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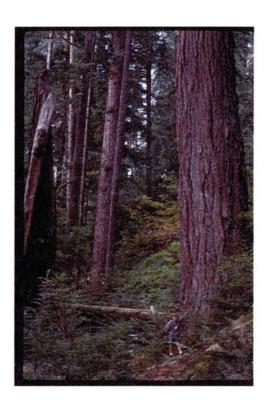


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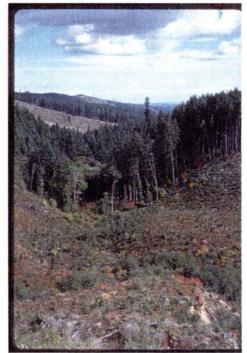
A Users Guide to

STANDCARB version 2.0:

A model to simulate the carbon stores in forest stands.







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Introduction



This user's guide describes the second version of STANDCARB, a model that is designed to simulate the dynamics of living and dead pools of carbon in a forest stand. STANDCARB 2.0 can be used to examine the effects that climate, tree species, succession, wildfire, timber harvest, site preparation, and regeneration success have on carbon dynamics at the stand level. These results are presented in ASCII output files that can be used to

produce carbon yield tables analogous to volume yield tables. While this model also estimates the mass and volume of boles that are removed by harvest, it does not track the fate of that harvested material. Another model should be used for that purpose (e.g., Harmon et al. 1996) to provide the total stand level carbon balance.

The majority of past models used to examine stand level carbon dynamics have been analytical models (Cooper 1983, Dewar 1991). While these models can be used to analyze many general aspects of carbon dynamics, they have difficulty with complicated or real life situations such as thinning and slash removal. Ecological process models (Cropper and Ewel 1987), while more realistic in terms of ecosystem processes than analytical models, are also limited because they can only simulate a fixed mixture of species. This means that fundamental changes such as species succession or replacement due to silvicultural activity cannot be included in these simulations. STANDCARB 2.0 was designed to overcome these restrictions by incorporating the successional features of a gap simulation model (Urban 1993, Urban et al. 1993) with an ecological process model (Harmon et al. 1990). It therefore constitutes a new type of hybrid model.

Temporally, STANDCARB is a difference model that operates on an annual time step for all variables, except those used to estimate the effects of climate on tree establishment, growth, and decomposition. These climate related variables are calculated on a monthly time step. In addition, while disturbances are simulated annually, there are arbitrary semiannual timesteps that occur once the normal growth and decomposition related processes are addressed.

Spatially, STANDCARB is designed to simulate the dynamics of a number of cells within a stand. Each cell represents the area occupied by a single, mature tree (or an area of approximately 0.04 ha). This approach allows the model to have flexibility in terms of species mixtures and/or tree ages, and allows the user to estimate the degree of spatial variation associated with a simulation. This approach is not designed, however, to simulate the actual location of cells on a landscape.

Because STANDCARB 2.0 is designed to operate at the stand level, it has incorporated finer levels of resolution within its computations using a meta-model approach. The meta-model approach is used to capture the overall response of more detailed simulation models of a phenomenon without all the computational burdens entailed in including the full model. For example, to simulate species to species interactions, STANDCARB 2.0 reduces individual to individual tree interactions found in a gap model to upper and lower tree layers. This allows shade tolerant species to replace shade intolerant species or for tree layers to shade out shrub and herb layers. In a similar manner the penetration of light through foliage is simplified from the detailed individual tree profiles found in gap models to a single layer that removes a fraction of the light depending upon foliage mass. The key point in understanding the use of meta-models is that they capture the key aspects of the behavior of interest, but not all aspects. If the question being asked involves the interaction of individuals, for example, then STANDCARB 2.0 may not be an appropriate model to use.

This users guide is designed to explain how to use the STANDCARB 2.0 model to investigate the effects of various types of forest management at the stand level on live and dead carbon stores. We first review the differences between STANDCARB 1.0 and STANDCARB 2.0, then provide installation instructions. This is followed by an overview of the objectives and structure of the model. Examples of facets of the model are given and this is followed by a description of the modules used to run simulations. A brief summary of each of the major sections of the model is then described with particular attention to the equations used for critical calculations. Finally, the types and structures of the input and output files are defined.

Before using the model a final word of caution is in order. STANDCARB 2.0 is a simulation model. As such, it represents our best representation of reality, but the results must be used with caution. There are many factors that may cause the projected results to deviate from what actually occurs. This is no different than the distinction between volume yield projections and the actual harvested volume. Bear in mind each simulation model has a number of tacit assumptions, and when these are not met, the projected results may be entirely misleading. For example, we assume that pathogens do not removed a significant amount of carbon, but in some stands this is not the case. It may also be the case that the simulations are correct in a relative sense but not in an absolute sense. When interpreting results bear in mind that relative differences will always be more robust than absolute differences. Finally, it must be kept in mind that simulation models are only tools to be used primarily for planning or understanding how system works. They are not a substitute for actual measurements of the actual forest carbon stores of a particular stand.

Changes in STANDCARB Version 2.0

The original version of the STANDCARB model (Ver. 1.0) was modified to make it more flexible, realistic, and convenient to use. These changes include:

- Additional silvicultural treatments such as the selection of species, herbicide treatment to remove species, and timber salvage have been added to the HARVEST module;
- 2) Species-specific harvested volumes are reported in the Volume.out file;
- 3) An estimate of the number of trees that are present at any time or that are harvested is computed by a new module called DENSITY and is reported in the Total.out and Volume.out files, respectively. This data can be used to determine the mean volume of trees and assign size-specific economic value;
- 4) Canopy interception was changed to account for canopy storage of water in the CLIMATE module;
- 5) A maximum fraction of cells that are colonized by trees can be set to mimic situations where tree cover is not complete. This was added to the PLANT module;
- 6) The addition of rotten heartwood or heart-rot to the GROWTH module and Live.out file;
- 7) A hydraulic limitation on Gross Primary Production that is based on tree height was added to the GROWTH module;
- 8) A change of mortality rates in the single-cell mode so that it converges on the multicell version was made in the MORTALITY module;
- 9) The stable soil pool was divided into stable pools that are specific to dead leaf, dead wood and stable soil;
- 10) A time lag between the production of detritus and the next recipent pool was added to the DECOMPOSE module. This includes the fall of snags, the decay of wood from a salvageable to unsalvageable state and the formation of stable pools;
- 11) Snags and logs were separated in the DECOMPOSE and CLIMATE modules to account for macroclimate differences between these two positions;
- 12) Sprouting of trees that are disturbed was addressed in a new module called SPROUT;
- 13) Multiple runs in a simulation was added with the output of each run appended within the output files;
- 14) The files used in each simulation run are now output in a file called Summary.out. The user can examine this file to see exactly what the settings were used for a given simulation.

In addition to these changes, there have been minor changes to the input and output files. Headers have been added to help the user determine what the columns represent. There have also been changes in the data contained within each file and therefore the user is advised to compare the new files with those from version 1.0 as the older files may not be compatible with version 2.0. The main changes in files have been for the parameter (PRM) and output files (OUT), however, some driver file formats have changed, particularly the Simul.dvr file. The extension of driver files have been changed from drv to dvr (to avoid overlapping a common file types used by Windows operating systems).

Installation Instructions for StandCarb version 2.0

STANDCARB version 2.0 has been built to run any of these operating systems: Windows 95, Windows 98, Windows NT.

 To use STANDCARB with data in different directories, the user should install STANDCARB in a directory that is in the user's PATH environment variable. This simplifies maintenance since there is only one copy of a version located on a computer.

This directory may either be an existing directory already in the PATH variable, or it may be a new directory that the user creates and adds to the variable. The user can name the directory whatever she wishes; the examples in the rest of these instructions will the sample directory "C:\apps\models".

2. Copy the program file "StandCarb-v2-0.exe" from the floppy disk to this PATH directory; for example,

```
C:\> copy A:\StandCarb-v2-0.exe C:\apps\models
```

- 3. If the user wishes to continue to have the previous version of STANDCARB (version 1.0) available, move its executable file from wherever it's located on the computer to the PATH directory where version 2.0 is. Use the same naming convention to distinguish between the different versions; therefore, version 1.0's executable file should be named "StandCarb-v1-0.exe".
- 4. Create a DOS batch file called "StandCarb.bat" in the PATH directory where the various version(s) of STANDCARB are located. The contents of this batch file should be:

```
@echo off
standCarb-v2-0.exe %1 %2 %3 %4 %5 %6 %7 %8 %9
```

This batch file allows the user to access the latest version of STANDCARB by simply using "StandCarb" at the DOS prompt, e.g.,

```
C:\some_data_directory> standCarb
```

If the user wants to access a particular version of STANDCARB, she can explicitly specify the version on the command line; for example,

```
C:\some data directory> standCarb-v1-0
```

5. In addition to running STANDCARB from the DOS prompt, the user can also start STANDCARB while viewing a data directory with Windows Explorer. The user first needs to copy the DOS batch file called "run_StandCarb.bat" from the floppy disk to the data directory. This batch file contains these lines:

```
@echo off
StandCarb
echo.
pause
```

This batch file invokes the batch file "StandCarb.bat" created in the previous step.

To run STANDCARB from Windows Explorer, the user simply double clicks on the "run_StandCarb.bat" file in the data directory. If the user should need to edit this batch file, select the file in the Explorer window, click the **right** mouse button, and select "Edit" from the pop-up menu. This will open the batch file with Windows Notepad accessory.

Model Overview

OBJECTIVES



The object of STANDCARB 2.0 is to simulate the accumulation of carbon over succession in mixed species, mixed aged forest stands. This version of the model is parameterized for stands in the Pacific Northwest. There is no reason, however, that it could not be used for other types of forests as well. The model can be used to investigate the stand level effects of various regeneration strategies, effects of thinning, herbiciding, salvage, patch cutting, tree

species replacement by design or by natural succession, site preparation, and wildfires.

The model provides output on seven live state variables, nine detritus (partially decomposed) state variables, three stable (highly decomposed) state variables, and three variables related to the volume harvested (see Output files section for more details). In addition, sums of the various state variables are output. The state variables are saved as means and standard errors of the mean for each year. Values for each cell for each year are deliberately not saved because the model is not designed to spatially distribute results over a landscape. In other words, STANDCARB 2.0 is not a landscape model, although it can be used to estimate the degree of variation within a stand.

BASIC APPROACH

The approach used in STANDCARB 2.0 is to utilize the features of a gap model to simulate species composition and the structure of an ecosystem "process" model to simulate the growth, mortality, and decomposition of plants within a plot. As with gap models, a simulation run does not consist of single plot. Rather a stand is simulated by running many replicate plots or cells which are then averaged to predict stand level values. If one chooses to use the single cell mode, the model is reduced to the approach of a typical ecosystem model. The user should be aware, however, that the single cell mode cannot always produce the same patterns as the multicell mode, in part, because the interaction of cells causes new behaviors to emerge.

STANDCARB has a number of levels of organization that it uses to estimate changes in carbon stores within a stand (Figure 1). At the highest level there are a number of cells, each which contains up to four layers of vegetation each having up to seven parts, nine

detrital **pools** and three stable soil carbon pools. The four layers of vegetation that can occur in each cell are upper trees, lower trees, shrubs, and herbs. The two tree layers can have different species, whereas the shrub and herb layers are viewed as each representing a single "species". Each cell can have any combination of layers except that lower trees can only occur when upper trees are present.

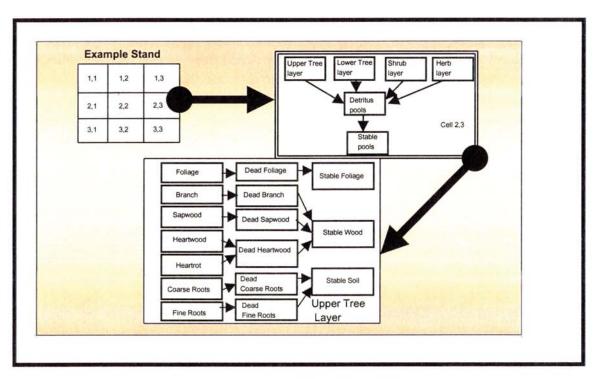


Figure 1. Overall conceptual strucure of STANDCARB 2.0.

Each of the layers can potentially have seven live **parts**: 1) foliage, 2) fine roots, 3) branches, 4) sapwood, 5) heartwood, 6) coarse roots, and 7) heart-rot. Of course to make the layers correspond to the actual structure of certain life forms, herbs are restricted from having woody parts and shrubs can not have heartwood or heart-rot (as they do not form a bole). All the live parts correspond to parts typically reported in the ecological literature with the exception of the bole. The later would be composed of sapwood, heartwood, and heart-rot. In our model heartwood includes the heartwood and the outer bark as these are non respiring, decay-resistant layers. The sapwood includes the sapwood and the inner bark layers as these are respiring and decompose relatively quickly compared to outer bark or heartwood. Heart-rot represents the portion of the heartwood that is being degraded by parasitic and saprophytic fungi inside the living trees.

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Each of the live parts of each layer contributes material to a corresponding detrital or dead pool. Thus foliage adds material to the dead foliage, fine roots to dead fine roots, branches to dead branches, sapwood to dead sapwood, heartwood and heart rot to dead heartwood, and coarse roots to dead coarse roots. Rather than have every plant layer in each cell have its own detrital pool, we have combined all the inputs from the layers of the cell to form a single detrital pool for each plant part. For example, the foliage from the four plant layers feeds into a single dead foliage pool. We have also separated dead sapwood and dead heartwood into snags versus logs so that the effects of position on microclimate can be modeled. Snags and logs are further divided into salvageable versus unsalvagable fractions so that realistic amounts of dead trees can be removed during simulated salvage operations. To introduce time lags into these detrital pools, we have divided each pool into cohorts. Finally, all the detritus pools in a cell can potentially add material to stable pools. The objective is to simulate a pool of highly decomposed material that changes slowly and is quite resistant to decomposition.

COMPUTING ENVIRONMENT.

STANDCARB 2.0 can be run in Microsoft WINDOWS 3.2, 95, or more advanced operating system. This version of the model is compiled using Visual C^{++} .

MODEL MODULE OVERVIEW

STANDCARB 2.0 consists of a number of modules which perform specific functions (Figure 2). The following section describes the general purpose of each module. A fuller description of each can be found under the Model Documentation section.

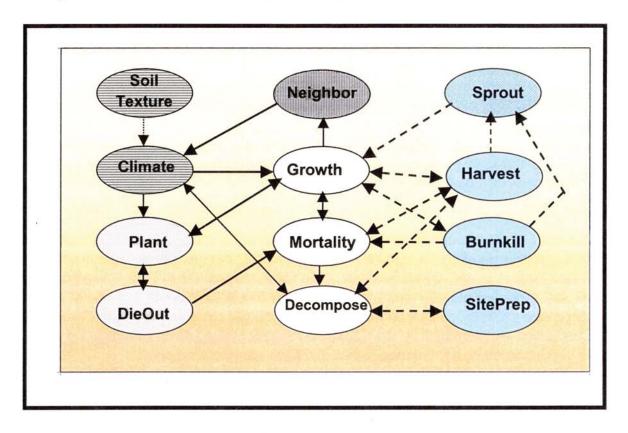


Figure 2. Modules and flow of information in STANDCARB 2.0. Dashed arrows indicate information flows that do not occur each timestep, whereas solid lines indicates those that do. Modules with similar shading perform similar tasks.

CLIMATE. The purpose of this module is to determine the effect of climate on tree species, growth, and decomposition. In addition to these functions, CLIMATE is used to calculate the angle of the sun used in the NEIGHBOR module.

SOILTEXTURE. This module is used to calculate the effects of soil texture, depth and rockiness on the water holding capacity of soils. These results are used by the CLIMATE module.

PLANT. This module determines which layers and tree species can be planted in a cell. Herb and shrub layers are planted into each plot based on a fixed probability influenced by the presence of a tree layer. The upper tree layer is planted before the lower tree layer. If a tree layer is planted this module also determines which species will establish. The

probability of a tree species colonizing a site is a function of shade tolerance, temperature, moisture limits, and the local abundance of a species in a life zone.

DIEOUT. The purpose of this module is to determine when the upper tree layer will completely dieout in a plot. This reflects the fact that above a certain tree age, each cell is dominated by a single tree. When this tree dies, the underlying tree layer grows faster and replaces the old upper tree layer. This in turn allows the establishment of new lower tree layer. Combined with PLANT, the DIEOUT module allow STANDCARB 2.0 to simulate species replacement during succession.

SPROUT. This module determines if a tree sprouts from its roots once it has died aboveground. For tree species unable to sprout, all parts die when the tree dies. For species capable of sprouting, there is a probability that the tree will survive in a cell even if the aboveground portions of the tree are killed by harvest, herbicide, and/or fire. If the tree sprouts then the belowground parts of the tree are kept alive and a small fraction of the foliage is allowed to survive so that the aboveground portions of the tree can regrow.

GROWTH. This module determines the rate that living plant parts grow in a cell. The living parts tracked by the GROWTH module include foliage, branches, sapwood, heartwood, heart-rot, coarse roots, and fine roots. In addition to these seven plant parts, this module computes the total live mass and the live bole volume. The rate of growth is dependent upon the amount of foliage within a cell and the maximum rate of net production as determined by the CLIMATE module. The growth of foliage for each layer is dependent on its light extinction rate and light compensation point.

MORTALITY. This module determines the rate of detrital production when a plot has not been harvested or burned. For foliage and fine roots, a fixed proportion is assumed to die each year. These proportions will be functions of the species (e.g., deciduous trees and herbs lose all their leaves each year). The proportion of boles, branches, and coarse roots lost to mortality or pruning is a function of the light environment, as calculated in GROWTH, so that as the light passing through the foliage of a layer approaches the light compensation point, the mortality rate reaches a maximum. The mortality function also determines the proportion of trees dying from natural causes that form snags versus logs. This is a function of the ecoregion and the age of the forest.

DECOMPOSE. This module determines the balance of inputs from normal mortality, harvesting and fires, and the losses from decomposition and fire. These balances are calculated for each of the eight detritus pools (dead foliage, dead fine roots, dead coarse roots, dead branches, dead sapwood, and dead heartwood; the latter two subdivided into snags and logs) and three stable pools (stable foliage, stable wood, and stable soil organic matter). In addition to these 11 pools, this module calculates total detritus (excludes stable pools), total stable, and total dead stores. MORTALITY, HARVEST, and BURNKILL are used to calculate detritus inputs. The rates of decomposition of each pool are determined by the species contributing detritus to a plot, and climatic effects as calculated in the CLIMATE module. Losses from fires are determined by the SITEPREP module.

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The user has the option to track detritus pools as cohorts or to combine all cohorts into one pool. The advantage of the cohort mode is that lags in the formation of stable pools or lags associated with the decomposition of sapwood and heartwood and snag fall can be accounted for during simulations. In the non-cohort mode there are no time lags, thus stable organic matter can form the first year after input into a detritus pool.

DENSITY. This module approximates the number of stems of trees. This approximation is based on the minus 3/2 thinning "law", although other factors such as the minimum number of trees possible and effects of thinning have also been taken into account.

HARVEST. This module determines if the plot is to be harvested, salvaged, or herbicided and the amount of live plant parts removed from the forest and the amount added to detrital pools. Types of harvest simulated are precommercial thinning, commercial thinning, clear-cut, and timber salvage harvest. Each of these harvest types can be conducted in a subset of the cells or in all the cells and in the case of live trees can be for one or more target species. For each simulation, the user can set three levels of utilization standards (the amount cut and removed). Only sapwood and heartwood (i.e., boles) either alive or dead can be removed from the simulated forest. In the case of salvage (i.e., removal of dead wood) the user can determine the size of the pieces to be salvaged as well as the extent of decay that is acceptable. All other living pools (leaves, branches, fine roots, and coarse roots) are transferred to the appropriate detrital pools after a harvest.

SITE PREP. This module determines the effect of site preparation following harvest on detrital pools. Three levels of detrital reduction can be specified in each simulation run. This module is also used to determine the effects of wildfires.

BURNKILL. This module is used to determine the amount of the living layers that is killed by site preparation fires or by wildfires. As with SITEPREP, three levels of fire severity can be specified in each simulation run.

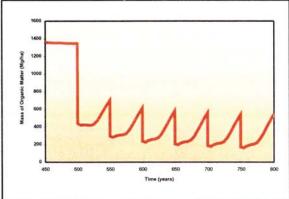
NEIGHBOR. The purpose of this module is to determine the overall light environment of a cell and the interaction with neighboring cells. The degree of blocking of direct and diffuse light is determined by the relative tree and topographic height of cells. Height of the upper tree layer is a function of the age of that layer in a cell.

Example Simulations

The following section illustrates features of the STANDCARB model using output from selected simulations. The model output files (i.e., ascii text format) were imported into a graphics software to produce the figures. Note that these figures are for illustrative purposes only and should not be used to estimate real carbon balances!

Comparing Silvicultural Strategies

The primary purpose of the STANDCARB model is to allow the user to compare the effect of various types of silvicultural treatments on carbon stores in forest ecosystems. For example, one might want to compare the effect clear cutting on a 50 year rotation to an old-growth ecosystem (Figure 3). These particular figures would be typical of a Douglas-fir forest of medium productivity. The results shown indicate that converting from an old-growth ecosystem to an intensively managed system would release carbon for a 200 year period.



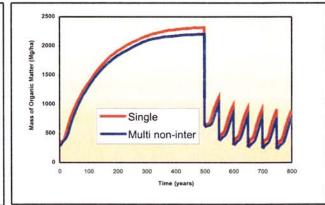


Figure 3. Effect of converting from old-growth to 50 year rotation on total organic matter stores.

Figure 4. Comparison of single cell and non-interactive multicell versions. Douglas-fir was the only species present in these simulations.

Single Cell Versus Multicell Versions

Although the single cell version of STANDCARB can be used to give a fast, preliminary idea of how a silvicultural treatment will store carbon, there are several advantages to using the multicell version of the model. The first is that species mixtures are allowed to change over time in the multicell version. The results of these two versions are quite similar when the species in the upper and lower tree layers are the same and the interactive, multicell mode is used (Figure 4). There are, however,

significant effects of cell to cell interactions (see below) that need to be considered. The single-cell version cannot mimic the effects of species succession (Figure 5).

Variation in the Multicell Version of STANDCARB

An important aspect of the multicell version is that it is stochastic. That is, when the model is run in this mode and given a new random number seed, it will produce a slightly different output each run (Figure 6). This element of "randomness" is important during forest development and important to recognize. By using the multicell version of the model and running a scenario with a new random number seed each time, one can generate "data" to test effects of treatment using statistics such as analysis of variance. Even if one does not wish to use statistics to test the outcome of the experiments it is still important to run the model at least 5 times to get an average response. Notice that in Figures 6 that each run generally parallels the mean value, but there are times when individual runs are quite a bit higher or lower than the mean.

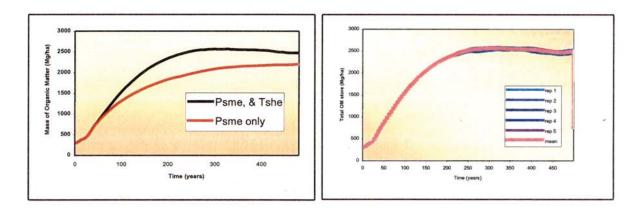
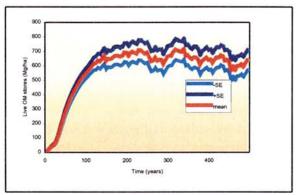


Figure 5. Multicell versions with Douglas-fir versus a mixture of Douglas-fir and western hemlock.

Figure 6. Multicell individual simulation runs and their mean.

Another feature of the multicell version of the model is that the internal variation of the stand being simulated can be computed (Figure 7). Internal variation is an important part of the multicell version and enters the simulation because cells can be colonized at different times by different species and/or the upper tree layer in cells can be replaced by lower trees at different times. This reflects the patchiness of a real forest, which is not the homogenous tree layer assumed in the single cell version. For most of the output files the mean as well as the standard error of the mean is computed. Figure 7 was prepared by adding and subtracting one standard error of the mean from the mean value. Notice that the variation about the mean increases with time in these figures, indicating that the formation of tree gaps caused by upper trees dying is causing

variation to increase. Plotting the standard errors of a single run is not the same as plotting multiple runs; therefore averaging several runs is the soundest strategy to assess the effect of a silvicultural treatment.



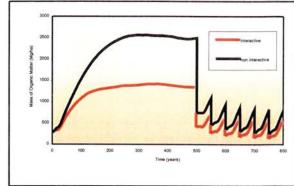


Figure 7. Live organic matter for a multicell simulation with mean and plus and minus a standard error for a single simulation run.

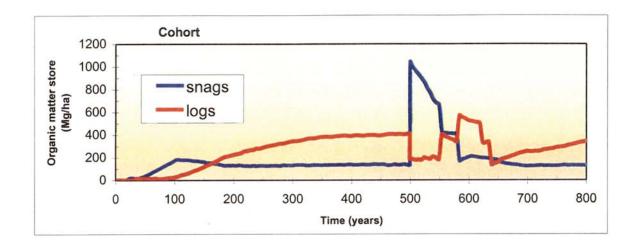
Figure 8. Comparison for multicell simulations with and without cell by cell interactions.

Interactive Versus Non-Interactive Mode

Within the multicell version of the STANDCARB model it is possible to run simulations that have the cells act independently (noninteractive mode) or to have the cells interact through shading. The latter mode is probably the most realistic, in that it allows cells with larger trees to shade cells with smaller trees. This might be important if a species, such as Douglas-fir, requires a certain sized opening to regenerate. In the non-interactive mode shade intolerant species might be able to replace themselves, however, when one cell can shade another this might not be the case. In the example presented here we find that for a cell width of 15 m, cell to cell interactions lead to a total carbon store that is substantially less than in the noninteractive mode (Figure 8).

Cohort versus Non-Cohort Mode

A new feature of STANDCARB 2.0 is that it allows the user to select using a cohort structure to follow decomposition dynamics. The advantage is that the cohort model allows for lag times to be included. For example, after a disturbance a large pulse of snags may be added. In the non-cohort mode this new detritus will start to contribute to the log pool the following year. In reality it may take many years before snags fall. The cohort mode allows one to track these changes cause by major disturbances more realistically (Figure 9).



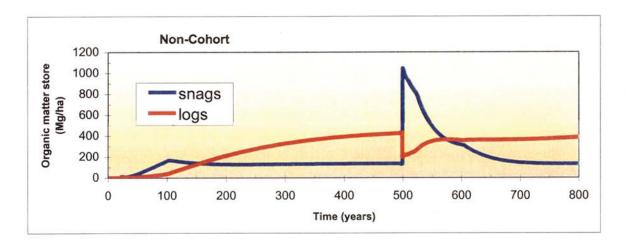


Figure 9. Contrast of cohort versus non-cohort modes for snags and logs. Notice that as long as disturbances are small the results are similar. Large pulses from a fire in year 500, however, are more realistically simulated by the cohort mode.

Model Documentation

This section describes each of the main model modules in detail. For each of the model modules we describe the overall purpose, the functions it contains as well as the computations used and the logic behind them, and the input data and parameters required.

Given that STANDCARB 2.0 is programmed in an object-oriented computer language, we have been able to use one Class of programming objects to compute changes in state variables at the cell, layer, part, and pool level depending upon the desired level of resolution. Rather than describe each of these levels, we have tried to describe the level that pertains to all the underlying levels. For example, the equation describing the balance of inputs and losses for all detritus layers is the same regardless of the cell number, species, layer, or detritus pool involved. We have therefore described this equation generically.

Naming Conventions.

The following conventions are used throughout this section:

- 1) All model modules are indicated by full capitalization of the name (e.g., CLIMATE).
- 2) All variables, parameters and state variables are indicated with capitalized letters for each significant part of a name (e.g., DeadBranch, TempOpt).
- 3) In cases where a variable or parameter could pertain to more than one living layer, plant part, detritus pool, or cohort, we have added the name of that layer, part, or pool to make the overall name (e.g., DeadBranchTempOpt).
- 4) When we are referring to a general set of calculations for all the living layers or detritus pools we have added *Layer*, *Part*, *Pool*, *Cohort*) to make the overall name (e.g., *Pool*TempOpt).
- 5) There are also a number of variables that apply to different time steps. We have therefore used the prefix *Hour* for variables calculated hourly, *Mon* for those calculated monthly, *Total* for those summed over a year, and *Annual* for those averaged over a year.

Model Module Descriptions

The following sections describe the calculations and assumptions of each module used in

The following sections describe the calculations and assumptions the STANCARB model.	of each module used in
CLIMATE	
SOILTEXTURE	
PLANT	
DIEOUT	
SPROUT	
GROWTH	
MORTALITY	
DECOMPOSE	
DENSITY	
HARVEST	
BURNKILL	
SITEPREP	·
NEIGHBOR	

CLIMATE



The purpose of CLIMATE is to estimate the effect of temperature, precipitation, and radiation on the establishment of tree species, growth of plants, and decomposition of detritus. The data used to drive these estimates are found in the Climate.dvr and Locate.dvr files.

This module contains 15 functions. The TempConvert and DegreeDays are calculated once at the start of each simulation and used

for all the cells in a stand. The functions that estimate interception (CanInterception, LogIntercept, ForFloorInterception, and Total Interception), water stores (PET & Transpire, WaterStore, and WaterPot), the effects of climate on decomposition (MoistDecayIndex, TempDecayIndex, and AbioticDecayIndex) as well as growth (TempProdIndex, MoistProdIndex, and ProdIndex) are calculated each month on each cell. The variables are named using differing prefixes depending upon the time step used and whether they are annual averages or totals. Variables calculated on a monthly time step have the prefix *Mon*. Variables that are averaged over the year have the prefix Annual, and those that are yearly totals have the prefix TotalAnnual.

The variables calculated in this module are used by the PLANT, GROWTH, DECOMPOSE, and NEIGHBOR modules. To keep the time step the same as used in these modules the output information has been converted to annual means or summaries depending on the variable.

TempConvert Function.

This function converts mean daily temperature based on a 24 hour period into the mean day time temperature required by the TempProdIndex function. Temperature is converted to the mean daytime temperature using the mean monthly 24 hour temperature (Temp24) and the mean maximum temperature (TempMax):

MonTempDay = 0.212* (MonTempMax-MonTemp24) + MonTemp24

where MonTempDay is the daytime temperature.

For the purposes of computing the respiration costs of living plant parts, the mean annual temperature (MeanAnnualTemp) is computed from the *Mon*Temp24 values.

DegreeDays Function.

This function computes the degree days for the site. This is computed once per simulation run. The degree days (DDays) is the sum of all temperatures for all the days exceeding 5.56 C. To compute DDays we first compute the mean daily temperature from the mean monthly values stored in the CLIMATE.dvr file. This is done by linearly interpolating between the midpoint of each month. The daily change in temperature between each month is:

TempChangeMon1 = Temp24Mon2-Temp24Mon1/JulianMon2-JulianMon1

where these are the daily temperatures (Temp24) for the respective months and the Julian day of the midpoint of months 1 and 2. Given the daily rate of change, the Julian day, and the mean monthly temperature the daily temperature (TempDaily) is computed:

TempDaily = TempMon1 + TempChangeMon1*(Julian-JulianMon1)

where Julian is the Julian day, and the other variables are as defined above. The total degree days is then computed by adding all the temperatures of the days exceeding 5.56 C.

CanInterception Function.

This function calculates the amount of canopy interception based upon the plant life-form, mean monthly precipitation, and the mass of foliage as calculated in the GROWTH module. Each layer occupying a cell is capable of intercepting precipitation (Figure 10).

The interception rate generally decreases with increasing precipitation (Rothacher 1963). This relationship is simulated by:

MonLayerCanIntRate = LayerCanopyInterMin +(1- LayerCanopyInterMin)*Exp(-0.75*MonLayerPrecip)

where Layer Canopy InterMin is the minimum interception per Mg of foliage as set by the user in the Grow Layer.prm file and MonLayer Precip is the amount of precipitation falling through a layer.

The interception by each layer also increases linearly with increasing foliage mass. This simulates the increase in interception observed with stand age and density (Ward and Robinson 1990). As leaf mass varies seasonally for some species, canopy interception also varies monthly depending on the life-form. Deciduous trees (i.e., those trees with a foliage turnover rate of 1.0 in the Mort.prm file), herbs, and shrubs have minimal interception (5%) during the non-growing season (i.e., the months of November through April). In contrast, evergreen trees have the potential for high interception year round. The

proportion of precipitation intercepted by foliage of all the layers in a given month and cell is:

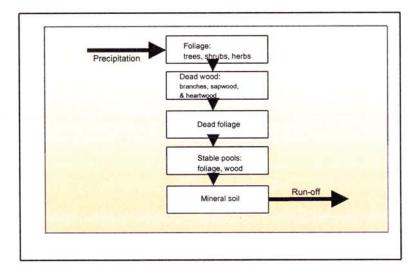
 $MonCanInterception = MonPrecip* \Sigma (MonLayerCanIntRate*LayerFoliage)$

where *Layer*Foliage is the mass of foliage for a particular layer in a cell. Canopy throughfall is the fraction of the precipitation that is not intercepted by the canopy:

MonCanThroFall=MonPrecip-MonCanInterception

where *Mon*CanThroFall is the amount of precipitation allowed to pass through the canopy each month and *Mon*Precip is the mean monthly precipitation as defined by the Climate.dvr file.

LogIntercept Function.



This function estimates the amount of interception from the deadwood pools including those associated with snags, logs, and stable wood from their mass as calculated in the DECOMPOSE module. It also adjusts the interception as a function of the maximum moisture content of the woody material.

Figure 10. Interception and stores of water in STANDCARB model.

The first step is to calculate the projected area of each dead wood pool from its mass:

PoolProArea = PoolAreaMassRatio*Pool/100

where *Pool*ProArea is the projected area in percent of the cell surface area, and *Pool*AreaMassRatio is the ratio of projected area to mass of the woody detrital pool. The latter parameters are found in the DecayPool.prm file. Pool can be either SnagSapwood, SnagHeartwood, LogSapwood, LogHeartwood, DeadBranches, or StableWood.

The next step is to calculate the amount of *Mon*CanThroFall intercepted by the woody detrital pools. The amount intercepted is a function of the maximum potential interception based on area (MaxPotInterceptionArea) and the maximum potential based on the storage capacity (MaxPotInterceptionCap). The maximum potential interception based on area is:

MaxPotInterceptionArea = PoolProArea * MonCanThroFall

where *Pool*ProArea is the projected area of a pool and *Mon*CanThroFall is the monthly canopy throughfall as calculated above. The maximum potential based on the storage capacity (MaxPotInterceptionCap) is calculated first by calculating the maximum storage capacity of the woody detritus pool:

MaxStoresCap = StoresMax- StoresAct

where the maximum possible water store is:

StoresMax=Pool*PoolMoistStoreMax/100

where *Pool*MoistStoreMax is set in the DecayPool.prmfile. The actual current water stores is:

StoresAct=Pool*MonPoolMoist/100

where *Mon*PoolMoist is calculated by the CLIMATE WaterStore function. The maximum potential interception based on storage capacity is:

MaxPotInterceptionCap=MaxStoresCap/100

assuming there are 100 Mg/ha of water in 1 cm of precipitation.

The amount of canopy throughfall (MonCanThroFall) intercepted by the woody detritus pools depends on the relationship of the maximum potentials based on area and storage capacity. If MaxPotInterceptionArea is less than or equal to MaxPotInteceptionCap then:

MonPoolInter=MaxPotInterceptionArea

If, on the other hand, MaxPotInterceptionArea is greater than MaxPotInterceptionCap, then:

MonPoolInter=MaxPotInterceptionCap

This relationship assures that the detritus pool can not absorb more water than the detritus pool can store. The last step is to calculate the amount of canopy throughfall that is passed

on to the forest floor. The amount added to the forest floor each month as log throughfall is:

 $MonLogThroFall = MonCanThroFall - \sum MonPoolInter$

The total interception by the dead woody pools is:

 $MonLogInteception = \sum MonPoolInter$

ForFloorInterception Function.

This function estimates the amount of interception by the dead foliage pool (DeadFoliage) as well as a stable carbon pool (StableFoliage) derived from dead foliage. Water is first removed by the DeadFoliage pool; whatever is passed through this layer is partially removed by the StableFoliage pool. The amount intercepted by each pool is a function of the mass as calculated in the DECOMPOSE module and the maximum moisture content of the detrital pool.

We assume that until a certain mass, these pools do not cover the cell surface completely. If these pools are less than or equal to 3 Mg/ha, the projected area is calculated as:

PoolProArea = PoolAreaMassRatio*Pool/100

where *Pool*ProArea is the projected area of either the dead foliage or stable pool and *Pool*AreaMassRatio defines the relationship between mass and projected area as defined in the DecayPool.prm file. If on the other hand the mass exceeds 3 Mg/ha then

PoolProArea=1.0

The amount intercepted by the dead foliage and stable foliage pool each month is a function of the maximum potential interception based on area (MaxPotInterceptionArea) and the maximum potential based on the storage capacity (MaxPotInterceptionCap). The maximum potential interception based on area is:

MaxPotInterceptionArea=PoolProArea*MonLogThroFall

where *Pool*ProArea is the projected area of a pool and *Mon*LogThroFall is the monthly log throughfall as calculated above. The maximum potential based on the storage capacity (MaxPotInterceptionCap) is calculated first by calculating the maximum storage capacity of the woody detritus pool:

MaxStoresCap = StoresMax- StoresAct

where the maximum possible water store is:

StoresMax=Pool*PoolMoistStoreMax/100

where *Pool*MoistStoreMax is set in the DecayPool.prm file. The actual current water stores is:

StoresAct=Pool*MonPoolMoist/100

where *MonPool*Moist is calculated by the CLIMATE WaterStore function. The maximum potential interception based on storage capacity is:

MaxPotInterceptionCap=MaxStoresCap/100

assuming there are 100 Mg/ha of water in 1 cm of precipitation.

The amount of log throughfall (MonLogThroFall) intercepted by these dead foliage related pools depends on the relationship of the maximum potentials based on area and storage capacity. If MaxPotInterceptionArea is less than or equal to MaxPotInteceptionCap then:

MonPoolInterception=MaxPotInterceptionArea

If, on the other hand, MaxPotInterceptionArea is greater than MaxPotInterceptionCap, then:

MonPoolInterception=MaxPotInterceptionCap

This relationship assures that these dead foliage related pools can not absorb more water than it can store. The amount added to the soil as throughfall from the dead foliage pool each month is:

MonForestFloorThroFall=MonLogThroFall-MonDeadFoliageInterception -MonStableFoliageInterception

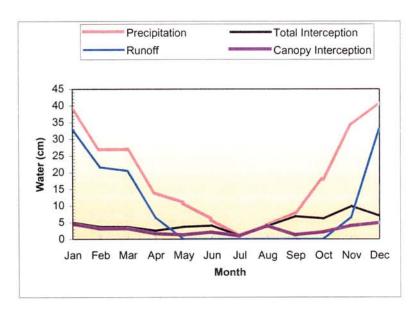
Total Interception Function.

This function calculates the total amount of precipitation intercepted by the canopy, above-ground dead woody detritus pools, and the dead foliage pool (Figure 11). The monthly total interception is:

MonTotalInterception=MonStableFoliageInterception +
MonDeadFoliageInterception+MonLogInteception+MonCanopyInterception

TotalAnnualInterception is the sum of all the monthly interception values.

PET & Transpire Function.



This function calculates the monthly total potential evapotranspiration (in cm) of the site using a modification of the Priestly-Taylor method (Bonan 1989). Total potential evapotranspiration for a month (MonPETTotal) is assumed to be proportional to the estimated solar radiation (MonSolRad), the monthly

Figure 11. Example of seasonal interception of water predicted by the STANDCARB model for an old-growth forest.

mean air temperature (MonTemp24 in C), and number of days in a month (MonthDay).

