

Updates for Selected Equations in the Red Alder Plantation Version of ORGANON

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Updates to Selected Equations in the Alder Plantation Version of ORGANON

1.0 Overview

When the red alder (*Alnus rubra*) plantation version of ORGANON (RAP-ORGANON) was first produced in 2011 (Hann et al. 2011), the oldest measured data from red alder plantations were 18 years total age, so the initial version of the model was envisioned to provide suitably accurate extrapolations of trees and stands simulated out to approximately 30 years, especially given the early peak of red alder diameter and height increment. Comparison of RAP-ORGANON projections to more recent measurements of the from the Hardwood Silviculture Cooperative (HSC) network of plots has found some inconsistencies, most notably significant underestimates of diameter increment in thinned stands, and overestimates of mortality rate in unthinned stands.

A refit of updated data sets was made in 2021, when two of the installations had been measured at 28 years of age. Since that time, an additional 4 installations have received a 23 year measurement, 2 have received a 25 year measurement, and 8 have received a 28 year measurement, providing data applicable to trees and stands near an appropriate rotation age. The equations in the original version of RAP-ORGANON were developed using data collected by both the HSC and Weyerhaeuser Company in order to increase sample size. The continued remeasurement of the HSC installations produced a modeling data set of a sufficient size and range to make the inclusion of the Weyerhaeuser Company data unnecessary. Dropping the Weyerhaeuser Company data in this reanalysis also meant that the differences in measurement protocols found between the two data sets, which complicated the original analysis, could now be avoided. Using the new data, the Center for Intensive forest Plantation Silviculture (CIPS) agreed to refit the equations using the existing model forms, or, if necessary, with some simple alteration to existing equations.

This report describes the expanded modeling data sets available to the reanalysis, and it provides new parameter estimates and, in some cases, new model forms for the following equations used in RAP-ORGANON: height-diameter equations, top-height and site-index equations, height to crown base equation, diameter increment equation, height increment equation, mortality rate equation, diameter and height increment residuals equations, and thinning effects upon diameter increment, height increment, and mortality rate equations. These updated equations are then compared to the original equations in order to illustrate differences. RAP-ORGANON equations not refit in this reanalysis are the maximum crown width equation, the largest crown width equation, the crown profile equation, the branch diameter equation, and the crown recession equation.

2.0 Red Alder Height-Diameter Equations

The height-diameter equation in RAP-ORGANON is used to impute missing tree heights (Hann et al. 2011). Two equation forms are used to characterize the relationship: The exponential equation form of Larsen and Hann (1987) predicts total tree height (H) from diameter at breast height (D). The equation form of Krumland and Wensel (1988) predicts H from D, the top height of the stand (H40), and the average D associated with the top height trees (D40). The exponential model form can be applied to any stand structure, while the Krumland and Wensel (1988) equation form is applicable to only even-aged stands/plantations. In general, the Krumland and Wensel (1988) will have better precision than the exponential model form in even-aged stands/plantations.

2.1 Data

Subsampling was used to measure heights on trees in the modeling data set. In the original analysis, the data for fitting the equations came from all of the undamaged and damaged subsampled trees on both the control (i.e., untreated) plots and those measurements taken before treatment on the thinned plots. In this reanalysis, the data was restricted to just the control plots. This action was taken because using just the control plot data produced a better fit to trees with D values above 10-inches than when the small size trees from the pre-thinning data was incorporated in the modeling data set. This improved behavior is important because the additional sampling on the HSC plots has increased the number of trees with D values above 10-inches from 371 in the original data set to 1226 in the revised modeling data set (an increase of 230-percent). Table 2.1 presents a summary of the data.

Table 2.1 Descriptive statistics for the modeling data set used in the height-diameter equations for plantation-grown red alder.

Attribute	Mean	Minimum	Maximum	Std. Deviation
Tree Attributes (Number of Observations = 36,359)				
H (ft.)	26.9	4.6	99.7	18.8
D (in.)	3.2	0.2	15.9	3.0
Plot/Measurement Attributes (Number of Observations = 569)				
H40 (ft.)	40.8	7.9	88.0	18.7
D40 (in.)	6.0	0.5	14.0	3.2

2.2. Data Analysis and Results

The exponential equation form is:

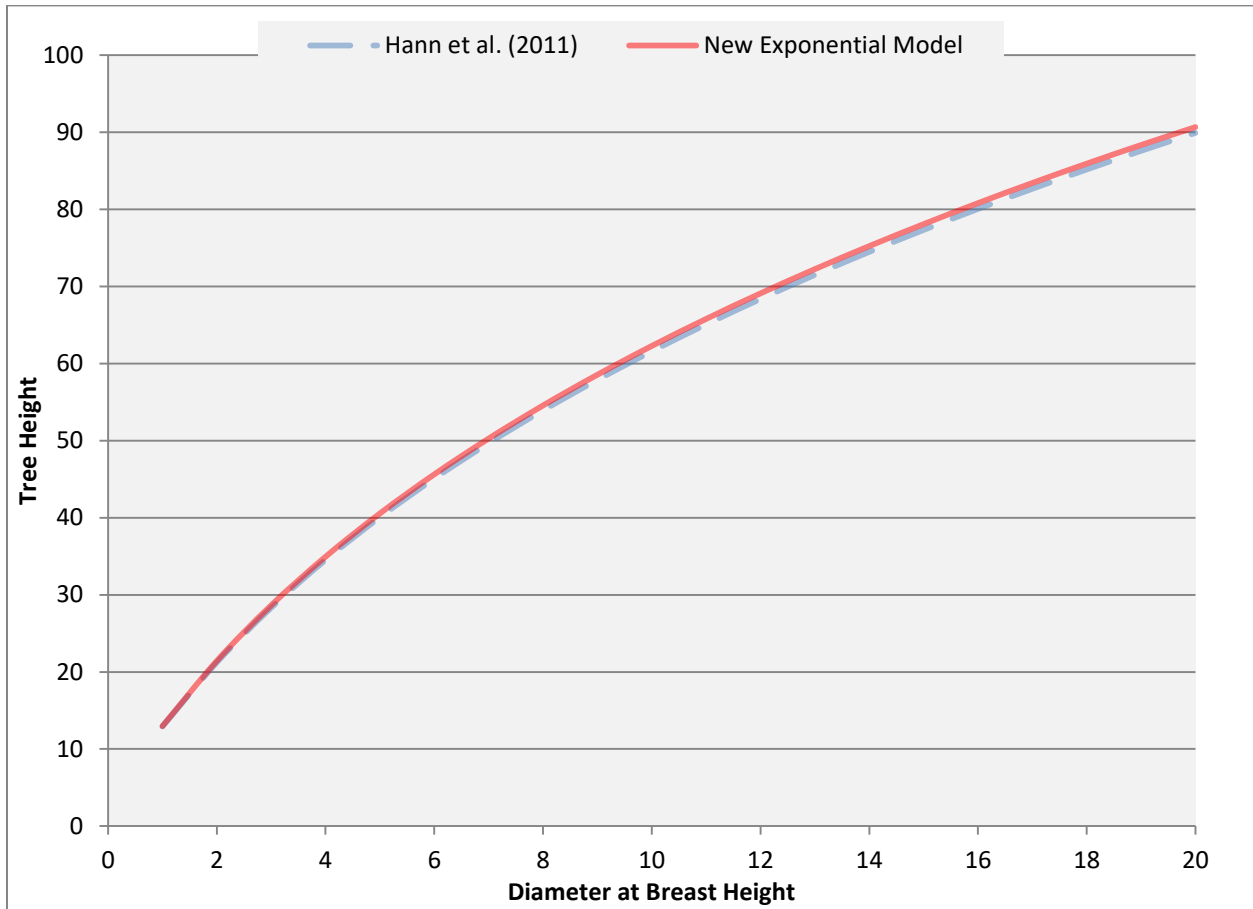
$$H = 4.5 + \exp(b_0 + b_1 D^{b_2}) \quad (2.1)$$

