



CO-OP REDWOOD YIELD RESEARCH PROJECT

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USERS GUIDE TO GENR

An Interactive Program to Generate Inventory Records
of Typical Young Growth Stands in Coastal California.

by

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I. Introduction

GENR is an interactive computer program that is designed to generate a one acre representation of a pure or mixed species, natural young growth evenaged stand typical of the north coast region of California. Only combinations of the following four species can be generated: redwood, Douglas fir, tanoak, and red alder.

The primary purpose of this program is to convert some general broad stand descriptors (input) into a plausible representative tree-by-tree inventory record for direct use by the CRYPTOS (I) program. (See Research Note No. 16).

As a secondary feature, GENR has some graphics capabilities which can be used to generate frequency diagrams of trees by two inch DBH classes and species thus allowing the user to get a visual picture of the population of trees being generated.

The analytical design of this program incorporates several models that were documented in previous research notes. Appendix I provides a summary of the procedures that are used. Appendix II contains an illustrative example of the program.

II. Program Environment

GENR was developed for use on the University of California's PDP 11/70 computers and was coded in standard Fortran IV. These computers use Fortran IV-PLUS compilers but special features of the Fortran IV PLUS language were not used to make adaptations to other computers as easy as possible. The program consists of about 500 lines of code.

This program assumes the keyboard is assigned input channel '5' and the screen is the output channel '6'. If you are going to save the tree information for use by CRYPTOS (I), you will be asked to input a file number where the information will be stored. For the U.C. PDP 11/70 computer, this number is in the range 1-3 or 11-15. If your entered number is 'xxx', the output file created will be called 'forxxx.dat.'

III. Using The Program

The program is basically self-explanatory since it is operated by responding to questions asked by the program. However, there are a few codes you will need to know.

You will initially be asked to enter a code designating the control species : a '1' is for redwood and a '2' is for Douglas fir. The control species is used as a base for estimating missing site index and age values for other species. (See Appendix I).

You will then be asked to input the following values for each of the previously mentioned species groups:

- a) stems/acre (TPA)
- b) site index (SI)
- c) average breast high age of dominants (Age)
- d) quadratic mean DBH (optional)
- e) number of tree records (NR) to be generated (optional)

A. Items to Note

- 1) Items 'b' and 'c' listed above are both required for the control species. If you fail to enter them, the program will mercifully give you another chance.
- 2) For any other species you wish to have as part of your stand (e.g. you have entered a stems/acre value of 25 or greater for the species) you may enter site index and age. If either or both of these are not entered, they will be estimated using the control species as a basis.
- 3) It is not necessary for the control species stems/acre value to be nonzero.
- 4) If quadratic mean DBH values are supplied for any species, Model II of Research Note 11 will be used in estimating diameter distributions. Otherwise, Model I will be used.
- 5) The number of tree records (NR) by species is defaulted to 15 if the stems per acre for any species is greater than 25. This value may be overridden on input with any value greater than or equal to 10. The following conventions are used:
 - a) If a species record number is entered in the range 1-9, it is changed to 10.
 - b) If the total number of records for all species is greater than 200, the program will start all over. So 200 is a maximum.
 - c) If the total number of records is greater than 65, a warning to the effect that your output file is unusable for CRYPTOS will be issued.

IV. Preliminary Output

The program will next print two tables. The first one displays the input information (or program-generated estimates if they were not entered) plus the estimated dominant height for each of the four species.

The second table is the result of the diameter distribution estimation process by species. The Y_i 's are DBH's at approximately the .89, .61, and .33 percentage points. 'a', 'b', 'c' are the Weibull diameter distribution parameters. If '(mod)' is printed, some adjustments were made in the parameters (See Research Note No. 11, Appendix IV). The

original values are under "originals". \bar{D} is the estimated quadratic mean DBH based on the Weibull estimates. It is approximately (exactly, if Model II is used) the same as listed under "First Stage Estimation".

V. Graphics

Next, you may look at DBH frequency diagrams by species. These are the species codes in this program:

- 0 - all trees
- 1 - Redwood
- 2 - Douglas fir
- 3 - Tanoak
- 4 - Alder

Entering a species code of '9' will allow you to exit from the graphics subroutine.

VI. Storing your stand for future use

Once graphics are completed, you have the option of (1) starting all over, (2) stopping, or (3) preserving your stand record for future use (in CRYPTOS (I) most likely). If option 3 is chosen you will be asked to input a file number that, for CRYPTOS (I) compatibility, must be in the range 1-3 or 10-15. The appropriate information will be stored in CRYPTOS (I) compatible format on this file. You will also have an opportunity to examine this tree file before storage procedures are completed.

Note:

If the original estimated value for the Weibull parameter 'a' (the minimum DBH) for any species is less than 1.0 inches, the program will issue a warning to the effect that you may wish to reconsider your decision to save this stand for future use. These stands represent an extrapolation far beyond the reasonable limits of the data used to construct the component models.

