

**VALIDATION of the USE of GENETIC GAIN
GROWTH RATE MULTIPLIERS ASSOCIATED
with BREEDING VALUES for DIAMETER
to PREDICT GROWTH**

**B. SHULA
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Report No. 95

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Stand Growth Modelling Cooperative

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EXECUTIVE SUMMARY

Genetic gain in growth has been expressed as an increase in the rate of basal area growth or ‘genetic gain multipliers’. The genetic gain growth rate multiplier approach offers a methodology, which removes the influence of confounding factors by utilising the predictive power of the original, baseline growth models. Such multipliers have been developed based on GF rating and incorporated into existing regional growth models. As an alternative to GF rating, multipliers for basal area have also been estimated using diameter breeding values (BV DBH).

Trials on sites represented by the CLAYSF, SANDS and NAIPRAD growth models were not used in the estimations of genetic gain multipliers either with GF ratings or BV DBH. This is because the methodology developed for calculating the multipliers was not valid for those regional growth models. Consequently, these datasets represent independent datasets available to validate the genetic gain growth rate multiplier approach.

The objectives of this report are:

- to document the validation of GF and BV DBH genetic gain growth rate multipliers using growth models not used to develop the multipliers, and
- to investigate if the use of genetic gain multipliers in growth models gives more accurate predictions of growth of improved seedlots, than baseline models.

There are eight Silviculture/Breed trial datasets situated in the growth modelling regions of Auckland Clays, West Coast Sands, and Hawkes Bay. Four sites (datasets) were chosen, one each from CLAYSF (CLAYS with fertiliser effects) and SANDS, and two from NAIPRAD growth model regions. These trials were selected for their uniformity, in that all plots had measurements starting at age 6 and ending at age 11 (i.e., a 5 year period), and they all remained at their planting stocking to age 11 (i.e., without any confounding effects of thinning or mortality).

Generalised results are that:

- In all cases, R^2 increased in multiplier implementation from base model (without the use of multipliers), through GF multiplier to BV DBH multiplier.
- For MTH, there was no difference with multiplier implementation, i.e., height multipliers were insignificant.
- For SPH, there were minor differences with multiplier implementation; R^2 values were >0.94 for all regional models.
- For BA and Volume, there were greater differences with multiplier implementation; R^2 was >0.8 for the NAIPRAD model, but generally <0.5 in the other models.
- GF and BV DBH genetic gain growth rate multipliers are valid to use in growth models not used to develop the multipliers.
- The use of genetic gain multipliers in growth models gives more accurate predictions of growth of improved seedlots, than baseline models.

INTRODUCTION

Background

Genetic gain in growth has been expressed as an increase in the rate of basal area growth or ‘genetic gain multipliers’. The genetic gain growth rate multiplier approach offers a methodology, which removes the influence of confounding factors by utilising the predictive power of the original, baseline growth models. Such multipliers have been developed and incorporated into existing regional growth models (SGMC Report 44, Carson et al. 1999). Originally these multipliers were estimated for height and basal area using data collected from the 1978, 1979 and 1980 series of genetic gain trials. There was only one seedlot of each of GF2, GF14 and GF22, and four local climbing select seedlots, GF7. All growth rates were compared to the base value of GF7.

Multipliers for basal area have since been estimated using diameter breeding values (BV DBH) (SGMC Report No.81, in prep) to predict genetic gain, as an alternative to GF ratings for all genetic gain and silviculture/breed trials with two or more increment periods. This new methodology developed a relationship of the basal area genetic gain growth rate multipliers to the given BV DBH of a seedlot. There were 35 different seedlots used at 18 sites, planted between 1978 and 1990 (SGMC Report No.100; Hayes 2001).

Rationale and significance

Trials on sites represented by the CLAYSF, SANDS and NAIPRAD growth models were not used in the estimations of genetic gain multipliers either with GF ratings or BV DBH. This is because the methodology developed for calculating the multipliers was not valid for those regional growth models. Consequently, these datasets represent independent datasets available to be used for validation of the genetic gain growth rate multiplier approach.

OBJECTIVES

The objectives of this report are:

- to document the validation of GF and BV DBH genetic gain growth rate multipliers using growth models not used to develop the multipliers, i.e., CLAYSF, SANDS, and NAPIRAD; and
- to investigate if the use of genetic gain multipliers in growth models gives more accurate predictions of growth of improved seedlots, than baseline models.

NOTATION

GF	= Growth and Form rating
BV DBH	= Breeding Value for Diameter
BA	= Basal Area per hectare
SPH	= Stems per hectare
MTH	= Mean Top Height
PSP	= Permanent Sample Plot
STD	= Standard Deviation
NI	= No modification, predictions with baseline model
YU	= Yes modification, predictions with GF multipliers
YI	= Yes modification, predictions with BV DBH multipliers

DATA

Origin

There are eight Silviculture/Breed trial datasets situated in the growth modelling regions of Auckland Clays, West Coast Sands, and Hawkes Bay (i.e., Gwavas, Glengarry, Mamaranui, Santoft, Tikokino, Tungrove, Tairua, and Woodhill forests). Four sites (datasets) were chosen, one each from CLAYSF (Clays with fertiliser effects) and SANDS, and two from NAPIRAD growth model regions. These trials were selected for their uniformity, in that all plots had measurements starting at age 6 and ending at age 11 (i.e., a 5 year period), and they all remained at their planting stocking to age 11 (i.e., without any confounding effects of thinning or mortality).

Description

Data extracted from the PSP database included:

Trial ID	Forest	Growth Model	Number of Plots	GF Rating	BV DBH	Initial & Final Stocking (stems/ha)
FR 7	Woodhill	SANDS	4	7	-2.97	500
			4	13(LI)	1.67	500
			4	14	1.37	500
			4	21	6.25	500
FR 10	Glengarry	NAPIRAD	2	7	-2.97	500
			2	13(LI)	1.67	500
			2	14	1.37	500
			6	16	2.95	1000
			2	21	6.25	500
FR 54	Mamaranui	CLAYSF	4	9(LI)	-1.54	500
			4	14	1.37	500
			2	17	3.76	200
			4	22	6.17	500
FR 57	Tikokino	NAPIRAD	6	7(LI)	-2.49	400, 500, 600
			4	17	3.89	400, 500, 600
			6	19	3.45	400, 500, 600

Variables, as applicable, were extracted from the Forest Research PSP database (**Appendix 1** provides the Structured Query Language, SQL, procedure) to be used as starting points for the GROPAK runs. A suitable input file was set up in column format with variables of plot_id, site index, GF and BV DBH ratings, age, basal area, stocking and mean top height. Actual data at both age 6 and age 11 was included in each dataset.

METHODS

The growth models in GROPAK had previously been modified to include the new genetic gain multipliers based on GF. To complete this validation study, the initial task was to rewrite the GWBASIC code for the three models CLAYSF, NAPIRAD and SANDS to also include the genetic gain growth rate multipliers based on BV DBH. With the need to run a large number of simulations, further modifications were required to enable the models to be run in batch mode. GROPAK was run with the appropriate revised growth model for each corresponding dataset. A new output file was produced with predicted variables at ending age 11 (i.e., a 5 year prediction period) for BA, SPH, MTH and Volume. This file was imported into SAS for statistical analysis.

For each of the data variables, the following statistics were calculated:

1. R^2
2. Mean difference
3. Mean % error
4. RMSE (root mean squared error)
5. Mean absolute difference
6. Mean absolute % error
7. Mean actual
8. Mean predicted
9. Actual STD (standard deviation)
10. Predicted STD (standard deviation).

The first 3 represent 'soft' validation assessors, as positive (+) and negative (-) errors accumulate, but have the opportunity to 'average out'. Conversely, statistics 4 - 6 represent 'hard' validation assessors, as errors (absolute or squared) are accumulated without the opportunity to 'average out'. Statistic 4 is a particularly 'hard' assessor, as the squaring of errors, penalises large errors, especially.

The R^2 statistic quantifies the departure of predicted values from actual values, relative to the departure of actual values from the mean actual value. This statistic, then, is sensitive to the range in prediction error (variation about zero error) and to the range in the actual data (variation about the mean actual value). A value of 1 identifies a perfect prediction model, while a value ≤ 0 , identifies a prediction model no-better-to-worse than using the mean.

The standard deviation statistics quantify the variation about the mean actual and mean predicted values, respectively.

Firstly, validation was carried out for each trial by predicted variable (SPH, BA, Volume and MTH), multiplier implementation (NI, YU, YI), and seedlot. The validation results were recorded for:

- GF7, 14, and 21 in trials FR7 (SANDS) and FR10 (NAPIRAD);
- GF9(LI), 14, and 22 in trial FR54 (CLAYSF); and
- GF7(LI), 17 and 19 in trial FR57 (NAPIRAD).

After the initial validation, the two trials in the NAPIRAD growth model region (FR10 and FR57) were combined to form one dataset with double the number of observations. The number of plots were:

- CLAYSF -14 plots
- SANDS -16 plots and

- NAPIRAD (combined) - 30 plots.

Finally, the analysis of the three growth model regions was combined for all seedlots, but still analysed by predicted variable and multiplier implementation.

RESULTS

Results by GF rating for each regional growth model are provided in **Appendices 5A-CLAYS; 5B-NAPIRAD (FR10); 5C-NAPIRAD (FR57); 5D-SANDS**. The results of the combined analysis are presented in **Tables 1-SPH, 2-BA , 3-Volume, and 4-MTH**. Summaries of validation statistics by growth model site are provided in **Tables 5-SPH, 6-BA, and 7-Volume**.

