



Northern California Forest Yield Cooperative

Department of Forestry and Resource Management

University of California, Berkeley, Ca. 94720

\$5.00

Research Note No. 11

April 15, 1985

STAG

A STAnd Generator for Mixed Species Stands

Version 2.0

by

Paul C. Van Deusen and Greg S. Biging

Abstract

STAG is an interactive computer program designed to provide estimates of missing tree characteristics encountered in processing inventory tree lists or to produce a hypothetical tree list based solely on stand descriptors. The completed tree lists (DBH, total height, crown ratio and tree weight for each tree) are used as input to the Northern California Forest Yield Cooperative growth simulator CACTOS ^{*/}. Thus, STAG serves as a preprocessor to CACTOS ensuring that all data sets destined for use in CACTOS are complete. There are several user specified options for modifying the way in which missing data are replaced with model estimates and for localizing predictive equations. This program is written in standard FORTRAN 77 code and is running on the University's Vax 11/780 computer system and IBM PC compatible personal computers.

^{*/} CACTOS is an acronym for CALifornia Conifer Timber Output Simulator. Special thanks goes to Peter J. Daugherty for his help in developing the user's guide, sample runstreams and improving the computer program, and to Vaughn Landrum for his programming assistance. Additionally, Lee C. Wensel is to be acknowledged for his help in guiding Paul Van Deusen's thesis research and study design. This research was supported in part by the Northern California Forest Yield Cooperative and McIntire-Stennis Project 3679-MS.

DISCLAIMER

This document and associated software was prepared as part of a project under the auspices of the University of California. The University of California nor any of their employees make any warranty, expressed or implied, or assumes any legal liability or responsibility for the accuracy, completeness, or usefulness of any information, product, or process disclosed. Reference herein to any specific commercial product, process, or service by trade name, trademark, manufacturer, or otherwise, does not necessarily constitute or imply its endorsement, recommendation, or favoring by the University of California. The views and opinions of authors expressed herein do not necessarily state or reflect those of the University of California thereof, and shall not be used for advertising or product endorsement purposes.

Table of Contents

Abstract	cover
I. Introduction to STAG	1
A. STAG routines	1
B. Special features of the options	2
C. Parameter updates	4
D. STAG prediction equations	5
II. STAG user's guide	9
A. Generating hypothetical stands	9
B. Generating values for missing data	11
C. Program termination messages	16
Literature cited	17
User Notes	18
Appendix 1	19
STAG sample runstreams	21

INTRODUCTION TO STAG

The Northern California Forest Yield Cooperative (NCFYC) stand generator for mixed species stands (STAG) provides for complete and partial generation of tree characteristics for the following eight species groups:

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 (but the equations were derived mainly from chinquapin and tanbark oak)
8	Black Oak (BO)	black oak

STAG is specifically designed to provide complete tree lists (DBH, total height, crown ratio, and tree weight for each tree) for input to the NCFYC growth simulator CACTOS. For information on the use of CACTOS see Wensel and Daugherty (1985).

A. STAG Routines

The theory behind STAG was developed as part of Paul Van Deusen's Ph.D. dissertation (1984), and the discussion herein concentrates on the applications of STAG. STAG provides for the following options:

OPTION 1) Generation of missing heights and /or crown ratios when tree DBH, stand basal area and plot elevation are known. Random errors can optionally be added to better simulate the variability found in nature.

OPTION 2) Complete generation of mixed species stands of trees. STAG generates diameters, heights, and crown ratios for each tree and requires the user to supply stand elevation, per acre basal area (>5.5 inches DBH) by

species and per acre number of trees (>5.5 inches DBH) by species. Random errors can be optionally added to the predicted heights and crown ratios.

OPTION 3) Generation of a hypothetical list of individual trees when only the numbers of trees by species and diameter classes are known. Through a process termed **distributional apportionment** (see chapter 6 of Van Deusen's dissertation), 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 of each generated tree (see Appendix I). 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.

B. Special Features of the Options

The STAG program expects the input data to be formatted the same as CACTOS stand description input files. Users may use the stand description entry program, ENTRY, to prepare files for STAG (see Res. Note #10, chapter 4). STAG, unlike CACTOS, allows four different types of height measurements: total heights, heights to a merchantable top (≤ 6.5 in.), or heights measured to whole (16.5 ft.) or half logs (8.25 ft.). Within a STAG file all heights must be of the same measurement standard. For the six major conifer species ^{1/} STAG, using a taper equation, solves for total

^{1/} The six major conifer species are Ponderosa Pine, Sugar Pine, Incense Cedar, Douglas-fir, White fir and Red Fir. NOTE: The height conversion process is not intended to encourage the measurement of other than total height. Rather, it is intended to allow the use of older inventory data.