MonPETTotal = CT*(MonTemp24 + TX)*MonSolRad*MonthDay/MonLatHeatVapor

The constants CT and TX are empirically derived and calculated after Jensen and Haise (1963):

CT = 1/[38-(2*Elev/305) + 380/SatVapPresMax-SatVapPresMin)]

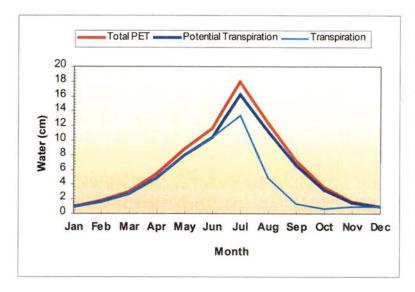
TX = 2.5 + (0.14*(SatVapPresMax-SatVapPresMin)) + Elev/550

where Elev is the elevation in meters, SatVapPresMin and SapVapPresMax are the saturation vapor pressures in mbars for the mean minimum (TempMeanMin) and mean maximum (TempMeanMax) daily temperatures for the warmest month of the year. The vapor saturation pressures are calculated from the appropriate air temperatures using Bosen's approximation (Bonan 1989). For example for the SatVapPresMin:

SatVapPresMin=33.8639*[($(0.00738*TempMeanMin+0.8072)^8$ - 0.000019*(1.8*TempMeanMin + 48) + 0.001316)]

MonLatHeatVapor is the latent heat of vaporization (cal) for each month and is calculated as follows:

MonLatHeatVapor = 597 - 0.568*MonTemp24



This means that each month has its own value of latent heat of vaporization.

To estimate the potential amount of transpiration by plants (MonPotenTrans), the total potential evapotranspiration (MonPETTotal) is reduced by the amount of evaporation from canopy interception and detritus pools:

Figure 12. Relationship of total potential evapotranspiration (PET), potential transpiration, and actual transpiration predicted by the STANDCARB model for an old-growth forest.

MonPotenTrans = MonPETTotal-MonCanInterception-MonDetritusEvaporation

MonPotenTrans is set so it cannot go below zero. If the interception and evaporation terms are larger than PET total then set PotenTrans to zero. This yields a monthly potential transpiration loss, assuming that leaf mass and soil water stores are at a maximum. The actual transpiration losses each month (*Mon*Transpiration) are controlled by the soil water stores and the foliage mass (Figure 12):

MonTranspiration=MonPotenTrans*(Mon-1)MoistProdIndex*(Foliage/FoliageMax)

where (Mon-1)MoistProdIndex is calculated in the MoistProdIndex function and is the value of the previous month, and Foliage is the total foliage mass for all layers and FoliageMax is the maximum total foliage mass possible in a cell (Figure 13). This is calculated for each layer from the light compensation point (LayerLightCompPoint) and the light extinction coefficient (LayerLightExtCoeff) for each layer in a cell. The first step is to calculate the maximum light a layer (LayerMaxLightAbsorb) can absorb assuming that the overlying layers are also at their maximum:

LayerMaxLightAbsorb=LayerLightIn-(LayerLightCompPoint/100)

where LayerLightIn is the light not absorbed by the overlying layers and LayerLightCompPoint is the light compensation point of the layer as defined in the Growth.prm file. In cases where the LayerLightIn is less than LayerLightCompPoint (when the overlying layers reduce light below the light compensation point of the layer in question), LayerMaxLightAbsorb is set equal to zero.

The maximum mass of foliage a layer can have, adjusted for the amount of light it can absorb is:

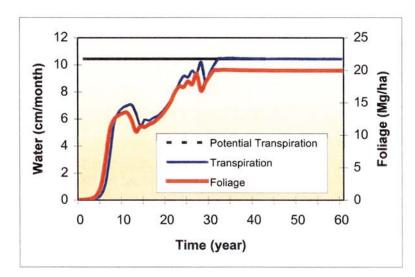
LayerFoliageMax = -Ln [LayerLightRemoved/LayerLightExtCoeff]

where LayerLightExtCoeff is the light extinction coefficient (defined in Growth.prm) and LayerLightRemoved is the amount of light removed by a layer:

LayerLightRemoved = (LayerLightIn-MaxLightAbsorbed)/LayerLightIn

The maximum foliage mass of all the plant layers is calculated as the sum of maximum foliage mass for all four layers in a cell:

FoliageMax = $\sum (Layer$ FoliageMax).



In cases where a tree species has not been planted in a cell the identity of the tree species is determined as follows. In the single of multicell versions, the parameters associated with the herb and shrub layers are taken from the Growth.prm file to solve the potential maximum leaf mass. For tree layers this is not possible because a specific tree species must be identified

Figure 13. Change in peak transpiration predicted by STANCARB over succession following rapid regeneration. The values are for the month of June, a period when soil limitations are minimal.

with each layer. In the single cell version of the model, the identity of the upper and lower tree layers is taken from the Simul.dvr file. In the case of the multicell version of the model, the species on the site that has the potential to have the maximum leaf mass is used until an actual species has been selected and planted.

WaterStore Function.

This set of functions determines the monthly moisture content of eight detritus pools, two surface stable pools (i.e., StableFoliage and StableWood), and the mineral soil. For all pools, the moisture content is computed monthly and represents the balance of inputs through precipitation and outputs via evaporation and/or transpiration.

Mineral Soil Subfunction.

This function computes the water stores in the mineral soil. Input to the mineral soil is whatever water has not been intercepted by the canopy, dead wood, surface stable pools, and the dead foliage pools.

MonSoilWaterIn=MonForestFloorThroFall

where MonSoilWaterIn is the amount of water added to the mineral soil layer in cm. The loss of water from the mineral soil will be controlled solely by the transpiration from plants, this assumes that there is always plant cover or forest floor cover. The overall balance of mineral soil water stores is therefore:

 $Mon\Delta SoilWat = MonSoilWaterIn-MonTranspiration$

The water stored in mineral soil for each month would be:

 $MonSoilWat = MonSoilWatOld + Mon\DeltaSoilWat$

where MonSoilWatOld is the water store in the soil the previous month. To keep the water potential and other indices from becoming undefined, the minimum value that MonSoilWat is allowed to have is 0.01.

To compute an overall water balance, runoff occurs when *Mon*SoilWat exceeds the SoilWaterMax (the maximum storage capacity of the soil based on its texture, rockiness, and depth as calculated by the SoilTexture module). The monthly runoff is therefore:

MonRunoff=MonSoilWat-SoilWaterMax

When runoff occurs the MonSoilWat is set to equal SoilWaterMax. If the monthly water store is less than or equal to the maximum then MonRunoff is set to zero.

The annual Runoff is the sum of all the monthly values (TotalAnnualRunoff). While this variable is not directly used in carbon budgets, it is a useful variable for model calibration.

The moisture content of the soil is calculated on a volumetric basis relative to the maximum water storage of the particular site being examined:

MonSoilMoist = 100*MonSoilWat/SoilWaterMax

where SoilWaterMax is the maximum amount of water (cm) a soil can hold as calculated in SOILTEXTURE.

Detrital Water Stores Subfunction.

This function calculates the balance of water stores for four detritus pools and two stable pools (Figure 14). The input of water into the DeadFoliage, DeadSapwood, DeadHeartwood, DeadBranch, StableFoliage and StableWood pools is equal to the amount intercepted:

MonPoolWaterIn=MonPoolInterception

DeadSapwood and Dead Heartwood are subdivided into snags and logs for water balance purposes. The loss of water each month from these pools is dependent upon the temperature and the amount of solar radiation received. The amount of solar radiation received each month is a function of the amount of light that passes through the foliage layer just above the detritus pool. Therefore for Deadfoliage, DeadBranch, StableFoliage, StableWood, and DeadSapwood and DeadHeartwood in logs the amount of radiation received is:

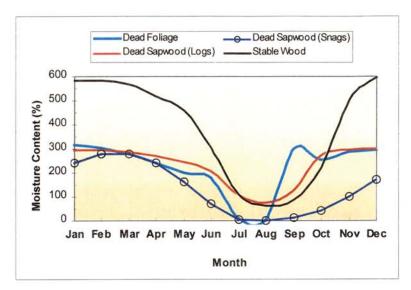
MonPoolRadiationInput=MonSolRad*HerbLightOut

where *MonPool*RadiationInput is the amount of radiation recieved by a detrital pool each month, *Mon*SolRad is the total amount of solar radiation recieved by a site each month (see Radiate.dvr file) and HerbLight is the fraction of light passing through the foliage of all plant layers each month. In the case of DeadSapwood and DeadHeartwood in snags the amount of light recieved is higher because of the greater height distribution of this material. Therefore:

MonSnagPoolRadiationInput=MonSolRad*UpperTreeLightOut

where *Mon*Snag*Pool*RadiationInput is the amount of radiation recieved by DeadSapwood and DeadHeartwood in snags each month and UpperTreeLightOut is the amount of radiation passing through the upper tree layer. The rate of drying is dependent on the evaporative demand for each detritus pool:

MonPoolEvapDemand=MonTemp24*MonPoolRadiationInput.



When MonTemp24 is negative, *MonPool*EvapDemand is set to 0 so that detritus pools do not directly gain water from the atmosphere. The rate that water is lost from each detrital pool is:

Figure 14. Seasonal changes in moisture content as predicted by STANDCARB of selected detritus and stable pools.

MonPoolRateWaterLoss = MonPoolEvapDemand*PoolDryingConstant

where *Pool*DryingConstant is found in the DecayPool.prm file. This parameter represents the rate of drying in a month when the temperature is 1 C and the radiation input is 1 cal m⁻² day⁻¹.

The overall rate of change for each of the detrital layers and surface stable pools is a function of the inputs versus loss through evaporation:

Mon \(\Delta Pool \) Water = Mon Pool \(\Delta a \) water \(\Lor \) Mon \(\Delta Pool \) Water \(\Lor \) ate \(\Delta a \) ate \(\Delta a \) water \(\Lor \) ate \(\Delta a \) water \(\Lor \) and \(\Delta a \) water \(\Delta a \)

The store of water in a pool for a given month is:

 $MonPoolWater = MonPoolWaterOld + Mon\DeltaPoolWater$

with the restriction that MonPoolWater can not be less than 0.

To calculate the effect of water stores in these detrital layers on the Moisture Decay Index functions, the values of water depth have to be converted to moisture content based on mass. The mass of water per hectare in 1 cm of depth is 100 Mg. Therefore each 1 cm of water stored in a detritus layer is:

MonPoolWaterMass=MonPoolWater*100

where *Pool* is any of the four detrital layers we are considering (DeadSapwood, DeadHeartwood, DeadBranches, and DeadFoliage). The moisture content for these pools would therefore be:

MonPoolMoist=100*MonPoolWaterMass/Pool.

where *Pool* is the mass of each detritus pool during the year being considered.

In this version of the model there are two layers in which the moisture content is not modeled using inputs and outputs. For the dead fine root pool (DeadFineRoot), the moisture content changes rapidly with the surrounding soil and humus. It is therefore assumed to be the same as for the StableFoliage pool. In the case of dead coarse roots (DeadCoarseRoot) the water balance is controlled by the moisture of the surrounding mineral soil (Chen 1999). We assume that the response time-lag over a monthly time step is minimal. When the soil is saturated we assume that the dead coarse roots reach their maximum moisture content. Therefore:

If MonSoilMoist = 100 then

MonDeadCRootMoist = DeadCRootMoistStoreMax

as defined in the DecayPool.prm file. When the moisture content of the mineral soil is less that saturated we assume the dead coarse roots and mineral soil are in equilibrium. However, since mineral soil moisture is expressed in volumetric terms and dead coarse roots in mass terms we must convert units:

If MonSoilMoist < 100 then

MonDeadCRootMoist = 2*MonSoilMoist

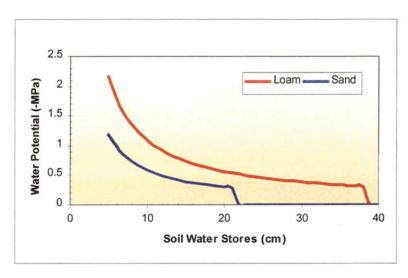
Finally, to calculate the potential transpiration losses from the mineral soil it is necessary to calculate the amount of water lost via evaporation from detritus and the surface stable pools (MonDetritusEvaporation):

 $MonDetritusEvaporation = \sum MonPoolRateWaterLoss.$

WaterPot Function.

This function converts the volumetric moisture content of soils to a xylem water potential. This relationship is represented by a reciprocal function modified by an asymptote:

MonWaterPot=CorrTerm*WaterPotAsym + (WaterPot1*(SoilWaterMax/MonSoilWat))

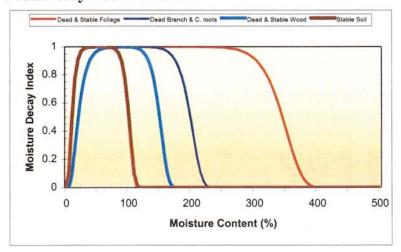


where *Mon*WaterPot is the predawn xylem water potential in MPa for a given month, *Mon*SoilWat is the monthly water store in soil, and SoilWaterMax is the maximum water stores in cm (Figure 15). The later variable is dependent upon the soil depth, rockiness, and texture and is calculated by SOILTEXTURE. The parameter WaterPotAsym

Figure 15. Relationship of water stores to water potential used by the STANDCARB model.

simulates the behavior of coarse textured soils that can yield considerable water without changing their water potential. WaterPot1 is the fraction of the water stores when WaterPot is equal to 1 MPa. When this water potential is reached moisture becomes limiting to transpiration and production. The values of WaterPotAsym and WaterPot1 are defined in the Soil.prm file. Finally, the term, CorrTerm, is used to correct for the fact that water potential does not increase appreciably from 0 when the soil is near saturation. CorrTerm is set equal to 0 if the ratio of *Mon*SoilWat/SoilWaterMax is greater to or equal to 0.9. Otherwise CorrTerm is set to 1.

MoistDecayIndex Function.



This function determines the way the moisture content (MonPoolMoist) of each pool influences the decomposition rate of the detrital layers for each month (Figure 16). For all layers we assume that moisture controls decomposition in two ways. The first is through matric potential which makes water unavailable for decomposers.

Figure 16. Response of decomposition to moisture content of selected detritus and stable pools. Note that all pools except stable soil are in percent moisture by weight, whereas stable soil is volumetric percent.

For most detrital forms, decomposition ceases when moisture content reaches the fiber saturation point. The second effect is caused by poor oxygen diffusion when the moisture content is too high (Hicks 2000). For most detrital layers this is not a problem, however, coarse wood respiration is often limited by this factor. We model the matric potential and diffusion limitation portions separately. For all detritus pools except the stable soil pool, the percent moisture content used is based on mass of water divided by dry mass of the substrate. For the stable soil pool, the percent moisture content is based on volume of water divided by volume of soil.

The equation for the matric potential limitation (MonMatricLimit) of each detrital pool or the stable soil pool for each month is:

 $\textit{MonPool} MatricLimit = (1-exp[-IncreaseRate*(\textit{MonPool} Moist + MatricLag)]) \\ MatricShape$

where MatricShape is a dimensionless number that determines when the Matric limit is reduced to the point that decay can begin to occur. The MatricLag parameter is used to offset the curve to the left or right. The IncreaseRate is the parameter determining the point at which the matric limitation ends. This parameter is determined from the minimum moisture content at which decay can occur:

IncreaseRate=3/MoistMin

The diffusion limitation (*Mon*DiffuseLimit) is designed to mimic the reduction in decomposition caused when the substrate becomes water saturated. Water saturation causes a reduction in oxygen diffusion reducing decomposition. This function remains at 1 until the maximum moisture content without diffusion limitations is reached. The function decreases to 0 when moisture content exceeds the maximum for decomposition to occur. This function is calculated for each detrital pool for each month:

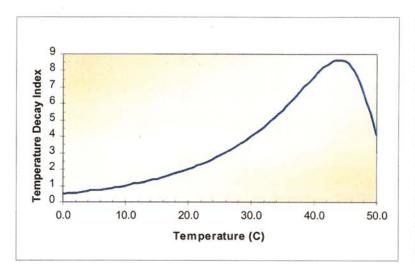
MonPoolDiffuseLimit = exp[-(MonPoolMoist/(MoistMax+DiffuseLag))DiffuseShape

where MoistMax is the maximum moisture content without diffusion limitations, DiffuseShape is a dimensionless number that determines the range of moisture contents where diffusion is not limiting, and DiffuseLag is a parameter used to shift the point when moisture begins to limit diffusion. These parameters are stored in the DecayPool.prm file.

The combined effect of matric and diffusion limitations for each detritus pool or for the stable soil pool for each month is:

MonPoolMoistDecayIndex=MonPoolMatricLimit*MonPoolDiffuseLimit

TempDecayIndex Function.



This function determines the effect of temperature on the decomposition rate of the detrital pools (Figure 17). The response to temperature has two components. The first part is an increase in respiration rate with temperature following a Q10 type curve. For each detritus pool and each month the value of the following equation will be solved as:

Figure 17. Response of decomposition to monthly temperature used in STANDCARB.

MonPoolTempIncrease = (PoolQ10((MonTemp24-10)/10))

where the respiration rate of the layer at 10 C is assumed to be 1.0, and *PoolQ10* is the rate respiration increases with a 10 C increase in temperature (see the DecayPool.prm file) and *Mon*Temp24 is the temperature of a given month.

The second part of the temperature response simulates the effect of a lethal temperature limit that arrests decomposer activity. This equation is given by:

MonPoolTempLimit = Exp[-(MonTemp24/(PoolTempOpt + PoolTempLag))PoolTempShape]

where *Pool*TempOpt is the optimum temperature for decomposition of a detritus pool and *Pool*TempLag and TempShape are parameters that determine the shape of the response curve as determined from the DecayPool.prm file.

The combined effects of these effects for each detritus pool for each month is given by MonPoolTempDecayIndex:

MonPoolTempDecayIndex = MonPoolTempIncrease*MonPoolTempLimit

AbioticDecayIndex Function.

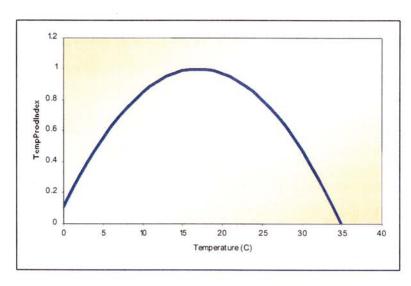
This function calculates the combined effects of temperature and moisture on the decomposition rate of each detrital pool and the stable soil pool for each month.

For each detritus pool or the stable soil pool the monthly abiotic decomposition index (MonPoolAbioticIndex) is

MonPoolAbioticIndex = MonPoolMoistDecayIndex*MonPoolTempDecayIndex

The mean annual AbioticIndex (*Pool*AnnualAbioticIndex) for each detritus pool or the stable soil pool is then used to control the decomposition rates in DECOMPOSE.

TempProdIndex Function.



This function determines the effect of temperature on net photosynthesis of each layer (Figure 18). The curve used to simulate this relationship is taken from Running and Coughlan (1988) and defines the mean daytime temperature (*Mon*TempDay; see TempConvert function above) response according to a minimum and maximum temperature compensation

Figure 18. Response of plant growth to monthly air temperature used in the STANDCARB model.

point (LayerTempMin and LayerTempMax) for each layer as defined in the Growth.prm file. If the mean daytime temperature exceeds either the minimum or maximum temperature compensation points of a layer, then the temperature production index (LayerTempProd) for a layer is set to zero. If the daytime temperature is within those limits then:

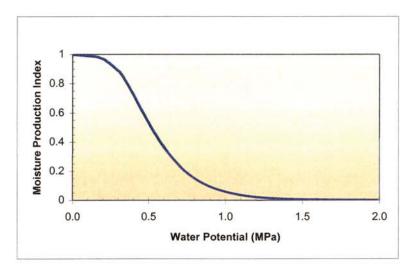
MonLayerTempProdIndex = (LayerTempMax-MonTempDay)*(MonTempDay-LayerTempMin)/(LayerTempMax-LayerTempOpt)*(LayerTempOpt-LayerTempMin)

where *MonLayer*TempProdIndex is a relative index of the response of each layer to a monthly daytime temperature (*Mon*TempDay).

The optimum temperature (LayerTempOpt) for a layer is defined as:

LayerTempOpt = (LayerTempMax-LayerTempMin)/2.

MoistProdIndex Function.



This function determines the effect of soil moisture on the production of live biomass (Figure 19). We assume there is no effect on production of live biomass when waterlogging occurs. In a future version of the model we hope to implement a reduction in production for soils in which the water potential is less than -0.1 MP. This would account for a

Figure 19. Response of plant growth to soil water potential used in the STANDCARB model. Note the units of soil water potential are actually negative, but have been transformed for display purposes.

more realistic assumption that poor drainage and waterlogging reduces production. The current equation giving the waterlogging response is:

MonWaterLoggingIndex = 1

where MonWaterLoggingIndex is the reduction of waterlogging on production.

In the current version of the model water becomes limiting when soil water potential (WaterPot) is below -0.3 MPa, the production rate decreases exponentially as a function of drought (Emmingham and Waring 1977). The equation describing this response is:

MonDroughtIndex = 1-(1-exp[-5*MonWaterPot])⁹

where *Mon*DroughtIndex is the reduction in production caused by drought. The overall effect of water potential on production (*Mon*MoistProdIndex) is:

MonMoistProdIndex = MonWaterLoggingIndex*MonDroughtIndex.

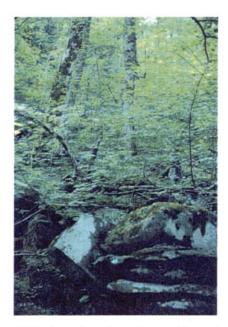
ProdIndex Function.

This function combines the monthly effects of moisture and temperature on the production rate of living biomass for each plant layer. In addition to indicating the response of production, it is also used to control the transpiration of the layers in the PET & Transpire functions. For each month the product of these two indices is computed:

MonLayerProdIndex = MonLayerTempProdIndex *MonMoistProdIndex

The mean annual production index (Annual Layer Prod Index) is then computed and used by the GROWTH module.

SOILTEXTURE



This module is used to estimate the maximum amount of water that can be stored in a soil profile for a site. It is invoked once at the beginning of each simulation. This estimate is based on the soil texture class, the depth of the soil in cm, and the percentage of the soil with fragments greater than 2 mm in size that is specified in the Locate.dvr file.

SoilTexture Function.

This function determines the maximum amount of water storage in a soil based upon the soil texture, depth, and rockiness. The output of this function is sent to CLIMATE and used in the WaterPot and WaterStores functions.

This function first determines the fraction of the soil that can store water between field capacity and the wilting point (SoilWaterMaxPer) based on the soil texture class specified by the Locate.dvr file. SoilWaterMaxPer is set for each soil texture class contained within the Soil.prm file.

The volume of rocks is used to decrease the overall water holding capacity. The fraction of the soil profile with fine soil (FineSoil) is calculated:

FineSoil = (100-Rocks)/100

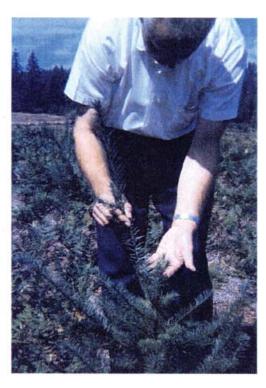
where Rocks is the percentage of the soil with fragments greater than 2 mm diameter as specified in the Locate.dvr file.

Finally, the depth of soil that can store water (SoilWaterMax) in cm is calculated from the soil texture, rock content, and soil depth (in cm):

SoilWaterMax=SoilWaterMaxPer*SoilDepth*FineSoil

where SoilWaterMaxPer is the percent of fine soil that can store water from field capacity to wilting point, SoilDepth is the depth of the soil (in cm) as defined in the Locate.dvr file, and FineSoil is the fraction of the soil that is fragments less than 2 mm diameter.

PLANT



This module plants the vegetation layers and selects the species of tree to be planted in a cell. The first step is to determine if the herb, shrub, upper tree layer or the lower tree layer is present in a cell. If a layer is missing from the cell, then the PlantLife function is used to determine if the layer will be planted. If all these layers are present in a cell then PLANT moves to the next cell to determine which layers are present and need to be planted.

The files required by this function are Estab.prm, TreeReg.prm, and EcoRegion.prm.

PlantLife Function.

The purpose of this function is to determine if a life form is to be planted in a cell. If a life form is to be planted, then the life form specific growth and decomposition parameters are imported into the GROWTH and DECOMPOSE modules for that cell. In the case of a tree layer being selected the PlantTree function is invoked to select a tree species.

Life forms (i.e., herb, shrub, and trees) have unequal chances of being selected to be planted. The probability a layer will be planted is defined in the Estab.prm file for up to four cases or regeneration scenarios. For any simulation only one of these four cases can be selected. The layer of trees that is planted is dependent on the presence of the upper tree layer. The lower tree layer can only be planted when an upper tree layer is present. The upper tree layer can only be planted when the cell has no trees on it.

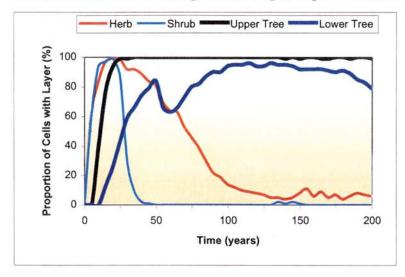
Time Step 1:	no layers planted	
Tree	Shrub	Herb
Time Step 5		
Tree	Shrub	None
Time Step 10	*	
Tree	None	None
Time Step 12:	all layers planted	
None	None	None

Figure 20. Examples of cumulative probability function showing a progression from no layers planted to all layers planted. The total length of each bar is 1.

Only one layer can be planted in a cell during each time step. To determine if a layer is to be planted, this function creates a cumulative probability function based on the probabilities of all the layers that have yet to be planted in a cell (Figure 20). The cumulative probability function can not exceed a value of 1.0 and is constructed by selecting the herb layer and assigning it a probability band from 0 to the probability specified in the Estab.prm file. The next layer is assigned a probability band from the high range of the first layer to the sum of the probabilities of the first and second layer. This process is continued until all the layers that have not been planted are considered. In many cases the summation of all the layer probabilities does not equal 1.0, and when this occurs the remaining probability band is assigned to "no layer" in that time step. After the cumulative probabilities are calculated for each layer, a random number is selected between 0 and 1. Whichever probability band the number falls into determines which layer is planted that time step. If no layer is selected, then the function moves on to the next cell to determine which layers to plant in that cell.

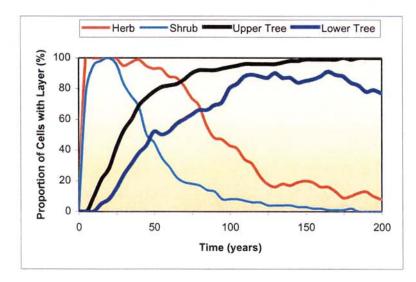
If a layer is selected for planting, then a message is sent to GROWTH module to make the mass of foliage for that layer a small positive number. Once the foliage mass is added the layer begins to grow and add biomass. Adjusting InitialFoliageMass (the value is specified in the GrowLayer.prm file) determines the length of time lag required for the layer to begin growing at a significant rate. Setting this parameter low increases the lag time, whereas increasing it decreases the lag time.

The probability of a layer establishing in a plot depends upon whether an upper tree layer exists. If there is no upper tree layer, then the probability of establishment that is used is EstOpenReg, where Reg is regeneration scenario. There are four regeneration scenarios present in the Estab.prm file: 1) natural fast, 2) natural slow, 3) artificial fast, and 4) artificial slow. If there is an upper tree layer present, then the probability of establishment that is used is EstClosedReg, where Reg is regeneration scenario.



The probabilities of establishment in the Estab.prm file are set so that herbs will tend to establish before shrubs and shrubs will establish before trees (Figures 21 & 22). The probability of trees establishing in the upper layer can be modified by the options selected in the Simul.dvr file. The

Figure 21. Example of plant layer colonization for artificial fast regeneration. Noninteractive multicell mode used.



probability of a life form establishing beneath a tree canopy layer (EstClosedReg) is always lower than the probability of establishing in the open (EstOpenReg).

MaxTreeCells Function.

There are cases where upper trees cannot occupy all the cells in a stand regardless of the amount of time that

Figure 22. Example of plant layer colonization for slow natural regeneration. Noninteractive multicell mode used.

expires. Examples would be woodland (e.g., grassland-forest combinations), savannas, high elevation treeline forest, and bog forest. In these cases it is possible to specify the

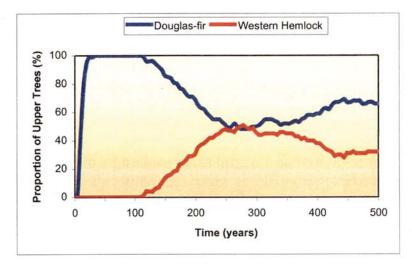
maximum percentage of the cells that can be occupied by trees in the Simul.dvr file. If the trees are removed by a disturbance, then the cells are colonized in a random sequence until the maximum percentage of trees is reached.

NOTE: Tests of this function have revealed that in simulations with mixed disturbance regimes (e.g., old-growth versus younger plantations) more cells will be colonized in the regime with the lowest mortality rates. This causes a spatial interaction and can cause departures as much as 20% from the expected carbon stores. This effect is highest when the maximum colonization is set to 50%.

PlantTree Function.

As specific species of the herb and shrub layers are not considered, it is not necessary to select which species herb or shrub should be planted. Trees, however, are treated on the species level. The PlantTree function selects which species can be planted. STANDCARB does not consider all the factors that control tree establishment. Rather the intent of the PlantTree function is to plant trees in proportion to their abundance in the various stages of

succession (Figure 23).



The first step is to determine the response of a species to individual environmental factors. These are then combined to estimate the probability of a tree species establishing in a plot (Prob*Species*) from the local abundance (LocalAbund as set in Ecoregion.prm) and tolerances to the abiotic

Figure 23. Example of replacement of Douglas-fir by western hemlock over succession. Noninteractive multicell mode was used.

environment of the site (DDayMax, DDayMin, TreeSoilMax, TreeSoilMin, LightMax, LightMin; as set in TreeReg.prm). The limits to abiotic factors are set for a species; however, the local abundance (LocalAbund) varies with the specific location within the Pacific Northwest.

Temperature Limits. A species may not be planted if the thermal environment of the site exceeds the limits of a tree species. If the degree day values (DDays) of a site determined from the DegreeDays function of the CLIMATE module are equal to or below the degree day minimum (DDayMin), or equal to or exceed the degree day maximum (DDayMax) for

a species, then its probability of establishment is set to zero (DDayLimit). If the DDays are within the limits then DDayLimit is set to one.

Soil Moisture Limits. A species of tree may also not be planted if the site is too dry or because it is too wet. For these calculation we use the absolute value of soil water potential as a indicator of soil moisture. (Note: when using soil water potential the wettest soil has the lowest water potential and the driest soil has the highest water potential). If the yearly maximum soil water potential (MaxMonWaterPot) calculated for a cell in the WaterPot function of the CLIMATE module is equal to or lower than the species minimum (TreeSoilMax), then the value of SoilLimit is set to zero. If the soil water potential exceeds the species minimum (TreeSoilMin) for more than 9 months, then SoilLimit is also set to zero. If the site soil water potential is within these limits, then SoilLimit is set to one.

Light Limits. A species of tree may not be able to establish within a cell if there is too much or too little light. In the former case, light *per se* may not be the limiting factor. Excessive heating or drying may be the actual mechanism involved. These problems are highly correlated, however, to high light levels. Minimum light levels are related to the species shade tolerance and light compensation point.

The light value used to determine the probability a tree can establish depends upon if it is being planted as an upper tree or as a lower tree layer. For upper trees the value of light that is considered is the amount entering a cell (UpperTreeLightIn). This may fall below full sunlight if adjacent cells contain taller trees that shade the cell being considered (see NEIGHBOR module). For lower trees the value of light that is considered is the amount passing through the upper tree layer (LowerTreeLightIn) as determined by the GROWTH module. If the light value considered in either case is within the limits during the time step a species is being selected, then the value of *Layer*LightLimit is set to 1. If the light is equal to the maximum and minimum light limits or exceeds these values, the value of *Layer*LightLimit is set to zero.

The second step in determining the probability of a tree species establishing in a cell is to calculate a species ranking:

RankSpecies = LocalAbund*DDayLimit*SoilLimit*LightLimit

These formulae do not allow a species to become established if the species is not present in the ecoregion or if the temperature, moisture, or light limits are exceeded.

The last step is to convert these ranks into proportions:

ProbSpecies = RankSpecies/RankAll

where *Species* is the value for a given tree species and *All* is the sum of the values of all the species.

Once these probabilities are estimated, a cumulative probability is calculated in a manner similar to that used for determining which layers are to be planted. A tree species is selected at random and then the probability band it occupies is set from 0 to the probability determined above (ProbSpecies1). The next species has a probability band from the first species to the sum of probabilities for the two species (ProbSpecies1+ ProbSpecies2) and so on until all the species have been considered. A random number is then generated to determine which species will be planted in a plot. Whichever band the random number falls within determines which tree species is planted in that cell.

DIEOUT



This module determines when a upper canopy layer in a cell will die out completely. The rational is that as long as the canopy layer is comprised of more than one individual, the death of a tree will not cause the species to vacate the upper tree layer of a cell. Once the upper canopy is dominated by a single individual, however, there is some chance (ProbDieOut) that a species will disappear from the cell. The parameters used to define when trees die

out (AgeMax and TimeClose) are contained within the Mort.prm file.

The parameters required by this module are stored in the Mort.prm file.

TimeThere Function.

This function calculates the time a species has occupied the upper tree layer in a cell. Because not all the trees are planted in year 0, there is a difference between the simulation time and the time a tree species occupies a cell. To determine if an upper canopy layer has a chance of dying out, the time the species is on the site must be calculated:

TimeThere=Time-TimePlant

where time is the simulation Time in years, TimePlant is the simulation time that a species was planted in a layer, and TimeThere is the number of years a species has occupied the upper canopy layer of a cell.

ProbDieOut Function.

This function calculates the chances an upper tree layer will die out and be replaced. The probability an upper tree layer will die out is a function of the time the species has occupied a cell. If the time since a species was planted in a cell (TimeThere) is less than TimeClose (defined in the Mort.prm file) then:

ProbDieOut = 0

If the time since a species was planted in a cell (TimeThere) is greater than or equal to TimeClose, then the probability is equal to:

ProbDieOut = ExtRate

where ExtRate is the annual probability that a species will die. This probability is calculated from the maximum age of the species (AgeMax) and the time required for a single tree to dominate a plot (TimeClose):

ExtRate = 4.61/(AgeMax-TimeClose)

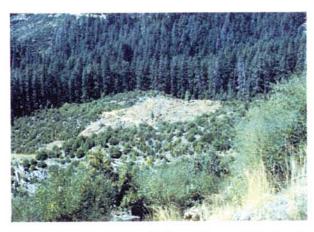
To determine if the upper canopy layer in a cell dies out, a random number is chosen. If this number is less than ProbDieOut then the species dies out of a cell.

Once the upper tree layer has died out of a cell, the lower tree layer, if present, becomes the upper tree layer. When a lower tree layer replaces an upper tree layer, the replacing layer is assumed to be 25 years of age. This partially compensates for the fact that the lower tree layer was planted prior to the death of the upper canopy layer. The time the replacing layer was planted is therefore estimated to be:

TimePlant = Time-25

where Time is the simulation time when the upper tree layer dies and 25 is the assumed value of TimePlant when the lower tree layer replaces the upper tree layer.

SPROUT



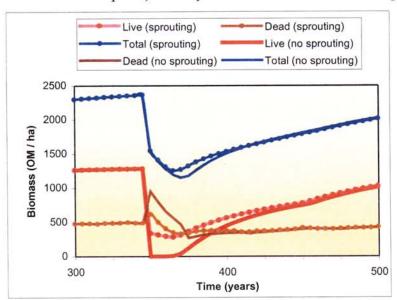
This module is invoked whenever layers in a cell are completely killed by a disturbance (i.e., fire, cutting, or herbicide). If upper trees are killed as a function of age in the DIEOUT module, then the trees cannot sprout. In all other cases of mortality, trees can sprout.

If the Sprout parameter in the TreeReg.prm file is zero, then the species can only reoccur if it recolonizes the cell. If, on the other hand, the Sprout parameter is set from 1 to 9,

the species has a possibility of remaining in the cell and start growing the following year. To calculate the probability that sprouting will occur the probability of sprouting (ProbSprout) is calculated as:

LayerProbSprout= [1-(LayerProbDeathHerbicide/100) *(LayerSprout/10]

where LayerSprout is any integer from 0 to 9 (with 0 meaning no sprouting ability and 9 means all stems sprout) and LayerProbDeathHerbicide is the probability of the layer dying



from herbicide treatment. This latter parameter is set to zero for cutting and fire, however, for herbicide treatment it is determined by the parameter %RootsDie in the Herbicide.prm file. This accounts for the fact that herbiciding can reduce the ability of species to survive, whereas other disturbances such as fire and cutting sprouting is based more on the species innate capacity to form sprouts.

Figure 24. Effect sprouting for the live, dead, and total organic matter stores after major disturbance. There are more live and total stores when trees can sprout.

To determine if a layer in a cell can sprout, the probability of sprouting is compared to a random number between 0 and 1. If the random number is less than or equal to the probability then the species survives; otherwise the species is removed from the cell.

In addition to determining if a species can stay in a cell following disturbance, sprouting also determines which parts are added to detritus pools (see BURNKILL and HARVEST modules). If a layer does not sprout, then all parts remaining after the disturbance are added to the appropriate detritus pools. If the layer does sprout, then only the aboveground parts are added to detritus pools, because the fine and coarse roots are assumed to survive. A small amount of foliage, equal to the amount added when layers are planted, is added to the cells where trees sprout. This allows the aboveground portions of the trees to eventually regrow following disturbance.

GROWTH



The purpose of this module is to calculate the mass of seven live pools of carbon: 1) foliage, 2) fine roots, 3) branches, 4) sapwood, 5) heartwood, 6) heart-rot, and 7) coarse roots. To avoid confusion with the corresponding detrital pools, we have referred to these live pools as **parts**. The functions in GROWTH are invoked each year for each cell.

This module is divided into eleven functions which perform specific tasks. These include: 1) Light Absorption and Foliage, 2) Fine Root, 3) Hydraulics, 4) Allocation, 5) Respiration, 6) Heartwood Formation, 7) Heart-rot, 8) Mortality, 9) Prune, 10) Live Stores, and 11) Volume. Each of these functions is invoked for each plant layer present in a cell.

The parts present depend on the plant layers present in a cell. Herbs are assumed to have leaves and fine roots only. Shrubs have leaves, fine roots, branches, sapwood, and coarse roots. Trees have leaves, fine roots, branches, sapwood, heartwood, heart-rot, and coarse roots. Boles are divided into three pools: sapwood, heartwood, and heart-rot. Sapwood and heart-rots represents respiring tissue, whereas heartwood represents non-respiring tissue. Heart-rot represents a part that is decomposing. Splitting the bole into these parts also allows one to have the decomposition of dead wood as a function of decay-resistance of the heartwood of the tree species growing in a plot.

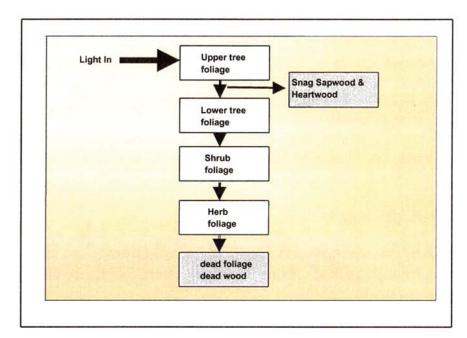
The mass of parts calculated in this module are in turn used by MORTALITY, CLIMATE, DECOMPOSE, DENSITY, HARVEST, and BURNKILL.