TABLE 1. SPH

Growth Region	NAPIRAD			CLAYSF			SANDS		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	30	30	30	14	14	14	16	16	16
r2	0.9911	0.9912	0.9911	0.9923	0.9918	0.991	0.948	0.9456	0.9464
mean difference	-4.518	-2.882	-1.891	1.26	2.783	3.62	-0.503	0.277	0.829
mean % error	-1.557	-1.229	-1.026	0.07	0.398	0.576	-0.118	0.048	0.167
rmse	15.05	14.942	15.001	8.77	9.05	9.468	7.014	7.174	7.12
mean absolute diff	12.101	12.246	12.49	8.046	8.116	8.399	5.341	5.738	5.943
mean absolute % error	2.988	2.986	3.022	1.825	1.831	1.884	1.16	1.248	1.295
mean actual	453.6	453.6	453.6	454.2	454.2	454.2	465.8	465.8	465.8
mean predicted	458	456	455	453	451	451	466	465	465
actual STD	162.1	162.1	162.1	104	104	104	32	32	32
predicted STD	157	156	155	101	101	100	32	32	32

TABLE 2. BA

Growth Region	NAPIRAD			CLAYSF			SANDS		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	30	30	30	14	14	14	16	16	16
r2	0.853	0.894	0.915	0.187	0.495	0.616	-0.426	-0.157	-0.065
mean difference	2.624	1.249	0.319	6.891	5.179	4.258	1.859	1.513	1.265
mean % error	6.481	2.173	-0.84	15.634	11.524	9.312	6.751	5.385	4.358
rmse	3.745	3.178	2.848	7.618	6.003	5.245	2.898	2.61	2.505
mean absolute diff	3.035	2.559	2.348	6.891	5.257	4.431	2.398	2.095	1.97
mean absolute % error	8.289	7.505	7.32	15.634	11.854	10.045	9.345	8.176	7.736
mean actual	35.2	35.2	35.2	43.1	43.1	43.1	24.7	24.7	24.7
mean predicted	32.6	34.0	34.9	36.2	37.9	38.8	22.9	23.2	23.5
actual STD	9.95	9.95	9.95	8.8	8.8	8.8	2.5	2.5	2.5
predicted STD	8.7	8.7	8.5	7.2	7.3	7.4	1.1	1.1	1.1

TABLE 3. Volume

Growth Region	NAPIRAD			CLAYSF			SANDS		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	30	30	30	14	14	14	16	16	16
r2	0.926	0.937	0.945	0.337	0.573	0.658	-1.119	-0.818	-0.674
mean difference	11.635	3.431	-1.954	46.882	34.99	28.539	20.005	17.972	16.505
mean % error	5.62	1.476	-1.385	15.37	11.259	9.027	11.977	10.692	9.723
rmse	21.329	19.697	18.441	54.693	43.9	39.293	25.613	23.723	22.763
mean absolute diff	16.745	14.994	14.132	46.882	35.885	31.243	21.389	19.357	18.479
mean absolute % error	7.623	6.885	6.637	15.37	11.842	10.402	13.058	11.774	11.262
mean actual	221.3	221.3	221.3	300.2	300.2	300.2	155.5	155.5	155.5
mean predicted	209.7	217.9	223.3	253.5	265.2	271.7	135.5	137.5	139
actual STD	79.9	79.9	79.9	69.7	69.7	69.7	18.2	18.2	18.2
predicted STD	82.3	83.3	82.7	61.3	62.7	63.5	8.4	8.4	8.4

TABLE 4. MTH

Growth Region	NAPIRAD			CLAYSF			SANDS		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	30	30	30	14	14	14	16	16	16
r2	0.6693	0.6693	0.6693	0.468	0.468	0.468	-0.3948	-0.3948	-0.3948
mean difference	-0.206	-0.206	-0.206	-0.058	-0.058	-0.058	1.196	1.196	1.196
mean % error	-0.806	-0.806	-0.806	-0.247	-0.247	-0.247	6.946	6.946	6.946
rmse	1.059	1.059	1.059	0.921	0.921	0.921	1.287	1.287	1.287
mean absolute diff	0.864	0.864	0.864	0.805	0.805	0.805	1.196	1.196	1.196
mean absolute % error	4.791	4.791	4.791	4.17	4.17	4.17	6.946	6.946	6.946
mean actual	17.8	17.8	17.8	19.4	19.4	19.4	17.2	17.2	17.2
mean predicted	18.0	18.0	18.0	19.5	19.5	19.5	16	16	16
actual STD	1.87	1.87	1.87	1.3	1.3	1.3	0.6	0.6	0.6
predicted STD	2.7	2.7	2.7	1.7	1.7	1.7	0.6	0.6	0.6

Table 5. Summary of SPH statistics by growth model site.

GROWTH MODEL SITE			Age increment 5 years (actual 6-11 years)		
	Prediction type	No. of plots	Mean Actual SPH m ² /ha	Mean Predicted SPH m ² /ha	Mean absolute % error
NAPIRAD 2 sites 7 seedlots GF 7,13,14, 17,19,21	Base model	30	453.6	458	2.99
	GF multiplier	30	453.6	456	2.99
	BV multiplier	30	453.6	455	3.02
CLAYSF 1 site 4 seedlots GF 9,14,17,22	Base model	14	454.2	453	1.83
	GF multiplier	14	454.2	451	1.83
	BV multiplier	14	454.2	451	1.88
SANDS 1 site 4 seedlots GF 7,13,14,21	Base model	16	465.8	466	1.16
	GF multiplier	16	465.8	465	1.24
	BV multiplier	16	465.8	465	1.30

Table 6. Summary of BA statistics by growth model site.

GROWTH MODEL SITE			Age increment 5 years (actual 6-11 years)		
	Prediction type	No. of plots	Mean Actual BA m ² /ha	Mean Predicted BA m ² /ha	Mean absolute % error
NAPIRAD 2 sites 7 seedlots GF 7,13,14, 17,19,21	Base model	30	35.2	32.6	8.3
	GF multiplier	30	35.2	34.0	7.5
	BV multiplier	30	35.2	34.9	7.3
CLAYSF 1 site 4 seedlots GF 9,14,17,22	Base model	14	43.1	36.2	15.6
	GF multiplier	14	43.1	37.9	11.9
	BV multiplier	14	43.1	38.8	10.0
SANDS 1 site 4 seedlots GF 7,13,14,21	Base model	16	24.7	22.9	9.3
	GF multiplier	16	24.7	23.2	8.2
	BV multiplier	16	24.7	23.5	7.7

Table 7. Summary of VOLUME statistics by growth model site.

GROWTH MODEL SITE			Age increment 5 years (actual 6-11 years)		
	Prediction type	No. of plots	Mean Actual VOL m ² /ha	Mean Predicted VOL m ² /ha	Mean absolute % error
NAPIRAD 2 sites 7 seedlots GF 7,13,14, 17,19,21	Base model	30	221.3	209.7	7.6
	GF multiplier	30	221.3	217.9	6.9
	BV multiplier	30	221.3	223.3	6.6
CLAYSF 1 site 4 seedlots GF 9,14,17,22	Base model	14	300.2	253.5	15.4
	GF multiplier	14	300.2	265.2	11.8
	BV multiplier	14	300.2	271.7	10.4
SANDS 1 site 4 seedlots GF 7,13,14,21	Base model	16	155.5	135.5	13.1
	GF multiplier	16	155.5	137.5	11.8
	BV multiplier	16	155.5	139.0	11.3

DISCUSSION

Overall results

- For all analyses of MTH there was no difference in any results between different prediction types, i.e., height multipliers are insignificant.
- For SPH, the R^2 values are >0.94 for all regional models.
- For BA and Volume, R^2 is >0.8 for the NAPIRAD model. In the other regions, R^2 is generally <0.5 .
- In all cases, R^2 increased in multiplier implementation from base model, through GF multiplier to BV DBH multiplier
- Comparing the individual NAPIRAD datasets showed a considerable improvement in R^2 with the combined dataset of 30 observations, particularly for BA and Volume. The following table shows the benefit of having more extensive datasets for better predictability.

R^2	NAPI 1 n = 14	NAPI 2 n = 16	NAPI combined n = 30
SPH	0.993	0.970	0.991
BA	0.318	0.696	0.887
VOL	0.507	0.674	0.936

- For SPH, the mean absolute % error for each regional model between the different multiplier implementations was very small (**Table 5**), but generally has an upward trend in multiplier implementation from base model, through GF multiplier to BV DBH multiplier.
- This was in contrast to both BA and Volume. In all cases, the mean absolute % error decreased significantly following a downward trend in multiplier implementation from base model, through GF multiplier to BV DBH multiplier (**Tables 6 & 7**).

CONCLUSION

Genetic gain growth rate multipliers developed using diameter breeding values (DBH BV) give better predictions of actual increase in diameter, even with growth models and on sites, which were not used to estimate the genetic gain multipliers for either GF or BV DBH.

REFERENCES

- Carson, S.D. and Dunlop, J.D. 1995. Validation of growth rate multipliers for the SANDS and NAPIRAD models. SGMC Report No. 44.
- Carson, S.D., O. Garcia, and J.D. Hayes. 1999. Realised gain and prediction of yield with genetically improved *Pinus radiata* in New Zealand. Forest Science 45(2): 186-200.
- Carson, S.D. and Hayes, J.D. in prep. The relationship of breeding values and genetic gain multipliers, and the validity of genetic predictions. SGMC Report No. 81.
- Hayes, J.D. 2001. Trials designed to quantify growth and yield gains from genetically improved radiata pine - Forth revision. SGMC Report No. 100.

