



## Computing the Components of Forest Growth and the Revisions for CACTOS version 4.5

by

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### Overview

A new procedure has been added to facilitate the comparison of actual growth and mortality observed on a sample plot with the growth and mortality predicted by the CACTOS (Wensel and Biging 1988) models. The procedure is accessed from the "go:" command level with "cp", which stands for compare. This comparison procedure is actually an attempt to make growth model validation (Bruce and Wensel 1988) more explicit for CACTOS. For data observed at a remeasurement, the procedure will compute the basal area in the four components survivor, ingrowth, mortality, and cut, and will also compute the basal area in the two components survivor and mortality for the predictions made by CACTOS (CACTOS does not predict ingrowth and it is assumed that any type of harvest can be simulated accurately) by species and totals so that direct comparison of the two predicted quantities with actual observation can be made.

Also new in CACTOS version 4.5 is an added feature to the "free harvest" (r3) routine. Now the user can specify the amount of timber to leave, as well as the amount to take.

The "stocks" (st) command and the "standing logs" (sl) command have also been made more consistent with each other. Both commands now give the user the option of writing the result to the report file as well as to the screen. This may have an effect on some existing batch files, but the batch command file generator (Meerschaert and Wensel 1990) correctly handles this change.

### New Compare Module

The new compare module performs a more detailed plot analysis than that which can be achieved with the COMPARE program (Meerschaert and Wensel 1987). The CACTOS compare module uses matched record stand description files as input. In this way, the growth components can be separated and then the growth models can be evaluated without the confounding effects of the mortality models, and *vice versa*.

The new compare routine requires two stand description files to operate. The first will represent the stand at the "initial" measurement, the second will represent the stand at the "final", or subsequent measurement. The two files must be matched, meaning that if tree 7, say, is on line 12 in the first stand description file, then tree 7 must be on line 12 in the final file. All ingrowth trees present in the final measurement but not in the first should follow (in any order) the trees that do



The California Conifer Timber Output Simulator

by

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American Forest Products	The Hearst Corp.
W.M. Beaty and Associates	Louisiana-Pacific Corp.(Elk Creek)
Champion International Corp.	Louisiana-Pacific Corp.(Feather Falls)
Crane Mills	Fiberboard Corp.
Roseburg Resources (Diamond)	Michigan-California Lumber Co.
Fruit Growers Supply	Sierra Pacific Industries
U.S.D.A. Forest Service (R5)	CA Dept. of Forestry & Fire Protection

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enter "return" to continue <return>

STARTUP PROGRAM

Type "pc" to get a list of commands

cactos:cf

INITIALIZATION ROUTINE

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

- CURRENT CONFIGURATION STATUS -

sk - Title page skip.....OFF  
cm - Cubic minimum diameter..... 0"  
ct - Cubic merch top..... 6.0"  
bm - Board foot minimum diameter..... 8.0"  
bt - Board foot merch top..... 6.0"  
yf - Yield flag.....ON  
fl - Print flag.....ON  
iq - Inhibit record quintupling.....OFF  
sp - Species grouping code.....1

initgo:sk

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

initgo:iq

Enter 0 to quintuple records (default)  
or 1 to inhibit quintupling : 1

initgo:ps

*Enter the configuration routine.*

*Title page skip switched on.*

*Record quintupling is switched off.*

*Current configuration status is reviewed for*

```
- CURRENT CONFIGURATION STATUS -
sk - Title page skip.....ON
cm - Cubic minimum diameter..... 1.0"
ct - Cubic merch top..... 6.0"
bm - Board foot minimum diameter..... 8.0"
bt - Board foot merch top..... 6.0"
yf - Yield flag.....ON
fl - Print flag.....ON
iq - Inhibit record quintupling.....ON
sp - Species grouping code.....1
```

initgo:af

Current configuration saved in:CACTOS.CNF

initgo:ex

Exiting initialization routine

cactos:pc

MAIN COMMANDS

-----

```
pc - print these commands
cf - enter configuration routine
go - enter interactive mode (*go: prompt)
ba - enter batch mode
cm - build command file for batch mode
br - branch to operating system
ex - exit program
```

cactos:go

Open the stand description file
Enter a file name here: 5p85.sd

Open the yield file
Enter a file name here: 5p85.yd

Open the report file
Enter a file name here: 5p85.rp

MAIN PROGRAM

-----

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

go:pc

correctness.

The current configuration is saved.

