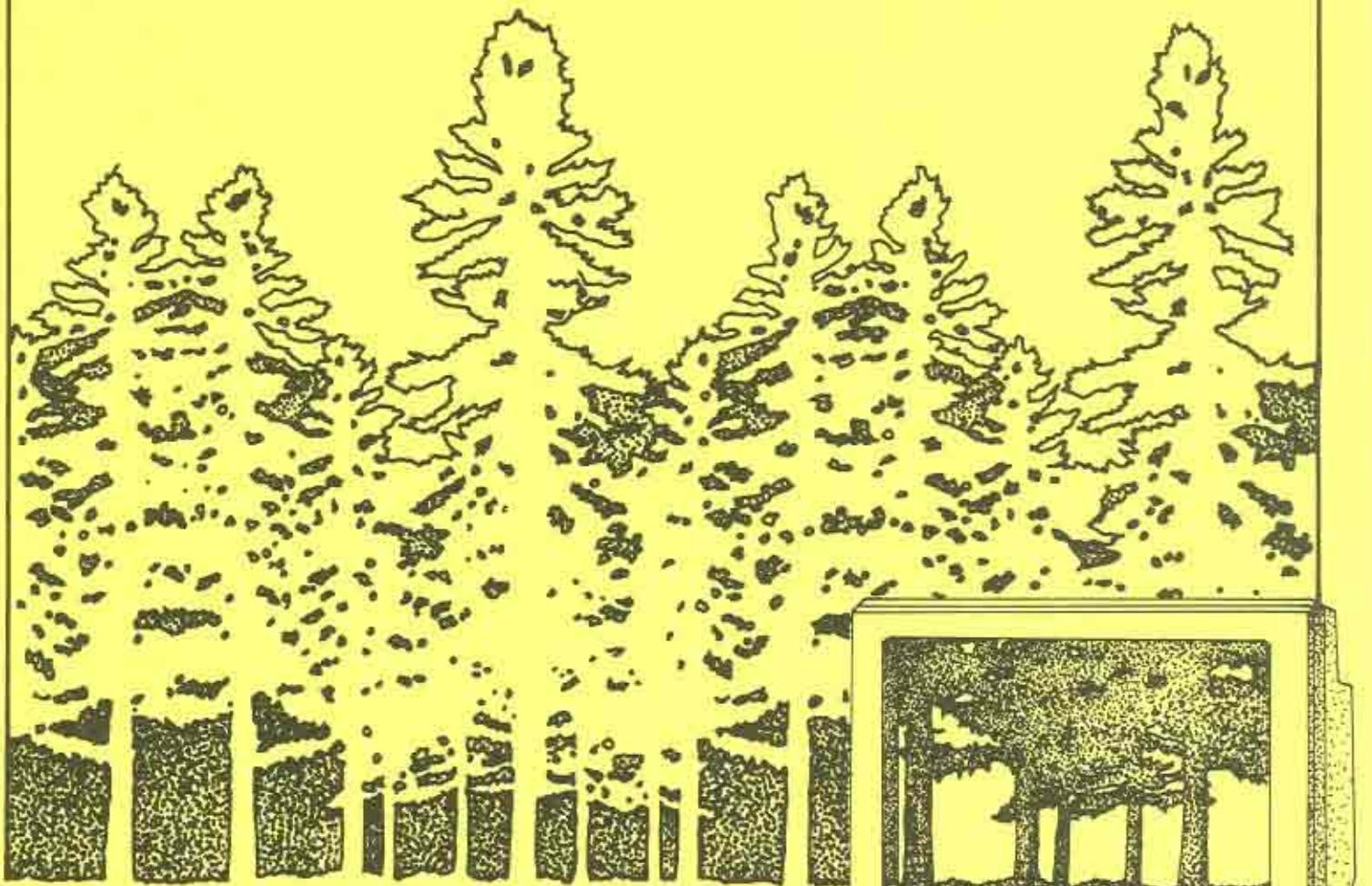


CACTOS USER'S GUIDE:

The California Conifer Timber Output Simulator



Agricultural Experiment Station
UNIVERSITY OF CALIFORNIA
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Summary

The computer simulator CACTOS is designed to model the changes that take place in young-growth conifer stands in the mixed-conifer region of northern California. CACTOS requires the user to enter a stand description and allows the user to perform various operations and print out various descriptive reports of the stand. This interactive program is written in standard FORTRAN 77 code. The current version is running on a Vax 11/780 computer system, IBM PC compatible personal computers, and the Apple Macintosh. To run the program, the user answers questions or issues two-letter commands. The list of commands available at any stage can be displayed by typing pc (for print commands).

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PREFACE

The release of the CACTOS program represents an important milestone in our cooperative efforts with representatives of the forest industries in California. However, this release is similar to giving birth. If CACTOS is to be useful in evaluating alternative management strategies, it must be carefully groomed as it grows from infancy to maturity. Both the estimates themselves and the way in which they are presented will need careful testing, adjustment, and retesting. Thus, the need for cooperation is not over.

The height growth estimates for version 3 are based upon the stem analysis data base which contains reliable height growth information on a limited number of samples. The diameter estimates are based on the more extensive permanent plot data base. At the time this document was prepared, the permanent plots were still being remeasured; thus the diameter growth information is limited to increment borings, and the height growth information not yet available. As the remeasurement data arrive, they will be used to validate and/or update the height growth estimates.

Improved mortality estimates, ingrowth models, productivity measures, and refined competition indices are but a few of the topics that still need further research. As the program components become available they will be added to CACTOS. The productive cooperative effort that is summarized in the CACTOS program should not cease with the first public release. Instead, there is still much to do and we still need your support.

ACKNOWLEDGMENTS

The CACTOS program represents the labors of many people for over 7 years. First, we owe thanks to **Bob Leatherman** of Champion International Corporation for lining up the support of our industry cooperators and then serving as the first chairman of the group of industry supporters. Without his initiative this project might never have gotten off the ground. He was followed in the chairmanship by **Art Stackhouse** of Southern Pacific Land Co. and then **Gary Nakamura** of Champion International, both of whom helped the project through difficult times. Also, I'd like to thank all of our industry cooperators who participated in our planning sessions and then went into the field to collect data according to the common standard agreed upon. These cooperators took a personal interest in making sure that the measurements were done correctly in the first place and, after the data were in machine readable form, patiently helped us with the editing.

The list of industry cooperators includes the foresters from the following companies: American Forest Products Co., Wm. Beaty and Associates, Champion International Corp., Crane Mills Lumber Co., Diamond Lands Corp., Fruit Growers Supply Co., The Hearst Corp., International Paper Co., Louisiana Pacific Corp., Michigan-California Lumber Co., and Santa Fe Pacific Timber Co. Special recognition is appropriate for **Duncan Brinkerhoff** of the Hearst Corporation. One of the charter members of the cooperative, Duncan was one of its most eager supporters.

Second, I'd like to thank **Bruce Krumland** and **Greg S. Biging** for sharing the responsibilities of formulating the procedures to be used in all aspects of the project. Bruce worked with me in producing the growth model, CRYPTOS, for the redwood region and then provided support in starting the project that led to the CACTOS program. In fact, with Bruce's help, the initial version of CACTOS came directly from CRYPTOS. Greg joined the project after it was started but took major responsibility for various parts of it, including the design of the stem analysis study and the construction of the volume equations and site index curves used by CACTOS.

I have been fortunate at all times to have at least one person employed on the project full time to provide continuity from day to day and to make sure that the details of the project were not neglected. **Robin Filion** worked on the project through much of the data collection and encoding phases. He was followed by **Jim Koehler** who, while he aided in the data collection and encoding phases, made his greatest contribution by spending countless hours in the "wee hours of the morning" detecting errors in the data sets, seeing to it that they were corrected, and then running the statistical analyses necessary to develop our prediction equations. **Peter Daugherty** was the principal programmer and maintained overall responsibility for the code until he began work on his Ph.D. degree. **Walter Meerschaert** revised the code for the version 3 upgrade and now has responsibility for the program code.

I'd like to thank all of the past and present employees of the project for their contributions to various parts of the project. **Ken Brown** did much of the data correction and helped with the harvest routines. **Paul VanDeusen** did the analyses leading to the formulation of the crown models used; he also developed the stand generation routines. **Jerry Ingersoll** assisted with portions of the coding, and **Mark Teply** helped develop the calibration procedures. **Jon Jue**, **Jeremy Fried**, **Ed Peggs**, and **Eugena Wong Seito** assisted with the ring measurements, data recording, or data editing. **Vaughan Landrum** and **Pamela Swartz** helped prepare the user's manual.

Finally, I'd like to thank all of those who supported this project over the past 7 years. The industry representatives who participated in the planning, collected field data, and obtained funding for the project are the ones who made all this possible.

Lee C. Wensel

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I. INTRODUCTION

CACTOS, the California Conifer Timber Output Simulator, is an interactive computer program designed to simulate the growth and partial harvests of conifer forest stands in northern California. The program, written in standard FORTRAN 77 code (ANSI, 1978), is operational on the following systems:

- (1) DEC VAX 11/780 under UNIX 4.2 BSD
- (2) Data General Mini-computers under AOS/VS
- (3) IBM-PC compatibles under MS-DOS v2.1 and above
- (4) Apple Macintosh personal computers

CACTOS is designed to provide the forestland manager with a means of predicting the changes that are likely to take place in a young-growth conifer stand, either due to the uninterrupted growth processes or as a result of interventions on the part of the forest manager. It is important for the CACTOS user to understand how the program is organized and how it operates. This understanding will not only make the program easier to use, but it should also make the results more meaningful. While the program is interactive, a complete reading of this manual is suggested for efficient and meaningful use of the simulator. An hour invested in reading this manual will pay for itself in savings of time and money when running the program.

The general structure of the CACTOS is illustrated in figure 1. These components are briefly described below and then treated in detail in subsequent sections.

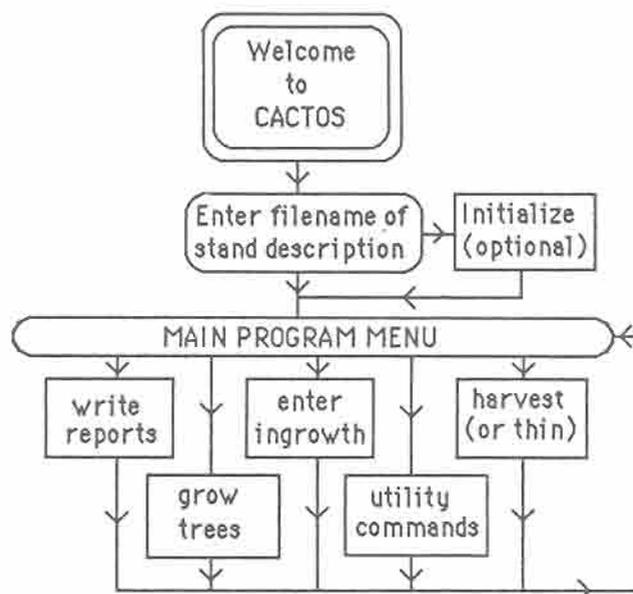


Figure 1. Structure of components of CACTOS

Stand description

A stand description consists of the site index and initial age (optional) of each species and a list of the trees representing the stand. The site index is used as a measure of the potential productive capacity of the stand, using the site relationships developed by Biging and Wensel (1985).

Each tree record in the stand description contains the following five items:

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

A detailed explanation of the stand description file is given in the section on sample input files, section IV. A., and an illustration of a stand description is given in Appendix A.

The above tree list represents the stand CACTOS uses throughout the 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. For example, if the sample wound up with greater or lesser density, under- or overabundance of certain species, larger or smaller trees, etc., the simulation results may not represent the stand the user intended.

Frequently, the user will want to model a stand without having all of these data items. Thus, external to CACTOS, provision has also been made to "fill in" the missing data using STAG, the STAnd Generator (VanDeusen and Biging 1985).

Initialization

There are other data items the user may wish to change in the program. These are optional items that specify the way in which the program output is structured, but they have little or nothing to do with the simulation of the stand development. Reasonable default values are set by the program so that the initialization process can be completely ignored until the user is familiar with the entire program operation. The initialization process is discussed in detail in section V. (The user may obtain a listing of the initialization commands by typing `pc` in response to the initialization prompt "initgo:".)

Main program menu

CACTOS is menu driven to make it "user friendly". The program is operated by either responding to questions from the program, or by typing a two-letter command in response to the main program menu prompt "go:". A complete list of the commands available from the main menu is provided when `pc` (print commands) is typed.

Generation of reports

Within the main program menu, provision is made to summarize the current stand in different ways. The options available range from a simple list of tree records to a log stock summary or yield/harvest summaries. One summary of particular interest is the `pf` command which displays the current stand profile, showing the average height and crown size by diameter class. Reports shown on the screen can be saved in a report file for later processing. Per-acre summaries of the 5-year growth, ingrowth, and harvest are automatically stored in the yield summary file.

Growth prediction

The actual growth prediction is done in response to the grow command, `gr`. At this point, the program computes the summary stand statistics, computes a density measure for each tree (depending upon the size of the tree in relation to the others in the stand), and accesses the various equations used to predict the changes in the tree characteristics for a user-specified number of 5-year growth cycles (Wensel and Koehler 1985). Thus the growth process actually changes the stand representation as given by the tree list. Individual tree growth detail and/or growth summaries for each growth cycle may be requested. Before or after the `gr` command is issued, the user can invoke commands to harvest part of the stand and/or to print out various stand summaries.

Calibration

User calibration of basal area and/or height may be specified. Calibration can be used to adjust the final growth prediction. Such adjustments may be necessary due to silvicultural activities, microsite, or any similar factor not specifically addressed in CACTOS. Users can implement this feature as an option from both the initialization routine and the main program. Calibration schemes are entered either through the keyboard or from an external file. A scheme may be applied at any point in stand growth simulation and for any number of growth cycles. Given this versatility, users can create and apply a variety of schemes. However, the degree of calibration is limited to prevent drastic alterations to the response surfaces of the growth models.

Ingrowth

For short-term simulations of growth, ingrowth (growth of trees to merchantable size) can be provided for by including smaller trees in the original stand description. However, for longer simulations, trees not otherwise provided for in the description may have to be entered to more accurately represent the stand development. These trees can be entered using the ingrowth command, `ig`. This command allows the user to enter tree descriptions from the keyboard or from a specified external file.

Utility commands

Utility commands allow the user to save the current stand description (either internally or externally) for later use. This permits more efficient generation of several alternative prescriptions for a single stand. These commands are discussed in more detail in Section III, Structure and Strategies.

Harvest options

Several harvest options provide the ability to perform thinning operations on the stand currently held in the computer memory in much the same patterns that one might harvest stands on the ground. This enables one to compare alternative simulations with the same starting data but with different thinning options.

II. PRELIMINARIES

This section gives a brief set of instructions for operating CACTOS on IBM PC compatible and Apple Macintosh personal computers. Be sure to make a backup copy of the program disk before running. Also, the user should be familiar with the basic file handling capabilities of the computer before running CACTOS.

II.A PC Version

The PC version of CACTOS is designed to operate on IBM PC compatible personal computers running under DOS v2.1 or later with a minimum of 256K of free memory (RAM), above that used by any resident software. CACTOS has been tested on the IBM PC and Compaq Plus computers. The program package is contained on a 5.25-inch floppy disk containing the executable code in a file called "cactos.exe," the coefficient file called "cofile," and several demonstration input files called "demo.sd," "demo.sg," "demo.ig," and "demo.cl." We recommend that the user make a backup copy of this disk prior to use.

The operating system (MS-DOS or PC-DOS) has a default limit of only nine files that can be opened at one time. Since some applications of CACTOS could exceed this number, the user should reset this number to 25 (or more). (See your system manual for instructions on how to do this, as it may vary among the various IBM PC-compatibles.) The method of operation varies, depending on the configuration of the user's personal computer. Possible configurations for single floppy drive, dual floppy drive, and hard drive systems are given here.

(1) Single floppy disk drive

The most efficient way to run CACTOS on a single disk drive machine is to have the executable file, "cactos.exe," and the coefficient file, "cofile," on one floppy disk (disk 1); and the input files on another disk (disk 2). To operate, insert disk 1 in the drive and type "cactos (return)" to invoke the program. When the logo appears on the screen, remove disk 1 from the drive and insert disk 2, the disk containing the input files, then proceed with the execution of the program. Operating CACTOS in this manner results in all the output files placed on disk 2. Thus, the user will have one disk with the executable program and one (or more) disk containing input/output files, thereby maximizing the storage space for input/output files.

(2) Dual floppy disk drives

The strategy for this configuration is similar to the single drive machines. Insert the disk with the executable file "cactos.exe" into drive A:. Insert the disk with the input files in drive B. In this case "cofile," the coefficient file, should be on the disk in drive B rather than on the disk with the executable file. To operate, the user should have prompt "B>" and type "a:cactos (return)." This command invokes CACTOS from the A drive while reading input files from and writing output files to the B drive.

(3) One floppy disk and one hard disk drive

The strategy for this configuration is to install CACTOS on the hard disk and to use floppy disks only to backup files produced. To install, insert the program disk into the floppy disk drive and copy all files to the hard disk, preferably into a directory created for this purpose (see the DOS manual for the "mkdir" command). Once the files are copied to the hard disk, remove the floppy and store in a safe place, as the program disk is not needed again unless the files on the hard disk are lost or damaged. To

operate, the user should have the hard disk drive prompt and be in the proper directory. Type "cactos (return)" to start the program. Input and output files are read from and written to the hard disk. It is strongly recommended that important output files be copied to floppy disk for backup.

CACTOS has the ability to search for its coefficient file "cofbin" in any user specified disk and/or directory besides the current or default. This is accomplished by typing the following DOS command before entering CACTOS:

```
SET COFBIN=path\COFBIN
```

where `path\` is the disk drive letter and DOS pathname describing the location of the coefficient file. Use of this option allows the user to run CACTOS from any directory while the sole copy of "cofbin" lies in a protected area apart from the work area. This DOS command can be placed in the user's "autoexec.bat" file to configure the system for CACTOS at system startup.

II.B Apple Macintosh personal computers

The Apple Macintosh version of CACTOS requires 512K of memory and operates basically the same as on the PC-compatibles. No special programming has been done to make use of the special features of the Macintosh's pull-down menus or mouse. Thus, users can readily exchange input and output files between the two systems. The program disk contains the CACTOS program file as well as a system file, coefficient file, and several demonstration files. The possible configurations of the system depend upon the number of disk drives available and include the following combinations:

(1) Single floppy disk system

CACTOS can be run from a single floppy drive with little or no disk swapping. The system file should be trimmed of unnecessary fonts and desktop applications and the Imagewriter file can be deleted, since printing the files is done separately by a word processing program. Thus, the following files are needed to run CACTOS:

<u>Name</u>	<u>Size</u>	<u>Kind</u>
CACTOS v3.1	182K	CACTOS program file
cofbin	4K	binary coefficient file (see section IV.F)
Finder	47K	Apple system finder file(size varies with version)
System	87K	Apple system file (size varies with options loaded)

This leaves about 75K available for data files.

2) Two floppy disk drives (or a hard disk drive)

Adding a second disk drive, or a hard disk, to the system increases the flexibility of CACTOS. One disk drive should be set up with the files listed above and any "utility" program files needed. The second disk drive is then used to load data disks. All file names specified for CACTOS contain the disk (or volume) name followed by a colon. For example, if the data disk volume is named "D1", the demonstration stand description file, yield summary, and report file are named "D1:demo.sd," "D1:demo.yd," and "D1:demo.rp," respectively. Any file names given without the disk drive (or volume) name are assumed to be on the program disk. Note that up to 15 characters can be used for the entire file name.

Be sure to check Appendix E. for further operational differences between the Macintosh version and other versions of CACTOS.

III. STRUCTURE AND STRATEGIES

The CACTOS program provides the user with a menu from which various operations may be selected to alter the user-supplied stand description. The menu allows the user to: (a) initialize or change the default program parameters which determine the minimum DBH, merchantable top diameter, species groupings, etc. used for summaries; (b) simulate changes in the stand description by growth, harvest, or ingrowth; and (c) prepare reports describing the stand at any point in time.