APPENDIX 1

Structured Query Language (SQL) Procedure to extract data from the PSP database

```
select P.PLOT_ID,  
       PLOTNAME=((CONVERT(VARCHAR(5), P.EXPNO)) +  
                 (CONVERT(VARCHAR(5),P.PLOTNO))+  
                 (CONVERT(VARCHAR(5), P.SUBPLOT))),  
       P.SITE_INDEX, C.GF_RATING, HT_ADJ_AGE,  
       SPH_LIVE, BA_LIVE, MTH, VOL_LIVE  
from PLOT_DESC P, PLOT_SUMMARY S,  
     CROP_DESC C, MEAS_DESC M, PLOTS_JUDY J  
where J.PLOT_ID=P.PLOT_ID  
      AND P.PLOT_KEY=S.PLOT_KEY  
      AND P.PLOT_KEY=C.PLOT_KEY  
      AND P.PLOT_KEY=M.PLOT_KEY  
      AND S.MEAS_KEY=M.MEAS_KEY  
      AND (HT_ADJ_AGE=6 OR HT_ADJ_AGE=11)
```

APPENDIX 2

CLAYSFERT MODEL revised to use GF or BV multipliers

```
2 rem DEFINIT I-K
4 O = 1
6 rem ***** AUCKLAND CLAYS GROWTH MODEL FOR RADIATA PINE"
8 rem ***** WITH PHOSPHORUS FERT EFFECTS INCLUDED"
10 rem *****
12 rem 12/99 => CUT-DOWN VERSION MODIFIED FOR BATCH INPUT AND USE OF BREEDING
VALUES
13 rem *****
14 REM ---- Dimension COEFFICIENT ARRAYS ----
15 REM
16 DIM QMODGF(4), PMODGF(4), gfval(4) : rem modified for genetic gain
17 DIM C(4, 4), CINV(4, 4), P(4, 4), PINV(4, 4), T(2, 4), TINV(2, 4), E(4), Y(4)
20 REM *****
21 REM ***** 'Initialise things *****
22 REM *****
32 sourcefile$ = "fr54clay.csv"
36 targetfile$ = "fr54clay.out"
37 REM open the files
38 OPEN "I", #1, sourcefile$
39 OPEN "O", #2, targetfile$
40 REM Read the input file
41 WHILE NOT EOF(1)
42 INPUT #1, ID, SITEIND, GF, BV, AGE1, AGE2, BA1, BA2, SPH1, SPH2, MTH1, MTH2, YORN$, IORU$
50 REM
43 rem set foliar to 0.15, i.e., start off at high
44 FOLIAR = 0.15
46 I$ = "##### ##.## ##.## ##### ##.## ##.## #####.##
#.####"
47 PRINT "PROCESSING PSP FR:"; ID
48 rem I$ = " ### ##.## ##### ##.## ##.## #####
#.####"
50 REM
51 REM ---- READ IN COEFFICIENTS ----
52 REM
800 RESTORE 960
810 FOR I = 1 TO 4: FOR J = 1 TO 4: READ C(I, J): NEXT J: NEXT I
820 FOR I = 1 TO 4: FOR J = 1 TO 4: READ CINV(I, J): NEXT J: NEXT I
830 FOR I = 1 TO 4: FOR J = 1 TO 4: READ P(I, J): NEXT J: NEXT I
840 FOR I = 1 TO 4: FOR J = 1 TO 4: READ PINV(I, J): NEXT J: NEXT I
900 REM *****
920 READ LAMBDA1, LAMBDA2, LAMBDA3, LAMBDA4, A1, A2, A3, A4, T0
940 REM *****
960 DATA .4340279, -.04897968, .5236111, -.09194972, 0, -
.3786075, 0, 0, 0, 0, .9152051, 0, 0, 0, 0, -.5028563
980 DATA 2.304, -0.298064, -1.318174, -0.4212975, 0, -
2.6412577, 0, 0, 0, 0, 1.092651, 0, 0, 0, 0, -1.9886397
1000 DATA 1, 65.9894021179, -.514022292927, -1.83644958922, 1.56546840498E-
4, 1, 2.58021893648E-5, -2.73701618813E-4, 0, 0, 1, 0, 0, 0, 1
1020 DATA 1.010438, -66.6782, 0.5211082, 1.837369, -1.581809E-4, 1.010438, -1.0738E-
4, -1.393269E-5, 0, 0, -1, 0, 0, 0, 0, -1
1040 DATA -1.31628916377, -1.35978362354E-2, -1, -27.17421044
1060 REM *****
1080 DATA 0, .780930226033, 42.7203823247, .9999999999
1100 REM *****
1120 DATA 0
1130 REM *****
1132 REM vvvvvv Modif. for genetic gains vvvvvv
1134 DATA 2, .96, .89, 7, 1, 1, 14, 1.048, 1.134, 22, 1.078, 1.220
1136 FOR i = 1 TO 4
1138 READ gfval(i), PMODGF(i), QMODGF(i)
1140 NEXT i
1142 rem
1155 DEF FNH (T, B) = (A3 * (1 - A1 * EXP(-B * (T - T0)))) ^ (1 / C33)
```

```

1156 DEF FNB (H, T) = -LOG((1 - H ^ C33 / A3) / A1) / (T - T0)'Where A1=1-(-
(HOC/A^C33))
1159 REM
1160 REM ***** CALC MEAN DBH
1180 REM DEF FNDBH (BAREA, STOCK) = 200 * SQR(BAREA / (3.1415 * STOCK))
1200 REM ****
1220 REM ****
1240 REM *** CLAYS MODEL V/B ratio regression, n=1090 r^2=0.96 ***
1260 REM ****
1280 REM DEF FNVOL (BAREA, STOCK, HEIGHT) = (.27587728# * HEIGHT + (-1.2774E-04
* (STOCK * HEIGHT) / BAREA) + 1.58809184#) * BAREA
1300 REM *****
1320 REM **** CLAYSFERT COEFFS FOR FERT EFFECTS ****
1340 AB = 1.25: BB = .0175: AH = 1.15: BH = .0105: CC = .04194: EC = EXP(-CC)
1360 REM *****
1380 REM *****
1400 ON ERROR GOTO 7720
1402 rem
1490 REM vvvvvv Modif. for genetic gains vvvvvv
1492 rem
1493 SITE=SITEIND
1494 K$ = YORN$ 'Y or N
1495 IF K$ = "" THEN 1494 ELSE GENETICGAIN$=CHR$(ASC(K$) AND 223)
1497 GOSUB 9000 '<<<< Modif. for genetic gains
1498 rem IF GENETICGAIN$ = "Y" THEN GOSUB 9000 ELSE IF GENETICGAIN$ <> "N" THEN
1494
1500 PRINT "YORN$=";YORN$;" IORU$=";IORU$
1502 PRINT "GF rating=";GF;" Data SiteIndex="; SITEIND
1599 REM
1600 IF O = 2 THEN PRINT : PRINT FOLIAR
1820 REM *****
1840 REM *** CLAYS Height Model No. 8 w/ N=114 & n=535 ***
1860 REM *****
1880 A = 60.49445: T0 = 0: C33 = .9152051: HOC = 2.726208
1900 IF O = 2 THEN PRINT : PRINT SITE; AGE; HEIGHT
1920 A1 = 1 - (-(HOC / A ^ C33))
1921 rem
1922 GOSUB 9500'<<<< Modif. for genetic gains
1930 rem IF GENETICGAIN$ = "Y" THEN GOSUB 9500'<<<< Modif. for genetic gains
3640 REM *****
3660 REM *** INITIALISE ***
3680 REM *****
3682 THRATIO = 1
3700 X = -(LOG((1 - (SITE / A) ^ C33) / A1) / (20 - T0))
3720 IF THRATIO = 1 THEN 3760
3740 THRATIO = (1 - (1 - THRATIO ^ C(4, 4)) * EXP(LAMBDA4 * YSTH * X)) ^ (1 /
C(4, 4))
3760 E(1) = EXP(LAMBDA1 * X)
3780 E(2) = EXP(LAMBDA2 * X)
3800 T3 = EXP(-X)
3820 T4 = EXP(LAMBDA4 * X)
3840 RISE = 0
3842 rem altered for psp input variables
3860 Y1 = BA1 ^ C(1, 1) * SPH1 ^ C(1, 2) * MTH1 ^ C(1, 3) * THRATIO ^ C(1, 4)
3880 Y2 = SPH1 ^ C(2, 2) - A2
3900 Y3 = MTH1 ^ C(3, 3) - A3
3920 Y4 = THRATIO ^ C(4, 4) - A4
3940 Z1 = P(1, 1) * Y1 + P(1, 2) * Y2 + P(1, 3) * Y3 + P(1, 4) * Y4
3960 Z2 = P(2, 1) * Y1 + P(2, 2) * Y2 + P(2, 3) * Y3 + P(2, 4) * Y4
3980 REM ***
4060 REM *****
4080 REM *** START SIMULATION ***
4100 REM *****
4102 PRINT " ID AGE MTH STOCKING BA DBH VOLUME
FOLIAR P"
4103 PRINT " (yrs) (m) (sph) (m2/ha) (cm) (m3/ha)
%"
4104 REM
4105 REM ---- APPLY VOLUME FUNCTION TO PSP INPUT DATA AT AGE1 and DISPLAY ---