The "go" routine is entered from which "cp" will be called. Enter the initial stand description file name here.

Print available commands.

=== MAIN COMMAND MENU ===

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  
 dp - display tree file                et - print elapsed time  
 dt - enter dia. dist. routine        pf - enter stand profile routine  
 dc - print dia. class table          st - print stock table  
 yd - print yield table                sl - print standing log table  
 cg - print current 5yr growth

--- Simulation Commands ---

gr - enter growth routine            ig - add ingrowth to tree file  
 ct - enter harvest routine           cl - initialize/reset user calibration  
 cp - enter growth comp. routine

--- File Utility Commands ---

cf - change output file number      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 table  
 ex - exit from program               br - branch to operating system

go:yd

YIELD SUMMARY: units = english

-----  
 Cofile version 4.12 10/16/89 Revised mortality coefs (Table 2)  
 stand label = 5P-0016 07-08-85

	min. DBH	merch top
cubic ft.	.0	6
board ft.	8.0	6

species	site	init. age
Sugar Pine	75.	0.
Cedar misc	47.	0.
DouglasFir	62.	0.
White Fir	62.	0.

species	et	dbar	tpa	basar	cvol	bdvol	bagro	cvgro	bdgro
Sugar Pine	.00	11.62	55.0	40.5	.78	3.24	.0	.00	.00
Cedar misc	.00	16.65	50.0	75.6	2.07	12.12	.0	.00	.00
DouglasFir	.00	9.85	40.0	21.2	.47	2.17	.0	.00	.00
White Fir	.00	19.52	75.0	155.8	5.59	32.87	.0	.00	.00
Totals	.00	15.63	220.0	293.1	8.91	50.41	.0	.00	.00

species	et	dbar	tpa	basar	cvol	bdvol	bagro	cvgro	bdgro
---------	----	------	-----	-------	------	-------	-------	-------	-------

go:dt

Print diameter distribution

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

The appearance of the main command menu has been changed slightly so that it all fits on one standard 25 line display screen.

New "cp" command.

Of course, all these commands perform their usual functions.

Note that it is the initial measurements that are processed.

To perform these operations on the new stand description, it must be accessed through the 'ns' command or as below by exiting and re-entering 'go' level.

Diameter Distribution  
elapsed time = .00 yrs  
All species combined

dbh	trees	15	30	45	60
0 - 2	0.				
2 - 4	40.				
4 - 6	0.				
6 - 8	50.				
8 -10	0.				
10-12	20.				
12-14	20.				
14-16	20.				
16-18	10.				
18-20	10.				
20-22	10.				
22-24	5.				
24-26	15.				
26-28	10.				
28-30	5.				
30-32	0.				
32-34	5.				
-----					
total	220.				

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

Table saved in report file.

go:cp

Begin Growth Prediction Validation Routine

Enter the number of 5 yr. growth cycles desired.

Note: for efficiency mortality will be ENABLED for the comparison regardless of configuration setting.

When finished, configuration file regains control.

Please enter number of cycles here: **1**

MORTALITY ON

Open the final stand description file

Enter a file name here: **5p90.sd**

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

Finished computing comparison summary.

Open the comparison summary file.

Enter a file name here: **5p85-90.cp**

Comparison summary saved in 5p85-90.cp

go:ex

Yield summary saved in 5p85.yd

Report summary saved in 5p85.rp

Stand was labeled: SP-0016 07-08-85

cactos:go

Open the stand description file

Enter a file name here: **5p90.sd**

*The growth comparison routine is called.*

*Enter the number of cycles desired for your data*

*Here is where we enter the new stand description file name.*

*Here we name the file to contain the comparison summary. The 'cp' extension is suggested.*

*Now let's "grow" the new stand to forecast conditions in the future.*

Open the yield file  
Enter a file name here: 5p90.yd

Open the report file  
Enter a file name here: 5p90.rp

This stand contains either pseudo-stochastic or status code information.  
Do you want to save this extra description information ?  
(y=yes,n=no) enter answer here: n

