Northern California Forest Yield Cooperative
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Research Note No. 34 September 16, 1991

The Forest Stand Generator (STAG) User's Guide

Version 4.0

by

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Abstract

The forest Stand Generator, STAG[2], estimates missing tree heights, height-to-crown base measurements, or both to produce complete stand descriptions comprised of complete individual tree records (height, diameter, live-crown-ratio, species, and tree expansion factor) for use in the conifer growth and yield simulator, CACTOS[3]. Complete stand descriptions are also produced from stand tables or from the summary statistics of elevation, basal area and number of trees per acre by species. By producing a complete stand description, STAG ensures that most forms of inventory data can be analyzed by CACTOS to estimate future growth and yield under a wide array of silvicultural regimes and management instruments.

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[2] **STAG** is an acronym for Forest STAnd Generator for Mixed Conifer Species © U.C. Regents 1984-1991.

[3] **CACTOS** is an acronym for CAlifornia Conifer Timber Output Simulator © U.C. Regents 1984-1991.

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Research conducted under AES project 3679-MS.

ACKNOWLEDGMENTS

The **STAG** program represents the collective efforts of many people over eight years. This work would not have been accomplished in a timely manner without the financial and technical support of the industry cooperators listed on page ii or without our new agency cooperators. The specification for the design of this study was guided, in a large part, by the industrial cooperators to take into account the type and quality of information that would be available to run **STAG**.

We would like to thank **Dr. Paul C. Van Deusen**, who is now at the Southern Forest Experiment Station in New Orleans, for sharing the responsibilities of formulating the procedures used to "fill in" missing data and for generating information based upon readily supplied summary statistics. Much of the theoretical work that is used as a basis for **STAG's** models and routines was developed as part of Paul's Ph.D. dissertation at Berkeley. Paul was also responsible for doing much of the original programming of the first version of **STAG**. Paul's excellent work and contributions to this project should be evident to anyone familiar with this work. We also would like to thank our friend and colleague **Dr. Lee C. Wensel** who provided valuable input on how this simulator could best be structured to maximize its utility and function.

Many good people have worked on this project who have had a direct bearing on the quality of the project. **Peter J. Daugherty** improved the computer coding and helped develop the user's guide and sample runstreams of version 2.0 of STAG. **Vaughn Landrum** assisted Peter in improving the computer program and helped develop the routine that allows merchantable height to be inputted to STAG. To these people our sincere thanks for a job well done.

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I. INTRODUCTION

The forests of northern California are characterized by stands of mixed species as well as mixed ages and sizes. Inventories of these stands usually contain diameter at breast height (DBH) for each tree with only occasional measurements of heights and crowns. In other instances, only stand summary statistics or stand table data are recorded, and hence, no individual tree information is available. However, the California Conifer Timber Output Simulation System, CACTOS, (Wensel and others (1986), Wensel and others (1987), Wensel and Biging (1987)), requires that species, diameter at breast height (DBH), tree height (H), height-to-crown base (HCB) or live crown ratio (LCR), and per acre expansion factor be supplied for each tree making up the stand description. To obtain the most accurate representation to project with CACTOS, these variables should be measured for all trees.

It is evident that forest managers need a means by which these data can be supplemented to form a complete stand description comprised of complete individual tree records, as described above, so that individual tree growth and yield projections can be performed on the stands of interest for all different levels of data availability. This paper will discuss the operation of the forest stand generator, STAG, designed to meet this need. The estimation procedures used in STAG to: (1) fill in missing measurements of tree height, height to the crown base, or both; (2) generate stands from summary statistics and, (3) convert stand table data, numbers of trees by DBH classes and species, to individual tree records are described in Biging and others (1991), and Van Deusen (1984).

STAG is written in standard FORTRAN 77 code (ANSI, 1974) and is operational on IBM-PC compatibles under MS-DOS v3.3 and higher. The general structure of STAG is illustrated in figure 1. The components are treated in detail in sections which follow.

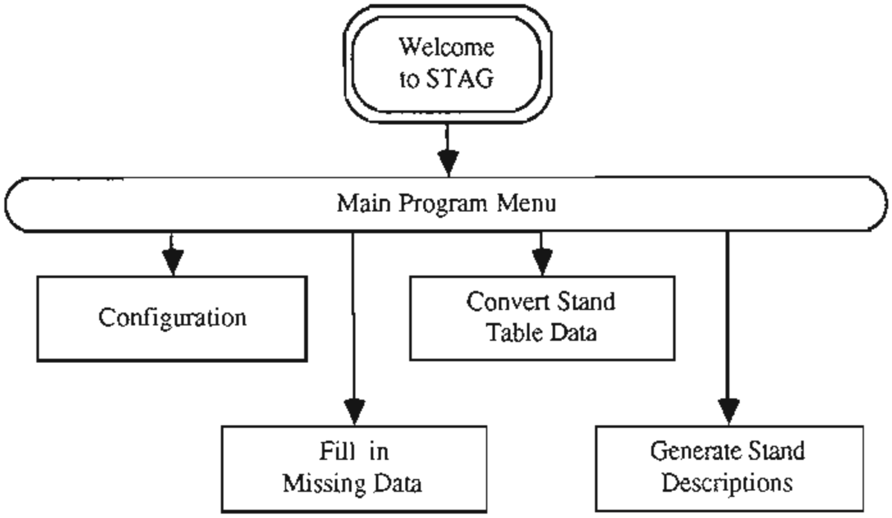

Figure 1. Structure of the components of STAG.

Menu Operation

STAG is a user-friendly, interactive program that makes use of menus, or command lists. Two-letter commands are entered from the keyboard at the various program prompts. Arguments to these commands can be entered to adjust the function of the routines invoked from their initial, default conditions. The command list can be displayed by typing `pc`, for print commands, at any of the program prompts. Only the commands available to the user within each routine are displayed. All of the commands are described in detail in section IV, Program Commands.

Stand Description

The stand description that STAG reads and/or creates has two types of records - header and tree records. The header records contain the stand label, number of tree records, elevation, and site and age of each species present. The complete individual tree record required by CACTOS includes the following five items:

(1) a two digit species code
(2) diameter at breast height in inches (DBH)
(3) total height in feet
(4) live crown ratio
(5) number of trees per acre represented by the tree record

This information comprises the tree list representing a stand that is created on output from STAG and which CACTOS uses for simulation. Since these data are frequently drawn from a sample, it is important that they be carefully examined to see that they really do represent the stand of interest.

The tree records in a stand description file may be incomplete, and STAG can fill in missing heights and crown ratios for these records. Alternatively a description may be of a stand table, where the entries are species, diameter class (diameter class intervals must be 2 inches or less), and number of trees per acre in that diameter class for a given species. Stand description files can be entered outside of STAG or CACTOS using either a standard text editor or Entry, the CACTOS System stand description entry program (Meerschaert and Wensel, 1987).

II. INPUT AND OUTPUT FILES

STAG accepts one type of user input file and produces four types of output files.

The input file recognized by STAG is:

(1) a CACTOS stand description file (Wensel, Daugherty and Meerschaert, 1986) that may be complete, or incomplete in one or more items discussed in detail under Section II.A.

The primary output file created by STAG is:

(1) a completed stand description file for use with the CACTOS individual tree growth simulation system.

Other output files which may be created by STAG include:

(2) externally saved stand description files, created by the **es** command, and used to save copies for later use of the stand description at the time the **es** command was invoked (optional).

(3) report files are created with the **rp** command and are used to save information selected by the user during the course of the simulation (optional). The report commands are discussed in section II.B. and IV.D.

(4) a file containing height coefficients which are updated using local data (optional)

All input and output files are referenced by file names chosen by the user. STAG allows up to 32 characters for a file name. The computer system you use may mandate different limits on file name lengths. Individual systems may support the use of path names as part of the file name.

The authors recommend adoption of a naming convention that gives each file name a root and an ending. The root indicates the stand being processed and the ending indicates the type of file. Root names are at the discretion of the user, but they should have a meaningful pattern developed to fit the application. In the examples that follow, the suffixes serve the function of indicating the process that was used in STAG to complete the stand description file.

.sd stand description file

.sda stand description created in STAG using the distributional apportionment process for converting stand table data to complete individual tree records

.sdm stand description which utilized the missing data routines of STAG to estimate missing values to complete individual tree records

.sdg stand description created in STAG using the stand generation routines to generate complete individual tree records

.sdu stand description created in STAG using the understory generation routines

.sdq stand description created in STAG using a dimunition quotient to create a negative exponential diameter distribution

.srp STAG report file

STAG has special filenames that are reserved and should be avoided by the user. These include: "exp1", "exp2", and "stbin". These reserved filenames are used for storing values used in stand generation and for storing user configuration parameters. Overwriting these files will prevent STAG from working properly.

Standard FORTRAN notation is provided here to describe the format of each line of input and output. Real numbers are expressed in the form rFw.d where w is the field width (total number of characters including blanks and decimal); d is the number of characters to the right of the decimal; and r is the number of times this format is repeated by this specification. An actual decimal point in the field overrides the number specified by d in Fw.d. Thus, the format 5F8.3 specifies 5 real numbers 8 characters wide with 3 places to the right of the decimal. Integer formats are of the form rIw, where w is the field width and r is the repeater. Character formats are of the form rAw, where w is the number of characters in the field and r is the repeater.