Initialization, or changing the default program parameters, is only allowed at the outset of a simulation run. Once a user exits the initialization routine (or declines to enter it) the user must rerun the program to change any program parameters. While becoming familiar with the operation of the program, the user may skip the initialization step. However, a clear understanding of the defaults will help the user to avoid the need to rerun a simulation to correct reporting defaults. See section V for a full discussion of the default parameters.

CACTOS produces two output files for every simulation run. The yield summary is produced automatically and contains summaries for all 5-year growth cycles, harvests, and ingrowth. The report file is an auxiliary output file. The program opens the report file and labels it with the stand identifier, site index, initial age of the stand, and the merchantability limits selected at the initialization stage. Any further additions to the report file are controlled by the user. Many of the user-requested reports (i.e., information produced by the "report" commands) may be routed to the report file. Commands that can be routed to the report file are identified by an asterisk on the command summary page (see Appendix F). The other report commands (i.e., ones that cannot be routed to the report file) are provided as aids for controlling the simulation. Report commands are discussed in more detail in sections VI and VII.

The program is also designed to allow efficient simulation of alternative prescriptions of a single stand. The generation of a complete yield stream and report for each prescription is accomplished by the save (sv) and restore (rt) commands. The sv command internally saves the stand description, yield summary, and report file as they exist at the time of command execution. Simulation of the first alternative can then be continued. The rt command automatically saves the yield summary and report file for the first alternative, and then prompts the user for names for the new yield summary and report file, which are restored to the condition existing when the sv command was issued. The stand description is also restored to the saved condition. Simulation of the next alternative can be continued from that point. The actual stand description resulting from the alternative prescription may be saved externally at the user's discretion, by using the es command. The externally saved stand description can be entered at a later time for further simulation by entering the ns command. In this case, the yield summary and report file start with the externally saved condition as the first entry.

Figure 2 illustrates the simulation of four alternative prescriptions for a single stand. Stand output for each prescription is saved at nodes 2, 3, 5, and 6 with the es (external save) command.

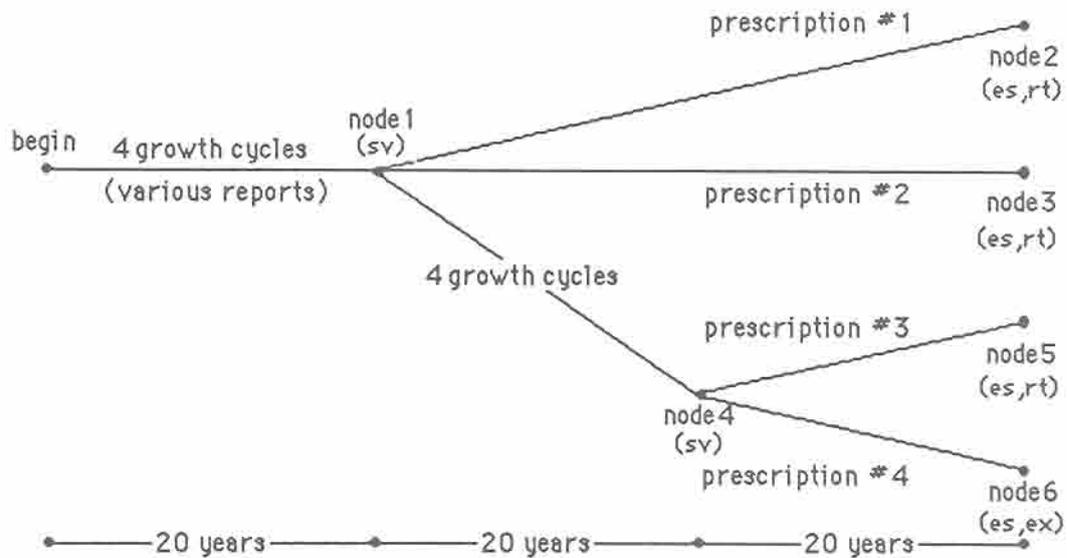


Figure 2. Simulation of four alternative prescriptions of a single stand

The nodes represent points where the *sv*, *rt*, or *es* commands are used. The lines represent other simulation commands issued to grow and thin the stand and to create various reports. Prescriptions 1 and 2 represent two different thinnings occurring after 20 years of growth. Prescriptions 3 and 4 represent two different thinnings occurring after 40 years of growth. Thus, after 60 years of simulation, the user ends up with four stands, each with a different stand history.

Finally, CACTOS allows the simulation of many stands during one entry into the program through the use of the *ns* (new stand) command. This command allows the entry of a new stand description input file without exiting the program. The previous stand's yield summary and report file are automatically saved, and the user is prompted for the names of the new stand description input file and the two output files. At this point the user is allowed to reenter the initialization routine to set program parameters. The *ns* command reinitializes the program parameters to their default values.

IV. INPUT AND OUTPUT FILES

CACTOS accepts four types of user input files and produces four types of output files. The input files recognized by CACTOS include:

- (1) a stand description file that provides the basic information about the stand to use in the simulation
- (2) an ingrowth file (optional) that can be used to enter ingrowth to the stand description at any point in simulation
- (3) a species grouping file (optional) that defines the manner in which the species are grouped for reporting purposes
- (4) a calibration file (optional) that provides adjustments to use in the growth simulation

The output files include:

- (1) the yield summary file is automatically updated by CACTOS as the simulation proceeds
- (2) the report file is used to save tables that are selected by the user during the course of the simulation
- (3) externally saved stand description files, created by the `es` command to save copies of the current stand description for later use
- (4) externally saved calibration scheme files, created during execution of the calibration `cl` command to save calibration schemes for later use

All input and output files are referenced by file names chosen by the user. CACTOS allows up to 32 characters in a file name. However, users are cautioned to observe limits placed on file names by the computer system they are using. Individual systems may support the use of path names as part of the file name. The authors strongly recommend adoption of the following, or similar, convention in naming files. The convention recommended 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. The ending names should be one of the following:

<code>.sd</code> stand description	<code>.cl</code> calibration
<code>.ig</code> ingrowth	<code>.fn</code> batch mode <i>filenames</i>
<code>.yd</code> yield summary	<code>.cm</code> batch mode command
<code>.rp</code> report	

Thus, "demo.sd" and "demo.yd" are the stand description and yield summary files for the stand "demo". Adoption of the above conventions allows for easy recognition of file types and efficient file management.

Several file names to avoid, since they are already used by CACTOS, are: "cofbin," "cofile," "isave1," "isave2," and "fort.xx," where xx is a number from 11 to 15, inclusive.

Standard FORTRAN notation is provided here to describe the format of each line of input. 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.

IV. A Stand description input file

After CACTOS has been invoked, the program welcomes the user to the program and requests a stand description input file name. This file name refers to the stand description input file of the stand the user wishes to simulate. The stand description input file must have the following structure:

- Line(1) Stand identifier and tree record count (format A20, I10). The stand identifier is composed of up to 20 alphanumeric characters and the rightmost digit of the tree record count is in column 30.
- 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). Site index 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 only and is not needed for the model to function.)
- 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):
- (1) species code (see below)
 - (2) DBH in inches
 - (3) total height in feet
 - (4) live crown ratio (decimal fraction)
 - (5) per-acre expansion (i.e. the number of trees per acre represented by this tree record)

Species Codes - The following species codes are used in CACTOS:

01 - ponderosa pine	08 - white pine
02 - sugar pine	09 - Jeffrey pine
03 - incense cedar	10 - miscellaneous conifer
04 - Douglas-fir	11 - chinquapin
05 - white fir	12 - black oak
06 - red fir	13 - tan oak
07 - lodgepole pine	14 - miscellaneous hardwood

Note: CACTOS has a maximum internal storage capacity of 500 tree records. If the number of tree records in the stand description input file is greater than 500, the program automatically terminates. The record quintupling process in the pseudo-stochastic procedure produces five tree records for each user-entered tree record. Therefore the effective limit on user-entered tree records is 100 records. Any stand description input file with more than 100 records results in a warning, notifying the user that the record quintupling process cannot proceed normally. The program will then quintuple as many records as memory allows, starting with the first tree record and proceeding through the records as ordered in the input file.

An example of a stand description input file is shown in Appendix A.

IV. B Ingrowth File

An ingrowth file may be used to add ingrowth to the stand description during the simulation. The ingrowth command is discussed in detail in section VI.C. The ingrowth file must have the following structure:

- Line (1) The number of ingrowth tree records (format I5).
- Line(2-end) The ingrowth tree records follow. Each record has the following five items (format 5F8.3, i.e. one line for each ingrowth tree record):
- (1) species code
 - (2) DBH in inches
 - (3) total height in feet
 - (4) live crown ratio (decimal fraction)
 - (5) per-acre weight (i.e., the number of trees per acre represented by this ingrowth tree record)

An example of an ingrowth file is shown in Appendix A.

IV. C Species grouping file

CACTOS allows user-defined species groups for summary reporting, specifying species to use in various reports, and for targeting species to cut. Implementation of this option is discussed in section V. The species grouping file specifies the species group names and species included in each group. The file must have the following structure:

- Line (1) The number of species groups desired (format I3).
- Line (2-end) List the species group records.
Each species group record contains the following items
(format A10,14I2; i.e., one line for each group):
- (1) the group name (up to 10 characters long), and
 - (2) the species codes of species that belong in that group

Note: No species may be included in more than one group, and each of the fourteen species codes must be assigned to a group.

An example of a species grouping file is shown in Appendix A.

IV. D User calibration file

The user calibration file, discussed in detail in Appendix D, contains a table of calibration factors entered by the user using the `cl` command. Calibration can be for the basal area growth and/or height growth and may be applied by species and by up to five diameter class ranges defined by the user. Users are cautioned not to use the calibration file to make such drastic changes in the growth rates so as to defeat the integrity of the growth equations. As a partial control on this, calibration is restricted to changes in the growth rates of no more than 20 percent. The calibration file contains calibration vectors for basal area and height models, with one line containing the size classes and the next line containing the corresponding calibration factor for each of the 14 permissible species:

- Line(1-28) Calibration vectors for basal area by species, two lines per species (format 2(5F8.2/)). The first line for each species contains the lower limit for each class; the second line contains the calibration factors corresponding to the lower limits in the first line.
- Line(29-56) Calibration vectors for height by species, two lines per species (format 2(5F8.2/)).

Indicator variables are also contained in this file. These variables tell the program how to interpret and apply the calibration scheme:

- Line(57) Three indicator variables (format 3I3). These variables instruct the program how to interpret the calibration scheme. The first variable indicates the models to calibrate. It has the value:
- 1 - basal area only
 - 2 - height only
 - 3 - both basal area and height

The second and third values indicate how basal area and height factors are entered. They have the values:

1 - all species together

2 - by individual species

Line(58-59) Fourteen indicator variables (format 2(14I3/)). These variables indicate if a specific species has a basal area (line 58) or height (line 59) calibration vector. These lines are significant, depending on the value of the second or third indicators on line 57. A one in this field indicates that a factor is present for that species.

Because of the complexity of these indicators and their effect on the meaning of the calibration vectors, users should not attempt to externally edit a calibration file. If calibration vectors and indicators are changed irrespective of each other, erroneous growth predictions can be produced. For this reason, the calibration command `cl` allows for keyboard entry of the calibration scheme and editing of an existing scheme. The program also allows for external saving of calibration schemes after keyboard entry.

An example of a user calibration input file is shown in Appendix A.

IV.E Coefficient files - "cofile" and "cofbin"

CACTOS requires that a file containing all of the coefficients for the equations used throughout the program be present. A file supplied with the program, "cofile," contains text (ASCII) representations of these coefficients. The first time CACTOS is run, "cofile" is read in and a machine-specific binary version is created. This new file is called "cofbin" and should be used instead of "cofile." The binary version loads much faster and takes up about one-third the space of the text version. Neither file should be altered in any way, as the normal operation of CACTOS is vitally dependent on these coefficients. Once "cofbin" has been created, the original file, "cofile" is no longer used by CACTOS. However if the binary file "cofbin" is not found on any subsequent run, CACTOS looks for "cofile" and recreates "cofbin" for future runs.

IV. F Output files

After the stand description file name has been entered, the program requests names for the yield summary and report file. The yield summary is created automatically during a simulation and contains the yield and periodic growth for each period in the simulation. The report file can be used to save various reports. When the program is terminated, the yield summary and report file are saved with the user-defined names. These files can then be printed or used for further analysis.

A stand description can be saved externally on an output file created by the `es` command. This command saves the stand description in a formatted file, with a user-supplied name, and it can be reentered as a stand description input file for further simulation. The `es` command may be issued at any point in the simulation. An externally saved stand description differs from a user stand description in that the record quintupling/pseudo-stochastic procedures may have been performed on the stand. An indicator variable is placed in an externally saved stand which causes the program to notify the user of this condition before performing further record quintupling/pseudo-stochastic procedures.

An externally saved user calibration scheme is an output file created as an option in the `cl` command. The external file saving capability serves as storage for calibration schemes after keyboard entry. These files may be retrieved at a later time for use in other simulations. The calibration file is also referenced by a user-supplied file name.

V. INITIALIZATION ROUTINE AND PROGRAM DEFAULTS

Once the user has entered file names for the stand description, the yield summary, and report file, the program gives the user the opportunity to enter the initialization routine to alter any of the program defaults. This is a one-time-only opportunity for the user to alter program parameters. The user chooses this option by entering "y", which results in the prompt:

initgo:

The initialization routine menu contains the following commands:

pc	print commands
cm	set cubic foot DBH minimum
ct	set cubic merchantable top
bm	set board foot DBH minimum
bt	set board foot merchantable top
sc	list species groups and current group indicator
sp	set species groups
su	list user defined species groups
fl	set print flag
yf	set yield flag
cl	set calibration scheme
iq	set record quintupling option
ex	return to main program

Explanation of commands

pc	Print the list of available <u>commands</u> and their functions.
cm	Print and allow changes in the current <u>minimum</u> DBH used in computing summary statistics for <u>cubic</u> foot volume. This minimum DBH is also used for computing the number of trees, the basal area, and the average (quadratic mean) DBH of the stand. Therefore, the cubic minimum DBH must be less than or equal to the board foot <u>minimum</u> DBH (default is 0 inch).
ct	Print and allow changes in the <u>merchantable top</u> limit for <u>cubic</u> foot volume estimation (may be 4 or 6 inches, default is 4 inches).
bm	Print and allow changes in the current <u>minimum</u> DBH used in computing summary statistics for <u>board</u> foot volumes (default is 8 inches).

- bt Same as the ct command, only it applies to board foot merchantable top (may be 6 or 8 inches; default is 6 inches). In estimating volumes, if a tree's DBH is less than the merchantable top limit, that tree is assigned a volume of zero.
- sc List available species group options, their indicator codes, and the option currently in effect.
- sp Combine species into several groups for use in summary reporting, designating species used in the various reports, and/or targeting species for harvesting. The following code indicators and groups are permissible:

<u>Code</u>	<u>Group</u>
0	Report by totals only (i.e., all species combined).
1	(This code is default.) No combining occurs. Reports are by individual species.
2	Make two groups for summary reporting: <ul style="list-style-type: none"> (1) Conifers - composed of all conifer species (2) Hardwoods - composed of all hardwood species.
3	Make nine groups for summary reporting: <ul style="list-style-type: none"> (1) white pines - (sugar and white pines) (2) yellow pines - (ponderosa and Jeffrey pines) (3) Douglas-fir - (Douglas-fir) (4) true fir - (red and white firs). (5) cedar - (cedar) (6) conifer misc - (lodgepole and miscellaneous conifers) (7) black oak - (black oak) (8) tan oak - (tan oak) (9) hardwood misc - (chinquapin and miscellaneous hardwoods).
4	Select user-defined grouping option. Any combination of up to 14 groups designated by the user in a species grouping file described in the input section. The program requests the name of the species-grouping input file.

Note: Regardless of the option chosen, totals are always reported. Species groups should only be used when actually needed, because their use slows the computation process.

- su Print out the user-defined species group names and the species included in the groups. This command is used to insure that the species grouping file was read in correctly.

- fl** Set print flag for nonexistent species groups in the yield summary. The choices are:
- 0 - Print a line of 0's if the species is not present
 - 1 - Do not print if the species is not present (default)
- yf** Set yield summary flag to indicate summary format. The choices are:
- 0 - By totals only
 - 1 - By the same criteria as specified with the **fl** and **sp** options (default)
- cl** Set up a user-defined calibration scheme for later implementation in the **gr** or growth simulation routine. When the **cl** command is entered the user is given three options for entry method:
- 0 - Cancel option and return to menu
 - 1 - Keyboard entry of calibration scheme
 - 2 - Entry from an external file

Keyboard entry of calibration scheme

When keyboard entry has been requested, the program asks the user which models to calibrate. The choices are:

- 1 - Basal area only
- 2 - Height only
- 3 - Both basal area and height

The program executes the next section once if option 1 or 2 is chosen (i.e., only one of the models is calibrated) or twice if option 3 is chosen (i.e., both models are calibrated).

Entering calibration vectors

The program first asks the user if the same basal area (height) calibration factors apply to all species. If the user answers "n" for no, the program asks for the codes of the species to include in the first calibration group. If the user answers "y" the calibration is for all species, the program skips the section for entering species codes.

The program then asks if the user wishes to enter calibration factors by diameter (height) classes. If "n" is entered, the program asks the user to enter the calibration factor. This calibration factor is applied to all species included in the group regardless of tree diameter (height). Growth adjustments are all relative to the model norm, hence the default calibration factor is 1.00 (i.e., 100 percent of model norm). Entering 1.12 would increase basal area (height) growth by 12 percent. CACTOS limits the range of adjustment between 0.8 and 1.2 (80 and 120 percent of model norm). If the user enters "y" for calibration by size class, the program asks the user for the number of size classes desired (2-5).

Classes are defined by a lower size limit and a corresponding calibration factor. The lower size limit for the first size class is set to 0.0 and the user is asked to enter the calibration factor for this limit. The program then asks for the lower DBH (height) limit and calibration factor for the 2nd, 3rd, 4th, and 5th size classes.

When size classes are used, the tree's DBH (height) determines the calibration factor applied. (See Appendix D for detailed discussion of application.) If calibration is done by species, the program asks if the user wants to enter another calibration group. The user may enter as many groups as desired by answering "y" to this question. The program repeats the section starting with the entering of species codes included in the nth group.

External-file entry of calibration scheme

When external-file entry is requested, the program asks the user for the name of the calibration file and attempts to locate it. If the file cannot be found (i.e., the wrong name was entered), the program notifies the user and requests the file name again. When the file is found, the program reads the calibration scheme contained in the file. If an error occurs while reading a calibration scheme, the program notifies the user and resets the program calibration to the default values.

Calibration summary

When entry of the calibration scheme is completed (either by keyboard or external file), the program prints a summary of the calibration scheme on the screen. We recommend that the user save this in the report file to provide documentation on user calibration.

Once a calibration scheme is designated, it may be applied as a user option in the gr command (see section VI. B for detailed instructions). Note that the calibration scheme is not automatically applied. The calibration may also be redesignated at any point in the simulation (see cl command discussion under main program, section IV. E). For further discussion on use, see Appendix D, which includes a flow diagram and a sample runstream.

iq Inhibit the record quintupling process in the pseudostochastic procedure. The pseudostochastic/record quintupling process performs a complex statistical error application to the tree records entered. The inhibiting of record quintupling should only be done after the user has developed an understanding of this process. For a detailed discussion of pseudo-stochastics in CACTOS see Koehler and Wensel (1985).

ex Exit the initialization routine and enter the main routine.

Note: If a command is not recognized, the program responds with an appropriate message and allows the user to reenter a command.