MAIN PROGRAM

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

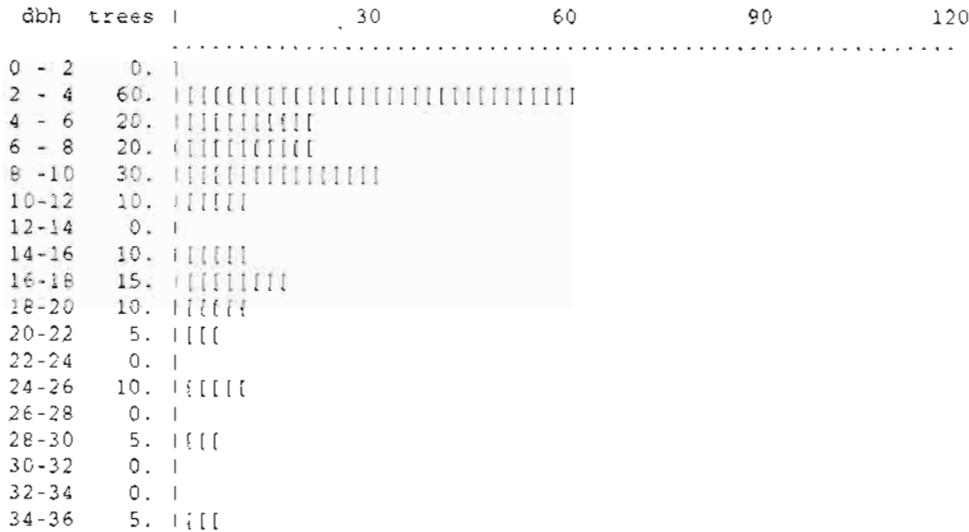
go:dt

Print diameter distribution

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

Diameter Distribution  
elapsed time = .00 yrs  
All species combined



total 200.

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

Table saved in report file.

go:gr

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: 2

Since we just used this stand description in the previous comparison, it contains tree status code information which we must discard.

Let's see a DBH distribution.

Now we just grow the stand as usual.

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  
etc.

Enter Record skip: 0

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

GROWTH SUMMARY - CYCLE = 1 elapsed time = 5.00  
species bagro cvgro bdgro  
-----  
Sugar Pine 4.6 .14 .67  
Cedar misc -2.5 -.07 -.45  
DouglasFir 5.1 .16 .92  
White Fir 5.9 .29 1.86  
Totals 13.1 .51 3.00

GROWTH SUMMARY - CYCLE = 2 elapsed time = 10.00  
species bagro cvgro bdgro  
-----  
Sugar Pine 5.1 .17 .99  
Cedar misc -2.5 -.07 -.36  
DouglasFir 5.6 .18 1.09  
White Fir 6.0 .32 2.08  
Totals 14.3 .59 3.80

Tree detail and/or summary info saved in report file.

go:dt

Print diameter distribution

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

Save a copy of the pre-  
dicted DBH distribution.



The output filenames are constructed exactly the same way as before: the prescription code is appended to the "root" of the initial stand description files appearing in the filenames file. If any of the files named in the filenames file are concatenated files, the comparison summaries for individual stands will appear concatenated in the output file with an asterisk (\*) separating them, much like concatenated yield files are created. The batch filename extension is "cp."

Note also that "final" stand description files containing status codes in columns 41-48 cannot themselves be batch processed as initial stand descriptions unless the '100' is removed from columns 70-72 of the stand description headers. Due to the structure of the CACTOS processing algorithms the status codes will be interpreted as basal area growth factors if the '100' is not removed. Obviously this will produce erroneous results.

### Specifying Amount to Leave in Harvest Option R3

A new feature has been added to the "free harvest" or r3 routine. The routine continues to function as before, but in addition the user can now specify the amount of timber to save.

#### Accessing the save option in r3

The new save option is accessed by preceding the amount to harvest with a minus ("-") sign. Thus, to save two trees in a particular dbh class the user would enter "-2", etc. Also, "minus zero" is different than "zero." Typing a minus in front of a zero denotes "save none", while a zero by itself denotes "cut none" as it did before. The following runstream should make the operation of the new options clear.

```

      MAIN PROGRAM
      -----
Type "pc" to get a list of available commands
Current output file is 32 (the screen)

gc:dc

      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: 0.50,10
```

*The title screen is edited here as it is the same as above.*

*Let's make a stand/stock table to see what we've got.*

Standing diameter class table -- et = .00 yrs  
table is totals by DBH class

-----  
stand label = Compare Demo 1.1  
All species combined  
-----

	stocks			growth			
	trees	basar	cfvol	bdvol	basar	cfvol	bdvol
0-10	100.0	18.35	.14	.50			
10-20	60.0	72.89	2.17	11.17			
20-30	10.0	33.15	1.10	6.25			
30-40	20.0	119.60	4.33	27.25			
40-50	5.0	53.76	1.62	9.58			
totals	195.0	297.74	9.35	54.76			