II.A. Stand description input file

STAG operates on stand description input files to accomplish any or all of the three objectives discussed in section III. A complete stand description input file must have the structure listed below, but an incomplete stand description may have missing values for total height and/or live crown ratio.

When working with stand table data the structure of the stand description is similar to that of a description file comprised of individual trees. However, in this case, the diameter entry represents the diameter class midpoint usually expressed in an integer value such as 12 or 14. Values for total height and live crown ratio are not required to form a description based upon these stand table data. See Table 1 for a summary of the data requirements for the stand description files when there is missing data and for converting stand table data. See Appendix A for an example of a stand description file.

Line(1) Stand description label, tree record count, elevation, and a number which indicates the file type (format A20, I10,I9,19X, I3). These file type indicators are shown here:

code	meaning
0 or 1	raw data file with all heights measured in feet to the tip of the tree
2	heights are in feet to the merchantable top
3	heights are in 16.5 foot logs above a 1.5 foot stump
4	heights are in 1/2 logs above a 1.5 foot stump

Line(2) Fifty year site indices for (in this order) ponderosa pine, sugar pine, incense cedar, Douglas-fir, white fir, red fir, lodgepole pine, white pine, Jeffrey pine, miscellaneous conifer, chinquapin, black oak, tan oak, and miscellaneous hardwoods (format 14F5.0). STAG does not use site index in any of its functions, but CACTOS uses site index extensively, therefore it must be entered for every species present. Zeros or blanks may be entered for species not present on the plot.

Line (3) Breast height ages for (in this order) ponderosa pine, sugar pine, incense cedar, Douglas-fir, white fir, red fir, lodgepole pine, white pine, Jeffrey pine, miscellaneous conifer, chinquapin, black oak, tan oak, and miscellaneous hardwood (format 14F5.0). Zeroes or blanks may be entered if actual values are unknown. (Age is a descriptive variable used in CACTOS only and is not needed for any of the models to function in either CACTOS or STAG.)

Line (4-end) Individual tree records follow, one per line. Each tree record should have the five items listed in Table 1 (format 5F8.3, i.e., one line for each tree record).

Table 1. Structure of stand description files for individual trees and for stand tables.

Stand description using individual trees	Stand description using stand table data
(1) species code (see Table 2)	(1) species code (see Table 2)
(2) DBH in inches	(2) diameter class midpoint
(3) total height in feet (optional)	(3) average total height in feet of trees in the diameter class (optional)
(4) live crown ratio[3] in decimal fraction (optional)	(4) live crown ratio in decimal fraction (optional)
(5) per-acre expansion factor	(5) per-acre expansion factor

[3] Live crown ratio is defined as (H-HCB)/H where H = total height and HCB = height-to-crown base, i.e. the proportion of height in which live branches can be found.

Fourteen species are recognized by STAG on input. These species are listed in Table 2.

Table 2. Species codes and names using in STAG.

Species Code	Common Name	Species Abbreviation	Scientific Name
01	ponderosa pine	PP	*Pinus ponderosa* (Laws.)
02	sugar pine	SP	*Pinus lambertiana* (Dougl.)
03	incense cedar	IC	*Libocedrus decurrens* (Torr.)
04	Douglas-fir	DF	*Pseudotsuga menziesii* (Mirb.) Franco
05	white fir	WF	*Abies concolor* (Gord. and Glend.) Lindl.
06	red fir	RF	*Abies magnifica* (A. Murr.)
07	lodgepole pine	LP	*Pinus contorta* (Dougl.)
08	white pine	WP	*Pinus monticola* (Dougl.)
09	Jeffrey pine	JP	*Pinus jeffreyi* (Grev. & Balf.)
10	miscellaneous conifers	MC	n.a.
11	chinquapin	CH	*Castanopsis chrysophylla* (Dougl.) A. DC.
12	black oak	BO	*Quercus kelloggii* (Newb.)
13	tan oak	TO	*Lithocarpus densiflorus* (Hook. & Arn.)
14	miscellaneous hardwoods	MH	n.a.

These species are grouped into 8 different species groups during the simulation process. These groups are listed in Table 3.

Table 3. Species groups used for modelling in STAG.

Sp. Group No.	Species Group Name	Species Group Abbreviation	Species Abbreviations and Codes Included in Group (See Table 2)
1	Ponderosa Pine	PP	PP(01), JP(09), LP(07)
2	Sugar Pine	SP	SP(02), WP(08)
3	Incense Cedar	IC	IC(03)
4	Douglas-fir	DF	DF(04), MC(10)
5	White Fir	WF	WF(05)
6	Red Fir	RF	RF(06)
7	Other Hardwoods	OH*	CH(11), TO(13), MH(14)
8	Black Oak	BO	BO(12)

*/ Other hardwoods includes all hardwoods except black oak. Howerver, the equations were derived mainly from chinquapin and tanbark oak.

II.B. Report File

In addition to the completed stand description files, one or more report file(s) may be generated by the user while inside any of the main STAG functions except the configuration routine. The report file provides the user with a means of saving information which describes, or summarizes the characteristics of the trees contained in the stand description file. Many of the important report commands contained in CACTOS have been incorporated into STAG. These include the following commands (described in detail in Section IV.D):

Command	Description
`pf`	graphs the stand profile of the trees in the stand description
`dt`	graphs the diameter distribution of the trees in the stand description
`st`	produces stock tables for the trees in the stand description

The report file is opened with the **rp** command. Any number of report files can be used during the course of a simulation, but only one may be open at a time. Reports can be saved in the report file by adding the argument **o=r** or **o=b** to the command used to generate the report (see section IV).

II.C. Updated Height Coefficient File

While in the missing data routine (**md**), you are able to update the coefficients of the height models (Biging and others, 1991) using either a pseudo-Bayesian or an adhoc technique for use on either the current stand descriptions or on others at a later time (see section III.A). To use the updated coefficients at a later time, you must place them in a special file recognized by STAG for this purpose. This can be accomplished by use of the update height coefficient command (**uh**) discussed in section IV.D. This file is a binary sequentially accessed file and is written and read by STAG very quickly.

III. USES OF STAG

The stand generator, STAG, is a sophisticated processor developed to ensure that data sets destined for use in the CACTOS projection system are complete. Since there are different levels of data availability, the stand generator was designed to: (1) fill in missing measurements of tree height and/or height to the crown base found in inventory field data; (2) convert stand table data, numbers of trees by DBH classes and species, to individual tree records, and (3) generate stands from summary statistics. Each of these capabilities is discussed in brief detail below.

III.A. Filling in Missing or Incomplete Data

Inventory field data collected by forest land managers for use with CACTOS often have missing values. The values may be missing at random, or missing because the sample design called for sub-sampling total height and/or live crown ratio. In either case, STAG is able to fill in missing height or live crown ratio variables. If desired, the user has the option of adding random errors to the estimates to reflect the variability found in the modelling data set.

When heights are sub-sampled, the available height data can be used to localize the height prediction model. This is accomplished using either an ad-hoc approach or a pseudo-Bayesian approach that adjusts the amount of change to the model parameters by a constant ratio between 0 and 1. Within the ad-hoc procedure, a weight of zero causes the update routine to abort (no update), while a weight of one places all the emphasis on the local sample to determine the coefficient values to be used for the height prediction equations. The pseudo-Bayesian approach is more conservative than the ad-hoc procedure. If the local sample is small then the updated coefficients for the height prediction equation are quite close to the database values. If, however, there is a large local sample, then the pseudo-Bayesian estimates are a compromise between the database values and those determined from the local sample. See Van Deusen (1984) and Biging and others (1991) for more information on the updating procedure.

STAG, unlike CACTOS, allows four different types of tree height measurements: 1) total heights; 2) heights to a merchantable top ($\leq$6.5 in.); 3) heights measured to whole (16.5 ft.) logs; or 4) heights measured to half logs (8.25 ft.). Within a STAG stand description file all heights must be of the same measurement standard. STAG uses a taper equation for the six major conifer species (species numbers 1-6) to solve for total height whenever height to a merchantable top or number of 16.5 ft. logs is supplied[4].

There are several cases when STAG does not estimate total height from merchantable height or number of logs. These cases include: 1) when taper equations do not exist for a species (note: there are no taper equations for any species other than the six major conifer species); 2) when the

[4] The height conversion process is not intended to encourage the measurement of anything other than total heights. Rather, it is intended to allow the use of older inventory data.

merchantable top is greater than 6.5 inches (total height predictions become inaccurate when the merchantable top is too large); and 3) when tree DBH is less than 8 inches (a tree is considered unmerchantable if its DBH is too small). In these cases, height is set to missing and can be filled in using the standard missing data techniques within STAG.