VI. MAIN PROGRAM

After initialization, the user enters the main program. In the main program, the user may issue commands to grow the stand, enter the harvest routine, and specify the reports to save in the report file. The prompt for the main program is:

go:

The main program menu contains the following commands:

Report Commands

- | | | | |
|------|--------------------------------|------|----------------------------------|
| • pi | print initial description | • pm | print DBH mins and merch tops |
| • sc | print current species group | • su | print user-defined species group |
| • dp | display tree file | • et | print elapsed time |
| • dt | enter DBH distribution routine | • pf | enter stand profile routine |
| • dc | print DBH class table | • st | print stock table |
| • yd | print yield table | • sl | print standing log table |
| • cg | print current 5-year growth | | |

Simulation Commands

- | | | | |
|------|-----------------------|------|-----------------------------------|
| • gr | enter growth routine | • ig | add ingrowth to tree file |
| • ct | enter harvest routine | • cl | initialize/reset user calibration |

File Utility Commands

- | | | | |
|------|---------------------------|------|--------------------------------|
| • wc | write coefficients | • es | external save of current stand |
| • sv | save current stand status | • ns | start over with new stand |
| • rt | restore stand saved by sv | • os | truncate yield summary |
| • ex | exit from program | • pc | print commands |

- Information from this command may be routed to the report file.

VI. A. Report commands

CACTOS has several report commands allowing the user to generate various descriptions of the stand during the simulation. Some of the reports can be saved in the report file if desired (these commands are identified in the command summary). The other report commands are available to aid the user in controlling the simulation. The information presented in these reports is automatically placed in the report file and/or yield summary.

Many of the report commands allow the user to specify the species to include in the report. In these cases, the program asks the user to enter the species choices. The alternatives are:

- 0 All species together
- 1 By one or more species
- 2 By one or more species group

If "0" is entered, a report including all species present is printed. If a "1" is entered, the program lists the species codes and asks the user to enter the codes of the species to include in the report, terminated with a "/". If a "2" is entered, the program lists the species group codes, and asks the user to enter the codes of the groups to include, terminated with a "/". The species choice is listed at the top of the report. However, this list of species is just a labeling convention and does not mean that all species listed are present in the stand. Thus, careful development of species lists results in greater clarity of the report summaries.

- pi Print initial stand description (i.e., stand identifier, site indices, and initial ages as supplied in the stand description input file). This initial description is automatically placed as a header in the yield summary and report file.

- pm Print cubic and board foot DBH minimums and merchantable tops. These limits are also placed as a header in the yield summary and report file.

- sc Print the current species group code and which species are included in the groups. This table may be placed in the report file. Note: This command does not print user-defined groups. If the user-defined grouping option is in effect, use the su command.

- su Print the user-defined species group names and the species included in the group if the option is in effect. This table may be placed in the report file.

- dp Display the current status of the tree record file (i.e., the tree records from the stand description file). The program requests a record skip causing the program to skip records when printing (e.g., entering "1" causes every tree record to be printed, entering "2" causes every second record to be printed, etc). This table may be placed in the report file. Note: The table saved in the report file will have the same record skip as the table printed to the screen.

- et Print the simulated elapsed time, in years passed since entering the stand. This command is a user aid and may not be routed to the report file. All reports list the elapsed time as part of the report header.

- dt Graph the current diameter distribution. The user controls the species to include in the graph as discussed earlier. Graphs created by this command may be saved in the report file.

pf Graph the current stand profile, 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.

dc Print a diameter class table showing current stocks and most recent five-year growth. The user controls the species to include in the table. After the species are entered, the program asks the user for the lower DBH limit, the upper DBH limit, and the class interval. The lower DBH limit sets the first class to include in the table. The first diameter class printed includes trees with DBH's from 0 inch to the DBH specified. The default is 0 inch DBH. The upper DBH limit sets the last class to include in the table. The last table entry includes all trees with a DBH greater than the upper DBH limit. The default is 50 inches DBH. The class interval sets the width of the diameter classes. The default is a two-inch class width. To choose the defaults, the user enters a "/" in response to the prompt. This table may be saved in the report file. After the user indicates whether or not to save the table, the program asks the user if more tables are desired. Entering a "0" returns the user to the main program prompt, "go:". Entering a "1" causes the table to be reprinted showing averages, rather than totals, by DBH classes. Entering a "2" converts the table to percentages, where the entries are a percent of the included species totals. Entering a "3" produces percentages, where the entries are a percent of the stand total.

The upper DBH limit is sometimes adjusted from the user-supplied input (a) to make the upper DBH limit an even multiple of the increment and (b) to insure that there are not more than 25 classes. The diameter class table is labeled "standing diameter class table" when the dc command is issued after a growth simulation (i.e., gr command). When the dc command is issued after a harvest simulation (see ct command, section VII) the table is labeled "Residual diameter class table." The growth figures listed in a "standing" diameter class table are the current five-year growth of the stand. The growth figures listed in a "residual" table include only that portion of growth attributable to the trees remaining (residual) after the harvest. For growth figures on trees removed by harvest, see harvest diameter class command, hc (section VII). If a diameter class table is produced at elapsed time of zero, the table is labeled "standing" (unless harvest is done at time zero) and does not include growth figures (unless ingrowth is added at time zero).

st Print the current stand inventory (stock table) indicating average DBH, stems/acre, basal area/acre, and cubic and board foot volumes/acre by the species groups set by the sp command. The information in this table is automatically placed in the yield summary after every change to the stand (i.e., after every growth cycle, harvest, and ingrowth entry), and may not be routed to the report file.

yd Print the current yield summary. This command is a user aid that allows the user to look at the yield summary without exiting the program.

sl Print the standing log inventory by two-inch diameter classes. The inventory reports volumes for: Yellow Pine, which includes ponderosa pine, lodgepole pine, and Jeffrey pine; White Pine, which includes sugar pine and white pine; True Fir, which includes white fir and red fir; Douglas-fir; and Cedar misc. The report is by 16-foot logs for cubic volumes and 16.5-foot logs for board foot volumes. Cubic volumes are estimated by Smalian's formula applied to one-foot segments of the log. Board volumes are estimated

using the Scribner board foot volume equation for logs with a top dib (diameter inside bark) greater than nine inches. For logs with a top diameter inside bark (dib) less than or equal to nine inches, Scribner factors are used to calculate log volume. All volumes reported by this command have been adjusted to be compatible with the volume equation totals. Also, the equation/taper ratio used to adjust the volumes is reported below the totals for each species group. The table may be saved in the report file.

A tree that does not contain at least one-half of a log is not included on either the cubic-foot or board-foot section of the table. Also the number of logs in the smaller dib classes may be different for cubic foot and board foot sections even when the same merchantability limits are used. This difference results from scaling top logs to the nearest foot for cubic foot volume, while scaling top logs to the nearest one-half log for board foot volume.

- og Print the current 5-year growth by species group as specified by the `sp` command. This information is contained in the yield summary, and may not be routed to the report file.

VI.B Growing trees - the `gr` command

After issuing the `gr` command, the user must specify the number of growth cycles to simulate, whether or not mortality and calibration are applied, and the level of detail to report.

Number of growth cycles

Growth estimates are computed in terms of 5-year growth cycles. Thus, a 40-year simulation is requested by specifying "8" growth cycles.

Mortality

The mortality option is "on" when the growth routine is entered. To turn the mortality option "off," place a minus sign in front of the number of cycles. A 40-year simulation without mortality is specified as "-8" growth cycles. The message "MORTALITY ON" or "MORTALITY OFF" reminds the user of the status of the mortality option. Also, the letter "M" is placed in the yield summary for any growth period to which mortality is applied.

Calibration

If a calibration scheme has been designated before issuing the `gr` command (see `cl` command, section V and VI.E), the program alerts the user and asks how the calibration should be applied. The form of this message depends on how the calibration scheme is designated. If only one model (either basal area or height) has been calibrated, the program asks the user if this calibration scheme should be applied to the number of growth cycles requested. If the user enters "y" for yes, the calibration factors are applied to designated growth predictions at the end of every five-year growth cycle entered. The user should take note of this compound process when designating and applying calibration schemes in CACTOS. If both basal area and height models have calibration schemes, the program gives the user the following application choices:

- 0 Do not apply calibration scheme
- 1 Apply basal area calibration scheme only
- 2 Apply height calibration scheme only
- 3 Apply both basal area and height calibration schemes

If a calibration scheme is applied to a given growth cycle, one of the following letter codes is placed in the yield summary for that growth period: "D" if only basal area is applied, "H" if only height is applied, or "B" if both calibrations are applied.

Tree detail and summary code

The program then asks if either individual tree growth detail or growth summary information is desired. If either option is desired, the user must enter "y" for yes. Entering "n" for no causes the program to grow the stand for the number of cycles requested. The prompt "go:" appears when the growth simulation is completed.

If "y" is entered, the program first requests a record skip for the individual tree growth detail. The choices are:

- 0 for no individual growth detail
- 1 for detail on every tree record
- 2 for detail on every second tree record
- etc.

After the tree detail record skip is entered, the program requests the growth summary code. The choices are:

- 0 for no summary
- 1 for summary by totals only
- 2 for summary by species groups as specified by sp command

After the summary code is entered, the program asks if the user wants the tree detail or summary information printed in the report file. The way the program routes the tree detail and summary to the report file differs from other report routing. The user cannot preview the tree detail or growth summary before making a decision to place the information in the report file.

VI. C Entering ingrowth - the ig command

CACTOS has no provision for internally generating ingrowth. Therefore the user may wish to enter additional tree records to better represent the stand development for longer simulations. To add more trees to the stand at some point in the simulation to represent, for example, sapling reproduction 10 to 15 years after a heavy harvest, the user enters the ig, ingrowth command. When the ig command is entered, the program requests an ingrowth input mode. The choices are:

- 1 Enter the ingrowth tree records from the keyboard
- 2 Enter the ingrowth tree records from an external file

If input mode 1 is chosen, the program asks the user for the number of ingrowth records to add to the stand. The program then asks the user for five items for each tree record. The items are: species code, DBH in inches, total height in feet, live crown ratio in decimal fraction, and the per-acre weight (i.e. the number of trees/acre the record represents).

If input mode 2 is chosen, the program asks the user for the ingrowth file name. When the file name is entered, the program reads the file and adds the ingrowth tree records to the internal stand representation.

Ingrowth is automatically recorded in the yield summary under the heading of "INGROWTH." The record lists ingrowth by the species groups specified by the `sp` command, and by totals. The next entry is "The Stand After Ingrowth." This entry lists the stand stocks and growth. The growth figures listed are for the current 5-year growth, plus ingrowth. Note: If ingrowth is entered immediately after a harvest, growth figures will include growth remaining after harvest plus ingrowth. After ingrowth input and recording in the yield summary are completed, the program informs the user that ingrowth has been completed and then returns the user to the main program's "go:" prompt. If an ingrowth species does not have a site index already present in the program (i.e., entered in the stand description file), the program prompts the user for the site index.

The user may use the `yd` command to view the yield summary, to ensure ingrowth has been properly recorded. The `dp` or display tree records command also provide a visual check on ingrowth input.

VI. D Harvest - the `ct` command

CACTOS allows the user to simulate harvesting or thinning and to produce reports on the harvest or thinning. To simulate a harvest, the user enters `ct`, the `cut` command. The harvest routine is a menu-driven routine like the initialization routine and main program. The harvesting routine is described in detail in section VII.

VI. E User calibration - the `cl` command

As mentioned in section V, the user calibration scheme may be redesigned at any point in the simulation by issuing the `cl` command in response to the "go:" prompt. If no calibration scheme exists in the program memory, the `cl` command behaves exactly as described in section V. However, if a calibration scheme is present and the user chooses to redesignate only one model (basal area or height), the other model remains as previously designated. If both models are redesignated or if a different external file is read, the complete scheme is replaced.

The use of the `ns`, new stand command, does not reinitialize the calibration scheme. The calibration scheme stored in memory remains there until replaced by the user or until the program is terminated.

VI. F Utility commands

CACTOS provides a number of utility commands that allow the user to: (1) efficiently generate alternative prescriptions for a single stand; (2) simulate many stands during one entry into the program; and (3) produce simple diagnostic reports. The first two functions use the `sv`, `rt`, `es`, and `ns` commands, which are discussed in section III Structure and Strategies. These commands are described below, along with the diagnostic commands.

- `sv` Internally save the current state of the stand. This command saves the stand description, the report file and the yield summary as they exist at the time of the execution of the `sv` command. Only one stand state may be in saved status at any time.

- rt** Internally restore the stand in saved status. The program first saves the current report file and yield summary, then requests names for another yield summary and another report file. Once these file names are entered, the program restores the stand description, the report file and the yield summary to the state existing at the time of the save.
- Note: If the user wishes to externally save the current stand description, the **es** command must be entered prior to the restore command, because the restore command destructively replaces the current stand description with the internally saved stand description.
- es** Externally save the current stand description. The program requests a file name for the externally saved stand description. The program formats the file so that the user can reenter the stand using the **ns** command or when first entering the program. In both cases, the report file and yield summary start with the stand description as the first entry.
- ns** Start over with a new stand. This command saves the current report file and yield summary, then requests a new stand description input file name. From this point on the program runs from the beginning, except that the welcome page is not printed. The user is allowed to enter the initialization routine, and must enter it if other than default parameters are desired, because the **ns** command reinitializes all parameters (with the exception of the calibration scheme and **r3** harvest parameters) to their default values. This command also deletes any stand in internal saved status.
- os** Omit (remove) any stand in internal saved status and reinitialize the yield summary and report file so that the current stand state is the first entry in the output files.
- cf** Change the output file number. The default output file number is 6 (i.e., the screen). This command allows the user to change this number to any number between 11 and 15. Implementing this command causes the output normally printed to the screen to be printed to a file named "fort.xx," where "xx" equals the user-entered file number. This command may be used for printing single reports or reports that cannot be routed to the report file. The file(s) "fort.xx" are saved at program termination. However, if the CACTOS program is run again and the same unit number is specified, any data stored in "fort.xx" is erased without warning. Caution: "fort.xx" files are intended for temporary use only.
- wc** Write coefficients. This command is for diagnostic purposes only. This command prints the coefficients read from the coefficient file, "cofile." This command may be used to insure that the program is correctly reading the coefficients.
- pc** Print the list of available commands.
- ex** Exit from the program. The program automatically saves the output files.

VII. HARVEST ROUTINE

When the `ct` command is executed, the user enters the harvest routine. The harvest routine initially requests a harvest label which is printed in the harvest section of the yield summary. This label may be up to 30 characters long and can be used to document the type of harvest simulated. The prompt in this routine is:

`cutgo:`

The harvest routine menu contains the following commands:

Harvest commands

- `pc` print harvest commands
 - `cf` change output file number
 - `dt` enter DBH distribution routine
 - `pf` enter stand profile routine
 - `st` print current stock table
 - `dc` print DBH class table
 - `r1` harvest - DBH control
 - `r2` harvest - Basal Area control
 - `r3` harvest - Free
 - `r4` harvest - Sanitation
 - `ih` print intermediate harvest since last `ih` call
 - `ch` print cumulative harvest since entering cut routine
 - `th` print total harvest since beginning simulation
 - `hc` print cumulative harvest DBH class table
 - `hl` print cumulative harvest log stock table
 - `ex` exit cutting routine
- information from this command may be routed to the report file.

Explanation of commands

The harvest routine is menu driven with two letter commands similar to the main program commands. Many of the commands are for producing reports on the stand or the harvest, and some of these reports may be placed in the report file. There are four harvest commands: `r1`, `r2`, `r3`, and `r4` which allow the user to alter the tree records to simulate a harvest. These commands ask the user for the species to cut, using the same conventions as for specifying species to include in reports.

- pc Print list of available harvest routine commands and their functions.
- dt Graph the current diameter distribution (same as in main program). This command is used to view the change in the diameter distribution resulting from a harvest.
- pf Graph the current stand profile (same as in the main program).
- st Print the current stand inventory (stock table) (same as in the main program).
- dc Print the diameter class table. If this command is issued prior to harvesting, it behaves exactly as described in the main program section. If the command is issued after harvest has occurred, the table will contain the residual trees (of the species specified) as they exist at the time the command is issued. The additional tables (e.g. percentages of the stand totals) are not offered until the user exits the harvest routine, as final stand conditions are not determined until then.
- r1 Harvest (remove) trees with DBH control. The program requests four values which specify the prescription:

- (1) The smallest diameter to cut (dl)
- (2) The largest diameter to cut (du)
- (3) The amount (decimal fraction) of the smallest diameter to cut (pl)
- (4) The amount (decimal fraction) of the largest diameter to cut (pu)

These values are entered on the same line, separated by commas. After entering these values, the user specifies the species to cut. The program then processes the tree records, ignoring trees if they are not the appropriate species. If the tree qualifies, the next sequence of events follow:

(a) If the tree diameter "d" is between "du" and "dl," its per acre weight is reduced by the fraction "x" where:

$$x = pl - \{(d - dl)/(du - dl)\} (pl - pu)$$

Hence, if $d = 12.0$, $du = 18.0$, $dl = 6.0$, $pu = 0.2$, and $pl = 0.8$, then:

$$x = 0.8 - \{(12 - 6)/(18 - 6)\} (0.8 - 0.2) = 0.5$$

and 0.5 times the tree record's per acre weight is cumulated as harvests.

(b) If the tree diameter, "d" is less than "dl," and "dl" is prefixed by a minus sign, all of the tree record's per acre weight is cumulated as harvest. The same is true for "d" greater than "du", and "du" prefixed with a minus sign.

(c) Otherwise, the tree record is not altered.

- r2 Harvest (remove) trees with Basal Area Control. This routine allows the user to specify harvest by basal area to cut or by basal area to leave (i.e., residual basal area). The program asks the user to specify which method to use. Entering a "0" indicates the basal

area specified is the amount to cut. Entering a "1" indicates the basal area specified is the amount to leave. The amount of basal area in the current stand is shown on the screen and the user is prompted to specify the amount of basal area to cut or to leave. The user is then prompted to specify the species included in the harvest. This harvest option is intended to mimic thinning from below or thinning from above. If a positive basal area is entered, the program mimics a thinning from below. The trees with the smallest $((DBH^{**} 1.5) * lcr)$ are removed first. This formula for tree selection removes the trees with the smallest DBH first, unless the live crown ratio (lcr) of the next largest tree is much smaller than the previous tree (e.g. a tree with a 10 inch DBH and 0.4 lcr will be cut before an 8 inch DBH tree with a lcr of 0.6). If a negative basal area is specified (i.e. prefixed by a minus sign), the program mimics a thinning from above. The trees with the largest values of $((DBH^{**}1.5)+++lcr)$ are removed first. Thus, a tree with a larger DBH is removed first unless the next smaller DBH tree has a much smaller live crown ratio. (Note: all trees with crown ratios of 0.6 or greater are treated as though they have crown ratios of 0.6.)

- r3 Free Harvest. This command invokes harvest option r3, designed to allow the user to simulate almost any type of harvest. Briefly, r3 allows the user to set up to 24 variable-width diameter classes; harvest in any of these classes; specify amount to cut by either number of trees or basal area, in either absolute amount or percent; and specify species to cut, as well as which tree characteristics to consider in selecting trees in a given class. The flexibility of this option requires some initial planning to fully utilize its capabilities. A detailed description and an example of r3 are in Appendix C.
- r4 Sanitation harvest. This harvest option removes trees in the stand with a live crown ratio less than or equal to the user-specified live crown ratio. The program requests the live crown ratio target and allows the user to specify the species to cut.
- Note: Any combination of the harvest options, (i.e., r1, r2, r3, and r4) can be executed successively to allow considerable flexibility in simulating harvest.
- ch Print cumulative harvest since the user entered the harvest routine. This table can be saved in the report file.
- ih The first time this command is executed, it behaves as a ch command. The next time it is executed, the ih command prints the intermediate harvest, which has occurred since the last time the ih command was executed. This table can be saved in the report file.
- th Print total harvests that have occurred since the beginning of the simulation. The commands ch and ih only report harvests that occur within a given entry into to the harvest routine. The th command reports all harvests that have occurred. This table can be saved in the report file during the simulation. The table is automatically placed at the end of the yield summary when the simulation is terminated (i.e. the last entry in the yield summary is the total amount harvested during the simulation by species groups as specified by the sp command).

