Northern California Forest Yield Cooperative
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STAG USER'S GUIDE:

The Forest STAnd Generator for Mixed Conifer Species in California

Version 3

by

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Abstract

The forest Stand Generator, STAG[1], estimates missing tree heights, height-to-crown base, or both to produce complete stand descriptions (height, diameter, live-crown-ratio, species, and tree expansion factor) for use in the conifer growth and yield simulator, CACTOS[2]. Complete 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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[1] STAG is an acronym for Forest STAnd Generator for Mixed Conifer Species © U.C. Regents

[2] CACTOS is an acronym for CAlifornia Conifer Timber Output Simulator © U.C. Regents

ACKNOWLEDGMENTS

The **STAG** program represents the collective efforts of many people over five years. This work would not have been accomplished in a timely manner without the financial and technical support of the industry cooperators listed on the front page of this manuscript or of 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 shared responsibilities in guiding Paul's thesis work and for having a clear vision of how this simulator could best be structured to maximize its utility and function. His support has helped us to produce a totally new architecture and design for STAG.

We have had many good people work on this project that 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. For version 3.0, **Timothy A. Robards** developed the new and efficient algorithms for parameter estimation of the Weibull distribution used in the stand generation routines. To all 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, Daugherty, and Meerschaert (1986), Wensel, Meerschaert, and Biging (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 number of trees per acre 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, 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) to convert stand table data, numbers of trees by DBH classes and species, to individual tree records are described in Biging and Robards (1987) and Van Deusen (1984).

STAG is written in standard FORTRAN 77 code (ANSI, 1978) and is operational on the following systems:

(1) IBM-PC compatibles under MS-DOS v2.1 and higher
(2) Apple Macintosh personal computers
(3) Data General Mini-computers under AOS/VS

The general structure of STAG is illustrated in figure 1. The components are treated in detail in sections which follow.

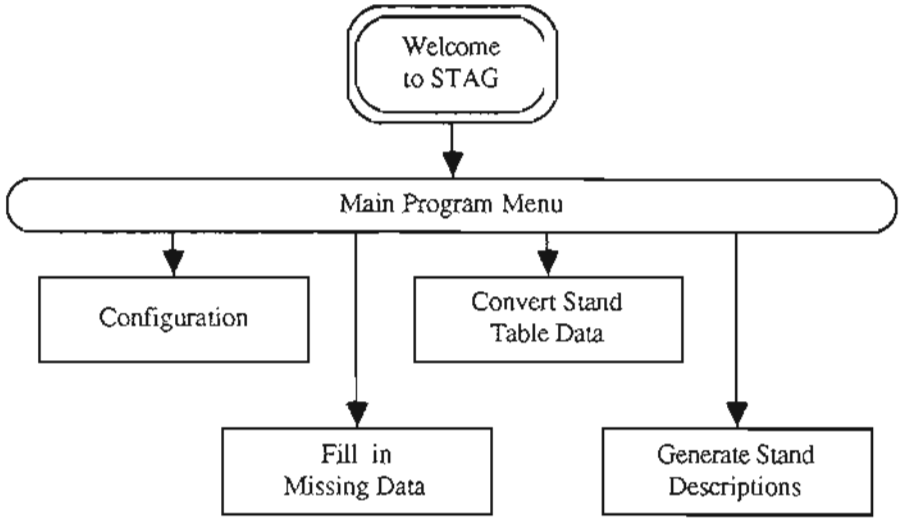

Figure 1. Structure of the components of STAG.

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.

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 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 may be incomplete, as STAG is designed to fill in missing heights and crown ratios. 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 that can be used for growth and yield projection in CACTOS

Other output files which can be created by STAG include:

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

(3) the report file used to save information selected by the user during the course of the simulation (optional). The report commands that can be selected are discussed in section II.B. and IV.D.

(4) a file containing height coefficients 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. Be aware that 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

.sdm stand description which utilized the missing data routines of STAG to estimate missing values

.sdg stand description created in STAG using the stand generation routines

.srp STAG report file

STAG has special filenames that are reserved and should be avoided by the user. These include: "exp1", "exp2", "exp1.low", "exp2.low", and "stbin". These reserved filename 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 an incomplete stand description input file and fills in missing data to provide a complete description. A complete stand description input file must have the structure presented below, but with an incomplete stand description values for total height and/or live crown ratio may be missing.