Equation (2.1) was fit to the data using weighted nonlinear regression and a weight of 1.0/D. The resulting parameter estimates and their standard errors are shown in Table 2.2. The weighted MSE for the fit was 11.10403. A comparison of the new fit to Equation (2.1) to the original fit is shown in Figure 2.1.

Table 2.2 Parameter estimates and their standard errors for Equation (2.1).

Parameter	Estimate	Standard Error
b_0	6.67791193	0.06325467
b_1	-4.54168226	0.06341754
b_2	-0.238681844	0.004159331

Figure 2.1. A comparison of predictions for Equation (2.1) using parameter estimates from Table 2.2 to those found in Hann et al. (2011).



The Krumland and Wensel (1988) equation form is:

$$H = 4.5 + (H40 - 4.5) \frac{\exp[b_0 D^{b_1 + b_2(H40 - 4.5)}]}{\exp[b_0 D40^{b_1 + b_2(H40 - 4.5)}]} \quad (2.2)$$

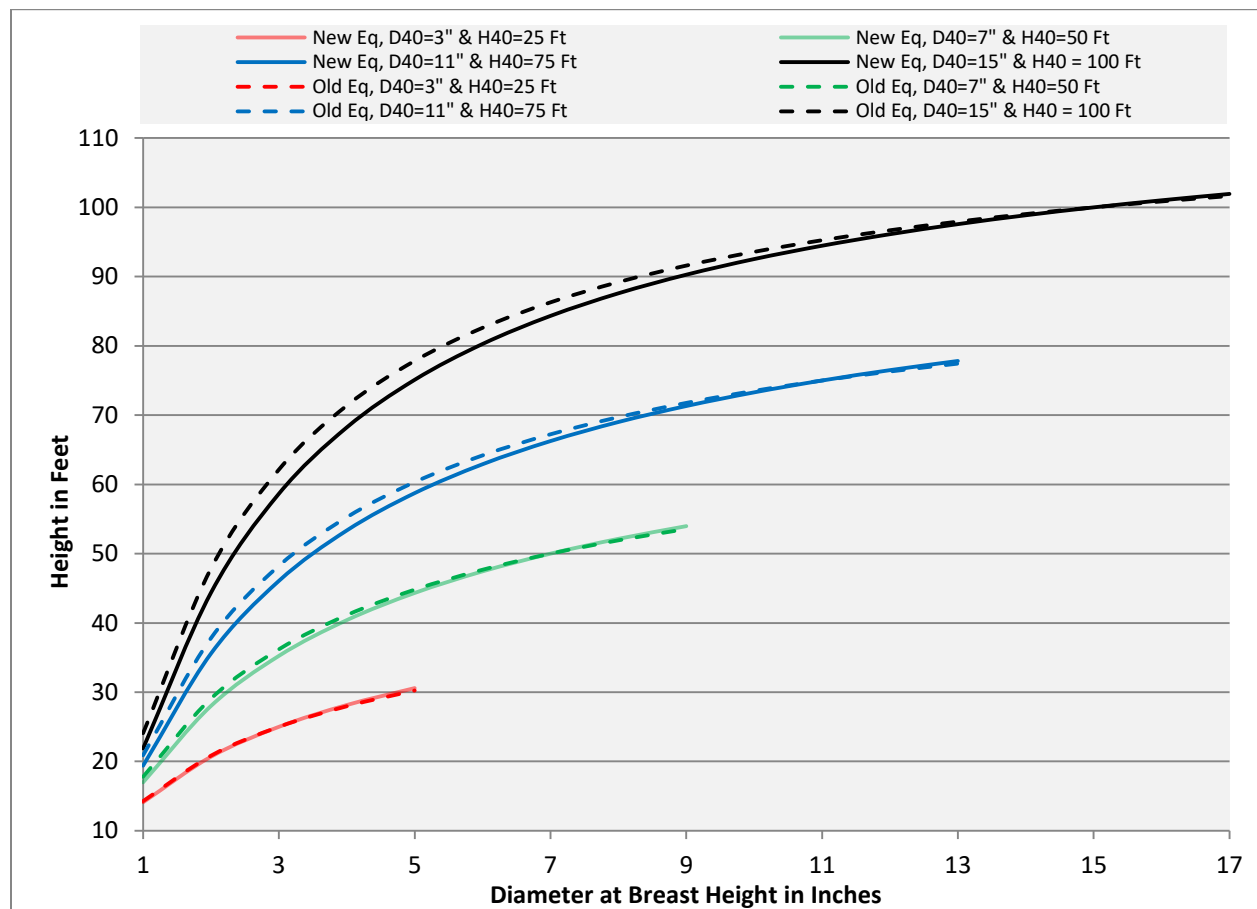
Equation (2.2) was fit to the data using weighted nonlinear regression and a weight of $1.0/D$. The resulting parameter estimates and their standard errors are shown in Table 2.3. The weighted MSE for the fit was 2.775793. A comparison of the new fit to Equation (2.2) to the original fit is shown in Figure 2.2 for four stands that span the size range found in the red alder modeling data

set: (1) D40 = 3" and H40 = 25', (2) D40 = 7" and H40 = 50', (3) D40 = 11" and H40 = 75', and (4) D40 = 15" and H40 = 100'.