VII. Limitations

The data used to develop the distribution equations used by GENR were somewhat deficient in the younger age classes and lower stocking levels. It is currently felt that if the quadratic mean DBH is not supplied by the user and consequently, it is estimated by the program, the resulting estimates will be too large for young sparsely stocked stands. Ignoring this problem gets compounded into overestimates of future yields if GENR is used to create an input file to CRYPTOS.

The following procedure can be used to correct for this problem. If you are supplying the mean quadratic DBH by species based on whatever local experience you have, you may ignore the rest of this section. Otherwise, a) Find the age and site index of your stand in Table 1. b)

If the total stems per acre of all species combined is less than the amount listed, use the corresponding mean quadratic DBH as model input. c) Otherwise, the program can be used "normally".

This table was prepared by iteratively generating stands and finding a stem count that corresponded to approximately 100 percent canopy cover at ground level. This is the stem count listed in the table along with the estimated mean quadratic DBH for this stocking level. Stands with lesser stocking levels were presumed to have the same average size.

Table 1. Minimal Stocking levels for which program
estimated quadratic mean DBH's are acceptable

REDWOOD					
SITE	Breast High Age				
INDEX	10	15	20	25	30
(STEMS PER ACRE/QUADRATIC MEAN DBH)					
90	450/4.32	160/7.01	100/9.68	75/11.75	65/13.33
100	360/4.90	135/7.60	85/10.35	65/12.47	55/14.18
110	300/5.44	115/8.17	75/10.98	59/13.13	50/14.19
120	250/5.97	100/8.37	67/11.59	53/13.81	45/15.66
130	210/6.51	87/9.28	61/12.17	48/14.49	41/16.41
140	185/7.03	80/9.76	56/12.75	44/15.15	38/17.12
DOUGLAS FIR					
SITE	Breast High Age				
INDEX	10	15	20	25	30
(STEMS PER ACRE/QUADRATIC MEAN DBH)					
90	430/2.82	150/6.05	95/3.31	72/10.07	59/11.54
100	310/3.19	120/6.65	30/8.49	62/10.76	52/12.28
110	228/3.82	105/7.13	70/9.51	55/11.40	46/13.01
120	190/4.26	95/7.58	63/10.03	50/12.01	42/13.70
130	165/4.63	33/8.01	57/10.54	45/12.61	38/14.40
140	145/4.97	75/8.40	53/11.00	42/13.17	35/15.06

Appendix I

ANALYTICAL SUMMARY OF THE PROCEDURES USED IN STAND GENERATION

The primary purpose of the stand generator is to convert some very broad stand descriptors of evenaged mixed species stands into a one acre representation of a plausible tree by tree inventory. The initial input by species is:

- a) fifty year breast high age base site index
- b) average breast high age of dominants
- c) stems per acre
- d) quadratic mean DBH (optional)
- e) record count (optional)

>From this information, a tree list is generated where each record has the following characteristics.

- a) species indicator code
- b) DBH
- c) total height
- d) live crown ratio
- e) per acre weight

A. Site-Age Adjustments

Initially, the site index and age of either redwood or Douglas fir must be specified. One of these species, which must have site index and age supplied, is designated as a control species. If a trees per acre value greater than 25 is supplied for any species and the site index and/or breast high age is not supplied, they will be estimated by procedures described in the Appendix of Research Note No. 11 with the control species used as a base.

B. Diameter Distribution Estimates

Site index, age, and stems per acre by species are all that is required to estimate parameters in the diameter distribution models described in Research Note No. 11. If the quadratic mean DBH is not supplied for any species group, Model I will be used. Otherwise, Model II will be utilized.

In cumulative form, the diameter distribution model is

$$F(d_i) = 1 - \exp[-((d_i - a)/b)^c]$$

where

$F(d_i)$ = Percentage of trees between "a" and "d_i" inches DBH for a particular species

a, b, c, = Species Specific Model parameters with "a" being the minimum DBH.

>From this expression the percentage of trees between d_i and d_j inches ($d_j > d_i$) can be computed as

$$\exp[-((d_i-a)/b)^c] - \exp[-((d_j-a)/b)^c]$$

C. Record Generation

By Program default, or user modification, the number of records (NR) for a particular species is internally available in the program along with the number of trees per acre (TPA). Tree diameters are generated for each of the NR records by dividing the range of diameters into NR equal intervals. For each tree diameter a weight w_i is computed to represent the number of trees per acre represented by tree 'i' with DBH_i, where $\sum w_i = \text{TPA}$.

The process is illustrated as follows:

- 1) As the upper limit of the Weibull distribution is infinity, a finite range (DMIN - DMAX) is established as the diameters corresponding to the cumulative probabilities of 2 and 99.5 percent respectively. These DBH's are estimated as

$$\text{DMAX} = a + b(-\log[.005])^{1/c}$$

$$\text{DMIN} = a + b(-\log[.995])^{1/c}$$

The asymmetry of the range maintains approximately the same average stand quadratic mean diameter after record generation.