```



```

4106 REM
4107 V1= (.27587728# * MTH1 + (-1.2774E-04 * (SPH1 * MTH1) / BA1) + 1.58809184#)
* BA1
4108 PRINT "ACTUAL AT TIME1"
4109 PRINT USING I$; ID, AGE1, MTH1, SPH1, BA1, 200 * SQR(BA1 / (3.1415 *
SPH1)), V1, FOLIAR
4380 REM PRINT USING I$; AGE, HEIGHT, STOCK, BAREA, FNDBH(BAREA, STOCK),
FNVOL(BAREA, STOCK, HEIGHT), FOLIAR
4420 REM *****
4472 AGE=AGE1
4474 KK=AGE2
4580 REM *****
4600 REM *** FORWARD
4620 REM *****
4640 FOR AGE = AGE + 1 TO KK
4660 IF RISE > 1E-09 THEN DB = AB - AB * BB / RISE * LOG(1 + RISE / (FOLIAR -
.06 + BB)): DH = AH - AH * BH / RISE * LOG(1 + RISE / (FOLIAR - .06 + BH)):
FOLIAR = FOLIAR + RISE: GOTO 4700
4680 DB = AB / CC * LOG((BB + FOLIAR - .06) / (BB + (FOLIAR - .06) * EC)): DH =
AH / CC * LOG((BH + FOLIAR - .06) / (BH + (FOLIAR - .06) * EC)): FOLIAR =
(FOLIAR - .06) * EC + .06
4700 RISE = 0
4720 Z1 = E(1) ^ DB * Z1: Z2 = E(2) ^ DB * Z2: Y3 = T3 ^ DH * Y3: Y4 = T4 ^
DH * Y4
4740 Y1 = PINV(1, 1) * Z1 + PINV(1, 2) * Z2 + PINV(1, 3) * Y3 + PINV(1, 4) *
Y4
4760 Y2 = PINV(2, 1) * Z1 + PINV(2, 2) * Z2 + PINV(2, 3) * Y3 + PINV(2, 4) *
Y4
4780 B = Y1 ^ CINV(1, 1) * (Y2 + A2) ^ CINV(1, 2) * (Y3 + A3) ^ CINV(1, 3) *
(Y4 + A4) ^ CINV(1, 4)
4800 N = (Y2 + A2) ^ (1 / C(2, 2))
4820 H = (Y3 + A3) ^ (1 / C(3, 3))
4840 THRATIO = (Y4 + A4) ^ (1 / C(4, 4))
4860 rem PRINT USING I$; AGE, HEIGHT, STOCK, BAREA, FNDBH(BAREA, STOCK),
FNVOL(BAREA, STOCK, HEIGHT), FOLIAR
4880 NEXT AGE
4882 REM
4884 REM ---- APPLY VOLUME FUNCTION TO PREDICTED AND ACTUAL DATA AT AGE2 ----
4886 REM
4888 AGE=AGE-1
5890 V=(.27587728# * H + (-1.2774E-04 * (N * H) / B) + 1.58809184#) * B
5892 PRINT "PREDICTIED AT TIME2"
5894 PRINT USING I$; ID, AGE, H, N, B, 200 * SQR(B / (3.1415 * N)), V, FOLIAR
5896 PRINT "ACTUAL AT TIME2"
5898 V2=(.27587728# * MTH2 + (-1.2774E-04 * (SPH2 * MTH2) / BA2) + 1.58809184#)
* BA2
5900 PRINT USING I$; ID, AGE2, MTH2, SPH2, BA2, 200 * SQR(BA2 / (3.1415 *
SPH2)), V2, FOLIAR
5902 REM
5903 REM ***** print output to file *****
5904 REM
5905 PRINT
#2, ID, SITEIND, SITE, USI, GF, BV, AGE1, AGE2, BA1, BA2, B, SPH1, SPH2, N, MTH1, MTH2, H, V1, V2, V
, YORN$, IORU$, FOLIAR
5906 rem
5907 PRINT "PRINTED PSP CODED FR "; ID; " TO FILE "; targetfile$
5908 PRINT STRING$(64, "=")
5909 IF INKEY$="" THEN 5909 ELSE : cls : PRINT "NEXT"
5910 WEND
5911 END : REM --- THE END ---
5940 REM *****
7700 REM ****
7720 REM *** ERROR TRAP
7740 REM ****
7760 PRINT : PRINT "WARNING: Input Error, or Value Out of Range (ERROR"; ERR;
"AT LINE"; ERL; ")."
7780 RESUME 7720
7800 REM ****
8999 REM vvvvvv Modif. for genetic gains vvvvvv
9000 REM --- Get Genetic Gain info ---

```

```

9001 REM
9002 PMODIFY = 1 'rem set ht modifier as 1, unless modified in following lines
9003 if YORN$="Y" and IORU$="I" then QMODIFY = (.0104*BV) + 1.103:goto 9200'calc
ba modifier
9005 if YORN$="N" and IORU$="I" then QMODIFY = 1:goto 9200 'don't use ba
modifier
9007 rem GF=14 then QMODIFY = 1.134:PMODIFY = 1.048:goto 9210'rem to check
against original CLAYSF model
9008 rem if GF=14 then PMODIFY = 1.048 ' rem to check against original CLAYSF
model
9009 rem
9010 rem --- default to original GRM routine using GF
9012 rem ---
9030 indx = 1
9040 rem IF gf < gfval(1) THEN PRINT "GF rating too low "; gf: goto 9000
9050 WHILE gfval(indx) <= GF
9060     IF gfval(indx) = GF THEN QMODIFY = QMODGF(indx): PMODIFY = PMODGF(indx):
goto 9200
9070     indx = indx + 1
9080     rem IF indx > 4 THEN PRINT "GF rating too high "; gf: goto 9000
9090 WEND
9100 PMODIFY = PMODGF(indx - 1) + (PMODGF(indx) - PMODGF(indx - 1)) * (GF -
gfval(indx - 1)) / (gfval(indx) - gfval(indx - 1))
9110 QMODIFY = QMODGF(indx - 1) + (QMODGF(indx) - QMODGF(indx - 1)) * (GF -
gfval(indx - 1)) / (gfval(indx) - gfval(indx - 1))
9200 rem
9210 LAMBDA1 = QMODIFY * LAMBDA1 / PMODIFY
9220 LAMBDA2 = QMODIFY * LAMBDA2 / PMODIFY
9272 PRINT "BV=";BV;" PMODIFY(ht)=";PMODIFY;" QMODIFY (ba)=";QMODIFY
9280 RETURN
9500 REM --- Modify site index, if necessary ---
9501 rem
9502 rem always using improved site index, so calc unimproved site index
9550 USI=FNH(20, FNB(SITE, 20) / PMODIFY)
9552 PRINT "The unimproved equivalent site index (USI) is"; USI : print
9600 RETURN
9610 REM ^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^
10000 REM ---- Adjust to different BASIC versions ----
10001 REM (GW-BASIC/BASICA, AMSTRAD PCW8256, MS-BASIC + ANSI)
10010 IF CSRLIN THEN 10012 ELSE 10014
10012 KEY OFF : CLS : GWBASIC% =1
10013 RETURN
10014 IF VERSION(0) THEN 10016 ELSE 10018
10016 PRINT CHR$(27)"H"CHR$(27)"J": OV$=CHR$(27)+"A"+CHR$(27)+"K"
10017 RETURN
10018 PRINT CHR$(27)"[2J": OV$=CHR$(27)+"[A"+CHR$(27)+"[K"
10020 RETURN
11000 REM - Overwrite previous line
11010 IF GWBASIC% THEN 11011 ELSE 11013
11011 LOCATE CSRLIN-1,1: PRINT SPC(78);: LOCATE CSRLIN,1
11012 RETURN
11013 PRINT OV$;
11020 RETURN

```

APPENDIX 3

NAPIRAD MODEL revised to use GF or BV multipliers

```
05 rem
10 rem PRINT TAB(10); "NAPIRAD GROWTH MODEL"
11 rem *****
12 rem 11/99 => CUT-DOWN VERSION MODIFIED FOR BATCH INPUT AND USE OF BREEDING
VALUES
13 rem *****
14 REM      ---- Dimension COEFFICIENT ARRAYS ----
15 REM
16 DIM C(4), CI(4), P(2,4), PI(2,4), T(2,4), TI(2,4), E(4), Y(4)
17 DIM QMODGF(4), PMODGF(4), gfval(4) : rem modified for genetic gain
20 REM *****
21 REM ***** 'Initialise things *****
22 REM *****
30 rem sourcefile$ = "fr10napN.csv" 'use to test against real NAPIRAD
32 sourcefile$ = "fr57napi.csv" 'use after testing checks out
36 targetfile$ = "fr57napi.out"
37 REM open the files
38 OPEN "I", #1, sourcefile$
39 OPEN "O", #2, targetfile$
40 REM Read the input file
41 WHILE NOT EOF(1)
42 INPUT #1, ID, SITEIND, GF, BV, AGE1, AGE2, BA1, BA2, SPH1, SPH2, MTH1, MTH2, YORN$, IORU$
50 REM
51 REM      ---- READ IN COEFFICIENTS ----
52 REM
64 RESTORE
65 FOR J=1 TO 4
66     READ C(J), CI(J)
67 FOR I=1 TO 2
68     READ P(I, J), PI(I, J)
69 NEXT I, J
70 READ C2, C3, C4, L1, L2, L3, L4, A2, A3, A4, T0
141 DATA 0.21878, 4.5708351, 1, 1.0048894, 1.18541E-4, -1.1912061E-4, -0.010177, -
0.087689335, 41.0463, -41.246968, 1, 1.0048894, 0.52866, -3.4655761, 0.164337, -
0.16433678, 1.94806E-5, -8.3266727E-17
142 DATA -0.012207, -0.048344618, -0.552258, 0.55225843, -6.54653E-5, 1.1102230E-16, -
0.53049, 0.69726, -1.1541, -0.475954, -0.00231584, -1, -26.1874, 0.592988, 18.1962, 1, 0
143 rem
144 REM vvvvvv Modif. for genetic gains vvvvvv
145 DATA 2, .96, .89, 7, 1, 1, 14, 1.048, 1.134, 22, 1.078, 1.220
146 FOR i = 1 TO 4
147     READ gfval(i), PMODGF(i), QMODGF(i)
148 NEXT i
149 rem
155 DEF FNH(T,B)=(A3*(1-EXP(-B*(T-T0))))^(1/C3)
156 DEF FNB(H,T)=-LOG(1-(H^C3)/A3)/(T-T0)
168 rem
169 I$ = "#####   ##.##   ##.##   ####   ##.##   ###.##   ####.##"
170 PRINT "PROCESSING PSP FR: "; ID
171 rem
175 rem vvvvvv 1. Modif. for genetic gains vvvvvv
176 S=SITEIND
205 K$ = YORN$ 'Y or N
207 IF K$= "" THEN 205 ELSE GENETICGAIN$=CHR$(ASC(K$) AND 223)
208 GOSUB 5000: GOSUB 5500 '<<<< Modif. for genetic gains
209 rem if GENETICGAIN$="Y" THEN GOSUB 5000: GOSUB 5500 '<<<< Modif. for genetic
gains
210 PRINT "YORN$="; YORN$; " IORU$="; IORU$
211 PRINT "GF rating="; GF; " Data SiteIndex="; SITEIND : print
212 rem
350 REM --- INITIALISE ---
351 rem
375 GOSUB 760
376 R2=1 'initialise crown closure
377 X=-LOG(1-S^C3/A3)/(20-T0)
```

```

378 IF R2=1 THEN 380 ELSE R2=(1-(1-R2^C4)*EXP(L4*Y2*X))^(1/C4)
380 E(1)=EXP(L1*X): E(2)=EXP(L2*X)
381 T3=EXP(-X): T4=EXP(L4*X)
382 FOR I=1 TO 2
383   FOR J=1 TO 4
384     T(I,J)=0: TI(I,J)=0
385   FOR K=1 TO 2
386     T(I,J)=T(I,J)+PI(I,K)*E(K)*P(K,J)
387     TI(I,J)=TI(I,J)+PI(I,K)*P(K,J)/E(K)
388   NEXT K,J
389   T(I,3)=T(I,3)+PI(I,3)*T3
390   TI(I,3)=TI(I,3)+PI(I,3)/T3
391   T(I,4)=T(I,4)+PI(I,4)*T4
392   TI(I,4)=TI(I,4)+PI(I,4)/T4
393 NEXT I
394 rem CHANGED TO USE PSP INPUT VARIABLES
395 Y(1)=BA1^C(1)*SPH1^C(2)*MTH1^C(3)*R2^C(4)
396 Y(2)=SPH1^C2-A2
397 Y(3)=MTH1^C3-A3
398 Y(4)=R2^C4-A4
409 rem
410 REM --- START ---
411 REM
412 PRINT "      ID      AGE      MTH      STOCKING      BA      DBH      VOLUME"
413 PRINT "              (yrs)      (m)      (sph)      (m2/ha)      (cm)      (m3/ha)"
414 REM
415 REM      ---- APPLY VOLUME FUNCTION TO PSP INPUT DATA AT AGE1 and DISPLAY ----
416 REM
417 V1=(.314183*MTH1+8.478338E-04*SPH1*MTH1/BA1+.361168)*BA1
418 PRINT "ACTUAL AT TIME1"
419 PRINT USING I$; ID, AGE1, MTH1, SPH1, BA1, 200 * SQR(BA1 / (SPH1 *
3.14159)), V1
420 REM
421 REM      ---- LOOP TO NEXT AGE ----
422 A=AGE1
423 K=AGE2
424 REM
425 REM - FORWARD
426 rem
427 FOR A=A+1 TO K
428   X=T(1,1)*Y(1)+T(1,2)*Y(2)+T(1,3)*Y(3)+T(1,4)*Y(4)
429   Y(2)=T(2,1)*Y(1)+T(2,2)*Y(2)+T(2,3)*Y(3)+T(2,4)*Y(4)
430   Y(1)=X: Y(3)=T3*Y(3): Y(4)=T4*Y(4)
431   B=Y(1)^CI(1)*(Y(2)+A2)^CI(2)*(Y(3)+A3)^CI(3)*(Y(4)+A4)^CI(4)
432   N=(Y(2)+A2)^(1/C2)
433   H=(Y(3)+A3)^(1/C3)
434   R2=(Y(4)+A4)^(1/C4)
435 NEXT A
436 REM
437 REM      ---- APPLY VOLUME FUNCTION TO PREDICTED AND ACTUAL DATA AT AGE2 ----
438 REM
439 A=A-1
440 V=(.314183*H+8.478338E-04*N*H/B+.361168)*B
441 PRINT "PREDICTED AT TIME2"
442 PRINT USING I$; ID, A, H, N, B, 200 * SQR(B / (N * 3.14159)), V
443 PRINT "ACTUAL AT TIME2"
444 V2=(.314183*MTH2+8.478338E-04*SPH2*MTH2/BA2+.361168)*BA2
445 PRINT USING I$; ID, AGE2, MTH2, SPH2, BA2, 200 * SQR(BA2 / (SPH2 *
3.14159)), V2
446 REM
447 REM ***** print output to file *****
448 REM
449 PRINT
450 #2,ID,SITEIND,S,USI,GF,BV,AGE1,AGE2,BA1,BA2,B,SPH1,SPH2,N,MTH1,MTH2,H,V1,V2,V,YO
RN$,IORU$
451 rem
452 PRINT "PRINTED PSP CODED FR ";ID;" TO FILE ";targetfile$
453 PRINT STRING$(64, "=")
454 IF INKEY$="" THEN 454 ELSE : cls : PRINT "NEXT"
455 WEND