Table 2.3 Parameter estimates and their standard errors for Equation (2.2).

Parameter	Estimate	Standard Error
b_0	-1.90918338	0.00689096
b_1	-0.361178787	0.002442016
b_2	-0.00483945572	0.0001606108

Figure 2.2. A comparison of predictions for Equation (2.2) using parameter estimates from Table 2.3 to those found for the old equation in Hann et al. (2011).



2.3 Discussion

Examination of Figure 2.1 shows that the expansion of the modeling data set to include trees with larger values of D and subsequently larger values of H has not substantially changed predictions from Equation (2.1). Examination of Figure 2.2 shows that the inclusion of D40 and H40 in an H/D equation produces the same predictions of H at the upper ends of D for all four stands. For the smallest stand, both the original version of Equation 2.2 and the new version of the equation overlay each other very closely across the full range of D. For the larger stands, the new version of Equation 2.2 predicts somewhat shorter trees than the original version between D values of 2" to 10". Given that the weighted MSE of Equation (2.1) is three times higher than

that of Equation (2.2), the usefulness of measuring D40 and H40 in evenaged plantations is clear when dubbing missing values of H.

2.4 Literature Cited

Hann, D.W., A.A. Bluhm, and D.E. Hibbs. 2011. Development and evaluation of the tree-level equations and their combined stand-level behavior in the red alder plantation version of ORGANON. Oregon State University, Department of Forest Engineering, Resources, and Management, Corvallis, Oregon. Forest Biometrics Research Paper 1. 127p.

Krumland, B.E. and L.C. Wensel. 1988. A generalized height-diameter equation for coastal California species. *Western Journal of Applied Forestry* 3: 113-115.

Larsen, D.R. and D.W. Hann. 1987. Height-diameter equations for seventeen tree species in southwestern Oregon. Forest Research Laboratory, Oregon State University, Corvallis. Research paper 49. 16 p.

3.0 Top-Height/Site Index Equation for Red Alder

The procedures and results from developing a top-height/site index (H40/SI) prediction equation for red alder plantations are described in detail in Weiskittel et al. (2009). The equation is used in RAP-ORGANON to predict the potential height increment of trees. When combined with the planting density (PDEN) correction equation, it is also employed by the users of RAP-ORGANON to calculate the appropriate SI for their input tree lists.

The Weiskittel et al. (2009) model was fit to data from several different data sets, but only one of these data sets, the HSC spacing installations, has received additional measurements in older ages since the original analysis. Therefore, the same procedures used by Weiskittel et al. (2009) were employed to re-estimate the parameters using data from only the 787 plot/measurements currently available from the HSC spacing plots.

Application of the Weiskittel et al. (2009) equation to the red alder plantation modeling data found that SI was under-predicted for plots with low planting densities (PDEN). Therefore, a refit of the PDEN correction equation for SI was also developed. The following is a summary of the new equations and how they can be used to predict H40/SI.

3.1 Data

After examining a number of alternative data structures used to model H40, Weiskittel et al. (2009) concluded that the usage of the non-overlapping forward difference data structure for the modeling data resulted in the most accurate and precise parameters for predicting H40. This data structure requires estimates of H40 for each stand age (A) measured on all plots. All trees on each plot were measured for diameter at breast height (4.5-feet) and a subsample of trees was measured for total height. Missing tree heights were imputed using a regional height-diameter equation developed for plantation grown red alder and then scaled to each plot's height measurements using simple linear regression through the origin similar to the approach of Hann and Hanus (2004). H40 at each age was then calculated as the mean height of the 40 largest trees per acre (based on diameter) that did not have height damage or other severe damage for each measurement period. The variable A was defined as the number of years since seed. The modeling data set requires the input of H40 at both the start and end of each growth period (H40₁ and H40₂, respectively) and the input of A at both the start and end of each growth period (A₁ and A₂, respectively). This process eliminated three observations from the data set. Table 3.1 provides a summary of the 784 observations remaining in the H40 modeling data set.

Table 3.1. Modeling data used to develop the H40/SI equation.

Attribute	Mean	Minimum	Maximum	Standard Deviation
H40 ₁ (ft.)	36.4	9.2	86.9	19.4
H40 ₂ (ft.)	48.6	13.8	95.8	18.4
A ₁ (yrs)	10.5	4	23	5.9
A ₂ (yrs)	14.5	5	28	6.7

Weiskittel et al. (2009) also found that low planting densities resulted in reduced estimates of SI. Modeling this behavior requires data on the relative SI (RSI) and PDEN for each plot, where RSI is the site index of the plot divided by the average SI for those plots on the installation with PDEN greater than 500 trees per acre. A summary of the 234 observations in the RSI modeling data set is found in Table 3.2.

Table 3.2. Modeling data used to develop the RSI equation.

Attribute	Mean	Minimum	Maximum	Standard Deviation
RSI	0.9656	0.6512	1.2049	0.1028
PDEN (#/Ac.)	652.2	72.0	1524.0	385.9

3.2 Top-Height/Site-Index Equation

The following GADA model form for the Schumacher equation used in Weiskittel et al. (2029) was fit to the non-overlapping forward difference data structure of the modeling data using nonlinear regression:

$$H40_2 = H40_1 \cdot e^{b_1(A_2^{b_2} - A_1^{b_2})} \quad (3.1)$$

Where,

- $H40_1$ = Measured H40 (i.e., top height) in feet at the start of the growth period
- $H40_2$ = Measured H40 (i.e., top height) in feet at the end of the growth period
- A_1 = Measured total stand age from seed at the start of the growth period
- A_2 = Measured total stand age from seed at the end of the growth period

The resulting parameter estimates and their standard errors are found in Table 3.3.

Table 3.3 Regression parameters for the red alder plantation site index equation:

Parameter	Estimate	Standard Error
b_1	-5.269144	0.04703208
b_2	-0.586430	0.01768175

The residual standard error for Equation (3.1) was 0.8913879, with an adjusted coefficient of determination (R_a^2) of 0.9681.

