](#) and [grids](#). Tree maps list individual trees and their attributes (X and Y coordinates, height, etc). Grid maps list some or all of the values held in each grid cell.

Usually, maps are produced as part of [detailed output files](#). These maps are written in the XML data format in plain text. They can be opened directly in a text editor, but due to the data format, it is probably not useful to do so.

Maps as output

The maps represent the model's data in a semi-raw state. You can feed the maps of a [detailed output file](#) directly into the [Data visualizer](#) in order to view them graphically.

Maps as input

If you have all of the tree and grid data from the model as maps, you have the complete data set upon which the simulation was based. This means you can use maps to recreate all or part of the model state and use it as a starting point for a new simulation, possibly with different parameter values. For more information on how to add map data to a parameter file, see [Adding to a parameter file](#).

If you wish to directly enter values for trees and grids, you can do so. For grids, you can enter or change grid values using the [Grid layer setup](#) window. Trees have their own tab-delimited text file format. For details on this format, see [tab-delimited tree maps](#).

Creating your own map analyses

If you would like to take the map data and analyze it in other ways, you can have the model interface output the values into a tab-delimited text format. For grid maps, you can do this in the Edit menu by choosing [Grid layer setup](#); for tree maps, choose [Tree Setup](#). (See those topics for exact instructions.) The tab-delimited text format is for your own use. SORTIE cannot accept it as input.

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Tab-delimited tree maps

You can use tab-delimited tree maps to directly enter tree map data. Tab-delimited text means that columns of data are separated by tabs. You can save files of this type in many programs, particularly spreadsheet programs like Microsoft Excel.

Requirements for 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.

Files must be in plain text with a ".txt" extension.

Using tree maps

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 Tree setup window.

SORTIE-ND will not alter your tab-delimited tree map file.

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 row in the file is assumed to be column headers and is ignored by SORTIE-ND.

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. 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 Tree setup window to view the list. (Case is important.)

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.

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.

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Files from versions of SORTIE prior to 6.01

If you used previous versions of SORTIE, you may have a collection of files you used for runs. This version of SORTIE can read some of those files. (If you have not used

previous versions of SORTIE, this topic is probably irrelevant for you.) Supported file types:

- **Harvest regime files (.hvr)**. A harvest regime file is a specification for harvest and planting for a run. A harvest regime file can be read in once a parameter file has been loaded. The parameter file must have the same species, and in the same order, as the file originally used to create the harvest regime file. In addition, the loaded parameter file must have a number of timesteps at least as large as the timestep of the last harvest or planting event. The old versions of SORTIE relied upon a hard-wired grid cell area for the harvest and planting specifications, while the new version may have a different resolution. SORTIE will make the conversion, but the areas of harvest and/or planting may be slightly different afterwards. To read a harvest regime file, use "File->Open file".
- **Output files (.out)**. Old output files can be viewed in the data visualization functions of the model.

Parameter files (.par). SORTIE-ND versions up to 6.04 support these parameter files. Later versions, including this one, do NOT support .par files. You can download and install a version of SORTIE-ND up to 6.04, and read this topic in its user manual for instructions on how to import your file. You can then save it into a SORTIE-ND parameter file, which can be opened by later SORTIE-ND versions.

Tree map files (.stmf). The format for tree map files from older versions of SORTIE is no longer supported. However, SORTIE-ND does support a different tab-delimited tree map file format. It is easy to manually convert any old .stmf files to the new format using a spreadsheet program such as Microsoft Excel.

All other file types are unsupported.

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Data Visualization

SORTIE runs produce output, which you can then use the SORTIE interface to view graphically. You can view 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 doing with that data. For more on output, including a guide on what to save, see the topic Output in SORTIE. In this document:

Loading an output file for data visualization
Displaying the data from a file
Viewing a chart's raw data
Viewing charts from a run as it progresses
Tips

For details on the chart types available, see [Output Chart Types](#).

Loading an output file for data visualization

You can load a file by choosing the menu option "File->Open Run Output". 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.

Displaying the data from a file

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 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.

Viewing a chart's raw data

You can save the raw data used to make any chart to a tab-delimited text file (suitable for viewing in spreadsheet 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 outout 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.

Viewing charts from a run as it progresses

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. Since SORTIE data visualization can only display the contents of output files, the first step in using this feature is to set up some output files to view. You can see more on individual chart types [here](#), so you can save the appropriate data for the charts you're interested in seeing. For more on the output file types and how to set them up, see either the [summary files](#) or the [detailed output files](#) topics.

2. Once you have completed a parameter file for your run and have set up your output, the next step is to create some output for SORTIE to analyze. 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. To view the output of the current run, it is recommended that you first pause the run. (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.) Then, 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.
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.

Tips

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.

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Output Chart Types

When you create output files, you can use SORTIE's [data visualization](#) capabilities to look at their data in various ways. SORTIE has several chart types that it can create from [detailed output files](#) and [summary output files](#). The chart types that you can view depend on the data you have saved in your output files.

[Customizing, saving, and printing the charts](#)
[Extracting the data to perform your own analyses](#)
[Line graphs](#)
[Histograms](#)
[Tree maps](#)
[Grid maps](#)
[Tables](#)

Customizing, saving, and printing the charts

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.

Extracting the data to perform your own analyses

If you want to perform your own analysis of the data in a detailed output file, you can translate it into tab-delimited text files that you can then open with a spreadsheet. See the topic [detailed output files](#) for instructions on how to do this.