```

```

556 END : REM --- THE END ---
759 REM
760 REM --- MODIFICATION ROUTINE ---
770 AL=- (LOG (1- (S/64.12584) ^C3) /20)
771 AL=AL^-.3972783
772 L1=L1*AL
773 L2=L2*AL
774 P (1,3)=P (1,3) *AL/ (L1-L3)
775 P (1,4)=P (1,4) *AL/ (L1-L4)
776 P (2,3)=P (2,3) *AL/ (L2-L3)
777 P (2,4)=P (2,4) *AL/ (L2-L4)
778 PI (1,3)=-(PI (1,1) *P (1,3) )-PI (1,2) *P (2,3)
779 PI (1,4)=-(PI (1,1) *P (1,4) )-PI (1,2) *P (2,4)
780 PI (2,3)=-(PI (2,1) *P (1,3) )-PI (2,2) *P (2,3)
781 PI (2,4)=-(PI (2,1) *P (1,4) )-PI (2,2) *P (2,4)
800 RETURN
801 REM
900 REM --- ERROR TRAP ---
901 REM
911 PRINT "Value out of range (error";ERR;"at line";ERL;")"
920 RESUME 801
922 REM
4999 REM vvvvvv Modif. for genetic gains vvvvvv
5000 REM --- Get Genetic Gain info ---
5001 REM
5100 PMODIFY = 1 'rem set ht modifier as 1 , unless modified below
5110 if YORN$="Y" and IORU$="I" then QMODIFY = (.0104*BV) + 1.103:goto 5200'calc
ba modifier
5112 if YORN$="N" and IORU$="I" then QMODIFY = 1:goto 5200 'don't use ba
modifier
5114 rem if GF=14 then QMODIFY = 1.134 ' rem to check against original NAPIRAD
model
5116 rem if GF=14 then PMODIFY = 1.048 ' rem to check against original NAPIRAD
model
5117 REM
5118 rem --- default to original GRM routine using GF
5119 rem ---
5120 indx = 1
5121 WHILE gfval(indx) <= GF
5122     IF gfval(indx) = GF THEN QMODIFY = QMODGF(indx): PMODIFY = PMODGF(indx):
goto 5200
5123     indx = indx + 1
5124 WEND
5125 PMODIFY = PMODGF(indx - 1) + (PMODGF(indx) - PMODGF(indx - 1)) * (GF -
gfval(indx - 1)) / (gfval(indx) - gfval(indx - 1))
5126 QMODIFY = QMODGF(indx - 1) + (QMODGF(indx) - QMODGF(indx - 1)) * (GF -
gfval(indx - 1)) / (gfval(indx) - gfval(indx - 1))
5200 rem
5210 BB=(-LOG (1- (S/64.12584) ^C3) /20) ^-.3972783
5220 P (1,3) = P (1,3) * ( (BB*QMODIFY/PMODIFY*L1-L3) / (BB*L1-L3) )
5230 P (1,4) = P (1,4) * ( (BB*QMODIFY/PMODIFY*L1-L4) / (BB*L1-L4) )
5240 P (2,3) = P (2,3) * ( (BB*QMODIFY/PMODIFY*L2-L3) / (BB*L2-L3) )
5250 P (2,4) = P (2,4) * ( (BB*QMODIFY/PMODIFY*L2-L4) / (BB*L2-L4) )
5260 L1 = QMODIFY*L1/PMODIFY
5270 L2 = QMODIFY*L2/PMODIFY
5272 PRINT "BV=";BV;" PMODIFY(ht)=";PMODIFY;" QMODIFY (ba)=";QMODIFY
5280 RETURN
5282 rem
5500 REM --- Modify site index, if necessary ---
5501 rem always use improved site index, so calc unimproved site index
5550 USI=FNH(20,FNB(S,20)/PMODIFY)
5552 PRINT "The unimproved equivalent site index (USI) is"; USI
5600 RETURN
5610 REM ^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^^
10000 REM ---- Adjust to different BASIC versions ----
10001 REM (GW-BASIC/BASICA, AMSTRAD PCW8256, MS-BASIC + ANSI)
10010 IF CSRLIN THEN 10012 ELSE 10014
10012 KEY OFF : CLS : GWBASIC% =1
10013 RETURN
10014 IF VERSION(0) THEN 10016 ELSE 10018

```

```
10016    PRINT CHR$(27)"H"CHR$(27)"J": OV$=CHR$(27)+"A"+CHR$(27)+"K"
10017 RETURN
10018    PRINT CHR$(27)"[2J": OV$=CHR$(27)+"[A"+CHR$(27)+"[K"
10020 RETURN
11000 REM - Overwrite previous line
11010 IF GWBASIC% THEN 11011 ELSE 11013
11011    LOCATE CSRLIN-1,1: PRINT SPC(78);: LOCATE CSRLIN,1
11012 RETURN
11013    PRINT OV$;
11020 RETURN
```