Equation (3.1) can be transformed to predict site index, uncorrected for PDEN, by:

$$SI_P = H40_M \cdot e^{b_1(20.0^{b_2} - A_M^{b_2})} \quad (3.2)$$

Where,

- SI_P = Predicted site index (H40 at a total stand age from seed of 20 years) in feet, uncorrected for planting density
- $H40_M$ = Measured H40 (i.e., top height) in feet

A_M = Measured total stand age from seed

Likewise, Equation (3.1) can be transformed into the following equation for predicting H40 from SI_M and A_M :

$$H40_P = SI_M \cdot e^{-b_1(20.0^{b_2} - A_M^{b_2})} \quad (3.3)$$

Where,

$H40_P$ = Predicted H40 (i.e., top height) in feet

SI_M = Measured site index (H40 at a total stand age from seed of 20 years) in feet, uncorrected for planting density

A graph of $H40_P$ over A_M using Equation (3.3) and both the parameters in Table 3.1 and the parameters in Hann et al. (2011) is found in Figure 3.1

Figure 3.1. Predicted H40 from Equation (3.3) using both the new parameters in Table 3.1 and the original parameters in Hann et al. (2011).

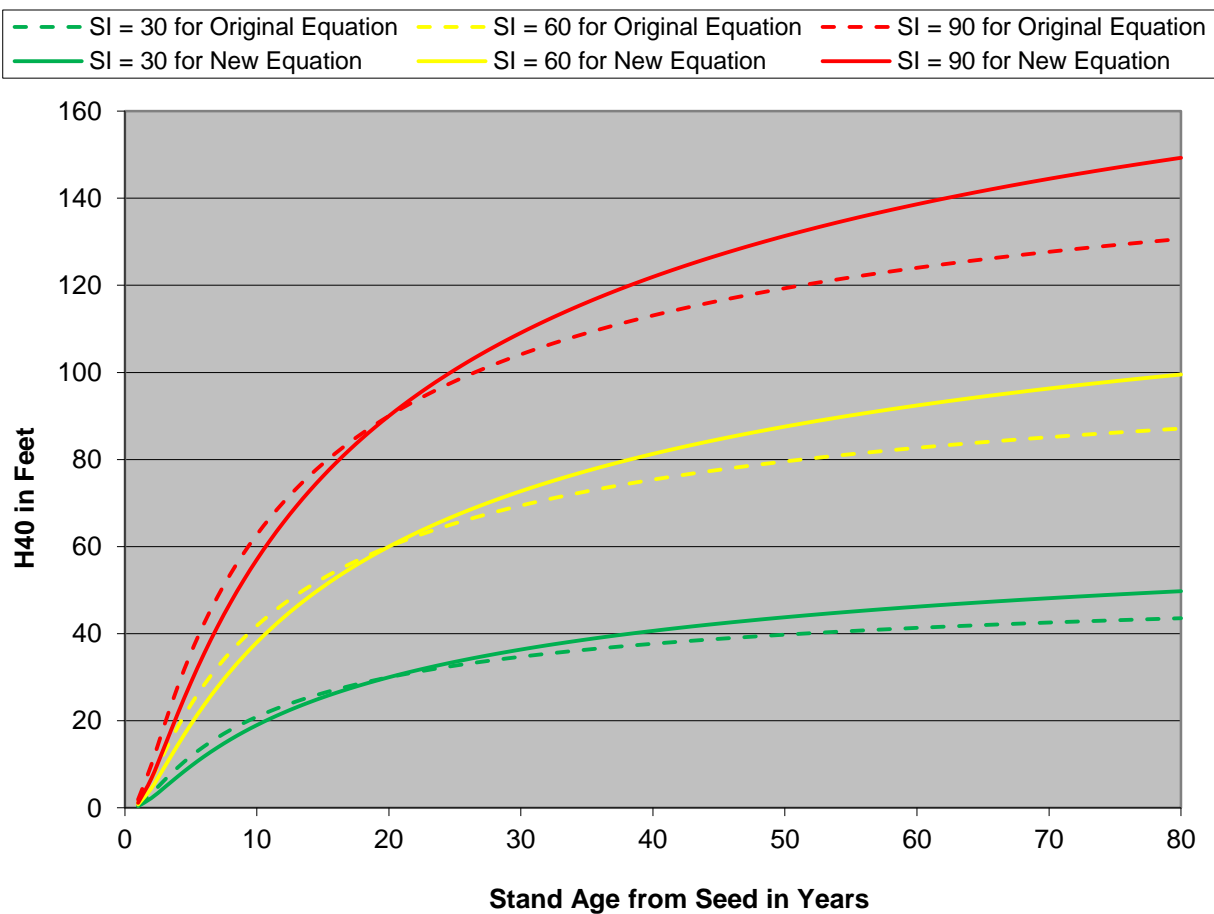
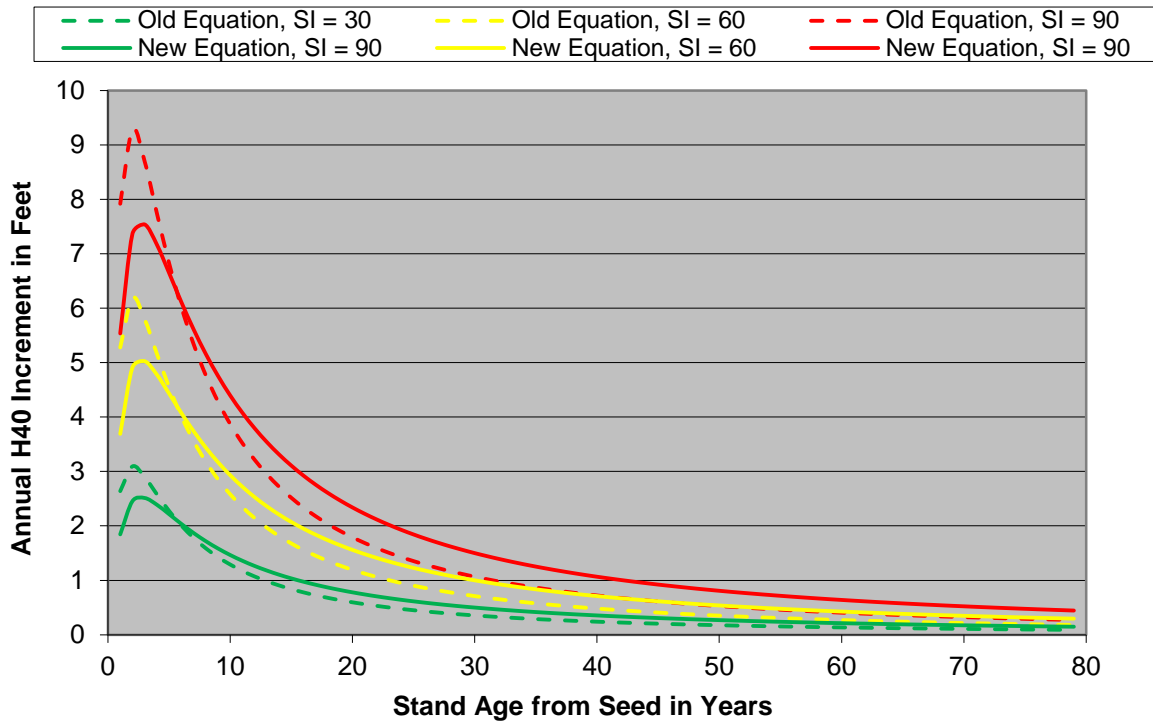


Figure 3.2 shows predicted annual H40 increment for the two sets of parameters.