The files directly used by the GROWTH module includes Growth.prm and GrowLayer.prm.

Light Absorption and Foliage Function

This function determines the growth of the foliage layers and the amount of light absorbed by them. Light is expressed in relative terms as a percentage of full sunlight. We assume that taller layers have a competitive advantage over shorter stature layers; if taller layers are present they will absorb light before underlying layers (Figure 25). In this model smaller stature layers do not have the ability to exclude potentially taller layers. This behavior can, however, be simulated by reducing the colonization rate of the taller layers in the PLANT module (see Estab.prm file). In addition to being reduced by taller layers, when the model is

run in the cell by cell interaction mode the light coming into a cell can be reduced by shading from surrounding cells (see NEIGHBOR).



The foliage mass of a layer (LayerFoliage) will not begin to grow until a small mass of foliage is added to the foliage part of a layer by PLANT. This allows the mass of foliage to increase at a rate dependent upon the amount of light that has not been absorbed. If a layer has not been planted then the foliage production rate (LayerFoliageProdRate) for each layer is set to 0.

Figure 25. Interception of light by plant layers. The shaded boxes are for pools influenced by light passing through the various layers.

Foliage production rate is an index that indicates the relative ability of foliage to produce more foliage. When this variable is 1, foliage increases at the maximum rate. When this variable is 0, foliage does not increase and when it is negative (i.e., an overlying layer establishes and absorbs light) the foliage mass decreases. Before a layer is planted the following condition is present:

The *Layer*FoliageProdRate=0

and

LayerFoliage=0

As soon as a layer is planted these variables are set:

FoliageProdEffic=1

and

Foliage=InitialFoliageMass

where InitialFoliageMass is the initial mass of foliage that is planted. InitialFoliageMass can be varied (See the GrowParm.prm file) to introduce a lag in the time required for a layer to grow significantly. By reducing this parameter one increases the lag in the growth of a layer.

Layers are able to increase their foliage mass until the light compensation point (LightCompPoint) for that layer or species of tree is reached. As overlying layers can absorb light, the growth of underlying layers can be far below that expected for full sunlight. This approach also allows the foliage of the underlying layers to change in response to an overlying layer dying out or to an overlying layer establishing.

The first step to calculate the rate that foliage increases is to convert LightCompPoint from a percentage to a proportion:

LayerLightCompPoint=LayerLightCompPoint/100

The next step is to calculate the potential maximum of light (*Layer*MaxLightAbsorb) that can be removed by each layer as a function of the amount of light that comes into the top of each layer and the light compensation point:

LayerMaxLightAbsorb=LayerLightIn-LayerLightCompPoint

where LayerLightIn is the relative fraction of full sunlight that reaches the top of a given layer. LayerMaxLightAbsorb is a dynamic variable and is calculated each time step because the amount of light removed by overlying layers or adjacent cells changes over time. To avoid possible cases where LayerMaxLightAbsorb could go negative (which happens if the light compensation point is larger than the light remaining from an overlying layer) LayerMaxLightAbsorb is restricted to be greater than 0.

The amount of light (Light) remaining at the base of the foliage of each layer is a function of the mass of foliage of that layer:

LayerLightOut=LayerLightIn*exp[-LayerLightExtCoeff*LayerFoliage]

where LayerLightOut is the light passed to an underlying layer and LayerLightExtCoeff is the light extinction coefficient for a layer. For trees, the latter parameter is a function of the species present in a cell. The light coming into an underlying layer equals the light passing through the overlying layer. The layers are set up so that the upper tree layer absorbs light first, what is left over is "passed" along to the lower tree layer, and that "passes" along what is left over to the shrub layer, and finally the shrub layer passes along what ever is left over to the herb layer. If the foliage mass of a layer is zero then no light is absorbed.

The next step is to calculate the light absorbed (LayerLightAbsorbed) by a layer:

LayerLightAbsorbed=LayerLightIn-LayerLightOut

The foliage production efficiency (*Layer*FoliageProdEffic) of a layer is assumed to decrease as the amount of light removed increases:

LayerFoliageProdEffic= 1-(LayerLightAbsorbed/LayerMaxLightAbsorb)2

This function means that as the amount of light removed by a layer increases, its ability to increase its foliage mass decreases. When the light absorbed equals the maximum that can be absorbed then the foliage production efficiency equals 0. If the light absorbed exceeds the maximum then the leaves die, that is FoliageProdEffic is negative.

The absolute foliage production rate (*Layer*FoliageProdRate) of a layer is a function of the foliage production efficiency (*Layer*FoliageProdEffic) and the maximum absolute rate of foliage increase (*Layer*FoliageProdRateMax) in full sunlight (as defined in the Growth.prm file):

Layer Foliage Prod Rate = Layer Foliage Prod Effic * Layer Foliage Prod Rate Max

The rate that foliage mass of each layer increases (LayerFoliageAlloc) is:

LayerFoliageAlloc=LayerFoliageProdRate*LayerFoliage

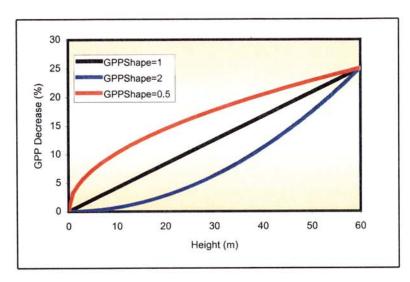
where LayerFoliage is the mass of foliage in a plant layer.

FineRoot Function.

This function calculates the production of fine roots. Although the dynamics of fine roots are quite complicated, there is little information to model these dynamics. We therefore assume that there is a fixed ratio (*Layer*FineRootFoliageRatio) between the mass of fine roots and foliage. This ratio is life-form specific (herbs, shrubs, and trees) and defined in the Growth.prm file. This assumption implies that the energy and nutrient gathering portions of plants are in balance. This ratio is assumed to be highest for herbs, intermediate for shrubs, and lowest for trees giving the highest allocation of biomass below ground for herbaceous plants and lowest for trees. The rate fine root mass for a layer can increase is therefore calculated from the foliage and this ratio:

 ${\it Layer} Fine Root Alloc = {\it Layer} Fine Root Foliage Ratio * {\it Layer} Foliage Alloc.$

Hydraulics Function.



The hydraulics function accounts for the fact that as plants increase in height the efficiency of leaves to photosynthesize decreases (Ryan and Yoder 1997). This leads to a decrease in Gross Primary Production (GPP) as trees age. Although this idea should still be considered a working hypothesis, we have included it in this version of the model to test its possible effects on carbon stores. This

Figure 26. Effect of tree height on reduction in gross primary production (GPP).

effect is only implemented for upper trees. The first step is to determine the coefficient (GPPDecreaseRate) describing the decline in GPP as height increases. This based on the maximum decrease in GPP (GPPDecreaseMax) that occurs are maximum tree height (HeightMax):

GPPDecreaseRate=GPPDecreaseMax/100*HeightMax^{GPPShape}

where GPPShape is a constant that determines if the decrease in GPP with height is linear, or quadratic in form (Figure 26). The predicted decrease for a given tree height (GPPDecrease) is given by:

GPPDecrease=GPPDecreaseRate *Height^{GPPShape}

where Height is the current height (m) of the upper tree in a cell as calculated in the NEIGHBOR module.

Allocation Function.

This function allocates production by the foliage to the woody plant parts: sapwood, branches, and coarse roots. There are several assumptions used in the calculation of sapwood, branch, and coarse root production. The first is that production of these parts is proportional to the mass of foliage of each layer. The second is that the proportions of allocation to bole (i.e., sapwood and heartwood), branches, and coarse roots are fixed. The latter assumption is based on the idea that these are structural elements that need to be

balanced to function properly. Although the allocation of production to these wood parts is fixed, this does not mean that the portions of woody parts is constant. This is because the pruning of branches and coarse roots, as calculated by MORTALITY, is a function of the amount of light absorbed by a cell. Therefore, cells with less light absorbed (and therefore less competition) will have more branches and coarse roots than those where the maximum amount of light has been absorbed.

The allocation to woody plant parts can be determined by two methods. The first is based on a calibration to yield curves. This will set the growth rate so that the wood volume matches that of a specified level of productivity or site index for a selected species. If this option is specified in the Simul.drv file, then the variable *Layer* GrowthRate is set to value referred to in the SiteIndex.prm file. *Layer* GrowthRate can be thought of as the ability of foliage to form woody tissues.

The second method used to determine the allocation to woody parts is to base the growth rate on climatic indices calculated in CLIMATE. If this option is specified in Simul.drv, then:

LayerGrowthRate=LayerAnnualProdIndex*LayerGrowthEffic

where LayerAnnualProdIndex is the effect of temperature and moisture on growth for a layer and LayerGrowthEffic is the growth efficiency for a layer as specified in the GrowLayer.prm file.

Regardless of the method used, the mass of production allocated from foliage to sapwood is:

LayerSapWoodAlloc=(1-GPPDecrease)*LayerGrowthRate*LayerFoliage

where GPPDecrease is the decrease in GPP due to hydraulic limitations (set equal to 0 for all layers except upper trees), <code>LayerSapWoodAlloc</code> is the mass of sapwood produced by a layer, <code>LayerFoliage</code> is the mass of foliage of a layer, and <code>LayerGrowthRate</code> is the ratio of wood mass produced to foliage mass. This relationship makes sapwood production reach a maximum when foliage mass is at a maximum. If foliage mass is reduced by thinning or shading then the rate of sapwood production will also be reduced.

The amount of production allocated to branches from foliage for trees and shrubs (LayerBranchAlloc) is equal to a fixed proportion of the rate of sapwood production for that layer. The parameter LayerBranchBoleRatio defines the ratio of branch to sapwood production. This parameter is set to give the proportions of a tree greater than 50 cm diameter at breast height as solved by biomass equations (Means et al. 1994). The mass of branches produced for a layer is therefore:

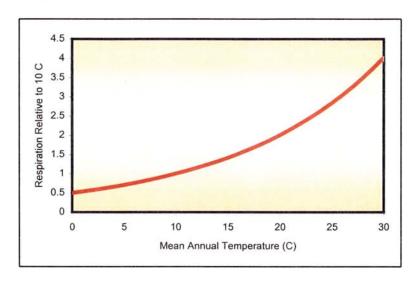
LayerBranchAlloc=LayerBranchBoleRatio*LayerSapWoodAlloc.

The mass of production allocated to coarse roots from foliage (LayerCoarseRootAlloc) for the tree and shrub layers is calculated in manner similar to branches:

LayerCoarseRootAlloc=LayerCoarseRootBoleRatio*LayerSapWoodAlloc

where *Layer*CoarseRootBoleRatio is the ratio of coarse root to sapwood production of a layer as defined in the Growth.prm file.

Respiration Function.



The purpose of this function is to estimate the respiration of the plant parts for each layer. Foliage, fine roots, branches, sapwood, heart-rot, and coarse roots all are capable of respiring. Heartwood is not capable of respiring. Due to the manner in which changes in foliage and fine mass are calculated, the respiration rates calculated here are used to give an estimate of the total

Figure 27. Response of live part respiration to mean annual temperature.

gross production. The respiration rates for branches, sapwood, heart-rot, and coarse roots are used to calculate the total gross production and to calculate the net production of those parts in the Live Stores function (see below). To give an estimate of gross production, the respiration losses of all plant parts except heartwood are estimated from their mass:

LayerPartResp=LayerPartRespRate*LayerPart.

where LayerPartResp is the mass of production that is respired by a plant part, LayerPartRespRate is the rate as a proportion of each part, and LayerPart is the mass of each part for a layer the previous time step. LayerPartRespRate is calculated as a function of the species and the mean annual ambient temperature (MeanAnnualTemp) for the site (see MeanAnnualTemp function in the CLIMATE module). For all plant parts the proportion of mass respired each year is:

LayerPartRespRate=LayerRespPart10 *Q10Part^((MeanAnnualTemp-10)/10)

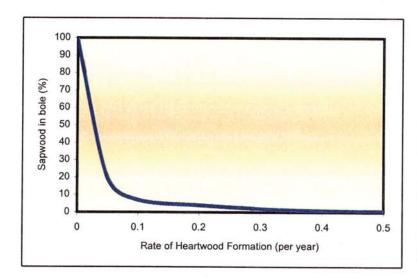
where *Layer*Resp*Part*10 is the respiration rate of the plant part at 10 C, Q10*Part* is the rate respiration increases with a 10 C increase in temperature and MeanAnnualTemp is the mean annual temperature (Figure 27).

For foliage, fine roots, branches, and coarse roots the fraction that is alive is constant among species and layers. In the case of sapwood, adjustments are made to *Layer*RespSapwood10 to reflect the fact that tree species have differing proportions of the sapwood that is alive. The respiration rate for sapwood contained in the GrowLayer.prm file is based on a living sapwood fraction of 5%. The rates used are based on respiration of lodgepole pine and Engelmann spruce (Ryan 1990). This base rate is adjusted by:

LayerRespSapwood10=LayerRespSapwood10*(LayerSapLive/5)

where *Layer*SapLive is the percentage of the sapwood of a layer that is alive. This parameter is stored in the Growth.prm file and is tree species specific based on the proportion of ray cells in sapwood (Panshin and de Zeeuw 1970).

Heartwood Formation Function.



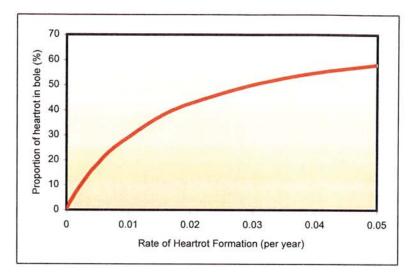
This function calculates the rate that heartwood is formed from sapwood for the tree layers. The mass transferred from sapwood to heartwood (LayerHeartWoodAlloc) for each tree layer is determined by the rate of heartwood formation (LayerRateHeartWoodForm) and the mass of sapwood (LayerSapWood) for the previous time step:

Figure 28. Effect of rate of heartwood formation on fraction of sapwood in boles.

LayerHeartWoodAlloc=LayerRateHeartWoodForm*LayerSapWood

LayerRateHeartWoodForm is parameterized so that the proportion of boles in sapwood matches the values in mature trees of the various tree species (Figure 28).

Heart-rot Function.



This function calculates the rate that heart-rot is formed from heartwood for the tree layers. For each species there is a characteristic time lag before heart-rots become a significant problem (Harmon et al. 1996b). This time lag (Heart-rotLag) is set in the Growth.prm file. If the time a layer has occupied a cell is less than the time lag, then no heartwood is allocated to heart-rot. If the time a layer

Figure 29. Effect of rate of heart-rot formation on fraction of bole in heart-rot.

has occupied a cell equals or exceeds this lag, then mass is transferred from heartwood to heart-rot (*Layer*Heart-rotAlloc) for each tree layer is determined by the rate of heart-rot formation (*Layer*RateHeart-rotForm) and the mass of heartwood (*Layer*HeartWood) from the previous time step:

LayerHeart-rotAlloc=LayerRateHeart-rotForm*LayerHeartWood

LayerRateHeart-rotForm is parameterized so that the proportion of boles in heart-rot matches the values in mature trees of the various tree species (Figure 29; Harmon et al. 1996b).

Mortality Function.

This function calculates the mass of all plant parts lost by normal mortality processes. Even without harvest or wildfire some of the trees are subject to mortality caused by competition (self thinning), wind, insects, and pathogens. It is assumed that when trees are subject to natural mortality, all the plant parts for that tree are added to detrital pools. The equation describing these losses is:

LayerPartMort=LayerMortalityRate*LayerPart

LayerMortalityRate is the proportion of trees dying and is calculated in MORTALITY and LayerPart is the mass of a layer from the previous time step. This parameter does not remain constant, but increases as the amount of light absorbed increases so that when the maximum amount of light is absorbed, the maximum mortality rate is reached. This mimics the increased competition among individuals as the canopy closes.

Prune Function.

This function calculates the mass of foliage, fine roots, branches, and coarse roots that are lost to litterfall, fine root turnover, or pruning. The mass of these plant parts for each layer lost to these processes is:

LayerPartPrune=LayerPartTurnoverRate*LayerPart

where LayerPartPrune is the mass of plant parts of a layer lost from normal foliage fall and pruning, LayerPart is the mass from the previous time step of the live part being considered, and LayerPartTurnoverRate is the fraction of the part for a layer that is pruned or replaced in a given year. LayerPartTurnoverRate has different names depending upon the plant part considered. FoliageTurnoverRate, FRootTurnoverRate, BranchPruneRate, and CRootPruneRate are used for foliage, fine roots, branches and coarse roots, respectively. All these variables are calculated in MORTALITY.

Live Stores Function.

This function calculates the mass of the plant parts after normal growth and mortality. The change in mass for each plant part caused by harvest and fire are calculated by HARVEST and BURNKILL, respectively. The balance of non-woody plant parts (i.e., foliage and fine roots) are calculated as follows:

LayerPart = LayerPartOld + LayerPartAlloc

Where LayerPartOld is the mass of the part from the previous year, and LayerPartAlloc is the mass of the plant part produced (for foliage this is LayerFoliageAlloc and for fine roots this is LayerFineRootAlloc).

For branches and coarse roots the mass in any year is:

 $\label{eq:LayerPart} LayerPart = LayerPart Old + LayerPart Alloc - LayerPart Resp- LayerPart Prune \\ - LayerPart Mort$

Where LayerPartOld is the mass of the part from the previous year, LayerPartAlloc is the mass of the plant part produced (for branches this is LayerBranchAlloc and for coarse roots this is LayerCoarseRootAlloc), LayerPart is the mass of plant part for that year, LayerPartResp is the mass respired, LayerPartPrune is the mass pruned, and LayerPartMort is the mass dying with boles because of normal mortality.

The mass of sapwood for a layer is calculated as:

 $\label{eq:Layer} Layer \mbox{SapWoodAlloc} - Layer \mbox{SapWoodAlloc} - Layer \mbox{SapWoodHeartWoodAlloc} - Layer \mbox{SapWoodMort}$ $- Layer \mbox{SapWoodHeartWoodAlloc} - Layer \mbox{SapWoodMort}$

where all the variables are the same as for branches and coarse roots except that LayerSapWoodHeartWoodAlloc is the mass of sapwood allocated to heartwood.

The mass of heartwood for a layer is calculated as:

 $\label{layer} Layer \mbox{HeartWoodOld} + Layer \mbox{HeartWoodAlloc} - Layer \mbox{HeartWoodMort-} \\ Layer \mbox{Heart-rotAlloc}$

where all the variables, except *Layer*Heart-rotAlloc, the allocation to heart-rot, are defined as for the other plant parts. In the case of heartwood *LayerPart*Alloc is *Layer*SapWoodHeartWoodAlloc, the mass of sapwood allocated to heartwood formation.

The mass of heart-rot for a layer is calculated as:

LayerHeart-rot=LayerHeart-rotOld + LayerHeart-rotAlloc -LayerHeart-rotResp -LayerHeart-rotMort

where all the variables are the same as above.

In addition to these plant parts the mass in boles for the upper or lower tree layers is calculated as

LayerBole=LayerSapwood+LayerHeartwood.

The total live mass is the sum of all the live parts:

LayerTotalLive=Σ LayerPart

where *LayerPart* is the mass of the part for each layer. In addition to these totals, the total mass of each part is also summed across all the layers.

Volume Function.

This function converts the mass of boles from a cell for a given year to wood volume. The volume of bole wood is estimated from the mass of live sapwood and heartwood, the fraction of boles in wood (WoodPer) and the wood density (WoodDen) for the given species in a cell and layer. The parameters WoodPer and WoodDen are stored in the Growth.prm file.

The total merchantable mass of boles for a tree layer in a cell is:

LayerWood=(LayerSapwood+LayerHeartwood)*WoodPer/100

where WoodPer is the percentage of the bole mass that is wood as opposed to bark (Wilson et al.1987). The volume of merchantable wood (*LayerVolume*) is calculated by dividing the wood mass (*LayerWood*) by the wood density (WoodDen):

LayerVolume=LayerWood/WoodDen

The values of wood density for each species is based on Marglin and Wahlgren (1972) and Wilson et al. (1987). Note the units for volume are m³ ha⁻¹.

MORTALITY



The purpose of this module is to calculate the mortality, pruning, and turnover rates of plant parts (foliage, fine roots, branches, sapwood, heartwood, heart-rot, and coarse roots) associated with normal growth processes. The rate that is calculated depends on the layer and the plant part being considered. These variables are used by the GROWTH and DECOMPOSE modules to adjust the live mass of parts or to calculate inputs to detritus pools.

Detritus inputs associated with either harvest or fire are calculated by HARVEST or BURNKILL, respectively.

During the course of normal growth, the mortality of sapwood, heartwood, and heart-rot occurs when a tree dies. In contrast, the mortality of foliage, fine roots, branches, and coarse roots occurs when a tree dies or when parts are pruned. That is, when the sapwood, heartwood, and heart-rot of tree dies, we assume that all the associated plant parts will also die. There is, however, some mortality of these non-bole plant parts even when a tree does not die caused by normal pruning and replacement.

The parameters required by this function are stored in the Mort.prm and Estab.prm files.

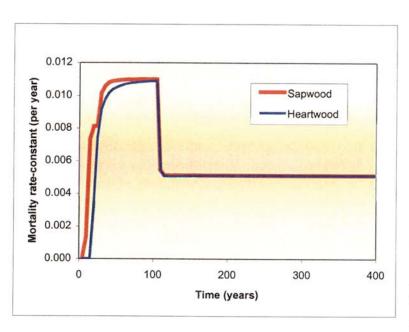
TreeMort Function.

This function determines the rate upper and lower trees die. The rate of tree mortality is dependent upon whether the single cell or multicell version of the model is being used, the tree layer involved, and the time an upper tree has occupied a cell. In the single cell version of the model, tree mortality occurs in the cell every year of the simulation. This is because the upper tree layer represents a population of trees and never becomes a single tree.

In the multicell version of the model tree mortality is calculated one of two ways depending on the time an upper tree has occupied a cell. In the case of the lower trees, mortality occurs each year of the simulation. In the case of upper trees, however, the layer may either represent a population or a single individual depending on the amount of time it has occupied the upper tree layer. For a given cell, upper tree mortality occurs each year that the time a species has occupied the upper canopy layer (TimeThere) is less than the age required for a single tree to occupy a cell (TimeClose). If the time a species occupies a cell is greater than TimeClose, then tree mortality is set to 0 until the DIEOUT function determines the species has died-out of a cell.

A major assumption used to calculate mortality rates is that as the amount of light absorbed by the stand increases, the mortality rate for trees increases. The amount of light absorbed is taken from the GROWTH module. For the single cell version and the multicell version when TimeThere is less than TimeClose:

LayerMortRate=MortMax*(LightAbsorbed/MaxLightAbsorb)



where LayerMortRate is the rate upper or lower trees die. LightAbsorbed is the amount of light absorbed by the layer, and MaxLightAbsorb is the maximum amount of light that can be absorbed by the tree layer. The later two variables are calculated by the GROWTH module. This function increases mortality as a positive function of the total amount of light removed, mimicking the phase of self thinning during the middle stages of stand development (Figure 30).

Figure 30. Change in the mortality rate-constant as a function of age. The decline after year 100 is due to switch from multiple to a single tree in the cells.

When TimeThere is greater than or equal to TimeClose two different approaches are used depending on whether the single cell or multicell version is selected. For the single cell version, LayerMortRate is gradually decreased from the value indicated by MortMax to the value determined by the DIEOUT module (ExtRate). This allows the single cell version to roughly match the change in mortality predicted by the multicell version. The rate of the conversion from one value to another is based on the rate that upper trees colonized the cells (EstOpenNF, EstOpenNS, EstOpenAF, EstOpenAS). Thus, if upper trees establish rapidly, the transition of mortality rates is rapid and vice versa.

For the multicell version the approach depends on whether the upper or lower tree layer is being considered. In the case of the upper tree layer, if the time a species has occupied an upper canopy layer (TimeThere) is equal or greater than the age required for a single tree to occupy a cell (TimeClose) then upper tree mortality rate can be either 0 or 1. If the upper tree layer does not die out (see DIEOUT module), then the upper tree mortality rate is:

UpperTreeMortRate=0

where UpperTreeMortRate is the mortality rate of the upper tree layer. If the DIEOUT module determines that the upper tree layer in a cell shall be replaced, mortality of the upper tree layer in this case occurs:

UpperTreeMortRate=1.0

In the case of the lower tree layer, LowerTreeMortRate is determined using the same equation as when TimeThere is less than TimeClose. This is based on the assumption that the lower tree layer always represents more than one tree per cell.

BranchPrune Function.

This function determines the rate that branches of upper and lower canopy trees and shrubs are lost via pruning. The rate branches are pruned (BranchPruneRate) is a positive function of the total amount of light removed and the maximum rate of pruning for an intact stand (BranchPruneMax):

BranchPruneRate = BranchPruneMax*(LightAbsorbed/MaxLightAbsorb)

where LightAbsorbed is the amount of light that is absorbed by a tree or shrub layer and MaxLightAbsorb is the maximum light available for the layer to absorb, as calculated in the GROWTH module.

Unlike the TreeMort function, branch pruning occurs for upper and lower canopy trees regardless of the time trees have been on a cell or whether the single or multicell versions are run. In the case of the multicell version, however, if the DIEOUT module determines if the upper tree layer dies out from a cell, then BranchPruneRate for the upper canopy layer is set equal to zero:

BranchPruneRate=0.

This method is used because when upper tree layers die out, the transfer of branches to dead branches is accounted for by the TreeMort function (see the GROWTH module description).

CRootPrune Function.

The rate coarse roots of upper and lower tress and shrubs are pruned is calculated by this function. The rate coarse roots are pruned (CRootPruneRate) is positive function of the total amount of light removed and the maximum rate of pruning for an intact stand (CRootPruneMax).

CRootPruneRate = CRootPruneMax*(LightAbsorbed/MaxLightAbsorb)

where LightAbsorbed is the amount of light that is absorbed by a tree layer and MaxLightAbsorb is the maximum light available for the layer to absorb as calculated in the GROWTH module.

As with branch pruning, coarse root pruning occurs for upper and lower canopy trees regardless of the time trees have been on a cell and whether the single or multicell versions are run. In the case of the multicell version, however, if the DIEOUT module determines if the upper tree layer dies out from a cell then CRootPruneRate for the upper canopy layer is set equal to zero:

CRootPruneRate=0.

This method is used because the transfer of coarse roots to dead coarse roots associated with trees dying out of a cell is accounted for by the TreeMort function (see the GROWTH module description).

Foliage Function.

This function determines which rate of foliage turnover used in DECOMPOSE. For all the plant layers the rate foliage is added to the DeadFoliage pool is defined by LeafTurnoverRate as stored in the Mort.prm file. If the upper tree layer dies out from a cell, then:

LeafTurnoverRate=0.

This method is used because the transfer of foliage to dead foliage associated with a tree dying out of a cell is accounted for by the TreeMort function.

FineRoot Function.

This function determines which rate of fine root turnover will be used by the DECOMPOSE module. For all the plant layers except the upper tree layer the rate fine roots are lost is defined by FineRootTurnoverRate as stored in the Mort.prm file. In the case where the upper tree layer in a cell is selected to die out by the DIEOUT module, then:

FineRootTurnoverRate=0.

This method is used because the transfer of fine roots to dead fine roots associated with a tree dying out of a cell is accounted for by the TreeMort function.

DECOMPOSE



This module is used to simulate the input, decomposition, and storage of carbon in detritus. All detritus **pools** are named after the corresponding live plant parts with the prefix Dead added. Six pools of detritus carbon are considered: 1) the **dead foliage** derived from foliage, 2) **dead fine roots** which can be either in the organic or mineral soil 3) **dead branches** (fine woody debris) derived from branches, 4) **dead sapwood** (one form of coarse woody debris), 5) **dead**

heartwood (another form of coarse woody debris), and 6) **dead coarse roots**. For computational purposes dead sapwood and dead heartwood are further subdivided into salvageable versus non-salvagable and snag versus log pools. All detritus pools can be in turn subdivided into **cohorts** of input so that lag times associated with decomposition can be accounted for. It is also possible to forgo the cohort structure and not account for lag times.

In addition to these detritus pools, the model simulates the dynamics of three stable pools (stable foliage, stable wood, and stable soil) that represent extremely decomposed organic matter. Despite the prefix stable, these pools do lose organic matter via decomposition, albeit at a very slow rate.

All of the plant layers can input detritus into the DECOMPOSE module, however, some life forms do not have certain woody parts and therefore do not contribute to the woody detritus pools. Herbs are assumed to contribute to the dead foliage and dead fine roots only. Shrubs contribute to the dead foliage, dead fine roots, dead branches, dead sapwood, and dead coarse roots. Finally, trees contribute to all the detritus pools including dead foliage, dead fine roots, dead branches, dead sapwood, dead heartwood, and dead coarse roots.

The inputs of material to the detritus pools comes from three potential sources: 1) normal litterfall and mortality, 2) thinning, herbicide use, and harvesting, and 3) fire killed plants. The first input is calculated by MORTALITY, the second by HARVEST, and the third by BURNKILL. Although pools receive inputs from the four plant layers, the input mass is aggregated and the substrate quality is averaged for each cell. The input of material into the stable pool is determined by the lag required to form this material.

The rate that each detritus pool decomposes and the time lag associated with transfers to other pools is determined by the species (as parameterized by the Decomp.prm file), and the climate as calculated by the CLIMATE module. Decomposition rates of the stable pools are determined by the values stored in the DecayPool.prm file as modified by climatic factors calculated by the CLIMATE module.

The stores of detritus calculated in the DECOMPOSE module are used by the CLIMATE module to calculate the interception of water by the dead foliage, woody detritus, and stable pools. Dead fine root, dead coarse root, and stable soil pools are assumed to not intercept water for water balance purposes.

The files directly used by this module are Decomp.prm and DecayPool.prm.

Detritus Input Function.

This function is used to calculate the total input into each of the detritus pools. The inputs of material to the detritus pools comes from three potential sources: 1) normal litterfall and mortality associated with self-thinning or the dying out of the upper tree layer, 2) thinning, herbicide use, and harvesting, and 3) fire killed plants. For any given year, the input can come from several of these sources. Each year the inputs from normal litterfall and mortality and upper tree die out are calculated first, and then additional inputs from harvesting or burning are added. The inputs from harvest and fire are calculated in separate time steps that represent a fraction of a year. This method is used to avoid possible conflicts in calculating the mass of pools.

Inputs to each of the detritus pools are calculated as follows where *Pool* represents a specific detritus pool, *Layer* represents a plant layer, and *Part* represents a plant part:

For the parts foliage, fine roots, branches, and coarse roots in cells not harvested or burned, the input is:

LayerPoolInput=PoolTurnoverRate*Part + MortRate*Part

where LayerPoolInput is the input mass from normal leaf fall and pruning for a particular layer and part, Part is the mass of the live part being considered, PoolTurnoverRate is the fraction of the part for a layer that is pruned or replaced in a given year, and MortRate is the mortality rate of trees. PoolTurnoverRate has different names depending upon the plant part considered; FoliageTurnoverRate, FRootTurnoverRate, BranchPruneRate, and CRootPruneRate are used for foliage, fine roots, branches and coarse roots, respectively. All these variables are calculated by MORTALITY. MortRate it is also calculated in MORTALITY and accounts for the input of non-bole parts associated with the mortality of entire trees. This includes the death of upper canopy trees that are selected to be replaced by the DIEOUT module.

For the parts sapwood, heartwood, and heart-rot, in cells not harvested or burned, the input is:

LayerPoolInput=MortRate*Part

where LayerPoolInput in this case is the input mass from sapwood, heartwood, or heart-rot of dying trees, Part is either sapwood, heartwood, or heart-rot mass, and MortRate is the

mortality rate of trees calculated in MORTALITY. As for the non-bole parts, MortRate includes the death of upper canopy trees that are selected to be replaced by the DIEOUT module.

Plant parts from layers can also be added to detritus pools when trees are harvested during thinning, herbicide use, or clear-cutting. These inputs are calculated after normal mortality inputs are calculated in a time step representing a fraction of a year (e.g., 12.2). If the trees in a cell are thinned, herbicided, or harvested then the inputs from foliage, fine roots, branches, sapwood, heartwood, and coarse roots are:

LayerPoolInput=PoolHarv

where *Pool*Harv is the amount of material generated from a layer as input to a detritus pool by harvest activities from HARVEST.

Finally, plant parts from layers can be added to detritus pools when plants are killed by site preparation or wildfires. These inputs are calculated after normal mortality inputs and harvest inputs are calculated in a separate time step that represents a fraction of a year (e.g., 12. 3). If plants in a cell are killed by fire, then the inputs from foliage, fine roots, branches, sapwood, heartwood, and coarse roots are:

LayerPoolInput=BurnInputPool

where BurnInputPool is the amount of plant parts killed by fire but not consumed as calculated by BURNKILL.

The total input to a pool (*Pool*Input) at any time step is the sum of all the inputs from the layers in a cell.

 $PoolInput = \sum (LayerPoolInput)$

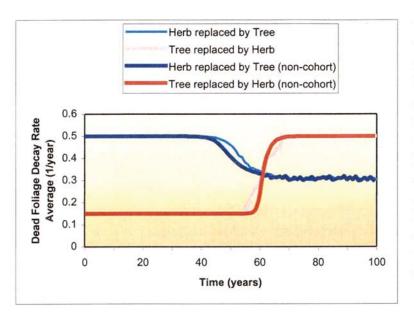
Detritus Substrate Effect Function.

This function calculates the effect of the substrate quality of the various inputs on the overall decomposition rate of a detritus pool. This function is invoked each time inputs are added to a cell. Thus it is possible to invoke this function three times in one year if normal growth, harvest, and fire occurs in a year.

The decomposition rate of each pool is dependent on the substrate quality of the inputs to that pool and the current substrate quality of the pool. The overall decomposition rate is a weighted average of the input and current stores. This has the dual effect of building in a system memory but allowing the decomposition rate to gradually change if the substrate quality of the inputs change (Figure 31)

The first step is to calculate the weighted average decomposition rates of the inputs of each pool from the herb, shrub, lower tree, and upper tree layers so that the layers with the largest inputs have the greatest impact on the decomposition rate:

InputDecayRate $Pool = \sum (LayerPoolInput*DecayRateLayerPart)/PoolInput$



where InputDecayRatePool is the weighted average decomposition rate of the inputs to a detritus pool, LayerPoolInput is the mass input of each plant part from a specific plant layer (e.g., herbs) to a detritus pool, PoolInput is the total input of all layers to a pool, and DecayRateLayerPart is the decomposition rate of a part for a layer at 10 C and when moisture is not limiting.

Figure 31. Response of decomposition rate-constant to a sudden change in substrate quality. The cohort mode is shown in the lighter lines.

For herb and shrub layers the latter parameter is fixed for the entire layer. For trees, however, this parameter is a function of the tree species occupying the particular tree layer. The values of DecayRateLayerPart are the values stored in the Decomp.prm file.

The second step is to calculate the weighted average decomposition rate from the average substrate quality of the inputs and the current material within the detritus pool. This step builds in a system memory and allows the decomposition rate of a detritus pool to change gradually when the substrate quality of the inputs change. Therefore one cannot change the decomposition rate of a detritus pool unless the change in substrate quality of the inputs is continued. The weighted average decomposition rate of each detritus pool is:

PoolDecayRateAvg=(InputDecayRatePool*PoolInput +OldPoolDecayRateAvg*Pool)/(PoolInput+Pool)

where *Pool*InputDecayRate and *Pool*Input are as above, Old*Pool*DecayRateAvg is the weighted average decomposition of each detritus pool from the past year, and *Pool* is the last year's mass of a particular detritus pool. An array of the values from the previous year containing Old*Pool*DecayRateAvg is stored and used to calculate the current value of *Pool*DecayRateAvg.

Position Function.

This function determines if woody detritus inputs from sapwood, heartwood, and heart-rot are added in the "position" of a snag or log. This dichotomy is important in that it determines the water balance of the woody detritus and hence the decomposition rate and the time it remains in a salvagable condition.

The proportion of sapwood, heartwood, and heart-rot that is added to the snag versus log pool depends on the location of the site, cause of mortality, the age of the trees in a cell, and the tree layer considered:

- 1) All lower trees dying from normal mortality processes are added to the snag pools.
- 2) All upper and lower trees dying from fire, associated with either wildfire or site preparation are added to the snag pools.
- 3) All woody parts of upper and lower trees that result from cutting operations are added to the log pools, whereas those killed by herbiciding are added as snags.

In addition, the proportion of snags dying from normal mortality causes is determined from the location as defined in the Ecoregion.prm file. Most trees die as snags early in stand development, however, the proportion of snags decreases as stands approach the old-growth phase. The proportion of snags also varies with location in the Pacific Northwest, with the the lowest proportion of snags along the wind-prone coastal zone, and the highest in the insect-prone interior zone (Franklin et al. 1987).

Salvage Function.

This function determines if woody detritus inputs from sapwood, heartwood, and heart-rot are sufficiently large or undecomposed to be considered merchantable in a timber salvage operation. All woody detritus input from either lower trees or heart-rot are considered unmerchantable, and therefore are added to either the non-salvagable log or snag pools. Upper trees that are less than the minimum mean tree volume (set in the Harvest.prm file) are also considered to be non-salvagable. All other woody detritus inputs are considered salvagable and input into either the salvageable snag (SalvSnagPart) or salvagable log (SalvLogPart) pools. The mean volume of trees that are dying is determined in the Density function of the Growth module.

Cohort Function.

This function determines the rate detritus is transfered from salvagable to non-salvagable pools, from snag to log pools, and to stable pools. In each case, a lag time occurs before these transfers can occur. That is, snags do not break into log pieces until a period of decomposition occurs. Likewise, woody detritus is merchantable until a large proportion of the material is decayed. A cohort data structure is used to introduce these lag time effects

(Figure 32). One can also choose to simulate detritus pools without a cohort structure by selecting this option in the Simul.drv file.

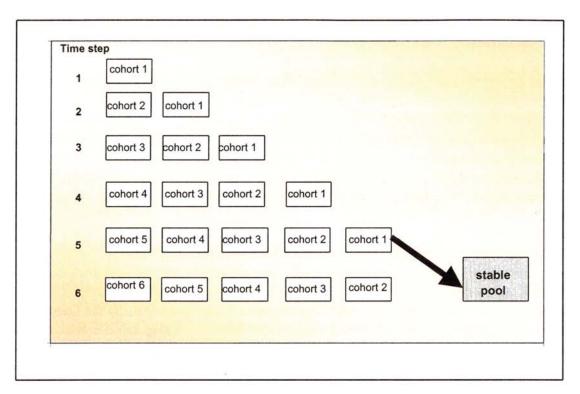


Figure 32. Development of cohort structure assuming a lagtime of 5 years and inputs of 6 years. After 6 years cohort 1 is added to the stable pool.

Cohorts are established for the appropriate detritus pools when input occurs. Each cohort is decomposed separately until the lag time required for the transfer has been exceeded. When this happens the remaining contents of the cohort are passed to the next detritus pool if a random number is less than or equal to the transfer rate set in the DecayPool.prm file. If the transfer is from salvagable to non-salvagable snags (i.e., SalvSnagLayer to SnagLayer), a new cohort is created to estimate the time until snag fall. If on the other hand the transfer is to non-salvagable logs (LogSapwood or LogHeartwood), then cohorts are formed to account for the lag time associated with the formation of the stable wood pool. Similar transfers occur for the formation of StableFoliage from DeadFoliage and StableSoil from DeadFineRoots and DeadCRoots. In addition to the mass of the cohort, the species is also transfered so that new time lags for the appropriate pool can be calculated.