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 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 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.

Histograms

The visualizer can produce a histogram for most tree and grid values in a detailed output file. 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.

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 DBHs of trees in a detailed output file. The tree map does not display seedlings.

The size of the tree circles corresponds to the size of its DBH. The color matches the species in the legend. If a tree is quite small, it may not show up on the map. If your trees do not show up well, you can change the relative sizes of the circles. To do this, enter a new value for the "DBH Scale Factor" and click the "Update Map" button. Larger values make the tree circles bigger; smaller values make them smaller.

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

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.

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 save DBH and tree volume (from the Tree volume calculator behavior), 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 = Volume(T)/(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).

Detailed output files can display specialized tables for the following grids:

- Harvest Results
- Mortality Episode Results
- Carbon Value
- Merchantable Timber Value
- Windstorm Results

If you wish to view these tables, set up your detailed output file to save all the data from your chosen grids.

Last updated: 22-Mar-2006 12:35 PM

Further reading

This list, along with reprints, is also available at www.sortie-nd.org.

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Glossary

Adult tree: A tree whose DBH is at least the minimum DBH for adulthood. See the [trees](#) topic for more.

Allometry: The relationships between various aspects of a tree's size and shape. See the [allometry](#) topic for more.

Basal area: The cross-sectional area of a tree trunk at 1.35 meters (DBH).

Batch: Grouping SORTIE runs together to automatically run consecutively. See the batch topic for more.

BC: British Columbia - Date Creek area, central BC. One of the primary SORTIE field sites. Submodels often contain a version whose simulations are based on field data from BC and are thus intended primarily to simulate BC conditions.

Behavior: A unit of work in the model which makes calculations and updates tree and grid data. A simulation consists of a chosen list of behaviors working in sequence. A behavior usually corresponds to a biological process. See the behaviors topic for more.

Canopy: The branches and leaves of a tree. Synonymous with crown.

Clear cut: A type of harvest.

Crown: The branches and leaves of a tree. Synonymous with canopy.

DBH: Diameter at Breast Height. The diameter of a tree's trunk at a height of 1.35 meters.

Deterministic: Not random; predictable.

Diameter at 10 cm: The diameter of a tree taken at a height of ten centimeters.

Fisheye photograph: A photograph taken with a fisheye lens, which captures a complete hemisphere in two dimensions. A fisheye photograph taken of the sky would see from horizon to horizon in all directions. See the light behaviors topic.

Gap: A small open area in a forest canopy.

Gap cut: A type of harvest.

GLI: Global Light Index. A measure of the amount of light that reaches a certain point in space, expressed as a percentage of full sun. See the light behaviors topic.

GMF: Great Mountain Forest, northwestern Connecticut. One of the primary SORTIE field sites. Submodels often contain a version whose simulations are based on field data from GMF and are thus intended primarily to simulate GMF conditions.

Grid: A way of storing data in SORTIE that varies over space. Grids are the same size as the plot and contain cells which can each contain several values. See the grids topic for more.

Grid cell: A single area in a grid object.

Harvest: Logging.

Julian day: A method for expressing dates. The days in the year are numbered consecutively from 1 to 365.

Juvenile tree: A seedling or sapling tree which has not yet reached adult status. See the trees topic for more.

Parameter file: A file with all of the settings and data needed to run SORTIE. See the parameter file topic for more.

Partial cut: A type of harvest.

Plot: SORTIE's underlying dimensions. See the plot topic for more.

Quadrat: A small grid cell.

Recruitment: The process by which seeds become seedlings.

Release: When a suppressed juvenile tree is exposed to higher light conditions, it is released. Release is characterized by a rapid increase in growth rate. See the growth behaviors topic for more.

Run: The process of the model receiving input and performing calculations for a specified number of timesteps. Synonymous with simulation.

Sapling: A tree at least 1.35 meters in height with a DBH less than the minimum adult DBH. See the trees topic for more.

Seedling: A tree less than 1.35 meters tall. See the trees topic for more.

Senescence: The slight increase in tree mortality seen among very old, very large trees. See the mortality behaviors topic for more.

Short output file: A type of output file which provides summary data for a run. Synonymous with summary output file. See the summary output file topic.

Silviculture: Forestry science. The management of tree harvesting and planting.

Simulation: The process of the model receiving input and performing calculations for a specified number of timesteps. Synonymous with run.

Stochastic: Chaotic, random. Stochastic processes in SORTIE generally make heavy use of the random number generator.

Submodel: In previous versions of the model, these were pieces of the SORTIE model designed to do a specific task in the simulation.

Subplot: A subarea of the plot chosen by the user. This subarea is tracked separately during data analysis.

Substrate: What seedlings germinate in - soil and the organic layers on top of it. See the substrate behaviors topic.

Summary output file: A type of output file which provides summary data for a run. Synonymous with short output file. See the summary output file topic.

Suppression: When juvenile trees are in persistently low light conditions, their growth slows considerably. This is suppression. Different species have different tolerances for suppression; some will die, while some can tolerate being suppressed for decades. See the growth behaviors topic for more.

Tab-delimited text file: An ASCII text file organized as a table, with columns separated by tabs and rows separated by returns.

Timestep: The basic unit of time in SORTIE. Timesteps are defined in years in the parameter file. The basic run cycle is repeated once per timestep. See the run setup and progression topic.

Torus: A donut shape. This is the shape of the forest in SORTIE. See the plot topic.

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