- hc Same as the dc command in the main program, except that the diameter class table is for harvested trees. As with the dc command, the user specifies the species to include. This table includes all trees, of requested species, harvested since entering the harvest routine, and the current 5-year growth removed by the harvest. This table may be saved in the report file.
- hl Same as the sl command in the main program, except that the report is for harvested logs. The table contains volume by logs for trees harvested since entering the harvest routine, and may be saved in the report file.
- ex Exit harvest routine, and return to main program. The program asks the user if a lag time is desired. This option mimics the lag time occurring between a thinning and the time the stand begins to respond. If "y" (for yes) is entered, the program requests the number of years of growth the stand "captures" in the next 5-year growth cycle. For example, if the user enters "4" then the stand captures 4 years of growth or 80 percent of the "normal" 5-year growth.
- If the user clearcuts the stand (i.e., removes all the trees), CACTOS allows the user to exit to the main program, but does not allow the simulation to continue. The user is given the choice to start over with a new stand or to exit the program. In either case, the yield summary and report file are saved. Between clearcutting the stand and exiting the harvest routine the program allows the generation of reports, but does not allow further harvesting. However, r3 is the only harvest option which informs the user that the stand has been clearcut.

VIII. VALIDATION OF PREDICTIONS

The individual tree growth prediction in CACTOS uses four models to predict change. These models predict (1) change in diameter, (2) change in height, (3) change in height to the crown base, and (4) mortality. The diameter and height growth models consist of a component for growth "potential," based primarily upon site index, and a component for "competition," based primarily upon CC66. (CC66 is the area of crowns on a "slice" taken from the stand at 66 percent of the tree's height.) This quantity is computed using crown models developed by VanDeusen and Biging (1984). The diameter and height growth models are presented in Wensel and Koehler (1985). The height to crown base recession model is a static model from the stand generator STAG (VanDeusen and Biging 1985). The diameter, height, and crown base models were developed from data collected by the Northern California Forest Yield Cooperative. The models show good predictive capability relative to the data base.

The data base contains no mortality data. CACTOS uses the mortality equation developed for Douglas-fir on the north coast of California (Krumland, Dye, and Wensel 1978).

Validation of the model by field testing is a crucial part of the program's development. As remeasurement of the permanent plots by Coop members occurs, these remeasurements can be used to calibrate and improve the predictive models. The collection of remeasurement data is necessary for validation of the model, and should allow for the fine tuning of the model to specific regions of California.

In field evaluation of the models, the users should keep in mind that the growth predictions are made by four individual growth equations. Users should look individually at the behavior of each of the four growth equations as well as how they interact with each other.

In summary, the current growth coefficients have only been tested against the data used to generate them. Until they are tested against independent data sets, they should be considered provisional. Users of CACTOS are encouraged to do their own testing of the predictions and to report the results to the authors.

IX. MISCELLANEOUS NOTES

Output definitions

The following is a list of captions and definitions:

et	elapsed time in years since the start of simulation
dbar	average stand quadratic mean DBH in inches
basar	basal area per acre in square feet
cfvol	cubic foot volume per acre in thousands
bdvol	scribner board foot volumes per acre in thousands (hardwoods not included)
tpa	trees (stems) per acre
bagro	five-year basal area growth per acre in square feet
cvgro	five-year cubic foot volume growth per acre in thousands
bdgro	five-year board foot volume growth per acre in thousands (hardwoods not included)

The following items apply to individual trees if lists are requested by the dp or gr command:

sp	species code
sg	species group code
DBH	tree diameter at breast height in inches
ht	total tree height in feet
cr	crown ratio expressed as a decimal fraction
exp	tree expansion factor (i.e. number of trees per acre represented)
dgro	current five-year DBH growth in inches
hgro	current five-year total height growth in feet
hcal	absolute fraction of normal height growth (does not include user calibration)
dcal	absolute fraction of normal basal area growth (does not include user calibration)

Notes

- (1) All growth estimates are net figures (gross growth minus mortality) and include trees that are part of the internal tree list growing into the size classes specified by the cm and bm program options. Ingrowth entered by the user is recorded in the yield summary and added to the growth figures only in the sections titled "STAND AFTER INGROWTH."
- (2) Harvest statistics are computed as the difference between the stand summaries taken before and after the harvest. The exception is the harvest dbar which is converted to the average diameter of the harvested trees.
- (3) Species codes are initially truncated to "real number" representations of integers in the range of 1-14. Tree records with species codes outside this range are deleted from the tree list on input.

X. ADVANCED TOPICS

X.A Growth period adjustment

CACTOS has an option which allows the user to report the amount of growth at any point less than 10 years elapsed time. This option is useful when the user wishes to compare the CACTOS growth projections with permanent plot growth measurements. The user implements this option by adding a "growth period adjustment value" (greater than zero and less than 10) to the first line of the stand description input file. The value should be placed in columns 46 through 50 inclusive (format F5.2; i.e., the decimal point occupies column 48). If the input file has the value "4.25" (indicating 4.25 growing seasons between measurements) in this location, CACTOS adjusts the elapsed time of the first growth period to 4.25 years. If the value is 6.5, CACTOS grows the stand for one 5-year growth period and adds a second growth cycle with an elapsed time of 1.5 years. Note that the second growth cycle is added automatically, thus growing the stand for one cycle with a growth period adjustment value greater than 5.0 results in two growth periods simulated.

A second use for this option occurs when the user wishes to align the projections of two or more stand descriptions measured at different points in time. In this case the growth period adjustment value represents the number of growing seasons elapsed between the time of measurement and some selected reference time. Implementation is the same as described above.

X.B Batch mode

CACTOS is capable of batch processing multiple stand descriptions through multiple prescriptions. This option is useful when the user wishes to run more than one stand description through the same set of simulations. The user invokes the batch mode by entering a "b" in response to the prompt 'enter "return" to continue' at the beginning of the program run.

When the user invokes the batch mode, CACTOS prompts the user for two file names, one file contains the "input filenames" and the other file contains the "batch commands". These are described below. After these two input files are successfully opened, the program asks the user to choose the output files to be produced by the simulation. In addition to the yield summary and report file, batch mode can produce a "tree list" file. This file is a sequentially accessed, unformatted (binary) file designed for post-processing. The tree list file is described below. The user has the option of producing any combination of these output files, by entering "y" or "n" in response to the prompt for each file type. The program then asks the user where the command prompts and other screen output should be printed during the batch operation. The user may choose an external file, the screen, or a scratch file for automatic deletion upon completion. As the simulation proceeds, the file name of the input file being processed is printed to the screen.

The Input filenames file

This input file contains the file names of the stand description input files to be processed (format A32 left justified). An example of an input filenames file (for the PC version) is shown below:

```
columns:
0      1      2      3 3
line 1234567890.....0.....0.2.....
1    demo1.sd
2    demo2.sd
3    demo3.sd
4    \stand1\meas1\input\demo4.sd
```

The above file tells the program that four stand descriptions (demo1.sd through demo4.sd) are to be simulated. The first three files are assumed to reside in the current directory, while the fourth file name specifies the directory in which the file is located.

In batch mode the output file names are automatically supplied by the program. The program takes the root name of the stand description file (the characters preceding the first period '.' or blank ' ') and appends a prescription code and extension to form an appropriate output file name. The prescription code is a five character code supplied by the user on the first line of the batch command file. The extensions are '.YD', '.RP', '.ES', and '.CTL' for the yield summary, report, external save, and tree list output files, respectively. As specified above, the stand description file name may be up to 32 characters long. The output file naming convention used in batch mode allows for a 23 character root name, a five character prescription code, and a four character extension (counting the period). Users should exercise care in the use of these conventions as some systems allow fewer than 32 characters in a file name. For example, DOS only allows an eight character root name and a four character extension. Thus, PC users should choose stand description file root names and prescription code lengths such that the combination does not exceed eight characters (e.g. a user could use a five character root name and a three character prescription code). PC users can use the rest of the allowable characters to specify directory location (path) of the file.

The output file names formed by the program have precedence over existing files. If a file with the same name already exists, it will be overwritten without warning. The exception to this convention occurs with the external save file. If a file with the same name exists, the externally saved stand description will be appended to the existing file. This exception allows for multiple execution of the external save, es, command. No separator code is placed between the externally saved stand descriptions because the first line of the description specifies the number of tree records that follow. Caution: In batch mode the file name of the external save file is supplied automatically; do not specify a file name in the command file.

Batch mode can use concatenated files for input and produce concatenated files for output. This is useful for running many inventory plots through the simulator, eliminating the need for keeping track of several sets of file names. The program automatically checks for concatenated files and processes all stand descriptions contained within each file. When concatenated files are used for input, the program automatically produces concatenated output files, appending the output associated with each new stand description to the appropriate output file. The program will place an asterisk in column 2 on a separate line between concatenated report files or yield summaries. These asterisks can be used later to separate the concatenated files for analysis. Likewise the number "999" is used as a separator in concatenated tree list files. No separator code is placed between concatenated externally saved stand description files.

Batch commands input file

This input file contains the commands and responses to prompts that define the simulation to run. The first line is reserved for the up to five character prescription code associated with the simulation (format A5 left justified). This code is used to form the output file names for a particular simulation. The second line must contain the value "y" or "n" (format A1). If the second line contains an "n", the program skips to the main program menu and expects the third line to be a main program command. If the second line contains a "y", the program enters the initialization routine and expects the third line to be an initialization command. The last line in a given set of simulation commands must contain either the main command ex or ns. The ex command causes termination of the simulation on one stand and initiation of the simulation on the next stand. The ns command tells the program to run the current stand through another set of simulation commands which follow the ns command. The lines that follow the ns command follow the same structure as the first set of commands, with the first line reserved for a new prescription code, the second line reserved for the initialization option choice, and so on. In this way multiple simulations can be stacked in the command file and executed in a single batch run. If the multiple simulation option is used

each set of commands must have an unique prescription code to prevent the overwriting of files from a previous simulation. The following is an example of a batch commands input file with a single set of simulation commands:

<u>command file</u>	<u>explanation</u>
RX2a	prescription code for forming output file names
y	enter initialization routine
iq.	set quintupling option (toggle)
1	inhibit quintupling option
ex.	exit initialization routine
dp.	display tree records
1	set record skip to one (i.e. display all tree records)
y	save the display tree record report in report file
gr.	enter grow routine
-001000100010002y .	grow for one cycle without mortality, skip tree detail/summary prompts, print growth detail with record skip of one, print summary by species groups, route tree detail/summary to report file
dp.	display tree records
1	set record skip to one
y	save the display tree record
es.	perform external save of stand
ex.	end simulation

This command file could be used to simulate stand descriptions for comparison with permanent plot growth data, if the stand description input files contain growth period adjustment values.

Some commands in the interactive version do not work in batch mode and/or serve no purpose for the batch version. The user-aid report commands (e.g. *et*, *pi*, *pm*, etc.) that cannot be routed to the report file serve no purpose because the user is not normally watching the screen during batch mode. The utility commands *cf*, *os*, *ns*, *sv*, and *rt* should not be used in batch mode. They produce undesirable results if attempted.

The Tree list output file

The tree list file is an output file designed for post-processing. It reports the growth and yield predictions at the finest level of detail, the tree record. Reporting predictions in terms of tree records allows for validation on an individual tree basis as well as production of customized summaries not available within the simulator.

The file contains all the information currently printed in the yield summary and also the tree list used to produce the summary. The first two lines of the file contains header information. The rest of the file contains yield sections, one for the initial stand condition and one for the stand condition after every

change simulated for the stand (i.e. one after each growth cycle, harvest, and ingrowth simulation). The file is a sequentially accessed, unformatted file. These file properties minimize the size of the file and the I/O processing time. The contents of the file are described below:

Header information:

<u>Line number</u>	<u>Information and variable type</u>	
1	Stand identifier (character*20)	
	Cubic ft. minimum D.B.H. (real)	These four variables specify the standards used in calculating the stand summaries.
	Cubic ft. merchantable top (integer)	
	Board ft. minimum D.B.H. (real)	
	Board ft. merchantable top (integer)	
2	Site by species (14 reals)	
	Age by species (14 reals)	

Yield section information:

<u>Line number</u>	<u>Information and variable type</u>
1	yield code (integer) 0 = initial stand condition, 1 = after growth cycle, 2 = after harvest, 3 = after ingrowth
2	elapsed time (real)
3	average stand diameter by species and total (15 reals) stems per acre by species and total (15 reals) basal area per acre by species and total (15 reals)
4	cubic volume per acre by species and total (15 reals) board volume per acre by species and total (15 reals)
5	basal area growth per acre by species and total (15 reals) cubic volume growth per acre by species and total (15 reals) board volume growth per acre by species and total (15 reals)
6	number (nrec) of tree records that follow (integer)

The next nrec lines contain tree record information (one line per tree record). Each line contains the species code, D.B.H., total height, live crown ratio, current per acre weight, diameter growth, height growth, per acre weight before mortality, and per acre weight before harvest for the tree record (9 reals). All real and integer variables in the tree list file are four byte variables.

The tree list file option should not be used with the species grouping option, because the tree list file does not preserve the species grouping codes and the stand summaries would not be interpretable.

The batch mode of CACTOS produces a batch report file with the name "batch.rp." This report file list all files processed by and all input processing errors that occur during a batch run. If an I/O error occurs the program termination message is ERRORS IN BATCH RUN. SEE "BATCH.RP". Errors in the batch command file can not be discovered by CACTOS prior to the execution of the simulation. Errors cause the program to either crash or behave unpredictably. Therefore, it is important to test the batch sequence interactively before starting a batch run.

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USER NOTES

APPENDICES

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APPENDIX A. SAMPLE INPUT FILES

Example of a CACTOS stand description input file.

Columns:

line	1	2	3	4	5	6	7
	1234567890	0	0	0	0	0	0
1	Demo Data Plot 9-79		27				
2	100.	0.	80.	90.	90.	0.	0.
3	30.	0.	30.	30.	0.	0.	0.
4	5.000	1.200	10.000	0.770	40.000		
5	5.000	7.400	41.000	0.780	10.000		
6	4.000	5.000	26.000	0.680	10.000		
7	5.000	9.900	41.000	0.240	10.000		
8	5.000	9.100	43.000	0.540	10.000		
9	3.000	7.800	35.000	0.880	10.000		
10	5.000	9.500	60.000	0.730	10.000		
11	3.000	9.700	43.000	0.530	10.000		
12	3.000	7.500	30.000	0.460	10.000		
13	5.000	8.500	39.000	0.410	10.000		
14	5.000	7.600	40.000	0.850	10.000		
15	1.000	14.900	82.000	0.560	5.000		
16	3.000	21.900	84.000	0.450	5.000		
17	4.000	19.600	97.000	0.540	5.000		
18	4.000	12.600	66.000	0.510	5.000		
19	1.000	25.500	107.000	0.350	5.000		
20	3.000	21.500	85.000	0.450	5.000		
21	1.000	12.400	79.000	0.630	5.000		
22	4.000	20.100	103.000	0.500	5.000		
23	4.000	22.500	96.000	0.500	5.000		
24	4.000	26.100	108.000	0.230	5.000		
25	3.000	17.400	61.000	0.430	5.000		
26	1.000	28.100	112.000	0.600	5.000		
27	4.000	20.600	105.000	0.570	5.000		
28	1.000	26.400	117.000	0.520	5.000		
29	4.000	20.200	100.000	0.650	5.000		
30	4.000	16.200	88.000	0.600	5.000		
	-----	-----	-----	-----	-----		
	SPECIES	DBH	HEIGHT	CROWN	PER ACRE		
	CODE	(INCHES)	(FEET)	RATIO	WEIGHT		

Example of CACTOS ingrowth file.

		column:																																		
		1					2					3					4																			
line		1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	6	7	8	9	0	1	2	3	4	5	6	7	8	9	0					
1		10																																		
2		5.000	6.000	20.000	0.450	5.000																														
3		3.000	8.000	26.000	0.520	5.000																														
4		4.000	7.100	24.000	0.450	5.000																														
5		4.000	6.500	21.000	0.480	5.000																														
6		5.400	8.500	24.000	0.460	5.000																														
7		3.000	7.500	26.000	0.550	5.000																														
8		3.000	6.400	29.000	0.470	5.000																														
9		5.000	8.200	26.000	0.370	5.000																														
10		5.000	7.200	24.000	0.530	5.000																														
11		5.000	9.200	36.000	0.490	5.000																														
		-----					-----					-----					-----					-----														
		SPECIES	DBH	HEIGHT	CROWN	PER ACRE																														
		CODE	(INCHES)	(FEET)	RATIO	WEIGHT																														

Example of a CACTOS species grouping file.

		column:										
		1					2					
line		1	2	3	4	5	6	7	8	9	0	
1		005										
2		all pines	0102070809									
3		true fir	0506									
4		doug fir	04									
5		resid con	0310									
6		hardwoods	11121314									
		-----					-----					
		GROUP	SPECIES									
		NAME	CODES									

Example of a CACTOS user calibration file.

This file was created using the runstream in Appendix D.

		column:					
		1		2	3	4	
line		1234567890	0	0	basal area calibration factors
1		0.00	6.00	10.00	30.00	30.00	<- diameter class lower limits and...
2		0.80	0.85	1.00	1.06	1.06	<- calibration factors for species 1
3		0.00	6.00	10.00	30.00	30.00	...
4		0.80	0.85	1.00	1.06	1.06	... likewise for species code 2
5		0.00	4.00	8.00	10.00	16.00	etc.
6		0.80	0.85	0.90	0.95	1.00	
7		0.00	12.00	22.00	22.00	22.00	
8		1.00	1.02	1.04	1.04	1.04	
9		0.00	4.00	4.00	4.00	4.00	
10		1.02	1.00	1.00	1.00	1.00	
11		0.00	4.00	4.00	4.00	4.00	
12		1.02	1.00	1.00	1.00	1.00	
13		0.00	6.00	10.00	30.00	30.00	
14		0.80	0.85	1.00	1.06	1.06	
15		0.00	6.00	10.00	30.00	30.00	
16		0.80	0.85	1.00	1.06	1.06	
17		0.00	6.00	10.00	30.00	30.00	
18		0.80	0.85	1.00	1.06	1.06	
19		0.00	4.00	8.00	10.00	16.00	
20		0.80	0.85	0.90	0.95	1.00	
21		0.00	6.00	20.00	20.00	20.00	
22		1.00	1.02	1.18	1.18	1.18	
23		0.00	6.00	20.00	20.00	20.00	
24		1.00	1.02	1.18	1.18	1.18	
25		0.00	6.00	20.00	20.00	20.00	
26		1.00	1.02	1.18	1.18	1.18	
27		0.00	6.00	20.00	20.00	20.00	
28		1.00	1.02	1.18	1.18	1.18	

Continued next page...

Example of a CACTOS user calibration file (continued).

line	column:												<u>height calibration factors</u>	
	1			2			3			4				
	1	2	3	4	5	6	7	8	9	0	1	2		
29		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	<-height class lower limit and...
30		1.07	1.07	1.07	1.07	1.07	1.07	1.07	1.07	1.07	1.07	1.07	1.07	<-calibration factor for species 1
31		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	...
32		1.07	1.07	1.07	1.07	1.07	1.07	1.07	1.07	1.07	1.07	1.07	1.07	...likewise for species code 2
33		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	etc.
34		1.02	1.02	1.02	1.02	1.02	1.02	1.02	1.02	1.02	1.02	1.02	1.02	
35		0.00	10.00	40.00	80.00	80.00	80.00	80.00	80.00	80.00	80.00	80.00	80.00	
36		1.00	1.02	1.04	1.06	1.06	1.06	1.06	1.06	1.06	1.06	1.06	1.06	
37		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
38		1.09	1.09	1.09	1.09	1.09	1.09	1.09	1.09	1.09	1.09	1.09	1.09	
39		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
40		1.09	1.09	1.09	1.09	1.09	1.09	1.09	1.09	1.09	1.09	1.09	1.09	
41		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
42		1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
43		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
44		1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
45		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
46		1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
47		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
48		1.02	1.02	1.02	1.02	1.02	1.02	1.02	1.02	1.02	1.02	1.02	1.02	
49		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
50		1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
51		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
52		1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
53		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
54		1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
55		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	
56		1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	
57		3	2	2										<- Indicator values that control
58		1	1	1	1	1	1	1	1	1	1	1	1	<- the operation and
59		1	1	1	1	1	1	0	0	0	1	0	0	<- interpretation of the above calibration factors see section IV.D.