III.B. Converting Stand Tables into Complete Tree Lists

Stand table information can be used to develop distributions from which individual trees and their accompanying dimensions (diameter, heights and crown ratios) can be generated. The created tree list has the property that reclassification of the diameters would reproduce the original stand table. Also, the sum of the tree weights of pseudo-individual trees within a diameter class equals the original tree weight from a diameter class of the stand table. The tree weight represents (in this case) the probability of the tree having actually been on the plot. This new tree list mimics the inherent variability found in inventory data and produces a list of trees having diameters different than the diameter class midpoints of the stand table. The procedure used to create the tree list completes the tree list by supplying height, crown ratio and tree weight (expansion factor) of each generated tree. In essence, this process produces a facsimile of a permanent plot using only the numbers of trees by diameter class and species. The resultant tree list is quite large, but is currently limited to be between 100-500 records. Converting stand tables into complete tree lists is only recommended when the width of the diameter classes is less than or equal to two inches so that an accurate portrayal of the diameter distribution can be obtained.

III.C. Generating Stand Descriptions

STAG has the additional ability of generating complete tree lists when only summary statistics are available to describe the stand of interest. This capability has obvious utility for transforming summary information into a form that can be used with the CACTOS individual tree growth simulation system. It also can be used to produce stand descriptions so that investigation of forest growth dynamics can be performed in the absence of field data observations. While this is not generally recommended, it can be important when the manager is evaluating the performance of stands that currently do not exist, but which he or she may wish to establish in the future. These hypothetical stands can easily be created within the interactive environment of STAG. Appendix B.4 gives a demonstration of how this interactive process can be used.

STAG requires certain information when either the Weibull or the negative exponential diameter distribution models are used. This information includes: stand elevation, basal area per acre by species, the number of trees per acre by species, and site index for each species of interest. In the case of the negative exponential diameter distribution the "Q value", or diminution quotient, must also be specified.

To keep the number of tree records for selected diameter classes manageable the understory data can be collapsed into classes for DBH, total height, and live-crown ratio by invoking the collapsing algorithm with the cu command issued from the sg routine.

Weibull distribution model

It is possible to iteratively generate various components of the stand using a Weibull diameter distribution until the user has built a stand matching the desired description. Each species that is represented in the overstory is considered to be a separate component, and the the understory in its entirety is considered to be another component.

Because stands of trees are often simulated for over 30 years with the CACTOS System it is essential to be able to generate an understory component that matures with relatively long simulations. When generating understories using the Weibull distribution the user is given several options. In one option the user specifies the information on the overstory such as the average diameter of trees over 5.5 inches in DBH, and the number of trees per acre greater than 5.5 inches in DBH. This information is used to generate a Weibull distribution for understory trees. Alternatively, the overstory trees can be used directly to predict the Weibull coefficients for the distribution of diameters of small trees. The user can then either specify directly the number of understory trees to generate, or they can use prediction models for estimating the number of small trees to be generated. The user must also specify the species composition.

Negative exponential distribution model

The user may also generate a diameter distribution for any species using the negative exponential distribution model by specifying the diminution quotient or "Q" value. When this model is employed, the user has the option either to generate understory trees of a given species simultaneously with the overstory trees, or to generate understory trees separately from the overstory as is done when using the Weibull distribution model.

IV. PROGRAM COMMANDS

STAG is operated by entering two letter commands at various descriptive prompts. Some commands will cause the program to prompt the user for further input, such as names for input and output files. These prompts can then be suppressed by entering arguments to the commands that can use them. For example, the name of the report file can be specified with the command **rp** as follows:

```
md:rp >demo.srp
```

This would automatically open the report file "demo.srp" and automatically overwrite it if it exists. These arguments are described in Table 4. The commands that take advantage of these arguments are described in the appropriate sections.

Table 4. Command Arguments used in STAG.

<table>
<tr><th>Argument</th><th>Use</th></tr>
<tr><td>>output</td><td>cause output to go to file "output", automatically overwriting file if it already exists</td></tr>
<tr><td>>>output</td><td>cause output to go to file "output", automatically append file if it already exists</td></tr>
<tr><td><input</td><td>cause input to come from file "input", if "input" does not exist, user will be prompted for another file</td></tr>
<tr><td>p=plist</td><td>cause operation to be performed on plots contained in plist. Plist is specified by listing the plots, starting at one for the first plot in memory, to be used in the operation. This list can specify ranges. For example, the following command will produce diameter distributions for the plots listed:

md: dt p=1,2,3,18,8-14,21-45

Note that the plots in plist do not have to appear in any special order.</td></tr>
<tr><td>s=slist</td><td>cause operation to be performed on species groups specified in slist. The same rules apply as for plist. Species groups are 1=PP, 2=SP, 3=IC, 4=DF, 5=WF, 6=RF,7=OH, and 8=BO. See Table 3.</td></tr>
<tr><td>o=s | r | b</td><td>cause output from procedure to be routed to the [s]creen, [r]eport file, or [b]oth. Specify only one letter for this argument.</td></tr>
<tr><td>nomore</td><td>cause ouput going to screen not to pause at each screenful of data.</td></tr>
</table>

IV.A. The Main Program

From the main program, the user can enter routines to "fill in" missing data, create a stand description based upon summary statistics, convert stand table data to individual tree data, or change the program configuration. The prompt in the main program is:

```
stag:
```

The main program menu contains the following commands:

cf enter the program configuration routine

ex exit from the program

da* [<input] [>|>>output]
enter the distributional apportionment routine which converts stand tables into complete individual tree lists

md* [<input] [>|>>output]
enter the missing data routine

pc print commands

sg [<input] [>|>>output]
enter the stand generation routine

* These routines can be run in interactive batch mode by adding the argument "b" to form dab and mdb.

IV.B. Special Features Available in STAG

Many commands require the use of input and output files. When prompted for a filename, a list of files on the current working directory can be obtained by entering a question mark "?" in response to the prompt "Enter a filename here:". Thus, if you do not recall the name of the input or output file requested, you can obtain a list of the files on your directory.

There is a special command, available at all of STAG's command prompts, that allows you to branch to DOS. The branch command, `br`, allows the user to return to DOS while STAG is temporarily suspended. This allows you, among other things, to run other programs, delete files or to get a current directory listing without having to exit the program and re-load your input file. To return to STAG from a branch, type `EXIT` at the DOS prompt. STAG will return to the routine from which it started.

IV.C. The Configuration Routine

The commands available to the user while within the configuration routine are summarized in Table 5.

The configuration routine allows the user to change default values of parameters that affect program output such as the cubic and board foot minimum DBH's used in report generation. The parameters have a default value which can be examined by typing `ps` (print current configuration status).

The user can redefine any of these parameters and can save the new configuration by using the `sc` (save current configuration command). At any time if the user wants to restore the original default parameters he or she may do so by using the `rc` (reset configuration parameters to their defaults). Thus no matter how many changes have been invoked, the `rc` command will restore the parameters to their condition when the program was purchased.

In a similar fashion the `rh` command can be used to reset the height equation parameters to their original default values. This feature would commonly be used after the height coefficients have been updated using the pseudo-Bayesian or ad hoc parameter update methods described in section III.A. In this case, the user may have used the updated coefficients to work with a particular dataset, but now wants to work with different data not requiring updated coefficient values.

The configuration routine menu uses the prompt "`config:`". The commands allowed within the configuration routine are described in Table 5.

Table 5. Summary of the commands available from within the configuration routine.

Command	Description of the command function
bm	Set the minimum DBH which contributes to board foot volume. Default: 8.0 inches.
bt	Set the board foot merchantable top diameter to a value of 6 or 8 inches. Default: 6.0 inches.
cm	Set the minimum DBH which contributes to cubic foot volume. Default: 0.0 inches.
ct	Set the cubic foot merchantable top diameter to a value of 4 or 6 inches. Default: 4.0 inches.
dc	Set the D-class width for stand tables to 1 or 2 inches. Default: 2 inches.
ex	Exit the configuration routine and return to the main menu.
hc	Set the highlight codes for displaying tree lists. The user may set highlight codes that accentuate the missing values and their estimates in the stand description files. The default value is reverse video.
mr	Set the maximum number of records created in the distributional apportionment and stand generation routines. The number of records created ranges from 100-500. If record quintupling is to be utilized in CACTOS, then **mr** should be set to 100 and **re** set to "off". Otherwise set **mr** to 500 and **re** to "ON" and STAG will create up to 500 tree records with random variation built into the tree list. Default: 500 records.
pc	Print the list of available commands.
ps	Print the current configuration status.
rc	Reset the configuration parameters to default values. If at any time the user wants to revert to the configuration supplied at the time of purchase of the program the **rc** command will accomplish this.
rh	Reset the height equation parameters to default values.
re	Set flag to add random errors to predictions. This command allows the user to add random errors to the predictions of height and or height-to-crown base used in the missing data routine (**md**). It is recommended that random errors routinely be added to the predictions. Default is ON.
sc	**[>output]** Save the current configuration. This command allows the user to tailor his/her configuration file and to save this configuration for future use in STAG. The new configuration will be in operation until another save (**sc**) is conducted or until reset to the default configuration parameters (**rc**) is invoked.
sk	Set the title page skip. The user can decide to print the title page or to forego printing the title page upon invoking STAG. Default is OFF (show title page).
uc	Set the understory collapsing feature to be invoked automatically. STAG will automatically reduce the number of generated understory records so that the overstory and understory records total to less than 500. This routine will automatically be invoked upon exiting the understory generation routine, using a predefined collapsing ratio (**ur**). Default is ON.
ur	Set the understory collapsing ratio. This command allows the user to specify the ratio of overstory to understory tree records actually retained in the stand description upon exiting the understory generation routine or when invoking the collapsing algorithm using the **cu** command within the **sg** routine. The ratio actually obtained after the collapsing algorithm finishes, however, depends on how similar the understory trees were to begin with. Default: 0.5 which is a ratio of one overstory to two understory trees.