APPENDIX 4

SANDS MODEL revised to use GF or BV Multipliers

```
110 rem PRINT TAB(10); "GROWTH MODEL FOR SAND DUNE GROWN RADIATA PINE"
227 rem *****
228 rem 11/99 => CUT-DOWN VERSION MODIFIED FOR BATCH INPUT AND USE OF BREEDING
VALUES
229 rem *****
230 REM
231 REM      ---- READ IN COEFFICIENTS ----
232 REM
233 DIM C(3), CI(3), P(2,3), PI(2,3), T(2,3), TI(2,3), E(3), Y(3)
253 DIM QMODGF(4), PMODGF(4), gfval(4) : rem modified for genetic gain
254 REM *****
255 REM ***** 'Initialise things *****
256 REM *****
264 rem sourcefile$ = "fr7sandy.csv"
265 rem targetfile$ = "fr7sandy.out"
266 sourcefile$ = "fr7sand.csv"
267 targetfile$ = "fr7sand.out"
284 REM open the files
285 OPEN "I", #1, sourcefile$
286 OPEN "O", #2, targetfile$
287 REM Read the input file
288 WHILE NOT EOF(1)
289 INPUT #1, ID, SITEIND, GF, BV, AGE1, AGE2, BA1, BA2, SPH1, SPH2, MTH1, MTH2, YORN$, IORU$
290 RESTORE
300 FOR J=1 TO 3
310     READ C(J), CI(J)
320     FOR I = 1 TO 2
330         READ P(I, J), PI(I, J)
340     NEXT I
350 NEXT J
360 REM
370 DATA 0.37126, 2.693565, -0.0026207542, -363.60426, 0.0002535113, 0.10337038
380 DATA -0.1374, -0.67332264, 0.45547471, 185.721867, 0.89172346, 1.0686244
390 DATA 0.5525, -1.7324273, 0.0016714637, 0.62661177, -0.00010155201, -
0.000064258801
430 DATA -0.54967, 0.85902, -0.020009, 0.000988626, -0.05547
440 DATA -0.058333776, 18.027792, 1.037854
442 READ C2, C3, L1, L2, L3, F2, F3, T0
445 L3o = L3 : REM save a copy of the original L3 before genetic gain
446 REM vvvvvvv Modif. for genetic gains vvvvvvv
447 DATA 2, .96, .89, 7, 1, 1, 14, 1.048, 1.134, 22, 1.078, 1.220
448 FOR i = 1 TO 4
449     READ gfval(i), PMODGF(i), QMODGF(i)
450 NEXT i
451 REM
452     PI=3.14159: FLAG=1
453 I$ = "#####   ##.##   ##.##   ####   ##.##   ###.##   ####.##"
500 REM
510 REM      ---- SELECT VOLUME FUNCTION COEFFS ----
520 REM
522 REM DONE FOR BATCH USING VOL FUNC NO. 6 (with stocking and for woodhill)
530 GOSUB 2300
540 REM
550 ON ERROR GOTO 2270
560 REM
580 REM
590 PRINT "PROCESSING PSP FR: "; ID
595 REM
600 REM ----- 1. Modif. for genetic gains -----
603 k$ = YORN$ 'y or n
605 IF K$ = "" THEN 603 ELSE GENETICGAIN$=CHR$(ASC(K$) AND 223)
606 GOSUB 5000 ELSE IF GENETICGAIN$<>"N" THEN 603
607 rem IF GENETICGAIN$="Y" THEN GOSUB 5000 ELSE IF GENETICGAIN$<>"N" THEN 603
608 PRINT "YORN$="; YORN$; " IORU$="; IORU$
610 REM
```

```

616 REM      ---- 2. Modif. for genetic gains ----
617 REM
618 S=SITEIND : FLAG=1 'Site Index from input file
657 GOSUB 5500
658 rem IF GENETICGAIN$="Y" THEN GOSUB 5500
659 PRINT "GF rating=";gf;" Data SiteIndex="; Siteind : print
660 REM
990 REM      ---- INITIALISE ----
1000 REM
1060 E(1)=EXP(L1) : E(2) = EXP(L2)
1070 T3 = EXP(L3)
1080 B3=-(L3*S^C3/(1-EXP(L3*(20-T0))))
1090 A2=F2*B3 : A3=F3*B3
1100 REM
1110 REM
1120 REM
1130 FOR I = 1 TO 2
1140     FOR J=1 TO 3
1150         T(I,J)=0
1160         TI(I,J)=0
1170         FOR K=1 TO 2
1180             T(I,J)=T(I,J)+PI(I,K)*E(K)*P(K,J)
1190             TI(I,J)=TI(I,J)+PI(I,K)*P(K,J)/E(K)
1200         NEXT K
1210     NEXT J
1220     T(I,3)=T(I,3)+PI(I,3)*T3
1230     TI(I,3)=TI(I,3)+PI(I,3)/T3
1240 NEXT I
1241 REM
1242 REM changed to use PSP input variables
1244 REM
1250 Y(1)=BA1^C(1)*SPH1^C(2)*MTH1^C(3)
1260 Y(2)=SPH1^C2-A2
1270 Y(3)=MTH1^C3-A3
1491 REM
1492 REM ***** START *****
1493 REM
1494 PRINT "      ID          AGE      MTH      STOCKING      BA      DBH      VOLUME"
1496 PRINT "      (yrs)      (m)      (sph)      (m2/ha)      (cm)      (m3/ha)"
1511 REM
1512 REM      ---- APPLY VOLUME FUNCTION TO PSP INPUT DATA AT AGE1 and DISPLAY ---
-
1514 REM
1516 V1=(A1+ B1*MTH1 +C1*SPH1 +D1*MTH1/SQR(SPH1) +E1*MTH1/SPH1) *BA1
1517 PRINT "ACTUAL AT TIME1"
1518 PRINT USING I$; ID, AGE1, MTH1, SPH1, BA1, 200 * SQR(BA1 / (SPH1 * PI)), V1
1520 REM
1530 REM      ---- LOOP TO NEXT AGE ----
1541 A=AGE1
1542 K=AGE2
1590 REM
1600 REM      ---- FORWARD ----
1610 REM
1620 FOR A=A+1 TO K 'original
1630     X=T(1,1)*Y(1)+T(1,2)*Y(2)+T(1,3)*Y(3)
1640     Y(2)=T(2,1)*Y(1)+T(2,2)*Y(2)+T(2,3)*Y(3)
1650     Y(1)=X
1660     Y(3)=T3*Y(3)
1670     B=Y(1)^CI(1)*(Y(2)+A2)^CI(2)*(Y(3)+A3)^CI(3)
1680     N=(Y(2)+A2)^(1/C2)
1690     H=(Y(3)+A3)^(1/C3)
1703 REM
1704 NEXT A
1705 REM      ---- APPLY VOLUME FUNCTION TO PREDICTED AND ACTUAL DATA AT AGE2 ----
1706 A=A-1
1714 V=(A1+ B1*H +C1*N +D1*H/SQR(N) +E1*H/N) *B
1720 PRINT "PREDICTED AT TIME2"
1722 PRINT USING I$; ID, A, H, N, B, 200 * SQR(B / (N * PI)), V
1724 PRINT "ACTUAL AT TIME2"
1726 V2=(A1+ B1*MTH2 +C1*SPH2 +D1*MTH2/SQR(SPH2) +E1*MTH2/SPH2) *BA2

```



```

1728 PRINT USING I$; ID, AGE2, MTH2, SPH2, BA2, 200 * SQR(BA2 / (SPH2 * PI)), V2
1730 REM
1731 REM ***** print output to file *****
1732 REM
1734 PRINT
#2, ID, SITEIND, S, USI, GF, BV, AGE1, AGE2, BA1, BA2, B, SPH1, SPH2, N, MTH1, MTH2, H, V1, V2, V, YO
RN$, IORU$
1736 PRINT "PRINTED PSP CODED FR ";ID;" TO FILE ";targetfile$
1738 PRINT STRING$(64, "=")
1740 IF INKEY$="" THEN 1740 ELSE : cls : PRINT "NEXT"
1742 WEND
1744 END : REM --- THE END ---
2240 REM
2250 REM ---- ERROR TRAP ----
2260 REM
2270 PRINT " Value out of range (error"; ERR; "at line";ERL;)"
2280 RESUME 2140
2290 REM
2300 REM ---- SELECT VOLUME FUNCTION ----
2310 REM
2315 IF VDONE = 1 THEN RETURN : REM don't select a volume function again
2317 VDONE = 1
2320 DATA 1.04764,0.30791,1.12946,0.30598,-0.000061765,0,0
2330 DATA 1.20888,0.2957,1.13061,0.30345,0,0,-1.57761
2340 DATA 0.91316,0.33674,0.99272,0.31368,0,0.3389,0
2350 DATA 0.2538,0.35454,0.16124,0.36681,0,-0.15484,0
2360 REM
2370 DIM VA(4,7)
2380 FOR I=1 TO 4
2390     FOR J=1 TO 7
2400         READ VA(I,J)
2410 NEXT J,I
2420 A1=VA(1,1) : B1=VA(1,2) : C1=0 : D1=0 : E1=0
2430 REM
2742 REM HARDWIRE A VOLUME FUNCTION USING WOODHILL WITH STOCKING
2743 REM
2744 NV=6
2750 IF NV<1 OR NV>8 THEN 2590
2760 IF NV>4 THEN NV=NV-4 : GOTO 2810
2770 A1=VA(NV,1)
2780 B1=VA(NV,2)
2790 C1=0 : D1=0 : E1=0
2800 RETURN
2810 A1=VA(NV,3)
2820 B1=VA(NV,4)
2830 C1=VA(NV,5)
2840 D1=VA(NV,6)
2850 E1=VA(NV,7)
2860 RETURN
2862 REM
4990 REM ----- Modif. for genetic gains -----
4995 REM
5000 REM --- Get Genetic Gain info ---
5100 PMODIFY = 1 'set ht modifier as 1, unless modified below
5105 rem QMODIFY = 1 : rem to check against original sands
model
5110 if YORN$="Y" and IORU$="I" then QMODIFY = (.0104*BV) + 1.103:goto
5200:'calc ba modifier
5112 if YORN$="N" and IORU$="I" then QMODIFY = 1:goto 5200:'don't use ba
modifier
5114 rem ---
5118 rem --- default to original GRM routine using GF
5119 rem ---
5120 indx = 1
5121 WHILE gfval(indx) <= GF
5122     IF gfval(indx) = GF THEN QMODIFY = QMODGF(indx): PMODIFY = PMODGF(indx):
goto 5200
5123     indx = indx + 1
5124 WEND

```

```

5125 PMODIFY = PMODGF(indx - 1) + (PMODGF(indx) - PMODGF(indx - 1)) * (GF -
gfval(indx - 1)) / (gfval(indx) - gfval(indx - 1))
5126 QMODIFY = QMODGF(indx - 1) + (QMODGF(indx) - QMODGF(indx - 1)) * (GF -
gfval(indx - 1)) / (gfval(indx) - gfval(indx - 1))
5200 REM
5210 L1 = QMODIFY*L1/PMODIFY
5220 L2 = QMODIFY*L2/PMODIFY
5230 PRINT "BV=";BV;" PMODIFY(ht)=";PMODIFY;" QMODIFY (ba)=";QMODIFY
5250 RETURN
5498 REM
5500 REM --- Modify site index, if necessary ---
5502 REM
5538 USI=S * ((1 - EXP( L3o * (20 - T0) )) / (1 - EXP( L3o * PMODIFY * (20 - T0
)))) ^ (1/C3)
5540 PRINT "The unimproved equivalent site index (USI) is"; USI
5560 RETURN
10000 REM ---- Adjust to different BASIC versions ----
10001 REM (GW-BASIC/BASICA, AMSTRAD PCW8256, MS-BASIC + ANSI)
10002 IF CSRLIN THEN
10003     KEY OFF: CLS: GWBASIC% = 1
10004     ELSE IF VERSION(0) THEN
10005         PRINT CHR$(27)"H"CHR$(27)"J": OV$=CHR$(27)+"A"+CHR$(27)+"K"
10006     ELSE
10007         PRINT CHR$(27)"[2J": OV$=CHR$(27)+"[A"+CHR$(27)+"[K"
10020 RETURN
11000 REM - Overwrite previous line
11001 IF GWBASIC% THEN
11002     LOCATE CSRLIN-1,1: PRINT SPC(78);: LOCATE CSRLIN,1
11003     ELSE
11004         PRINT OV$
11005 RETURN

```

APPENDIX 5A

CLAYSFERT MODEL - results for 12 plots (i.e., results exclude 2 plots of GF 17).