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 below for a summary of the data requirements for the stand description files when there is missing data and for converting stand table data and 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 indicators are shown in the following table:

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

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 has the following five items (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

There are fourteen species that STAG recognizes on input. These species are listed in Table 2.

Table 2. Species codes and names using in STAG.

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

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

[3] Live crown ratio is defined as (H-HCB)/H where H=total height and HCB=height-to-crown base.

Table 3. Species groups used for modelling in STAG.

Group No.	Species Group	Species Included in Group
1	Ponderosa Pine (PP)	ponderosa pine, jeffrey pine, lodgepole pine
2	Sugar Pine (SP)	sugar pine, white pine
3	Incense Cedar (IC)	incense cedar
4	Douglas-fir (DF)	Douglas-fir, miscellaneous conifers
5	White Fir (WF)	white fir
6	Red Fir (RF)	red fir
7	Other Hardwoods (OH)	all hardwoods except black oak (note that the equations were derived mainly from chinquapin and tanbark oak)
8	Black Oak (BO)	black oak

II.B. Report File

In addition to the completed stand description files, one or more report files 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:

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 Robards, 1987) 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 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 of these cases, 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 a pseudo-Bayesian approach or an ad-hoc 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 (1983) and Biging and Robards (1987) for more information on the updating procedure.

STAG, unlike CACTOS, allows four different types of tree height measurements: total heights, heights to a merchantable top ($\leq$6.5 in.), or heights measured to whole (16.5 ft.) or half logs (8.25 ft.). Within a STAG stand description file all heights must be of the same measurement standard. For the six major conifer species (species group numbers 1-6) STAG, using a taper equation, solves 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 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 techniques within STAG.

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

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 tree list so produced 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. This procedure also 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. This procedure 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 projection system. It also can be used to produce stand descriptions so that investigation of forest growth dynamics can be performed in the absence of data. While this is not a generally recommend procedure, it can be important when the manager is evaluating the performance of stands that currently do not exist, but which he or she may whish to establish in the future. These hypothetical stands can easily be created within the interactive environment of STAG. It is possible to iteratively generate various components of the stand until the user has built a stand matching the desired description. See Appendix B for a demonstration of how this interactive process can be used. The information required to create a stand description 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.

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 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

Argument	Use
>output	cause output to go to file "output", automatically overwriting file if it already exists.
>>output	cause output to go to file "output", automatically append file if it already exists.
<input	cause input to come from file "input", if "input" does not exist, another file will be prompted for.
p=plist	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 listy can include ranges. For example, the following command will produce diameter distributions for the plots listed: `md:dt p=1,2,3,8-14,18,21-45` Note that the plots listed in *plist* do not have to appear in any special order.
s=slist	cause operation to be performed on species specified in *slist*. The same rules apply for *slist* as apply for *plist*.
o=s | r | b	cause output from procedure to be routed to the [s]creen, [r]eport file, or [b]oth. Specify only one letter for this argument.
nomore	cause output going to screen not to stop at each screenful of data.

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 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 working directory from which it started.

IV.C. The configuration routine

The commands available to the user while within the configuration routine are summarized below 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 to default parameters. 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-Bayes or ad hoc parameter update methods described under the section on missing data. In this case, the user may have used the updated coefficients to work with a particular set of data, but now wants to work with different data not requiring updated coefficient values.

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

The configuration routine menu uses the prompt "config:" and contains the following commands:

Command	Description of the command function
`bm`	Set the board foot minimum DBH. The default value is 8.0 inches.
`bt`	Set the board foot merchantable top to a value of 6 or 8 inches. The default value is 6 inches.
`cm`	Set the cubic foot minimum DBH. The default value is 0.0 inches.
`ct`	Set the cubic foot minimum DBH. The default value is 8.0 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 routine. 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 500 tree records with random variation built into the tree list.
`pc`	Print the list of available commands.
`ps`	Print the current configuration status.
`rc`	Reset to default the configuration parameters. 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 to default the height equation parameters.
`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.
`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).
`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.

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. The commands available to the user varies by the particular routine that is in effect. Table 6 summarizes the palette of commands available within the three data manipulation routines.

Table 6. Command summary for the data manipulation routines.