IV.D. Data Manipulation Routines.

The primary routines in STAG are for filling in missing data, generating stand descriptions and converting stand tables into complete tree lists. These routines are called from the main routine by typing **md**, **sg**, or **da**, respectively. For these three main commands (**mg**, **sg**, or **da**), the input and output conventions are listed in Table 6a.

Table 6a. Input and output conventions for **mg**, **sg**, or **da**.

Routine	Options	
md	[<input]	[>l>>output]
sg	-	[>l>>output]
da	[<input]	[>l>>output]

The commands available to the user varies by the particular routine that is in effect (**md**, **sg**, or **da**). Table 6b summarizes the commands available within the three main routines.

Table 6b. Command summary for the data manipulation routines available within **md**, **sg**, or **da**.

Command	Command Options [listed in brackets] and Description of the command function	Routines from which the command can be invoked
ab	- no command options -	md sg da
	Abort without saving the tree list (stand description). This allows the user to exit the current routine without having estimated the missing values for height and height-to-crown base for individual trees.	
cu	- no command options -	sg
	Collapse the understory tree records. This feature allows the user to reduce the number of understory tree records so that the number of overstory plus understory tree records is less than a user specified number of records which must be ≤500. It is invoked by the user while in the sg routine, and allows the user to specify a DBH below which tree records will be collapsed into classes for DBH, height and crown ratio according to a specified collapsing ratio (see **ur** in Table 5).	
da	[p=plist]	da
	Invoke the distributional apportionment routine which converts stand tables into complete individual tree lists.	

Table 6b continued.

Command	Command Options [listed in brackets] and Description of the command function	Routines from which the command can be invoked
dp	[r=skip] [o=s|r|b] [s=slist] [p=plist] [nomore] [<input] Display the tree list(s). This command allows the user to display on the screen each tree's value for species, DBH, total height, live crown ratio and tree expansion factor. If the highlight codes are specified in the configuration command to, say, reverse video then the missing values are highlighted. After invoking the **md** command to "fill in" missing data, the estimates of the tree's dimensions that are "filled in" are highlighted. Tables created by this command may be saved in the report file.	md sg da
dq	- no command options - Create a negative exponential diameter distribution for a given species on the generated plot. The distribution is specified by knowing the diminution quotient or "Q" value. When prompted for species information you can enter a "?" to see a list of species and species codes.	sg
dt	[o=s|r|b] [s=slist] [p=plist] [nomore] Graph the diameter distribution of the plot(s). The user controls the species to be included in the graph. Graphs created by this command may be saved in the report file.	md sg da
es	[>|>>output] Externally save the stand description file that is currently in memory. Plots saved using **es** may be reopened as input for the **md** and **da** routines.	md sg da
ex	- no command options - Exit the missing data routine and save the tree list.	md sg da
md	[p=plist] Invoke the missing data routine. When the command **md** is invoked the program will automatically check for missing heights and height-to-crown base measurements in the tree list for all trees >1.5" in DBH. It will then "fill in" these missing values with estimates based upon statistical models developed for coniferous forests from a diverse geographic region in northern California. In the missing data routine height estimates can be localized to a specific data set using the **uh** command which updates the height coefficients using the currently loaded plots and employing a Bayesian approach or an adhoc weighting scheme. Thus, the user has control over the method in which missing heights are estimated. For more detail see the section on the **uh** command.	md
pc	- no command options - Print a list of the available commands.	md sg da

Table 6b continued.

Command	Command Options [listed in brackets] and Description of the command function	Routines from which the command can be invoked
pf	[o=s|r|b] [s=slist] [p=plist] [nomore]	md sg da
	Graph the crown profile of the plot(s), showing the average tree height and crown length by diameter class. The user controls the species to graph. If species is not specified then all species are used in producing the graph. Graphs created by this command may be saved in the report file.	
rh	- no command options -	md
	Reset the height coefficients to the default values supplied with the program.	
rp	[>|>>output]	md sg da
	Open a report file.	
rt	- no command options -	md sg da
	Restore internally saved plots. Plots saved using the **sv** command can be restored by the user. This may be useful, when the user initially saves the files before invoking the missing data routine. If the user does not like the results after using the adhoc method of updating height coefficients, then the plots can be restored to their condition prior to filling in missing data using the updated height coefficients.	
rx	[<input]	md
	Read a coefficient file saved externally with the **uh** command. The coefficient file contains the parameter values for the height model for each species group (1-8) that STAG recognizes. See Table 3.	
sg	- no command options -	sg
	Add a species to the generated plot. This feature allows the user to generate a stand description for multiple species using a Weibull diameter distribution. Trees generated are greater than 5.5 inches at DBH. When prompted for species information you can enter a "?" to see a list of species and species codes.	
st	[o=r|s|b] [p=plist]	md sg da
	Print the stock table for each plot indicating quadratic mean DBH (Dq), number of stems/acre (N/ac), basal area/acre (BA), and cubic and board foot volumes/acre (in 1000's - MCF and MBF, respectively) by species groups. Tables created by this command may be saved in the report file.	
sv	- no command options -	md sg da
	Internally save the plots in memory (stand description). Stand descriptions saved in this fashion can be restored using the `rt` command.	

Table 6b continued.

Command	Command Options [listed in brackets] and Description of the command function	Routines from which the command can be invoked
uh	[>output] Update the height coefficients using the current plots to localize the relationships and externally save these values. When the **uh** command is issued the user must decide if a pseudo-Bayesian or adhoc parameter update method is to be employed.	**md**
ug	- no command options - Add understory trees to the generated plot. This feature allows the user to generate an understory stand description for multiple species using a Weibull diameter distribution. Trees generated are less than 11.0 inches at DBH. If **uc** is set to ON then the number of understory tree records will be reduced so that the total number of tree records will be less than 500. The degree of collapsing which takes place depends on the **ur** setting (see Table 5).	**sg**

IV.E. Interactive Batch

The **md** and **da** commands called from the main menu prompt **stag:** can be run in batch mode. This is useful when the stand table expansion or missing data routines need to be invoked, but no reports are needed or wanted. To run these routines in batch mode, the user types in the command **mdb** or **dab** followed by the input and output file specifications. The files are specified as **<input_file** and **>output_file** where the user supplies the correct names. The program then opens the input and output files, runs the appropriate routines on the input data, and writes the converted results to the output file.

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APPENDIX A. SAMPLE STAND DESCRIPTION INPUT FILES

A.1. Stand Description with Missing Data

```
Column
....+....1....+....2....+....3....+....4....+....5....+....6....+....7
missing data demo            29      4500
  100.  95.  70.  90.  85.   0.  89.   0.  76.   0.  79.   0.   0.  70.
    0.   0.   0.   0.   0.   0.   0.   0.   0.   0.   0.   0.   0.   0.
    1.       6.5   40.        0.         2.647
    1.      10.7    0.        0.         2.670
    1.      18.8  100.        0.         1.281
    2.       8.4    0.        0.         2.453
    2.      10.2   49.        0.         4.799
    2.      14.6   75.        0.         2.465
    2.      16.3   81.        0.         1.928
    3.      36.0  138.        0.         0.446
    3.      38.2  152.        0.         0.458
    3.      42.5  150.        0.         0.205
    3.      44.0  145.        0.         0.237
    4.      46.9    0.        0.         0.465
   11.       6.5    0.        0.        35.354
   14.       6.4    0.        0.        24.757
    5.       8.6    0.        0.        10.628
    5.      10.4    0.        0.         3.549
    5.      16.3    0.        0.         1.485
    5.      18.2    0.        0.         0.822
    5.      20.4    0.        0.         0.843
    7.      22.5    0.        0.         0.320
    7.      26.7    0.        0.         0.354
    7.      28.4    0.        0.         0.343
    7.      30.4    0.        0.         0.512
    9.      34.8    0.        0.         0.555
   11.      36.6    0.        0.         0.326
   11.      38.5    0.        0.         0.549
    2.      40.2    0.        0.         0.348
    2.      44.3    0.        0.         0.554
    2.      50.8    0.        0.         0.325
```

A.2. Stand Description for Distributional apportionment

```
Column
....+....1....+....2....+....3....+....4....+....5....+....6....+....7
dist. app. plot 1             10     4500
  100. 100.    0.    0.    0.    0.    0.    0.    0.    0.    0.    0.    0.    0.
   40.  50.    0.    0.    0.    0.    0.    0.    0.    0.    0.    0.    0.    0.
      1.000  10.000      .000      .000  10.000
      1.000  12.000      .000      .000  10.000
      1.000  14.000      .000      .000  10.000
      1.000  16.000      .000      .000  10.000
      1.000  18.000      .000      .000  10.000
      2.000  14.000      .000      .000  10.000
      2.000  16.000      .000      .000  10.000
      2.000  18.000      .000      .000  10.000
      2.000  20.000      .000      .000  10.000
      2.000  22.000      .000      .000  10.000
dist. app. plot 2             12     4500
      0. 100.    0. 110.   99.    0.    0.    0.    0.    0.    0.    0.    0.    0.
      0.  50.    0.  10.    0.    0.    0.    0.    0.    0.    0.    0.    0.    0.
      5.000   6.000      .000      .000  20.000
      5.000   8.000      .000      .000  20.000
      5.000  10.000      .000      .000  20.000
      5.000  12.000      .000      .000  20.000
      5.000  14.000      .000      .000  20.000
      2.000  14.000      .000      .000  10.000
      2.000  16.000      .000      .000  10.000
      2.000  18.000      .000      .000  10.000
      2.000  20.000      .000      .000  10.000
      2.000  22.000      .000      .000  10.000
      4.000  24.000      .000      .000   5.642
      4.000  26.000      .000      .000   8.456
```