height whenever height to a merchantable top or number of 16.5 ft. logs is supplied. 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). If multiple stand descriptions (plots) are read in, a determination of the type of tree heights recorded on the first plot is made and used for subsequent plots. Thus, height must be measured to the same standard on each plot of a multiple plot file for STAG. If no heights or live crown ratios are present in the file, either Option 1 (Generation of missing heights and/or live crown ratios) can be used to supply estimates of the missing values using predictive equations based upon the permanent plot data base (see Appendix 1), or alternatively, Option 3 (Distributional apportionment) can be used to "fill in" missing data. However, if Option 3 is chosen, the data is treated as diameter class data and the complete tree list generated will not contain the original data points, but rather pseudo-individual trees within plus or minus one inch of the original diameter (see Appendix 1). Thus, when you only want to "fill in" missing heights and/or crown ratios use Option 1. When Option 1 is used, the program will allow the input file to contain multiple stand descriptions (i.e. plots). Thus missing heights and/or crown ratios can be generated for more than one stand description in a single STAG run. Distributional apportionment (Option 3) is allowed only if one stand description (i.e. plot) at a time is read in.

Random (Stochastic) Errors

When using Option 1 or Option 2 you can either make a deterministic or a stochastic prediction of missing values. Choosing random errors means that a stochastic value will be added to the prediction to reflect that an individual tree's dimensions cannot be predicted with certainty. Thus, a random value will be added or subtracted from the prediction (see Appendix 1). The random value is drawn from a normal distribution with mean zero and variance proportional to the predicted value. If random errors are not requested, then the missing value is set equal to the model prediction (deterministic prediction). If random errors are not added, all predicted heights and crown ratios will be identical for a given diameter of a particular species, given that basal area and elevation are the same.

C. Parameter Update for Height Predictive Equations

The program allows for parameter update procedures which are discussed in chapters 3 and 5 of Van Deusen's dissertation. These procedures allow the user to adjust several parameters of the height prediction equation (the intercept and slope coefficient for the square root of DBH) to conform to a subsample of measured heights and diameters which they would input. The parameter update procedures are:

0 = None This option means to use the default parameter values given in tables 1 and 2.

1 = Pseudo Bayes Specifying this option is equivalent to estimating the height equation parameters from your local data and forming a weighted average of these local parameters with the program's default parameters. The weights are functions of the estimated variance of the estimated parameters.

2 = ADHOC Local parameter values are estimated and new parameters (parm) are formed as follows:

$$\text{new parm} = K * (\text{local parm}) + (1-K) * (\text{default parm})$$

The value of K must be between 0 and 1 and is supplied by the user. If K=1 then the local data totally determines the new parameter value.

In general, the ADHOC method should be used when the user can translate their degree of confidence in the local height data into a value between 0 and 1. Use the Pseudo-Bayes method when you are uncertain about the local data, because this procedure is conservative in adjusting the program's default parameter values. Use the default parameter values (no update) when the local data is poor.

Updated parameters of the height prediction equation can be saved and used as input for later runs. However, multiple updates are not allowed as the procedure was not developed for this purpose. If parameters are to be saved it would make sense to base them on a number of plots from a particular region or timber type. The program currently allows 50 plots to be read in at one time. All of this information can then be used in updating the height equation parameters.

D. STAG Prediction Equations

The total height (H) prediction equation for trees ≥ 5.5 inches DBH is:

$$[1] \quad H = b_0 + b_1\sqrt{D} + b_2\sqrt{B} + b_3E^2$$

where,

b_0, b_1, b_2, b_3 , are species specific coefficients give in Table 1

D = tree DBH (in.)

B = stand basal area (sq. ft.) in trees > 5.5 inches, and

E = elevation (ft.)

Note that during the parameter update procedure only b_0 and b_1 can be localized to conform to a subsample of measured heights and diameters.

Table 1: Coefficients estimates by species group for equation [1]

Species Group	$S_{y,x}$ (ft)	N	b_0	b_1	b_2	b_3
PP	12.1	712	-38.15	28.01	1.53	-8.205E-7
SP	11.7	712	-38.70	28.49	1.04	-6.212E-7
IC	10.0	712	-28.29	21.74	0.84	-5.941E-7
DF	11.9	712	-33.09	27.57	1.04	-5.516E-7
WF	10.9	712	-46.61	30.29	1.15	-5.863E-7
RF	10.8	418	-39.09	28.88	0.77	-4.392E-7
OH	13.5	287	-44.99	18.56	2.36	-5.290E-9
BO	13.9	287	-11.77	15.10	1.57	-6.021E-7

The predicted height of trees less than 5.5 inches at DBH, although not presented here, is constrained to be between 4.5 feet and the height of a 5.5 inch DBH tree as predicted by equation [1] (see dissertation pages 19 and 20).