Command	Options of the command (listed parenthetically) / Description of the command function	Routines from which the command can be invoked
ab		**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.	
da	[p=plist]	**da**
	Invoke the distributional apportionment routine which converts stand tables into complete tree lists.	
dp	[r=skip] [o=s|r|b] [s=slist] [p=plist] [nomore] [<input] [>output]	**md sg da**
	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.	
dt	[o=s|r|b] [s=slist] [p=plist] [nomore]	**md sg da**
	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.	
ex		**md sg da**
	Exit the missing data routine and save the tree list.	
md	[p=plist]	**md**
	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. 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.	

Table 6 continued.

Command	Options of the command (listed parenthetically) / Description of the command function	Routines from which the command can be invoked
pc		md sg da
	Print a list of the available commands.	
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. Graphs created by this command may be saved in the report file.	
rh		md
	Reset the height coefficients to the default values supplied with the program.	
rp	[>|>>output]	md sg da
	Open a report file.	
rt		md sg da
	Restore internally saved plots. Plots saved using the sv command can be restored by the user. This can be useful, say, when the users initially save the files before invoking the missing data routine. If after using, say, the adhoc method of updating height coefficients the user does not like the results 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 that STAG recognizes.	
sg		sg
	Add a species to the generated plot. This feature allows the user to generate a stand description for multiple species. 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(s) indicating average DBH, stems/acre, basal area/acre, and cubic and board foot volumes/acre by species groups. Tables created by this command may be saved in the report file.	

Table 6 continued.

Command	Options of the command (listed parenthetically) / Description of the command function	Routines from which the command can be invoked
sv		md sg da
	Internally save the plots in memory (stand description). Stand descriptions saved in this fashion can be restored using the **rt** command.	
uh	[>output]	md
	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.	

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
line    |1234567890123456789012345678901234567890123456789012345678901234567890
   1    |plot num 1                    29      4500
   2    | 100.  95.  70.  90.  85.                                          70.
   3    |   0.   0.   0.   0.   0.                                          0.
   4    |   1.000   6.000  40.300   0.      2.600
   5    |   1.000  10.000   0.      0.      2.600
   6    |   1.000  18.000 100.900   0.      1.200
   7    |   2.000   8.000   0.      0.      2.400
   8    |   2.000  10.000  49.900   0.      4.700
   9    |   2.000  14.000  75.600   0.      2.400
  10    |   2.000  16.000  81.200   0.      1.900
  11    |   2.000  36.000 138.900   0.      0.400
  12    |   2.000  38.000 152.100   0.      0.400
  13    |   2.000  42.000 150.000   0.      0.200
  14    |   2.000  44.000 145.700   0.      0.200
  15    |   2.000  46.000   0.      0.      0.400
  16    |   3.000   4.000   0.      0.     35.300
  17    |   3.000   6.000   0.      0.     24.700
  18    |   3.000   8.000   0.      0.     10.600
  19    |   3.000  10.000   0.      0.      3.500
  20    |   3.000  16.000   0.      0.      1.400
  21    |   3.000  18.000   0.      0.      0.800
  22    |   3.000  20.000   0.      0.      0.800
  23    |   3.000  22.000   0.      0.      0.300
  24    |   3.000  26.000   0.      0.      0.300
  25    |   3.000  28.000   0.      0.      0.300
  26    |   3.000  30.000   0.      0.      0.500
  27    |   3.000  34.000   0.      0.      0.500
  28    |   3.000  36.000   0.      0.      0.300
  29    |   3.000  38.000   0.      0.      0.500
  30    |   3.000  40.000   0.      0.      0.300
  31    |   3.000  44.000   0.      0.      0.500
  32    |   3.000  50.000   0.      0.      0.300
```

A.2.. Stand description for Distributional Apportionment