The time lags for transfer from salvagable to non-salvagable woody detritus, and from snags to logs, and from detritus to the stable pools is set in the Decomp.prm file. The time lags in this file represent the years required under optimum conditions for decomposition. These times are adjusted downward for sub-optimal temperature or moisture regimes:

PoolTimeLag = PoolTimeLagOptimum / PoolAnnualAbioticDecayIndex

where *Pool*TimeLag is the time lag in the particular environment, *Pool*AnnualAbioticDecayIndex is the combined effects of temperature and moisture on decomposition, and *Pool*TimeLagOptimum is the time lag under optimum temperature and moisture conditions.

If the non-cohort version of the model is run, then a constant proportion of the pool is transferred each year regardless of the timing of inputs. This transfer rate (*Pool*TransferRate) is determined from the time lag and rate of transfer noted in the DecayPool.drv file as well as the decomposition rate of the material involved. The relationship used approximates the values that would result from the cohort version if the inputs were constant. This approximation is based on a weighted average of the mass contributing to the transfers (that is after the lagtime is exceeded) versus the total mass of material in the detritus pool. Assuming constant input, the total mass in a detritus pool that is not contributing to the transfers is:

PoolNonTransferMass = 1/(PoolDecayRateAvg*PoolAbioticDecayIndex) * (1- exp[-PoolDecayRateAvg*PoolAbioticDecayIndex*PoolTimeLag])

where *Pool*DecayRateAvg is the average substrate quality as determined by the Detritus Substrate Effect function and *Pool*AbioticDecayIndex is the annual index of abiotic effects as determined by CLIMATE. The mass of the pool contributing to the transfers to the next pool is equal to:

PoolTransferMass=PoolInputTransferMass/ [(PoolDecayRateAvg*PoolAbioticDecayIndex)+PoolTransferRate]

where PoolInputTransferMass is the mass that remaining after the lagtime is exceeded:

PoolInputTransferMass=

exp[-PoolDecayRateAvg*PoolAbioticDecayIndex*PoolTimeLag].

The total mass of the pool is:

PoolTotalMass=PoolNonTransferMass + PoolTransferMass

The transfer rate for a pool is then the weighted average of the period without transfers versus those with transfers. Since the period without transfers has a rate of 0 regardless of its mass the average transfer rate is:

PoolMeanTransferRate=PoolTransferRate*PoolTransferMass/PoolTotalMass

where *Pool*TransferRate is the value specified in the DecayPool.drv file. The end result is that in the non-cohort version the mean annual transfer rate is used. This rate is computed each year and therefore varies as substrate quality and climatic variables change.

Detritus Decomposition Function.

This function calculates the decomposition rate and mass of detritus lost from decomposition. Decomposition rate is calculated from the substrate effect (see Detritus Substrate Effect function above) and the effects of abiotic factors, temperature, solar radiation warming, and moisture as calculated in the CLIMATE module. The rate of decomposition losses from all the detritus pools is:

PoolCohortDecay=PoolCohortDecayRateAvg*PoolAnnualAbioticDecayIndex

where *PoolCohort*Decay is the realized decomposition rate of a detritus pool cohort, *PoolCohort*DecayRateAvg is the substrate quality determined rate when temperature is 10 C and moisture is not limiting, and *PoolAnnualAbioticDecayIndex* is the combined effects of temperature and moisture on decomposition as calculated in the AbioticDecayIndex function of CLIMATE modules.

The mass of detritus lost via decomposition in a year from a pool is:

PoolCohortDecayLoss=PoolCohortDecay*Pool

where *PoolCohort*DecayLoss is the mass lost via decomposition, *PoolCohort*Decay is the realized decomposition rate of a pool, and *PoolCohort* is the mass of a detritus pool cohort.

Stable Transfer Function.

This function transfers mass from cohorts that have exceeded the time lag required to form stable organic matter. Once the time lag for the given climate and species has been reached, a random number from 0 to 1 is selected and compared to the TransferRate indicated in the DecayPool.prm file. If the random number is lower or equal than the transfer rate, then the entire mass in this cohort is transferred to the appropriate stable pool (StableFoliage, StableWood, or StableSoil):

StableTransferPool=CohortPool

where StableTransfer*Pool* is the mass transferred to the stable pool and CohortPool is the mass of a detritus pool cohort. If the random number is greater than the transfer rate then no mass is moved to the stable pools.

Detritus Stores function.

This function is used to calculate the change in the mass of detritus stores each year. The balance for each detritus pool is the inputs minus the losses from decomposition and transfers to the stable pools. Losses from fire are calculated by SITEPREP. The overall rate of change for a detritus pool is:

∆PoolCohort=PoolCohortInput -PoolCohortDecayLoss-StableTransferPool

where *PoolCohort*Input is calculated in the Detritus Input function, *PoolCohort*DecayLoss is calculated in the Detritus Decomposition function, and StableTransfer*Pool* is as defined above.

The mass in a give detritus pool for a given year is therefore:

Pool= $OldPool + \Delta Pool$

where Pool is the mass in particular detritus pool, OldPool is the value for the previous year, and $\Delta Pool$ is as above.

Stable Soil Function.

This function controls the input and decomposition of stable organic matter. These represent three very stable pools in the model and should not change greatly over time unless the forest is removed for extensive periods. These include: 1) StableFoliage, which is derived from dead foliage (similar to O2 horizons), 2) StableWood, which is derived from logs and branches (similar to brown-rotted wood), and StableSoil, which is derived from dead fine and coarse roots (similar to mineral soil organic matter). The intent of this function is not to consider all the factors that control stable fractions and predict the stores of stable carbon a priori. Other models are more appropriate for these types of estimates. Rather the intent is to mimic the slow changes in stores in these pools.

Because the decomposition parameters of stable pools are difficult to measure, these parameters may have to be changed for each particular site. We recommend that they be estimated by running the model and comparing to the values expected for each ecosystem being examined. If the inputs of detritus to the stable pools are constant and the estimated stable pool approximates the store expected for particular site, then the decomposition rates for these pools are probably correct. To see if inputs to the stable pools are constant one can examine the Mort.Dgn file. If the inputs are constant and the stable pool is increasing, then the decomposition rates are probably too low. If the inputs are constant and the stable pool is decreasing, then the decomposition rates are probably too high. The user should change the value of StableDecayRate in the DecayPool.prm file until it converges on the target level of the stable pool being calibrated.

The equation describing the inputs to the stable pools is the sum of all the various inputs from detritus pools:

Stable Pool Input = Σ Stable Transfer Pool

where StableTransfer*Pool* is the transfer rate from each of the detritus pools as calculated in the Stable Transfer function.

As with the detritus pools, the decomposition rate-constant of each stable pool (StablePoolDecay) is a function of the substrate and abiotic effects:

Stable Pool Decay = Stable Pool Decay Rate * Stable Pool Annual Abiotic Decay Index

where Stable *Pool* Annual Abiotic Decay Index represents the combined effects of temperature and moisture calculated by CLIMATE, and Stable *Pool* Decay Rate is the rate of decomposition of a pool at 10 C when moisture conditions are not limiting.

The overall rate of change for each pool is:

∆Stable*Pool*=Stable*Pool*Input-Stable*Pool*Decay

The stores for this pool in a given year are:

Stable $Pool = Old Stable Pool + \Delta Stable Pool$

where OldStablePool is the mass for the previous year and Δ StablePool is calculated as above.

CoarseWoodyDebris Aggregation Function.

Coarse woody debris is comprised of many detritus pools, including snags versus logs, sapwood versus heartwood, and salvagable versus non-merchantable material. If the cohort mode is selected these pools are tracked in separate cohorts to introduce time lags. These cohorts are summed, however, to estimate climate effects on decomposition into the following pools:

 $TotalSalvSnagPool = \sum SalvSnagPoolCohort$

 $TotalSnagPool = \sum SnagPoolCohort$

 $TotalSalvLogPool = \sum SalvLogPool\ Cohort$

 $TotalLogPool = \sum LogPoolCohort$

where TotalSalvSnagPool and TotalSalvLogPool represent the sapwood and heartwood mass in salvageable snags and log, respectively; TotalSnagPool and TotalLogPool is the sapwood and heartwood mass in the unsalvageable log sapwood or heartwood pools, respectively; and PoolCohort indicates the mass in a particular cohort of a pool.

For the purposes of reporting carbon or organic matter stores, these values are futher aggregated into dead sapwood and dead heartwood pools:

DeadPool = TotalSnagPool +Total LogPool

where Pool is either sapwood or heartwood.

Detritus Aggregation Function.

Other detritus pools that have been broken into cohorts to introduce time lags are summed to estimate climate effects on decomposition and to report mass values. DeadFoliage, DeadFineRoot, and DeadCRoots are aggregated:

 $DeadPool = \sum PoolCohort$

where Dead*Pool* is the total mass of the detritus pool and *PoolCohort* indicates the mass in a particular cohort of a pool. As stable pools are not tracked using cohorts, there is no need to sum them across cohorts.

Total Stores Function.

This function calculates the total mass of detritus pools and total mass of stable carbon. These values are reported in the Total.out file.

DENSITY



(LayerDensity) each year is:

This module estimates the number of trees per cell for each layer using a variation of the -3/2 power law (Yoda et al. 1963). Given that STANDCARB does not track individuals, we have assumed that as biomass increases, the number of trees decreases. The density of trees

LayerTreeDensity=InitialTreeDensity * (LayerSapwood+LayerHeartwood+LayerHeart-rot) -1.5

Where Layer is either upper tree or lower tree, and the InitialTreeDensity is dependent on the width of the cells, TimeClose, and the level of site productivity (Table 1). The value of InitialTreeDensity is set so that one tree is left when TimeClose is reached. InitialTreeDensity is related to the MaxTreeDensity parameter in Simul.dvr input file. In fact, they are the same quantity, but have different units: MaxTreeDensity is trees/cell whereas InitialTreeDensity is trees/ha:

InitialTreeDensity = MaxTreeDensity / CellsPerHectare

Where

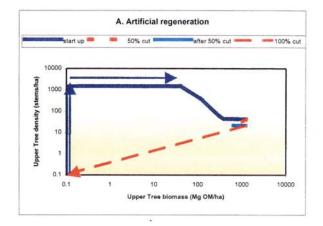
CellsPerHectare = $(1/\text{CellWidth}^2) * (10,000 \text{ m}^2/\text{ha})$

and CellWidth is from Simul.dvr.

If the sum of sapwood, heartwood, and heart-rot are zero, then the tree density is zero.

In addition to thinning caused by competition, disturbance can reduce density. After disturbances such as harvest or fire, the density of trees is reduced below that predicted from biomass. In those cases, tree density remains constant until it equals the value predicted by the biomass relationship (Figure 33). It will then proceed to be reduced as described by the -3/2 power law. If the disturbance reduces the number of individuals below a density of 1 ha⁻¹, then post disturbance density in a cell may not change. In the single cell mode, if the disturbance would reduce the density to below 1 ha⁻¹, then the density and biomass are set to zero. In the case of the multicell mode, the post disturbance density is either set to zero or left as it was before the disturbance. In this mode the density is set to zero if a random number between 0 and 1.0 is less than the probability of being disturbed. The probability of being disturbed is equal to the proportion of the trees in the cell that was supposed to be

stand level as specified in the HarvInt.drv file, however, rather than all cells being disturbed, only a fraction are disturbed such that no cell has less than 1 tree ha⁻¹.



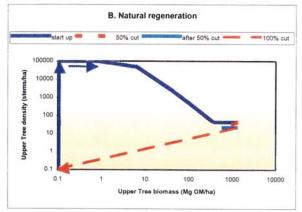


Figure 33. Decrease in density predicted by STANDCARB for upper and lower trees following: A. artificial regeneration and B. natural regeneration. The arrows indicate the direction of change; a 100% restarts the cycle with low biomass and low density.

In addition to disturbance effects, it is also possible for density and biomass of the lower tree layer to decrease simultaneously due to suppression from the upper trees. This would happen if the foliage in the upper tree layer increases. To simulate this process, density of lower trees is decreased in proportion to biomass decreases calculated by GROWTH. This prevents lower tree density from increasing when decreased light is the cause of a decrease in biomass.

Table 1. Initial tree density values to be used for natural regeneration as a function of bole growth efficiency, cell width, and TimeClose variables. If your system does not have the values of these parameters specified in the table, use linear extrapolation to estimate the appropriate value.

CellWidth (m) BoleGrowth Efficiency					
	0.19	0.66	1.0		
TimeClose = 50 years					
10	46000	245000	465000		
15	20000	100000	235000		
20	10000	65000	120000		
25	6500	42000	80000		
TimeClose = 100 years					
10	135000	880000	1600000		
15	59500	380000	710000		
20	34000	220000	400000		
25	20000	140000	255000		
TimeClose = 150 years					
10	180000	1160000	2180000		
15	79500	515000	850000		
20	45000	290000	540000		
25	28700	185000	347000		

HARVEST



The purpose of this module is to determine if a cell is to be harvested and to reallocate the carbon in the living and dead pools depending upon the type and utilization standards of the harvest used as well as the ability of a species to sprout. The output variables of this module are used to modify the state variables in the GROWTH and the DECOMPOSE modules. HARVEST is invoked the year a harvest is specified and can be for any number of cells or species.

HARVEST calculations are made following the calculation of changes associated with normal growth and decomposition.

The utilization standards (i.e., fraction of the bole removed) for each type of harvest is defined by the Harvest.drv file. The schedule of harvests is given in the HarvInt.drv file. Finally, the pattern of cells and species that are cut in a given harvest cycle is specified in the CutPatt.drv file.

If harvesting occurs on a cell in a given simulation year, then the HARVEST module determines which activity is to occur as defined by the HarvInt.drv file. Possible activities include: precommercial thinning, commercial thinning, herbicide, timber salvage, and clear-cut harvest. These activities may be performed on the upper or lower tree layer, separately or together. Moreover, it is possible, at least for the live trees, to specify that all or only a subset of species are to be harvested. Precommercial thinning is defined as a thinning of the trees where all the bole material is left on the site as slash. In a commercial thinning, a proportion of the boles in a cell is removed. In herbiciding trees are killed and left standing. In timber salvage, snags and logs in the salvageable classes can be removed. Finally, in a clear-cut all the bole material for a cell is cut.

When the single cell mode of the model is used, the treatment occurs on that cell. When the multicell version of the model is used, it is possible for the treatment to occur on all the cells or a subset of cells depending upon the pattern indicated in the HarvPat.drv file. Thus specifying clear-cut harvest in the multicell version does not necessarily mean that all the cells are clear-cut. Depending on the density of trees, HARVEST may remove different fractions of the trees than specificied. This occurs when the tree density left after disturbance would be less than 1 tree ha⁻¹. Since this possibility cannot occur, harvest activities are set to 100% when an activity would leave fewer than 1 tree ha⁻¹ for the single cell mode. In the multicell mode, cells with 1 tree ha⁻¹ are selected randomly for total

harvest. This allows the original proportion described in HarvInt.drv to be killed, but for no cell to have less than 1 tree ha⁻¹.

All the harvest activities result in the production of detritus that is removed from the GROWTH module and added to the decomposition pools in the DECOMPOSE module. In addition, some of the bole material is removed as harvested mass.

The files used by this module is Harvest.drv and HarvInt.drv.

Convert Function.

This function converts the parameters from the Harvest.prm file from percentages to proportions:

AmtCut = AmtCut/100

AmtTake=AmtTake/100

where AmtCut is the fraction of the tree bole volume that is cut and AmtTake is the fraction of the boles that are cut that is taken as harvested material.

Harvest Function.

Once the type and timing of a harvest treatment has been determined from the HarvInt.drv file the Harvest function calculates the amount of sapwood and heartwood mass removed, the mass of sapwood and heartwood left in tops and stumps, and the mass of other detritus or slash created by the harvest. Regardless of the type of harvest specified, the mass plant parts remaining after harvest is calculated as:

PartNew = AmtCut*PartOld

where

PartNew and PartOld are the masses of plant parts after and before the harvest.

Sapwood and heartwood can be removed from the site during harvest. The mass of sapwood and heartwood that is removed (*Part*Taken) from a cell is calculated as:

PartTaken = AmtCut*AmtTake*Part

where AmtCut is the proportion of the tree biomass cut and AmtTake is the proportion of the bole mass that is harvested and exported from the site as forest products, and *Part* is either sapwood or heartwood mass. In most cases, AmtTake for precommercial thinning is set to zero.

We have used the convention that the input of detritus mass associated with harvest is named for the detritus pool with the addition of Harv (e.g., sapwood left to decompose after harvest is called DeadSapwoodHarv). The amount of sapwood and heartwood mass added to the DeadSapwood and DeadHeartwood pools due to harvesting is calculated as:

PoolHarv = AmtCut*(1-AmtTake)*Part

where *Pool* is either DeadSapwood or DeadHeartwood, and *Part* is either Sapwood or Heartwood mass, respectively.

For other plant parts such as branches and coarse roots, the model assumes there is no export from the site. The mass of the non-bole parts transferred to their appropriate dead pool by commercial thinning is calculated as:

PoolHarv = AmtCut*Part

where *Pool* is the detrital pool the material is being added to (i.e., DeadFoliage, DeadFineRoots, DeadBranch, and DeadCoarseRoots) and *Part* is the corresponding plant part mass (i.e., Foliage, FineRoots, Branches, and CoarseRoots). An exception is when a species is capable of sprouting. Whenever AmtCut is 1.0 and the Sprout module determines that a harvested layer can sprout then foliage is set to the amount used when a layer is planted. This allows the layer to begin growing again after harvest. If the species sprouts (as determined by the Sprout module), then AmtCut is set to 0 for roots. This allows the below-ground parts to survive the disturbance.

Volume Function.

This function converts the mass of boles harvested from a cell for a given year to wood volume. The volume of bole wood removed in harvest is estimated from the sapwood and heartwood mass removed and the fraction of boles in wood (WoodPer), and the wood density (WoodDen) for the given species harvested in a cell. The parameters WoodPer and WoodDen are stored in the Growth.prm file.

The total mass removed in boles for a tree layer in a cell is:

Harvest=SapwoodTaken + HeartwoodTaken

The mass of wood (Wood) in the harvested boles is:

Wood=Harvest*WoodPer/100

where WoodPer is the percentage of the bole mass that is wood as opposed to bark (Wilson et al.1987). The volume of wood (HarvVol) is calculated by dividing the wood mass (Wood) by the wood density (WoodDen):

HarvVol=Wood/WoodDen

The values of wood density for each species is based on Marglin and Wahlgren (1972) and Wilson et al. (1987).

Harvest Density Function.

This function calculates the number of stems harvested in each layer based on the proportion of volume that is harvested (AmtCut):

LayerHarvestDensity = LayerDensity * AmtCut

where LayerHarvestDensity is the layer number of trees removed from a layer and LayerDensity is the number of trees in a layer prior to treatment as determined by the GROWTH module. This assumes that each tree is the same volume. An adjustment is also made to the total density to account for the loss of trees from harvest:

LayerActDensity = LayerOld Density-LayerHarvestDensity

where LayerActDensity is the actual tree density of the layer and LayerOldDensity is the density just before the harvest occurs.

BURNKILL



This module determines the amount of live vegetation that is killed and consumed by a fire. The purpose of this module to reduce the amount of live carbon in the GROWTH module and to transfer some of this material to the DECOMPOSE module as fire-killed detritus inputs. Not all the live vegetation killed by fire is necessarily transferred to detritus; some is consumed by the fire itself. Moreover, in the case of sprouting species, the roots may survive the fire. BURNKILL is invoked the year a fire is specified, but the calculations occur after normal growth and decomposition calculations have been made for that year. If a harvest has been specified for a year, then the BURNKILL calculations are performed after the harvest calculations

The type of fire may be a management burn or wildfire. The amount that the live plant parts and

layers is reduced is described in the BurnKill.prm file. The BurnKill.prm file is set up so that as the fire intensity increases from light to hot the fraction of each of the vegetation layers (herbs, shrubs, upper trees, and lower trees) killed by fire increases. The fraction of plant material that is consumed by fire also increases with fire intensity. Above- and below-ground plant parts can be consumed by fire to different degrees. We have set the parameters so that below-ground parts have less material consumed than above-ground parts for a given fire intensity. The user selects the timing and type of burn in the HarvInt.dry or the WFireInt.dry files.

Depending on the density of trees, BURNKILL may kill slightly different fractions of the trees than specificied by the user. This result occurs when the tree density left after disturbance would be less than 1 tree ha⁻¹. In the single cell mode, mortality is set to 100% when fire would leave fewer than 1 tree ha⁻¹ (since this possibility cannot occur in nature). In the multicell mode, cells with 1 tree ha⁻¹ are selected randomly for total mortality. This creates surviving proportion described in WfireInt.drv or HarvInt.drv, but since the process is random an exact match is unlikely.

BurnKill function.

This function determines the proportion of each part of each layer remaining after a fire occurs. The first step is to determine when and what type of fire occurs in a cell as determined by the HarvInt.drv file or by the WFireInt.drv file. A site preparation fire is assumed to occur the year of a harvest. Site preparation fires may occur after thinning, although usually these types of fires are not used. As with SITEPREP, only one of three types of fires can occur in a given year: light, medium or hot fires.

The fraction of the above-ground live mass of a part of a layer surviving (Surv*Part*) after a fire is:

SurvPart = (1-AboveKill/100)*Part

where AboveKill is the percentage of above-ground parts killed by the fire (determined from the BurnKill.prm file), and *Part* is the mass of the above-ground part (i.e., foliage, branches, sapwood, and heartwood) in question. An exception occurs when AboveKill is 100% and it is determined that the tree in the cell sprouts (see SPROUT module). In this case *Layer*Foliage is set to the same value as when a layer is planted. This allows the layer to begin growing again in the cell following the fire. These calculations are performed for each of the layers in a cell.

The fraction of the below-ground live mass of a part surviving (SurvPart) after a fire is:

SurvPart=(1-BelowKill/100)*Part

where BelowKill is the fraction of below-ground parts killed by the fire (determined from the BurnKill.prm file), and *Part* is the mass of the below-ground part (i.e., fine roots and coarse roots) in question. An exception is when a species is capable of sprouting. If the species sprouts after fire (determined in the SPROUT module), then BelowKill is set to 0. These calculations are performed for each of the layers in a cell.

The mass of above- and below-ground parts killed (KillPart) is calculated as:

KillPart=Part-SurvPart

where *Part* refers to a specific plant part of a layer in a cell. This quantity is deducted from the live mass of the parts for each layer of each cell in the GROWTH module.

Consume function.

This function calculates the of mass plant parts that is consumed by fire. Above- and below-ground parts have different portions of parts consumed by fire. For above-ground parts the mass consumed (Consum*Part*) is:

Consum*Part* = AboveBurn*Kill*Part*/100

where AboveBurn is the percentage of the above-ground parts that are killed by fire that are combusted (determined from the BurnKill.prm file), and *Part* is the mass of the above-ground part (i.e., foliage, branches, sapwood, and heartwood) in question. These calculations are performed for each of the layers in a cell.

For below-ground parts the mass consumed (ConsumPart) is:

Consum*Part*=BelowBurn*Kill*Part*/100

where BelowBurn is the percentage of the below-ground parts that are killed by fire that are combusted (determined from the BurnKill.prm file), and *Part* is the mass of the below-ground part (i.e., foliage, branches, sapwood, and heartwood) in question. These calculations are performed for each of the layers in a cell.

The mass of above- and below-ground parts added to the appropriate detrital pool in DECOMPOSE (BurnInputPool) is calculated as:

BurnInputPool=KillPart-ConsumPart

where *Pool* refers to a specific detrital pool in a cell. This quantity is added to the appropriate detrital pool of each cell in the DECOMPOSE module.

Density Function.

In addition to reducing the amount of live biomass, fires kill individual trees. These effects are calculated by the Density function by assuming that all the trees in a layer have the same volume:

LayerActDensity = LayerOldDensity*(1-AboveKill)/100

where *Layer*ActDensity is the actual number of trees ha⁻¹ after the fire, AboveKill is the percentage of above-ground parts killed by the fire (determined from the BurnKill.prm file), and *Layer*OldDensity is the density of trees ha⁻¹ before the fire.

SITEPREP



The purpose of this function is to reduce the amount of dead material in the DECOMPOSE module to reflect the losses caused by fire. The type of fire may be a management broadcast burn or a wildfire. SITEPREP is invoked the year a fire is specified, but the calculations occur after normal growth and decomposition calculations have been made for that year. If a harvest has been specified for a year, then the SITEPREP calculations are performed

after the harvest calculations. SITEPREP only reduces the parts of detrital pools that existed before the fire in question occurs. Thus detritus that is created the same year from harvest or death from fire are not reduced by SITEPREP.

The amount that the detrital pools are reduced is described in the SitePrep.prm file. The SitePrep.prm file is set up so that as fire intensity increases from light to hot, the fraction of each of the above-ground detrital pools removed by fire increases. In contrast, it is assumed that the dead coarse roots and the stable soil pools do not decrease when there is a fire. The user selects the timing and type of burn in the HarvInt.drv or the WFireInt.drv file.

SitePrep Function.

This function determines the proportion of each detrital pool remaining after a fire occurs. The first step is to determine when and what type of fire occurs in a cell as determined by the HarvInt.drv file or by the WFireInt.drv file. A site preparation fire occurs the same year as the harvest. One can have site preparation fires following any type of harvest. We assume that site preparation fires, however, will usually follow clearcutting but not thinning. One of three types of fires can occur in a given year: light, medium, or hot fires. To calculate the amount removed in each of the detrital pools after fire (*Pool*FireLoss), the fraction remaining is multiplied by the mass of the pool:

PoolFireLoss=(1-BurnRemaining/100)*Pool

where *Pool* is the mass of a given detrital pool (i.e., dead foliage, dead branches, dead sapwood, dead heartwood, dead fine roots, dead coarse roots, stable foliage, stable wood, or stable soil), *Burn*Remaining is the percent remaining after a fire of type *Burn*. The latter parameter is determined from the SitePrep.prm file.

If a fire does not occur in a given cell on a given year then:

PoolFireLoss=0.

The detritus pool mass is then reduced to account for these fire losses:

PoolNew=PoolOld-PoolFireLoss

where PoolNew and PoolOld are the detritus pool mass after and before the fire, respectively.

NEIGHBOR



The purpose of this module is to simulate the interaction between the cells regarding light. The main interaction between cells is therefore one of shading. The degree of shading is determined by the relative heights of trees in cells and the distance between cells. No attempt is made to realistically model the height distribution or profile of foliage in canopies in NEIGHBOR. Rather, it is assumed that foliage extends from the ground to the tree top and that foliage mass is evenly distributed over this height. While real

foliage profiles are more complex, this simplifying assumption represents many common situations such as well stocked stands. It is most likely to have problems in situations where tree stocking is very low or cell to cell variation in tree heights is high.

There are two aspects of shading considered: 1) the blocking of indirect or diffuse radiation and 2) the blocking of direct radiation. Diffuse radiation can be blocked on all sides, whereas direct radiation is blocked on the east, south, and west facing directions.

The degree of blocking of radiation inputs for direct and diffuse radiation is based on the height difference between the cell in question and the adjacent cell. The height is estimated from the age of the upper tree layer in each cell.

The cell arrangement is a rectangular grid (Figure 34). This means that each cell will have four immediate neighbors. The distance across a cell (CellWidth) represents a horizontal distance. The slope corrected area represented by each cell is therefore fixed. All cells are referenced using two numbers to indicate their position on the X and Y coordinates. These are RowNum and ColNum, respectively. "Looking" uphill, Cell 1,1 is in the uppermost left corner of the stand. This means the direction the sides of the cells face is across and up and down slope. The direction the sides face, with respect to true north will therefore depends on the aspect of the stand.

In addition to the simulated stand, the height of a boundary forest is followed. The boundary forest is basically the surrounding stand. Its height must be followed and used to shade cells on the edge of the simulated stand to avoid unrealistic boundary effects.

This module depends on information from the DIEOUT module to determine the age of the upper tree layer. The height of the tree layer is determined by parameters described in the Growth.prm file. This module also depends on the Radiate.drv file to calculate the height

of the sun at various times of the day for a site. Finally it depends on the Locate.dvr file to determine the relative elevations of the cells to each other and the sun from the slope and aspect.

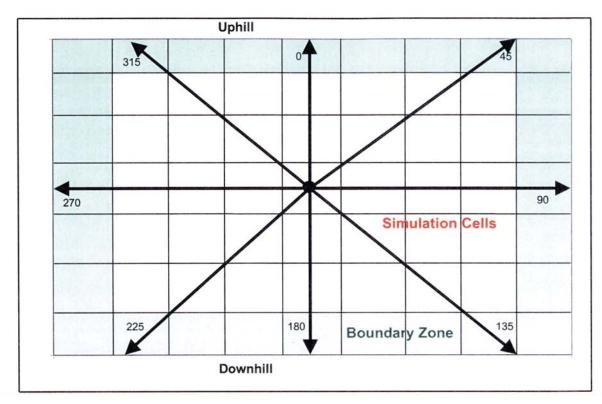


Figure 34. Arrangement of cells in STANDCARB multicell mode. Simulation cells are surrounded by a boundary zone with heights specified by the user. The arrows indicate the directions of transects used to determine shading effects.

Boundary Function.

This function is invoked once each simulation and is used to define the location and condition of the forest surrounding the simulated stand. As with all models that simulate shading effects, STANDCARB must address the so-called boundary problem. This is caused by the fact that cells respond to shading from surrounding cells, but on the boundaries the shading effect is ambiguous. Is the surrounding stand, for example, shorter or taller or the same as the simulated stand? Each boundary condition could lead to different responses of the simulated stand. To avoid this problem the user has to select the age of the surrounding stand. There are three options for the boundary forest (set by the user in Simul.dvr file):

- 1) No forest, if this selected then the tree height and age in the surrounding boundary cells is set to zero. This would be most likely to be used to simulate a remnant forest surrounded by agriculture land or development.
- 2) Old-growth forest, if this is selected then the height in the surrounding boundary cells is set to the maximum height (HeightMax) of the dominant tree species (see the Growth.prm file). This situation would best match a staggered setting cutting pattern.
- 3) The same age as the simulated stand, if this is selected then the height is increased assuming the age of the forest in the surrounding cells is the same as the average of the trees in the simulated stand. The height is calculated as in the Tree Height function below. This situation would be used to simulate a stand with "infinite" extent.

The two numbers defining the location of the boundary cells are calculated from the number of rows and columns selected by the user. The lower boundary forest locations is defined by using -1 for RowNum, the upper most boundary forest is defined by adding 1 to the highest RowNum of the simulated stand, etc.

Direction Function.

This function is used to adjust the angle of the transect lines used to estimate shading effects. These lines are used to sample the angle between a particular cell and its surrounding cells (Figure 24). With respect to the uphill direction, the angles of the transect lines are 0, 45, 90, 180, 225, 270, and 315 degrees. To estimate the effects of removing direct radiation, these transect lines must be referenced to the true azimuth and not the uphill direction.

The first step in making this adjustment is to estimate the azimith offset (Offset) between the uphill direction and south:

Offset = Aspect-180

The corrected transect line angle is:

CorrectedLineAngle = Offset + LineAngle

where LineAngle is the direction the transect line faces with respect to the uphill direction (0, 45, 90, 135, 180, 225, 270, or 315).

Local Elevation Function.

This function determines the local elevation differences of the cells from the slope steepness. Assuming that a stand is always rectangular in shape, the rows of cells will determine how far one has traveled in horizontal distance in the uphill direction.

Assuming that the first row is the lowest point of the stand the relative elevation of the cells in a row (RowRelElev) is:

RowRelElev = (CellWidth/100)*RowNumb*SlopeSteep

where RowNumb is the difference between the lowest and highest row number of the cells, SlopeSteepness is the slope steepness of the site in percent as defined by the Locate.dvr file, and CellWidth represents the maximum crown width of a mature tree. The later parameter is set at 20 m in this version of the model.

TreeHeight Function

The height of the crown in a cell will be determined from the age of the upper canopy layer. A Chapman-Richards equation will be used to predict the height from the age since planting of the upper canopy layer:

TreeHeight=HeightMax * (1 -exp [-HeightRate*Age]) HeightShape

where HeightMax is the maximum height of a species, HeightRate is the rate at which the maximum is reached, and HeightShape is the parameter that reduces height growth early in the life of a tree. These parameters are stored in the Growth.prm file. Age will be the time since the upper tree layer was planted in a cell. For the boundary cells, Age will represent one of the three conditions outlined above.

In the case of cells where a lower tree layer replaces an upper tree layer, the age of the new upper tree layer must be adjusted. Setting the age to zero when the tree layer replacement occurs will underestimate the height, because the lower tree layer has been growing slowly under the upper tree layer. Conversely using the time since planted as a lower tree would give the layer too much height. Therefore when a lower tree layer replaces an upper tree layer the age will be set at 25 years and then incremented as for the original upper tree layer (see the DIEOUT module).

TotalHeight Function.

This function is used to determine the total height of the trees in cells including the effects of topography. The total height difference between two cells is:

TotalHeight = TreeHeight + RelElevRow

Cell Select Function.

This function is used to establish an array of cells that need to be considered for shading effects. The idea is that although each cell has the potential to shade every other cell, only a subset of cells will lie along the transect directions that will be sampled (see Direction

a subset of cells will lie along the transect directions that will be sampled (see Direction function above). For each cell the surrounding cells that need to be examined will depend upon the transect line being considered. To avoid confusion we will refer to the transect lines by the direction they face with respect to the uphill direction.

For the 0 line the cells to be considered are selected by keeping ColNum constant and increasing the RowNum by 1 until a boundary cell is reached. For the 180 line the cells to be considered are selected by keeping ColNum constant and decreasing the RowNum by 1 until a boundary cell is reached. For the 90 line the cells to be considered are selected by keeping RowNum constant and increasing the ColNum by 1 until a boundary cell is reached. For the 270 line the cells to be considered are selected by keeping RowNum constant and decreasing the ColNum by 1 until a boundary cell is reached.

For lines on the diagonal the method is slightly more complex. For the 45 line the cells are selected by increasing both the RowNum and ColNum by 1 until a boundary cell is reached. For the 225 line the cells are selected by decreasing both the RowNum and ColNum by 1 until a boundary cell is reached. For the 135 line the cells are selected by increasing the ColNum by 1 and decreasing the RowNum by 1 until a boundary cell is reached. Finally, for the 315 line, the cells are selected by increasing RowNum by 1 and decreasing ColNum by 1 until a boundary cell is reached.

Distance Function.

This function determines the horizontal distance between two cells. This variable is then used to compute the angle between the canopies of two cells to determine shading effects. The first step is to calculate the difference in X and Y coordinates for the cells:

ColDiff=ColNum2-ColNum1

RowDiff=RowNum2-RowNum1

where these are the row and column numbers for cells 1 and 2. The horizontal distance between the centers of the cells is:

CellDist = CellWidth* $(ColDiff^2 + RowDiff^2)^{0.5}$

DiffuseShading Function.

The purpose of this function is to determine the fraction of the sky that is obscured by the trees in surrounding cells. The angle (in radians) between the top of tree layer in the cell of question and the eight adjacent cells which form the largest angle in the eight transects will be computed as:

DiffuseShadeAngle=arctan [(TotalHeightCell2-TotalHeightCell1)/CellDist]

where TotalHeightCell2 is the height of the upper tree layer in the adjacent cell, TotalHeightCell1 is the height of the upper tree layer in the cell in question and CellDist the distance from the center of one cell to the cell forming the largest angle.

The angle of the sky open to diffuse light would therefore be

DiffuseOpenAngle=1.57 - DiffuseShadeAngle.

After DiffuseOpenAngle is calculated for each of the 8 transects, they are summed up and divided to estimate the fraction of the sky that is obscured by adjacent trees:

DiffuseOpen = SDiffuseOpenAngle /12.5664.

This number is then used to reduce the MonDiffuseSolRadSlope that can enter a plot.

DirectShading Function.

This function estimates the effects of cells lying on the transects to the east, southeast, south, southwest, and west on the input of direct radiation to the cell. This function uses the angles calculated in the DiffuseShading Function to estimate the amount of direct radiation blocked. These angles are compared to mean altitude angle of the sun along each transect. The mean altitude angle of the sun on each transect is calculated from the transect direction and the mean altitude angle of the sun when it is due south (or solar noon). The Solar class of modules calculates this variable and stores it in the Radiation.dvr file.

The first step is to calculate the mean solar altitude angle for each transect:

TransectSolarAltAngle =

- SolarAltAngleSouth* cos (CorrectedLineAngle*ExpFactor+PhaseAdj)

where SolarAltAngleSouth is the solar altitude angle when the sun is due south, CorrectedLineAngle is the angle the transect faces (see Direction function above), ExpFactor and PhaseAdj are factors used to correct for the fact the sun does not always rise or set at due east. ExpFactor is calculated from the average azimuth angle when the sun rises (SunriseAzimAngle):

ExpFactor = (SunriseAzimAngle - 180)/90

and is used to rescale the angle between south and the azimuth angle of the sunrise. PhaseAdj is used to adjust the phase of the cosine wave so that the highest value is always at 180 degrees (due south). It is calculated as:

PhaseAdj = 0.0349* (90-SunriseAzimAngle)

TransectSolarAltAngle is then compared to the angle between the heights of the cell in question and the adjacent cell. If the solar altitude angle is smaller than (DiffuseShadeAngle) then the value of a variable indicating the direction (e.g., E, SE, S, SW, W) will be set to 1. If the sun angle exceeds the tree height angles then this variable is set equal to 0. To calculate the fraction of the direct light reaching the cell these variables are weighted by their importance in adding radiation:

DirectOpen=1-E*0.035 + SE*0.27 + S*0.39 + SW*0.27 + W*0.035

where E, SE, S, SW, and W indicate the effect of direct radiation blocking from those directions. For example, if direct light is blocked from all the directions then DirectOpen is zero. If on the other hand direct light is blocked from just the south then DirectOpen is 0.39.

Setting the CellWidth Parameter.

When running the interactive, multicell version the response of the model is sensitive to the value of CellWidth that is selected (Figure 35). One consideration is that the cell width should reflect the density found in a mature stand. When TimeClose is reached the density of trees should approximate the values found in published stand tables. One can compute the value of CellWidth that gives the desired density as follows:

TreeDensity = 1/(CellWidth*CellWidth/10000)

where CellWidth is the width of the cell.

Another consideration is that CellWidth also determines the minimum light that is possible. For example, the larger the cells the higher the minimum light that can reach the forest floor. Assuming that a single cell is surrounded by old-growth trees, and that approximately 50% of the light is diffuse, yields the values presented in Table 2. This is an important consideration because each species has a minimum light that it can establish under--if the CellWidth is too large, this effect will not be realized in the interactive mode.

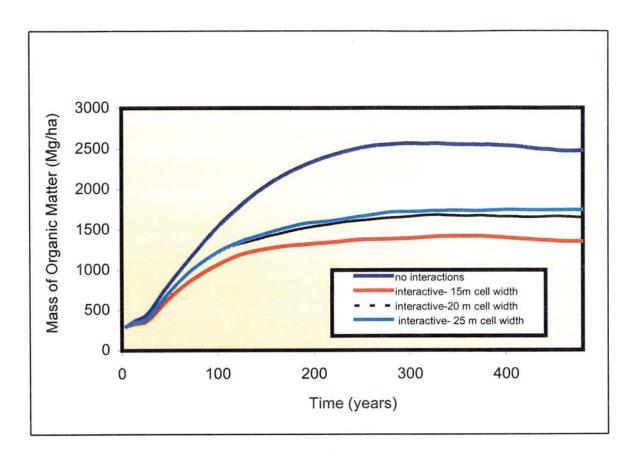


Figure 35. Effect of cell width on total organic matter stores using the multicell mode.