Figure 3.2. Predicted annual H40 increment from Equation (3.2) using both the new parameters in Table 3.1 and the original parameters in Hann et al. (2011).



Examination of Figures 3.1 and 3.2 shows that the new parameters predict somewhat lower values of H40, and its increment, before the base age of 20 years since seed and substantially higher values of H40, and its increment, after the base age of 20 years when compared to the original model.

3.3 Planting Density Correction Equation for Site Index

Weiskittel et al. (2009) reported that the parameters of Equation (3.1) did not vary by planting density. Therefore, predictions of H40 from Equation (3.3) (and the height increment model used in RAP-ORGANON that incorporates H40 increment) use the measured SI value for the stand without correction for planting density (PDEN) (Weiskittel et al. 2009). This means that the development path of H40 over time on low density stands of a specified SI value is the same as the development path of H40 over time on high density stands with the same specified SI value.

However, it has been found that the equations for HCB, diameter increment, mortality rate equation, etc. are more highly correlated to values of SI that have been corrected for PDEN (Hann et al. 2011). Therefore, the predictions from Equation (3.2) must be corrected for PDEN values under approximately 500 trees per acre (Hann et al. 2011). To do this first requires the development of an equation that predicts relative site index (*RSI*) using the following model form:

$$RSI = 1.0 - b_3 e^{(b_4 \times PDEN^{1.5})} \quad (3.4)$$

Where,

RSI = The SI of the plot divided by the average SI for those plots on the installation with PDEN greater than 500.

The equation's parameters and their standard errors are found in Table 3.4.

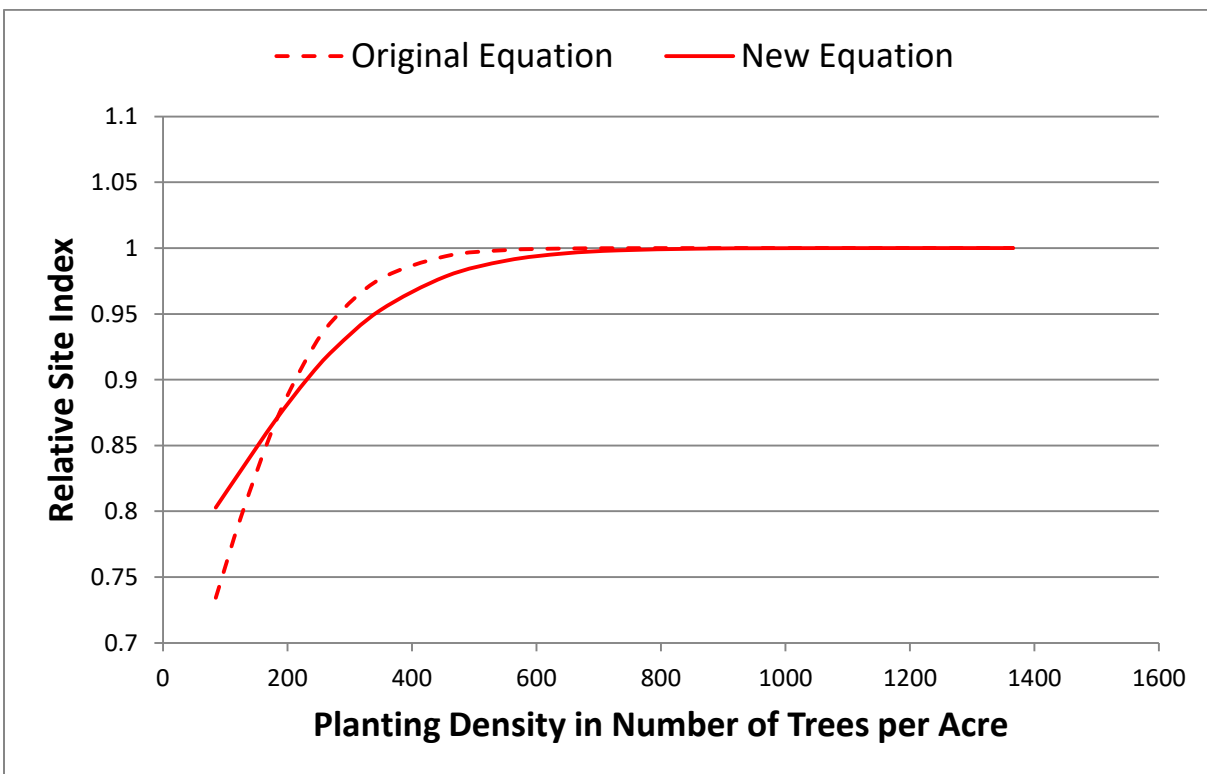
Table 3.4 Regression parameters, and their standard errors, for the relative site index correction Equation (3.4).

Parameter	Estimate	Standard Error
b_3	0.23951149	0.03984259
b_4	-0.00024883	0.00004880

The residual standard error for Equation (3.4) was 0.00746, with a R_a^2 of 0.2941.

Figure 3.3 illustrates the behavior of Equation (3.4) using both the original parameters of Weiskittel et al. (2009) and the new parameters found in Table 3.4. Examination of Figure 3.3 shows that the new equation predicts somewhat larger values of RSI than the original equation up to a PDEN value of approximately 180 trees per acre and then somewhat smaller values of RSI for PDEN values above 180 trees per acre. Both parameterizations predict a value of RSI greater than 0.99 for PDEN densities greater than approximately 550 trees per acre.

Figure 3.3 Graph of predicted relative site index (RSI) plotted over planting density for both the original equation of Weiskittel et al. (2009) and the new equation parameters found in Table 3.4.



Using Equation (3.4), a PDEN corrected site index (SI_C) value can be calculated by:

$$SI_C = SI/RSI_P$$

Where,

RSI_p = Predicted relative SI from Equation (3.4)

RAP-ORGANON uses values of both SI_C and PDEN when creating the .INP file in ORGEDIT.EXE. SI_C is also used in ORGEDIT.DLL for calibrating the HCB and diameter increment equations, and it is used in ORGRUN.DLL to project the inputted stand into the future.