APPENDIX B. SAMPLE RUNSTREAMS

B.1. Configuration Routine

```
                    WELCOME TO

     SSSSS   TTTTTTTT    AAA      GGGGG
    SS   SS  TTTTTTTT   A   A    GGGGGGG
    SS          TT     AA   AA   GG
     SSSSS      TT     AAAAAAA   GG  GGG
         SS     TT     AA   AA   GG    G
    SS   SS     TT     AA   AA   GGGGGGG
     SSSSS      TT     AA   AA    GGGGG


        The STAnd Generator for mixed conifers


                    version 4.0
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              enter "return" to continue


        The STAnd Generator for mixed conifers

                        by
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  Walter J. Meerschaert, Paul C. Van Deusen, Timothy A. Robards,
                and Eric C. Turnblom
         Department of Forestry and Resource Management
            University of California, Berkeley

     A Product of the Northern California Forest Yield Coop.

American Forest Products            The Hearst Corp.
W.M. Beaty and Associates, Inc.     Louisiana-Pacific Corp. (Elk Creek)
Champion International Corp.        Louisiana-Pacific Corp. (Feather Falls)
Crane Mills                         Michigan-California Lumber Co.
Fibreboard Corporation              Pacific Gas & Electric Co.
Fruit Growers Supply Co.            Roseburg Resources Co. (Diamond Lands)
Georgia Pacific Corp. (Martell)     Sierra Pacific Industries

U.S.D.A. Forest Service (R5)        CA Dept. of Forestry & Fire Protection

         Research conducted under AES project 3679-MS.


              enter "return" to continue
```

This is the header with title page skip OFF (see below).

[Whenever simply entering a "carriage return" accomplishes our goal, its entry is implied].

```
          MAIN PROGRAM
          ------------
   Type "pc" to get a list of commands



stag: cf
```

Enter the configuration routine (responses the user would type appear in **bold** characters).

```
          CONFIGURATION ROUTINE
          ------------- -------

   Type "pc" to get a list of available commands.

        - CURRENT CONFIGURATION STATUS -
```

Current status is printed automatically.

```
   re - Add random errors................ON
        Height coefficients.............DEFAULT
   sk - Title page skip..................OFF
   dc - DBH class width used in d.a...... 2.0"
   mr - Max. number of records in d.a....500
   cm - Cubic minimum diameter...........  .0"
   ct - Cubic merch top.................. 4.0"
   bm - Board foot minimum diameter...... 8.0"
   bt - Board foot merch top............. 6.0"
   uc - auto. understory compression.....ON
   ur - understory compression ratio.....  .5
   hc - Highlight Code................... 3


config:pc
```

Print available commands.

```
        CONFIGURATION COMMANDS
        ------------- --------

   bm - set board foot minimum DBH
   bt - set board foor merchantable top
   cm - set cubic foot minimum DBH
   ct - set cubic foot merchantable top
   dc - set DBH class width used in "distributional apportionment"
   ex - exit configuration routine
   hc - set highlight codes for displaying tree lists
   mr - set max. number of records created in "distributional apportionment"
   pc - print commands
   ps - print current configuration status
   rc - reset to default configuration parameters
   rh - reset to default height equation parameters
   re - set flag to add random errors to predictions
   sc - save current configuration
   sk - set title page skip
   uc - set automatic understory tree record compression
   ur - set ratio of tree records saved in "u.g." (overstory:understory)

        OPTIONS: [>or>>output] [<input]
```

These options are for routines that use files.

```
config:bm

 Board foot min. DBH =  8.0 enter new: 8.0
```

Set minimum DBH contributing to board foot volume.

```
config:bt

 Board foot merch top =  6 in.- enter new (6 or 8): 6
```

Set merchantable top diameter for board foot volume.

```
config:cm

 Cubic min. DBH =    .0 enter new;
 (must be less than board ft DBH min.): 4.0
```

Set minimum and merchantable diameters for cubic foot volume analogously.

```
config:ct

 Cubic merch top =  4 in. - Enter new (4 or 6): 4
```

```
config:mr

 Maximum number of records produced in dist. app. is 500
 Enter new maximum (100-500): 100
```

Set the maximum number of records produced in distributional apportionment.

```
config:re

 Current random error flag is set to 1
 Enter new flag value (1=add random errors, 0=don't): 1
```

In this example we want to make sure random errors are added to height and crown estimates.

```
config:sk

 Title page skip is currently 0 enter new (0=print,1=skip): 1
```

Set the title page skip for future runs.

```
config:ur

 The ratio of the number of overstory tree records to the
 number of understory tree records is  .5 -
 Enter new value (0.1 - 4.0): 1.0
```

Ratio of overstory to understory tree records desired is 1:1.

```
config:uc

 Automatic understory tree record compression is ON.
    Enter new setting (0=OFF,1=ON): 0
```

Turn off automatic invocation of understory collapsing algorithm.

```
config:ps

       - CURRENT CONFIGURATION STATUS -

   re - Add random errors................ON
        Height coefficients.............DEFAULT
   sk - Title page skip..................ON
   dc - DBH class width used in d.a...... 2.0"
   mr - Max. number of records in d.a....100
   cm - Cubic minimum diameter........... 4.0"
   ct - Cubic merch top.................. 4.0"
   bm - Board foot minimum diameter...... 8.0"
   bt - Board foot merch top............. 6.0"
   uc - auto. understory compression.....OFF
   ur - understory compression ratio..... 2.0
   hc - Highlight Code................... 3
```

Print status of the new configuration to check our choices.

```
config:sv

   Current configuration saved in: stbin
```

Save the current configuration in the reserved STAG file named "STBIN."

```
config:ex

 Exiting initialization routine


stag: ex
stag: user termination
```

B.2. Filling in Missing Data

```
STAG version 4.0  August 26, 1991
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Release number: #####

          MAIN PROGRAM
          ------------
  Type "pc" to get a list of commands
```

Header with title skip ON.

```
stag: md

     FILL IN MISSING DATA
     ---- -- ------- ----


Open the plot data input file
Enter a file name here: mddemo.sd

Open the output tree list file
Enter a file name here: mddemo.sdm
```

Input filename is requested. Note the use of the suggested conventions for naming files.

```
Reading  29 tree records from : missing data demo

Read in     1 plots containing      29 tree records

There were     20 missing heights, and     29 missing crowns

Type "pc" to get a list of commands
```

```
md:md

Filling in missing data on: missing data demo
```

Fill in missing data.

```
md:dp
```

Display the tree list.

```
Display tree records
  plot label : missing data demo

 no.  sp   dbh   ht    cr     exp
-----------------------------------
   1  PP   6.5   40.  .355   2.647
   2  PP  10.7   61.  .508   2.670
   3  PP  18.8  100.  .499   1.281
   4  SP   8.4   38.  .242   2.453
   5  SP  10.2   49.  .316   4.799
   6  SP  14.6   75.  .513   2.465
   7  SP  16.3   81.  .461   1.928
   8  IC  36.0  138.  .451    .446
```

Notice that the filled in data are highlighted.

```
  9    IC  38.2  152.  .390     .458
 10    IC  42.5  150.  .437     .205
 11    IC  44.0  145.  .397     .237
 12    DF  46.9  155.  .234     .465
 13    CH   6.5   38.  .462   35.354
 14    HW   6.4   30.  .282   24.757
 15    WF   8.6   43.  .349   10.628
 16    WF  10.4   44.  .442    3.549
 17    WF  16.3   77.  .384    1.485
 18    WF  18.2   86.  .358     .822
 19    WF  20.4   92.  .297     .843
 20    LP  22.5   99.  .365     .320
 21    LP  26.7  100.  .303     .354
 22    LP  28.4  113.  .443     .343
 23    LP  30.4  105.  .355     .512
 24    JP  34.8  112.  .312     .555
 25    CH  36.6   90.  .213     .326
 26    CH  38.5   90.  .226     .549
 27    SP  40.2  140.  .372     .348
 28    SP  44.3  149.  .387     .554
 29    SP  50.8  165.  .305     .325
```

```
md:rp

 Open the report file
 Enter a file name here: demo.srp
 Report file in use named: demo.srp
```

Open a report file named demo.srp, overwriting if it already exists.

```
md:pf  o=b  s=1

       Print stand profile

Plot label : missing data demo
species = PP

                     feet above ground
 DBH   Trees |     24     48     72     96    120    144    168    192    216    240
             |.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
2 - 4     0. |
4 - 6     0. |
6 - 8     3. |=====>>>>
8 -10     0. |
10-12     3. |=======>>>>>>>>
12-14     0. |
14-16     0. |
16-18     0. |
18-20     1. |=============>>>>>>>>>>>
------------
total     7.


   Graph saved in report file
```

Display a plot profile, using species code 1 (PP), send output to both the screen and the report file.

```
md:dt  s=1,2

       Print diameter distribution

Plot label : missing data demo
species = PP SP

 dbh  trees |             15             30             45             60
            |..............|..............|..............|..............|
2 - 4    0. |
4 - 6    0. |
6 - 8    3. |111
8 -10    2. |11
10-12    7. |1111111
12-14    0. |
14-16    2. |11
16-18    2. |11
18-20    1. |1
20-22    0. |
22-24    0. |
24-26    0. |
26-28    0. |
28-30    0. |
30-32    0. |
32-34    0. |
34-36    0. |
36-38    0. |
38-40    0. |
40-42    0. |
42-44    0. |
44-46    1. |1
46-48    0. |
48+      0. |
------------
total   19.
```

Print a diameter distribution to the screen (default), use species 1 and 2 (PP and SP).

```
md:st
```

Print a stock table.