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: 0

go:ct

#### HARVEST ROUTINE

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

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

cutgo:r3

WELCOME TO FREE CUTTING

How many diameter classes to establish? (max= 24): 5  
What is the upper DBH limit for the 1st DBH class?: 10  
What is the upper DBH limit for the 2nd DBH class?: 20  
What is the upper DBH limit for the 3rd DBH class?: 30  
What is the upper DBH limit for the 4th DBH class?: 40  
What is the upper DBH limit for the 5th DBH class?: 50  
What is the upper DBH limit for the 6th DBH class?: 100

Enter maximum fraction of total BA which may be cut:1.0

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 : 0

You may remove either trees or basal area by  
considering the following:

(1)-- smallest dbh in the class  
(2)-- live crown ratio  
(3)--lcr and dbh

Enter option to use: 3

*Enter the harvest module  
as always.*

*Enter 'r3' as always.*

*Set up DBH classes  
almost as usual. Note  
the explicit inclusion of  
a class to "catch" all the  
50+ trees. This is very  
important in batch mode  
not really for the inter-  
active mode.*

*Here also, specifying  
"1.0" as the max  
fraction to cut is im-  
portant for batch mode  
not so much so for  
interactive mode (see  
below).*

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

Enter 1 or 2 : 1

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

Enter 1 or 2 : 1

How many DBH classes to operate in (1- 6) ? : 6

Initial total basal area = 297.74 sq.ft./ac.

Current basal area = 297.74 sq.ft./ac.

.00 % of the initial basal area has been cut.

diameter class :	1	2	3	4	5	6
upper limit :	10.0	20.0	30.0	40.0	50.0	100.0

Enter DBH class to harvest 1st ( 1,2,3, etc): 6

How many trees to harvest ?

Trees in this class = .00

Enter amount here: -2

Initial total basal area = 297.74 sq.ft./ac.

Current basal area = 297.74 sq.ft./ac.

.00 % of the initial basal area has been cut.

diameter class :	1	2	3	4	5	6
upper limit :	10.0	20.0	30.0	40.0	50.0	100.0

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

How many trees to harvest ?

Trees in this class = 5.00

Enter amount here: -2

Initial total basal area = 297.74 sq.ft./ac.

Current basal area = 265.49 sq.ft./ac.

10.83 % of the initial basal area has been cut.

diameter class :	1	2	3	4	5	6
upper limit :	10.0	20.0	30.0	40.0	50.0	100.0

Enter DBH class to harvest 3rd ( 1,2,3, etc): 4

How many trees to harvest ?

Trees in this class = 20.00

Enter amount here: -4

Initial total basal area = 297.74 sq.ft./ac.

Current basal area = 170.37 sq.ft./ac.

42.78 % of the initial basal area has been cut.

diameter class :	1	2	3	4	5	6
upper limit :	10.0	20.0	30.0	40.0	50.0	100.0

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

How many trees to harvest ?

Trees in this class = 10.00

Enter amount here: -10

Initial total basal area = 297.74 sq.ft./ac.

Current basal area = 170.37 sq.ft./ac.

42.78 % of the initial basal area has been cut.

*Attempt to save more trees than are present. Note that saving trees that aren't there has no effect.*

*Save two trees in class five. Of course, a realistic request is processed and the basal area is decremented accordingly.*

*Save four trees in class four.*

*Save 10 trees in class three.*

```
diameter class :   1   2   3   4   5   6
  upper limit :  10.0 20.0 30.0 40.0 50.0 100.0
```

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

How many trees to harvest ?  
Trees in this class = 60.00  
Enter amount here: -10

Initial total basal area = 297.74 sq.ft./ac.  
Current basal area = 117.09 sq.ft./ac.  
60.68 % of the initial basal area has been cut.

```
diameter class :   1   2   3   4   5   6
  upper limit :  10.0 20.0 30.0 40.0 50.0 100.0
```

Enter DBH class to harvest 6th ( 1,2,3, etc): 1

How many trees to harvest ?  
Trees in this class = 100.00  
Enter amount here: -20

You have finished harvesting. Normal termination.  
Basal area harvested is 189.57 sq.ft./ac. or 63.67 % of total basal area.  
Remaining basal area = 108.17 sq.ft./ac.