3.4 Literature Cited

Hann, D.W., A.A. Bluhm, and D.E. Hibbs. 2011. Development and evaluation of the tree-level equations and their combined stand-level behavior in the red alder plantation version of ORGANON. Oregon State University, Department of Forest Engineering, Resources, and Management, Corvallis, Oregon. Forest Biometrics Research Paper 1. 127p.

Hann, D.W. and M.L. Hanus. 2004. Evaluation of nonspatial approaches and equation forms used to predict tree crown recession. Canadian Journal of Forest Research 34, 1993-2003.

Weiskittel, A.R., D.W. Hann, D.E. Hibbs, T.Y. Lam, and A.A. Bluhm. 2009. Modeling top height growth of red alder plantations. Forest Ecology and Management 258: 323-331.

4.0 Height-to-Crown-Base Equation for Red Alder

Two equations for predicting height to crown base (HCB) in feet are needed in ORGANON (Hann et al. 2011). The first equation is developed with a data set that includes all trees with measured HCB on the control plots and it is used in RAP-ORGANON to impute missing measurements of HCB. The second equation is developed with a control plot data set that includes only undamaged trees with measured HCB and it is used in RAP-ORGANON to predict crown recession via the indirect method of Hann and Hanus (2004).

4.1 Data

Subsampling was used by the HSC to measure HCB on the research plots. The HSC defined HCB as the lowest contiguous live whorl in which at least 3/4 of the branches in the whorl were alive. Furthermore, the HSC used point of branch insertion rather than bottom of foliage in their definition. Tree and stand attributes used in the HCB equation include total tree height (H), tree diameter at breast height (D), crown competition factor in larger D trees (CCFL), stand basal area per acre (BA), and SI_C calculated by Equations (3.2) and (3.4). Table 4.1 presents the means, minimums, maximums, and standard deviations for the tree and stand attributes used to form the response and predictor variables for all trees on the untreated plots, including the control plots and the pretreatment measurements on the thinned plots. Table 4.2 presents the means, minimums, maximums, and standard deviations for the tree and stand attributes used to form the response and predictor variables for just undamaged trees on just the control plots.

Table 4.1 Descriptive statistics for the modeling data set used in the HCB equation for all red alder trees on the control plots with measured HCB.

Attribute	Mean	Minimum	Maximum	Standard Deviation
Tree Level attributes (N=35,371)				
HCB (ft.)	10.8	0.1	74.8	13.5
H (ft.)	27.1	4.6	99.7	18.9
CCFL (%)	99.8	0.0	559.1	108.7
D (in.)	2.3	0.2	15.9	3.0
Plot/Measurement Level Attribute (N=569)				
BA (ft. ² /ac.)	53.6	0.1	170.7	43.8
Plot Level Attribute (N=97)				
SI_C (ft.)	64.2	39.1	84.2	11.3

Table 4.2 Descriptive statistics for the modeling data set used in the HCB equation for just undamaged red alder trees on the control plots with measured HCB.

Attribute	Mean	Minimum	Maximum	Standard Deviation
Tree Level attributes (N=31,808)				
HCB (ft.)	11.1	0.3	74.8	13.7
H (ft.)	28.0	4.6	99.7	19.2
CCFL (%)	97.5	0.0	559.1	106.3
D (in.)	3.4	0.2	15.9	3.0
Plot/Measurement Level Attribute (N=569)				
BA (ft. ² /ac.)	53.6	0.1	170.7	43.8
Plot Level Attribute (N=97)				
SI _C (ft.)	64.2	39.1	84.2	11.3

4.2 Data Analysis and Results

The following weighted model form of Hann et al. (2011) was fit to both the all tree HCB data set and the undamaged tree HCB data set using nonlinear regression:

$$(HCB-1.7)/(H-1.7) = \{1 + \text{EXP}[b_0 + b_1 \cdot H + b_2 \cdot \text{CCFL} + b_3 \cdot \ln(\text{BA}) + b_4 \cdot (D/H) + b_5 \cdot (\text{SI}_C - 4.5)]\}^{-1} \quad (4.1)$$

The value of 1.7 in Equation (4.1) was the estimated HCB when BA approaches zero.

The resulting parameter estimates and the standard errors of the parameter estimates for Equation (4.1) fit to all 35,371 observations on the control plots with measured values of HCB are presented in Table 4.3.

Table 4.3. Parameter estimates and the standard errors of the parameter estimates for Equation (4.1) fit to all 35,371 observations on the control plots with measured values of HCB.

Parameter/Statistic	Estimate	Standard Error
b ₀	3.72868895	0.05936679
b ₁	-0.0161856525	0.0006276532
b ₂	-0.00207572032	0.00006400438
b ₃	-1.12363537	0.01530648
b ₄	6.13894263	0.1972781
b ₅	0.0267941365	0.00055038

The weighted mean squared error (MSE) was 0.01788202 and the weighted adjusted coefficient of determination (R_a^2) was 0.7608 for this fit to Equation (4.1).

The resulting parameter estimates and the standard errors of the parameter estimates for Equation (4.1) fit to the 31,808 undamaged trees on the control plots with measured values of HCB are presented in Table 4.4.

Table 4.4. Parameter estimates and the standard errors of the parameter estimates for Equation (4.1) fit to the 31,808 undamaged trees on the control plots with measured values of HCB.

Parameter/Statistic	Estimate	Standard Error
b ₀	3.61362558	0.06051048
b ₁	-0.0185967549	0.0006449976
b ₂	-0.00212746874	0.00006450116
b ₃	-1.0732265	0.015575
b ₄	5.94837586	0.1993464
b ₅	0.0276233607	0.0005594343

The weighted MSE was 0.01707272 and the weighted R_a^2 was 0.7677 for this fit to Equation (4.1).

HCB is predicted by the following equation for both data sets using parameters in Tables 4.3 or 4.4:

$$HCB = \{H-1.7\} \times \{1 + \text{EXP}[b_0 + b_1 \cdot H + b_2 \cdot \text{CCFL} + b_3 \cdot \ln(\text{BA}) + b_4 \cdot \ln(\text{D}/\text{H}) + b_5(\text{SI}_C-4.5)]\}^{-1} + 1.7 \quad (4.2)$$

4.3 Discussion

A comparison between the parameters from the original analysis (Hann et al. 2011) to the new parameters from this analysis was done by calculating the percent change that occurred between the new and original parameters for both the fit to all trees and the fit to just undamaged trees (Table 4.5).