STOCK TABLE

Plot label = missing data demo

species	Dq	N/ac	BA	MCF	MBF
Pond. Pine	14.68	7.	8.4	.26	1.42
Sugar Pine	18.06	13.	22.9	.80	5.42
Cedar misc	39.27	1.	11.3	.42	3.55
DouglasFir	33.12	2.	11.9	.47	3.33
White Fir	11.24	17.	11.9	.28	1.22
Chinquapin	8.70	36.	15.0	.45	.00
H.W. misc	6.40	25.	5.5	.04	.00
Totals	12.52	102.	87.0	2.71	14.94

```
md:es  >>mddemo.es

 Saving tree list for plot : missing data demo
```

Save what's in memory to the file "mddemo.es", automatically appending if it exists.

```
md:uh

 What kind of height parameter update do you want?

    [0] none
    [1] pseudo-bayes
    [2] adhoc

 Enter here: 1

 Open the coefficient output file
 Enter a file name here: mddemo.uh
 Coefficients saved in file: mddemo.uh
```

Height equation coefficient update using local data.

```
md:rx  <mddemo.uh

 Height coefficients read from file: mddemo.uh
```

This shows how the updated coefficients would be used in a later run. STAG already recognizes the updated coefficients for this run.

```
md:rh

 Height coefficients reset to default
```

This is how to reset the height coefficients to default values.

```
md:ex

 Saving tree list for plot : missing data demo

stag:ex
stag: user termination
```

"ex" quits and saves the plots in memory, "ab" quits butr aborts changes to the plots in memory.

B.3. Distributional Apportionment

```
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Release number: #####

          MAIN PROGRAM
          ------------
  Type "pc" to get a list of commands
```

```
stag: da <dademo.sd >dademo.sda

     DISTRIBUTIONAL APPORTIONMENT
     -------------- ------------

 Reading  10 tree records from : dist. app. plot 1

 Reading  12 tree records from : dist. app. plot 2

 Read in     2 plots containing      22 tree records

 Type "pc" to get a list of commands
```

Enter distributional apportionment routine, use dademo.sd as input, route output to dademo.sda.

```
da:dp

 Display tree records
   plot label : dist. app. plot 1

  no.  sp   dbh   ht    cr     exp
----------------------------------
   1   PP  10.0    0.  .000  10.000
   2   PP  12.0    0.  .000  10.000
   3   PP  14.0    0.  .000  10.000
   4   PP  16.0    0.  .000  10.000
   5   PP  18.0    0.  .000  10.000
   6   SP  14.0    0.  .000  10.000
   7   SP  16.0    0.  .000  10.000
   8   SP  18.0    0.  .000  10.000
   9   SP  20.0    0.  .000  10.000
  10   SP  22.0    0.  .000  10.000
 - more plots -
```

Look at stand tables loaded into memory.

(A carriage return is entered here to resume paused output).

Display tree records

plot label : dist. app. plot 2

no.	sp	dbh	ht	cr	exp
1	WF	6.0	0.	.000	20.000
2	WF	8.0	0.	.000	20.000
3	WF	10.0	0.	.000	20.000
4	WF	12.0	0.	.000	20.000
5	WF	14.0	0.	.000	20.000
6	SP	14.0	0.	.000	10.000
7	SP	16.0	0.	.000	10.000
8	SP	18.0	0.	.000	10.000
9	SP	20.0	0.	.000	10.000
10	SP	22.0	0.	.000	10.000
11	DF	24.0	0.	.000	5.642
12	DF	26.0	0.	.000	8.456

```
da:da

 Creating tree list from stand table on plot : dist. app. plot 1
 dist: re-iterating to reduce number of records

 Creating tree list from stand table on plot : dist. app. plot 2
 dist: re-iterating to reduce number of records
```

Create the stand descriptions.

```
da:dp  p=1  nomore


 Display tree records
   plot label : dist. app. plot 1

  no.  sp   dbh   ht    cr     exp
-----------------------------------
   1   PP  10.5   45.  .524    .765
   2   PP   9.3   36.  .255    .691
   3   PP   9.6   51.  .739    .597
   4   PP  10.6   52.  .556   1.299
   5   PP   9.7   51.  .429   1.397
   6   PP   9.3   54.  .200    .637
   7   PP  10.6   56.  .573   1.134
   8   PP  10.8   60.  .475   1.438
   9   PP  10.1   57.  .253    .780
  10   PP  11.0   73.  .660    .506
  11   PP  11.0   73.  .647    .755
  12   PP  12.7   47.  .541    .679
  13   PP  12.2   53.  .514    .949
  14   PP  12.6   47.  .212    .569
  15   PP  11.6   55.  .641    .930
  16   PP  11.6   55.  .515   1.554
  17   PP  11.6   62.  .391   1.114
  18   PP  12.3   73.  .660    .661
  19   PP  12.3   69.  .576   1.313
  20   PP  12.2   65.  .435   1.111
  21   PP  11.7   77.  .649    .561
  22   PP  12.8   82.  .467    .558
  23   PP  13.4   63.  .449   1.200
  24   PP  13.7   63.  .427   1.119
  25   PP  13.5   68.  .644    .577
  26   PP  13.0   67.  .515   1.530
  27   PP  14.7   74.  .504   1.695
  28   PP  14.0   69.  .231    .798
  29   PP  14.9   78.  .606   1.014
  30   PP  13.7   81.  .526   1.325
  31   PP  14.3   81.  .407    .742
  32   PP  15.5   57.  .380    .654
  33   PP  16.5   71.  .543   1.038
  34   PP  16.3   71.  .459   1.497
  35   PP  15.4   70.  .344    .927
  36   PP  16.9   78.  .608    .996
  37   PP  15.3   76.  .519   1.716
  38   PP  16.8   83.  .431   1.268
  39   PP  16.6   86.  .501   1.016
  40   PP  16.1   94.  .422    .887
```

Look at the new list of trees for the first plot without pausing after a screenful of data is displayed.

41	PP	17.5	66.	.375	.862
42	PP	17.8	74.	.352	.690
43	PP	18.1	84.	.668	.626
44	PP	18.9	79.	.496	1.423
45	PP	17.9	81.	.351	1.368
46	PP	18.7	77.	.163	.553
47	PP	18.1	89.	.603	1.208
48	PP	17.6	85.	.452	1.378
49	PP	17.3	92.	.339	.669
50	PP	17.3	104.	.628	.521
51	PP	18.4	95.	.520	.702
52	SP	14.6	59.	.603	.565
53	SP	14.6	58.	.415	1.325
54	SP	14.2	62.	.393	1.122
55	SP	14.0	69.	.545	1.595
56	SP	14.0	70.	.395	1.805
57	SP	14.3	72.	.354	.737
58	SP	13.1	80.	.659	.854
59	SP	14.6	81.	.533	1.288
60	SP	14.9	76.	.386	.709
61	SP	15.2	59.	.527	.544
62	SP	16.6	57.	.356	.574
63	SP	16.3	68.	.563	1.066
64	SP	15.8	65.	.433	1.517
65	SP	16.0	68.	.289	.787
66	SP	16.8	81.	.658	.902
67	SP	15.7	82.	.572	1.727
68	SP	15.3	81.	.343	1.206
69	SP	16.4	87.	.582	.869
70	SP	16.1	86.	.386	.808
71	SP	17.9	66.	.487	.522
72	SP	17.6	65.	.435	.932
73	SP	17.7	72.	.248	.607
74	SP	18.6	77.	.570	.680
75	SP	18.3	76.	.433	1.657
76	SP	18.6	77.	.287	1.456
77	SP	17.8	89.	.525	1.296
78	SP	17.5	89.	.410	1.520
79	SP	17.3	86.	.303	.644
80	SP	18.2	104.	.564	.687
81	SP	20.1	84.	.516	1.164
82	SP	19.7	79.	.374	1.278
83	SP	20.9	87.	.583	1.359
84	SP	19.9	95.	.483	2.006
85	SP	19.0	86.	.248	1.081
86	SP	19.6	103.	.618	.703
87	SP	20.2	96.	.451	1.398
88	SP	20.5	101.	.454	1.012
89	SP	21.6	81.	.360	.703
90	SP	22.5	85.	.533	.895
91	SP	21.8	85.	.431	1.663
92	SP	22.2	91.	.359	1.128
93	SP	21.1	101.	.633	.672
94	SP	21.9	102.	.482	1.699
95	SP	23.0	103.	.446	1.548
96	SP	22.2	111.	.559	.764
97	SP	23.0	114.	.497	.928

```
da:ex

 Saving tree list for plot : dist. app. plot 1

 Saving tree list for plot : dist. app. plot 2


stag:ex
stag: user termination
```

The results seem acceptable, let's quit.