```
        Column
                 1         2         3         4         5         6         7
line    12345678901234567890123456789012345678901234567890123456789012345678901234567890
  1     dist. app. plot 1                  10     4500
  2      100. 100.   0.   0.   0.   0.   0.   0.   0.   0.   0.   0.   0.   0.   0.
  3       40.  50.   0.   0.   0.   0.   0.   0.   0.   0.   0.   0.   0.   0.   0.
  4         1.000  10.000    .000    .000  10.000
  5         1.000  12.000    .000    .000  10.000
  6         1.000  14.000    .000    .000  10.000
  7         1.000  16.000    .000    .000  10.000
  8         1.000  18.000    .000    .000  10.000
  9         2.000  14.000    .000    .000  10.000
 10         2.000  16.000    .000    .000  10.000
 11         2.000  18.000    .000    .000  10.000
 12         2.000  20.000    .000    .000  10.000
 13         2.000  22.000    .000    .000  10.000
 14     dist app plot 2                    12     4500
 15         0. 100.   0. 110.  99.   0.   0.   0.   0.   0.   0.   0.   0.   0.   0.
 16         0.  50.   0.  10.   0.   0.   0.   0.   0.   0.   0.   0.   0.   0.   0.
 17         5.000   6.000    .000    .000  20.000
 18         5.000   8.000    .000    .000  20.000
 19         5.000  10.000    .000    .000  20.000
 20         5.000  12.000    .000    .000  20.000
 21         5.000  14.000    .000    .000  20.000
 22         2.000  14.000    .000    .000  10.000
 23         2.000  16.000    .000    .000  10.000
 24         2.000  18.000    .000    .000  10.000
 25         2.000  20.000    .000    .000  10.000
 26         2.000  22.000    .000    .000  10.000
 27         4.000  24.000    .000    .000   5.642
 28         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 3.2
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                  enter "return" to continue


          The STAnd Generator for mixed conifers

                             by
                   Greg S. Biging    Lee C. Wensel

     Walter J. Meerschaert, Paul C. Van Deusen, and Timothy A. Robards
              Department of Forestry and Resource Management
                   University of California, Berkeley
          A Product of the Northern California Forest Yield Coop.

                        Industry Members

American Forest Products          The Hearst Corp.
Beaty and Associates              Louisiana-Pacific Corp.(Elk Creek)
Champion International Corp       Louisiana-Pacific Corp. (Feather Falls)
Crane Mills Lumber Co.            Louisiana-Pacific Corp. (Sonora)
Diamond Land Co.                  Michigan-California Lumber Co.
Fruit Growers Supply              Santa Fe Pacific Timber Co.

Research conducted under AES projects 3679-ms and 3815-ms.


                  enter "return" to continue


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

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

```
stag:cf
```

Enter the configuration routine.

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

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

         - CURRENT CONFIGURATION STATUS -

   re - Add random errors.................ON
        Height coefficients..............DEFAULT
   sk - Title page skip..................OFF
   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"
   hc - Highlight Code................... 3
```

Current status is printed automatically.

```
config:pc
```

Print commands.

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

   bm - set board foot minimum DBH
   bt - set board foot merchantable top
   cm - set cubic foot minimum DBH
   ct - set cubic foot merchantable top
   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

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

These options are available on routines that use files.

```
 config:bm
```

Set the board foot minimum DBH.

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

config:bt
```

Set the board foot merchantable top.

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

config:cm
```

Set the cubic foot minimum DBH.

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

```
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


config:re


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


config:sk

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


config:sc


Current configuration saved in: STBIN



config:ex

 Exiting initialization routine


stag:ex

stag: user termination
```

Set the cubic foot merchantable top.

Set the max. number of records produced in distributional apportionment.

Set flag to add or not to add random errors to height and crown estimates.

Set the title page skip for future runs.

Save the current configuration in the STAG file "stbin".

B.2. Filling in Missing Data

```
 STAG version 3.2    July 27, 1987
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 Release number: 00000

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

Header with title skip.

```
stag:md

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

Enter missing data routine.

```
 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.out

 Reading  29 tree records from : missing data demo

 Read in     1 plots containing      29 tree records

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

Specify input and output files.

```
md:md

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

Fill in missing data.

```
md:dp

 Display tree records
   plot label : missing data demo

  no.   sp    dbh    ht     cr      exp
-----------------------------------------
   1    PP    6.5    40.  .494     2.64
   2    PP   10.7    53.  .430     2.670
   3    PP   18.8   100.  .454     1.281
   4    SP    8.4    43.  .432     2.453
   5    SP   10.2    49.  .419     4.799
   6    SP   14.6    75.  .434     2.465
   7    SP   16.3    81.  .426     1.928
   8    IC   36.0   138.  .413      .446
   9    IC   38.2   152.  .421      .458
  10    IC   42.5   150.  .397      .205
  11    IC   44.0   145.  .382      .237
```

Display the tree list.

Notice that the filled in data are highlighted.