Table 2. Density r	reached at time close as determ	nined by the width of the cells used.
Cell Width (m)	Density (numbers ha ⁻¹)	Minimum Light (% full sunlight)
5	400	2-3
6	278	2-3
7	205	3-4
8	156	3-5
9	123	4-6
10	100	4-6
11	83	5-6
12	69	5-7
13	59	5-7
14	51	6-8
15	44	6-8
16	39	7-9
17	35	7-9
18	31	7-9
19	28	8-10
20	25	8-10

INPUT AND OUTPUT FILES

INPUT FILES

File Header

In version 2.0, a new file header has been designed for the input files. The header's format is the same for all the input files for consistency to aid both the user and the program. Here is an example of the new file header:

Program StandCarb
Data_File EcoRegions
Version 2

The new file header has three lines:

- 1. The "Program" line specifies the name of the program the input file is associated with. For this model, the name must be "StandCarb".
- The "Data_File" line contains the file code which identifies the file's type and format. The file code is a single word or a phrase with no spaces, e.g., "Site parameters".
- 3. The "Version" line identifies which format version the file uses. The version is a positive integer. This allows a program to distinguish between different versions of an input file when its format changes.

Because file information is now contained in this new file header, the information does not need to be repeated on each row in a data table.

Currently, only four input files use the new file header: two original input files with simulation parameters ("Simul.dvr") and tree regeneration parameters ("TreeReg.prm"), and two new input files with ecoregion parameters ("EcoRegion.prm") and herbicide parameters ("Herbicide.prm"). In the future, all the input files will be updated to use the new file header.

Comment lines

Each input file using the new file header also allows the user to place comments throughout the file. The comments can be used to document the data in the file. A common use of comments is to provide headings for columns in a data table.

Each line of text in a comment starts with the character ">". When reading the file, the program simply ignores all the comment lines.

PARAMETER FILES

This section describes the files containing the parameters needed to run the model. For the most part these files should require minor adjustments to make the model simulate most common situations. All the files that contain parameters end with the extension **PRM**.

For each class of model modules the files needed are described. Next the parameters are defined and the units indicated. The file format in terms of columns is flexible, however, the parameters must be listed in the order shown.

Finally, an example of each file is given.

Table 3. List of parameter files required to run the StandCarb model.			
File Name	Purpose		
Estab.prm	sets rates that layers establish		
EcoRegion.prm	defines the relative abundance of tree species in various ecoregions, and		
	the proportion of snags versus logs formed		
TreeReg.prm	defines which tree species can establish		
Growth.prm	sets species attributes of growth		
GrowLayer.prm	sets layer attributes of growth		
Mort.prm	sets species attributes of litter formation and mortality		
Decomp.prm	sets species attributes of decomposition		
DecayPool.prm	sets detritus pool attributes of decomposition		
BurnKill.prm	sets levels of fire mortality for each plant layer		
SitePrep.prm	sets levels of fuel reduction for each detritus pool		
Harvest.prm	defines the level of removal given a harvest		
Herbicide.prm	sets the ability of trees to recover from herbiciding		
Soil.prm	sets characteristics of soil texture classes		
SiteIndex.prm	sets the level of productivity for a site index of a tree species		

Estab.prm

This file indicates the probability that the different life forms (e.g., herbs, shrubs, and trees) have of entering a cell. This file is used by PLANT.

There are four regeneration scenarios parameterized: 1) NF-natural fast, 2) NS-natural slow, 3) AF- artificial fast, and 4) AS- artificial slow. Probabilities for each regeneration scenario are given for with and without an upper tree layer. If an upper tree layer is present then the Closed probabilities are used. If the upper tree layer is not present then the Open probability is used. Note that for any regeneration scenario and upper tree layer status (i.e., Open or Closed), the probabilities can not sum to a value exceeding 1.0.

The parameters in order they occur in the file are:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 1 indicates this is the Estab.prm file.

Layer: refers to the layer of living vegetation. Three names are valid: herb, shrub, or tree. Tree is used to indicate the parameters for upper and lower tree layers.

Natural Fast Open: establishment probability for natural open, fast regeneration (year⁻¹). For trees this would apply to the upper tree layer.

Natural Fast Closed: establishment probability for natural closed, fast regeneration (year⁻¹). For trees this would apply to the lower tree layer.

Natural Slow Open: establishment probability for natural open, slow regeneration (year⁻¹). For trees this would apply to the upper tree layer.

Natural Slow Closed: establishment probability for natural closed, slow regeneration (year¹). For trees this would apply to the lower tree layer.

Artificial Fast Open: establishment probability for artificial open, fast regeneration (year⁻¹). For trees this would apply to the upper tree layer.

Artificial Fast Closed: establishment probability for artificial closed, fast regeneration (year ¹). For trees this would apply to the lower tree layer.

Artificial Slow Open: establishment probability for artificial open, slow regeneration (year¹). For trees this would apply to the upper tree layer.

Artificial Slow Closed: establishment probability for artificial closed, slow regeneration (year⁻¹). For trees this would apply to the lower tree layer.

Example of Estab.prm file::

Establishment probabilities for layers - StandCarb model

			Natura	1			Artifi	cal		
Model	File		Fast		Slow		Fast		Slow	
#	#	Layer	Open	Closed	Open	Closed	Open	Closed	Open	Closed
ML02	1	Herb	0.500	0.250	0.600	0.300	0.600	0.300	0.600	0.300
ML02	1	Shrub	0.300	0.150	0.300	0.150	0.300	0.150	0.300	0.150
ML02	1	Tree	0.200	0.050	0.030	0.050	0.600	0.050	0.100	0.050

EcoRegion.prm

This file defines the various ecoregions recognized by the model. Each ecoregion's definition includes the relative abundances of tree species, and the proportions of snags versus logs that mortality yields.

File Header

This file uses the new file header. The file code is "EcoRegions", and the version is 1.

EcoRegion table

After the file header comes a data table defining the ecoregions. The table has the following columns:

EcoRegion: the name of ecoregion. The name must a single word or a phrase with no spaces.

% Snags Open Canopy: the proportion of upper trees dying as snags when the age of the trees in a cell is less than TimeClose (%).

% Snags Closed Canopy: the proportion of upper trees dying as snags when the age of the trees in a cell is greater than or equal to TimeClose (%).

Local Abundances: the name of the column in the table of local abundances that's associated with this ecoregion. The name must be a single word or a phrase with no spaces.

Local abundance table

After the ecoregion table comes a data table with relative local abundances for the ecoregions. The first line in the table starts with the phrase "Local_Abundances"; following this phrase are the column headings used in the ecoregion table.

Each row in the abundance table starts with the name of a tree species. The name must appear in the table of tree species in the tree-regeneration file ("TreeReg.prm"). The rest of the columns on the row specify that species' local abundances. Local abundances are relative within a column, and range from 0 (not present) to 99 (very abundant). The minus sign (i.e., "-") is an alternative to using 0 to denote a particular species is not present.

Example of EcoRegion. prm file:

Program StandCarb
Data_File EcoRegions
Version 1

>		% Snags		
>		Open	Closed	Local
>	EcoRegion	Canopy	Canopy	Abundances
	CA_CoastRange	90	30	coast_range
	CA_CascadesWest	90	50	cascades
	OR_CascadesWest	90	50	cascades
	OR CascadesEast	90	80	cascades
	OR CoastRange	90	30	coast range
	WA CascadesWest	90	50	cascades
	WA CascadesEast	90	80	cascades
	Other	90	60	Other

Local_Abundances	coast_range	cascades	Other
Abam	10	10	-
Abco	-	1	-
Abgr	1	1	_
Abla	-	1	-
Abpr	10	10	-
Acma	1	1	_
Alru	H =	10	-
Arme	1	1	-
Cach	5	5	_
Cade	_	1	-
Pila	·-	1	-
Pimo	1	1	_
Pien	_	1	_
Potr	2	2	_
Prem	5	5	_
Psme	50	10	10
Quga	12 	1	-
Thpl	20	5	_
Tshe	40	10	10
Tsme	·	10	-

TreeReg.prm

This file is used by PLANT to determine the tree species that can grow on a given site. These parameters are specific to a given location within the Pacific Northwest.

File Header

This file uses the new file header. The file code is "Tree_Regeneration_Parms", and the version is 1.

Regeneration-parameter table

After the file header comes a data table containing the regeneration parameters for various tree species. The table has the following columns:

Species: the species that the parameters describe. Species abbreviations are after Garrison (19??) and can be in any order.

Light Max: the maximum amount of light a species can establish under (percent of full sunlight)

Light Min: the minimum amount of light a species can establish under (percent of full sunlight)

DegreeDays Max: the degree day maximum that a species can establish under (degrees C)

DegreeDays Min: the degree day minimum that a species can establish under (degrees C)

WaterPot Min: minimum water potential under which a tree species can establish itself. If this value is exceeded for more than 9 months of the year then a species can not establish itself in a cell because the soil is too moist (MPascals)

WaterPot Max: maximum water potential that a tree species can tolerate during establishment (MPascals)

Sprout: ability of a tree species to sprout with 0 meaning no sprouting and 1-9 meaning species can sprout (the value increases with a species ability to form sprouts).

Version 2

Example of Treereg.prm file:

Program StandCarb

Data_File Tree_Regeneration_Parms

Version 1

> >	Species	Light_ Max	Min	Degree! Max	Days Min	Wate: Max	rPot Min	Sprout
	Abam Abco Abgr Abla Abpr Abma Acma Alru Arme Cach Cade Lide Pico Pila Pimo Pipo Pien	0.80 0.95 0.90 1.00 1.00 1.00 1.00 1.00 1.00 1.00	0.05 0.10 0.10 0.50 0.50 0.25 0.90 0.75 0.75 0.25 0.90 0.75 0.25 0.90 0.75	3095 2640 2640 1200 1854 1854 2810 3370 3095 3500 3500 3500 3500 3500 3500 350	625 990 990 350 885 920 810 625 900 900 400 350	2.0 2.5 2.0 1.8 2.0 2.0 1.0 2.5 2.5 2.5 2.5 2.7 1.7	0.10 0.10 0.10 0.10 0.10 0.10 0.05 0.05	0 0 0 0 0 9 5 9 9 0 9 0 0 0 0 0
	Pisi Potr Prem Psme Quga Sese Thpl Tshe Tsme	1.00 1.00 1.00 0.90 1.00 0.80 0.90 1.00	0.50 0.90 0.90 0.50 0.50 0.25 0.25 0.05	2000 3500 3500 3095 2880 2500 3095 3095 1475	400 900 600 625 975 600 625 625 555	1.5 1.0 2.0 2.0 2.5 1.5 1.7	0.05 0.05 0.10 0.20 0.20 0.10 0.05 0.10	0 9 9 0 9 9 0 0 0

Growth.prm

This file contains the species and understory parameters to describe the growth of foliage, branches, sapwood, heartwood, and roots. Most of these parameters are used by GROWTH. Temperature minimum and maximum are used by CLIMATE. WoodPer and WoodDen are used by HARVEST. HeightMax, HeightRate, and HeightShape are used by NEIGHBOR.

The parameters in the order they occur in the file are:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 3 indicates this is the Growth.prm file

Species: the species or understory layer that the parameters describe. Species abbreviations are after Garrison and can be in any order. Herb and shrub are included as non-tree species.

Light Comp Point: light compensation point for a species of tree or understory layer (%)

Light Ext Coeff: light extinction coefficient for a species of tree or understory layer (ha Mg⁻¹). This is the point at which additional leaves can not survive.

Foliage Prod Rate Max: maximum rate of foliage production (dimensionless). This parameter is the rate leaves of a species can create more foliage.

Fine Root Foliage Ratio: fine root mass to foliage mass ratio (dimensionless).

Sap Live: fraction the sapwood that is alive (% sapwood volume).

Rate Heart Wood Form: rate of heartwood formation from sapwood (year -1).

Branch Bole Ratio: branch mass to bole mass ratio (dimensionless). Used to allocate production to branches.

Coarse Root Bole Ratio: coarse root mass to bole ratio (dimensionless). Used to allocate production to coarse roots.

Temp Min: minimum temperature for net photosynthesis of a species or life form (C)

Temp Max: maximum temperature for net photosynthesis of a species or life form (C)

Wood Pcnt: the percentage of the bole that is wood (%)

Wood Density: the density of wood in the bole (Mg m⁻³)

Height Max: the maximum height of a tree species (m)

Height Rate: the rate the maximum height of a tree species is reached as a function of age (year⁻¹).

Height Shape: introduces a lag in the height growth curve (dimensionless).

Heart-Rot Lag: the number of years before heart-rot appears in the bole of a species (years).

Heart-Rot Rate Form: the rate that heart-rot is formed from heartwood (year-1).

Example of Growth.prm file:

Growth parameters for species - StandCarb model version 2

Rot	Rate	Form	0.000	0.000	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.020	0.010	0.010	0.005	0.020	0.010	0.010	0.010	0.010	0.010	0.010	0.025	0.020	0.010	0.010	0.010	0.010	0.020	
Heart-Rot		Lag	0	0	20	20	20	20	20	20	20	25			100							100	20	20	100	100	_	200	100	_
н		Shape	1.0	1.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	2.0	0.020
	Height	te	0 0.015	0 0.015	60 0.015	60 0.015				60 0.015	30 0.015	30 0.015	30 0.015				40 0.015					90 0.015	45 0.015	20 0.015	90 0.015		99 0.015	60 0.015	85 0.015	5 2.0 100
		Pont Density	0.45	0.45	0.40	0.35	0.35	0.31	0.37	0.36	0.44	0.37	0.60	09.0	0.35	09.0	0.38	0.34	0.35	0.38	0.33	0.37	0.31	0.47	0.45	09.0	0.38	0.32	0.42	60 0.01
	Wood	Pcnt	0.0	0.0	90.0	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	0.06	90.0	0.06	0.06	0.06	0.06	0.06	90.0	0.06	0.42
		Max	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	0
	Temp	Min	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7 90.0
Coarse		Ratio	0.000	1.500	0.750	0.770	0.770	1.200	0.720	0.650	0.380	0.550	0.950	0.900	1.000	1.000	0.900	0.900	0.900	0.570	0.850	0.800	0.500	0.500	0.620	1.250	0.770	1.500	0.520	0 37
Branch	Bole	Ratio	0.000	1.500	0.500	0.500	0.500	0.900	0.350	0.480	0.220	1.500	0.850	0.850	0.500	006.0	0.350	1.900	1.900	0.330	0.400	0.350	0.500	0.500	0.110	0.950	0.250	0.550	0.340	0.650
Rate				0.000	0.039									0.059	0.105	0.059	0.024			0.011	0.043	0.039	0.059	0.059	0.059		0.102	0.102	0.022	2 0.850
	Sap	Live	00.0	00.0	09.9	9.50	6.70	5.70	09.9	09.9	18.50	13.70	13.70	12.20	8.90	12.20	5.70	5.70	09.9	6.80	5.90	7.30	9.60	16.40	7.40	30.00	7.90	6.90	8.80	0 0.022
e Fine Root	Foliage	Ratio	0.75	0.50	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33	0.33 8.80
Foliage	Rate	Max	2.00	1.20	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.75	0.50	0.50	0.50	0.50	0.50	0.35	0.35	0.55	0.50	0.50	0.75	0.50	0.85	0.50	0.50	0.50	09.0).50 (
	Ext	Coeff	0.23	0.40	0.15	0.15	0.15	0.15	0.15	0.15	0.32	0.32	0.32	0.32	0.15	0.32	0.15	0.15	0.15	0.15	0.15	0.15	0.32	0.32	0.15	0.32	0.15	0.15	0.15	.15 (
ight	Comp	oint	2				10																				2	10	2	10
I	Comp	Species F	Herb	Shrub	Abam	Abco	Abgr	Abla	Abpr	Abma	Acma	Alru	Arme	Cach	Cade	Lide	Pico	Pila	Pimo	Pipo	Pien	Pisi	Potr	Prem	Psme	Quga	Sese	Thpl	Tshe	Tsme
	File	#	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
	Model	#	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02 3

GrowLayer.prm

This file is used to describe the response of the living layers to temperature. These parameters are all used in GROWTH. The parameters in the order they occur in the file are:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 4 indicates this is the GrowLayr.prm file

Layer: refers to the layer of living vegetation. Valid values are "Herb", "Shrub", "LTree" (for lower tree), and "UTree" (for upper tree).

Foliage Q10: rate foliage respiration increases with 10 C increase (dimensionless).

Foliage Resp10: respiration rate of leaves at 10 C (year-1).

FineRoot Q10: rate fine root respiration increases with 10 C increase (dimensionless).

FineRoot Resp10: respiration rate of fine roots at 10 C (year⁻¹).

Sapwood Q10: rate sapwood respiration increases with a 10 C change in temperature (dimensionless).

Sapwood Resp10: respiration rate of sapwood ar 10 C (year ⁻¹). Based on 5% of the sapwood being alive; species are adjusted from this rate based on SapAlive parameter in Growth.prm.

Branch Q10: rate branches respiration increases with a 10 C change in temperature (dimensionless).

Branch Resp10: respiration rate of branches at 10 C (year -1).

CRoot Q10: rate coarse roots respiration increases with a 10 C change in temperature (dimensionless).

CRoot Resp10: respiration rate of coarse roots at 10 C (year -1).

HeartRot Q10: rate heart-rot respiration increases with a 10 C change in temperature (dimensionless).

HeartRot Resp10: respiration rate of heart-rot at 10 C (year -1).

Initial Foliage Mass: mass of leaves that is added to Foliage when a layer is planted or resprouts (Mg ha⁻¹).

Canopy Inter Min: the minimum ratio of the mass of leaves to the amount of canopy interception $(mass^{-1})$.

Bole Growth Effic: the bole growth efficiency in terms of mass of sapwood produced per unit mass of foliage when moisture and temperature are not limiting (dimensionless).

Example of GrowLayer.prm file:

ole	rowth	0.00 0.50 1.00
		0.006 0 0.006 0 0.006 1
Initial	Foliage Mass	0.01 0.01 0.01
	Rot Resp10	2.000 0.000 2.000 0.000 2.000 0.010 2.000 0.010
	Resp10	0.000 0.050 0.017 0.017
	CRoot Q10	2.000 0.000 2.000 0.050 2.000 0.017 2.000 0.017
	Resp10	0.000 0.050 0.017
	Branch Q10 F	2.000 0.000 2.000 0.050 2.000 0.017 2.000 0.017
	sesp10	0.000 0.050 0.017
	Sapwood Q10	2.000 0.000 2.000 0.050 2.000 0.017 2.000 0.017
	ot Resp10	0.500 0.500 0.500
S	FineRoot Q10 Resp10	2.000 0.500 2.000 0.500 2.000 0.500 2.000 0.500
t layer	sp10	
or plan rsion 2	Foliage Q10 Re	2.000 0.500 2.000 0.500 2.000 0.250 2.000 0.250
Growth parameters for plant layers Standcarb model, version 2	Layer	Herb Shrub LTree UTree
paramarb mod	File #	4444
Growth	Model File #	ML02 ML02 ML02 ML02

Mort.prm

This file describes the maximum rates of mortality and branch pruning for woody layers of living plants, the time that a tree species needs to have its crown to reach cell size, and the lifespan of the trees.

Mortality and branch pruning parameters are used in MORTALITY. The time a trees crown needs to reach cell size, and the lifespan of the trees are used in DIEOUT.

The parameters in the order they occur in the file are:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 5 indicates this is the Mort.prm file

Species: the species or understory layer that the parameters describe. Species abbreviations are after Garrison and can be in any order.

Mort Max: mortality rate of a tree species when the maximum amount of light is absorbed (year⁻¹).

Branch Prune Max: pruning rate of branches of a tree species when the maximum amount of light is absorbed (year⁻¹).

Coarse Root Prune Max: pruning rate of coarse roots of a tree species when the maximum amount of light is absorbed (year⁻¹).

Time Close: the time required for the tree species to have is crown area equal the cell area (years).

Age Max: the maximum age of the tree species (years).

Turnover-Rate Foliage: turnover rate of leaves for a species or understory layer (year-1).

Turnover-Rate Fine Root: fine root turnover rate for a species or understory layer (year⁻¹).

Version 2

Example of Mort.prm file:

Mortality parameters - StandCarb model version 2

				Branch	Coarse Root			m.,	. Datas
Model	File		Mort	Prune	Prune	Time	7.00	Turnove	-Rates Fine
#	#	Species		Max	Max	Close	Age Max	Foliago	
ш	π	phecies	Max	Max	Max	CIOSE	Max	Foliage	Root
ML02	5	Herb	0.000	0.000	0.000	0	0	1.000	0.500
ML02	5	Shrub	0.010	0.020	0.010	0	0	0.500	0.500
ML02	5	Abam	0.010	0.020	0.005	100	500	0.200	0.500
ML02	5	Abco	0.010	0.020	0.005	100	500	0.200	0.500
ML02	5	Abgr	0.007	0.020	0.005	100	500	0.200	0.500
ML02	5	Abla	0.007	0.020	0.005	100	200	0.200	0.500
ML02	5	Abpr	0.010	0.020	0.005	100	500	0.200	0.500
ML02	5	Abma	0.010	0.020	0.005	100	500	0.200	0.500
ML02	5	Acma	0.018	0.020	0.005	100	200	1.000	0.500
ML02	5	Alru	0.018	0.020	0.005	50	120	1.000	0.500
ML02	5	Arme	0.010	0.020	0.005	50	150	0.333	0.500
ML02	5	Cach	0.018	0.020	0.005	50	150	0.333	0.500
ML02	5	Cade	0.010	0.020	0.005	100	900	0.200	0.500
ML02	5	Lide	0.018	0.020	0.005	50	150	0.333	0.500
ML02	5	Pico	0.010	0.020	0.005	100	400	0.333	0.500
ML02	5	Pila	0.012	0.020	0.005	100	500	0.333	0.500
ML02	5	Pimo	0.012	0.020	0.005	100	500	0.333	0.500
ML02	5	Pipo	0.012	0.020	0.005	100	600	0.333	0.500
ML02	5	Pien	0.010	0.020	0.005	150	500	0.200	0.500
ML02	5	Pisi	0.010	0.020	0.005	100	600	0.250	0.500
ML02	5	Potr	0.018	0.020	0.005	75	150	1.000	0.500
ML02	5	Prem	0.020	0.020	0.005	25	100	1.000	0.500
ML02	5	Psme	0.011	0.020	0.005	120	1200	0.200	0.500
ML02	5	Quga	0.010	0.020	0.005	100	300	1.000	0.500
ML02	5	Sese	0.005	0.020	0.005	150	1500	0.200	0.500
ML02	5	Thpl	0.010	0.020	0.005	100	1000	0.200	0.500
ML02	5	Tshe	0.013	0.020	0.005	100	600	0.250	0.500
ML02	5	Tsme	0.010	0.020	0.005	100	600	0.200	0.500

Decomp.prm

This file defines the decomposition rates of all the detrital pools except StableFoliage, StableWood, and StableSoil. The decomposition rate of the latter pools are defined in the DecayPool.prm file.

All the parameters are specific to a species of tree or to the shrub or herb layers that are producing detritus. All the parameters are used in DECOMPOSE. The parameters in the order they occur in the file are:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 6 indicates this is the Decomp.tab file

Species: the species or understory layer that the parameters describe. Species abbreviations are after Garrison and can be in any order.

Decay-Rate Foliage: foliage decay rate based upon leaf lignin/nitrogen ratio at 10 C and no moisture limitations (year⁻¹).

Decay-Rate Fine Root: fine root decay rate based upon the lignin/nitrogen ratio of the layers at 10 C and optimum moisture conditions for a species or understory layer (year⁻¹).

Decay-Rate Coarse Root: coarse root decay rate for a species or understory layer at 10 C and optimum moisture conditions (year⁻¹).

Decay-Rate Sap Wood: rate sapwood decay of a species at 10 C and moisture optimum for a species or understory layer (year-1).

Decay-Rate Heart Wood: rate heartwood decay of a species at 10 C and moisture optimum (year ⁻¹).

Decay-Rate Branch: decay rate of dead branches at 10 C and optimum moisture conditions (year⁻¹).

Optimum-Lag Snag Fall: the average number of years for a snag to fall under optimum decomposition conditions (years).

Optimum-Lag Salv: time that the average piece is salvagable under optimum conditions for decomposition (years)

Optimum-Lag Stable Wood: the time required for stable wood to form under optimum decomposition conditions (years)

Optimum-Lag Stable Foliage: the time required for the stable foliage pool to form under optimum decomposition conditions (years)

Optimum-Lag Stable Soil: the time required for stable soil organic matter to form under optimum decomposition conditions (years)

Example of Decomp.prm file:

Decomposition parameters - StandCarb model

2.77																											
Soil	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
Stable-Pools Wood Foliage	5 2	2	5	2	2	2	2	2	2	5	2	2	2	2	2	2	2	2	2	2	5	2	2	2	2	2	2
Stabl Wood	10	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20	20
Optimum-Lag Snag Fall Salv	00	2	2	2	2	2	2	2	2	2	2	20	2	2	10	10	2	2	2	2	2	20	10	30	20	2	2
Optimu Snag Fall	00	10	10	10	10	10	10	2	2	10	10	20	10	10	20	20	10	10	10	2	2	30	10	30	30	20	10
Branch	0.000	.10	٦.		۲.	1.	٦.	.1	۲.	.1	٦.	۲.	4	٦.	٦.	۲.	4	٦.	.1	۲.	۲.	٦.	.1	.1	.10	.15	Γ.
Heart	0.000	.05	.05	0.	.05	.05	.05	.05	.05	.01	.01	.00	.01	.02	.02	.02	0.020	.05	.05	.05	00.	.02	.05	.00	0.005	.07	.05
Sap Wood	0.000	0.050	°.	0.	0.	°.	°.	°.	°	0.	°.	°.	°.	0.050	0.050	0.050	0.050	0.050	0.050	0.050	0.050	0.070	0.100	0.050	0.050	0.070	0.050
Coarse	0.000		.10	٦.	۲.	۲.	.10	۲.	.15	.10	.10	٦.	۲.		.10	۲.	۲.	۲.		۲.	۲.	Η.	۲.		۲.		.10
rtes Fine Root	0.500	٦.	۲.	٦.	۲.	۲.	۲.	1.	۲.	1.	۲.	1.	۲.	٦.	٦.	۲.	۲.	۲.	٦.	۲.	٦.	۲.	.1	۲.	۲.	۲.	٦.
Decay-Rates Fin Foliage Roo	0.500	7	7	٦.	۲.	۲.	1.	2	2	.2	2	٦.	2	۲.	1.	7	۲.	۲.	٦.	2	2	4	2	۲.	۲.	۲.	Τ.
Species	Herb	Abam	Abco	Abgr	Abla	Abpr	Abma	Acma	Alru	Arme	Cach	Cade	Lide	Pico	Pila	Pimo	Pipo	Pien	Pisi	Potr	Prem	Psme	Quqa	Sese	Thpl	Tshe	Tsme
File #	9 9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
Model #	ML02 ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02

DecayPool.prm

This file defines the response of each detrital layer (e.g., dead foliage) to moisture and temperature (Q10's and moisture limits) and also has the transfer rates to the stable soil organic matter pool.

TempOpt, MoistMin, MoistMax, Drying Constant, AreaMassRatio, and MoistStoreMax are used by CLIMATE. SoilTransfer*Pool* and SoilDecayRate are used by DECOMPOSE objects.

The parameters in the order they occur in the file are:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 7 indicates this is the DcayPool.prm file.

Pool: detrital pool the parameter values describe. Valid names include: DeadFoliage, DeadFineRoot, SalvSnagSapwood, SalvSnagHeartwood, SnagSapwood, SnagHeartwood, SnagHeartwood, LogSapwood, LogHeartWood, DeadBranch, DeadCRoot, StableFoliage, StableWood, and StableSoil.

Q10: rate at which the decomposition rate for a pool increases with a 10 C increase in temperature (dimensionless).

Temp Opt: temperature optimum for decay (C).

Moist Min: moisture minimum for decay (% water weight to dry weight for all pools except StableSoil which is in volume of water to volume of soil)

Moist Max: moisture maximum for decay (% water weight to dry weight for all pools except StableSoil which is in volume of water to volume of soil)

Transfer Rate: transfer rate to another pool for the detrital pool once the time lag associated with a process (e.g., formation of stable organic matter) has been exceeded (year-1).

Stable Decay Rate: rate at which the stable pools decompose (year⁻¹).

Area Mass Ratio: ratio of projected area to mass of a pool (% area Mg mass-1)

Moist Store Max: the maximum moisture content that a pool can store before becoming completely saturated (% water weight to dry weight for all pools except StableSoil which is in volume of water to volume of soil).

Matric Shape: parameter that determines the shape of the matric limitation (i.e., when detritus is too dry) curve (dimensionless).

Matric Lag: parameter that determines the difference between the minimum moisture content and the response to excessive drying (%)

Diffuse Shape: parameter that determines the shape of the diffusion limitation curve (dimensionless)

Diffuse Lag: parameter that determines the difference between the maximum moisture content and the decline in the diffusion limitation curve (%)

Temp Shape: parameter that determines the shape of the excessive temperature limitation curve (dimensionless)

Temp Lag: parameter that determines the difference between the maximum temperature and the decline due to excessive temperature (C)

Drying Constant: the rate at which a pool dries at a temperature of 1 C and a solar radiation in put of 1 cal cm⁻² month⁻¹ (cm² degrees⁻¹ cal ⁻¹).

Example of DecayPool.prm file:

	rying	00150	00000	00025	00075	00025	000075	00025	000075	00025	00150	00000	00100	00100	00000
	ПО	0		0	0	0	0	0	0	0	0	0	0	0	0
	Temp Shape Lag	4	4 4	4	4	4	4	4	4	4	4	4	4	4	4
	Temp	15	T -	12	15	15	15	15	15	15	15	15	15	15	15
	se_ Lag	4	4 4	4	4	4	4	4	4	4	4	4	4	4	4
	Diffuse Shape Lag	15	15	15	15	15	15	15	15	15	15	15	15	15	15
	Lag	0	00	0	0	0	0	0	0	0	0	0	0	0	0
	Matric Shape Lag	5.0	0.0	2.0	5.0	5.0	5.0	5.0	5.0	5.0	5.0	2.0	5.0	5.0	2.0
Moist	Store	300	300	200	300	200	300	200	300	200	200	200	400	009	100
Area	Mass Ratio	20.00	0.00	0.02	0.02	0.02	0.10	0.10	0.10	0.10	0.10	0.00	20.00	0.10	00.0
Stable	Decay Rate	0.0000	00000	0.0000	0.0000	0.0000	0.0000	0.000.0	0.000.0	0.000.0	0.000.0	0.000.0	0.2000	0.2000	0.0120
	fer	-			_	-	_	_			_	_	_	_	_
	Transfer Rate	0.300	0.300	0.150	0.15	0.150	0.150	0.150	0.07	0.07	0.150	0.150	0.000	0.000	00000
	Max	350	150	150	150	150	150	150	150	150	200	190	350	150	100
	Moist	30	30	30	30	30	30	30	30	30	30	30	30	30	15
	Temp Opt	45	45	45	45	45	45	45	45	45	45	45	45	45	45
e pools	010	2.000	2.000	2.000	2.000	2.000	2.000	2.000	2.000	2.000	2.000	2.000	2.000	2.000	2.000
Parameters for dead and stable pool Standcarb model, version 2	Pool	DeadFoliage	DeadFineRoot	SalvShadHeartWood 2.000	SnaqSapWood	SnagHeartWood	SalvLogSapWood	SalvLogHeartWood	LogSapWood	LogHeartWood	DeadBranch	DeadCRoot	StableFoliage	StableWood	StableSoil
ters arb	File #	7	Г г	7	7	7	7	7	7	7	7	7	7	7	7
Parame	Model File	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02

BurnKill.prm

This file describes the fraction of the live layers that is killed given a fire of certain serverity. These parameters are used in BURNKILL and occur in the following order:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 8 indicates this is the Burnkill.prm file.

Layer: refers to the layer of living vegetation. Valid names include herb, shrub, utree, and ltree.

Fire Intensity: type of fire occurring. Valid names include Hot, Medium, and Light.

%-Killed Above: proportion of above-ground parts (foliage, branches, sapwood, and heartwood) killed by the fire (%).

%-Killed Below: proportion of below-ground parts (fine roots and coarse roots) killed by the fire (%).

%-Burned Above: proportion of the above-ground parts that are killed by fire that are combusted (%).

%-Burned Below: proportion of the below-ground parts that are killed by fire that are combusted (%).

Example of Burnkill.prm file:

Burn and Kill parameters for fires - StandCarb model

Model	File		Fire	NG 74 - 1		%-Burr		
#	#	Layer	Intensity	Above	Below	Above	Below	
ML02	8	Herb	Hot	100	100	100	50	
ML02	8	Shrub	Hot	100	100	100	10	
ML02	8	LTree	Hot	100	100	10	5	
ML02	8	UTree	Hot	100	100	5	2	
ML02	8	Herb	Light	100	100	100	0	
ML02	8	Shrub	Light	50	50	50	0	
ML02	8	LTree	Light	80	80	5	0	
ML02	8	UTree	Light	10	10	1	0	
ML02	8	Herb	Medium	90	90	100	25	
ML02	8	Shrub	Medium	75	75	75	5	
ML02	8	LTree	Medium	90	90	7	2	
ML02	8	UTree	Medium	50	50	2	1	

SitePrep.prm

This file describes the amount of detritus removed by various types of fires. These parameters are used by the SITEPREP class of objects and occur in the following order:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 9 indicates this is the SitePrep.prm file.

Pool: refers to the pool of detritus. Valid names include: DeadFoliage, DeadFineRoot, SnagSapWood, SnagHeartWood, LogSapWood, LogHeartWood, DeadBranch, DeadCRoot, StableFoliage, StableWood, and StableSoil.

Light Burn: amount remaining after a light intensity fire (percent)

Medium Burn: amount remaining after a medium intensity fire (percent)

Hot Burn: amount remaining after a hot intensity fire (percent)

Example of SitePrep.prm file:

Site Prep parameters - StandCarb model

Model #	File #	Pool	Light Burn	Medium Burn	Hot Burn
ML02	9	DeadFoliage	75.0	50.0	0.0
ML02	9	DeadFineRoot	100.0	75.0	0.0
ML02	9	SnagSapWood	100.0	85.0	50.0
ML02	9	LogSapWood	95.0	75.0	10.0
ML02	9	SnagHeartWood	100.0	95.0	75.0
ML02	9	LogHeartWood	100.0	90.0	50.0
ML02	9	DeadBranch	75.0	50.0	0.0
ML02	9	DeadCRoot	100.0	100.0	50.0
ML02	9	StableSoil	100.0	100.0	100.0
ML02	9	Stablefoliage	100.0	50.0	5.0
ML02	9	Stablewood	100.0	50.0	5.0

Harvest.prm

This driver file describes the amount of trees cut, the fraction of the bole removed, and the fraction left on the site as slash. It also determines the severity of herbiciding, and the minimum mean tree volume that can be salvaged. This information is used by the HARVEST module.

The variables in the order of their appearance in the file are as follows:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 10 indicates this is the Harvest.prm file

Treatment: harvest treatment used with **PCom** as precommercial thinning, **Com** as commercial thinning, and **CCut** as clear-cut. Salvage removals of dead woody detritus pools are indicated by **Salv**. The abbreviations of these treatments is fixed.

Utilization Standards

There are three utilization standards: Low, Medium, and High. Each utilization standard has two parameters:

For PCom, Com, and CCut treatments:

%-Cut: the fraction of the tree boles that are cut under the specific utilization standards (%volume).

%-Taken: the fraction of the boles that are taken under the specific utilization standards (% of volume).

For Salv treatment:

%-Taken: the fraction of total salvagable material removed (% mass).

MinVol: the minimum mean tree volume that is removed (cubic decimeters).

Example of Harvest.prm file:

Harvest parameters - StandCarb model

Model File	e Treatment		ation %-Taken		m zation <u> </u>		zation %-Taken	
ML02 10 ML02 10 ML02 10	PCom Com CCut	5 5 80	0 50 80	10 10 95	0 90 90	20 20 98	0 95 95	
		Low Utiliz %-Take	ation_ n MinVol		um ization <u></u> ken MinVo		n Lization_ aken MinV	ol
ML02 10	Salv	50	100	75	5 50	10	00 25	

Herbicide.prm

This file determines the survival of trees after herbiciding. Note these are the treatments for the cells that are herbicided and do not necessarily pertain to all the cells.

File Header

This file uses the new file header. The file code is "Herbicide_Parms", and the version is 1.

Effectiveness table

After the file header comes a data table containing the parameters for various level of herbicide effectiveness. The table has the following columns:

Level of Effectiveness: One of these levels: low, medium, high

% Treated: the fraction of the tree boles subjected to the given herbicide treatment (% of mass).

% Taken: the fraction of the treated boles that are taken from the site (%).

% Roots Die: the fraction of the treated trees whose roots die (%).

Example of Herbicide.prm:

Program

V	ersion 2				
	Level of Effectiveness	% Treated	% Taken	% Roots	Die
5	21200021011000	110000	2011011	1,0000	

StandCarb

Data File Herbicide Parms

LOW	100	O	50
medium	100	0	75
high	100	0	100

Soil.prm

This file contains the data for various types of soils in terms of their depth and maximum moisture holding capacity. This information is used by the CLIMATE and SOILTEXTURE classes of objects.

The variables in the order of their appearance in the file are as follows:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 11 indicates this is the Soil.prm file.

Soil Texture: indicates the soil texture. Valid names include: sand, loamysand, sandyloam, loam, siltloam, silt, sandyclayloam, clayloam, siltyclayloam, sandyclay, siltyclay, and clay.

Water PotAsym: a pararmeter that modifies the moisture retention curve so that sandier soils will release more moisture with a smaller change in the water potential (MPa).

Water Pot1: the fraction of the water stores when the water potential is equal to 1 MPa.

SoilWater MaxPer: the maximum fraction of the soil depth that can hold water from field capacity to the wilting point (%).

Example of Soil.prm file:

Soil parameters for StandCarb model

Model #	File #	Soil Texture	Water PotAsym	Water Pot1	SoilWater MaxPer
ML02 ML02 ML02 ML02 ML02 ML02 ML02 ML02	11 11 11 11 11 11 11 11 11	sand loamySand sandyLoam loam siltLoam silt sandyClayLoam clayLoam siltyClayLoam sandyClay siltyClay	0.00 0.01 0.02 0.03 0.04 0.05 0.06 0.07 0.08 0.09 0.10	0.25 0.25 0.25 0.25 0.25 0.25 0.25 0.25	25.0 35.0 35.0 45.0 50.0 50.0 50.0 50.0 45.0 60.0
ML02	11	clay	0.11	0.25	60.0

SiteIndex.prm

This file contains the bole growth efficiencies in terms of mass of sapwood produced per unit mass of foliage for the commercial tree species growing in the Pacific Northwest. These parameters are used by the Growth objects and are set so that bole mass and volume accumulation matches a site index related volume table.

The variables in the order of their appearance in the file are as follows:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 12 indicates this is the SiteIndex.prm file.

Site Index Species: the species that is to be used to determine the level of productivity. Species abbreviations are after Garrison and can be in any order.

Site-1 High: the bole growth efficiency to match a high site index 1 productivity (dimensionless).

Site-1 Med: the bole growth efficiency to match a medium site index 1 productivity (dimensionless).

Site-1 Low: the bole growth efficiency to match a low site index 1 productivity (dimensionless).

Site-2 High: the bole growth efficiency to match a high site index 2 productivity (dimensionless).

Site-2 Med: the bole growth efficiency to match a medium site index 2 productivity (dimensionless).

Site-2 Low: the bole growth efficiency to match a low site index 2 productivity (dimensionless).

Site-3 High: the bole growth efficiency to match a high site index 3 productivity (dimensionless).

Site-3 Med: the bole growth efficiency to match a medium site index 3 productivity (dimensionless).

Site-3 Low: the bole growth efficiency to match a low site index 2 productivity (dimensionless).

Site-4 High: the bole growth efficiency to match a high site index 4 productivity (dimensionless).

Site-4 Med: the bole growth efficiency to match a medium site index 4 productivity (dimensionless).

Site-4 Low: the bole growth efficiency to match a low site index 4 productivity (dimensionless).

Site-5 High: the bole growth efficiency to match a high site index 5 productivity (dimensionless).