The height-to-crown-base (HCB) prediction equation is:

$$[2] \quad HCB = H \left[1 - e^{-(c_0 + c_1 \ln(B) + c_2 D/H)^2} \right]$$

where,

H = the total tree height (ft.)

B = stand basal area (sq.ft.) in trees > 5.5 inches DBH

D = tree DBH (in.)

ln = natural log

c_0, c_1, c_2 are species specific coefficients given in Table 2

Table 2: Coefficients estimates by species group for equation [2]

Species Group	$S_{y,x}$ (ft)	N	c_0	c_1	c_2 ^{2/}
PP	11.5	706	0.895	0.046	-1.543
SP	11.1	706	0.619	0.035	0
IC	9.6	706	0.532	0.050	0
DF	11.8	706	0.534	0.086	-1.147
WF	11.3	706	0.403	0.069	0
RF	11.3	407	0.892	0	-.458
OH	10.2	281	0.606	0.047	0
BO	10.7	281	0.825	0.8E-6	0

Further information on the development of the equations [1] and [2] can be found in Van Deusen's (1984) dissertation, chapter 2.

^{2/} For five species groups (SP, IC, WF, OH, and BO), the coefficient C_2 was estimated to be zero, thus reducing the predicted height-to-crown-base to total height times a constant where the constant is a function of stand basal area. When live crown ratios of individual trees are calculated for these species, the formula $LCR=1-(HCB/H)$ reduces to $LCR=1-(HK/H)$ or $LCR=1-K$, where K is a constant dependent on the stand basal area. Thus, for each of these species the predicted live crown ratio will be a constant varying by species. To induce variability into the prediction of live crown ratios, the user must select random (stochastic) errors when generating data for use in CACTOS simulations.

The equation used to convert merchantable height (MH) to total height (H) for the six major conifer species is derived from a sigmoid taper equation (Biging, 1983). The equation is:

$$[3] \quad H = \frac{MH(\lambda)^3}{[1 - \exp((d/D - b_1)/b_2)]^3}$$

where,

$$\lambda = 1 - \exp(-b_1/b_2)$$

H=the estimated total tree height (ft.)

D=the tree DBH (in.)

d=the merchantable top diameter (< 6.5")

MH=the height to the merchantable top diameter (ft.)

$\exp(x)$ =2.71828... raised to a power of 'x'

b_1, b_2 are species specific coefficients given in Table 3

Table 3: Coefficients estimates by species for equation [3]

Species	N	b_1	b_2
PP	2014	1.019589	0.335666
SP	692	1.06932	0.415632
IC	541	1.071343	0.472157
DF	1588	1.029288	0.334012
WF	2645	1.092615	0.365295
RF	312	1.075880	0.353784

If the heights of trees are entered as number of logs, the program first converts these to heights to the given merchantable top using equation [4], and then uses equation [3] to predict total heights. The equation to estimate height to the merchantable top (MH) is given by:

$$[4] \quad MH = [SH + LL/2] + (NLOGS)(LL)$$

where,

SH = stump height of the tree = 1.5 ft.

LL = log length in feet (16.5 or 8.25 feet)

NLOGS = the number of logs of length LL for a tree

When diameter distributions are generated, the truncated Weibull is used. A separate Weibull is fit to each species, and it is also possible to generate each species diameter distribution from more than one Weibull. This allows for multi-modal distributions within a species group. See chapter 4 of Van Deusen's dissertation (1984) for discussion on generating diameter distributions with the Weibull.

II STAG USER'S GUIDE

STAG, the **ST**And **G**enerator for mixed conifers is written in FORTRAN 77 code. The program is designed to be minimally interactive, requiring little input from the user. The program is started by entering "**stag**".

The program will first welcome the user to the stand generator with a short description of its capabilities. The program will then ask the user to choose from three options: (see runstream 1)

- "0" to make a stand
- "1" to stop
- "2" to read a file

If the user enters a "1" the program is terminated. This choice allows the user to immediately exit the program after starting it. If the user enters a "0", the program executes the section for generating a hypothetical stand that can be used as a stand description in **CACTOS**, the **CA**lifornia **C**onifer **T**imber **O**utput **S**imulator.

A. Generating Hypothetical Stands

After the user has entered a "0" to make a stand, the program will ask the user for a plot name which can be up to 20 characters long (see runstream 2). The plot name is analogous to the stand identifier in a CACTOS stand description. After entering the plot name, the user will be asked to enter the elevation of the plot (see runstream 3). After the elevation is entered the program begins a loop which allows the user to enter the required stand information species by species. For each species included in the hypothetical stand, the user is required to enter the species code (1 to 14, the same code as used in CACTOS ^{3/}), the basal area per acre (sq. ft.) of the species in trees greater than 5.5 inches DBH, and the number of trees greater than 5.5 inches DBH per acre in that species (see runstream 4). After this information is entered for the first species, the program will ask the user to enter the site index (coop site) for the species as CACTOS requires site index. The stand generator does not use the site index in its calculations.