TRIAL: FR54 - Mamaranui Forest

VARIABLE SPH									
Seedlot	GF9			GF14			GF22		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	4	4	4	4	4	4	4	4	4
r2	0.481	0.481	0.932	0.897	0.895	0.893	0.84	0.814	0.801
mean difference	6.229	6.731	8.026	-0.841	0.967	1.747	0.93	3.682	4.425
mean % error	1.251	1.353	1.616	-0.294	0.07	0.228	0.204	0.76	0.91
rmse	7.848	8.26	8.364	10.801	10.882	11.009	8.375	9.021	9.33
mean absolute diff	7.255	7.487	8.163	10.589	10.613	10.621	7.747	7.729	8.047
mean absolute % error	1.459	1.511	1.645	2.143	2.127	2.119	1.556	1.554	1.62
mean actual	492.5	492.2	492.5	494.8	494.8	494.8	494.8	494.8	494.8
mean predicted	486	486	484	496	494	493	494	491	490
actual STD	12.6	12.6	12.6	38.8	38.8	38.8	24.2	24.2	24.2
predicted STD	10.0	10.0	10.0	29.0	28.0	28.0	28.0	28.0	27.0

VARIABLE BA									
Seedlot	GF9			GF14			GF22		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	4	4	4	4	4	4	4	4	4
r2	-3.739	-3.001	-1.461	-13.47	-8.876	-7.215	-28.12	-11.782	-8.603
mean difference	5.151	4.625	3.267	9.222	7.422	6.652	8.081	5.196	4.421
mean % error	11.729	10.505	7.342	18.619	14.972	13.412	17.479	11.232	9.554
rmse	5.749	5.283	4.143	9.688	8.004	7.299	8.256	5.469	4.74
mean absolute diff	5.151	4.625	3.267	9.222	7.422	6.652	8.081	5.196	4.421
mean absolute % error	11.727	10.505	7.342	18.619	14.972	13.412	17.479	11.232	9.554
mean actual	43.1	43.1	43.1	49.5	49.5	49.4	46.2	46.2	46.2
mean predicted	38	38.5	39.9	40.3	42.1	42.8	38.2	41	41.8
actual STD	3.1	3.05	3.05	2.94	2.94	2.94	1.77	1.77	1.77
predicted STD	2.1	2.1	2.1	4.1	4.1	4.1	2.4	2.4	2.4

VARIABLE Volume									
Seedlot	GF9			GF14			GF22		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	4	4	4	4	4	4	4	4	4
r2	-2.415	-1.72	-0.882	-11.495	-7.667	-6.301	-12.903	-5.897	-4.515
mean difference	28.965	26.658	17.005	64.296	51.352	45.816	58.672	38.601	33.217
mean % error	8.536	8.601	5.358	18.54	14.881	13.316	18.117	11.877	10.214
rmse	39.4	36.646	30.483	68.748	57.258	52.551	61.785	43.517	38.913
mean absolute diff	28.965	26.658	21.122	64.296	51.352	45.816	58.672	38.601	33.217
mean absolute % error	8.536	8.601	6.689	18.54	14.881	13.316	18.117	11.887	10.214
mean actual	299.2	299.2	299.2	353.5	353.5	353.5	323	323	323
mean predicted	268.8	272.5	282.2	289.2	302.1	307.7	264.3	284.4	289.8
actual STD	25.7	25.7	25.7	22.5	22.5	22.5	19.1	19.1	19.1
predicted STD	24.1	24.2	24.5	47.8	48.9	49.4	24.5	25.3	25.4

VARIABLE MTH									
Seedlot	GF9			GF14			GF22		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	4	4	4	4	4	4	4	4	4
r2	-6.966	-6.966	-6.966	0.308	0.308	0.308	-1.886	-1.886	-1.886
mean difference	-0.512	-0.512	-0.512	-0.017	-0.017	-0.017	0.205	0.205	0.205
mean % error	-2.647	-2.647	-2.647	-0.006	-0.006	-0.006	0.987	0.987	0.987
rmse	0.944	0.944	0.944	0.914	0.914	0.914	1.001	1.001	1.001
mean absolute diff	0.767	0.767	0.767	0.782	0.782	0.782	0.943	0.943	0.943
mean absolute % error	3.932	3.932	3.932	3.922	3.922	3.922	4.788	4.788	4.788
mean actual	19.5	19.5	19.5	20.25	20.25	20.25	19.65	19.65	19.65
mean predicted	20.0	20.0	20.0	20.3	20.3	20.3	19.4	19.4	19.4
actual STD	0.39	0.39	0.39	1.27	1.27	1.27	0.68	0.68	0.68
predicted STD	0.9	0.9	0.9	1.9	1.9	1.9	1.1	1.1	1.1

APPENDIX 5B

NAPIRAD MODEL - results for 6 plots (i.e., results exclude 8 plots of GF 13 (LI) and 16).

TRIAL : FR10 - Glengarry Forest

VARIABLE SPH

Seedlot	GF7			GF14			GF21		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	2	2	2	2	2	2	2	2	2
r2	0.598	0.598	0.441	-	-	-	0.752	0.737	0.723
mean difference	9.151	9.151	11.214	-0.55	1.395	2.231	-0.598	2.227	3.178
mean % error	1.924	1.924	2.268	-0.117	0.297	0.476	-0.23	0.386	0.592
rmse	9.515	9.515	11.214	10.078	10.103	10.224	10.217	10.517	10.782
mean absolute diff	9.515	9.515	11.214	10.063	10.005	9.978	10.199	10.279	10.303
mean absolute % error	1.924	1.924	2.268	2.146	2.133	2.127	2.23	2.219	2.216
mean actual	495	495	495	469	469	469	459.5	459.5	459.5
mean predicted	485	485	484	470	468	467	460	457	456
actual STD	21.1	21.1	21.1	0	0	0	28.99	28.99	28.99
predicted STD	21.0	21.0	21.0	14.0	14.0	14.0	15.0	14.0	14.0

VARIABLE BA

Seedlot	GF7			GF14			GF21		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	2	2	2	2	2	2	2	2	2
r2	-3140.1	-3140.1	-1718.1	-12.03	-7.47	-5.83	-147.3	-77.71	-59.47
mean difference	4.712	4.712	3.423	5.88	4.733	4.246	6.875	5.002	4.379
mean % error	10.477	10.477	7.608	12.891	10.37	9.3	14.667	11.516	9.346
rmse	4.764	4.764	3.524	5.903	4.759	4.274	6.88	5.013	4.393
mean absolute diff	4.712	4.712	3.423	5.88	4.733	4.246	6.875	5.002	4.379
mean absolute % error	10.477	10.477	7.608	12.891	10.37	9.3	14.667	11.516	9.346
mean actual	44.9	44.9	44.9	45.5	45.5	45.5	46.9	46.9	46.9
mean predicted	40.3	40.3	41.5	39.7	40.8	41.3	40	41.9	42.5
actual STD	0.12	0.12	0.12	2.31	2.31	2.31	0.79	0.79	0.79
predicted STD	0.9	0.9	1.1	1.6	1.6	1.6	1.2	1.3	1.3

VARIABLE Volume

Seedlot	GF7			GF14			GF21		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	2	2	2	2	2	2	2	2	2
r2	-179.97	-179.97	-80.25	-2.97	-0.104	0.566	-51.46	-20.29	-13.04
mean difference	22.109	22.109	13.815	16.84	8.777	5.355	34.851	21.998	17.73
mean % error	7.61	7.61	4.76	5.532	2.891	1.77	10.916	6.88	5.544
rmse	23.54	23.54	15.77	16.89	8.91	5.588	35.12	22.37	18.165
mean absolute diff	22.109	22.109	13.815	16.84	8.777	5.355	34.851	21.998	17.73
mean absolute % error	7.61	7.61	4.76	5.532	2.891	1.77	10.916	6.88	5.544
mean actual	291.2	291.2	291.2	305.3	305.3	305.3	318.7	318.7	318.7
mean predicted	269.1	269.1	277.4	288.5	296.5	299.9	283.9	296.7	301
actual STD	2.5	2.5	2.5	12	12	12	6.9	6.9	6.9
predicted STD	13.9	13.9	13.2	13.9	14.1	14.2	0.7	1.1	1.2

VARIABLE MTH

Seedlot	GF7			GF14			GF21		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	2	2	2	2	2	2	2	2	2
r2	-131.64	-131.64	-131.64	-126.32	-126.32	-126.32	-363.82	-363.82	-363.82
mean difference	-0.609	-0.609	-0.609	-1.669	-1.669	-1.669	-0.836	-0.836	-0.836
mean % error	-3.194	-3.194	-3.194	-8.504	-8.504	-8.504	-4.195	-4.195	-4.195
rmse	1.152	1.152	1.152	1.693	1.693	1.693	0.955	0.955	0.955
mean absolute diff	0.978	0.978	0.978	1.669	1.669	1.669	0.836	0.836	0.836
mean absolute % error	5.156	5.156	5.156	8.504	8.504	8.504	4.195	4.195	4.195
mean actual	18.9	18.9	18.9	19.65	19.65	19.65	19.95	19.95	19.95
mean predicted	19.5	19.5	19.5	21.3	21.3	21.3	20.8	20.8	20.8
actual STD	0.14	0.14	0.14	0.21	0.21	0.21	0.07	0.07	0.07
predicted STD	1.5	1.5	1.5	0.2	0.2	0.2	0.6	0.6	0.6