APPENDIX B. SAMPLE RUNSTREAM

Boldface indicates user entry.

Italic indicates reference in User's Guide.

WELCOME TO

```

      CCCCC      AAAA      CCCCC      TTTTTTTTT      OOOO      SSSSS
CCCCCCC      AA  AA      CCCCCC      TTTTTTTTT      OOOOOO      SS  SS
CC           AA  AA      CC           TT           OO  OO      SS
CC           AAAAAAAAA      CC           TT           OO  OO      SSSSS
CC           AA  AA      CC           TT           OO  OO      SS
CCCCCCC      AA  AA      CCCCCC      TT           OOOOOO      SS  SS
CCCCC      AA  AA      CCCCC      TT           OOOO      SSSSS
```

The California Conifer Timber Output Simulator
Version 3.2

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enter "return" to continue

The California Conifer Timber Output Simulator

by

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Ken Brown, Walter J. Meerschaert, and Mark E. Tply
Department of Forestry and Resource Management
University of California, Berkeley

A Product of the Northern California Forest Yield Cooperative

American Forest Products	The Hearst Corp.
Beaty and Associates	Louisiana-Pacific Corp. (Sierra)
Champion International Corp.	Louisiana-Pacific Corp. (Sonora)
Crane Mills Lumber Co.	Michigan-California Lumber Co.
Diamond Land Co.	Santa Fe Pacific Timber Co.
Fruit Growers Supply	University of California, Berkeley

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

enter "return" to continue

Open the stand description file
Enter a file name:**demo.sd** *IV-A pg.10*

Open the yield file
Enter a file name:**demo.yd** *IV-F pg.13*

Open the report file
Enter a file name:**demo.rp** *IV-F pg.13*

In this program, if the computer is waiting for a command
it will give you a prompt that is:

go: If you are in the main program
initgo: If you are in the initialization routine
cutgo: If you are in the cutting routine.

Do you want to enter the initialization routine,
to change any of the initial (default) control options? (y=yes):y

INITIALIZATION ROUTINE

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

initgo:cm *V pg.14*

Cubic min. DBH = 0.0 enter new;
(must be less than board ft DBH min.):0.0

initgo:ct *V pg.14*

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

initgo:bm *V pg.14*

Board foot min. DBH = 8.0 enter new:8.0

initgo:bt *V pg.15*

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

initgo:sp *V pg.15*

SPECIES GROUP CODES

- 0 - totals only
- 1 - all 14 permissible codes
- 2 - 1) conifers
2) hardwoods
- 3 - 1) white pines 6) con. misc.
2) yellow pine 7) black oak
3) douglas fir 8) tan oak
4) true fir 9) h.w. misc.
5) cedar misc.
- 4 - user defined grouping option
(see user guide for implimentation procedures)

Current code is 1

Enter new code, (0,1,2,3,4):4

Open the species grouping file
Enter a file name:demo.sg

IV-C pg.12

(Use "su" command to check species groups.)

initgo:fl

V pg.16

Print flag = 1 can be either:
0) - print a line of zeros if species not present
1) - do not print if species not present (default)

Enter 0 or 1 :1

initgo:yf

V pg.16

Yield flag = 1 can be either:
0) - by totals only
1) - by criteria specified by "fl" and "sp" options (default)

Enter 0 or 1 :1

initgo:ex

V pg.17

Exiting initialization routine

MAIN PROGRAM

Type "pc" to get a list of available commands
Current output file is 6 (the screen)

go:pi

VI-A pg. 19

Initial Description

stand label = Demo Data Plot 9-79

species	site	age
Pond. Pine	100.	30.
Cedar misc	80.	30.
DouglasFir	90.	30.
White Fir	90.	0.

go:pm

VI-A pg. 19

	min.dbh	merch top
cubic ft.	0.0	4
board ft.	8.0	6

go:sc

VI-A pg. 19

SPECIES GROUP CODES

0 - totals only

1 - all 14 permissible codes

2 - 1) conifers
2) hardwoods

3 - 1) white pines 6) con. misc.
2) yellow pine 7) black oak
3) douglas fir 8) tan oak
4) true fir 9) h.w. misc.
5) cedar misc.

4 - user defined grouping option
(see user guide for implimentation procedures)

Current code is 4

Do you want this table placed in the report file? (y=yes):n

go:su

VI-A pg. 19

USER DEFINED GROUPS

```

-----
all pines :
  Pond. Pine
  Sugar Pine
  L.P. Pine
  White Pine
  Jeff. Pine
true fir :
  White Fir
  Red Fir
doug fir :
  DouglasFir
resid con :
  Cedar misc
  Con. misc
hardwoods :
  Chinquapin
  Black Oak
  Tan Oak
  H.W. misc

```

Do you want this table placed in the report file? (y=yes):y

Table saved in report file.

go:dp

VI-A pg. 19

Display tree records

Total records = 135 enter record skip:10

Tree record

Record skip = 10 elapsed time = 0.00 yrs

no.	sp	dbh	ht	cr	exp	hcal	dcal	sg
1	WF	1.2	10.	0.77	17.64	1.000	1.000	2.
11	WF	7.6	40.	0.85	4.41	1.000	1.000	2.
21	DF	26.1	108.	0.23	2.06	1.000	1.000	3.
31	WF	1.2	10.	0.77	4.87	1.500	1.000	2.
41	WF	9.9	41.	0.24	1.04	1.000	2.008	2.
51	IC	7.8	35.	0.88	1.30	1.515	1.000	4.
61	IC	7.5	30.	0.46	0.95	1.000	2.068	4.
71	WF	7.6	40.	0.85	1.22	1.500	1.000	2.
81	DF	19.6	97.	0.54	0.55	1.000	1.868	3.
91	PP	25.5	107.	0.35	0.99	1.293	1.000	1.
101	DF	20.1	103.	0.50	0.55	1.000	1.868	3.
111	DF	26.1	108.	0.23	0.72	1.449	1.000	3.
121	DF	20.6	105.	0.57	0.55	1.000	1.868	3.
131	DF	20.2	100.	0.65	0.72	1.449	1.000	3.

Do you want this table placed in the report file? (y=yes):n

Begin Growth Routine

MORTALITY ON

Enter the number of 5 yr. growth cycles desired

Note: a "-" (minus) prefix shuts off mortality for all cycles entered.
Enter number of cycles here:3

Do you want either individual tree growth detail
or summary info printed?(y=yes):y

Individual tree detail Record skip:

- 0 for no detail
- 1 for detail on every tree record
- 2 for detail on every 2nd tree record
- ect.

Enter Record skip:10

Summary codes:

- 0 for no summary
- 1 for summary by totals only
- 2 for summary by species groups

Enter summary code:2

Do you also want the tree detail or summary info
to be printed to the report file?(y=yes):y

TREE GROWTH DETAIL - elapsed time = 5.00 yrs
sp dbh ht cr exp hcal dgro hgro dcal

sp	dbh	ht	cr	exp	hcal	dgro	hgro	dcal
WF	9.0	43.	0.42	4.2	1.00	0.46	4.5	1.00
DF	23.4	101.	0.50	2.0	1.00	0.91	5.2	1.00
WF	1.4	12.	0.73	4.5	0.63	0.22	1.8	1.00
WF	10.1	45.	0.27	1.6	1.00	0.18	4.4	0.37
IC	8.3	37.	0.84	1.6	0.60	0.47	1.7	1.00
IC	7.6	33.	0.42	1.6	1.00	0.13	2.7	0.39
WF	8.1	43.	0.83	1.6	0.63	0.46	2.9	1.00
DF	20.0	102.	0.53	0.8	1.00	0.41	5.2	0.42
PP	26.3	111.	0.35	0.8	0.65	0.84	4.2	1.00
DF	20.5	108.	0.49	0.8	1.00	0.42	5.1	0.42
DF	26.9	111.	0.24	0.8	0.61	0.84	2.9	1.00
DF	21.0	110.	0.56	0.8	1.00	0.44	5.0	0.42
DF	21.2	103.	0.65	0.8	0.61	1.01	3.2	1.00

GROWTH SUMMARY - CYCLE = 1 elapsed time = 5.00

species bagro cvgro bdgro

all pines	4.9	0.31	2.27
true fir	1.7	0.08	0.46
doug fir	7.1	0.40	2.69
resid con	2.9	0.10	0.64
Totals	16.6	0.88	6.07

TREE GROWTH DETAIL - elapsed time = 10.00 yrs

sp dbh ht cr exp hcal dgro hgro dcal

WF	9.4	48.	0.43	4.0	1.00	0.44	4.2	1.00
DF	24.3	106.	0.49	2.0	1.00	0.89	5.0	1.00
WF	1.6	14.	0.70	3.3	0.63	0.22	1.8	1.00
WF	10.3	50.	0.29	1.5	1.00	0.17	4.2	0.37
IC	8.7	38.	0.80	1.5	0.60	0.46	1.6	1.00
IC	7.8	35.	0.39	1.5	1.00	0.13	2.6	0.39
WF	8.5	46.	0.80	1.5	0.63	0.43	2.7	1.00
DF	20.4	107.	0.52	0.8	1.00	0.40	4.9	0.42
PP	27.2	115.	0.36	0.8	0.65	0.82	4.0	1.00
DF	20.9	113.	0.48	0.8	1.00	0.41	4.8	0.42
DF	27.8	114.	0.24	0.8	0.61	0.81	2.8	1.00
DF	21.5	115.	0.55	0.8	1.00	0.43	4.8	0.42
DF	22.2	106.	0.64	0.8	0.61	0.97	3.0	1.00

GROWTH SUMMARY - CYCLE = 2 elapsed time = 10.00

species bagro cvgro bdgro

all pines	5.0	0.32	2.46
true fir	1.6	0.08	0.52
doug fir	7.2	0.42	2.91
resid con	2.9	0.10	0.67
Totals	16.7	0.92	6.56

TREE GROWTH DETAIL - elapsed time = 15.00 yrs

sp dbh ht cr exp hcal dgro hgro dcal

WF	9.8	52.	0.43	3.9	1.00	0.41	4.0	1.00
DF	25.2	111.	0.49	2.0	1.00	0.88	4.7	1.00
WF	1.9	15.	0.68	2.6	0.63	0.22	1.8	1.00
WF	10.4	54.	0.30	1.5	1.00	0.16	4.0	0.37
IC	9.2	40.	0.77	1.5	0.60	0.45	1.5	1.00
IC	7.9	38.	0.37	1.4	1.00	0.13	2.4	0.39
WF	8.9	48.	0.79	1.4	0.63	0.40	2.5	1.00
DF	20.8	112.	0.51	0.8	1.00	0.39	4.7	0.42
PP	27.9	119.	0.36	0.8	0.65	0.80	3.8	1.00
DF	21.3	117.	0.48	0.8	1.00	0.41	4.5	0.42
DF	28.5	116.	0.24	0.8	0.61	0.77	2.7	1.00
DF	21.9	119.	0.54	0.8	1.00	0.42	4.5	0.42
DF	23.1	109.	0.64	0.8	0.61	0.94	2.9	1.00

Print diameter class table

How to specify species to be included ?

- 0 - All species together
- 1 - By one or more species
- 2 - By one or more species groups

Enter 0, 1, or 2 :2

The species group codes are:

- 1: all pines
- 2: true fir
- 3: doug fir
- 4: resid con
- 5: hardwoods

Enter codes of groups to be included
(separated by commas, terminated by "/"):2/

Enter lower dbh limit (default=0),
upper dbh limit (default=50),
and class interval (default=2");
(separated by commas).Enter a "/" to choose defaults:/

Standing diameter class table -- et = 15.00 yrs
table is totals by DBH class

stand label = Demo Data Plot 9-79
species groups = true fir

	stocks				growth			
	trees	basar	cfvol	bdvol	basar	cfvol	bdvol	
0- 2	13.2	0.24	0.00	0.00	0.00	0.00	0.00	
2- 4	1.9	0.06	0.00	0.00	0.01	0.00	0.00	
4- 6	0.0	0.00	0.00	0.00	0.00	0.00	0.00	
6- 8	1.4	0.49	0.01	0.00	0.00	0.00	0.00	
8-10	23.4	10.62	0.22	0.77	0.40	0.03	0.16	
10-12	26.2	16.94	0.40	1.59	0.91	0.05	0.26	
12-14	1.9	1.66	0.04	0.17	0.20	0.01	0.04	

totals	67.9	30.01	0.67	2.53	1.52	0.08	0.45	

Do you want this table placed in the report file? (y=yes):

Table saved in report file.

Do you want more tables?

- 0: exit
- 1: average tree by DBH class
- 2: percentages of species group total
- 3: percentages of all species total

More? Enter 0,1,2, or 3:3

Standing diameter class table -- et = 15.00 yrs
 table is percentages of all species total

stand label = Demo Data Plot 9-79
 species groups = true fir

	stocks				growth		
	trees	basar	cfvol	bdvol	basar	cfvol	bdvol
0- 2	7.3	0.08	0.00	0.00	0.00	0.00	0.00
2- 4	1.0	0.02	0.00	0.00	0.08	0.00	0.00
4- 6	0.0	0.00	0.00	0.00	0.00	0.00	0.00
6- 8	0.8	0.17	0.12	0.00	0.00	0.09	0.00
8-10	13.0	3.81	2.37	1.44	2.34	2.75	2.30
10-12	14.6	6.08	4.32	2.95	5.40	5.24	3.76
12-14	1.0	0.59	0.44	0.32	1.16	0.75	0.54
totals	37.9	10.76	7.23	4.70	8.98	8.83	6.60

Do you want this table placed in the report file? (y=yes):y

Table saved in report file.

go:st

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STOCK TABLE

elapsed time = 15.00 years

species	dbar	tpa	basar	cfvol	bdvol
all pines	25.23	24.	83.6	3.35	21.23
true fir	9.00	68.	30.0	0.67	2.53
doug fir	20.89	47.	111.1	4.15	24.49
resid con	15.60	41.	54.1	1.15	5.55
Totals	16.88	179.	278.8	9.32	53.80

go:yd

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YIELD SUMMARY: units = english

stand label = Demo Data Plot 9-79

	min. DBH	merch top
cubic ft.	0.0	4
board ft.	8.0	6

species	site	init. age
Pond. Pine	100.	30.
Cedar misc	80.	30.
DouglasFir	90.	30.
White Fir	90.	0.

species	et	dbar	tpa	basar	cvol	bdvol	bagro	cvgro	bdgro
all pines	0.00	22.42	25.0	68.5	2.38	13.85	0.0	0.00	0.00
true fir	0.00	6.79	100.0	25.2	0.42	1.09	0.0	0.00	0.00
doug fir	0.00	18.11	50.0	89.4	2.89	15.77	0.0	0.00	0.00
resid con	0.00	13.61	45.0	45.5	0.86	3.61	0.0	0.00	0.00
Totals	0.00	13.80	220.0	228.6	6.55	34.33	0.0	0.00	0.00
all pines	5.00	23.36	24.7	73.4	2.69	16.12	4.9	0.31	2.27
true fir	5.00	7.65	84.4	26.9	0.51	1.56	1.7	0.08	0.46
doug fir	5.00	19.04	48.8	96.5	3.29	18.47	7.1	0.40	2.69
resid con	5.00	14.28	43.5	48.4	0.96	4.26	2.9	0.10	0.64
Totals	5.00	14.94	201.3	245.2	7.44	40.40	16.6	0.88	6.07
all pines	10.00	24.30	24.4	78.4	3.01	18.58	5.0	0.32	2.46
true fir	10.00	8.36	74.7	28.5	0.59	2.08	1.6	0.08	0.52
doug fir	10.00	19.97	47.7	103.7	3.71	21.37	7.2	0.42	2.91
resid con	10.00	14.95	42.1	51.3	1.05	4.92	2.9	0.10	0.67
Totals	10.00	15.95	188.8	261.9	8.36	46.95	16.7	0.92	6.56
all pines	15.00	25.23	24.1	83.6	3.35	21.23	5.2	0.34	2.65
true fir	15.00	9.00	67.9	30.0	0.67	2.53	1.5	0.08	0.45
doug fir	15.00	20.89	46.7	111.1	4.15	24.49	7.4	0.44	3.12
resid con	15.00	15.60	40.8	54.1	1.15	5.55	2.8	0.10	0.62
Totals	15.00	16.88	179.4	278.8	9.32	53.80	16.9	0.96	6.84
species	et	dbar	tpa	basar	cvol	bdvol	bagro	cvgro	bdgro

go:sl

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Print log table

Standing log inventory

stand = Demo Data Plot 9-79

elapsed time = 15.00

Cubic volume (MCF/ac) by log size

sp.	Yellow Pines		White pines		True fir		Douglas Fir		Cedar misc.	
dib	logs	cvol	logs	cvol	logs	cvol	logs	cvol	logs	cvol
4	17.4	0.05	0.0	0.00	46.0	0.12	34.8	0.09	37.6	0.10
6	15.1	0.07	0.0	0.00	49.0	0.23	22.6	0.12	16.0	0.07
8	18.3	0.14	0.0	0.00	37.4	0.28	24.0	0.19	16.8	0.13
10	16.6	0.18	0.0	0.00	3.0	0.03	30.3	0.33	5.9	0.07
12	17.7	0.26	0.0	0.00	0.0	0.00	31.9	0.48	9.3	0.14
14	14.8	0.29	0.0	0.00	0.0	0.00	29.8	0.60	12.1	0.26
16	11.3	0.29	0.0	0.00	0.0	0.00	27.4	0.70	2.4	0.06
18	12.2	0.39	0.0	0.00	0.0	0.00	25.2	0.80	8.0	0.26
20	11.9	0.46	0.0	0.00	0.0	0.00	13.3	0.51	0.9	0.04
22	13.3	0.62	0.0	0.00	0.0	0.00	3.3	0.15	0.0	0.00
24	6.9	0.38	0.0	0.00	0.0	0.00	3.3	0.17	0.0	0.00
26	3.3	0.20	0.0	0.00	0.0	0.00	0.0	0.00	0.0	0.00
28	0.6	0.04	0.0	0.00	0.0	0.00	0.0	0.00	0.0	0.00
Totals		3.35		0.00		0.67		4.15		1.15
eqn/taper		0.99		0.00		1.15		1.01		0.99

Board volume (MBF/ac) by log size

sp.	Yellow Pines		White pines		True fir		Douglas Fir		Cedar misc.	
dib	logs	bdvol	logs	bdvol	logs	bdvol	logs	bdvol	logs	bdvol
6	24.4	0.50	0.0	0.00	52.4	1.35	40.9	0.84	36.6	0.72
8	8.4	0.24	0.0	0.00	28.1	1.00	9.5	0.30	0.7	0.02
10	19.1	1.03	0.0	0.00	3.0	0.17	30.0	1.61	9.7	0.54
12	17.0	1.35	0.0	0.00	0.0	0.00	32.0	2.66	7.3	0.55
14	16.5	1.99	0.0	0.00	0.0	0.00	29.1	3.55	12.8	1.55
16	10.4	1.77	0.0	0.00	0.0	0.00	28.2	4.61	2.5	0.44
18	12.1	2.62	0.0	0.00	0.0	0.00	25.7	5.57	7.2	1.50
20	11.0	2.97	0.0	0.00	0.0	0.00	11.8	3.19	0.9	0.24
22	12.5	4.16	0.0	0.00	0.0	0.00	2.7	0.92	0.0	0.00
24	6.9	2.78	0.0	0.00	0.0	0.00	3.3	1.24	0.0	0.00
26	3.3	1.48	0.0	0.00	0.0	0.00	0.0	0.00	0.0	0.00
28	0.6	0.32	0.0	0.00	0.0	0.00	0.0	0.00	0.0	0.00
Totals		21.23		0.00		2.53		24.49		5.55
eqn/taper		1.00		0.00		1.28		1.00		0.97

Do you want this table placed in the report file? (y=yes):n

Current (past) 5 years growth - elapsed time = 15.

species	bagro	cvgro	bdgro
all pines	5.2	0.34	2.65
true fir	1.5	0.08	0.45
doug fir	7.4	0.44	3.12
resid con	2.8	0.10	0.62
Totals	16.9	0.96	6.84

go:ig

VI-C pg. 22

Ingrowth input mode:

- 1) - enter ingrowth trees from the keyboard
- 2) - enter ingrowth trees from an external file

Enter 1 or 2 :1

Enter number of ingrowth records :

Enter ingrowth tree record items

no.	sp	dbh	ht	cr	exp

	x	xx.x	xxx	.xx	xx.x

1	5	2.6	25	.45	10.0

Ingrowth added to tree records and yield summary.

go:ig

VI-C pg. 22

Ingrowth input mode:

- 1) - enter ingrowth trees from the keyboard
- 2) - enter ingrowth trees from an external file

Enter 1 or 2 : 2

Open the ingrowth file

Enter file name here:demo.ig

Ingrowth added to tree records and yield summary.

go:sv

VI-F pg. 23

Internally saving stand, please wait...