Table 4.5. Percent change from the original parameters of Hann et al. (2011) across predictor variables, and associated parameters, of Equation (4.1) for both the fit to the all trees data set and to the undamaged trees data set.

Parameter	Predictor Variable	% Change from Original Parameters of Hann et al. (2011)	
		All Trees	Undamaged Trees
b ₀	Intercept	-6.5	-3.1
b ₁	H	-16.1	-13.7
b ₂	CCFL	+17.7	+28.4
b ₃	ln(BA)	+0.5	+0.8
b ₄	D/H	-13.9	-20.4
b ₅	SI-4.5	+11.5	+9.2

The parameter on H (i.e., b₁) displayed the largest negative % change between the new parameters in Tables 4.3 and 4.4 and the original parameters of Hann et al. (2011) for the all trees data set, while the parameter on D/H (i.e., b₄) displayed the largest negative % change for the undamaged trees data set. The second largest negative % change saw a reversal of these results with the parameter on D/H (i.e., b₄) displayed the next largest negative % for the all trees data set, while the parameter on H (i.e., b₁) displayed the next largest negative % change for the undamaged trees data set. Finally, the smallest negative % change occurred on the intercept (i.e., b₀) for both data sets.

The parameter on CCFL (i.e., b_2) displayed the largest positive % change between the new parameters in Tables 4.3 and 4.4 and the original parameters of Hann et al. (2011) for both data sets. The second largest positive % change in the parameters occurred for the parameter on the (SI-4.5) (i.e., b_5) variable for both data sets. Finally, the smallest positive % change occurred on the parameter for the $\ln(\text{BA})$ variable (i.e., b_3) for both data sets.

These changes are the result of adding additional modeling data for the control plots with larger values of H and CCFL, changes to SI from a new equation, and the elimination of untreated trees on the thinned plots from the modeling data set.

4.4 Literature Cited

Hann, D.W., A.A. Bluhm, and D.E. Hibbs. 2011. Development and evaluation of the tree-level equations and their combined stand-level behavior in the red alder plantation version of ORGANON. Oregon State University, Department of Forest Engineering, Resources, and Management, Corvallis, Oregon. Forest Biometrics Research Paper 1. 127p.

Hann, D.W. and M.L. Hanus. 2004. Evaluation of nonspatial approaches and equation forms used to predict tree crown recession. Canadian Journal of Forest Research 34:1993-2003.

5.0 Annual Diameter Increment Equation for Red Alder

The diameter increment (ΔD) equation used in RAP-ORGANON is a function of tree and plot attributes (Hann et al. 2011). The tree attributes include diameter at breast height (D), crown ratio (CR), and basal area per acre in larger trees (BAL). The plot attributes include site index corrected for planting density (SI_C) predicted by Equations (3.2) and (3.4) and basal area per acre (BA) for each growth period. In this revision, the parameters were predicted using a weighted nonlinear regression fit to periodic annual increment (PAI) data, where the periodic annual variables were determined for the central year of the growth period using linear interpolation. Therefore, the predictor variables used in this analysis were D, CR, BAL, BA at the start of the central, annual growth period, and SI_C of the plot. As with the development of previous ORGANON diameter growth rate equations, predicted ΔD was used as a weight for each observation.

5.1 Data

The data used in this reanalysis uses only the modeling data from the control plots, which differs from the original analysis which used both the modeling data from the control plots and the pretreatment measurements on the thinned plots. The pretreatment measurements on the thinned plots consisted exclusively of small trees and it was felt that this subsample of the population was adequately represented by the early measurements on the control plots. A description of the resulting ΔD modeling data set is found in Table 5.1.

Table 5.1 Descriptive statistics for the modeling data set used in the central PAI procedure to fit the annual ΔD equations for plantation grown red alder.

Attribute	Mean	Minimum	Maximum	Std. Deviation
Tree Level Attributes: N = 17,122				
ΔD (in.)	0.40	-0.54	1.93	0.29
D (in.)	5.4	0.2	16.7	3.1
CR	0.63	0.07	0.99	0.22
BAL (ft. ² /ac.)	29.22	0.00	160.0	31.88
Plot/Measurement Level Attribute: N = 484				
BA (ft. ² /ac.)	61.00	0.46	164.41	44.46
Plot Level Attribute: N = 97				
SI_C (ft.)	64.2	39.1	84.2	11.3

5.2 Data Analysis and Results

Hann et al. (2011) used the following general model form to characterize the ΔD of red alder growing in plantations:

$$\Delta D = e^{\sum_{i=0}^6 b_i X_i} + \varepsilon_{\Delta D} \quad (5.1)$$

Where,

$$\begin{aligned} X_0 &= 1.0 \\ X_1 &= \ln(D + 1.0) \\ X_2 &= D \\ X_3 &= \ln[(CR + 0.2)/1.2] \\ X_4 &= \ln(SI - 4.5) \\ X_5 &= BAL/\ln(D + K) \\ X_6 &= BA^{1/2} \end{aligned}$$

In the original analysis, K was set to 1.0. However, the usage of $D + 1.0$ is problematic in X_5 because the $\ln(D + 1.0)$ approaches zero as D approaches zero which results in X_5 approaching infinity. To avoid this problem, the value of K was changed to 2.8. This modification makes the $\ln(D + 2.8)$ term approach one as D approaches zero.

Equation (5.1) with the revised X_5 was fit to the ΔD modeling data using weighted nonlinear regression with a weight of the reciprocal of predicted ΔD . The resulting parameter estimates and their standard errors are found in Table 5.2

Table 5.2 Parameter estimates and their standard errors for the red alder plantation ΔD Equation (5.1).

Parameter	Estimate	Standard Error
b_0	-3.82892681	0.06407541
b_1	0.675980965	0.01949952
b_2	-0.146294494	0.003535964
b_3	1.33546052	0.02087329
b_4	0.828183586	0.0147564
b_5	-0.0222607698	0.0003780143
b_6	-0.0351133186	0.002202004

5.3 Discussion

Graphs of predictions from Equation (5.1) are found in Figures 5.1 to 5.4. Figure 5.1 displays the maximum predicted ΔD for an open-grown tree plotted across D for SI values of 40, 60, and 80-feet. For each SI value, an open-grown tree was simulated by setting CR to 1.0, BAL to 0.0, and BA to the tree's basal area per acre (i.e., $BA = 0.005454154 \times D^2$). Figure 5.2 exhibits the multiplicative modifier for adjusting the predicted maximum ΔD to the tree's measured CR. Figure 5.3 shows the multiplicative modifier for adjusting the predicted maximum ΔD to the tree's measured BAL and D . Figure 5.4 presents the multiplicative modifier for adjusting the predicted maximum ΔD to the plot's measured BA.