B.4. Stand generation

```
 STAG version 4.0  August 26, 1991
 (c) Copyright 1986-1991
 The Regents of the University of California
 Release number: #####

           MAIN PROGRAM
           ------------
   Type "pc" to get a list of commands


stag:  sg  >sgdemo.sdg
```

Enter the stand generation routine, automeatically over-writing the file "sgdemo.sdg" if it exists.

```
     MAKE A HYPOTHETICAL PLOT DESCRIPTION
     ---- - ------------ ---- -----------


 Enter a plot description (20 char max): sg demo plot

 Enter the elevation of this plot:  3500

 Type "pc" to get a list of commands



sg:sg
```

Start generating species with some small white fir.

```
        *** MAKE ALL ENTRIES PER ACRE ***
 All tree weights = 1, the number of tree records will be
 the same as the number of trees specified

 Enter the following information:
    species code.................(1-14)
    basal area (>6 inches).......(5-400)
    number of trees(>6 inches)...(5-500)
```

White fir, 50 ft^2 BA. 170 trees/acre. site index 88.

```
 Enter here (separated by commas-? for species list):5,50,150

 Enter the site index of this species: 88

   Species.................White Fir
   Quadratic mean DBH...... 7.8
   Predicted average DBH... 7.6
   Number of trees > 6"....150
```

```
  [RETURN] Generate species, [R]etry, or [A]bort :

 Developing weibull distribution ...

 Filling in diameters ...

    Total plot basal area...  50.
    Total number of trees... 150

 Filling in missing data on: demo sg plot


sg:dt

      Print diameter distribution

Plot label : demo sg plot
All species combined

 dbh  trees |              30             60             90            120
            |..............|..............|..............|..............|
0 - 2    0. |
2 - 4    0. |
4 - 6   17. |111111111
6 - 8   83. |111111111111111111111111111111111111111111
8 -10   40. |11111111111111111111
10-12   10. |11111
------------
total  150.


sg:sv

 Internally saving current plot information


sg:sg

        *** MAKE ALL ENTRIES PER ACRE ***
 All tree weights = 1, the number of tree records will be
 the same as the number of trees specified

 Enter the following information:
    species code.................(1-14)
    basal area (>6 inches).......(5-400)
    number of trees(>6 inches)...(5-350)

 Enter here (separated by commas-? for species list):1,200,100

 Enter the site index of this species: 99

   Species.................Pond. Pine
   Quadratic mean DBH......19.1
   Predicted average DBH...17.8
   Number of trees > 6"....100

   [RETURN] Generate species, [R]etry, or [A]bort :r
```

Generate species with a carriage return.

Total height and crown lengths are automatically estimated.

Look at the results in a diameter distrubution plot.

Save the tree list internally so we can come back to this point without starting over.

Now let's add some residual pine trees.

Ponderosa pine, 200 ft^2 BA, 100 trees per acre, site index 99.

Mean DBH is 17.8 inches.

We don't like the size of the trees, they are

```
       *** MAKE ALL ENTRIES PER ACRE ***

All tree weights = 1, the number of tree records will be
the same as the number of trees specified

Enter the following information:
   species code.................(1-14)
   basal area (>6 inches).......(5-400)
   number of trees(>6 inches)...(5-350)

Enter here (separated by commas-? for species list):1,200,70

Enter the site index of this species: 99


  Species.................Pond. Pine
  Quadratic mean DBH......22.9
  Predicted average DBH...21.5
  Number of trees > 6".... 70

  [RETURN] Generate species, [R]etry, or [A]bort :r

       *** MAKE ALL ENTRIES PER ACRE ***
All tree weights = 1, the number of tree records will be
the same as the number of trees specified

Enter the following information:
   species code.................(1-14)
   basal area (>6 inches).......(5-400)
   number of trees(>6 inches)...(5-350)

Enter here (separated by commas-? for species list):1,200,40

Enter the site index of this species: 99


  Species.................Pond. Pine
  Quadratic mean DBH......30.3
  Predicted average DBH...29.1
  Number of trees > 6".... 40

  [RETURN] Generate species, [R]etry, or [A]bort :

Developing weibull distribution ...

Filling in diameters ...

   Total plot basal area... 250.
   Total number of trees... 190

Filling in missing data on: demo sg plot
```

too small.

We try for larger trees by decreasing trees/acre.

Avg. DBH is 21.5".

Avg. DBH still seems too small.

Avg. DBH is 29.1".

This is what we think we want.

Let's look at the result.

```
sg:dt

       Print diameter distribution

Plot label : demo sg plot
All species combined

 dbh  trees |             30             60             90             120
            |..............|..............|..............|..............|
0 - 2    0. |
2 - 4    0. |
4 - 6   17. |111111111
6 - 8   83. |111111111111111111111111111111111111111111
8 -10   41. |111111111111111111111
10-12   10. |11111
12-14    0. |
14-16    1. |1
16-18    4. |11
18-20    1. |1
20-22    2. |1
22-24    2. |1
24-26    3. |11
26-28    4. |11
28-30    1. |1
30-32    4. |11
32-34    3. |11
34-36    2. |1
36-38    6. |111
38-40    3. |11
40-42    1. |1
42-44    0. |
44-46    1. |1
46-48    1. |1
------------
total  190.

sg:rt

 Restoring plot information
```

We decide that this really isn't what we wanted, so we go back to the internally saved tree list start over.

```
andsg:dt

       Print diameter distribution

Plot label : demo sg plot
All species combined

 dbh  trees |             30             60             90             120
            |..............|..............|..............|..............|
0 - 2    0. |
2 - 4    0. |
4 - 6   17. |111111111
6 - 8   83. |111111111111111111111111111111111111111111
8 -10   40. |11111111111111111111
10-12   10. |11111
------------
total  150.
```

```
sg:sg

       *** MAKE ALL ENTRIES PER ACRE ***
All tree weights = 1, the number of tree records will be
the same as the number of trees specified

Enter the following information:
   species code................(1-14)
   basal area (>6 inches).......(5-400)
   number of trees(>6 inches)...(5-350)

Enter here (separated by commas-? for species list):1,200,70

Enter the site index of this species: 99


  Species.................Pond. Pine
  Quadratic mean DBH......22.9
  Predicted average DBH...21.5
  Number of trees > 6".... 70

  [RETURN] Generate species, [R]etry, or [A]bort :

Developing weibull distribution ...

Filling in diameters ...

   Total plot basal area... 250.
   Total number of trees... 220

Filling in missing data on: demo sg plot
```

We will put the pine in using a quadratic mean diameter of 22.9" found above.

```
sg:dt  nomore
```

Look at the results.

```
            Print diameter distribution

Plot label : demo sg plot
All species combined

 dbh   trees |              30             60             90             120
             |..............|..............|..............|...............|
0 - 2    0.  |
2 - 4    0.  |
4 - 6   17.  |111111111
6 - 8   84.  |111111111111111111111111111111111111111111
8 -10   40.  |11111111111111111111
10-12   13.  |1111111
12-14    4.  |11
14-16    8.  |1111
16-18    6.  |111
18-20    1.  |1
20-22   11.  |111111
22-24    9.  |11111
24-26    7.  |1111
26-28    5.  |111
28-30    1.  |1
30-32    9.  |11111
32-34    2.  |1
34-36    3.  |11
------------
total  220.
```

```
sg:pf  nomore

       Print stand profile

Plot label : demo sg plot
All species combined

                 feet above ground
 DBH  Trees |    24    48    72    96   120   144   168   192   216   240
            |.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
0 - 2    0. |
2 - 4    0. |
4 - 6   17. |====>>>>>>>
6 - 8   84. |=====>>>>>>
8 -10   40. |======>>>>>>>>
10-12   13. |=======>>>>>>>>>
12-14    4. |========>>>>>>>>>>>
14-16    8. |==========>>>>>>>>>>>
16-18    6. |===========>>>>>>>>>>>>>
18-20    1. |=========>>>>>>>>>>>>>>>>>>
20-22   11. |============>>>>>>>>>>>>>>
22-24    9. |=============>>>>>>>>>>>>>
24-26    7. |==============>>>>>>>>>>>>>>>
26-28    5. |===============>>>>>>>>>>>>>>>>
28-30    1. |================>>>>>>>>>>>>>>>>>>
30-32    9. |=================>>>>>>>>>>>>>>>
32-34    2. |==================>>>>>>>>>>>>>>
34-36    3. |===================>>>>>>>>>>>>>>>>
------------
total  220.
```

For another dimension we can also look at the stand profile.

```
sg:st


          STOCK TABLE
          -----------
 Plot label = demo sg plot


  species        Dq     N/ac     BA      MCF     MBF
  -----------------------------------------------------

  Pond. Pine   23.25     70.   206.4    7.84   47.98
  White Fir     7.77    150.    49.4    1.02    2.00
  Totals       14.60    220.   255.8    8.85   49.98
```