Stand saved internally;

Saving yield summary and report file, please wait...

Yield summary and report file saved.

Save completed.

go:gr

VI-B pg. 21

Begin Growth Routine

MORTALITY ON

Enter the number of 5 yr. growth cycles desired

Note: a "-" (minus) prefix shuts off mortality for all cycles entered.
Enter number of cycles here:3

Do you want either individual tree growth detail
or summary info printed?(y=yes):n

go:st

VI-A pg. 20

STOCK TABLE

elapsed time = 30.00 years

species	dbar	tpa	basar	cfvol	bdvol

all pines	27.99	23.	100.0	4.45	30.34
true fir	9.67	85.	43.4	1.04	4.18
doug fir	21.80	53.	136.9	5.60	35.07
resid con	15.60	50.	67.0	1.48	7.54
Totals	17.34	212.	347.3	12.56	77.14

go:es

VI-F pg. 24

External save of stand

Open the external save file
Enter a file name:demo.es

Saving stand please wait...

Stand saved in file demo.es

go:rt

VI-F pg. 24

Yield summary saved in demo.yd
Report summary saved in file demo.rp

Open the yield file
Enter a file name:demo1.yd

Open the report file
Enter a file name:demo1.rp

Restoring stand to saved status, please wait...
Stand restored to saved status;
Restoring report file to saved status, please wait...
Report file restored to saved status;
Restoring yield summary to saved status, please wait...
Yield summary restored to saved status.
Restoration completed.

go:ct

VI-D pg. 23

HARVEST ROUTINE

Enter harvest label (up to 30 char):demo harvest

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

cutgo:r1

VII pg. 26

Harvest with DBH control

Values needed: 1) Smallest dia. to be cut
2) Largest dia. to be cut
3) Amount (decimal fraction) of smallest dia. to be cut
4) Amount (decimal fraction) of largest dia. to be cut

Enter values (separated by commas):0.0,10.0,0.5,0.7

How to specify species to be harvested ?

- 0 - All species together
- 1 - By one or more species
- 2 - By one or more species groups

Enter 0, 1, or 2 :0

Harvest completed.

cutgo:r2

VII pg. 26

Harvest with Basal Area Control

How would you like to harvest?

- [0] Specify basal area to cut.
- [1] Specify basal area to leave.

Enter here :0

Stand Basal Area is 270.9 sq.ft./acre

Enter basal area to cut :-50.0

How to specify species to be harvested ?

- 0 - All species together
- 1 - By one or more species
- 2 - By one or more species groups

Enter 0, 1, or 2 :1

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 the codes of species to be harvested
(separated by commas, terminated with a "/"):1/

Harvest completed.

cutgo:r4

VII pg. 27

Sanitation harvest

This routine will remove all trees that have a live crown ratio
equal to or below the user specified live crown ratio;

Specify live crown ratio target:.35

How to specify species to be harvested ?

- 0 - All species together
- 1 - By one or more species
- 2 - By one or more species groups

Enter 0, 1, or 2 :0

Harvest completed.

cutgo:ch

VII pg. 27

CUMULATIVE HARVESTS

elapsed time = 15.00 years

species	dbar	tpa	basar	cfvol	bdvol
all pines	29.47	11.	50.0	2.08	13.63
true fir	8.06	56.	19.8	0.34	1.10
doug fir	16.58	16.	24.5	0.88	5.47
resid con	8.67	22.	8.9	0.11	0.26
Totals	13.45	105.	103.3	3.41	20.46

Do you want this table placed in the report file? (y=yes):n

cutgo:ih

VII pg. 27

INTERMEDIATE HARVESTS

 elapsed time = 15.00 years

species	dbar	tpa	basar	cfvol	bdvol
all pines	29.47	11.	50.0	2.08	13.63
true fir	8.06	56.	19.8	0.34	1.10
doug fir	16.58	16.	24.5	0.88	5.47
resid con	8.67	22.	8.9	0.11	0.26
Totals	13.45	105.	103.3	3.41	20.46

Do you want this table placed in the report file? (y=yes):n

cutgo:r2

VII pg. 26

Harvest with Basal Area Control

How would you like to harvest?

[0] Specify basal area to cut.

[1] Specify basal area to leave.

Enter here :1

Stand Basal Area is 191.4 sq.ft./acre

Enter basal area to leave:150

How to specify species to be harvested ?

0 - All species together

1 - By one or more species

2 - By one or more species groups

Enter 0, 1, or 2 :0

Harvest completed.

cutgo:st

VII pg. 26

STOCK TABLE

 elapsed time = 15.00 years

species	dbar	tpa	basar	cfvol	bdvol
all pines	23.55	10.	29.2	1.13	6.97
doug fir	22.71	29.	83.0	3.14	18.42
resid con	23.03	13.	37.9	0.91	4.83
Totals	22.95	52.	150.0	5.17	30.22

cutgo:ih

VII pg. 27

INTERMEDIATE HARVESTS

elapsed time = 15.00 years

species	dbar	tpa	basar	cfvol	bdvol
all pines	14.45	4.	4.4	0.14	0.63
true fir	8.63	47.	19.1	0.42	1.59
doug fir	10.22	11.	6.2	0.15	0.61
resid con	10.13	21.	11.7	0.16	0.47
Totals	9.58	83.	41.4	0.87	3.31

Do you want this table placed in the report file? (y=yes):n

cutgo:hc

VII pg. 28

Print diameter class table

How to specify species to be included ?

- 0 - All species together
- 1 - By one or more species
- 2 - By one or more species groups

Enter 0, 1, or 2 :0

Enter lower dbh limit (default=0),
upper dbh limit (default=50),
and class interval (default=2");
(separated by commas).Enter a "/" to choose defaults:/

Harvest diameter class table -- et = 15.00 yrs
 table is totals by DBH class
 note: growth figures include ingrowth if harvested

 stand label = Demo Data Plot 9-79
 All species combined

	stocks				growth		
	trees	basar	cfvol	bdvol	basar	cfvol	bdvol
0- 2	13.2	0.24	0.00	0.00	0.00	0.00	0.00
2- 4	11.9	0.43	0.00	0.00	0.38	0.00	0.00
4- 6	1.4	0.22	0.00	0.00	0.00	0.00	0.00
6- 8	39.7	9.98	0.10	0.00	7.66	0.06	0.00
8-10	58.5	24.91	0.37	1.15	8.54	0.11	0.37
10-12	35.1	22.81	0.49	1.84	1.21	0.06	0.29
12-14	4.3	3.89	0.10	0.40	0.31	0.01	0.06
14-16	6.4	7.56	0.23	1.04	0.45	0.03	0.16
16-18	0.0	0.00	0.00	0.00	0.00	0.00	0.00
18-20	1.4	2.70	0.05	0.23	0.08	0.00	0.03
20-22	0.0	0.00	0.00	0.00	0.00	0.00	0.00
22-24	0.0	0.00	0.00	0.00	0.00	0.00	0.00
24-26	0.0	0.00	0.00	0.00	0.00	0.00	0.00
26-28	4.2	17.16	0.68	4.26	0.68	0.05	0.41
28-30	8.0	36.57	1.50	9.75	2.11	0.14	1.14
30-32	2.1	10.99	0.45	3.00	0.87	0.05	0.43
32-34	1.2	7.18	0.31	2.09	0.78	0.04	0.37
totals	187.2	144.63	4.27	23.76	23.07	0.57	3.26

Do you want this table placed in the report file? (y=yes):y

Table saved in report file.

cutgo:dc

VII pg.26

Print diameter class table

How to specify species to be included ?

- 0 - All species together
- 1 - By one or more species
- 2 - By one or more species groups

Enter 0, 1, or 2 :0

Enter lower dbh limit (default=0),
 upper dbh limit (default=50),
 and class interval (default=2");
 (separated by commas).Enter a "/" to choose defaults:/

Residual diameter class table -- et = 15.00 yrs
 table is totals by DBH class
 note: growth figures include ingrowth

 stand label = Demo Data Plot 9-79
 All species combined

	stocks				growth		
	trees	basar	cfvol	bdvol	basar	cfvol	bdvol
14-16	1.0	1.09	0.03	0.14	0.07	0.00	0.02
16-18	5.2	8.13	0.26	1.29	0.57	0.03	0.19
18-20	6.9	13.69	0.38	1.92	0.93	0.04	0.28
20-22	4.2	10.43	0.38	2.18	0.51	0.03	0.23
22-24	20.0	58.71	2.07	12.06	3.66	0.21	1.49
24-26	8.7	29.31	0.94	5.47	2.05	0.10	0.73
26-28	2.8	11.16	0.39	2.39	0.94	0.04	0.32
28-30	0.8	3.98	0.17	1.08	0.09	0.01	0.08
30-32	2.5	13.50	0.56	3.69	0.83	0.05	0.43
totals	52.2	150.00	5.17	30.22	9.65	0.52	3.77

Do you want this table placed in the report file? (y=yes):y

Table saved in report file.

cutgo:h1

VII pg. 28

Print log table

Harvest log inventory

stand = Demo Data Plot 9-79

elapsed time = 15.00

Cubic volume (MCF/ac) by log size

sp.	Yellow Pines		White pines		True fir		Douglas Fir		Cedar misc.	
dib	logs	cvol	logs	cvol	logs	cvol	logs	cvol	logs	cvol
4	11.6	0.03	0.0	0.00	62.3	0.18	22.6	0.06	36.7	0.11
6	7.9	0.04	0.0	0.00	54.0	0.26	2.9	0.01	11.8	0.06
8	11.1	0.09	0.0	0.00	37.4	0.29	5.7	0.04	6.6	0.05
10	7.9	0.08	0.0	0.00	3.0	0.03	7.4	0.08	1.4	0.02
12	11.3	0.17	0.0	0.00	0.0	0.00	6.2	0.09	0.8	0.02
14	6.7	0.14	0.0	0.00	0.0	0.00	2.9	0.06	0.6	0.02
16	8.8	0.22	0.0	0.00	0.0	0.00	3.3	0.08	0.0	0.00
18	8.9	0.28	0.0	0.00	0.0	0.00	4.4	0.14	0.0	0.00
20	7.7	0.29	0.0	0.00	0.0	0.00	4.9	0.20	0.0	0.00
22	10.0	0.45	0.0	0.00	0.0	0.00	2.2	0.10	0.0	0.00
24	5.3	0.28	0.0	0.00	0.0	0.00	3.3	0.17	0.0	0.00
26	1.6	0.10	0.0	0.00	0.0	0.00	0.0	0.00	0.0	0.00
28	0.6	0.04	0.0	0.00	0.0	0.00	0.0	0.00	0.0	0.00
Totals		2.22		0.00		0.75		1.03		0.27
eqn/taper		0.99		0.00		1.16		1.00		1.20

Board volume (MBF/ac) by log size

sp.	Yellow Pines		White pines		True fir		Douglas Fir		Cedar misc.	
dib	logs	bdvol	logs	bdvol	logs	bdvol	logs	bdvol	logs	bdvol
6	15.1	0.32	0.0	0.00	56.5	1.50	11.4	0.22	21.1	0.45
8	4.5	0.13	0.0	0.00	28.1	1.01	2.1	0.07	0.7	0.03
10	8.8	0.45	0.0	0.00	3.0	0.18	5.2	0.26	1.4	0.09
12	12.3	0.99	0.0	0.00	0.0	0.00	6.9	0.56	0.8	0.09
14	8.4	1.07	0.0	0.00	0.0	0.00	2.2	0.28	0.6	0.08
16	7.9	1.36	0.0	0.00	0.0	0.00	4.1	0.66	0.0	0.00
18	8.8	1.93	0.0	0.00	0.0	0.00	3.6	0.74	0.0	0.00
20	6.8	1.84	0.0	0.00	0.0	0.00	4.9	1.32	0.0	0.00
22	9.2	3.03	0.0	0.00	0.0	0.00	2.2	0.74	0.0	0.00
24	5.3	2.09	0.0	0.00	0.0	0.00	3.3	1.23	0.0	0.00
26	1.6	0.73	0.0	0.00	0.0	0.00	0.0	0.00	0.0	0.00
28	0.6	0.32	0.0	0.00	0.0	0.00	0.0	0.00	0.0	0.00
Totals		14.26		0.00		2.69		6.07		0.74
eqn/taper		1.00		0.00		1.29		0.99		1.11

Do you want this table placed in the report file? (y=yes):y

Table saved in report file.

cutgo:ex

VII pg.28

Do you wish to implement a lag time for response to thin? (y=yes):n

Exiting harvest routine.
Returning to main program.

go:yd

VI-A pg.20

YIELD SUMMARY: units = english

stand label = Demo Data Plot 9-79

	min. DBH	merch top
cubic ft.	0.0	4
board ft.	8.0	6

species	site	init. age
Pond. Pine	100.	30.
Cedar misc	80.	30.
DouglasFir	90.	30.
White Fir	90.	0.

species	et	dbar	tpa	basar	cvol	bdvol	bagro	cvgro	bdgro
all pines	0.00	22.42	25.0	68.5	2.38	13.85	0.0	0.00	0.00
true fir	0.00	6.79	100.0	25.2	0.42	1.09	0.0	0.00	0.00
doug fir	0.00	18.11	50.0	89.4	2.89	15.77	0.0	0.00	0.00
resid con	0.00	13.61	45.0	45.5	0.86	3.61	0.0	0.00	0.00
Totals	0.00	13.80	220.0	228.6	6.55	34.33	0.0	0.00	0.00
all pines	5.00	23.36	24.7	73.4	2.69	16.12	4.9	0.31	2.27
true fir	5.00	7.65	84.4	26.9	0.51	1.56	1.7	0.08	0.46
doug fir	5.00	19.04	48.8	96.5	3.29	18.47	7.1	0.40	2.69
resid con	5.00	14.28	43.5	48.4	0.96	4.26	2.9	0.10	0.64
Totals	5.00	14.94	201.3	245.2	7.44	40.40	16.6	0.88	6.07 M
all pines	10.00	24.30	24.4	78.4	3.01	18.58	5.0	0.32	2.46
true fir	10.00	8.36	74.7	28.5	0.59	2.08	1.6	0.08	0.52
doug fir	10.00	19.97	47.7	103.7	3.71	21.37	7.2	0.42	2.91
resid con	10.00	14.95	42.1	51.3	1.05	4.92	2.9	0.10	0.67
Totals	10.00	15.95	188.8	261.9	8.36	46.95	16.7	0.92	6.56 M
all pines	15.00	25.23	24.1	83.6	3.35	21.23	5.2	0.34	2.65
true fir	15.00	9.00	67.9	30.0	0.67	2.53	1.5	0.08	0.45
doug fir	15.00	20.89	46.7	111.1	4.15	24.49	7.4	0.44	3.12
resid con	15.00	15.60	40.8	54.1	1.15	5.55	2.8	0.10	0.62
Totals	15.00	16.88	179.4	278.8	9.32	53.80	16.9	0.96	6.84 M

APPENDIX C. HARVEST OPTION R3

The harvest command `r3` calls the "free" harvest subroutine. This interactive option gives the user considerable flexibility in simulating harvest. Using `r3`, one can easily create up to 24 variable-width diameter classes, each available for harvesting. Harvesting can be done by species groups, specified species, or all species. Harvesting may be done in units of trees or square feet of basal area, and may also be specified as a fraction of the number of trees or square feet of basal area available for harvesting. User-specified overall cutting limits are used to prevent accidental over-harvesting. The user can also specify which tree characteristic(s) to consider when removing trees.

Harvesting under `r3` is designed to give the user freedom to regulate the cutting parameters. To give the user a flexible routine, a moderate amount of interaction is required. A flowchart detailing the program/user interaction is given on the next page. To initialize `r3`, the user must respond to questions when prompted by CACTOS. The program also indicates the form of the response required.

The harvest specification consists of two phases: (1) the program initialization, and (2) the actual harvest specification. Once initialized, `r3` allows multiple harvests and even allows the user to go back and change the specifications given in the initialization cycle. The initialization and harvesting phases are described below, and a sample runstream is given to illustrate the operation of `r3`.

Initialization

The "free" harvest option is called by entering the harvest routine with the `ct` (or `cut`) command and choosing the option `r3` in response to the harvest prompt, "cutgo:". The user then sets the basic pattern for the way the harvest will be specified.

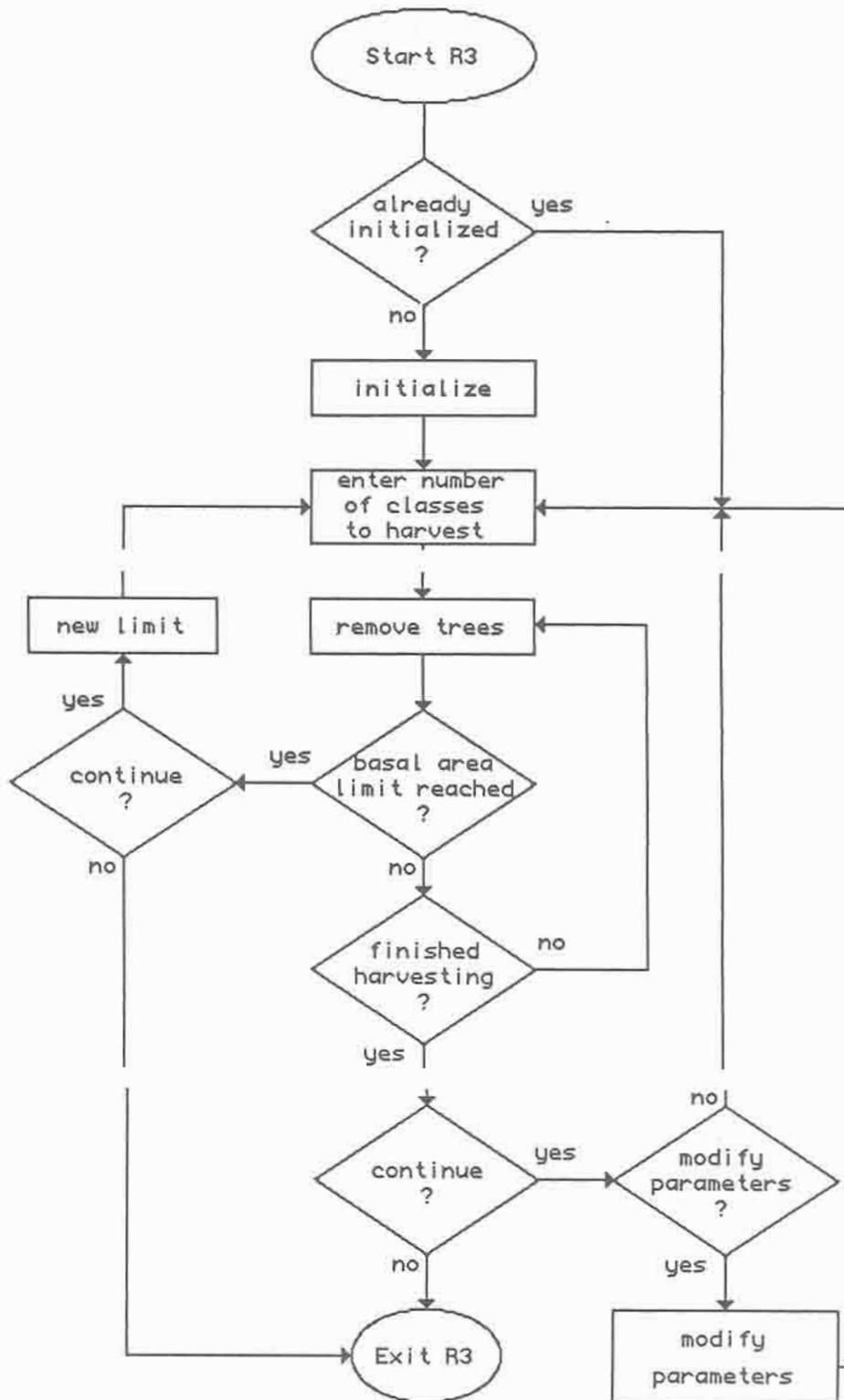
Diameter classes. Up to 24 variable-width diameter classes may be requested. The number of classes desired is requested, followed by a prompt for the upper limits of each DBH class, specified in ascending order. The lower limit for the first diameter class is zero inch. If the upper limit for the last diameter class does not include the largest tree in the tree list, an additional diameter class is automatically created. This ensures that every tree in the stand can be harvested.