```
  12    DF  46.9  154.  .236     .465
  13    CH   6.5   26.  .338   35.354
  14    HW   6.    25.  .338   24.757
  15    WF   8.6   46.  .401   10.628
  16    WF  10.4   54.  .396    3.549
  17    WF  16.3   78.  .373    1.485
  18    WF  18.2   85.  .365     .822
  19    WF  20.4   92.  .356     .843
  20    LP  22.5   92.  .371     .320
  21    LP  26.7  104.  .352     .354
  22    LP  28.4  108.  .345     .343
  23    LP  30.4  113.  .337     .512
  24    JP  34.8  124.  .319     .555
  25    CH  36.6   80.  .267     .326
  26    CH  38.5   83.  .264     .549
  27    SP  40.2  140.  .337     .348
  28    SP  44.3  149.  .327     .554
  29    SP  50.8  163.  .312     .325
```

```
md:rp  >demo.rp

 Report file in use named: demo.rp
```

Open a report file named demo.rp, 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
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, use 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
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    0. |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

           STOCK TABLE
           -----------
 Plot label = missing data demo

  species       dbar     tpa   basar   cfvol  bdvol
  ---------------------------------------------------

  Pond. Pine   14.68      7.     8.4     .26    1.51
  Sugar Pine   18.06     13.    22.9     .80    5.39
  Cedar misc   39.27      1.    11.3     .42    3.55
  Douglas Fir  33.12      2.    11.9     .47    3.37
  White Fir    11.24     17.    11.9     .29    1.28
  Chinquapin    8.70     36.    15.0     .39     .00
  H.W. misc     6.40     25.     5.5     .03     .00
  Totals       12.52    102.    87.0    2.67   15.11
```

Print a stock table.

```
md:es  >>mddemo.es
```

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

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

```
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
```

Parameter update using local data.

```
md:rx  <mddemo.uh
```

This is how you would use the updated coefficients in a later run. STAG already has the updated coefficients in memory for this run.

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

```
md:rh
```

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

```
Height coefficients reset to default
```

```
md:ex
```

"ex" quits and saves the plots in memory, "ab" quits and aborts the plots in memory so no save occurs.

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

stag:ex

stag: user termination
```

B.3. Distributional Apportionment

```
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Release number: 00000

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

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

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

```
     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
```

```
da:dp
```

Look at stand tables loaded into memory.

```
 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
```

```
 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

 Creating tree list from stand table on plot : dist. app. plot 2
```

Create the stand descriptions.

```
da:dp  p=1

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

  no.  sp   dbh    ht     cr      exp
-------------------------------------
   1   PP    9.0    45.   .599    2.128
   2   PP    9.2    55.   .418    3.272
   3   PP   10.8    63.   .742     .871
   4   PP   10.1    56.   .519    3.666
   5   PP   10.0    58.   .333     .062
   6   PP   11.8    55.   .370     .113
   7   PP   12.1    64.   .753     .219
   8   PP   12.8    64.   .567    6.238
   9   PP   11.6    62.   .350     .794
  10   PP   11.3    66.   .579    1.922
  11   PP   12.3    70.   .370     .714
  12   PP   14.0    58.   .429     .379
  13   PP   14.0    59.   .297     .251
  14   PP   15.0    73.   .558    3.000
  15   PP   14.3    68.   .353    5.491
  16   PP   14.4    79.   .670     .144
  17   PP   13.7    83.   .470     .736
  18   PP   15.8    65.   .600     .223
  19   PP   15.7    73.   .440    2.210
  20   PP   16.6    67.   .232     .100
  21   PP   15.8    76.   .549     .174
  22   PP   16.8    82.   .522    6.189
  23   PP   16.2    80.   .363     .963
  24   PP   16.7    93.   .546     .098
  25   PP   16.2    91.   .504     .044
```