Site-5 Med: the bole growth efficiency to match a medium site index 5 productivity (dimensionless).

Site-5 Low: the bole growth efficiency to match a low site index 5 productivity (dimensionless).

Example of SiteIndex.prm file:

Bole growth efficiencies for Site Indexes - StandCarb model

		Low	0.25	0.18	0.15	0.32	0.25	0.40	0.30	0.33	0.30	
	5	Med	0.27	0.24	0.20	0.38	0:30	0.48	0.36	0.44	0.35	
	Site-	High Me	30	30	25	42	35	99	41	0.51	38	
		Гом	0.33	0.36	0.31	0.47	0.41	0.65	0.47	0.61	0.42	
	4	Med	0.40	0.42	0.37	0.51	0.45	0.75	0.52	0.68	0.51	
	Site-	High Me	48	48	43	24	22	84	28	0.79	29	
		Low	0	0	0	0	0	0	0	0.88	0	
	3	Med	0.66	0.59	0.55	0.60	0.75	1.00	0.74	0.98	0.73	
	Site-	High Me	0.74	0.65	0.62	0.64	0.89	1.13	0.81	1.06	0.84	
		Low	0	0	0	0	1	1.	0	1,11	0	
	-2	Med	0.90	0.75	0.75	0.71	1.22	1.35	0.92	1.21	1.07	
	Site-	High Me	1.01	0.80	0.83	0.76	1.45	1.44	0.97	1.27	1.23	
		Гом	i,	0	0	0	H	i,	ij.		ij	
	ij	Med								1.50		
	Site-	High M	1.15	1.00	1.10	0.92	1.92	1.70	1.11	1.60	1.60	
Site		Species										
	File	#	12	12	12	12	12	12	12	12	12	
	Model	#	ML02									

Med High Low \geq Med High 9/ Table 4. Correspondence between site index classes and site index values (height in feet at 50 years of age). Site Class Class Low Med High Low Med High Low High Med Picea sitchensis³ Abies concolor1 Abies grandis² Species

Low >

Pinus contorta4

Pinus monticola5

Pinus pondersosa6

Pseudotsuga menziesi⁷

equoia sempervirons⁸

Tsuga heterophylla9

1-Schumacher 1926, 2-Cochran 1979, 3-Meyer 1937, 4-Dahm 1964, 5-Haig 1932, 6-Meyer 1938. 7-McArdle and Meyer 1930, 8-Lundquist and Palley, and 9-Barnes 1962.

Driver Files

These files are also used to parameterize each simulation run. They differ, however, from the parameter files in that they are not constant but change from run to run. We therefore refer to these as driver files. The extension of these files is **DVR**, a change from version 1 as Windows uses the extension DRV. The driver files required to run the StandCarb model are outlined in Table 5.

For each, the model module needing the file is described. Next the parameters are defined and the units indicated. The format in terms of columns is flexible, however, the parameters must be listed in the order shown.

Table 5. List of driver files required to run StandCarb model and the function of each file.				
File Name	Function			
Simul.dvr	defines the characteristics of a simulation run			
Locate.dvr	Locate.dvr defines the physical characteristics of site such as aspect			
Climate.dvr	defines the precipitation and temperature regime of site			
Radiate.dvr	defines the solar radiation and sun angles for a site			
HarvInt.dvr	defines the timing and type of harvest and cutting in stand			
CutPatt.dvr	defines the spatial patterns of the harvests or cuts.			
WFireInt.dvr	defines the timing and severity of wildfires			
WFPatt.dvr	defines the spatial patterns of wildfires			

Simul.dvr

This file is used to define the overall nature of a simulation run. It defines the number of cells, the length of time the model is run, the time layers are planted (in the single cell version), whether diagnostic files are to be output, the type of output files to be output, and other aspects of the particular run.

File Header

This file uses the new file header. The file code is "Simulation_Parms", and the version is 1.

SpeciesUpper: for single cell version, the tree species in the upper tree layer.

SpeciesLower: for single cell version, the tree species in the lower tree layer.

SiteName: name of the site being examined in the simulations.

GrowthMethod: the method used to determine the growth rate of plants.

Valid selections include Climate or SiteIndex. If Climate is selected then the rate of growth is solved from climatic indices. If SiteIndex is used then the growth rate matches that required to mimic a volume table.

SiteIndexSpecies: the species the growth should match if the SiteIndex growth method is selected.

SiteIndex: the site index level being selected. Valid levels include: Site1High, Site1Medium, Site1Low, Site2High, Site2Medium, Site2Low, Site3High, Site3Medium, Site4Low, Site5High, Site5Medium, Site5Low.

Regen: the regeneration scenario to be used. Valid names include: NF (natural fast), NS (natural slow), AF (artifical fast), and AS (artificial slow).

MaxTreeDensity: the maximum tree density for natural regeneration scenarios (trees / ha)

MaxTreeCells: the maximum fraction of cells that can be colonized by trees. Set this less than 100% if partial stocking is occurring at the site due to excess water, drought, snow and ice damage, etc (percent).

#ofRows: the number of rows in stand (integer > 0).

#ofCols: the number of columns in stand (integer > 0).

#ofReps: the number of simulation replications to be run (integer > 0).

TimeEnd: the number of years the simulation is to run (years).

Interval: the number of years that results are output. The smallest interval is 1 year.

CellWidth: the width of the cell to be used in determining the distance between trees (m). This correspondes to the width of a mature tree.

TimeHerb: for single cell version the time the herb layer is planted.

TimeShrub: for single cell version the time the shrub layer is planted.

TimeUpper: for single cell version the time the upper tree layer is planted.

TimeLower: for single cell version the time the lower tree is planted.

Border: the type of border to be used in the Neighbor calculations. Valid names include: None, Same, and Old.

NeighborOnOff: determines if the cells interact spatially (ON) or are independent spatially (OFF) (0 = OFF, 1 = ON).

Cohort: determines if the detritus pools are simulated with (ON) or without (OFF) the cohort structure that accounts for time lags (0 = OFF, 1 = ON).

Restart: determines if layers can restart after disturbance in the single cell version of model. A 1 makes the layers restart after disturbance that reduces their biomass to 0. A 0 indicates the layers will not restart once their biomass is reduced to zero.

PETReduction: the amount of potential evapotranspiration that is lost via evaporation (%).

InitialSoilCarbon: an estimate of the stable soil carbon (Mg ha⁻¹). This reduces the time needed to calibrate the stable soil pool.

Units: determines whether the mass values are output as organic matter or carbon. Valid codes are OM (organic matter) or C (carbon).

GPP_DecreaseMax: determines the maximum decrease in Gross Primary Production (GPP) that occurs when upper trees reach their maximum height (%).

GPP_Shape: determines the shape of the response of GPP to height. The number must be positive. A value of 1 gives a linear response, a value of < 1 gives the highest response at the lowest heights and a value > 1 gives the largest response for the tallest heights.

DiagnosticsMode: a 1 indicates that only diagnostic files are to be output, a 0 indicates only output files of states variables are output, and 10 indicates both diagnostic and output files are to be output.

PlantDiag: a 1 indicates that diagnostic files on the frequency of cells in layers and tree species are to be output. In this mode, the layers and species are planted, but not allowed to die out. A 0 means that this diagnostic is not run.

DieOutDiag: a 1 indicates that diagnostic files on the frequency of cells in layers and tree species are to be output. In this mode, the layers are planted for 100 years and then there is no planting or replacement after that time. A 0 means that this diagnostic is not run.

ReplacementDiag: a 1 indicates that diagnostic files on the frequency of cells in layers and tree species are to be output. In this mode, layers and species are planted, dieout, and are replaced similar to the normal simulation runs. A 0 means that this diagnostic is not run.

DensityDiag: a 1 indicates that the diagnostic file on the mean tree density for each layer is to be output. A 0 means that this diagnostic is not run.

InterceptionDiag: a 1 indicates the interception values for the canopy and detrital pools, and monthly runoff will be output. These are for the temperature, precipitation, soil, and radiation conditions of the site. A 0 means that this diagnostic is not run.

WaterBalanceDiag: a 1 prints out the moisture content of the detrital pools and soil. These are for the temperature, precipitation, soil, and radiation conditions of the site. A 0 means that this diagnostic is not run.

TranspirationDiag: a 1 prints out the potential transpiration and the actual transpiration. These are for the temperature, precipitation, soil, and radiation conditions of the site. A 0 means that this diagnostic is not run.

TempResponseDiag: a 1 indicates that the response of growth, plant respiration, and decomposition to temperature is to be output. In this mode a systematic progression of temperature values is used (0-50 C by 1 C increments) rather than the values in the Climate.dvr file. A 0 means that this diagnostic is not run.

DetritalMoistureDiag: a 1 indicates that the response of decomposition to moisture is to be output. In this mode a systematic progression of moisture values is used (0-500 % by 5 % increments) rather than the values computed from the WaterBalance functions. A 0 means that this diagnostic is not run.

AbioticResponseDiag: a 1 indicates that the combined response of growth and decomposition to temperature and moisture is to be output. These are for the temperature,

precipitation, soil, and radiation conditions of the site. A 0 means that this diagnostic is not run.

LightDiag: a 1 indicates that the light entering and leaving a cell will be printed out for each time step. A 0 means that this diagnostic is not run.

RespirationDiag: a 1 indicates that the losses from respiration and the mass of the respiring pools is to be output. A 0 means that this diagnostic is not run.

MortalityDiag: a 1 indicates the mass of mortality from all sources (pruning, mortality, thinning, dieout, fire) is to be output. A 0 means that this diagnostic is not run.

SubstrateQualityDiag: a 1 indicates that the portion of the decomposition rate of each pool that is dependent on substrate quality (PoolDecayRateAvg) is printed out. A 0 means that this diagnostic is not run.

WaterPotRespDiag: a 1 indicates that the response of water potential and growth to soil water stores will be output. A 0 means that this diagnostic is not run.

SpeciesDiag: a 1 indicates that the species of the upper-tree layer and the lower-tree layer for each cell will be output. A 0 means that this diagnostic is not run.

NeighborDiag: a 1 indicates that the fraction of full diffuse, direct, and total radiation will be printed out for a selected year. A 0 means that this diagnostic is not run.

YearNeighbor: indicates the year that the Neighbor Diagnostic is to be performed.

RandomNumSeed: a random number used to seed the random number generator (integer)

Example of Simul.dvr file

Program Data_File Version	StandCarb Simulation_Parms 1		
SpeciesUppe SpeciesLowe		psme tshe	
SiteName		testsite1	
GrowthMetho SiteIndexSp SiteIndex		Siteindex psme Site3Medium	
Regen MaxTreeDen: MaxTreeCel		af 189482 100	
<pre>#ofRows #ofCols</pre>		10 10	
#ofReps TimeEnd Interval		5 1000 5	
CellWidth		25	
TimeHerb TimeShrub TimeUpper TimeLower		1 5 5 15	
Border		same	
NeighborOn Cohort Restart	Off	1 1 1	
PET_Reduct InitialSoi Units		10 304 C	
GPP_Decrea GPP_Shape	seMax	0 1	
Diagnostic PlantDiag DieOutDiag		10 0 0	

ReplacementDiag	0
DensityDiag	0
InterceptionDiag	0
WaterBalanceDiag	0
TranspirationDiag	0
TempResponseDiag	0
DetritalMoistureDiag	0
AbioticResponseDiag	0
LightDiag	0
RespirationDiag	0
MortalityDiag	1
SubstrateQualityDiag	0
WaterPotRespDiag	0
SpeciesDiag	0
NeighborDiag	0
YearNeighbor 10	0
RandomNumSeed -85	2

Locate.dvr

This file defines the location and site characteristics of the forest to be simulated.

The variables in the order of their appearance in the file are as follows:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 22 indicates this is the Locat.dvr file.

Site Name: the name of the particular site being simulated.

Soil Texture: the soil texture class of the site. The valid names of textures are: sand, loamysand, sandyloam, loam, siltloam, silt, sandyclayloam, clayloam, siltyclayloam, sandyclay, siltyclay, and clay.

Ecoregion: the ecoregion that the site occurs in. This determines the species of trees that will be present. Must be one of the names that are defined in the ecoregions parameter file ("EcoRegion.prm")

Long: the longitude of the site to the nearest degree (degree).

Lat: the latitude of the site to the nearest degree (degree).

Elev: the elevation above mean sea level of the site (meters).

Aspect: the compass direction that the site is sloping toward (degrees).

Slope Steep: the steepness of the site in percent slope (%).

Soil Depth: the depth of the soil for rooting of plants (cm).

Rocks: the percentage of the soil profile that has fragments of rock >2mm in diameter (%).

Drainage Factor: the ability of the site to drain water if the slope is equal to 0. Defined as the proportion of potential runoff that can be removed in 1 month (%).

Example of Locate.dvr file:

Locate driver file for StandCarb

Drainage Factor	100	100	50	20
Rocks	2	2	2	2
Soil Depth	100	100	100	100
Slope	0	0	0	0
As	180			
Elev	300	100	1000	3000
Lat	40	39	44	44
nong	123			
Ecoregion	Other	CA CoastRange	OR CascadesWest	OR_CascadesEast
Soil Texture	loam	loam	loam	loam
Site Name	default	testsite1	testsite2	testsite3
File #	22	22	22	22
Model #	ML02	ML02	ML02	ML02

Climate.dvr

This driver file contains the climatic information required to calculate the effects of climate on establishment, growth, and decomposition. These variables are used by the CLIMATE module.

The variables in the order of their appearance in the file are as follows:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 23 indicates this is the Climate.dvr file

Month: the abbreviation of month of the year staring with Jan and ending with Dec.

Temp Min: the mean monthly minimum temperature (C).

Temp Max: the mean monthly maximum temperature (C).

Temp 24-hr: the mean monthly temperature for the entire 24 hour day (C).

Precip: the mean monthly total precipitation (cm).

Example of Climate.dvr file:

Climate driver file - StandCarb

Model	File		Temp			
#	#	Month	Min	Max	24-hr	Precip
ML02	23	Jan	-1.5	3.20	0.30	39.0
ML02	23	Feb	-0.20	7.00	2.70	27.0
ML02	23	Mar	0.10	9.40	3.80	27.0
ML02	23	Apr	1.70	14.60	7.40	14.0
ML02	23	May	4.40	19.30	11.70	11.0
ML02	23	Jun	7.30	23.30	14.90	6.0
ML02	23	Jul	9.00	28.70	18.30	1.0
ML02	23	Aug	8.60	28.00	17.40	4.0
ML02	23	Sep	6.30	24.10	13.50	8.0
ML02	23	Oct	3.40	15.80	8.10	18.0
ML02	23	Nov	0.70	7.50	3.50	34.0
ML02	23	Dec	-0.90	3.6	1.10	41.0

Radiate.dvr

This driver file contains the radiation and sun angle information required to calculate the effects of radiation on establishment, growth, and decomposition. These variables are used by the Neighbor and Climate modules. These data are calculated using the SolarRad program (Harmon and Marks 1995; http://www/fsl.orst.edu/lter/datafr.htm).

The variables in the order of their appearance in the file are as follows:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 24 indicates this is the Radiate.dvr file

Month: the abbreviation of the month of the year starting with Jan and ending with Dec. The code Year indicates the daily mean radiation averaged over the year and the yearly weighted average for the sun angles.

Solar Radiation Diffuse: mean daily diffuse solar radiation for a given site (cal cm⁻² day⁻¹). To calculate the monthly radiation multiply this number by the number of days in the month. For the year, this is the daily mean for the year. To calculate the yearly radiation multiply the year value by 365.

Solar Radiation Direct: mean daily direct solar radiation for a given site (cal cm⁻² day⁻¹). To calculate the monthly radiation multiply this number by the number of days in the month. For the year, this is the daily mean for the year. To calculate the yearly radiation multiply the year value by 365.

Solar Radiation Total: mean daily total solar radiation for a given site (cal cm⁻² day⁻¹). To calculate the monthly radiation multiply this number by the number of days in the month. For the year, this is the daily mean for the year. To calculate the yearly radiation multiply the year value by 365.

Sunrise Azimuth Angle: the azimuth angle of the sun at sunrise for each month (degrees from south). The year value is the weighted average, weighted by total radiation recieved each month.

Solar Alt-Angle South: solar altitude angle when the sun is directly south (degrees from the horizon) The year value is the weighted average, weighted by total radiation recieved each month.

Version 2

Example of Radiate.dvr file:

Radiation driver file - StandCarb

Model	File		Solar Ra	diation		Sunrise Azimuth	Solar Alt-Angle
#	#	Month	Diffuse	Direct	Total	Angle	South
ML02	24	Jan	92.78	51.11	143.90	71.30	29.08
ML02	24	Feb	125.47	83.93	209.39	78.88	37.04
ML02	24	Mar	167.30	118.54	285.84	87.98	47.58
ML02	24	Apr	207.88	180.51	388.39	98.01	59.42
ML02	24	May	233.74	234.26	468.00	106.60	68.79
ML02	24	Jun	231.63	308.88	540.50	110.97	73.09
ML02	24	Jul	145.10	552.26	697.36	108.99	71.18
ML02	24	Aug	191.46	310.35	501.81	101.59	63.46
ML02	24	Sep	174.19	189.08	363.26	91.87	52.22
ML02	24	Oct	136.80	104.75	241.54	81.85	40.40
ML02	24	Nov	100.48	59.15	159.63	73.30	31.09
ML02	24	Dec	83.78	44.42	128.20	69.09	26.95
ML02	24	Year	157.55	186.44	343.99	97.03	57.89

HarvInt.dvr

This file describes the intervals and tree layers that are affected, the type of action, the degree of utilization, and the type of site preparation that is used. These parameters are used by the HARVEST, SALVAGE, and SITEPREP modules. For each action there are four variables to describe the action taken. The year, the layer (i.e., upper or low tree) that is affected, the type of utilization standard used (amount of bole removed), and the type of site preparation fire used. The years indicate when various actions are taken, to have a treatment occur more than once use another line. If one treatment is invoked more than another, put a zero in the treatments that are not used. Also if fire is not used then use a zero to indicate no fire.

The variables in the order of their appearance in the file are as follows:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 26 indicates this is the HarvInt.dvr file.

Harvest Types

There are three types of cutting treaments: precommercial thinning, commercial thinning, and clear-cut. For each of these cutting treatments, there are these columns:

Interval UTree: time of cutting treament of the upper tree layer (years).

Interval LTree: time of cutting treament of the upper tree layer (years).

Util: the utilization standards used in the cutting treament (see the Harvest.prm file for the definitions of these levels). Valid codes for levels are: 1- low utilization, 2-medium utilization, and 3-high utilization (0 can be used for a treatment that's not being used).

FireType: the type of fire used after the cutting treatment. For site preparation fires the valid codes for the type of fire are: 0- no fire, 1-light fire, 2-medium fire, and 3-hot fire.

Salvage Int: time of salvage operation (years).

Salvage Util: the ulization standards used in the salvage operation. The variable considered is the amount of potentially salvagable wood removed and the mean minimum tree volume (see Harvest.prm file).

Herbicide UTree Int: the time herbicide treatment is used on upper tree layer (years). The species to be selected are indicated in the CutPatt.dvr file.

Herbicide UTree Effect: the level of effectiveness of the herbicide treatment on upper tree layer. 1- low effectiveness, 2-medium utilization, and 3-high utilization (0 can be used for a treatment that's not being used).

Herbicide UTree Int: the time herbicide treatment is used on lower tree layer (years). The species to be selected are indicated in the CutPatt.dvr file.

Herbicide UTree Effect: the level of effectiveness of the herbicide treatment on lower tree layer. 1- low effectiveness, 2-medium utilization, and 3-high utilization (0 can be used for a treatment that's not being used).

Example of HarvInt.dvr file:

Harvest Interval driver file - StandCarb

				3	3	Э
			Int	0	0	0
		UTree	Int Effect	0 1	0 1	0 1
		Salvage	Int Util	0 2	0 2	400 2
		Fire	Type	0	0	0
			Util	3	3	3
Cut		val	UTree LTree	300	0	0
Clear-Cut		Interval		300	0	0
		Fire	Type	0	7	0
			Util	Э	٦	ж
ccial	lo.	ral	UTree LTree	0	0	0
Commercial		Interval	UTree	0	350	0
		Fire	Type	0	0	0
al			Util	1	1	,
Pre-Commercial		ra1	UTree LTree Util	0	0	0
Pre-Co		Inter	UTree	0	0	0
	side	File	#	26	26	26
	Herbic	Model File Interval	# Effect	ML02	ML02	ML02

CutPatt.dvr

This file describes the cutting or herbiciding pattern of the cells and takes the form of a row by column pattern to indicate the pattern of cells that are thinned or clear-cut.

Cut Pattern

Year: Specifies the simulation year that this cutting pattern should be used. Multiple years should be separated by commas.

Species: Identifies the tree species that should be cut. Multiple species should be separated by commas. If a cell does not contain one of the given species, it is not harvested. The word "All" can be used to denote that all tree species should be harvested. Note: This parameter should **not** be used if the cut pattern is for a salvage harvest.

Cell pattern

Each row of cells in the stand is represented by a separate line of 0's and 1's. The first row corresponds to the uppermost (uphill) portion of the stand and the first column corresponds to the lefthand side of the stand as one looks uphill. If a cell has a value of 1 it is to have the treatment, if the cell has a value of 0 it does not receive the treatment.

Example of CutPatt.dvr file:

Cut Pattern driver file for StandCarb

ML02 27

Yea	r	300,	350
Spe	cie	s al	1
1	0	1	1
0	1	0	1
1	0	1	0
0	1	0	1
Yea	r	400	
1	1	1	1
1	1	1	1
1	1	1	1
1	1	1	1

WFireInt.dvr

This driver file describes the time and severity of wildfires that burn through the stand. This file allows one to specify if the fires are light, medium or hot. The severity of the fire effects the amount of live layers killed and the amount of detritus burned away. These variables are used in the BURNKILL and SITEPREP classes of objects.

The years indicate when various fires occur. To have more than one fire of a type occur use another line. If one fire type is invoked more than another, put a zero in the treaments that are not used.

The variables in the order of their appearance in the file are as follows:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 25 indicates this is the WFireInt.dvr file.

Lite Fire: year that a light fire occurs (year).

Med Fire: year that a medium fire occurs (year).

Hot Fire: year that a hot fire occurs (year).

Example of WFireInt.dvr file:

WildFire Interval driver file - StandCarb

Model #	File #	Lite Fire	Med Fire	Hot Fire
ML02	25	50	0	250
ML02	25	100	0	0
ML02	25	150	0	0

WFPatt.dvr

This file describes the wild fire burn pattern of the cells and takes the form of a row by column pattern to indicate the pattern of cells that are burned by a wildfire.

Cut Pattern

Year: Specifies the year that this cutting pattern should be used for. Multiple years should be separated by commas.

Cell pattern

Each row of cells in the stand is represented by a separate line of 0's and 1's. The first row corresponds to the uppermost (uphill) portion of the stand and the first column corresponds to the lefthand side of the stand as one looks uphill. If a cell has a value of 1 it is burned, if the cell has a value of 0 it does not burn.

Example of WFPatt.dvr file:

Wildfire pattern driver file - StandCarb

ML12 28

Yea	ar 50)							
1		0	0	1	1	0	0	1	1
1	1	0	0	1	1	0	0	1	1
0	0	1	1	0	0	1	1	0	0
0	0	1	1	0	0	1	1	0	0
1	1	0	0 1 1 0 0	1	0 1 1	0	0	1	1
0 0 1 1 0 0 1	1 0 0 1 1 0 0	0 1 1 0 0 1 1 0	0	0 1 1 0 0		1 0 0 1 1 0	1 0 0 1 1 0	1 0 0 1 1 0 0	1 0 0 1 1 0 0
0	0	1	1 1 0 0	0	0 0 1	1	1	0	0
0	0	1	1	0	0	1	1	0	0
1	1	0	0	1	1	0	0	1	1
1	1	0	0	1	1	0	0	0	0
	11	- 0	200						
rea	ar I:	50, .	200	_					
1	1	1	1	1	1	1	1	1	1
1	1	1	1	1	1	1	1	1	1
1	1	1	1	1	1	1	1	1	1
1	1	1	1	1	1	1	1	1	1
1	1	1	1	1	1	1	1	1	1
1	1	1	1	1	1	1	1	1	1
1	1	1	1	1	1	1	1	1	1
1	ar 15 1 1 1 1 1 1 1 1	50, 3	1 1 1 1 1 1 1 1	1 1 1 1 1 1	1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1 1 1	1 1 1 1 1 1 1
1	1	1	1	1	1	1	1	1	1
1	1	1	1	1	7	7	7	1	1

Output Files

These files represent the standard output files that each model simulation generates. All output files have the extension **OUT**. Each file is composed of two parts: 1) a header section that describes the format of the data and 2) the output data itself.

The output file format in terms of columns is flexible, however, the parameters must be listed in the order shown. An example of each file is given.

Table 6. List of out	put files currently available for STANDCARB model.
File Name Total.out	Purpose total organic matter or carbon values for live, dead, and stable pools
Live.out	total organic matter or carbon values for live pools
Dead.out	total organic matter or carbon values for dead pools
DeadWood.out	total organic matter or carbon values for all dead wood pools
Stable.out	total organic matter or carbon values for stable pools
Volume.out	volume, age, density, and height of tree layers

Total.out

This file has the totals of the organic matter or carbon stores and the volume harvested. This is the most commonly used output file for assessing overall effects of treatments on stores of organic matter or carbon. When the single cell version of the model is used only the mean stores are output and the standard error is set to zero. When the multicell version is used then the mean and the standard error are output.

The variables defined in the order they appear in the file are:

Model #: ML02 indicates this file is output for STANDCARB.

File #: 31 indicates this is the Total.out file

Time: simulation year. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, a state variable will be output for the time Year.1. Then the effects of harvest or wildfire will be calculated and output for the time Year.2. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.3. If a wildfire occurs during the year of harvest, then the effects of this disturbance will be calculated and output for time Year.4. This allows one to directly track the changes in stores for each disturbance in a given year.

TotalLive Mean: mean of the total live carbon for all the cells (Mg ha⁻¹). Includes boles, branches, leaves, fine roots, and coarse roots for herbs, shrubs, upper trees ,and lower trees.

TotalLive StdErr: standard error of the total live carbon for all the cells (Mg ha⁻¹). Includes all live forms as above.

TotalDead Mean: mean of the total detritus or dead carbon for all the cells (Mg ha⁻¹). Includes dead foliage, dead fine roots, dead coarse roots, dead branches, dead sapwood, and dead heartwood. This is the fraction of dead material that is expected to change significantly with varying silvicultural treatment.

TotalDead StdErr: standard error of the total detritus or dead carbon for all the cells (Mg ha⁻¹). Includes all the dead pools described above.

TotalStableMean: mean of the stable pools (Mg ha⁻¹). Includes stablefoliage, stablewood, and stablesoil.

TotalStable StdErr: standard error of the stable pools (Mg ha⁻¹). Includes all the stable pools described above.

Volume: the total cubic volume excluding bark of upper and lower trees (cubic meters ha⁻1).

Density: the mean density of live trees (number ha⁻¹).

Harvest: the harvest made during each year of bole volume excluding bark (cubic meters ha-1).

Example of Total.out file:

Total.out

	Harvest	00.0	00.00	00.00	00.00	00.00	00.00	00.0	00.00	00.00	0.00	0.00	0.00	00.0	00.00	00.00	00.00	1241.58	00.00	00.00	00.00	00.00	00.00	16.57	00.00	00.00	00.00	00.00	00.0	00.00	3.86
	Density	1333.33	2296.70	850.96	833.56	727.19	467.34	463.83	719.59	613.19	429.45	663.31	623.61	575.04	541.71	688.75	614.72	11.15	873.74	928.54	1030.20	486.64	256.80	255.60	66.19	355.63	855.03	995.68	-	832.89	832.89
	Volume	0.07	34.87	210.48	380.98	537.26	675.60	797.80	906.62	1010.04	1109.85	1372.21	416	1458.29	306	1350.95	1387.29	169.15	160.62	325.77	499.41	632.73	737.38	704.23	3	8.3	2	4.3	1.	530.59	530.59
	StdErr	258.31	228.12	00	185.94	169.49	155.53	146.27	139.81	133.35	128.43	109.91	108.50	108.35	106.97	103.81	101.28	101.28	112.42	118.22	138.90	131.70	127.90	127.90	127.90	124.09	122.73	120.33	131.05	132.41	132.41
TotalStable	Mean	273.98	241.95	212.74	197.22	179.77	164.96	155.14	148.30	141.44	136.22	116.58	115.08	114.93	113.46	110.10	107.43	107.43	119.24	125.39	147.33	139.69	$^{\circ}$	35	35	31	130.18	127.62	139.00	140.44	140.44
Ē	StdErr			1.75				3.35	3	6.	3.49	41.20	37.48	34.99	58.05	46.66	42.73	18.45	43.32	38.51	36.88	32.52	29.41	29.21	28.85	26.45	24.65	36.83	38.25	63.97	37.70
TotalDead	Mean	8.13	33,38	51.73	57.71	70.32	88.10	0	123.19	143.54	9	236.55	220.28	206.47	257.32	234.82	222.13	486.55	354.88	266.10	234.90	238.95	244.58	256.48	278.66	262.98	260.02	306.91	282.46	326.11	263.35
	StdErr	2.93	3.10	4.17	6.49	8.44	10.35	11.18	11.73	11.17	8.16	109.74	107.08	103.57	117.56	115.23	113.76	33.47	21.46	23.70	18.18	13.81	10.87	9.93	9.04	7.38	6.10	60.13	74.26	83.01	83.01
TotalLive	Mean	23.63	47.81	114.05	192.52	259.98	314.73	361.61	400.66	436.06	470.62	722.96	755.77	787.35	713.03	742.89	768.50	66.72	83.76	164.83	247.75	308.49	353.07	337.25	305.60	348.81	384.70	337.01	340.28	281.54	281.54
5	Time	10.0	20.0	30.0	40.0	50.0	0.09	70.0	80.0	0.06	100.0	250.0	260.0	270.0	280.0	290.0	300.1	300.2	310.0	320.0	330.0	340.0	350.1	350.2	350.3	360.0	370.0	380.0	390.0	400.1	400.4
File	#	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
Model	#	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	MT.02	MI.02	MI.02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02

Live.out

This output file contains the organic matter or carbon stores for all the live components of the vegetation. When the single cell version of the model is used only the mean stores are output and the standard error is set to zero. When the multicell version is used then the mean and the standard error are output.

The variables defined in the order they appear in the file are:

Model #: ML02 indicates this file is output for STANDCARB.

Output #: 32 indicates this is the Live.out file

Time: simulation year. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, a state variable will be output for the time Year.1. Then the effects of harvest or wildfire will be calculated and output for the time Year.2. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.3. If a wildfire occurs during the year of harvest, then the effects of this disturbance will be calculated and output for time Year.4. This allows one to directly track the changes in stores for each disturbance in a given year.

Foliage Mean: mean of the total foliage organic matter or carbon for all the cells (Mg ha⁻¹).

Foliage StdErr: standard error of the total foliage organic matter or carbon for all the cells (Mg ha⁻¹).

FineRoot Mean: mean of the total fine root organic matter or carbon for all the cells (Mg ha⁻¹).

FineRoot StdErr: standard error of the total fine root organic matter or carbon for all the cells (Mg ha⁻¹).

Branch Mean: mean of the total branch organic matter or carbon for all the cells (Mg ha⁻¹).

Branch StdErr: standard error of the total branch organic matter or carbon for all the cells (Mg ha⁻¹).

Sapwood Mean: standard error of the total sapwood organic matter or carbon for all the cells (Mg ha⁻¹).

Sapwood StdErr: standard error of the sapwood organic matter or carbon for all the cells (Mg ha⁻¹).

Heartwood Mean: standard error of the total heartwood organic matter or carbon for all the cells (Mg ha⁻¹).

Heartwood StdErr: standard error of the heartwood organic matter or carbon for all the cells (Mg ha⁻¹).

CoarseRoot Mean: mean of the total coarse root organic matter or carbon for all the cells (Mg ha⁻¹).

CoarseRoot StdErr: standard error of the total coarse root organic matter or carbon for all the cells (Mg ha⁻¹).

HeartRot Mean: standard error of the total heart-rot organic matter or carbon for all the cells (Mg ha⁻¹).

HeartRot StdErr: standard error of the heart-rot organic matter or carbon for all the cells (Mg ha⁻¹).

Version 2

Example of Live.out file:

# # StdErr				FineRoot		Branch		Sapwood		Heartwood	9	CoarseRoot	ot	
	Time	Mean	StdErr	Mean	StdErr	Mean	StdErr	Mean	StdErr	Mean	StdErr	Mean	StdErr	Mean
ML02 32	10.0	5.082	0.631	9.306	2.046	3,358	0.769	2.470	0.576	000.0	0.000	3.410	0.781	0.000
ML02 32	20.0	8.247	0.442	8.146	0.332	5.976	1.741	12.809	0.930	0.705	0.127	11.930	1.133	0.000
ML02 32	30.0	8,385	0.182	6.732	0.489	6.214	0.306	39.078	1.317	13,509	0.946	40.130	1.674	000.0
ML02 32	40.0	9.421	0.167	7.077	0.349	11.281	0.911	56.528	2,101	38.412	1.422	69.798	2.226	0.000
ML02 32	50.0	9.557	0.172	7.412	0.647	15.823	1.379	66.740	2.938	66.825	1.792	93.624	2.873	0.000
ML02 32	0.09	9.383	0.275	809.9	0.015	19,189	1.669	72.605	3.406	95.125	2.176	111.820	3.313	000.0
ML02 32	70.0	9.517	0.237	7.149	0.521	21.546	1.870	76.030	3.717	121.884	2.499	125.484	3.644	0.000
ML02 32	80.0	9.729	0.157	7.161	0.376	23.234	1.939	78.271	3.744	146.521	2.821	135.748	3.844	0.000
ML02 32	0.06	9.831	0.112	6.503	0.064	25.035	1.698	81.135	3.141	169,120	3.073	144.436	3.547	0.000
ML02 32	100.0	9.978	0.008	6.585	0.005	27.070	1.046	84.684	1.682	190.051	3.122	152.257	2.552	0.000
ML02 32	110.0	9.979	0.007	6.586	0.005	28,333	0.637	86.595	0.885	205,586	2.624	157.928	.1.822	3.709
ML02 32	120.0	9.979	900.0	6.586	0.004	29.104	0.388	87.602	0.466	202.843	1.979	162.013	1.302	22.861
ML02 32	130.0	086.6	0.005	6.587	0.004	29.849	0.243	89.202	0.330	203.744	1.708	167.406	1.135	39.213
ML02 32	140.0	9.981	0.005	6.587	0.003	31,459	0.155	93.522	0.211	221.975	1.580	182.424	0.995	56.905
1.234 ML02 32	150.0	9.981	0.004	6.588	0.003	32,587	0.098	95.465	0.115	240.523	1.365	194.823	0.788	74.706
ML02 32	160.0	8.277	1.063	5.463	0.702	29,259	2.563	81.020	9.541	204.841	33.354	166.547	23.978	92.160
32	170.0	8.724	0.904	5.758	0.597	30.569	2.221	83,696	8.792	218.498	35.019	174.873	24.483	87.920
2 32	180.0	8.814	0.711	5.813	0.471	31.086	1.742	81.390	8.236	202.790	41.626	163.961	27.489	88.900
ML02 32	190.0	8.858	0.681	5.846	0.450	33.311	1.102	85.625	6.545	214.828	42.636	171.866	26.669	99,991
ML02 32	200.0	9.288	0.477	6.135	0.314	35.724	0.930	90.051	4.635	226.586	43.192	179.523	25,380	111.003
ML02 32	210.0	9.308	0.458	6.144	0.303	37.373	1.402	92.748	3.568	237.878	43.385	185.557	24,382	121.851
ML02 32	220.0	9.581	0.292	6.321	0.194	38.802	1.874	95.029	2.589	248.466	43.357	190.715	23,395	132.475
ML02 32	230.0	9.017	0.687	5.948	0.454	38.089	3.429	89.841	7.169	221.570	48.024	172.315	26.975	120.697
ML02 32	240.0	9.116	0.659	6.019	0.435	40.400	3.996	94.110	6.954	229.849	48.206	178.603	25.752	130,887
ML02 32	250.0	9.230	0.632	960.9	0.418	42.968	4.857	98.418	7.357	237.292	48.394	185.667	24.264	143.288

156.400	169.234	151.899	162,387	172.654	7.734	6.077	4.871	3.898	3.119	2.496	2.372	2.136	1.712	1.370	7.489	17.432	24.161	24.161
22.832	21.261	25.353	24.164	23.296	10.541	4.324	5.725	4.330	3.114	2.270	2.057	1.897	1.424	1.085	18.177	22.816	25.515	25.515
192,403	198.577	180.689	187.143	192.227	11.182	14.803	42.094	70.553	91.441	106.391	101.638	91.360	104.690	115.753	101.929	102.066	82.196	82.196
48.442	48.311	51.102	50.792	50.380	7.056	3.963	5.323	5.943	5.901	5.562	5.208	4.606	4.204	3.787	12,691	15,598	17.913	17.913
244.331	251.098	216.911	223.281	229.487	16.214	11.088	17.998	30.729	46.380	62,565	59.707	54.185	68.189	82.152	69.815	65.993	50.382	50.382
7.910	7.696	10.912	10.494	10.341	9.751	8.496	7.818	4.446	2.398	1.342	1.240	1.736	1.203	0.740	16.830	19.742	20.796	20.796
101.997	105.190	100.924	105.081	107.500	23.253	26.856	58.016	85.800	101.258	109.490	104.613	95.240	104.102	110.872	94.537	91.453	73.422	73.422
5.657	6.105	7.183	7.397	7.596	5.292	2.651	3.195	2.093	1.297	0.823	0.749	0.930	0.684	0.463	8.919	10.734	11.563	11.563
45.275	47.363	47.298	49.654	51.247	5.614	9.400	25.194	40.237	49.759	55.598	53.119	48.349	53.799	58.016	990.09	48.962	39.239	39,239
0.400	0.212	0.453	0.436	0.420	0.634	1,918	1.000	0.023	0.020	0.020	0.041	0.037	0.020	0.018	978.0	0.495	0.964	0.964
6.107	6.316	6.092	6.104	6.119	0.672	8.389	7.254	6.579	6.574	6.574	6.282	5,653	6.485	6.575	5,251	5.994	5.174	5.174
909.0	0.318	0.686	0.659	0.636	0.916	0.809	0.192	0.033	0.031	0.030	0.063	0.157	0.031	0.027	1,353	0.916	1.337	1,337
9.253	9.573	9.215	9.245	9.271	2.054	7.146	9.405	9.948	9.958	096.6	9.517	8.676	9.832	9.959	7.924	8.377	6.962	6.962
260.0	270.0	280.0	290.0	300.1	300.2	310.0	320.0	330.0	340.0	350.1	350.2	350.3	360.0	370.0	380.0	390.0	400.1	400.4
32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32
ML02	ML02	ML02	39.987 ML02	40.981 ML02	41.956 ML02	Z.610 ML02	2.190 ML02	1.754 ML02	1.403 ML02	1.123 ML02	0.898 ML02	0.853 ML02	0.768 ML02	ML02	ML02	1.873 ML02	4.489 ML02	7.476 ML02 7.476

Dead.out

This output file contains all the data for the detrital pools. When the single cell version of the model is used only the mean stores are output and the standard error is set to zero. When the multicell version is used then the mean and the standard error are output.

Note that the stable pools are now placed in their own output file ("Stable.out")

The variables defined in the order they appear in the file are:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 33 indicates this is the Dead.out file

Time: simulation year. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.1. Then the effects of harvest or wildfire will be calculated and output for the time Year.2. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.3. If a wildfire occurs during the year of harvest, then the effects of this disturbance will be calculated and output for time Year.4. This allows one to directly track the changes in stores for each disturbance in a given year.