Maximum basal area to cut. The maximum fraction of total basal area which may be cut is specified by the user. The user may not wish to remove more than a certain fraction of the total basal area in a stand. The decimal fraction specified by the user is used as a cutoff for harvesting. If the limit is reached, a message appears on the screen and the user is given the option of continuing or stopping the harvest.

Species to cut. Cutting may be done by (1) all species, (2) individual species, or (3) species groups. As with the other harvest options, `r3` recognizes species "targets" when removing trees.

Cut by DBH, crown, or both. Removal may be prioritized by considering (1) smallest dbh, (2) live crown ratio, or (3) live crown ratio and dbh. The routine prioritizes removals in each diameter class by first removing (1) small trees, (2) trees with poor live crown ratios, or (3) trees with low values for $(lcr * dbh ** 1.5)$. The third option is used to prioritize removals similar to the field, where one considers both dbh and live crown ratio when removing trees.

Figure C.1: Flowchart of Harvest Option R3.



How to cut. The user may harvest by tree (option 1) or by basal area (option 2), specifying either the number of trees or the square feet of basal area to remove. Diameter class statistics are reported in the units used for cutting.

Actual units or relative units. Harvest may be specified in either (1) absolute or (2) fractional terms. By specifying absolute terms, the user gives the number of trees or square feet of basal area to be removed. Fractions are specified as a decimal proportion of the amount available for removal.

Number of DBH classes to cut. This entry establishes the number of times the user is asked for cutting information. The user cannot operate in more diameter classes than created.

Harvesting

Once initialized, *r3* asks the user in which diameter class to cut. If three diameter classes have been established (>0-16", >16-22", and >22-30"), and the user wishes to operate in the 22-30" class, entering "3" calls up the third diameter class for harvesting. Stand and diameter class statistics are then reported in the form specified during initialization. The user enters the amount to cut (i.e. a fraction of all the trees available, a percentage of square feet or basal area, etc.) and *r3* starts cutting. All harvesting proceeds normally unless the cutting specifications exceed the user-defined limit. If the limit is reached, a message is printed allowing the user to continue or to stop the harvesting session (continuation requires a new upper limit set on cutting). If all harvesting proceeds normally, a "normal termination" message appears at the end of the session. The user may then choose to stop or to continue harvesting. Stopping returns the user to the "cutgo:" prompt. Should the user choose to continue, the program asks if the user wishes to harvest with the same initialization or a modified one. Modifying allows the user to change any number of the initialization parameters. Harvesting can then continue as before.

Following is a sample run showing the majority of *r3*'s features.

Example of harvest option R3.

Boldface indicates user entry.

Italics indicates helpful annotations.

WELCOME TO

```

      CCCCC   AAAA   CCCCC   TTTTTTTTT   OOOO   SSSSS
CCCCCCC   AA  AA   CCCCCC   TTTTTTTTT   OOOOOO   SS  SS
CC        AA  AA   CC        TT        OO   OO   SS
CC        AAAAAAA   CC        TT        OO   OO   SSSSS
CC        AA  AA   CC        TT        OO   OO   SS
CCCCCCC   AA  AA   CCCCCC   TT        OOOOOO   SS  SS
      CCCCC   AA  AA   CCCCC   TT        OOOO   SSSSS
```

The California Conifer Timber Output Simulator
Version 3.3

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```

enter "return" to continue:1
demo.sd
demo.yd
demo.rp
```

*Enter names of
input and output
files, supressing
prompts.*

MAIN PROGRAM

Type "pc" to get a list of available commands
Current output file is 6 (the screen)

go:ct

*Enter Harvest
routine.*

HARVEST ROUTINE

Enter harvest label (up to 30 char): **example of harvest routine r3**

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

cutgo:pf

Stand Profile

Print stand profile

How to specify species to be graphed ?
0 - All species together
1 - By one or more species
2 - By one or more species groups

Enter 0, 1, or 2 : 0

Enter option to use: 3

Consider lcr and dbh when removing trees

How to cut? by tree (1) or by BA (2)

Enter 1 or 2 : 1

Removals in units of number of trees

Cut in absolutes (1) or percentages (2) ?

Enter 1 or 2 : 2

Removals by fraction of total number of trees

How many dia classes to operate in (1- 5) ? : 5

Harvest in 5 classes

Initial total basal area = 228.58 sq.ft./ac.

Current basal area = 228.58 sq.ft./ac.

0. % of the initial basal area has been cut.

diameter class :	1	2	3	4	5
upper limit :	4.0	10.0	18.0	24.0	30.0

*Harvest in 1st dia
class, remove 50%
of trees in this
class.*

Enter dia class to harvest 1st (1,2,3, etc): 1

How many trees to harvest ?

Trees in this class = 40.00

Enter amount here: .5

Initial total basal area = 228.58 sq.ft./ac.

Current basal area = 228.42 sq.ft./ac.

0.07 % of the initial basal area has been cut.

diameter class :	1	2	3	4	5
upper limit :	4.0	10.0	18.0	24.0	30.0

Enter dia class to harvest 2nd (1,2,3, etc): 2

Harvest in 2nd class

How many trees to harvest ?

Trees in this class = 100.00

Enter amount here: .1

Initial total basal area = 228.58 sq.ft./ac.

Current basal area = 227.06 sq.ft./ac.

0.67 % of the initial basal area has been cut.

diameter class :	1	2	3	4	5
upper limit :	4.0	10.0	18.0	24.0	30.0

Enter dia class to harvest 3rd (1,2,3, etc): 3

Harvest in 3rd class

How many trees to harvest ?

Trees in this class = 25.00

Enter amount here: .0

Initial total basal area = 228.58 sq.ft./ac.
Current basal area = 227.06 sq.ft./ac.
0.67 % of the initial basal area has been cut.

diameter class : 1 2 3 4 5
upper limit : 4.0 10.0 18.0 24.0 30.0

Enter dia class to harvest 4th (1,2,3, etc): 4

Harvest in 4th class

How many trees to harvest ?
Trees in this class = 35.00
Enter amount here: .1

Initial total basal area = 228.58 sq.ft./ac.
Current basal area = 218.23 sq.ft./ac.
4.53 % of the initial basal area has been cut.

diameter class : 1 2 3 4 5
upper limit : 4.0 10.0 18.0 24.0 30.0

Enter dia class to harvest 5th (1,2,3, etc): 5

Harvest in 5th class

How many trees to harvest ?
Trees in this class = 20.00
Enter amount here: .5

You have finished harvesting. Normal termination.
Basal area harvested is 46.65 sq.ft./ac. or 20.41 % of total basal area.
Remaining basal area = 181.92 sq.ft./ac.

Do you want to continue harvesting?(yes= y): y

Continue harvesting

The harvesting routine is initialized. You may
(1)-- Continue harvesting without changing parameters
(2)-- Modify harvest routine parameters
Enter 1 or 2 : 2

Modify parameters

---Menu for Changing Parameters---

- (1) End Harvest Routine
- (2) Start Harvesting Again
- (3) Adjust Diameter Classes
- (4) Change Species Keys
- (5) Change Key for Sort
- (6) Change Removal Limit
- (7) Cut by Tree or B.A.?
- (8) Absolutes or Percentages?

Which option?: 4

Change species targets

How to specify species to be harvested ?

- 0 - All species together
- 1 - By one or more species
- 2 - By one or more species groups

Enter 0, 1, or 2 : 1

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 the codes of species to be harvested
(separated by commas, terminated with a "/"): 1/

---Menu for Changing Parameters---

- (1) End Harvest Routine
- (2) Start Harvesting Again
- (3) Adjust Diameter Classes
- (4) Change Species Keys
- (5) Change Key for Sort
- (6) Change Removal Limit
- (7) Cut by Tree or B.A.?
- (8) Absolutes or Percentages?

Which option?: 7

Modify removal units

How to cut? by tree (1) or by BA (2)

Enter 1 or 2 : 2

---Menu for Changing Parameters---

- (1) End Harvest Routine
- (2) Start Harvesting Again
- (3) Adjust Diameter Classes
- (4) Change Species Keys
- (5) Change Key for Sort
- (6) Change Removal Limit
- (7) Cut by Tree or B.A.?
- (8) Absolutes or Percentages?

Which option?: 8

*Change way to
specify cut amount.
Cut in absolutes.*

Cut in absolutes (1) or percentages (2) ?

Enter 1 or 2 : 1

---Menu for Changing Parameters---

- (1) End Harvest Routine
- (2) Start Harvesting Again
- (3) Adjust Diameter Classes
- (4) Change Species Keys
- (5) Change Key for Sort
- (6) Change Removal Limit
- (7) Cut by Tree or B.A.?
- (8) Absolutes or Percentages?

Which option?: 2

Resume harvesting

How many dia classes to operate in (1- 5) ? : 2

Harvest in two classes

Initial total basal area = 228.58 sq.ft./ac.

Current basal area = 181.92 sq.ft./ac.

20.41 % of the initial basal area has been cut.

diameter class :	1	2	3	4	5
upper limit :	4.0	10.0	18.0	24.0	30.0

Enter dia class to harvest 1st (1,2,3, etc): 5

Harvest in 5th class

How much basal area to harvest ?

B.A. in this class = 40.5

You are harvesting by species groups.

There is 40.5 sqr ft. of basal area available for cutting

Enter amount here: 30.5

*Reached 30% limit
set earlier, set new
limit.*

You have reached the allowed limit!

Do you wish to continue? (y=yes)

(If you answer n for no, you will exit R3): y

Enter a new fraction of total BA for removal: .4

Initial total basal area = 228.58 sq.ft./ac.

Current basal area = 160.00 sq.ft./ac.

30.00 % of the initial basal area has been cut.

diameter class :	1	2	3	4	5
upper limit :	4.0	10.0	18.0	24.0	30.0

Enter dia class to harvest 2nd (1,2,3, etc): 5

*Harvest in 5th class
again*

How much basal area to harvest ?

B.A. in this class = 18.6

You are harvesting by species groups.

There is 18.6 sqr ft. of basal area available for cutting

Enter amount here: 12.6

You have finished harvesting. Normal termination.

Basal area harvested is 81.17 sq.ft./ac. or 35.51 % of total basal area.

Remaining basal area = 147.40 sq.ft./ac.

Do you want to continue harvesting?(yes= y) : n

Quit harvesting

cutgo:pf

*Print another stand
profile to see the
effects of the cut.*

How much basal area to harvest ?

B.A. in this class = 6.0

You are harvesting by species groups.

There is 6.0 sq ft. of basal area available for cutting

Enter amount here: 6.0

You have finished harvesting. Normal termination.

Basal area harvested is 6.00 sq.ft./ac. or 4.07 % of total basal area.

Remaining basal area = 141.40 sq.ft./ac.

Do you want to continue harvesting?(yes= y): n

Exit from R3

cutgo:pf

*Get another profile
to see the effects
of the cut*

Print stand profile

How to specify species to be graphed ?

0 - All species together

1 - By one or more species

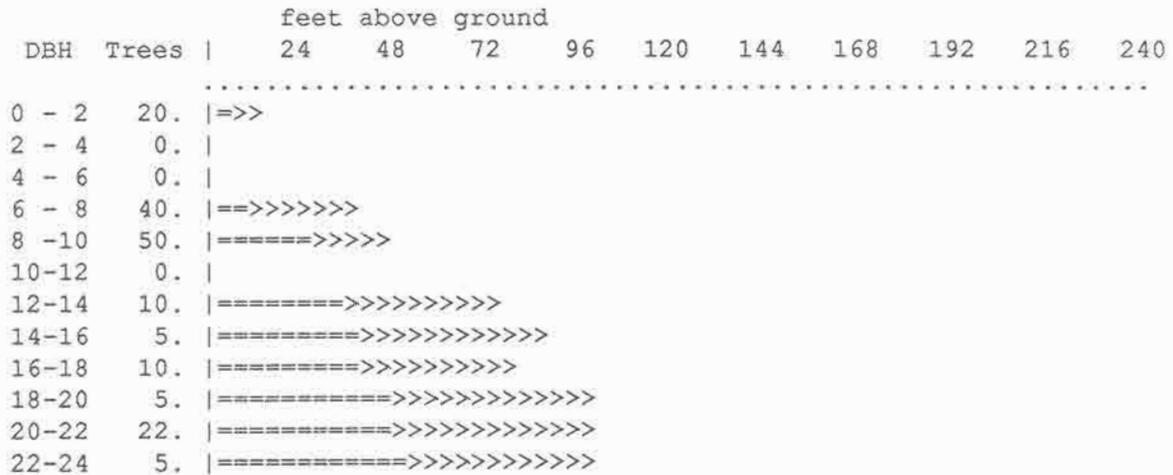
2 - By one or more species groups

Enter 0, 1, or 2 : 0

Stand Profile

elapsed time = 0. yrs

All species combined



total 167.

do you want this graph placed in the report file? (y=yes): n

cutgo:ex

*Exit harvest routine
continue with
simulation.*

APPENDIX D: SPECIFYING CALIBRATION FACTORS

The calibration option, *cl*, gives users a flexible tool for adjusting height and/or basal area growth predictions for perceived differences between predicted and actual growth rates. It is assumed that growth is of the same form as that predicted by CACTOS, but of a higher or lower magnitude. Thus, adjustments are expressed as percentages using calibration factors. It is likely that differences may not occur stand-wide, or even occur equally among the components of tree growth. Hence, this option allows the user to specify calibration factors for basal area and/or height growth by any combination of species and/or appropriate size classes. Such a designation is referred to as the calibration scheme.

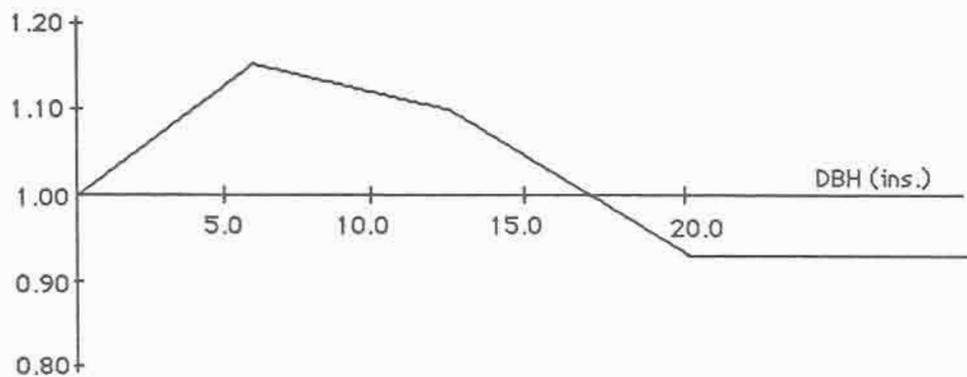
Calibration schemes are applied to growth predictions at any time in growth simulation and for any duration of growth periods. In calibrated runs, growth estimates are adjusted after each 5-year growth period, and subsequent predictions are based on the adjusted diameters and/or heights. Calibration in this manner is a compound process, and the calibration factors in a specified scheme should reflect this.

The decision process required of the user in *cl* enables efficient keyboard designation if the calibration scheme is known beforehand. Figure D.1 presents the process schematically, and a more detailed explanation is in section V. Only one scheme can reside internally in CACTOS, thus if the user wishes to change schemes during a simulation, *cl* must be reentered for redesignation.

A linear function is used to assign factors to individual tree records based on tree size at the beginning of a growth period. Using designated factors and size limits (hereafter referred to as a vector), specific factors are determined by linear interpolation between these values. By convention, the first size limit in a vector is 0 (inch or foot), for which the user supplies a factor. The last designated size limit is the lower limit of the last size class. Hence, the last factor applied as a constant to all trees larger than this limit. For example, suppose the following vector is designated for sugar pine basal area growth:

<u>Size</u>	<u>Factor</u>
0.0'	1.00
6.0'	1.15
12.5'	1.10
20.0'	0.94

The graph of sugar pine's calibrations specified by this vector would be as follows:



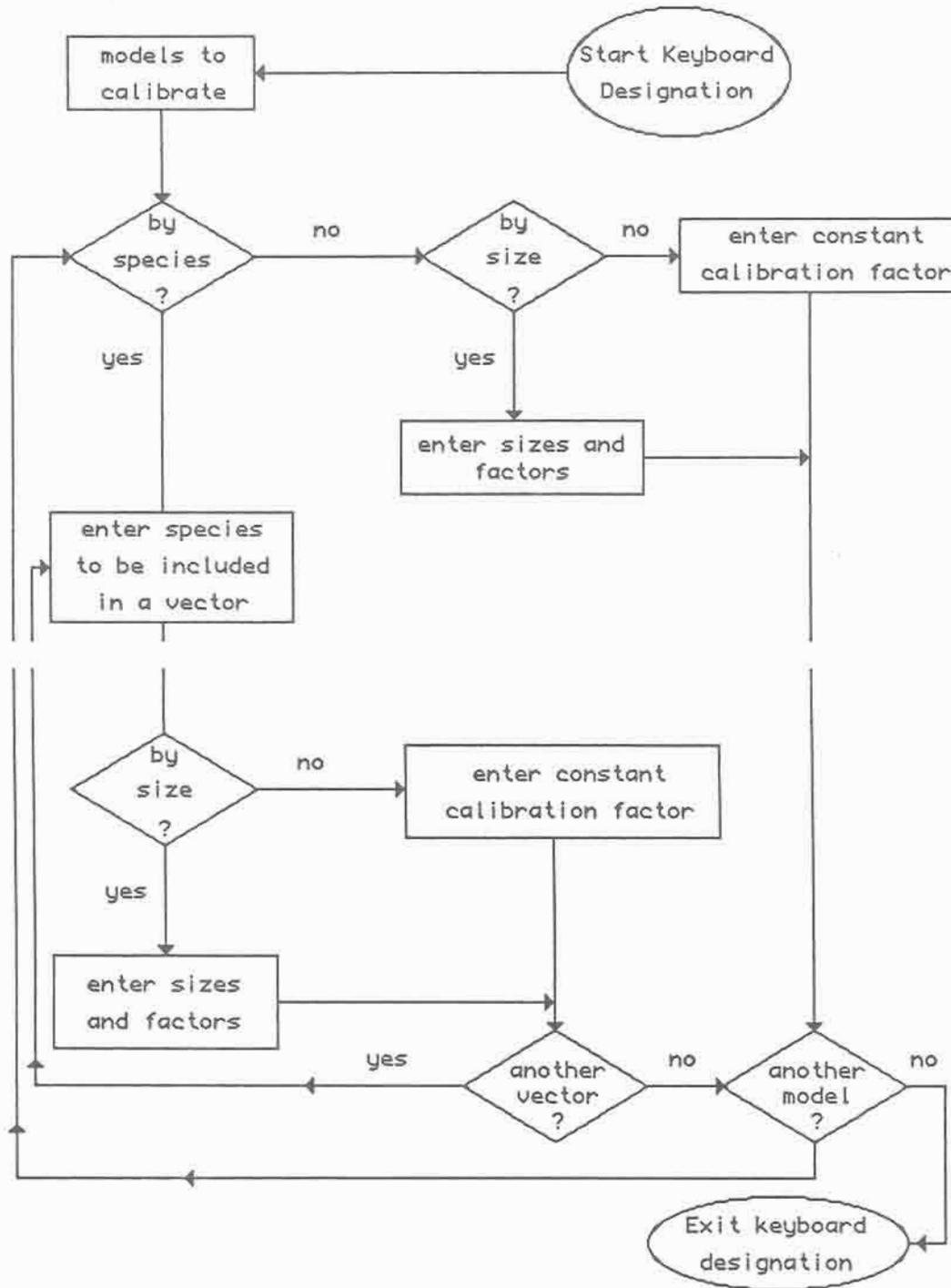
In the case where one calibration factor is applied to all size trees of a species, this graph would be a horizontal line.

There are a few reasonable restrictions on the calibration procedure. To preserve the integrity of the CACTOS response surfaces, growth predictions may be adjusted by no more than plus or minus 20 percent. Size designations are limited to the significant size variables (i.e., only diameter size limits are allowed for basal area calibration, and only total heights for height calibration). Specifying otherwise is functionally unsound for CACTOS. Finally, to keep the schemes manageable, users are limited to five sizes per calibration vector (more than needed because calibration should be done broadly and with large amounts of sample data.)

User discretion and available data determine the adequacy of calibration schemes. Once successful schemes are developed, they may be stored externally in formatted files through `cl`. Retrieval of a file for use in growth simulation is also done in `cl`.

The versatility of the calibration option is great and proficiency will come with use. The following sample runstream illustrates how to designate a calibration scheme and to apply it in growth simulations.

Figure D.1: User Calibration Decision Process Flowchart.



SAMPLE CALIBRATION RUNSTREAM

Boldface indicates user entry.

WELCOME TO

```
      CCCCC      AAAA      CCCCC      TTTTTTTT      OOOO      SSSSS
CCCCCCC      AA  AA      CCCCCC      TTTTTTTT      OOOOOO      SS  SS
CC           AA   AA  CC           TT           OO   OO  SS
CC           AAAAAAA  CC           TT           OO   OO  SSSSS
CC           AA   AA  CC           TT           OO   OO      SS
CCCCCCC      AA   AA  CCCCCC      TT           OOOOOO      SS  SS
      CCCCC      AA   AA      CCCCC      TT           OOOO      SSSSS
```

version 3.3

The California Conifer Timber Output Simulator

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```
enter "return" to continue;1
demo.sd
demo.yd
demo.rp
```

In this program, if the computer is waiting for a command it will give you a prompt that is:

```
go:           If you are in the main program
initgo:       If you are in the initialization routine
cutgo:        If you are in the cutting routine
```

Do you want to enter the initialization routine,
to change any of the initial (default) control options? (y=yes):y

INITIALIZATION ROUTINE

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

```
initgo:c1
```

Calibration Entry Routine

How to enter calibration scheme?