Before we add an understory component, let's examine a stock table.

```
sg:ug

 Use current stand to predict understory? (y/n): y


 All tree weights = 1, the number of tree records will be
 the same as the number of trees specified (rounded to nearest integer)

 Enter the following information:
    minimum diameter class............(1- 5)
    maximum diameter class............(minimum dbh class- 5)

 Enter here (separated by commas): 1,5

 Developing weibull distribution ...


    Predicted number of trees in understory ..........218

    Approximate 95% prediction interval .......[  5, 430]

 Would you like to change this number? (y/n): n


 The default species composition (in percent) for the Ponderosa pine
 forest type is as follows:
   ponderosa pine......50.0
   sugar pine.......... 5.0
   incense cedar.......15.0
   Douglas-fir......... 5.0
   white fir...........25.0
   red fir.............  .0

 Enter new percentages (separated by commas) or
 Return for default:


   Quadratic mean DBH of overstory (>6")...14.6
   Number of trees in overstory (>6")......220
   Number of trees in understory ( 1- 5")..218
   Understory proportion in PP.............50.0
   Understory proportion in SP............. 5.0
   Understory proportion in IC.............15.0
   Understory proportion in DF............. 5.0
   Understory proportion in WF.............25.0
   Understory proportion in RF.............  .0
   [RETURN] Generate species, [R]etry, or [A]bort :

 Filling in diameters ...

    Total plot basal area... 269.
    Total number of trees... 438

 Filling in missing data on: demo sg plot
```

Begin the understory generation routine, using the stand just generated to predict the understory.

STAG automatically determines the current overstory/ understory boundary (5" in this case).

Predicting the number of understory trees from overstory conditions is at best imprecise. Thus, a 95% confidence interval is offered to guide this decision.

The choices we have made are summarized before the understory trees are actually generated.

(Recall that we turnned OFF automatic understory collapsing with "uc" in the configuration routine, therefore it is not performed upon exiting ug).

```
sg:dt  nomore

       Print diameter distribution

Plot label : demo sg plot
All species combined

 dbh   trees |              30             60             90             120
             |..............|..............|..............|..............|
0 - 2    42. |111111111111111111111
2 - 4   113. |11111111111111111111111111111111111111111111111111111111
4 - 6    80. |1111111111111111111111111111111111111111
6 - 8    84. |111111111111111111111111111111111111111111
8 -10    40. |11111111111111111111
10-12    13. |1111111
12-14     4. |11
14-16     8. |1111
16-18     6. |111
18-20     1. |1
20-22    11. |111111
22-24     9. |11111
24-26     7. |1111
26-28     5. |111
28-30     1. |1
30-32     9. |11111
32-34     2. |1
34-36     3. |11
------------
total  438.
```

We've decided that we don't need so much detail on the stand below 11" DBH. Invoke the collapse understory routine.

```
sg:cu

   Please enter an integer DBH below which
   tree records will be collapsed:11


   Combining (collapsing) similar understory tree records ...
```

Collapsing is still governed by ratio set with "ur" in "cf".

```
   After collapsing tree records:

    Basal area (>6")........... 256.
    Basal area (all trees)..... 269.
    Number of trees (>6")...... 220
    Number of trees (total).... 438
    Number of tree records..... 116
```

A summary of the collapsing algorithm results is printed.

```
sg:dp  r=3  nomore


 Display tree records
   plot label : demo sg plot

  no.  sp   dbh   ht    cr     exp
----------------------------------
   1   WF  11.1   56.  .613   1.000
```

Let's display a few records to examine how the tree expansion factors have changed from the original 1 tree/ac.

4	PP	22.0	114.	.625	1.000
7	PP	16.0	92.	.640	1.000
10	PP	16.4	97.	.585	1.000
13	PP	22.0	107.	.504	1.000
16	PP	11.7	66.	.614	1.000
19	PP	22.6	109.	.430	1.000
22	PP	30.4	128.	.431	1.000
25	PP	23.0	100.	.545	1.000
28	PP	21.7	104.	.591	1.000
31	PP	11.0	79.	.614	1.000
34	PP	17.6	101.	.474	1.000
37	PP	22.0	117.	.634	1.000
40	PP	35.5	141.	.498	1.000
43	PP	14.4	80.	.485	1.000
46	PP	21.2	107.	.600	1.000
49	PP	26.7	127.	.554	1.000
52	PP	15.3	80.	.423	1.000
55	PP	30.2	133.	.504	1.000
58	PP	24.5	127.	.522	1.000
61	PP	27.5	127.	.480	1.000
64	PP	14.3	81.	.634	1.000
67	PP	27.1	125.	.497	1.000
70	PP	26.8	112.	.520	1.000
73	PP	1.7	16.	.767	34.000
76	PP	3.6	23.	.516	4.000
79	PP	4.1	38.	.718	31.000
82	SP	3.5	25.	.473	1.000
85	SP	4.5	39.	.674	1.000
88	IC	3.9	18.	.495	7.000
91	DF	2.2	15.	.435	1.000
94	DF	3.2	21.	.668	1.000
97	WF	1.9	18.	.570	5.000
100	WF	2.6	26.	.691	3.000
103	WF	4.1	34.	.556	13.000
106	WF	6.3	36.	.685	15.000
109	WF	7.7	45.	.416	15.000
112	WF	7.9	56.	.712	12.000
115	WF	10.0	62.	.457	6.000

sg:**st**

Print a stock table to see the impact of adding the understory.

STOCK TABLE

Plot label = demo sg plot

species	Dq	N/ac	BA	MCF	MBF
Pond. Pine	14.69	179.	210.8	7.89	47.98
Sugar Pine	1.30	12.	.1	.00	.00
Cedar misc	1.42	37.	.4	.00	.00
DouglasFir	2.53	6.	.2	.00	.00
White Fir	6.86	204.	52.4	1.05	1.29
Totals	10.51	438.	263.9	8.94	49.27

```
sg:ex

 Saving tree list for plot : demo sg plot


stag:sg  >sgdemo.sdq

     MAKE A HYPOTHETICAL PLOT DESCRIPTION
     ---- - ------------ ---- -----------


 Enter a plot description (20 char max): dq demo plot

 Enter the elevation of this plot: 3500

 Type "pc" to get a list of commands



sg:dq

        *** MAKE ALL ENTRIES PER ACRE ***
 All tree weights = 1, the number of tree records will be
 the same as the number of trees specified (rounded to nearest integer)

 Enter the following information:
    species code.................(1-14)
    minimum diameter class.......(1-99)
    maximum diameter class.......(minimum diameter class-99)
    diameter class increment.....(integer)

 Enter here (separated by commas-? for species list):1,2,24,2

 Enter the site index of this species: 88

 Do you know q? (y/n): y

 Enter Q: 1.5

 Do you know the number of trees
 in the largest diameter class? (y/n): y

 Enter the number of trees
 per acre in the largest diameter class: 1.2


   Species................................Pond. Pine
   Q......................................1.500
   Total basal area.......................  90.
   Minimum diameter class.................    2
   Maximum diameter class.................   24
   Diameter increment.....................    2
   Number of trees in max. diameter class.. 1.20

   [RETURN] Generate species, [R]etry, or [A]bort :
```

We're satisfied with results, exit and save stand description.

Let's go back to the stand generation routine.

Let's generate trees using the negative exponential distribution.

Note that this distribution can be used for modelling both over- and understory components.

We Created a DBH distribution for ponderosa pine with 1.5 for the diminution quotient (Q).

```
 Developing negative exponential distribution ...

 Filling in diameters ...

    Total plot basal area...  90.
    Total number of trees... 308

 Filling in missing data on: dq demo plot


sg:dt

       Print diameter distribution

Plot label : dq demo plot
All species combined

 dbh  trees |             30             60             90             120
            |..............|..............|..............|..............|
0 - 2   56. |1111111111111111111111111111
2 - 4   78. |111111111111111111111111111111111111111
4 - 6   68. |1111111111111111111111111111111111
6 - 8   30. |111111111111111
8 -10   25. |1111111111111
10-12   21. |11111111111
12-14   14. |1111111
14-16    9. |11111
16-18    4. |11
18-20    2. |1
20-22    1. |1
------------
total  308.


sg:pf

       Print stand profile

Plot label : dq demo plot
All species combined

                 feet above ground
 DBH  Trees |     24    48    72    96   120   144   168   192   216   240
            |.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
0 - 2   56. |=>>>
2 - 4   78. |=>>>>
4 - 6   68. |===>>>>
6 - 8   30. |=====>>>>>
8 -10   25. |=======>>>>>
10-12   21. |========>>>>>>>
12-14   14. |=========>>>>>>>
14-16    9. |==========>>>>>>>>>
16-18    4. |===========>>>>>>>>>>
18-20    2. |=============>>>>>>
20-22    1. |=============>>>>>>>>>
------------
total  308.
```

Examine the results by printing the DBH distribution and by printing the stand profile.

```
sg:ex

 Saving tree list for plot : dq demo plot


stag:ex
stag: user termination
```

Exit and save stand description.