Do you want to continue harvesting?: n

cutgo:ex

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

Exiting harvest routine.  
Returning to main program.

go:dc

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: 0,100,10

*Save ten trees in class two.*

*Save 20 trees in class one.*

*Exit r3 as usual.*

*Take a look at what's left.*

*Make the upper limit high enough to include all the trees.*

```

Residual diameter class table -- et = .00 yrs
table is totals by DBH class
-----
stand label = Compare Demo 1.1
All species combined
-----
                stocks                growth
-----
| trees | basar | cfvol | bdvol || basar | cfvol | bdvol ||
-----
0-10| 20.0 | 9.44 | .14 | .50 ||
10-20| 10.0 | 19.61 | .67 | 3.66 ||
20-30| 10.0 | 33.15 | 1.10 | 6.25 ||
30-40| 4.0 | 24.48 | .75 | 4.60 ||
40-50| 2.0 | 21.50 | .65 | 3.83 ||
-----
totals| 46.0 | 108.17 | 3.30 | 18.84 ||

```

*Note that only the classes containing trees printed.*

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

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: **0**

go:ex

Yield summary saved in demoSave.YD  
Report summary saved in demoSave.RP

### Considerations for batch operation

As noted in the side bar in the above runstream example, several considerations must be mentioned for successful batch runs using r3 with the new save option. When prompted for the number of classes to make, be sure to make enough to include all of your data which will appear on any of the plots run through that prescription. This can be accomplished as noted above by giving the largest class an upper limit that is larger than the largest tree likely to be encountered on any of your plots. Similarly, by specifying a maximum fraction of the total basal area to harvest of 1.00, the batch job is assured to run to completion. If anything less is specified, the risk is run that a stand will be encountered where the given prescription will attempt to harvest too much, and the remainder of the batch job will be garbled. This may, of course, result in some meaningless prescriptions for certain stands, but the onus is on the user to check the output for this, and perhaps re-run these stands interactively where there is much more control over the harvesting.

### Corrections to the "st" and "sl" Options in Batch Mode

Both the "st" (stocks) and "sl" (standing logs) commands now prompt the user if the result should be written to the report file as well as the screen.

#### Accessing the commands

The commands are accessed as before, the following runstream shows the prompts for writing the output of each command to the report file.

MAIN PROGRAM

Type "pc" to get a list of available commands  
 Current output file is 32 (the screen)

go:st

Issue the 'st' command.

STOCK TABLE

-----  
 elapsed time = .00 years

species	dbar	tpa	basar	cfvol	bdvol
Sugar Pine	31.76	15.	82.5	3.00	18.77
Cedar misc	39.33	10.	84.4	2.56	15.34
DouglasFir	30.40	5.	25.2	.95	5.84
White Fir	10.84	165.	105.7	2.84	14.81
Totals	16.73	195.	297.7	9.35	54.76

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

Query to send to report file.

Table saved in report file.

go:sl

Issue the 'sl' command.

Print log table

Standing log inventory

-----  
 stand = Compare Demo 1.1  
 elapsed time = .00

Cubic volume (MCF/ac) by log size

sp.	Yellow Pines	White pines	True fir	Douglas Fir	Cedar misc.
dib	logs	logs	logs	logs	logs
	cvol	cvol	cvol	cvol	cvol
4	.0	.0	.0	.0	.0
6	.0	14.4	74.7	2.2	8.1
8	.0	.0	55.0	5.0	.0
10	.0	10.0	35.0	.0	5.0
12	.0	5.0	25.0	5.0	5.0
14	.0	15.0	30.0	.0	5.0
16	.0	5.0	15.0	5.0	.0
18	.0	10.0	.0	5.0	10.0
20	.0	10.0	5.0	.0	.0
22	.0	5.0	.0	5.0	10.0
24	.0	10.0	.0	5.0	.0
26	.0	.0	.0	.0	5.0
28	.0	10.0	.0	.0	5.0
30	.0	.0	.0	.0	.0
32	.0	.0	.0	.0	.0
34	.0	.0	.0	.0	5.0
Totals	.00	3.00	2.84	.95	2.56
eqn/taper	.00	.98	1.07	.98	1.01