^{3/} codes: 1=PP, 2=SP, 3=Ced. Misc., 4=DF, 5=WF, 6=RF, 7=LPP, 8=WP, 9=JP, 10=Con. Misc., 11=Chin., 12=BO, 13=TO, 14=H.W. Misc. Refer to page 1 to see how STAG places species into groups.

Once the site index is entered, the program will print out the quadratic mean of the species $(\frac{\sum DBH^2}{n})^{0.5}$, the predicted average DBH $(\frac{\sum DBH}{n})$, the species code, and the number of trees for that species (see runstream 5). The program will then give the user three options (see runstream 6):

- "1" to try again
- "2" to stop
- "3" to continue

Entering "1" allows the user to reenter the information for that species. Entering "2" allows the user to stop or terminate the program. Entering "3" tells the program to continue the generation of the hypothetical stand.

If a "3" is entered, the program will respond with "Developing Weibull distribution, please wait...", and then print out the total stand basal area and total number of trees per acre (see runstream 7). The program will then give the user 3 options: (see runstream 8)

- "1" to add a species
- "2" to abort
- "3" to save the stand

Entering "2" allows the user to terminate the program. Entering a "1" causes the program to repeat the section for entering species information for the next species (see runstream 9). Entering "3" causes the program to exit the loop for entering the species information and begin the section for saving the stand description. After "3" has been entered the program will ask the user to enter "1" to add random errors or "0" to not add random errors (see runstream 10). After the question is answered the program will ask the user to enter "1" to save the file or "0" to abort or terminate the program (see runstream 11). If a "1" is entered, the program will ask the user to enter a filename for the file (see runstream 12). A filename ending in ".sd" is recommended as discussed in the section on input and output files in the CACTOS User's Guide. When the file name is entered, the program saves the hypothetical stand under the entered filename and then terminates.

Notes on generating hypothetical stands:

- 1) The basal area entered for any species must be in the range of 5 to 400 sq.ft./acre or else the program will respond with "basal area out of range" and then ask the user to reenter the information.

2) The number of trees greater than 5.5 inches DBH for any species must be in the range of 5 to 1000 trees/acre or else the program will respond with "number of trees out of range" and then ask the user to reenter the information.

3) If the average basal area per tree (basal area/number of trees) for a species in the hypothetical stand is less than 0.2 or greater than 13.0 the program will respond with "average tree too small, try again" or "average tree too large, try again" respectively, and then ask the user to reenter the information. This program check requires average tree DBH to be between 6.0 inches ($0.2 \text{ ft}^2 \text{ BA}$) and 49.0 inches ($13.0 \text{ ft}^2 \text{ BA}$), keeping the generated stand within the range of the data used to develop the procedure.

4) The hypothetical stand generator produces a tree record for each tree per acre (e.g. If the stand has 250 trees/acre, the stand generator will produce a stand description with 250 tree records each with a per acre weight of 1 tree/acre). As CACTOS presently accepts only 500 tree records, stands with more than 500 trees/acre greater than 5.5 inches in DBH should not be generated.

5) Since the hypothetical stand generator produces one tree record for each tree in the stand, the record-quintupling process in CACTOS may not be able to completely quintuple all records. Hence it is strongly recommended that random errors are added to the hypothetical stand during generation (see runstream 10).

B. Generating Values for Missing Data

If, when the stand generator is first started, the user chooses option "2", the program will begin the section for reading in a file that contains one or more plots, i.e. stand descriptions (see runstream 13).

STAG reads in files that have the same format as CACTOS stand description input files (see Res. Note #10, chapter 4). STAG requires an additional integer variable, elevation, which is placed in line one, column 35 through 39 inclusive (the complete format for line one is: 10A2, 110, 4x, 15 for the stand identifier, tree record count, and elevation of the stand).

The ENTRY program (see Res. Note #10) for CACTOS can prepare files for the stand generator. The ENTRY program asks the user if the stand description is going to be run through STAG before use in CACTOS. If so, the program requests the stand elevation. The rest of the procedure is identical to a stand description entry. The user must enter "0" (the number zero) for any missing heights or live crown ratios. The user also has the option of entering tree height as either total height, height to a merchantable top (≤ 6.5 in.) or height in 16.5 ft. logs, measured to the whole or half log. However, if the file contains heights other than total height, the file must be run through STAG prior to use in CACTOS. STAG can also read files which contain a number of stand descriptions one after another (the theoretical limit is up to 50 plots with 1000 tree records in total). Files of this type can be prepared using a computer editor to join together stand description files. All height measurements in these files must be to the same standard, since STAG determines the type of height measurement based upon the input from the first stand description.