- 2) The constant DC is computed as

$$\text{DC} = [\text{DMAX} - \text{DMIN}] / \text{NR}$$

- 3) For any species tree record i ($i=1, \text{NR}$), the DBH assigned is

$$\text{dbh}_i = \text{DMIN} + (i)\text{DC} - \text{DC}/2$$

- 4) The per acre weight assigned to the i^{th} species record is

$$w_i = \{F(a+(i)\text{DC}) - F(a+(i-1)\text{DC})\}(\text{TPA})(1/.975)$$

- 5) Average DBH of the trees in the top 20% of the diameter distribution for a species (D_m) is obtained by numerically integrating the estimated diameter distribution model.
- 7) Using D_m , assigned DBH's, average height of dominants estimated by site index curves, and the models presented in Research Notes 8 and 12, total heights are then assigned to each record.
- 8) Model C-1 in Research Note No. 15 is then used to estimate crown ratios.

Appendix II

AN ILLUSTRATIVE EXAMPLE

This appendix contains an illustrative example of the output produced by GENR. In the following listing, circled items are typed in on the keyboard. Uncircled items and queries are produced internally by the program. Freehand annotations inscribed within boxes are intended to be documentations of program functions.

The following example uses redwood as a control species and generates a stand with a redwood site index of 100 and a breast high age of twenty years. A total stem count of 300 trees per acre is specified divided equally between redwood, douglas fir, and tanoak.

agen.out

INVOKE PROGRAM

REDWOOD COOP STAND GENERATOR

enter control species (i1) 1

REDWOOD IS THE CONTROL

enter stand descriptors by species

(xxx denotes an integer input field)

(xx.x denotes a real field with a decimal point)

	tpa	si	age	don	nr
	xxxx	xxx	xxx	xx.x	xxx
redwood	100	100	20		
doug fir	100				
tan oak	100				
alder					

BASIC STAND DESCRIPTION

FIRST STAGE ESTIMATES AND DESCRIPTION

	rdwd	dfir	tok	alder
	-----	-----	-----	-----
stems	100.	100.	100.	0.
sites	100.	127.	70.	91.
ages	20.	16.	18.	20.
dbars	9.5	6.9	5.0	0.0
doa-ht	52.1	53.8	31.6	62.6

ESTIMATED STAND CHARACTERISTICS

DISTRIBUTION ESTIMATES

	percentiles			parameters			originals			
	y1	y2	y3	a	b	c	a	b	c	Δ(D)
redwood	12.3	8.6	6.2	1.21	7.03	1.57(reg)	1.21	7.03	1.57	8.57
doug fir	9.7	7.0	5.2	0.75	5.93	1.95(reg)	0.75	5.93	1.95	6.63
tan oak	7.5	5.6	4.4	0.91	4.54	2.14(reg)	0.91	4.54	2.14	5.30

you can now look at graphs - type a 9 to quit

enter species code (0 for all species) 0

LOOK AT ALL SPECIES

sp dbn height cr-rat exp

sp	dbn	height	cr-rat	exp
1.	1.74	14.82	0.72	5.24
1.	2.82	20.99	0.68	9.56
1.	3.90	26.08	0.66	11.37
1.	4.97	30.47	0.65	11.83
1.	6.05	34.34	0.64	11.40
1.	7.12	37.83	0.64	10.41
1.	8.20	41.01	0.64	9.11
1.	9.28	43.94	0.64	7.70
1.	10.35	46.67	0.64	6.32
1.	11.43	49.21	0.64	5.05
1.	12.51	51.61	0.64	3.94
1.	13.58	53.87	0.65	3.00
1.	14.66	56.01	0.65	2.24
1.	15.73	57.35	0.66	1.64
1.	16.81	57.35	0.66	1.13
2.	1.14	15.59	0.82	1.91
2.	1.92	23.01	0.76	5.27
2.	2.69	28.66	0.72	7.99
2.	3.47	33.23	0.70	9.91
2.	4.25	37.06	0.69	10.93
2.	5.03	40.36	0.68	11.23
2.	5.81	43.26	0.67	10.77
2.	6.59	45.83	0.67	9.78
2.	7.36	48.15	0.67	8.47
2.	8.14	50.25	0.67	7.01
2.	8.92	52.18	0.67	5.57
2.	9.70	53.96	0.68	4.25
2.	10.48	55.61	0.68	3.13
2.	11.26	57.14	0.68	2.21
2.	12.03	58.58	0.69	1.51
4.	1.19	8.36	0.47	1.13
4.	1.74	11.68	0.47	3.78
4.	2.30	14.56	0.47	6.42
4.	2.86	17.12	0.47	8.67
4.	3.41	19.42	0.47	10.29
4.	3.97	21.52	0.47	11.14
4.	4.52	23.45	0.47	11.21
4.	5.08	25.24	0.48	10.60
4.	5.64	26.91	0.48	9.47
4.	6.19	28.48	0.48	8.02
4.	6.75	29.95	0.48	6.46
4.	7.30	31.35	0.48	4.96
4.	7.86	32.67	0.49	3.63
4.	8.42	33.93	0.49	2.54
4.	8.97	34.79	0.49	1.69

enter output file number - i2 (0 for no save) 01

enter up to 20 characters as a stand identifier

20 yr. mixed stand

stand saved on file 1

enter 1(quit), 2(save stand), 3(start all over) 1

stop

store on file "1"

STOP