Look at the new list of trees for the first plot.

```
  26    PP  17.5   66.  .344    .048
  27    PP  18.0   78.  .468   3.462
  28    PP  17.5   79.  .306   2.748
  29    PP  18.3   92.  .567   1.175
  30    PP  18.0   87.  .433   2.566
  31    SP  14.1   59.  .435    .637
  32    SP  14.2   61.  .421    .268
  33    SP  14.1   65.  .560   2.968
  34    SP  14.7   73.  .478   5.649
  35    SP  13.0   77.  .619    .045
  36    SP  14.1   79.  .456    .433
  37    SP  15.3   67.  .488    .374
  38    SP  15.5   66.  .407   2.555
  39    SP  15.8   69.  .230    .054
  40    SP  15.6   81.  .580    .131
  41    SP  16.7   83.  .484   5.993
  42    SP  16.7   77.  .351    .847
  43    SP  15.7   92.  .566    .046
  44    SP  17.2   70.  .500    .050
  45    SP  17.6   82.  .508   4.308
  46    SP  18.3   80.  .408   2.198
  47    SP  18.7   87.  .497   1.045
  48    SP  18.1   87.  .451   2.400
  49    SP  19.9   75.  .501    .233
  50    SP  19.5   78.  .386    .378
  51    SP  19.1   93.  .524    .890
  52    SP  20.7   94.  .443   7.569
  53    SP  20.1   88.  .279    .204
  54    SP  21.0  103.  .544    .618
  55    SP  19.8  100.  .355    .108
  56    SP  23.0   93.  .541    .081
  57    SP  21.4   94.  .490   3.018
  58    SP  22.3   87.  .357    .356
  59    SP  22.0  103.  .476   4.024
  60    SP  21.9  102.  .364   2.480
  61    SP  22.5  110.  .454    .041
```

```
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
```

Looks good, let's quit.

```
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Release number: 00000

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

```
stag:sg
```

Enter the stand generation routine.

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

 Open the output tree list file
 Enter a file name here:sgdemo.sd

 Enter a plot description (20 char max):demo s. g. plot

 Enter the elevation of this plot:3500

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

Start generating species with some small white fir.

```
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)...(5-500)

 Enter here (separated by commas):5,50,170

 Enter the site index of this species:88


   Species.................White Fir
   Quadratic mean DBH...... 7.3
   Predicted average DBH... 7.5
   Number of trees > 6"....170

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

white fir
50 ft^2 BA
170 TPA
site index 88.

```
 Developing Weibull distribution ...

 Filling in diameters ...

    Total plot basal area...  50.
    Total number of trees... 170

 Filling in missing data on: demo s. g. plot
```

Look at the results in a diameter distribution plot.

```
sg:dt

       Print diameter distribution

Plot label : demo s. g. plot
All species combined

 dbh   trees |             30             60             90
             ..................................................
0 - 2     0. |
2 - 4     0. |
4 - 6    27. |11111111111111
6 - 8   101. |11111111111111111111111111111111111111111111111111
8 -10    41. |11111111111111111111
10-12     1. |1
------------
total   170.
```

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

```
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)...(5-330)

 Enter here (separated by commas):1,200,100

 Enter the site index of this species:99


   Species.................Pond. Pine
   Quadratic mean DBH......19.1
   Predicted average DBH...18.7
   Number of trees > 6"....100
```

Now lets add some residual pine trees.

ponderosa pine
200 ft^2 BA
100 TPA
site index 99.

Av. DBH is 18.7 in.

```
[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)...(5-330)

Enter here (separated by commas):1,200,50

Enter the site index of this species:99


  Species.................Pond. Pine
  Quadratic mean DBH......27.1
  Predicted average DBH...26.5
  Number of trees > 6".... 50

  [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)...(5-330)

Enter here (separated by commas):1,200,25

Enter the site index of this species:99


  Species.................Pond. Pine
  Quadratic mean DBH......38.3
  Predicted average DBH...38.0
  Number of trees > 6".... 25

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

Developing Weibull distribution ...

Filling in diameters ...

   Total plot basal area... 250.
   Total number of trees... 195

Filling in missing data on: demo s. g. plot
```

We don't like the size of the trees, we try to make them larger by decreasing the number of trees per acre.

Av. DBH is 27.1 in.

Av.DBH is still not large enough.

Av.DBH is 38.3 in.