STAG generates missing data for two types of stand descriptions: A) where the stand description is a diameter class table (i.e. where only the number of trees per diameter class by species is known); and B) where the stand descriptions (tree lists) are missing one or more heights and/or live crown ratios, but the tree DBH's are known. These two types are treated differently, so each will be covered separately. STAG will not accept stand descriptions (tree lists) with missing or incorrect species codes, missing diameters, or missing per acre weights. Additionally, the program will issue a warning for live crown ratios that are negative or greater than 1.0.

B1. When only the number of trees per diameter class by species is known

A file of this type would contain a tree record for each DBH class for each species that contained trees. A record would contain species code, diameter class (e.g. 2.0 for the 2 inch class), zeros for total height and live crown ratios, and the number of trees per acre in that class.

After the user requests that a file be read (by entering "2", see runstream 13), the program will ask the user to enter the filename (see runstream 14). After the file is located, the program will ask which height coefficients are to be used (see runstream 15). The choices are:

- "0" use the program's default coefficients
- "1" read coefficients from a file

If the user has not saved updated coefficients from a previous run, the user must enter "0" (see runstream 15). Saving updated coefficients will be discussed later. The program will then read in the stand description and report what it has read. For example, "Read from file tstplot.sd 10 tree records from 1 plots. 10 heights are missing 10 crowns are missing" (see runstream 16).

If all heights and crowns are missing, as would be the case with a diameter class table, and only one plot was read in, the program will ask the user to choose between distributional apportionment and generation of missing values only. Distributional apportionment spreads the trees in each diameter class across the range of the class. For plots where only the number of trees by diameter class by species is known, distributional apportionment is strongly recommended. Therefore, plots of this type should be read in one at a time. After a "1" is entered for distributional apportionment, the user is asked to enter the number of tree records (range of 100-500) to be created (see runstream 17). Choosing 500 tree records is computationally faster than choosing a lesser number of records, but the quintupling feature of CACTOS must be switched off since CACTOS accepts no more than 500 tree records. Conversely, choosing 100 tree records takes more computational time, but CACTOS can completely quintuple the 100 tree records. For values less than 500, CACTOS will be able to only partially quintuple the records up to the 500 tree record maximum. After specifying the target number of tree records STAG develops the diameter distribution, reiterating if necessary to reduce the number of tree records to the user-specified target number (see runstream 17). Note, however, that STAG never precisely hits the target number of individual tree records. When complete, the program will ask the user to enter "1" to save the file or "0" to abort or terminate the program (see runstream 18). Entering "1" causes the program to request a filename (see runstream 19), and then save the newly created file under the filename entered.

When saving a file created by STAG, the user may specify a new filename or the same filename as the file read in. In the later case the program will ask if the user wants to overwrite that file. If "y" is entered for "yes" the program will write the new file over the previous file, destroying the previous file. An example of this procedure is shown later.

B2. When one or more heights and/or crown ratios are missing, but tree DBH is known

A file of this type could range from having only a few heights and/or crown ratios missing to the special case of having all heights and crowns missing. The distinction of this type of file is that tree DBH is known, preferably to the nearest tenth of an inch, whereas in a diameter class file, diameter is known only to the nearest inch (or two inches). The procedures for reading in a file of this type are the same (see runstream 20). In this example the program responds with "Read from file twoplots.sd 143 tree records from 2 plots 9 heights are missing 9 crowns are missing". The program then asks what kinds of heights were measured (runstream 21). The choices are:

- 1=Total height (ft.)
- 2=Height above ground to merchantable top (ft.)
- 3=Height in 16.5 ft. logs above a 1.5 ft. stump, measured to whole log
- 4=Height in 16.5 ft. logs above a 1.5 ft. stump, measured to half log

If 2,3, or 4 is entered, the program will ask what merchantable top diameter was used. Refer to "special features of the options" in the Introduction to STAG for a discussion of the use and limitations of estimating total height from log height or merchantable height. The program will not perform a height parameter update if total heights are not entered. If the heights entered are total heights (option 1 above) the program asks what kind of height parameter update is desired (see runstream 22). The choices are:

- "0" for no update
- "1" for a pseudo-bayes update
- "2" for an adhoc update

These choices have been discussed previously, and in this example an adhoc update is chosen with the local data given a weight of 0.3 (see runstream 23). The program then updates the height coefficients and then asks if random errors are desired (see runstream 24) ^{4/}. The program then asks the user to enter "1" to save the file or "0" to abort (see runstream 25). This example shows the procedure for having the newly

^{4/} The use of random errors does not effect the updated height coefficients.

created file written over the file read in (see runstream 26). In this case the original file "twoplts.sd" with 9 missing heights and 9 missing crowns is replaced by a new file called "twoplts.sd" with no missing heights or crowns.