sp.	Yellow Pines	White pines	True fir	Douglas Fir	Cedar	misc.				
dib	logs	bdvol	logs	bdvol	logs	bdvol				
6	.0	.00	16.9	.34	94.1	1.96	6.3	.14	8.3	.19
8	.0	.00	.0	.00	26.6	.79	.0	.00	.0	.00
10	.0	.00	9.7	.58	44.8	2.75	.0	.00	4.1	.24
12	.0	.00	5.0	.49	15.0	1.43	5.0	.42	4.2	.33
14	.0	.00	10.0	1.21	30.0	3.97	.0	.00	5.0	.57
16	.0	.00	10.0	1.79	15.0	2.64	5.0	.75	.0	.00
18	.0	.00	5.0	1.02	.0	.00	5.0	1.08	10.0	1.95
20	.0	.00	10.0	2.72	5.0	1.27	.0	.00	.0	.00
22	.0	.00	5.0	1.46	.0	.00	5.0	1.46	10.0	3.23
24	.0	.00	10.0	3.88	.0	.00	5.0	1.98	.0	.00
26	.0	.00	.0	.00	.0	.00	.0	.00	5.0	2.23
28	.0	.00	10.0	5.29	.0	.00	.0	.00	5.0	2.66
30	.0	.00	.0	.00	.0	.00	.0	.00	.0	.00
32	.0	.00	.0	.00	.0	.00	.0	.00	.0	.00
34	.0	.00	.0	.00	.0	.00	.0	.00	5.0	3.94
Totals	.00		18.77		14.81		5.84		15.34	
eqn/taper	.00		.97		1.06		.94		.95	

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

Table saved in report file.

go:ex

Yield summary saved in demo\_rxl.YD  
Report summary saved in demo\_rxl.RP

Query to send to report file.

### Considerations for batch operation

Batch files created previously with the command file generator may not work properly. The command file generator now correctly handles the request to write output to the report file for both the 'st' and the 'sl' commands.

### Literature cited

- Bruce, D. and Wensel, L.C.  
1988. Modelling forest growth: Approaches, definitions, and problems. In: Forest Growth Modelling and Prediction. Proceedings of the IUFRO conference, 23-27 August, 1987, Minneapolis, MN (A. Ek, S. Shifley and T. Burk, editors). General Technical Report NC-120, USDA Forest Service, North Central Forest Expt. Stn., St. Paul, MN 55108.
- Meerschaert, W.J. and Wensel, L.C.  
1990. CACTOS (version 4.2): Batch command file generator. Research Note No. 22 (revised), Northern California Forest Yield Cooperative, Univ. California, Berkeley, CA 94720.
- Turnblom, E.C. and Wensel, L.C.  
1992. PCBridge: A data reformatting utility for bridging PERMCHEK files with CACTOS stand description files version 2.2. Research Note No. 35, Northern California Forest Yield Cooperative, Univ. California, Berkeley, CA 94720.

Wensel, L.C. and Biging, G.S.

1988. The CACTOS system for individual-tree growth simulation in the mixed conifer forests of California. In: Forest Growth Modelling and Prediction. Proceedings of the IUFRO conference, 23-27 August, 1987, Minneapolis, MN (A. Ek, S. Shifley and T. Burk, editors). General Technical Report NC-120, USDA Forest Service, North Central Forest Expt. Stn., St. Paul, MN 55108.

### Appendix 1

#### Contents of initial stand description for comparison

.....	1.....	2.....	3.....	4.....	5.....	6.....	7.....	8.....
5P-0016	07-08-85	33	4640		.00			0
0.	75.	47.	62.	62.	0.	0.	0.	0.
0.	0.	0.	0.	0.	0.	0.	0.	0.
5.000	25.900	106.000	.547	5.000	.000			
5.000	13.000	58.000	.534	5.000	.000			
2.000	13.900	58.000	.569	5.000	.000			
5.000	12.800	64.000	.531	5.000	.000			
4.000	3.600	18.000	.667	20.000	.000			
5.000	16.700	83.000	.590	5.000	.000			
2.000	20.400	90.000	.522	5.000	.000			
4.000	19.900	92.000	.793	5.000	.000			
3.000	33.200	119.000	.471	5.000	.000			
4.000	14.400	62.000	.726	5.000	.000			
2.000	7.600	29.000	.655	10.000	.000			
3.000	27.900	93.000	.473	5.000	.000			
2.000	6.400	29.000	.690	10.000	.000			
5.000	18.700	69.000	.594	5.000	.000			
5.000	26.100	113.000	.496	5.000	.000			
5.000	23.500	111.000	.414	5.000	.000			
2.000	7.400	37.000	.784	10.000	.000			
3.000	3.300	12.000	.500	20.000	.000			
3.000	6.700	37.000	.784	10.000	.000			
2.000	11.600	58.000	.362	5.000	.000			
2.000	14.800	62.000	.677	5.000	.000			
2.000	14.700	76.000	.684	5.000	.000			
4.000	7.800	46.000	.739	10.000	.000			
3.000	10.400	47.000	.660	5.000	.000			
5.000	16.200	78.000	.462	5.000	.000			
5.000	25.300	115.000	.348	5.000	.000			
5.000	13.100	60.000	.417	5.000	.000			
3.000	25.500	97.000	.474	5.000	.000			
5.000	28.700	130.000	.600	5.000	.000			
5.000	21.900	94.000	.468	5.000	.000			
5.000	11.200	53.000	.623	5.000	.000			
5.000	15.100	61.000	.295	5.000	.000			
5.000	10.800	62.000	.355	5.000	.000			