This is what we think we want.

```
sg:dt

       Print diameter distribution

Plot label : demo s. g. plot
All species combined

 dbh  trees |             30             60             90
            ..................................................
0 - 2    0. |
2 - 4    0. |
4 - 6   27. |111111111111111
6 - 8  101. |1111111111111111111111111111111111111111111111111111
8 -10   41. |11111111111111111111
10-12    1. |1
12-14    0. |
14-16    0. |
16-18    0. |
18-20    0. |
20-22    0. |
22-24    0. |
24-26    0. |
26-28    1. |1
28-30    1. |1
30-32    1. |1
32-34    0. |
34-36    2. |11
36-38    5. |111
38-40    5. |111
40-42    4. |11
42-44    2. |1
44-46    3. |11
46-48    1. |1
------------
total  195.


sg:rt

 Restoring plot information
```

Look at the result.

We decided that this really isn't what we wanted, so we went back to the internally saved tree list and started over from there.

```
sg:dt

       Print diameter distribution

Plot label : demo s. g. plot
All species combined

 dbh   trees |             30              60              90
             ..................................................
0 - 2     0. |
2 - 4     0. |
4 - 6    27. |111111111111
6 - 8   101. |1111111111111111111111111111111111111111111111111111
8 -10    41. |11111111111111111111
10-12     1. |1
------------
total   170.
```

We will put the pine in at the middle diameter estimate we found above.

```
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)...(5-330)

 Enter here (separated by commas):1,200,50

 Enter the site index of this species:99


   Species.................Pond. Pine
   Quadratic mean DBH......27.1
   Predicted average DBH...26.5
   Number of trees > 6".... 50

   [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 s. g. plot
```

```
sg:dt

       Print diameter distribution

Plot label : demo sg plot
All species combined

 dbh  trees |             30              60              90
            ..................................................
2 - 4    0. |
4 - 6    0. |
6 - 8    3. |11
8 -10    6. |111
10-12   24. |111111111111
12-14   70. |11111111111111111111111111111111111
14-16   59. |1111111111111111111111111111111
16-18    8. |1111
------------
total  170.
```

We will put the pine in at the middle diameter estimate we found above.

```
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)...(5-330)

 Enter here (separated by commas):1,200,50

 Enter the site index of this species:99


   Species.................Pond. Pine
   Quadratic mean DBH......27.1
   Predicted average DBH...26.5
   Number of trees > 6".... 50

   [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
```

```
sg:dt

        Print diameter distribution


Plot label : demo s. g. plot
All species combined

 dbh  trees |             30             60             90
            ..................................................
0 - 2    0. |
2 - 4    0. |
4 - 6   27. |111111111111111
6 - 8  101. |1111111111111111111111111111111111111111111111111111111
8 -10   41. |11111111111111111111
10-12    1. |1
12-14    1. |1
14-16    2. |1
16-18    2. |1
18-20    3. |11
20-22    3. |11
22-24    5. |111
24-26    3. |11
26-28   15. |11111111
28-30    4. |11
30-32    6. |111
32-34    4. |11
34-36    1. |1
36-38    1. |1
-----------
total  220.
```

Look at the results again.

```
sg:pf

       Print stand profile

Plot label : demo s. g. plot
All species combined

                  feet above ground
 DBH   Trees |    24    48    72    96   120   144   168   192
             ..................................................
0 - 2     0. |
2 - 4     0. |
4 - 6    27. |====>>>>>>
6 - 8   101. |=====>>>>>>
8 -10    41. |======>>>>>>>>
10-12     1. |=======>>>>>>>>>
12-14     1. |========>>>>>>>>>>>
14-16     2. |=========>>>>>>>>>>>>
16-18     2. |==========>>>>>>>>>>>>
18-20     3. |==========>>>>>>>>>>>>>
20-22     3. |===========>>>>>>>>>>>>>
22-24     5. |============>>>>>>>>>>>>>>
24-26     3. |=============>>>>>>>>>>>>>>
26-28    15. |==============>>>>>>>>>>>>>>
28-30     4. |===============>>>>>>>>>>>>>>>
30-32     6. |================>>>>>>>>>>>>>>>
32-34     4. |=================>>>>>>>>>>>>>>>>
34-36     1. |==================>>>>>>>>>>>>>>>>
36-38     1. |===================>>>>>>>>>>>>>>>>
------------
total  220.
```

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

```
sg:ex

 Saving tree list for plot : demo s. g. plot

stag:ex

stag: user termination
```

When we like what we see, we can quit , note that we can also do an external save at any point and then go back to a previously internally saved condition.