Since a height coefficients update was done, the program asks if the user wants to save the updated coefficients. In this example the updated coefficients are saved in a file called "coef" (see runstream 27). NOTE: this example saves updated coefficients based on only two plots. In practice a combined data set of all the plots in a region or timber type should be used when updated coefficients are to be saved.

The next runstream shows an example where the updated coefficients saved in file "coef" are used to generate missing data. When the program asks which height coefficients are to be used, the user enters "1" to have them read from a file (see runstream 28). In this example "coef" is entered in as the filename (see runstream 29). NOTE: updated coefficients are saved in a free formatted file. Care should be taken to make sure updated coefficient files are not altered, as the program may not catch changes that will result in errors. Updated coefficients should only be used for stands from the same region or timber type that was used to update the coefficients originally.

A special case of missing heights and crown ratios is when all heights and live crown ratios are missing but actual tree DBH is known, usually to the nearest 1/10th inch. If a file of this type is read in by itself, the program cannot distinguish the file from a diameter class distribution, and will therefore ask if the user wants distributional apportionment. In this case the recommended response is "0" for generation of missing values only. If two or more of these types of plot are combined in a single file, the program recognizes that only missing value generation is desired, and skips the section on distributional apportionment.

C. Program Termination Messages

When STAG is terminated, a message is printed to the screen after the word "stop". The messages and their meaning are as follows:

<u>MESSAGE</u>	<u>Meaning</u>
DUMMY	STAG program started then immediately terminated
FINISH	Program run to completion, all files saved
COEFFICIENTS TRASHED	Program run to completion, newly created file saved, but updated height coefficients are not saved
ABORT1-READ ERROR	A fatal error is encountered in reading in stand description. An additional error statement will precede this message telling where the error has occurred
ABORT2-DELETE FILE	Program run to completion, but newly created file is not saved
ABORT3-INTERRUPT ABORT4-INTERRUPT	Program terminated in mid-generation of a complete stand. Can occur at two different points. See runstream 6 and 8 for where the aborts are initiated.
MAKNUM	Error occurred in subroutine MAKNUM
ERRORH	Error occurred in subroutine ERRORH
ERRORC	Error occurred in subroutine ERRORC

Literature Cited

- Biging, Greg S. 1983. Volume tables for young-growth mixed conifers of Northern California based upon the stem analysis data. Part I: Volume tables for mixed conifers. Part II: Taper equations for mixed conifers. (Revised draft). Research Note #7. Northern Calif. Forest Yield Cooperative, Dept. of Forestry and Resource Mgmt., Univ. of Calif., Berkeley. 59 pages.
- Van Deusen, Paul C. 1984. Complete and partial generation of tree characteristics for mixed species stands. Ph.D. dissertation, Univ. of California, Berkeley. 122 pages.
- Wensel, Lee C. and Peter J. Daugherty. 1985. **CACTOS** User's Guide: The **CA**lifornia **C**onifer **T**imber **O**utput **S**imulator. Version 1.0. Research Note #10. Northern California Forest Yield Cooperative, Dept. of Forestry and Resource Mgmt., Univ. of Calif., Berkeley. 98 pages.

User Notes

Any user comments about problems discovered in, or enhancements wanted to this user manual and associated software should be in writing to Greg Biging at the Department of Forestry and Resource Management, University of California, Berkeley, California 94720.

APPENDIX 1

OPTION 1: Generation of missing heights and/or live crown ratios.

Example of a file with missing heights and live crown ratios:

```

stagtest1                11      4500
110.  0.  0. 100.  0.  0.  0.  0.  0.  0.  0.  0.  0.  0.
 50.  0.  0.  50.  0.  0.  0.  0.  0.  0.  0.  0.  0.  0.
  1.000 10.400 56.000 0.500 10.000
  1.000 12.500  0.      0.      10.000
  1.000 14.200 72.000  0.      10.000
  1.000 15.700 75.000 0.450 10.000
  1.000 20.300 95.000 0.630 10.000
  4.000  8.500  0.      0.      10.000
  4.000 12.500 65.000  0.      10.000
  4.000 15.600 85.000 0.560 10.000
  4.000 16.800  0.      0.      10.000
  4.000 22.300  0.      0.      10.000
  4.000 24.500 105.000 0.540 10.000
    
```

Example output when above file is run through STAG, using:
 Deterministic prediction (no random errors)

```

stagtest1                11      4500
110.  0.  0. 100.  0.  0.  0.  0.  0.  0.  0.  0.  0.  0.
 50.  0.  0.  50.  0.  0.  0.  0.  0.  0.  0.  0.  0.  0.
  1.    10.4    56.0    0.500 10.000
  1.    12.5    63.8    0.505 10.000
  1.    14.2    72.0    0.506 10.000
  1.    15.7    75.0    0.450 10.000
  1.    20.3    95.0    0.630 10.000
  4.     8.5    49.5    0.549 10.000
  4.    12.5    65.0    0.569 10.000
  4.    15.6    85.0    0.560 10.000
  4.    16.8    82.1    0.581 10.000
  4.    22.3    99.3    0.601 10.000
  4.    24.5   105.0    0.540 10.000
    
```