Dead-Foliage Mean: mean of the dead foliage organic matter or carbon for all the cells (Mg ha⁻¹).

Dead-Foliage StdErr: standard error of the dead foliage organic matter or carbon for all the cells (Mg ha⁻¹).

Dead-FineRoot Mean: mean of the dead fine root organic matter or carbon for all the cells (Mg ha⁻¹).

Dead-FineRoot StdErr: standard error of the dead fine root organic matter or carbon for all the cells (Mg ha⁻¹).

Dead-Branch Mean: mean of the dead branch organic matter or carbon for all the cells (Mg ha⁻¹).

Dead-Branch StdErr: standard error of the dead branch organic matter or carbon for all the cells (Mg ha⁻¹).

Dead-Sapwood Mean: mean of the total dead sapwood organic matter or carbon for all the cells (Mg ha⁻¹).

Dead-Sapwood StdErr: standard error of the total dead sapwood organic matter or carbon for all the cells (Mg ha⁻¹).

Dead-Heartwood Mean: mean of the total dead heartwood organic matter or carbon for all the cells (Mg ha⁻¹).

Dead-Heartwood StdErr: standard error of the total dead heartwood organic matter or carbon for all the cells (Mg ha⁻¹).

Dead-CoarseRoot Mean: mean of the dead coarse root organic matter or carbon for all the cells (Mg ha⁻¹).

Dead-CoarseRoot StdErr: standard error of the coarse root organic matter or carbon for all the cells (Mg ha⁻¹).

Version 2

Example of Dead.out file:

11.252	10.719	25.877	16.202	13.018	194.063	102.618	35.853	8.937	11.499	13.855	18.607	28.885	19.638	15.944	27.668	21.292	38.454	38.454
37.057	35.654	42.177	40.780	39.702	35.542	37.519	33.654	30.887	28.795	27.064	26.930	26.463	24.889	23.533	20.191	22.494	28.779	18.906
136.332	125.790	156.057	146.992	139.742	159.047	156.272	146.746	140.366	136.889	135.188	136.678	142.375	138.320	137.811	152.504	143.441	142.719	105.718
3,385	3.038	7,398	6.410	5.920	5.474	13.379	11.418	8.718	6.889	5.418	5.497	5.816	4.395	3.329	15.081	15.966	18.175	11.614
31.229	27.598	31.857	28.585	25.993	30.729	39.464	38.651	37.992	40.337	43.464	45.903	54.431	52.036	51.918	69.440	69.209	86.062	60.303
0.745	0.785	1.246	0.919	1.120	866.6	4.573	1.747	0.557	0.595	0.427	0.623	0.969	0.330	0.201	4.668	3.817	8.754	8.754
10.164	10.413	12.086	11.684	11.849	57.482	31.283	16.655	13.418	13.568	15.963	18.441	18.551	17.472	18.218	23.790	19.785	27.975	27.975
1.281	1.098	0.719	1.351	1.362	1.876	1.732	1.290	0.469	0.160	0.183	0.187	0.187	0.271	0.164	0.895	1.922	2.129	2.129
19.231	19.602	19.479	19.208	19.258	24.705	14.826	16.776	20.296	21.283	20.986	21.278	21,907	21.094	21.512	19.411	17.214	17.480	17.480
0.859	0.654	0.483	0.840	0.882	1.617	1.085	0.885	0.273	0.185	0.381	0.384	0.316	0.330	0.324	0.730	1.351	1.628	1.628
12.069	12.349	11.968	12.144	12.271	20.523	10.420	11.416	13.889	15.375	15.125	15.568	12,509	14.414	14.619	14.094	11.522	13.419	13.419
260.0	270.0	280.0	290.0	300.1	300.2	310.0	320.0	330.0	340.0	350.1	350.2	350.3	360.0	370.0	380.0	390.0	400.1	400.4
ML02 33	1.254 ML02 33	1.237 ML02 33	14.424 ML02 33	4.768 ML02 33	ML02 33	ML02 33	ML02 33	6.343 ML02 33	1.009 ML02 33	0.609 ML02 33	0.487 ML02 33	0.901 ML02 33	1.028 ML02 33	0.481 ML02 33	0.360 ML02 33	9.832 ML02 33	ML02 33	18.620 ML02 33 18.620

DeadWood.out

This output file contains all the data for the dead wood pools. When the single cell version of the model is used only the mean stores are output and the standard error is set to zero. When the multicell version is used then the mean and the standard error are output.

The variables defined in the order they appear in the file are:

Model #: ML02 indicates this file is output for STANDCARB.

File #: 35 indicates this is the DeadWood.out file

Time: simulation year. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.1. Then the effects of harvest or wildfire will be calculated and output for the time Year.2. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.3. If a wildfire occurs during the year of harvest, then the effects of this disturbance will be calculated and output for time Year. If a wildfire occurs during the year of harvest, then the effects of this disturbance will be calculated and output for time Year.04. This allows one to directly track the changes in stores for each disturbance in a given year. 4. This allows one to directly track the changes in stores for each disturbance in a given year.

Salvagable-Snag Mean: mean of the salvagable snag organic matter or carbon for all the cells (Mg ha⁻¹).

Salvagable-Snag StdErr: standard error of the salvagable snag organic matter or carbon for all the cells (Mg ha⁻¹).

Non-Salvagable-Snag Mean: mean of the non-salvagable snag organic matter or carbon for all the cells (Mg ha⁻¹).

Non-Salvagable-Snag StdErr: standard error of the non-salvagable snag organic matter or carbon for all the cells (Mg ha⁻¹).

Salvagable-Log Mean: mean of the salvagable log organic matter or carbon for all the cells (Mg ha⁻¹).

Salvagable-Log StdErr: standard error of the salvagable log organic matter or carbon for all the cells (Mg ha⁻¹).

Non-Salvagable-Log Mean: mean of the non-salvagable log organic matter or carbon for all the cells (Mg ha^{-1}).

Non-Salvagable-Log StdErr: standard error of the non-salvagable log organic matter or carbon for all the cells (Mg ha⁻¹).

Version 2

Example of DeadWood.out file:

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-LogStdErr	0.	0.911						0.899						•		9	4.55	2.67	21.924	0	2	28.325	÷	6	7	5	9	6.7	.9	5.1	4.41	.69	8.37	.7	10.748
Non-Salvagable-Log Mean StdE	900.0	0.888	6.058	6.936											7.013	6.494		5.225	46.329		6.009		1.752	3.372	3.654	8.620	4.135	4.197		9.302	7.816	207	8.478	6.040	86.040
StdErr		0.004	0.101	0.328	0.652	1.054	1.524	2.047	2.596	3,160	3.749	4.313	4.715	4.363	4.060	7.94	9	25.883	. 90	30.932	9.04	9.04	4	-	5	4	8	8.60	.57	7.8	7.11	2	2.97	2.5	8.143
Salvagable-Log Mean	0.000	0.007	.28			3.151		6.130			11.241		14.144	3.08	2.17	42,419		6	40.282	6	0		9	4	8	8	8	2	21.880	6	8	3	7	•	11.559
14	0.013	2.895	9.	1.447	8	1.448	2.319	3.588	5.349	7.553	0		7	1.63	25.062	32,131	29.885	35,514	32.787	30.553	28.613	28,613	26.802	22.821	39.946	36.194	33.857	33.857	33,939	32.038	30.852	26.347	28.059	25.642	25.642
Non-Salvagable-Snag Mean StdEr	0.022	4.862	4.174			3.213	5.290	8,356	(4)	20.503	9.19	0	53.063	64.551	8	65.819	61.823	75.664	70.201	64.493	60.208	60.208	47.536	28.772	51.748	49.523	~	50.188	50.611	52.880	0	53.923	0	9.0	59.061
nag StdErr	0.000	0.032	0.910	2.978	5.926	9.507	13.503	17.586	21.312	24.723	27.747	29.942	29.843	22.868	15.973	31.898	30.357	4.379		36.583	34.937	34.937	36.282	31.865	5.696	7.362	9.031	9.031	14.280	13.407	11.440	27.818	24.568	29.447	7.362
Salvagable-Snag Mean S	0.000	0.065	2.591	8.805	-	8	0	52,685	3	4	3	6	6	8		7		3	31.103	29.772	29.088	29.088	39.501	38.733	14.423	20.529	26.096	26.096	40.644	38.770	33.702	47.576	36.344	7	9.361
Time		20.0								00	10.	20.	30.	40.	150.0	250.0	.09	70.	280.0	90.	00	00.	10.	20.	30.	40.	50.	50.	50.	60.	70.	80.	90.	00.	00
File #	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35																				35
Model #	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02	ML02						

Stable.out

This output file contains all the data for the stable pools. When the single cell version of the model is used only the mean stores are output and the standard error is set to zero. When the multicell version is used then the mean and the standard error are output.

The variables defined in the order they appear in the file are:

Model #: ML02 indicates this file is output for STANDCARB.

File #: 36 indicates this is the Stable.out file

Time: simulation year. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.1. Then the effects of harvest or wildfire will be calculated and output for the time Year.2. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.3. If a wildfire occurs during the year of harvest, then the effects of this disturbance will be calculated and output for time Year.4. This allows one to directly track the changes in stores for each disturbance in a given year.

Stable-Foliage Mean: mean of the stable foliage organic matter or carbon for all the cells (Mg ha⁻¹). This pool is analogous to the O2 layer.

Stable-Foliage StdErr: standard error of the stable foliage pool organic matter or carbon for all the cells (Mg ha⁻¹).

Stable-Wood Mean: mean of the stable wood pool organic matter or carbon for all the cells (Mg ha⁻¹).

Stable-Wood StdErr: standard error of the stable wood organic matter or carbon for all the cells (Mg ha⁻¹).

Stable-Soil Mean: mean of the stable soil organic matter or carbon for all the cells (Mg ha⁻¹).

Stable-Soil StdErr: standard error of the stable soil organic matter or carbon for all the cells (Mg ha⁻¹).

Example of Stable.out file:

Stable.out

Version 2

Model	File		Stable-Foli	age	Stable-Wood		Stable-Soil	
#	#	Time	Mean	StdErr	Mean	StdErr	Mean	StdErr
	26	10.0	0.011	0 000	0.000	0.000	077 061	0 005
ML02	36	10.0	0.014	0.008	0.000			0.297
ML02	36	20.0	0.413	0.094	0.000	0.000	241.540	0.454
ML02	36	30.0	1.200	0.139		0.031	211.392	0.402
ML02	36	40.0	3.005	0.277		0.826	191.443	0.745
ML02	36	50.0	4.431	0.541		0.332	172.644	0.925
ML02	36	60.0	6.451	1.084	1.012	0.163	157.499	1.127
ML02	36	70.0	6.881	0.815	1.516 2.524	0.587		1.680
ML02	36	80.0	7.558	1.018	2.524	0.952	138.213	2.117
ML02	36	90.0	7.944	0.959	2.382 1.071	0.558		2.792
ML02	36	100.0	9.556	0.792	1.071	0.171	125.589	3.299
ML02	36	110.0	9.927	0.508	0.500	0.052	121.720	2.868
ML02	36	120.0	9.606	0.469	0.389	0.040	120.593	2.816
ML02	36	130.0	9.787	0.455	0.452	0.053	118.013	2.699
ML02	36	140.0	9.993	0.585	0.565	0.069	116.671	2.862
ML02	36	150.0	9.534	0.334		0.036	113.979	2.337
ML02	36	160.0	10.060	0.509	0.705	0.066	111.304	1.844
ML02	36	170.0	9.705	0.367	0.705	0.123	108.249	1.615
ML02	36	180.0	9.342	0.748	1.324	0.118	112.073	7.252
ML02	36	190.0	8.476	0.806	2.523	0.267	107.963	5.770
ML02	36	200.0	8.690	0.853	3.932	0.254	108.776	4.322
ML02	36	210.0	8.888	0.403	4.898 6.039	0.448	104.960	3.263
ML02	36	220.0	9.132	0.546	6.039	0.730	102.329	2.431
ML02	36	230.0	9.623	0.486	6.896	0.976	100.965	1.821
ML02	36	240.0	9.476	0.497	8.382	0.938	98.938	1.316
ML02	36	250.0	9.032	0.612	10.343	1.105	97.206	1.873
ML02	36	260.0	9.137	0.651	10.938	1.092	95.007	2.170
ML02	36	270.0	9.267	0.579		0.862	93.674	1.761
ML02	36	280.0	10.688	0.517	10 670	0 722	92.090	2.332
ML02	36	290.0	9.852	0.393		0.995	90.714	2.366
ML02	36	300.1	9.762	0.846	8.042	1.204	89.621	2.469
ML02	36	300.2	9.762	0.846		1.204		2.469
ML02	36	310.0	15.441	1.474	7.965	1.320	95.837	3.276
ML02	36	320.0	8.935	1.203	7.401	1.149		10.898
ML02	36	330.0	8.837	1.003	5.527	0.613	132.962	9.358
ML02	36	340.0	9.419	0.374	6.769	0.887	123.506	8.551
ML02	36	350.1	11.162	0.679		0.544	119.264	7.006
ML02	36	350.2	11.162	0.679	5.229	0.544	119.264	7.006
ML02	36	350.3	11.162	0.679		0.544	119.264	7.006
ML02	36	360.0	10.215	0.608	5.887	0.801	115.514	6.269
ML02	36	370.0	11.267	0.549		0.373	114.293	5.812
ML02	36	380.0	10.904	0.525		0.257	113.496	4.938
ML02	36	390.0	11.726	0.622	14.979	10.358	112.294	4.637
ML02	36	400.1	8.796	1.061	17.730	8.739	113.912	6.532
ML02	36	400.1	8.796	1.061	17.730	8.739	113.912	6.532
MLUZ	30	400.4	0.790	1.001	11.130	0./39	113.912	0.33

Volume.out

This file gives the cubic volume and the amount of volume that was harvested in a given year. In addition, the species, mean age, height, and tree density before and after harvest of each tree layer are output as indicators of wood value. When the single cell version of the model is used only the mean stores are output and the standard error is set to zero. When the multicell version is used then the mean and the standard error are output.

The variables defined in the order they appear in the file are:

Model #: ML02 indicates this file is input for STANDCARB.

File #: 34 indicates this is the Volume.out file

Time: simulation year. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.1. Then the effects of harvest or wildfire will be calculated and output for the time Year.2. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.3. If a wildfire occurs during the year of harvest, then the effects of this disturbance will be calculated and output for time Year.4. This allows one to directly track the changes in stores for each disturbance in a given year.

Layer: the tree layer that was harvested ("UT" = upper tree, "LT" = lower tree)

Species: the species that was harvested. If the value of Volume is 0, this means that none of the selected species was present in the stand.

Volume: mean volume of wood living in stand at the time of harvest (cubic meters ha⁻¹).

Density: mean density of the tree layer before harvest (numbers ha⁻¹).

Harvest Volume: volume of trees actually harvested (cubic meters ha⁻¹).

Harvest Density: the number of trees that were harvested in the layer (numbers ha⁻¹).

Height: height of harvested trees (m).

Age: approximate age of trees harvested, based on the upper tree layer (years).

Treatment: type of harvest treatment used.

% Cut: precent of tree that are cut in a cell (%).

% Taken: percent of the boles cut that is removed (%)

% Cells Cut: percent of cells that were cut by a particular treatment (%). This may be less that the proportion defined in CutPatt, drv if a selected species does not occur in all the cells.

Util: the utilization level that was specified.

Fire Type: the fire type used for site preparation.

Example of Volume.out file:

,	rire	one	none	one	one	ite	ite	ouc
•	Util 1		high no			ń	(H)	
	% Cells	44.4 h			Acres :			
ं	* & Taken C	95.0	95.0	95.0	95.0	50.0	50.0	75.0
	% Cut	0.86	0.86	0.86	0.86	5.0	5.0	75.0
	Treatment	ccut	ccut	ccut	ccut	com	com	salv
	Age	291.3	0.0	126.4	0.0	74.1	0.0	NA
	Height	7.78	0.0	46.9	0.0	33.9	0.0	NA
	nsity	7	0	16	581	1	0	NA
	Harvest Volume Density	757.3	0.0	398.8	85.5	16.6	0.0	8.7
	e Density	7	0	19	589	26	231	NA
	Volume De	797.1	0.0	500.1	0.06	736.3	1.1	34.7
	Species	Psme	Psme	Tshe	Tshe	Tshe	Tshe	NA
	Layer	UT	LT	UT	LT	UT	LT	NA
	Time	300.2	300.2	300.2	300.2	350.2	350.2	400.4
.out	File #	34	34	34	34	34	34	34
Volume.out	Model #	ML02	ML02	ML02	ML02	ML02	ML02	ML02

Diagnostic Files

The diagnostic files are used to examine specific subfunctions of the model for parameterization or trouble shooting purposes. The extension on these files is DGN. Diagnostic files are output when selected in the Simul.drv file.

Table 7. List of diagnostic files available to check the STANDCARB model behavior.										
File Name	Purpose									
Plant.dgn	checks the rate layers and species are planted in cells									
DieOut.dgn	checks the rate species die out of cells									
Replace.dgn	checks the rate species are replaced during succession									
Density.dgn	outputs the mean tree density of the stand									
Intercpt.dgn	outputs the interception of water by detrital pools and the canopy									
WaterBal.dgn	outputs the moisture content of the detrital pools and soil									
Transpir.dgn	outputs the transpiration of water									
TempResp.dgn	response of decomposition and respiration to temperature									
MoistResp.dgn	response of detrital pool and soil decomposition to moisture									
WPotResp.dgn	response water potential and plant production to soil water									
AbioResp.dgn	outputs indices of decomposition and growth									
Light.dgn	outputs light interception by foliage of plant layers									
Resp.dgn	outputs the respiration and mass of live plant parts									
Mort.dgn	outputs detritus production (litterfall)									
SubQual.dgn	outputs substrate quality of detritus added to detritus pools									
Species.dgn	outputs upper and lower tree species, and upper tree height and									
	age for each cell									
Neighbor.dgn	outputs radiation for each cell for a given year									

Plant.dgn

This diagnostic file gives the number of cells occupied by plant layers (herb, shrub, upper tree, and lower tree) and tree species in each tree layer. For this diagnostic, the model allows layers and species to be planted, but does not allow them to die out. Therefore once a layer of species occupies a cell, it can not be removed. This diagnostic is only available for multicell simulation runs.

Time: year being simulated. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.01. Then the effects of harvest or wildfire will be calculated and output for the time Year.02. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.03.

NumHerb: number of cells with herbs.

NumShrubs: number of cells with shrubs.

NumUpperTrees: number of cells with upper trees.

NumLowerTrees: number of cells with lower trees.

Species specific data then repeats in the following order:

Species: species abbreviation.

SpeciesTotal: total number of cells that has the named species. If a species occurs in the upper or lower tree layers or both layers of a cell it gets a value of 1. This variable indicates the presence or absence of a species in a cell.

SpeciesNumUTrees: number of cells that has the named species in upper tree layer.

SpeciesNumLTrees: number of cells that has the named species in lower tree layer.

Example of Plant.dgn file:

Plant.dgn

Time, NumHerbs, NumShrubs, NumUpperTrees, NumLowerTrees, Species, SpeciesTotal, SpeciesNumUTrees, SpeciesNumLTrees

10.0 ABPR CACH POTR PREM PSME	99 11 3 2 3 42	96 11 3 2 3 42	61 0 0 0 0	0	
20.0 ABPR ACMA CACH PIMO POTR PREM PSME THPL TSHE	100 18 2 8 2 4 8 76 1 2	79 14 1 6 0 4 7 68 0	100 6 1 2 2 0 1 19 1	34	
30.0 ABAM ABGR ABPR ACMA CACH PIMO POTR PREM PSME THPL TSHE	97 5 1 18 1 7 2 4 7 79 1	0 0 14 1 6 0 4 7 68 0	100 5 1 7 0 1 2 0 0 12 1 20	49	
40.0 ABAM ABGR ABPR ACMA CACH PIMO POTR PREM PSME THPL TSHE	89 5 1 15 1 6 1 4 7 77 1 37	0 0 14 1 6 0 4 7 68 0	100 5 1 3 0 0 1 0 0 9 1 37	57	
50.0 ABAM ABGR ABPR ACMA CACH PIMO POTR PREM PSME THPL TSHE	71 5 1 15 1 6 1 4 7 75 1 54	0 0 0 14 1 6 0 4 7 68 0	100 5 1 1 0 0 1 0 0 7 1 54	70	

DieOut.dgn

This diagnostic file gives the number of cells occupied by plant layers (herb, shrub, upper tree, and lower tree) and tree species in each tree layer. For this diagnostic, the model allows layers and species to be planted, but does not allow them to be replaced when they die out of a cell. Therefore once a layer of species dies out of a cell, it can not be replaced. This diagnostic is only available for multicell simulation runs.

Time: year being simulated. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.01. Then the effects of harvest or wildfire will be calculated and output for the time Year.02. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.03.

NumHerb: number of cells with herbs.

NumShrubs: number of cells with shrubs.

NumUpperTrees: number of cells with upper trees.

NumLowerTrees: number of cells with lower trees.

Species specific data then repeats in the following order:

Species: species abbreviation.

SpeciesTotal: total number of cells that has the named species. If a species occurs in the upper or lower tree layers or both layers of a cell it gets a value of 1. This variable indicates the presence or absence of a species in a cell.

SpeciesNumUTrees: number of cells that has the named species in upper tree layer.

SpeciesNumLTrees: number of cells that has the named species in lower tree layer.

Example of DieOut.dgn file:

DieOut.dgn

Time, NumHerbs, NumShrubs, NumUpperTrees, NumLowerTrees, Species, SpeciesTotal, SpeciesNumUTrees, SpeciesNumLTrees

10.0 ABPR CACH POTR PREM PSME	99 11 3 2 3 42	96 11 3 2 3 42	61 0 0 0 0	0
20.0 ABPR ACMA CACH PIMO POTR PREM PSME THPL TSHE	100 18 2 8 2 4 8 76 1	79 14 1 6 0 4 7 68 0	100 6 1 2 2 0 1 19 1	34
30.0 ABAM ABGR ABPR ACMA CACH PIMO POTR PREM PSME THPL TSHE	87 4 1 18 1 7 2 4 7 77 77 2	0 0 14 1 6 0 4 7 68 0	100 4 1 6 0 1 2 0 0 9 2	44
40.0 ABAM ABGR ABPR ACMA CACH PIMO POTR PREM PSME THPL TSHE	69 7 15 16 1 4 6 76 2	0 0 14 1 6 0 4 6 68 0	99 7 1 2 0 0 1 0 0 8 2 31	52
50.0 ABAM ABGR ABPR ACMA CACH PIMO POTR PREM PSME THPL TSHE	60 6 1 15 1 6 1 4 4 74 1 36	0 0 14 1 6 0 4 4 68 0	97 6 1 0 0 1 0 0 6 1 36	52

Replace.dgn

This diagnostic file gives the number of cells occupied by plant layers (herb, shrub, upper tree, and lower tree) and tree species in each tree layer. For this diagnostic, the model allows layers and species to be planted and die out as in the normal simulation run. This diagnostic is only available for multicell simulation runs.

Time: year being simulated. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.01. Then the effects of harvest or wildfire will be calculated and output for the time Year.02. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.03.

NumHerb: number of cells with herbs.

NumShrubs: number of cells with shrubs.

NumUpperTrees: number of cells with upper trees.

NumLowerTrees: number of cells with lower trees.

Species specific data then repeats in the following order:

Species: species abbreviation.

SpeciesTotal: total number of cells that has the named species. If a species occurs in the upper or lower tree layers or both layers of a cell it gets a value of 1. This variable indicates the presence or absence of a species in a cell.

SpeciesNumUTrees: number of cells that has the named species in upper tree layer.

SpeciesNumLTrees: number of cells that has the named species in lower tree layer.

Example of Replace.dgn file:

Replace.dgn

Time, NumHerbs, NumShrubs, NumUpperTrees, NumLowerTrees, Species, SpeciesTotal, SpeciesNumUTrees, SpeciesNumLTrees

10.0 ABPR CACH POTR PREM PSME	99 11 3 2 3 42	96 11 3 2 3 42	61 0 0 0 0	0
20.0 ABPR ACMA CACH PIMO POTR PREM PSME THPL TSHE	100 18 2 8 2 4 8 76 1 2	79 14 1 6 0 4 7 68 0	100 6 1 2 2 0 1 19 1	34
30.0 ABAM ABGR ABPR ACMA CACH PIMO POTR PREM PSME THPL TSHE	97 5 1 18 1 7 2 4 7 79 1	0 0 14 1 6 0 4 7 68 0	100 5 1 7 0 1 2 0 0 0 12 1 20	49
40.0 ABAM ABPR ACMA CACH POTR PREM PSME TSHE	88 2 14 1 6 4 5 77 35	0 0 14 1 6 4 5 69	100 2 2 0 0 0 0 8 34	46
50.0 ABAM ABPR ACMA CACH POTR PREM PSME TSHE	73 2 14 1 6 4 75 55	1 0 14 1 6 4 4 70	100 2 0 0 0 0 0 5 54	61

Density.dgn

This file contains the mean numbers of trees per layer for each output interval.

Time: year being simulated. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.01. Then the effects of harvest or wildfire will be calculated and output for the time Year.02. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.03.

UTreeDensity: the mean number of trees in the upper tree layer (number ha⁻¹).

LTree Density: the mean number of trees in the lower tree layer (number ha⁻¹).

Example of Density.dgn file:

Density.dgn

Year, U'	TreeDensi	ty, LTreeDensity 0.00
2.0	0.00	0.00
4.0	0.00	0.00
6.0	0.00	0.00
7.0	0.00	0.00
8.0	333.33	0.00
9.0	833.33 1333.33	0.00
11.0 12.0	1500.00 1500.00	0.00
13.0	1500.00	0.00 166.67
15.0	1500.00	166.67
16.0	1500.00	166.67
17.0	1500.00	166.67
18.0	1500.00	333.33
19.0	1500.00	333.33
20.0	1463.38	333.33 333.33
22.0	1036.75	333.33
23.0	743.96	500.00
24.0	535.29	496.39
25.0	409.65	662.65
26.0	327.80	505.12
27.0	271.13	491.67
28.0	230.01	487.92
29.0	199.03	484.84
30.0	174.97 155.83	481.87 338.42
32.0	140.27	333.33
33.0	127.40	333.33
34.0	116.61	500.00
35.0	107.44	500.00
36.0	99.56	666.67
37.0	92.72	666.67
38.0	86.74	833.33
39.0	81.46 76.78	1000.00
41.0	72.60	1166.67
42.0	68.84	1320.90
43.0	65.45	1301.94
44.0	62.37 59.57	1274.58 1243.65
46.0	57.01	1385.63
47.0	54.67	1365.52
48.0	52.51	1348.86
49.0	50.51	1334.85
50.0	48.66	1322.92

Intercpt.dgn

This file contains the interception values for the canopy and detrital pools and monthly runoff for the temperature, precipitation, soil, and radiation conditions of the site. This diagnostic is only available for the single cell version of the model.

Year: the year of simulation. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.01. Then the effects of harvest or wildfire will be calculated and output for the time Year.02. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.03.

Month: month being simulated

Temp24: temperature for month (C)

Prec: precipitation for month (cm)

SolRad: total solar radiation form month (cal cm2 month)

CanInterception: canopy interception for the month (cm)

DeadBranchInterception: interception of dead branch pool for the month (cm)

SnagSapwoodInterception: interception of snag sapwood pool for the month (cm)

LogSapwoodInterception: interception of log sapwood pool for the month (cm)

SnagHeartwoodInterception: interception of snag heartwood pool for the month (cm)

LogHeartwoodInterception: interception of log heartwood pool for the month (cm)

StableWoodInterception: interception of stable wood pool for the month (cm)

DeadFoliageInterception: interception of the dead foliage pool for a month (cm)

StableFoliageInterception: interception of stable foliage pool for the month (cm)

TotalInterception: total interception for the month (cm)

Runoff: water exceeding soil water holding capcity for each month (cm)

Example Intercpt.dgn file:

Intercpt.dgn

Year, Month, Temp24, Precip, SolRad, CanIntercept,
DeadBranchIntercept, SnagSapwoodIntercept, LogSapwoodIntercept,
SnagHeartwoodIntercept, LogHeartwoodIntercept,
StableWoodIntercept, DeadFoliageInterception, StableFoliageIntercept,
TotalIntercept, Runoff

	00.0	0.00	00.00	0.00	0.00	0.00	0.00	0.00	0.00	00.0	0.00	0.00	0.00	0.00	00.0	0.00	00.00	00.00	0.00	00.0	0.00	0.00	0.00	00.00	4	0.00	00.00	0.00	00.00	0.00	0.00	00.00	00.0	00.0	00.0	00.0	00.0	
	3.958	2.811	2.751	1.455	966.0	1.506	1.000	3.431	0.893	1.590	3.485	4.171	5.380	3.729	3.729	1.981	1.390	2.106	1.000	4.000	1.754	2,115	4.756	5.672		5.263	3.748	3.516	2.041	2.007	2.744	1.000	4.000	3.015	3.191	5,533	6.004	
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.000	0.000	0.001	0.002	0.000	0.000	0.008	0.000	0.001	0.000		0.003	0.000	000.0	0.000	0.034	0.101	0.000	0.000	0.347	0.014	0.038	0.010	
	0.007	0.076	0.016	0.036	0.091	0.149	0.000	0.421	0.000	0.170	0.040	0.018	0.004	0.005	0.017	0.033	0.083	0.139	0.000	0.000	0.432	0.004	0.061	0.015	1	0.008	0.049	0.030	0.059	0.150	0.249	0.000	000.0	0.749	0.002	0.110	0.027	
	0.000	000.0	000.0	000.0	000.0	000.0	000.0	000.0	000.0	000.0	000.0	0.000	000.0	0.000	000.0	000.0	000.0	000.0	000.0	000.0	000.0	000.0	000.0	0.000	2000000	0.000	0.003	0.001	0.002	0.005	0.002	000.0	0.000	0.003	0.008	0.016	0.004	
	0.000	000.0	000.0	000.0	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	00000	0.000	000.0	5 25 5 5 5	0.001	0.017	0.003	900.0	0.015	0.027	0.000	0.000	0.130	0.019	0.010	0.003	
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		0.008	0.049	0.036	0.069	0.180	0.098	0.000	0.000	0.168	0.401	0.757	0.434	
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.001	0.000	0.000		0.001	0.001	0.003	900.0	0.015	0.018	0.000	0.000	0.031	0.073	0.016	0.003	
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.060	0.042	0.032	0.022	0.017	0.007	0.000	0.000	0.012	0.029	0.053	0.063		0.566	0.392	0.193	0.186	0.159	0.064	0.000	0.000	0.109	0.261	0.494	0.595	
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.002	0.000	0.000	0.013	0.033	0.036	0.000	0.000	0.060	0.115	0.009	0.007		0.004	0.000	0.016	0.029	0.074	0.068	0.000	0.000	0.115	0.254	0.017	0.015	
	3.951	2.735	2,735	1.418	0.905	1.357	1.000	3.010	0.893	1.420	3.444	4.153	5.314	3.679	3.679	1.913	1.254	1.921	1.000	4.000	1.242	1.966	4.633	5.587		4.673	3.235	3,235	1.685	1.377	2.117	1.000	4.000	1.364	2.157	4.074	4.913	
	143.90	209.39	285.84	388.39	468.00	540.50	697.36	501.81	363.26	241.54	159.63	128.20	143.90	209.39	285.84	388.39	468.00	540.50	697.36	501.81	363.26	241.54	159.63	128.20		143.90	209.39	285.84	388.39	468.00	540.50	697.36	501.81	363.26	241.54	159.63	128.20	
	39.00	27.00	27.00	14.00	11.00	00.9	1.00	4.00	8.00	18.00	34.00	41.00	39.00	27.00	27.00	14.00	11.00	6.00	1.00	4.00	8.00	18.00	34.00	41.00		39.00	27.00	27.00	14.00	11.00	6.00	1.00	4.00	8.00	18.00	34.00	41.00	
•	0.30	2.70	3.80	7.40	11.70	14.90	18.30	17.40	13.50	8.10	3.50	1.10	0.30	2.70	3.80	7.40	11.70	14.90	18.30	17.40	13.50	8.10	3.50	1.10		0.30	2.70	3.80	7:40	11.70	14.90	18,30	17.40	13.50	8.10	3.50	1.10	
) 12								7 (
	10	10	10	10	10	10	10	10	10	10	10	10	20	20	20	20	20	20	20	20	20	20	20	20		100	100	100	100	100	100	100	100	100	100	100	100	ĺ

WaterBal.dgn

This file contains the moisture content of the detrital pools and soil. These are for the temperature, precipitation, soil, and radiation conditions of the site. This diagnostic is only available for the single cell version of the model.

Year: year of simulation. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.01. Then the effects of harvest or wildfire will be calculated and output for the time Year.02. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.03.

Month: month being simulated

Temp24: temperature for month (C)

Prec: precipitation for month (cm)

SolRad: total solar radiation for month (cal cm2 month):

DeadFoliageMoist: moisture content of the dead foliage pool for each month (% mass basis).

DeadFineRootMoist: moisture content of the dead fine root pool for each month (% mass basis).

DeadBranchMoist: moisture content of the dead branch pool for each month (% mass basis).

SnagSapwoodMoist: moisture content of the snag sapwood pool for each month (% mass basis).

LogSapwoodMoist: moisture content of the log sapwood pool for each month (% mass basis).

SnagHeartwoodMoist: moisture content of the snag heartwood pool for each month (% mass basis).

LogHeartwoodMoist: moisture content of the log heartwood pool for each month (% mass basis).

DeadCRootMoist: moisture content of the dead coarse root pool for each month (% mass basis).

StableFoliageMoist: moisture content of the stable foliage pool for each month (% volumetric basis).

StableWoodMoist: moisture content of the stable wood pool for each month (% volumetric basis).

StableSoilMoist: moisture content of the stable soil pool for each month (% volumetric basis).

Example WaterBal.dgn file:

WaterBal.dgn

Year, Month, Temp24, Precip, SolRad, DeadFoliageMoist, DeadFineRootMoist, DeadBranchMoist, SnagSapwoodMoist, LogSapWoodMoist, SnagHeartWoodMoist, LogHeartWoodMoist, DeadCRootMoist, StableFoliageMoist, StableWoodMoist, StableSoilMoist

Transpir.dgn

This diagnostic outputs the monthly transpiration caused by foliage of all layers. This diagnostic is only available for the single cell version of the model.

Year: year of simulation. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.01. Then the effects of harvest or wildfire will be calculated and output for the time Year.02. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.03.

Month: month being simulated

Temp24: temperature for month (C)

Prec: precipitation for month (cm)

SolRad: total solar radiation form month (cal cm2 month):

PETTotal: the potential evapotranspiration of the site based on temperature and radiation (cm)

PotenTrans: the potential transpiration if foliage mass is at its maximum in a cell and soil water supply is not limiting (cm).

Transpiration: actual transpiration given the current foliage mass and soil water potnetial (cm). Actual transpiration can be limited by a low foliage mass or low soil moisture.

Example Transpir.dgn file:

Transpir.dgn

Year, Month, Temp24, Precip, SolRad, PETTotal, PotenTrans, Transpiration

10 10 20 20 20 20 20 20 20 20 20 20 20 20 20	1 2 3 4 5 6 7 8 9 10 11 12 12 3 4 5 6 7 8 9 10 11	0.30 2.70 3.80 7.40 11.70 14.90 18.30 17.40 13.50 8.10 3.50 1.10 0.30 2.70 3.80 7.40 11.70 14.90 18.30 17.40 13.50 8.10 3.50 7.40 11.70	39.00 27.00 27.00 14.00 11.00 6.00 1.00 4.00 8.00 18.00 34.00 41.00 27.00 14.00 11.00 6.00 1.00 4.00 8.00	159.63	1.009 1.792 3.033 5.390 8.812 11.608 17.985 12.463 7.283 3.640 1.591 1.009 1.792 3.033 5.390 8.812 11.608 17.985 12.463 7.283 3.640 1.591	0.908 1.613 2.730 4.851 7.931 10.447 16.186 11.216 6.555 3.276 1.432 0.904 0.908 1.613 2.730 4.851 7.931 10.447 16.186 11.216 6.555 3.276 1.432	1.127	
100 100 100 100 100 100 100 100 100 100	12 3 4 5 6 7 8 9 10 11 12	1.10 0.30 2.70 3.80 7.40 11.70 14.90 18.30 17.40 13.50 8.10 3.50 1.10	41.00 39.00 27.00 27.00 14.00 11.00 6.00 1.00 4.00 8.00 18.00 34.00 41.00	128.20 143.90 209.39 285.84 388.39 468.00 540.50 697.36 501.81 363.26 241.54 159.63 128.20	1.004 1.009 1.792 3.033 5.390 8.812 11.608 17.985 12.463 7.283 3.640 1.591 1.004	0.904 0.908 1.613 2.730 4.851 7.931 10.447 16.186 11.216 6.555 3.276 1.432 0.904	0.823 0.908 1.613 2.730 4.851 7.931 10.447 13.797 5.592 1.642 1.317 1.166 0.904	

TempResp.dgn

This file contains the response of decomposition, plant respiration, and growth to temperature assuming a systematic progression of temperature values is used (0-50 C by 1 C increments) rather than the values in the Climate.drv file.

Temperature: temperature (C)

DeadFoliageTmpDcayIndx: value of index for response to temperature of dead foliage pool (dimensionless).

DeadFRootTmpDcayIndx: value of index for response to temperature of dead fine root pool (dimensionless).

DeadBranchTmpDcayIndx: value of index for response to temperature of dead branch pool (dimensionless).

SalvSnagSapTmpDcayIndx: value of index for response to temperature of salvageable snag sapwood pool (dimensionless).

SalvLogSapTmpDcayIndx: value of index for response to temperature of salvageable log sapwood pool (dimensionless).

SalvSnagHeartTmpDcayIndx: value of index for response to temperature of salvageable snag heartwood pool (dimensionless).

SalvLogHeartTmpDcayIndx: value of index for response to temperature of salvageable log heartwood pool (dimensionless).

DeadCRootTmpDcayIndx: value of index for response to temperature of dead coarse root pool (dimensionless).

StableFoliageTmpDcayIndx: value of index for response to temperature of stable foliage pool (dimensionless).

StableWoodTmpDcayIndx: value of index for response to temperature of stable wood pool (dimensionless).

StableSoilTmpDcayIndx: value of index for response to temperature of stable soil pool (dimensionless).

FRootRespRate: value of the respiration rate for fine roots of the upper tree layer (year⁻¹).

BranchRespRate: value of the respiration rate for branch of the upper tree layer (year-1).

SapwoodRespRate: value of the respiration rate for sapwood of the upper tree layer (year-1).

CRootRespRate: value of the respiration rate for coarse roots of the upper tree layer (year 1).