Contents of final stand description for comparison

	1	2	3	4	5	6	7	8
5P-0016	08-21-90	35	4640	.00				100
0.	75.	47.	62.	62.	0.	0.	0.	0.
0.	0.	0.	0.	0.	0.	0.	0.	0.
5.000	.000	.000	.000	20.000	3.000			
5.000	.000	.000	.000	20.000	3.000			
2.000	.000	.000	.000	20.000	3.000			
5.000	.000	.000	.000	20.000	2.000			
4.000	4.500	22.000	.727	20.000	1.000			
5.000	18.300	89.000	.618	5.000	1.000			
2.000	.000	.000	.000	20.000	3.000			
4.000	21.500	101.000	.812	5.000	1.000			
3.000	34.100	119.000	.471	5.000	1.000			
4.000	15.900	68.000	.750	5.000	1.000			
2.000	9.300	32.000	.625	10.000	1.000			
3.000	28.400	93.000	.473	5.000	1.000			
2.000	7.000	30.000	.700	10.000	1.000			
5.000	19.500	70.000	.600	5.000	1.000			
5.000	.000	.000	.000	20.000	3.000			
5.000	24.200	111.000	.414	5.000	1.000			
2.000	8.200	40.000	.800	10.000	1.000			
3.000	3.400	12.000	.500	20.000	1.000			
3.000	7.000	37.000	.730	10.000	1.000			
2.000	.000	.000	.000	20.000	2.000			
2.000	16.600	72.000	.653	5.000	1.000			
2.000	16.500	87.000	.701	5.000	1.000			
4.000	8.800	51.000	.725	10.000	1.000			
3.000	10.900	50.000	.580	5.000	1.000			
5.000	16.900	84.000	.405	5.000	1.000			
5.000	.000	.000	.000	20.000	2.000			
5.000	.000	.000	.000	20.000	2.000			
3.000	25.900	100.000	.490	5.000	1.000			
5.000	.000	.000	.000	20.000	3.000			
5.000	.000	.000	.000	20.000	3.000			
5.000	11.700	57.000	.544	5.000	1.000			
5.000	15.700	66.000	.348	5.000	1.000			
5.000	.000	.000	.000	20.000	3.000			
2.000	2.400	11.000	.636	20.000	4.000			
3.000	2.600	13.000	.231	20.000	4.000			

## Appendix 2

COMPARISON SUMMARY

Cofile version 4.12    10/16/89    Revised mortality coeffs (Table 2)

init. stand label= 5P-0016    07-08-85    in: 5p85.sd  
 final stand label= 5P-0016    08-21-90    in: 5p90.sd

	min. DBH	merch top
cubic ft.	.0	6
board ft.	8.0	6

species	site	init. age
Sugar Pine	75.	0.
Cedar misc	47.	0.
DouglasFir	62.	0.
White Fir	62.	0.

species	initial BA	et	----- surv.	Observed ingr.	final mort.	BA cut	---- Pred. surv.	final mort.	BA
Sugar Pine	40.52	5.00	26.00	.63	3.67	16.62	24.02	1.24	
Cedar misc	75.61	5.00	79.17	.74	.00	.00	78.61	5.25	
DouglasFir	21.19	5.00	25.93	.00	.00	.00	25.00	.06	
White Fir	155.80	5.00	53.72	.00	26.60	80.20	54.05	3.03	
Totals	293.12	5.00	184.82	1.37	30.27	96.82	181.68	9.59	M