Example output when first file is run through STAG, using:
 Stochastic prediction (random errors added)

```

stagtest1                11      4500
110.  0.  0. 100.  0.  0.  0.  0.  0.  0.  0.  0.  0.  0.
 50.  0.  0.  50.  0.  0.  0.  0.  0.  0.  0.  0.  0.  0.
  1.    10.4    56.0    0.500 10.000
  1.    12.5    69.7    0.311 10.000
  1.    14.2    72.0    0.521 10.000
  1.    15.7    75.0    0.450 10.000
  1.    20.3    95.0    0.630 10.000
  4.     8.5    58.2    0.653 10.000
  4.    12.5    65.0    0.399 10.000
  4.    15.6    85.0    0.560 10.000
  4.    16.8    85.4    0.647 10.000
  4.    22.3    99.9    0.476 10.000
  4.    24.5   105.0    0.540 10.000
    
```

indicates generated values

OPTION 3: Distributional apportionment

Example of a file that contains a diameter distribution:

```
stagtest2                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  0.  0.  10.000
 1.000 12.000  0.  0.  10.000
 1.000 14.000  0.  0.  10.000
 1.000 16.000  0.  0.  10.000
 1.000 18.000  0.  0.  10.000
 2.000 14.000  0.  0.  10.000
 2.000 16.000  0.  0.  10.000
 2.000 18.000  0.  0.  10.000
 2.000 20.000  0.  0.  10.000
 2.000 22.000  0.  0.  10.000
```

Example output when first file is run through STAG, using:
Distributional apportionment (Option 3)

```
stagtest2                91      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.   10.4  43.7  0.816  1.058  --
  1.   10.9  41.3  0.592  1.039  |
  1.    9.8  46.1  0.797  0.921  |
  1.   10.4  53.0  0.645  1.684  |
  1.   10.9  51.2  0.505  1.588  |
  1.    9.9  51.1  0.127  0.634  |
  1.   10.1  55.1  0.702  0.809  |
  1.   10.7  58.8  0.406  1.253  --
  1.   11.0  62.5  0.324  1.014
  1.   11.8  53.9  0.796  0.821
  1.   12.6  47.3  0.487  1.260
  1.   13.0  53.8  0.446  0.926
  1.   11.5  65.0  0.616  1.306
  1.   12.9  59.4  0.463  1.747
  1.   13.0  63.5  0.437  1.157
  1.   12.9  68.1  0.487  1.006
  1.   12.8  72.3  0.448  1.098
  1.   11.8  67.9  0.219  0.678
  1.   13.9  61.7  0.650  1.175
  1.   14.1  56.4  0.414  1.321
  1.   14.0  58.0  0.248  0.683
  1.   13.3  65.4  0.696  0.862
  1.   13.7  68.9  0.619  1.501
  1.   14.2  73.2  0.428  1.415
  1.   14.9  66.9  0.252  0.715
  1.   14.2  84.2  0.590  0.659
  1.   13.7  82.4  0.496  0.909
  1.   14.1  75.8  0.402  0.762
  1.   15.9  61.0  0.620  0.783
  1.   16.4  63.3  0.473  0.714
```

These tree records represent
---the trees contained in the
first diameter class listed
in the above file.

Note: Only 30 out of 91 tree records shown.

STAG RUNSTREAM

= user entry

= reference number from text

This runstream demonstrates generation of a hypothetical stand.

% stag

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

Copyright 1985 The Regents of the University of California

enter "return" to continue

The STAnd Generator for mixed conifers

by

Paul C. VanDeusen Greg S. Biging Lee C. Wensel

P. J. Daugherty and V. Landrum
Department of Forestry and Resource Management
University of California, Berkeley

A Product of the Northern California Forest Yield Cooperative
Industry Members

American Forest Products
Beaty and Associates
Champion International Corp
Crane Mills Lumber Co.
Diamond Land Co.
Fruit Growers Supply

The Hearst Corp.
Louisiana-Pacific Corp. (Elk Creek)
Louisiana-Pacific Corp. (Feather Falls)
Louisiana-Pacific Corp. (Sonora)
Michigan-California Lumber Co.
Southern Pacific Land Co.