APPENDIX 5C

NAPIRAD MODEL - results for 16 plots (i.e., no plots excluded)

TRIAL: FR57 - Tikokino Forest

VARIABLE SPH

Seedlot	GF7			GF17			GF19		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	6	6	6	4	4	4	6	6	6
r2	0.974	0.974	0.975	0.972	0.972	0.972	0.939	0.944	0.944
mean difference	-6.31	-6.31	-5.12	-2.61	-1.28	-0.72	-11.99	-10.69	-10.39
mean % error	-1.77	-1.77	-1.49	-0.90	-0.55	-0.41	-4.48	-4.09	-4.01
rmse	14.85	14.85	14.47	12.97	12.91	12.93	18.44	17.85	17.73
mean absolute diff	11.93	11.93	12.04	9.64	10.39	10.71	15.59	15.43	15.39
mean absolute % error	2.97	2.97	2.97	2.67	2.85	2.93	5.34	5.23	5.20
mean actual	413.7	413.7	413.7	375.8	375.8	375.8	331.0	331.0	331.0
mean predicted	420	420	419	378	377	376	343	342	341
actual STD	100.6	100.6	100.6	88.8	88.8	88.8	82.4	82.4	82.4
predicted STD	96	96	96	85	84	84	72	71	71

VARIABLE BA

Seedlot	GF7			GF17			GF19		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	6	6	6	4	4	4	6	6	6
r2	0.592	0.592	0.775	0.623	0.739	0.673	0.680	0.780	0.742
mean difference	2.36	2.36	0.59	1.66	-0.56	-1.51	1.70	-0.78	-1.35
mean % error	7.12	7.12	0.47	4.73	-4.06	-7.84	4.34	-4.74	-6.81
rmse	3.58	3.58	2.66	3.17	2.64	2.95	3.03	2.51	2.72
mean absolute diff	2.68	2.68	2.07	2.15	2.36	2.79	2.71	1.88	2.05
mean absolute % error	8.66	8.66	7.36	7.09	9.34	11.56	9.45	7.95	8.85
mean actual	27.35	27.35	27.35	25.99	25.99	25.99	28.2	28.2	28.2
mean predicted	25.0	25.0	26.8	24.3	26.6	27.5	26.5	29.0	29.6
actual STD	6.14	6.14	6.14	5.96	5.96	5.96	5.86	5.86	5.86
predicted STD	3.4	3.4	3.6	2.9	3.0	3.0	3.2	3.4	3.4

VARIABLE Volume

Seedlot	GF7			GF17			GF19		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	6	6	6	4	4	4	6	6	6
r2	0.490	0.490	0.716	0.450	0.746	0.776	0.737	0.848	0.825
mean difference	17.92	17.92	8.67	15.97	4.35	-0.64	10.01	-3.26	-6.28
mean % error	9.94	9.94	3.77	9.65	1.68	-1.75	4.88	-3.85	-5.84
rmse	24.59	24.59	18.36	21.76	14.78	13.89	16.32	12.39	13.33
mean absolute diff	18.26	18.26	13.09	15.97	9.82	11.76	13.40	10.93	11.04
mean absolute % error	10.22	10.22	7.46	9.65	5.59	7.41	8.06	7.87	8.26
mean actual	154.4	154.4	154.4	149.4	149.4	149.4	156.6	156.6	156.6
mean predicted	136.5	136.5	145.7	133.5	145.1	150.1	146.6	159.9	162.9
actual STD	37.7	37.7	37.7	33.9	33.9	33.9	34.9	34.9	34.9
predicted STD	20.3	20.3	21.2	21.1	21.9	22.3	21.5	22.6	22.8

VARIABLE MTH

Seedlot	GF7			GF17			GF19		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	6	6	6	4	4	4	6	6	6
r2	-1.541	-1.541	-1.541	-1.746	-1.746	-1.746	0.184	0.184	0.184
mean difference	0.59	0.59	0.59	0.92	0.92	0.92	0.11	0.11	0.11
mean % error	3.56	3.56	3.56	5.44	5.44	5.44	0.72	0.72	0.72
rmse	0.81	0.81	0.81	1.42	1.42	1.42	0.48	0.48	0.48
mean absolute diff	0.62	0.62	0.62	1.29	1.29	1.29	0.38	0.38	0.38
mean absolute % error	3.78	3.78	3.78	7.77	7.77	7.77	2.41	2.41	2.41
mean actual	16.1	16.1	16.1	16.5	16.5	16.5	16.0	16.0	16.0
mean predicted	15.5	15.5	15.5	15.6	15.6	15.6	15.9	15.9	15.9
actual STD	0.56	0.56	0.56	0.99	0.99	0.99	0.58	0.58	0.58
predicted STD	0.4	0.4	0.4	1.2	1.2	1.2	0.8	0.8	0.8

APPENDIX 5D

SANDS MODEL - results for 12 plots (i.e., excludes 4 plots of GF 13 (LI)).

TRIAL: FR7 - Woodhill Forest

VARIABLE

SPH

Seedlot	GF7			GF14			GF21		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	4	4	4	4	4	4	4	4	4
r2	0.926	0.926	0.932	0.977	0.962	0.95	0.924	0.934	0.934
mean difference	-6.91	-6.91	-6.111	3.287	4.201	4.592	-1.562	-0.121	0.362
mean % error	-1.558	-1.558	-1.384	0.7	0.894	0.978	-0.302	-0.001	0.1
rmse	12.274	12.274	11.821	3.294	4.209	4.6	5.019	4.685	4.669
mean absolute diff	10.41	10.41	10.112	3.287	4.201	4.592	4.764	4.671	4.64
mean absolute % error	2.26	2.26	2.25	0.7	0.894	0.978	0.99	0.979	0.974
mean actual	256.8	256.8	456.8	469.5	469.5	469.5	477.3	477.3	477.3
mean predicted	466	466	463	466	465	465	479	477	477
actual STD	52.2	52.2	52.2	25.0	25.0	25.0	21.1	21	21.2
predicted STD	53.0	53.0	52.0	25.0	25.0	25.0	25.0	25.0	25.0

VARIABLE

BA

Seedlot	GF7			GF14			GF21		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	4	4	4	4	4	4	4	4	4
r2	0.537	0.537	0.5	-2.222	-1.674	-1.463	-9.536	-5.754	-4.725
mean difference	-0.147	-0.147	-0.507	2.978	2.572	2.397	2.44	1.815	1.604
mean % error	-1.573	-1.573	-3.156	11.035	9.443	8.758	9.425	7.008	6.192
rmse	1.882	1.882	1.955	3.642	3.317	3.184	2.729	2.185	2.012
mean absolute diff	1.678	1.678	1.689	2.978	2.572	2.397	2.44	1.815	1.604
mean absolute % error	7.226	7.226	7.474	11.035	9.443	8.753	9.425	7.008	6.192
mean actual	23.1	23.1	23.1	25.7	25.7	25.7	25.9	25.9	25.9
mean predicted	23.3	23.3	23.6	22.7	23.1	23.3	23.4	24.1	24.3
actual STD	3.2	3.2	3.2	2.3	2.3	2.3	0.97	0.97	0.97
predicted STD	1.1	1.1	1.0	0.6	0.6	0.6	1.6	1.6	1.6

VARIABLE

Volume

Seedlot	GF7			GF14			GF21		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	4	4	4	4	4	4	4	4	4
r2	0.402	0.402	0.457	-4.135	-3.499	-3.245	-9.854	-7.289	-6.519
mean difference	6.699	6.699	4.563	27.218	24.813	23.779	23.662	20.036	18.811
mean % error	3.441	3.441	1.936	16.133	14.633	13.988	14.714	12.442	11.674
rmse	15.626	15.626	14.889	31.615	29.593	28.743	25.817	22.562	21.488
mean absolute diff	12.236	12.236	12.295	27.218	24.813	23.779	23.662	20.036	18.811
mean absolute % error	7.765	7.765	7.976	16.133	14.633	13.988	14.714	12.442	11.674
mean actual	145	145	145	161.8	161.8	161.8	160	160	160
mean predicted	138.3	138.3	140.4	134.6	137.0	138.0	136.3	140	141.2
actual STD	23.3	23.3	23.3	16.1	16.1	16.1	9	9	9
predicted STD	7.2	7.2	7.1	6.2	6.2	6.2	11.9	11.9	11.9

VARIABLE

MTH

Seedlot	GF7			GF14			GF21		
	Multiplier implementation			Multiplier implementation			Multiplier implementation		
	NI	YU	YI	NI	YU	YI	NI	YU	YI
n total	4	4	4	4	4	4	4	4	4
r2	-4.446	-4.446	-4.446	-27.88	-27.88	-27.88	-8.368	-8.368	-8.368
mean difference	1.057	1.057	1.057	1.235	1.235	1.235	1.227	1.227	1.227
mean % error	6.133	6.133	6.133	7.174	7.174	7.174	7.202	7.202	7.202
rmse	1.107	1.107	1.107	1.317	1.317	1.317	1.425	1.425	1.425
mean absolute diff	1.057	1.057	1.057	1.235	1.235	1.235	1.227	1.227	1.227
mean absolute % error	6.133	6.133	6.133	7.174	7.174	7.174	7.202	7.202	7.202
mean actual	17.1	17.1	17.1	17.2	17.2	17.2	16.8	16.8	16.8
mean predicted	16.0	16.0	16.0	16.0	16.0	16.0	15.6	15.6	15.6
actual STD	0.55	0.55	0.55	0.28	0.28	0.28	0.54	0.54	0.54
predicted STD	0.2	0.2	0.2	0.5	0.5	0.5	0.5	0.5	0.5