- 0 - exit calibration routine
- 1 - enter from keyboard
- 2 - enter from an external file

Enter 0,1, or 2 :1

What model(s) are to be calibrated?

- 1 - Basal Area only
- 2 - Height only
- 3 - Both Basal Area and Height

Enter 1,2, or 3 :3

Section for entering Basal Area calibration

Are the same Basal Area calibration factor(s) to be applied to ALL species? (y=yes,n=no) :n

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 the codes of the species to be included in the

1st Basal Area calibration group,
(separated by commas,terminated by a "/"):1,2,7,8,9/

Do you want to enter calibration factors by dia size classes?

(y=yes,n=no):y

How many dia size classes are wanted? Range is 2 to 5 classes.

Entering 1 is the same as not requesting dia size classes.

Enter here:4

The lower dia limit for the 1st size class is 0.0.

Please enter the corresponding calibration factor in decimal fraction,
(entering 1.12 increases growth by 12 %):0.8

Enter the lower dia limit and calibration factor for the 2nd size class.

Enter here (separated by a comma):6.0,0.85

Enter the lower dia limit and calibration factor for the 3rd size class.

Enter here (separated by a comma):10.0,1.0

Enter the lower dia limit and calibration factor for the 4th size class.

Enter here (separated by a comma):30.0,1.06

Do you want to enter another calibration group?

(y=yes,n=no):y

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 the codes of the species to be included in the
2nd Basal Area calibration group,
(separated by commas,terminated by a "/"):3,10/

Do you want to enter calibration factors by dia size classes?
(y=yes,n=no):y

How many dia size classes are wanted? Range is 2 to 5 classes.
Entering 1 is the same as not requesting dia size classes.
Enter here:5

The lower dia limit for the 1st size class is 0.0.
Please enter the corresponding calibration factor in decimal fraction,
(entering 1.12 increases growth by 12 %):0.8
Enter the lower dia limit and calibration factor for the 2nd size class.
Enter here (separated by a comma):4.0,0.85
Enter the lower dia limit and calibration factor for the 3rd size class.
Enter here (separated by a comma):8.0,0.90
Enter the lower dia limit and calibration factor for the 4th size class.
Enter here (separated by a comma):10.0,0.95
Enter the lower dia limit and calibration factor for the 5th size class.
Enter here (separated by a comma):16.0,1.00

Do you want to enter another calibration group?
(y=yes,n=no):y

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 the codes of the species to be included in the
3rd Basal Area calibration group,
(separated by commas,terminated by a "/"):4/

Do you want to enter calibration factors by dia size classes?
(y=yes,n=no):y

How many dia size classes are wanted? Range is 2 to 5 classes.
Entering 1 is the same as not requesting dia size classes.
Enter here:3

The lower dia limit for the 1st size class is 0.0.
Please enter the corresponding calibration factor in decimal fraction,
(entering 1.12 increases growth by 12 %):1.00
Enter the lower dia limit and calibration factor for the 2nd size class.
Enter here (separated by a comma):12.0,1.02
Enter the lower dia limit and calibration factor for the 3rd size class.
Enter here (separated by a comma):22.0,1.04

Do you want to enter another calibration group?
(y=yes,n=no):y

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 the codes of the species to be included in the
4th Basal Area calibration group,
(separated by commas, terminated by a "/"):5,6/

Do you want to enter calibration factors by dia size classes?
(y=yes,n=no):y

How many dia size classes are wanted? Range is 2 to 5 classes.
Entering 1 is the same as not requesting dia size classes.
Enter here:2

The lower dia limit for the 1st size class is 0.0.
Please enter the corresponding calibration factor in decimal fraction,
(entering 1.12 increases growth by 12 %):1.02
Enter the lower dia limit and calibration factor for the 2nd size class.
Enter here (separated by a comma):4.0,1.00

Do you want to enter another calibration group?
(y=yes,n=no):y

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 the codes of the species to be included in the
5th Basal Area calibration group,
(separated by commas, terminated by a "/"):11,12,13,14/

Do you want to enter calibration factors by dia size classes?
(y=yes,n=no):y

How many dia size classes are wanted? Range is 2 to 5 classes.
Entering 1 is the same as not requesting dia size classes.
Enter here:3

The lower dia limit for the 1st size class is 0.0.
Please enter the corresponding calibration factor in decimal fraction,
(entering 1.12 increases growth by 12 %):1.00
Enter the lower dia limit and calibration factor for the 2nd size class.
Enter here (separated by a comma):6.0,1.02
Enter the lower dia limit and calibration factor for the 3rd size class.
Enter here (separated by a comma):20.0,1.18

Do you want to enter another calibration group?
(y=yes,n=no):n

Section for entering Height calibration

Are the same Height calibration factor(s) to be applied to ALL species? (y=yes,n=no) : n

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 the codes of the species to be included in the 1st Height calibration group, (separated by commas,terminated by a "/"):1,2/

Do you want to enter calibration factors by ht size classes? (y=yes,n=no):n

Please enter the calibration factor in decimal fraction, (entering 1.12 increases growth by 12 %) :1.07

Do you want to enter another calibration group? (y=yes,n=no):y

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 the codes of the species to be included in the 2nd Height calibration group, (separated by commas,terminated by a "/"):3,10/

Do you want to enter calibration factors by ht size classes? (y=yes,n=no):n

Please enter the calibration factor in decimal fraction, (entering 1.12 increases growth by 12 %) :1.02

Do you want to enter another calibration group? (y=yes,n=no):y

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 the codes of the species to be included in the 3rd Height calibration group, (separated by commas,terminated by a "/"):4/

Do you want to enter calibration factors by ht size classes? (y=yes,n=no):y

How many ht size classes are wanted? Range is 2 to 5 classes. Entering 1 is the same as not requesting ht size classes. Enter here:4

The lower ht limit for the 1st size class is 0.0.
 Please enter the corresponding calibration factor in decimal fraction,
 (entering 1.12 increases growth by 12 %):1.00
 Enter the lower ht limit and calibration factor for the 2nd size class.
 Enter here (separated by a comma):10.0,1.02
 Enter the lower ht limit and calibration factor for the 3rd size class.
 Enter here (separated by a comma):40.0,1.04
 Enter the lower ht limit and calibration factor for the 4th size class.
 Enter here (separated by a comma):80.0,1.06

Do you want to enter another calibration group?
 (y=yes,n=no):y

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 the codes of the species to be included in the
 4th Height calibration group,
 (separated by commas,terminated by a "/"):5,6/

Do you want to enter calibration factors by ht size classes?
 (y=yes,n=no):n

Please enter the calibration factor in decimal fraction,
 (entering 1.12 increases growth by 12 %):1.09

Do you want to enter another calibration group?
 (y=yes,n=no):n

CALIBRATION SUMMARY

Calibration Vectors for: Basal Area

Pond. Pine		Sugar Pine		Cedar misc		DouglasFir		White Fir	
size	factor	size	factor	size	factor	size	factor	size	factor
0.0	0.80	0.0	0.80	0.0	0.80	0.0	1.00	0.0	1.02
6.0	0.85	6.0	0.85	4.0	0.85	12.0	1.02	4.0	1.00
10.0	1.00	10.0	1.00	8.0	0.90	22.0	1.04	4.0	1.00
30.0	1.06	30.0	1.06	10.0	0.95	22.0	1.04	4.0	1.00
30.0	1.06	30.0	1.06	16.0	1.00	22.0	1.04	4.0	1.00

Red Fir		L.P. Pine		White Pine		Jeff. Pine		Con. misc	
size	factor	size	factor	size	factor	size	factor	size	factor
0.0	1.02	0.0	0.80	0.0	0.80	0.0	0.80	0.0	0.80
4.0	1.00	6.0	0.85	6.0	0.85	6.0	0.85	4.0	0.85
4.0	1.00	10.0	1.00	10.0	1.00	10.0	1.00	8.0	0.90
4.0	1.00	30.0	1.06	30.0	1.06	30.0	1.06	10.0	0.95
4.0	1.00	30.0	1.06	30.0	1.06	30.0	1.06	16.0	1.00

Chinquapin		Black Oak		Tan Oak		H.W. misc	
size	factor	size	factor	size	factor	size	factor
0.0	1.00	0.0	1.00	0.0	1.00	0.0	1.00
6.0	1.02	6.0	1.02	6.0	1.02	6.0	1.02
20.0	1.18	20.0	1.18	20.0	1.18	20.0	1.18
20.0	1.18	20.0	1.18	20.0	1.18	20.0	1.18
20.0	1.18	20.0	1.18	20.0	1.18	20.0	1.18

Calibration Vectors for: Height

Pond. Pine		Sugar Pine		Cedar misc		DouglasFir		White Fir	
size	factor	size	factor	size	factor	size	factor	size	factor
0.0	1.07	0.0	1.07	0.0	1.02	0.0	1.00	0.0	1.09
0.0	1.07	0.0	1.07	0.0	1.02	10.0	1.02	0.0	1.09
0.0	1.07	0.0	1.07	0.0	1.02	40.0	1.04	0.0	1.09
0.0	1.07	0.0	1.07	0.0	1.02	80.0	1.06	0.0	1.09
0.0	1.07	0.0	1.07	0.0	1.02	80.0	1.06	0.0	1.09

Red Fir		Con. misc	
size	factor	size	factor
0.0	1.09	0.0	1.02
0.0	1.09	0.0	1.02
0.0	1.09	0.0	1.02
0.0	1.09	0.0	1.02
0.0	1.09	0.0	1.02

Do you want this summary placed in the report file? (y=yes):y

Summary placed in the report file

Do you want to save this calibration scheme in an external file?
(y=yes,n=no):y

Open the calibration file
Enter a file name here:demo.cl

Calibration scheme saved in file: demo.cl

initgo:ex

Exiting initialization routine

MAIN PROGRAM

Type "pc" to get a list of available commands
 Current output file is 6 (the screen)

go:gz

Begin Growth Routine

MORTALITY ON

Enter the number of 5 yr. growth cycles desired

Note: a "-" (minus) prefix shuts off mortality for all cycles entered.

Enter number of cycles here:1

Both Basal Area and Height calibration schemes are present.

How do you want them applied for the 1 growth cycles requested ?

- 0 - Do not apply any calibration scheme
- 1 - Apply Basal Area calibration scheme only
- 2 - Apply Height calibration scheme only
- 3 - Apply both Basal Area & Height calibration schemes

Enter 0, 1, 2, or 3 :3

Do you want either individual tree growth detail
 or summary info printed?(y=yes):n

go:yd

YIELD SUMMARY: units = english

stand label = test stand

	min. DBH	merch top
cubic ft.	0.0	4
board ft.	8.0	6

species	site	init. age
Pond. Pine	110.	50.
Sugar Pine	125.	55.
Cedar misc	73.	48.
DouglasFir	94.	50.

species	et	dbar	tpa	basar	cvol	bdvol	bagro	cvgro	bdgro
Pond. Pine	0.00	15.36	150.0	193.0	6.03	30.69	0.0	0.00	0.00
Sugar Pine	0.00	16.18	150.0	214.1	8.47	47.03	0.0	0.00	0.00
Totals	0.00	15.77	300.0	407.1	14.50	77.72	0.0	0.00	0.00
Pond. Pine	5.00	15.95	146.0	202.6	6.59	34.36	9.5	0.55	3.67
Sugar Pine	5.00	17.30	146.2	238.6	9.78	56.21	24.5	1.31	9.18
Totals	5.00	16.64	292.2	441.2	16.37	90.57	34.0	1.87	12.85 B M
species	et	dbar	tpa	basar	cvol	bdvol	bagro	cvgro	bdgro

go:ex

Yield summary saved in demo.yd
Report summary saved in demo.rp

APPENDIX E. MACINTOSH ADDENDUM

There are a few places in CACTOS where information requested by the program must be entered by the user in a form different from that specified in the User's Guide. These differences involve the way certain entries are made in batch mode and from the keyboard.

Formatted keyboard and batch command input:

The program has two distinct types of keyboard input: formatted and list-directed. With list-directed input, the program expects complete input of all items listed in the program source code. With formatted input, the user may enter a subset of that information. List-directed input is used in the program where there must be a complete user input, such as where the computer asks the user for a choice of several options, and there is no default. Formatted input, on the other hand, allows the user to input a variable amount of information, for example, where the user is entering the species targets for harvests and graphic routines.

In some implementations, the computer running CACTOS allows commas to be inserted in-between formatted inputs, on other systems, there must be a complete filling out of the entry. The Apple Macintosh version has the latter characteristic. For this implementation, the user should be aware of the following prompts and their expected input:

Page 24: When setting species targets, the computer expects a formatted input of species codes (format 14I3). Here, instead of entering 02,04,06... the user needs to enter 002004006... which completely fills in the "I3" format (I3 stands for an integer number with three digits and no decimal point). It is not necessary to fill in all 14 species codes, only those desired for output need be specified. This input format is necessary in responses to prompts when harvesting, printing diameter distributions and stand profiles, and when printing diameter class tables.

Page 27: In the growth routine, the user may wish to enter all or part of the information required at the prompt for the number of cycles desired. The program expects the format 4I4,A1 (four consecutive integers, four digits wide, followed immediately by a single character). These are for the number of growth cycles desired (positive for mortality on, negative for mortality off), followed by a 1 for suppression of further growth routine screen prompts. Thus, growing the current stand for one cycle without mortality, no screen prompts, record skip of two, with summaries by totals only, all printed in the report file would be specified at the number of cycles prompt as: -001000100010001y. Alternatively, growing the current stand for 4 cycles with mortality and no tree detail or summary printed, the response would be: 00040001.

Page 41: In batch mode, when specifying labels for harvest operations, the program expects the format A30, a 30-character label, in the batch command file. The entire 30 character field must be filled in for proper operation. The extra characters may be blanks, but ensure at least 30 characters, including blanks, in the command file for this label entry. To ensure enough characters, place a "dummy" character in column 31 on the line where the label is to occur. The two changes listed above also apply to batch mode.

APPENDIX F. COMMAND SUMMARY

INITIALIZATION COMMANDS

- pc - print commands
- cm - set cubic foot DBH min.
- ct - set cubic merch top
- bm - set board foot DBH min.
- bt - set board foot merch top
- sc - list species groups and current group indicator
- sp - set species groups
- su - list user defined species groups
- fl - set print flag
- yf - set yield flag
- cl - set user calibration scheme
- iq - set record quintupling option
- ex - return to main program

MAIN COMMANDS

- pc - print commands

Report Commands

- | | |
|------------------------------------|-------------------------------------|
| pi - print initial description | pm - print DBH mins & merch tops |
| • sc - print current species group | • su - print user defined sp. group |
| • dt - enter DBH dist. routine | • pf - enter stand profile routine |
| • dc - print DBH class table | st - print stock table |
| yd - print yield summary | • sl - print standing log table |
| cg - print current 5 yr growth | |

Simulation Commands

- | | |
|-----------------------------|--|
| • gr - enter growth routine | ig - add ingrowth to tree file |
| ct - enter harvest routine | • cl - initialize/reset user calibration |

File Utility Commands

- | | |
|----------------------------------|-------------------------------------|
| wc - write coefficients | es - external save of current stand |
| sv - save current stand status | ns - start over with new stand |
| rt - restore stand saved by "sv" | os - truncate yield summary |

- ex - exit from program

HARVESTS COMMANDS

- pc - print harvest commands
 - cf - change output file number
 - dt - enter DBH distribution routine
 - pf - enter stand profile routine
 - st - print current stock table
 - dc - print DBH class table
 - r1 - harvest - DBH control
 - r2 - harvest - Basal Area control
 - r3 - harvest - Free
 - r4 - harvest - Sanitation
 - ih - print intermediate harvest since last "ih" call
 - ch - print cumulative harvest since entering cut routine
 - th - print total harvest since beginning simulation
 - hc - print cumulative harvest DBH class table
 - hl - print cumulative harvest log stock table
 - ex - exit cutting routine
- - information from this command may be routed to the report file.

ERROR REPORTING PROCEDURE

The programs in the CACTOS system have been tested extensively prior to their release. However, you may encounter problems we have not encountered in our testing. If so, we'd appreciate hearing from you.

Problems you might encounter fall into two categories: application errors and design errors. Application errors result from using the programs outside the range of conditions intended. Where possible, the programs should alert you to such improper use and ask you to change your specifications. However, the programs will let you do some things that are possible on the computer but meaningless in practice.

Design errors occur when you try to do an operation which should be possible, but it fails. These errors are the ones of primary importance to us, because they may represent a failure of the program. Thus, we ask you to give us a detailed accounting of the problem so that we can reproduce it in our lab and correct it.

Please send the following items to us if you encounter a problem with one of the programs in the CACTOS system:

- (a) A printed copy of the screen contents showing the error.
- (b) A detailed list of the commands that led to the error. (In CACTOS, the best way to do this is to make a batch file.)
- (c) A copy of the diskette containing:
 - (1) the stand description or other data file used,
 - (2) the program that is giving you trouble, and
 - (3) any other relevant input and output files.
- (d) Your name, address, and telephone number.

The materials that you send to us for tracing errors should be copies. You should retain a copy so that we can discuss the runstream with you if necessary. These materials will be discarded when the problem is solved.

Your comments and suggestions concerning the programs in the CACTOS system are welcome. It is through this interaction that we can offer the best possible programs for your use.

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