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

enter "return" to continue, "1" to skip intro page;

```

Enter 0 to make a stand, 1 to stop, 2 to read a file:  | 1 |
Enter up to a 20 character plot name:  | 2 |
Enter elevation (integer) of plot example  | 3 |
Remember all entries should be per acre, the tree
weights=1 on the plot prosaically called example
Enter the following species (not stand) information:
species code, basal area (> 6 inch), n of trees >6"
The species codes are:
01=PP 02=SP 03=Ced.misc 04=DF 05=WF 06=RF 07=LPP
08=WP 09=JP 10=Con.misc 11=Chin 12=BO 13=TO 14=H.W.misc.
Enter here (separated by commas):  | 4 |
Enter the site index of this species (cactus needs it ): 
Quadratic mean= 19.1495
Predicted average dbh= 18.0952 | 5 |
Species code= 1
Number of trees= 75
Enter 1 to try again, 2 to stop, 3 to continue:  | 6 |
Developing weibull distribution, please wait ...
Total stand basal area= 150.000
Total n of trees= 75 | 7 |
Enter 1 to add a species, 2 to abort, 3 to save stand :  | 8 |
Enter the following species (not stand) information:
species code, basal area (> 6 inch), n of trees >6"
The species codes are:
01=PP 02=SP 03=Ced.misc 04=DF 05=WF 06=RF 07=LPP
08=WP 09=JP 10=Con.misc 11=Chin 12=BO 13=TO 14=H.W.misc.
Enter here (separated by commas): 
Enter the site index of this species (cactus needs it ): 
Quadratic mean= 15.1390
Predicted average dbh= 14.4320 | 9 |
Species code= 4
Number of trees= 80
Enter 1 to try again, 2 to stop, 3 to continue: 
Developing weibull distribution, please wait ...
Total stand basal area= 250.000
Total n of trees= 155
Enter 1 to add a species, 2 to abort, 3 to save stand : 
Enter 1 to add random errors, 0 not to :  | 10 |
Enter 1 to save the file, 0 to abort !:  | 11 |
Enter a filename for the file:  | 12 |
STOP: FINISH

```

This runstream demonstrates distributional apportionment.

%

WELCOME TO

STAG

Enter 0 to make a stand, 1 to stop, 2 to read a file:

13

Enter the input filename:

14

Which height coefficients? 0=default 1=read from file, enter here:

15

Read from file tstplot.sd 10 tree recs from 1 plots

10 heights are missing

10 crowns are missing

16

Enter 1) for distributional apportionment,
0) for generation of missing values only
enter 0 or 1:

Enter the number of tree records desired (100-500):

17

Developing distribution, please wait...

Routine dist re-iterates to reduce number of recs

Enter 1 to save the file, 0 to abort !:

18

Enter a filename for the file:

19

STOP: FINISH

This runstream demonstrates the Ad-hoc Parameter update procedure.

% stag

WELCOME TO

STAG

Enter 0 to make a stand, 1 to stop, 2 to read a file: 2

Enter the input filename: twoplots.sd

Which height coefficients? 0=default 1=read from file, enter here: 0

Read from file twoplots.sd 143 tree recs from 2 plots

9 heights are missing
9 crowns are missing

What kinds of heights were measured?

1 = Total height (feet)
2 = Height above ground to merchantable top (feet)
3 = Height in 16.5 ft. logs above a 1.5 ft. stump, measured to whole log
4 = Height in 16.5 ft. logs above a 1.5 ft. stump, measured to half log
enter 1, 2, 3, or 4: 1

What kind of height parameter update do you want?

0= none, 1= pseudo-bayes, 2= adhoc

Enter 0, 1, or 2 : 2

Enter k-value for ad hoc update, remember if k=0
the local data gets no weight, if k=1 the local data gets
all the weight, and you can choose any k from 0 to 1

Enter k-value here: .3

Enter 1 to add random errors, 0 not to : 1

Enter 1 to save the file, 0 to abort !: 1

Enter a filename for the file: twoplots.sd

A file with that name already exist.

Do you want to overwrite twoplots.sd ?(y=yes): y

Enter 1 to save updated coefficients 0 to stop: 1

Enter a filename for the file: coef

STOP: FINISH

This runstream demonstrates the use of previously saved coefficients.

%

WELCOME TO

STAG

Enter 0 to make a stand, 1 to stop, 2 to read a file:

Enter the input filename:

Which height coefficients? 0=default 1=read from file, enter here:

| 28 |

Enter the input filename:

| 29 |

Reading your height coefficients from file coef

Read from file twoplots.sd 143 tree recs from 2 plots

9 heights are missing

9 crowns are missing

What kinds of heights were measured?

1 = Total height (feet)

2 = Height above ground to merchantable top (feet)

3 = Height in 16.5 ft. logs above a 1.5 ft. stump, measured to whole log

4 = Height in 16.5 ft. logs above a 1.5 ft. stump, measured to half log

enter 1, 2, 3, or 4:

Enter 1 to add random errors, 0 not to :

Enter 1 to save the file, 0 to abort !:

Enter a filename for the file:

STOP: FINISH