Example of TempResp.dgn file:

TempResp.dgn

Temp, DeadFoliageTmpDcayIndx, DeadFRootTmpDcayIndx, DeadBranchTmpDcayIndx, SalvSnagSapTmpDcayIndx, SalvLogSapTmpDcayIndx, SalvSnagHeartTmpDcayIndx, SalvLogHeartTmpDcayIndx, DeadCRootTmpDcayIndx, StableFoliageTmpDcayIndx, StableWoodTmpDcayIndx, StableSoilTmpDcayIndx, FRootRespRate, BranchRespRate, SapwoodRespRate, CRootRespRate

600	600	010	010	011	012	013	014	015	016	017	018	020	021	022	024		136	146	156	167	179	192	206	221	237	254	272	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0											0.		
0.009	0.009	0.010	0.010	0.011	0.012	0.013	0.014	0.015	0.016	0.017	0.018	0.020	0.021	0.022	0.024		0.136	0.146	0.156	0.167	0.179	0.192	0.206	0.221	0.237	0.254	0.272	
0.009	0.009	0.010	0.010	0.011	0.012	0.013	0.014	0.015	0.016	0.017	0.018	0.020	0.021	0.022	0.024	19/03/2015	0.136	0.146	0.156	0.167	0.179	0.192	0.206	0.221	0.237	0.254	0.272	
0.250	0.268	0.287	0.308	0.330	0.354	0.379	0.406	0.435	0.467	0.500	0.536	0.574	0.616	0.660	0.707		4.000	4.287	4.595	4.925	5.278	5.657	6.063	6.498	6.964	7.464	8.000	
0.500	0.536	0.574	0.616	0.660	0.707	0.758	0.812	0.871	0.933	1.000	1.072	1.149	1.231	1.320	1.414		7.628	8.003	8.323	8.554	8.651	8.561	8.229	7.610	989.9	5.492	4.131	
0.500	0.536	0.574	0.616	0.660	0.707	0.758	0.812	0.871	0.933	1.000	1.072	1.149	1.231	1.320	1.414											5.492		
0.500	0.536	0.574	0.616	0.660	0.707	0.758	0.812	0.871	0.933	1.000	1.072	1.149	1.231	1.320	1.414											5.492		
0.500	0.536	0.574	0.616	0.660	0.707	0.758	0.812	0.871	0.933.	1.000	1.072	1.149	1.231	1.320	1.414		7.628	8.003	8.323	8.554	8.651	8.561	8.229	7.610	6.686	5.492	4.131	
0.500	0.536	0.574	0.616	0.660	0.707	0.758	0.812	0.871	0.933	1.000	1.072	1.149	1.231	1.320	1.414		7.628	8.003	8.323	8.554	8,651	8.561	8.229	7.610	989.9	5.492	4.131	
0.500	0.536	0.574	0.616	0.660	0.707	0.758	0.812	0.871	0.933	1.000	1.072	1.149	1,231	1,320	1.414		7.628	8.003	8.323	8.554	8.651	8.561	8.229	7.610	989.9	5.492	4.131	
0.500	0.536	0.574	0.616	0.660	0.707	0.758	0.812	0.871	0.933	1.000	1.072	1.149	1.231	1.320	1.414		7.628	8.003	8.323	8.554	8.651	8.561	8.229	7.610	6.686	5.492	4.131	
0.500	0.536	0.574	0.616	0.660	0.707	0.758	0.812	0.871	0.933	1.000	1.072	1.149	1.231	1.320	1.414		7.628	8.003	8.323	8.554	8.651	8.561	8.229	7.610	6.686	5.492	4.131	
0.500	0.536	0.574	0.616	0.660	0.707	0.758	0.812	0.871	0.933	1.000	1.072	1.149	1.231	1.320	1.414		7.628	8.003	8.323	8.554	8.651	8.561	8.229	7.610	6.686	5.492	4.131	
0.500	0.536	0.574	0.616	0.660	0.707	0.758	0.812	0.871	0.933	1.000	1.072	1.149	1.231	1.320	1.414		7.628	8.003	8.323	8.554	8.651	8.561	8.229	7.610	6.686	5.492	4.131	
0.500	0.536	0.574	0.616	0.660	0.707	0.758	0.812	0.871	0.933	1.000	1.072	1.149	1.231	1.320	1.414		7.628	8.003	8.323	8.554	8.651	8.561	8.229	7.610	6.686	5.492	4.131	
0.0	1.0	2.0	3.0	4.0	5.0	0.9	7.0	8.0	0.6	0.0	1.0	2.0	3.0	4.0	5.0		0.0	11.0	12.0	13.0	14.0	15.0	0.9	17.0	18.0	19.0	0.00	

MoistResp.dgn

This file contains the response of decomposition to moisture assuming a systematic progression of moisture values is used (0-500 % by 5 % increments) rather than the values computed from the WaterBalance functions.

Moisture: moisture of the detrital pool or soil (%)

DeadFoliageMoistDcayIndx: value of index for response to moisture of dead foliage pool (dimensionless).

DeadFRootMoistDcayIndx: value of index for response to moisture of dead fine root pool (dimensionless).

DeadBranchMoistDcayIndx: value of index for response to moisture of dead branch pool (dimensionless).

SnagSapMoistDcayIndx: value of index for response to moisture of snag sapwood pool (dimensionless).

LogSapMoistDcayIndx: value of index for response to moisture of log sapwood pool (dimensionless).

SnagHeartMoistDcayIndx: value of index for response to moisture of snag heartwood pool (dimensionless).

LogHeartMoistDcayIndx: value of index for response to moisture of log heartwood pool (dimensionless).

DeadCRootMoistDeayIndx: value of index for response to moisture of dead coarse root pool (dimensionless).

StableFolMoistDcayIndx: value of index for response to moisture of stable foliage pool (dimensionless).

StableWoodMoistDcayIndx: value of index for response to moisture of stable wood pool (dimensionless).

StableSoilMoistDcayIndx: value of index for response to moisture of stable soil pool (dimensionless).

Example of MoistResp.dgn file:

MoistResp.dgn

Moisture, DeadFoliageMoistDcayIndx, DeadFRootMoistDcayIndx, DeadBranchMoistDcayIndx, SnagSapMoistDcayIndx, LogSapMoistDcayIndx, SnagHeartMoistDcayIndx, LogHeartMoistDcayIndx, DeadCRootMoistDcayIndx, StableFolMoistDcayIndx, StableFolMoistDcayIndx,

0.000	0.775	0.967	0.995	0.998	0.999	1.000	00000	0.000	0.000	0.000	0.000	000.0	0.000	000.0	000.0	0.000	0.000
0.000	0.283	0.652	0.858	0.912	0.946	0.967	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.283	0.652	0.858	0.912	0.946	0.967	0.000	0.000	0.000	0.000	0.000	000.0	0.000	0.000	0.000	0.000	0.000
0.000	0.283	0.652	0.858	0.912	0.946	0.967	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.283	0.652	0.858	0.912	0.946	0.967	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.283	0.652	0.858	0.912	0.946	0.967	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.283	0.652	0.858	0.912	0.946	0.967	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.283	0.652	0.858	0.912	0.946	0.967	000.0	0.000	0.000	0.000	000.0	0.000	0.000	00000	0.000	0.000	0.000
0.000	0.283	0.652	0.858	0.912	0.946	0.967	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.283	0.652	0.858	0.912	0.946	0.967	900.0	0.003	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
0.000	0.283	0.652	0.858	0.912	0.946	0.967	000.0	000.0	0.000	000.0	000.0	0.000	000.0	0.000	0.000	000.0	0.000
5.00	15.00	25.00	35.00	40.00	45.00	50.00	450.00	455.00	460.00	465.00	470.00	475.00	480.00	485.00	490.00	495.00	500.00

WPotResp.dgn

This diagnostic file indicates the response of water potential and plant growth to soil water stores.

SoilWater: water stores in soil (cm)

WaterPotential: water potential of the soil (Mpascals).

MoistProdIndex: moisture production index of the upper trees (dimensionless).

Example of WPotResp.dgn file:

WPotResp.dgn

SoilWater, WaterPotential, MoistProdIndex

5.000 6.000 7.000 8.000 9.000 10.000 11.000 13.000 14.000 15.000 16.000 17.000 18.000	2.168 1.811 1.557 1.366 1.217 1.099 1.002 0.921 0.852 0.793 0.743 0.698 0.659 0.624 0.592	0.120 0.158 0.199 0.243 0.289 0.334	
20.000	0.564	0.424	
96.000 97.000 98.000 99.000 100.000	0.000 0.000 0.000 0.000 0.000		

AbioResp.dgn

This file contains the response of decomposition and growth to the combined effects of temperature and moisture. These indices are calculated using the temperature, precipitation, soil, and radiation conditions of the site. This diagnostic is only available for the single cell version of the model.

Year: year being simulated. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.01. Then the effects of harvest or wildfire will be calculated and output for the time Year.02. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.03.

Month: month being simulated

Temp24: temperature for month (C)

Prec: precipitation for month (cm)

SolRad: total solar radiation for month (cal cm2 month):

DeadFoliageAbioticDecayIndex: value of the abiotic decay index that combines the effects of moisture and temperature on the dead foliage decomposition rate (dimensionless).

DeadFineRootAbioticDecayIndex: value of the abiotic decay index that combines the effects of moisture and temperature on the dead fine root decomposition rate (dimensionless).

DeadBranchAbioticDecayIndex: value of the abiotic decay index that combines the effects of moisture and temperature on the dead branch decomposition rate (dimensionless).

SnagSapwoodAbioticDecayIndex: value of the abiotic decay index that combines the effects of moisture and temperature on the snag sapwood decomposition rate (dimensionless).

LogSapwoodAbioticDecayIndex: value of the abiotic decay index that combines the effects of moisture and temperature on the log sapwood decomposition rate (dimensionless).

SnagHeartwoodAbioticDecayIndex: value of the abiotic decay index that combines the effects of moisture and temperature on the snag heartwood decomposition rate (dimensionless).

LogHeartwoodAbioticDecayIndex: value of the abiotic decay index that combines the effects of moisture and temperature on the log heartwood decomposition rate (dimensionless).

DeadCRootAbioticDecayIndex: value of the abiotic decay index that combines the effects of moisture and temperature on the dead coarse root decomposition rate (dimensionless).

StableSoilAbioticDecayIndex: value of the abiotic decay index that combines the effects of moisture and temperature on the stable soil decomposition rate (dimensionless).

StableWoodAbioticDecayIndex: value of the abiotic decay index that combines the effects of moisture and temperature on the stable wood decomposition rate (dimensionless).

StableFoliageAbioticDecayIndex: value of the abiotic decay index that combines the effects of moisture and temperature on the stable foliage decomposition rate (dimensionless).

ProdIndexHerb: value of the abiotic production index for herbs that combines the effects of moisture and temperature on the growth rate (dimensionless).

ProdIndexShrub: value of the abiotic production index for shrubs that combines the effects of moisture and temperature on the growth rate (dimensionless).

ProdIndexLTree: value of the abiotic production index for lower trees that combines the effects of moisture and temperature on the growth rate (dimensionless).

ProdIndexUTree: value of the abiotic production index for upper trees that combines the effects of moisture and temperature on the growth rate (dimensionless).

Example AbioResp.dgn file:

AbioResp.dgn

Year, Month, Temp24, Precip, SolRad, DeadFoliageAbioticDecayIndex, DeadFineRootAbioticDecayIndex, DeadBranchAbioticDecayIndex, SnagSapwoodAbioticDecayIndex, LogSapwoodAbioticDecayIndex, SnagHeartWoodAbioticDecayIndex, LogHeartWoodAbioticDecayIndex, DeadCRootAbioticDecayIndex, StableSoilAbioticDecayIndex, StableFoliageAbioticDecayIndex, ProdIndexHerb, ProdIndexShrub, ProdIndexLTree, ProdIndexUtree

0.000 0.096 0.352 0.466 0.732 0.921 0.626 0.745 0.978	0.000 0.096 0.352 0.732 0.785 0.494 0.248 0.705 0.775
000000000000000000000000000000000000000	0.000 0.096 0.352 0.466 0.732 0.494 0.248 0.401 0.796 0.775
0.000 0.096 0.352 0.466 0.732 0.761 0.626 0.745 0.978	000000000000000000000000000000000000000
0.000 0.096 0.352 0.466 0.732 0.921 0.626 0.745 0.978	000000000000000000000000000000000000000
0.000 0.000 0.001 0.485 1.383 1.775 0.424 1.159 0.152	0.000 0.000 0.000 0.161 1.365 1.777 1.642 0.033 0.009
000000000000000000000000000000000000000	0.000 0.000 0.000 0.000 1.762 1.655 0.000 0.000
0.293 0.346 0.373 0.479 0.646 1.075 1.771 1.670 1.272 0.503 0.366	0.293 0.346 0.373 0.479 0.646 1.356 1.777 1.666 1.274 0.867
0.105 0.124 0.134 0.232 0.657 1.759 1.669 1.266 0.181	0.105 0.124 0.134 0.172 0.232 1.271 1.666 1.274 0.849
0.417 0.000 0.000 0.000 0.000 1.023 1.308 0.000 0.000	0.000 0.000 0.000 0.000 0.763 1.763 0.000 0.000
0.507 0.601 0.619 0.827 0.000 0.000 0.300 0.802 0.637	0.000 0.000 0.000 0.002 0.0852 1.667 1.273 0.872
0.510 0.000 0.000 0.000 0.000 1.775 1.664 1.187 0.000	0.000 0.000 0.000 0.000 1.768 1.664 1.231 0.000
0.510 0.601 0.601 0.552 0.000 0.000 0.005 0.095 0.664	0.000 0.000 0.000 0.166 1.399 0.002 0.306 0.822 0.636
0.475 0.318 0.541 0.541 1.124 1.404 0.060 0.164 0.660	0.246 0.409 0.522 0.813 1.123 1.404 0.006 0.006 0.608 0.426
0.010 0.051 0.243 0.775 1.114 1.775 1.383 1.258 0.689 0.364	0.000 0.003 0.064 0.666 1.112 1.777 1.642 0.769 0.722
0.508 0.575 0.637 0.833 1.125 1.125 1.256 1.275 0.610	0.495 0.576 0.635 0.833 1.125 1.404 0.001 1.177 0.870 0.607
143.90 209.39 285.84 388.39 468.00 540.50 697.36 501.81 363.26 241.54 1159.63	143.90 209.39 285.84 388.39 468.00 5540.50 697.36 241.81 159.63
39.00 27.00 27.00 11.00 6.00 1.00 4.00 8.00 41.00	39.00 27.00 27.00 11.00 6.00 6.00 4.00 8.00 34.00 41.00
0.30 2.70 3.80 7.40 11.70 14.90 18.30 13.50 8.10 3.50	0.30 2.70 3.80 7.40 11.70 14.90 18.30 17.40 13.50 8.10
10 10 10 10 10 10 10 10 10 10 10 10 10 1	100 2 100 3 100 4 100 5 100 6 100 7 100 9 100 10 100 10

Light.dgn

This file contains the light entering and leaving each plant layer in a cell for each output interval. This diagnostic can be used with the single cell or multicell version of the model. In the case of the multicell version, the mean of all the cells is output.

Time: year being simulated. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.01. Then the effects of harvest or wildfire will be calculated and output for the time Year.02. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.03.

UTreeLightIn: the fraction of full sunlight that enters a cell (dimensionless). In case of the multicell, interactive version the light entering a cell can be reduced by neighboring cells.

LTreeLightIn: fraction of full sunlight that passes through the upper tree foliage and into the lower tree layer (dimensionlesss).

ShrubLightIn: fraction of full sunlight that passes through the lower tree foliage and into the shrub layer (dimensionlesss).

HerbLightIn: fraction of full sunlight that passes through the shrub foliage and into the herb layer (dimensionlesss).

HerbLightOut: fraction of full sunlight that passes through the herb foliage (dimensionlesss).

Example of Light.dgn file:

Light.dgn

Year, UTreeLightIn, LTreeLightIn, ShrubLightIn, HerbLightIn, HerbLightOut

1 2 3 4 5 6 7 8 9 10 11 2 13 14 15 16 17 18 19 20 21 22 23 24 25 25 26 27 27 27 27 27 27 27 27 27 27 27 27 27	1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 1.000 0.999 0.999 0.999 0.999 0.999 0.999 0.999 0.999 0.999	1.000 1.000 1.000 1.000 1.000 1.000 0.999 0.997 0.995 0.995 0.998 0.969 0.944 0.900 0.827 0.717 0.573 0.419 0.288 0.200 0.151 0.126 0.114	1.000 1.000 1.000 1.000 1.000 1.000 1.000 0.999 0.997 0.995 0.999 0.983 0.969 0.944 0.900 0.826 0.715 0.570 0.416 0.285 0.196 0.146 0.122 0.112	0.999 0.997 0.993 0.985 0.967 0.931 0.863 0.759 0.645 0.553 0.478 0.410 0.351 0.294 0.288 0.279 0.268 0.260 0.251 0.225 0.186 0.146 0.122 0.112	0.998 0.994 0.984 0.959 0.895 0.751 0.532 0.345 0.227 0.172 0.146 0.129 0.113 0.091 0.078 0.074 0.070 0.061 0.052 0.048 0.046 0.045 0.045 0.053 0.050
26 27 28 29 30	0.998 0.998 0.998 0.998 0.998	0.107 0.104 0.102 0.101 0.101	0.105 0.103 0.102 0.101 0.100	0.105 0.103 0.102 0.101 0.100	0.059 0.058 0.054 0.058 0.050
31 32 33 34 35	0.998 0.998 0.998 0.998 0.998	0.100 0.100 0.100 0.100 0.100	0.099 0.099 0.098 0.097 0.095	0.099 0.099 0.098 0.096 0.095	0.055 0.057 0.051 0.056 0.058
36 37 38 39 40 41	0.998 0.998 0.998 0.998 0.998	0.100 0.100 0.100 0.100 0.100	0.093 0.091 0.090 0.089 0.089	0.093 0.091 0.090 0.089 0.088 0.088	0.054 0.059 0.053 0.060 0.055 0.049
42 43 44 45 46 47 48 49	0.998 0.998 0.998 0.998 0.998 0.998	0.100 0.100 0.100 0.100 0.100 0.100 0.100	0.088 0.087 0.086 0.084 0.082 0.080 0.077	0.088 0.087 0.086 0.084 0.082 0.080 0.077	0.060 0.055 0.057 0.061 0.051 0.054 0.052
49 50	0.998	0.100	0.074	0.074	0.057

Resp.dgn

This file contains the losses from respiration and the mass of the respiring pools for each output interval. This diagnostic can be used with the single cell or multicell version of the model. In the latter case, the output variables represent a mean of all the cells.

Time: year being simulated. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.01. Then the effects of harvest or wildfire will be calculated and output for the time Year.02. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.03.

FoliageMass: mass of foliage (Mg ha⁻¹).

FoliageResp: mass of foliage allocation respired (Mg ha⁻¹ yr⁻¹).

FineRootMass: mass of fine roots (Mg ha⁻¹).

FineRootResp: mass of fine root allocation respired (Mg ha⁻¹ yr⁻¹).

BranchMass: mass of branches (Mg ha⁻¹).

BranchResp: mass of branch allocation respired (Mg ha⁻¹ yr⁻¹).

SapwoodMass: mass of sapwood (Mg ha⁻¹).

SapwoodResp: mass of sapwood allocation respired (Mg ha⁻¹ yr⁻¹).

CoarseRootMass: mass of coarse roots (Mg ha⁻¹).

CoarseRootResp: mass of coarse root allocation respired (Mg ha⁻¹ yr⁻¹).

Example of Resp.dgn file:

Resp.dgn

Year, FoliageMass, FoliageResp, FineRootMass, FineRootResp, BranchMass, BranchResp, SapwoodMass, SapwoodResp, CoarseRootMass, CoarseRootResp

1.0	0.007	0.002	0.005	0.000	0.003	0.000	0.002	0.000	0.003	0.000
2.0	0.026	0.006	0.023	0.002	0.011	0.000	0.008	0.000	0.011	0.000
3.0	0.077	0.016	0.075	0.010	0.031	0.001	0.021	0.000	0.031	
4.0										0.001
	0.216	0.044	0.226	0.034	0.076	0.001	0.052	0.000	0.076	0.001
5.0	0.609	0.117	0.653	0.102	0.175	0.003	0.120	0.000	0.175	0.003
6.0	1.588	0.318	1.760	0.295	0.387	0.008	0.268	0.000	0.388	0.008
7.0	3.122	0.809	3.831	0.797	0.807	0.018	0.561	0.000	0.809	0.018
8.0	4.415	1.594	6.302	1.733	1.492	0.037	1.051	0.000	1.500	0.037
9.0	4.838	2.298	8.122	2.851	2.368	0.068	1.700	0.000	2.391	0.068
10.0	5.082	2.589	9.306	3.675	3.358	0.107	2.470			
								0.000	3.410	0.108
11.0	5.258	2.773	9.758	4.211	4.443	0.152	3.354	0.000	4.538	0.154
12.0	5.064	2.921	9.170	4.415	5.596	0.201	4.345	0.001	5.756	0.204
13.0	5.047	2.894	8.229	4.149	6.773	0.253	5.430	0.002	7.029	0.259
14.0	5.056	2.930	7.481	3.723	7.901	0.306	6.587	0.003	8.305	0.314
15.0	5.214	2.947	7.164	3.385	8.919	0.356	7.816	0.006	9.555	0.369
16.0	5.401	3.003	7.049	3.241	9.805	0.401	9.178	0.012	10.816	0.420
17.0	5.801	3.055	7.100	3.189	10.512	0.440	10.769	0.022	12.145	0.466
18.0	6.448	3.172	7.240	3.212						
					10.927	0.469	12.688	0.040	13.570	0.507
19.0	7.288	3.341	7.259	3.276	9.170	0.482	13.227	0.070	13.224	0.538
20.0	8.063	3.549	7.188	3.225	5.860	0.394	12.644	0.116	11.751	0.471
21.0	8.658	3.749	7.514	3.167	2.913	0.233	12.802	0.180	11.138	0.333
22.0	9.046	3.936	8.122	3.313	2.079	0.086	15.124	0.258	13.090	0.215
23.0	8.869	4.093	8.362	3.646	2.637	0.032	18.938	0.344	16.699	0.201
24.0	9.098	4.013	8.557	3.784	3.192	0.041	22.583	0.431	20.337	0.257
25.0	8.838	4.117	8.375	3.871	3.740	0.049	26.043	0.514	23.978	0.313
26.0	8.879	3.999								
			8.343	3.789	4.255	0.058	29.134	0.593	27.456	0.369
27.0	9.041	4.018	8.520	3.758	4.763	0.065	32.059	0.663	30.927	0.422
28.0	8.884	4.092	8.561	3.855	5.252	0.073	34.741	0.730	34.311	0.476
29.0	9.186	4.019	8.875	3.874	5.723	0.081	37.194	0.791	37.602	0.528
30.0	9.021	4.157	9.003	4.015	6.177	0.088	39.436	0.847	40.802	0.578
31.0	8.941	4.083	8.412	4.073	6.592	0.095	41.362	0.898	43.737	0.628
32.0	9.176	4.046	8.630	3.805	7.022	0.101	43.263	0.942	46.773	0.673
33.0	9.208	4.152	8.440	3.905	7.448	0.108	45.025	0.986	49.737	
34.0	8.973	4.167								0.720
			8.006	3.819	7.876	0.115	46.678	1.026	52.642	0.765
35.0	9.138	4.060	8.086	3.622	8.311	0.121	48.244	1.064	55.496	0.810
36.0	9.123	4.135	8.171	3.659	8.753	0.128	49.735	1.101	58.303	0.854
37.0	9.250	4.128	7.650	3.697	9.197	0.135	51.150	1.136	61.056	0.897
38.0	9.031	4.186	7.837	3.461	9.635	0.141	52.479	1.169	63.746	0.939
39.0	9.156	4.088	8.246	3.546	10.061	0.148	53.714	1.201	66.364	0.981
40.0	9.424	4.144	8.593	3.731	10.472	0.155	54.855	1.230	68.907	1.021
41.0	9.006	4.264	8.896	3.888	10.868	0.161	55.911	1.257	71.378	1.060
42.0	9.403	4.076	9.410	4.025	11.254	0.167	56.896	1.283	73.782	1.098
43.0	9.189	4.255	8.899	4.258	11.634					
						0.173	57.828	1.306	76.130	1.135
44.0	9.035	4.159	8.727	4.026	12.015	0.179	58.725	1.329	78.431	1.171
45.0	9.404	4.088	9.295	3.949	12.405	0.185	59.613	1.351	80.701	1.207
46.0	9.338	4.256	9.409	4.206	12.814	0.191	60.513	1.372	82.955	1.241
47.0	9.481	4.226	9.321	4.257	13.245	0.197	61.441	1.395	85.200	1.276
48.0	9.420	4.290	9.283	4.217	13.700	0.204	62.403	1.418	87.443	1.311
49.0	9.438	4.263	8.986	4.200	14.180	0.211	63.403	1.442	89.686	1.345
50.0	9.789	4.271	8.517	4.066	14.687	0.218	64.445			
50.0	5.109	1.211	0.51/	4.000	14.00/	0.218	04.445	1.468	91.932	1.380

Mort.dgn

This file contains the mass of mortality from all sources (pruning, mortality, thinning, dieout, fire) for each output interval. This diagnostic can be used with the single cell or multicell version of the model. In the latter case, the output variables represent a mean of all the cells.

Time: year being simulated. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.01. Then the effects of harvest or wildfire will be calculated and output for the time Year.02. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.03.

DeadFoliageInput: mass of foliage added to the dead foliage pool (Mg ha⁻¹ yr⁻¹)

DeadFRootInput: mass of fine roots dying and being added to the dead fine root pool (Mg ha⁻¹ yr⁻¹)

DeadBranchInput: mass of branches dying and being added to the dead branch pool (Mg ha⁻¹ yr⁻¹)

SalvSnagSapInput: mass of sapwood dying and being added to the salvagable-snag sapwood pool (Mg ha⁻¹ yr⁻¹)

NonSalvSnagSapInput: mass of sapwood being added to the non-salvagable-snag sapwood pool (Mg ha⁻¹ yr⁻¹)

SalvLogSapInput: mass of sapwood being added to the salvagable-log sapwood pool (Mg ha⁻¹ yr⁻¹)

NonSalvLogSapInput: mass of sapwood being added to the non-salvagable-log sapwood pool (Mg ha⁻¹ yr⁻¹)

SalvSnagHeartInput: mass of heartwood dying and being added to the salvagable-snag heartwood pool (Mg ha⁻¹ yr⁻¹)

NonSalvSnagHeartInput: mass of heartwood being added to the non-salvagable-snag heartwood pool (Mg ha^{-1} yr^{-1})

SalvLogHeartInput: mass of heartwood being added to the salvagable-log heartwood pool (Mg ha⁻¹ yr⁻¹)

NonSalvLogHeartInput: mass of heartwood being added to the non-salvagable-log heartwood pool (Mg ha^{-1} yr^{-1})

DeadCRootInput: mass of coarse roots dying and being added to the dead coarse roots pool (Mg ha^{-1} yr^{-1})

Example of Mort.dgn file:

Mort.dgn

0.000 0.040 0.042 0.048 0.051 0.054 0.057 0.000 0.063 0.066 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.001 0.384 0.411 0.439 0.466 0.466 0.522 0.550 0.578 0.606 0.000 0.057 0.058 0.059 0.060 0.061 0.062 0.063 0.063 0.000 Time, DeadFoliageInput, DeadFRootInput, DeadBranchInput, 0.549 0.560 0.570 0.579 0.589 0.608 0.618 0.629 0.641 0.000 0.000 0.009 0.016 0.023 0.032 0.053 0.075 0.088 1.934 0.042 0.064 0.106 0.000 0.000 SalvSnagHeartInput, NonSalvSnagHeartInput, SalvLogHeartInput, NonSalvLogHeartInput, SalvSnagSapInput, NonSalvSnagSapInput, SalvLogSapInput, NonSalvLogSapInput, 0.000 0.000 0.000 0.000 0.001 0.005 0.015 0.065 0.096 0.129 0.165 0.202 0.238 0.238 0.313 0.326 0.338 0.350 0.361 0.340 2.268 3.731 0.372 0.384 0.397 0.410 0.424 0.440 0.000 0.000 0.000 0.001 0.007 0.173 0.173 0.675 1.589 2.366 3.188 4.337 4.107 3.738 3.570 3.523 3.335 3.058 3.136 3.984 3.505 3.007 3.365 3.465 3.465 3.642 4.143 4.287 0.002 0.008 0.024 0.068 0.196 0.563 1.489 2.925 4.085 4.366 4.263 4.1874.233 4.405 2.722 2.978 2.954 2.927 2.685 2.794 2.794 2.689 2.525 2.433 4.645 DeadCRootInput 1.0 2.0 3.0 3.0 4.0 6.0 6.0 10.0 111.0 113.0 114.0 116.0 116.0 20.0 40.0 41.0 42.0 43.0 444.0 445.0 445.0 447.0 447.0 50.0

0.112 0.138 0.164

0.187 0.212 0.243 2.300 3.935

0.000 0.000 0.000 0.000 0.001 0.003 0.010 0.025 0.044 0.065 1.064 1.105 1.145 1.183 1.220 1.257 1.293 1.330

1.403 1.439

SubQual.dgn

This file contains the decomposition rate of each pool that is based only on substrate quality (*Pool*DecayRateAvg) for each annual time step. The effects of temperature and moisture are output by the AbioResp.dgn file. The SubQual diagnostic can be used with the single cell or multicell version of the model. In the latter case, the output variables represent a mean of all the cells.

Time: year being simulated. If a harvest activity or fire occurs in a given year several lines of output will be generated for that year. After the "normal" growth and decomposition processes have occurred, state variable will be output for the time Year.01. Then the effects of harvest or wildfire will be calculated and output for the time Year.02. If an addition disturbance occurs (e.g., site preparation fire after harvest), then the effects of the disturbance will be calculated and output for time Year.03.

DeadFoliageDcayRateAvg: the combined substrate quality effects of all the dead foliage pools (year⁻¹).

DeadFRootDcayRateAvg: the combined substrate quality effects of all the dead fine root pools (year⁻¹).

DeadBranchDcayRateAvg: the combined substrate quality effects of all the dead branch pools (year⁻¹).

SalvSnagSapDcayRateAvg: the combined substrate quality effects of all the salvagable snag sapwood pools (year⁻¹).

NonSalvSnagSapDcayRateAvg: the combined substrate quality effects of all the non-salvagable snag sapwood pools (year⁻¹).

SalvLogSapDcayRateAvg: the combined substrate quality effects of all the salvagable log sapwood pools (year⁻¹).

NonSalvLogSapDcayRateAvg: the combined substrate quality effects of all the non-salvagable log sapwood pools (year⁻¹).

SalvSnagHeartDcayRateAvg: the combined substrate quality effects of all the salvagable snag heartwood pools (year⁻¹).

NonSalvSnagHeartDcayRateAvg: the combined substrate quality effects of all the non-salvagable snag heartwood pools (year⁻¹).

SalvLogHeartDcayRateAvg: the combined substrate quality effects of all the salvagable log heartwood pools (year⁻¹).

NonSalvLogHeartDcayRateAvg: the combined substrate quality effects of all the non-salvagable log heartwood pools (year⁻¹).

DeadCRootDcayRateAvg: the combined substrate quality effects of all the dead coarse root pools (year⁻¹).

Example of SubQual.dgn file:

SubQual.dgn

Year, DeadFoliageDcayRateAvg, DeadFRootDcayRateAvg, DeadBranchDecayRateAvg, SalvSnagSapDcayRateAvg, NonSalvSnagSapDcayRateAvg, SalvLogSapDcayRateAvg, NonSalvLogSapDcayRateAvg, SalvSnagHeartDcayRateAvg, NonSalvSnagHeartDcayRateAvg, SalvLogHeartDcayRateAvg, NonSalvLogHeartDcayRateAvg, DeadCRootDcayRateAvg,

0.000 0.022 0.044 0.056 0.067 0.100 0.100 0.100 0.100 0.100 0.100 0.100 0.100 0.100	0.137 0.138 0.139 0.139 0.140
0.000 0.000 0.000 0.000 0.000 0.000 0.003 0.015 0.015 0.015 0.015	0.015 0.015 0.015 0.015 0.015
	000000000000000000000000000000000000000
0.000 0.000 0.000 0.000 0.000 0.003 0.015 0.015 0.015 0.015	0.015 0.015 0.015 0.015 0.015
	000000000000000000000000000000000000000
0.000 0.000 0.000 0.017 0.022 0.022 0.039 0.050 0.050 0.050 0.050 0.050	0.050 0.050 0.050 0.050 0.050
	000000000000000000000000000000000000000
0.000 0.011 0.022 0.028 0.033 0.039 0.044 0.050 0.050 0.050 0.050 0.050 0.050	0.050 0.050 0.050 0.050
000000000000000000000000000000000000000	0000000
0.000 0.022 0.044 0.056 0.067 0.100 0.100 0.100 0.100 0.100 0.100 0.100 0.100 0.100	0.147 0.148 0.148 0.149 0.149
0.000 0.022 0.044 0.056 0.067 0.100 0.100 0.100 0.100 0.100 0.100 0.100 0.100	0.137 0.138 0.139 0.139 0.140
0.268 0.366 0.368 0.368 0.377 0.424 0.424 0.427 0.427 0.433 0.433 0.433 0.433 0.433 0.433	0.269 0.266 0.264 0.258 0.258
1.0 2.0 3.0 4.0 6.0 6.0 7.0 8.0 10.0 11.0 11.0 11.0 115.0 115.0 116.0	45.0 46.0 47.0 48.0 50.0

Species.dgn

This file outputs the species of the upper-tree layer and the lower-tree layer for each cell in the stand for each output interval. It also outputs the height and age of the upper tree layer. Each row of the stand, the value of each output variable is printed on a separate line. This file is used to check if the regeneration of species is consistent with the shading expected from adjacent cells.

Year: current year in the simulation run.

UTree Species: the species in the cell's upper tree layer. If no species is present in this layer, then NULL is printed.

LTree Species: the species in the cell's lower tree layer. If no species is present in this layer, then NULL is printed.

UTree Height: the height of the cell's upper-tree layer (m).

UTree Age: the age of the cell's upper tree layer (years since planted).

Example of Species.dgn file:

Species.dgn

UTree Species, LTree Species, UTree Height, UTree Age

	270									
Year:	100									
Psme	Psme	Abpr	Psme	Psme	Acma	Psme	Tshe	Psme	Tshe	
Tshe	Tshe	Tshe	Tshe	Tshe	Psme	Tshe	NULL	Tshe	Tshe	
48			49		16	49			28	
88	90	89	90			90	34	10.000	57	
00	30	0,5	50	50		50	01	0,5	0,	
Psme	Abpr	Psme	Psme	Psme	Tshe	Tshe	Psme	Psme	Abpr	
Tshe	Tshe	Tshe	Tshe	Tshe	Tshe	NULL	Tshe	Tshe	Tshe	
50			49			37			33	
91	91	90	89	90				77	90	
Psme	Abpr	Psme	Abpr	Psme	Psme	Psme	Abpr	Psme	Psme	
		Tshe								
50			12.75	67500000			100000000000000000000000000000000000000		49	
91	90	90	90	91	89	89	90	90	90	
Ahnr	Peme	Psme	Ahnr	Peme	Peme	Deme	Peme	Peme	Ahnr	
Tehe	Teho	Tshe	Tehe	Teho	Tehe	Teho	Tehe	Tehe	Tehe	
33	48	49				50			33	
90		2 2 2 2 2 2 2 2					90	91	90	
90	88	90	90	8 /	90	91	90	91	90	
Psme	Psme	Psme	Psme	Psme	Psme	Psme	Psme	Psme	Tshe	
		Tshe								
48			47			48		50	17	
87	91	88	86					91	39	
		Psme								
Tshe	Tshe	Tshe	Tshe					NULL		
50	49	50	49				1010	4	50	
91	90	91	90	92	37	89	89	16	91	
Domo	Maha	Psme	Ahnr	Aham	Domo	Domo	Ahnr	Ahnr	Dotr	
Take	MULT	Tshe	Mobi	MITT	Tahe	Taha	Mobil	Taba	Domo	
48		-								
87	57	88	88	34	91	91	89	91	89	
Psme	Psme	Psme	Psme	Psme	Cach	Tshe	Psme	Psme	Psme	
		Tshe								
48									49	
88			88						75705780	
Cach	Psme	Psme	Psme	Psme	Abpr	Psme	Psme	Psme	Psme	
		Tshe								
16										
88	89	90	87	90	92	89	89	90	87	
Peme	Peme	Psme	Peme	Peme	Psme	Ahnr	Peme	Peme	Pame	
		NULL								
49										
89				100			277.07	0.707.0	91	
09	90	91	9 I	00	90	91	40	90	91	

Neighbor.dgn

This file contains the fraction of full diffuse, direct, and total radiation out for all the cells in a selected year. The radiation data are printed in separate matrices; each matrix contains a specific-type of radiation data for every cell in the stand. The value following the heading for the type of radiation report is the amount received when there is no shading.

The file also contains the tree height (m) of the upper-tree layer for every cell in the selected year.

Example of Neighbor.dgn file:

188 74 172 169 172 98 153 67 89 1 93 130 52 97 160 66 160 97 165 1 122 168 157 100 85 53 63 159 167 1 179 161 157 157 159 160 160 101 53 1 180 158 158 87 158 128 159 127 149 1 179 71 157 93 91 160 101 72 116 182 161 159 161 167 80 105 118 106 158 174 170 115 112 82 117 170 171 1 82 59 69 83 105 182 112 171 86 1	Slope: 0.00 Aspect: 180.00 Bo th Angle: 97.03 Solar Altitude	
188 74 172 169 172 98 153 67 89 1 93 130 52 97 160 66 160 97 165 1 122 168 157 100 85 53 63 159 167 1 179 161 157 157 159 160 160 101 53 1 180 158 158 87 158 128 159 127 149 1 179 71 157 93 91 160 101 72 116 182 161 159 161 167 80 105 118 106 158 174 170 115 112 82 117 170 171 1 82 59 69 83 105 182 112 171 86 1	iation: 157.55	
Direct Rediction: 106 44	172 169 172 98 153 6 52 97 160 66 160 9 157 100 85 53 63 15 157 157 159 160 160 10 158 87 158 128 159 12 157 93 91 160 101 7 159 161 167 80 105 11 170 115 112 82 117 17	7 89 118 7 165 183 9 167 136 1 53 158 7 149 180 2 116 73 8 106 95 0 171 187
Direct Radiation: 186.44	ation: 186.44	
186 101 186 186 186 173 186 73 123 1 123 180 0 173 186 173 186 173 186 1 180 186 186 187 73 0 0 186 186 1 186 186 186 186 186 186 173 0 1 186 186 186 186 186 186 173 0 1 186 186 186 186 186 173 186 173 173 1 186 186 186 186 173 123 180 173 180 186 186 173 173 101 173 186 186 1	186 186 186 173 186 7 0 173 186 173 186 17 186 173 73 0 0 18 186 186 186 186 18 186 173 186 173 186 17 186 173 173 186 173 17 186 186 186 173 123 18 186 173 173 101 173 18	3 123 173 3 186 186 6 186 180 3 0 180 3 173 186 3 173 123 0 173 50 6 186 186

Example of Neighbor.dgn file (continued):

Total	Radiat	ion:	343.9	9					
110	308	329	316	299	336	368	329	367	358
374	174	358	356	358	271	340	140	212	291
216	310	52	270	346	240	347	271	352	370
302	355	344	274	158	53	63	346	353	316
365	348	344	344	345	346	3,47	274	53	338
366	344	344	261	344	302	346	301	322	366
365	144	344	266	264	346	274	246	289	196
369	348	346	347	354	253	228	297	280	145
338	361	356	289	286	183	290	356	358	374
255	59	69	256	279	369	285	358	260	285
Tree H	eight								
14.8	60.3	68.7	66.5	61.9	73.5	85.1	74.6	82.3	77.6
85.2	26.2	85.1	85.1	85.1		79.0	34.2		60.6
45.7	66.8	10.0	56.8	85.2		85.1	56.8		85.1
63.1	85.0	85.1	56.8	45.7	13.0	21.1	85.1		67.5
84.9	85.2	85.0	84.9	85.1	85.2	84.9	56.3		75.3
85.2	85.1	85.2	53.9	85.3	75.0	85.1	64.0	75.7	85.2
84.9	50.4	85.0	58.9	52.6	85.2	43.6	26.8	55.1	30.5
85.0	85.1	84.9	85.0	85.2	28.7	48.1	57.8	51.7	44.1
73.7	85.1	85.1	59.2	55.1	31.8	57.8	8.3	85.1	84.9
35.9	13.6	21.8	31.8	45.7	85.1	56.8	79.9	45.2	54.3

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