Figure 5.1 Maximum predicted ΔD for an open grown tree with a measured D and SI. An open grown tree was simulated by setting CR to 1.0, BAL to 0.0, and BA to the basal area per acre of the tree (i.e., $BA = 0.005454154 \times D^2$) for both the new parameters and the original parameters in Hann et al.(2011).

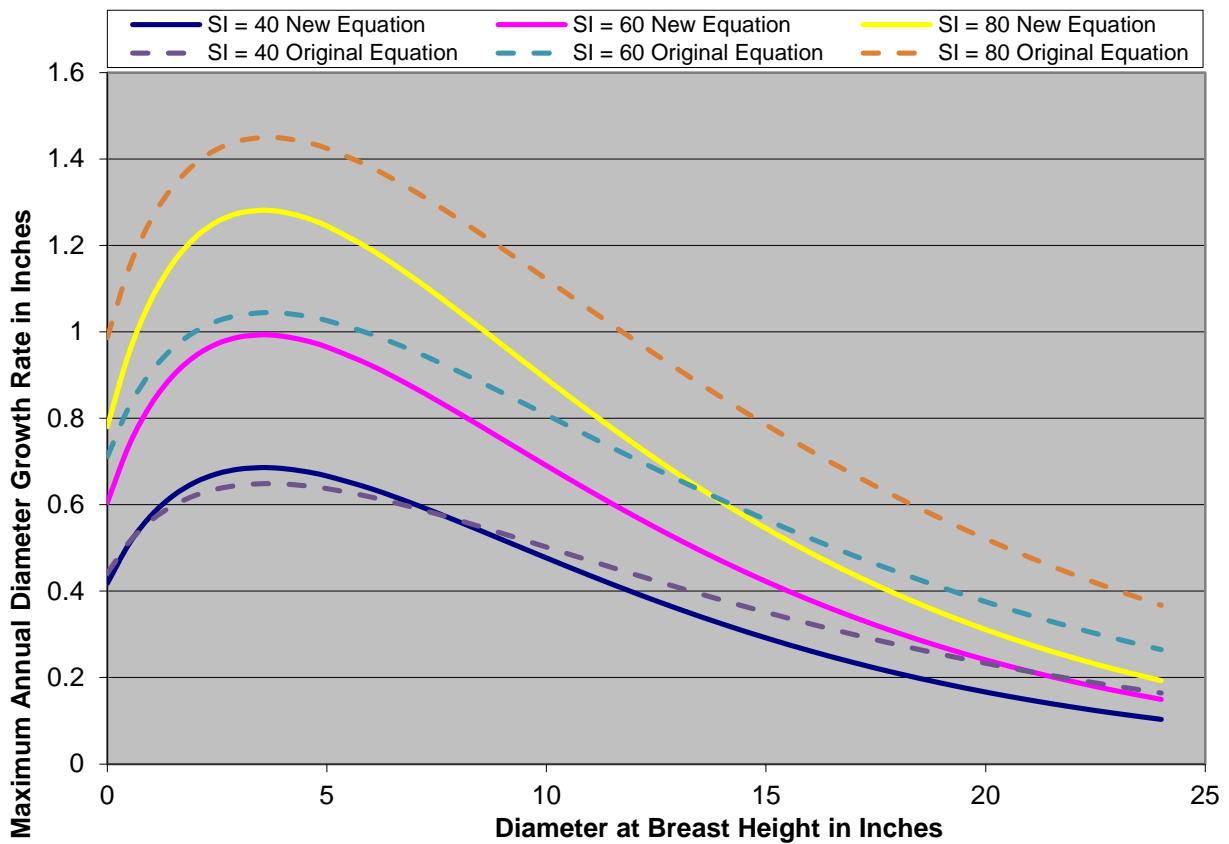


Figure 5.2 Multiplicative modifier for adjusting the predicted maximum ΔD to the measured crown ratio of the tree for both the new parameters and the original parameters in Hann et al. (2011).

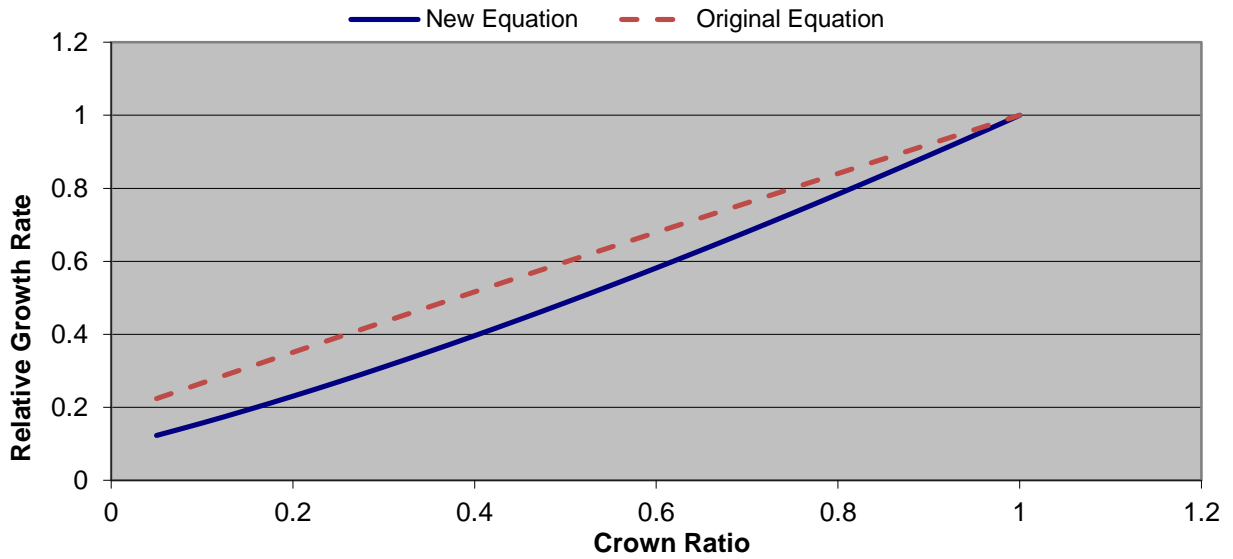


Figure 5.3 Multiplicative modifier for adjusting the predicted maximum ΔD to the measured basal area in larger diameter trees for the tree and diameter at breast height (D) for both the new parameters and the original parameters in Hann et al. (2011).

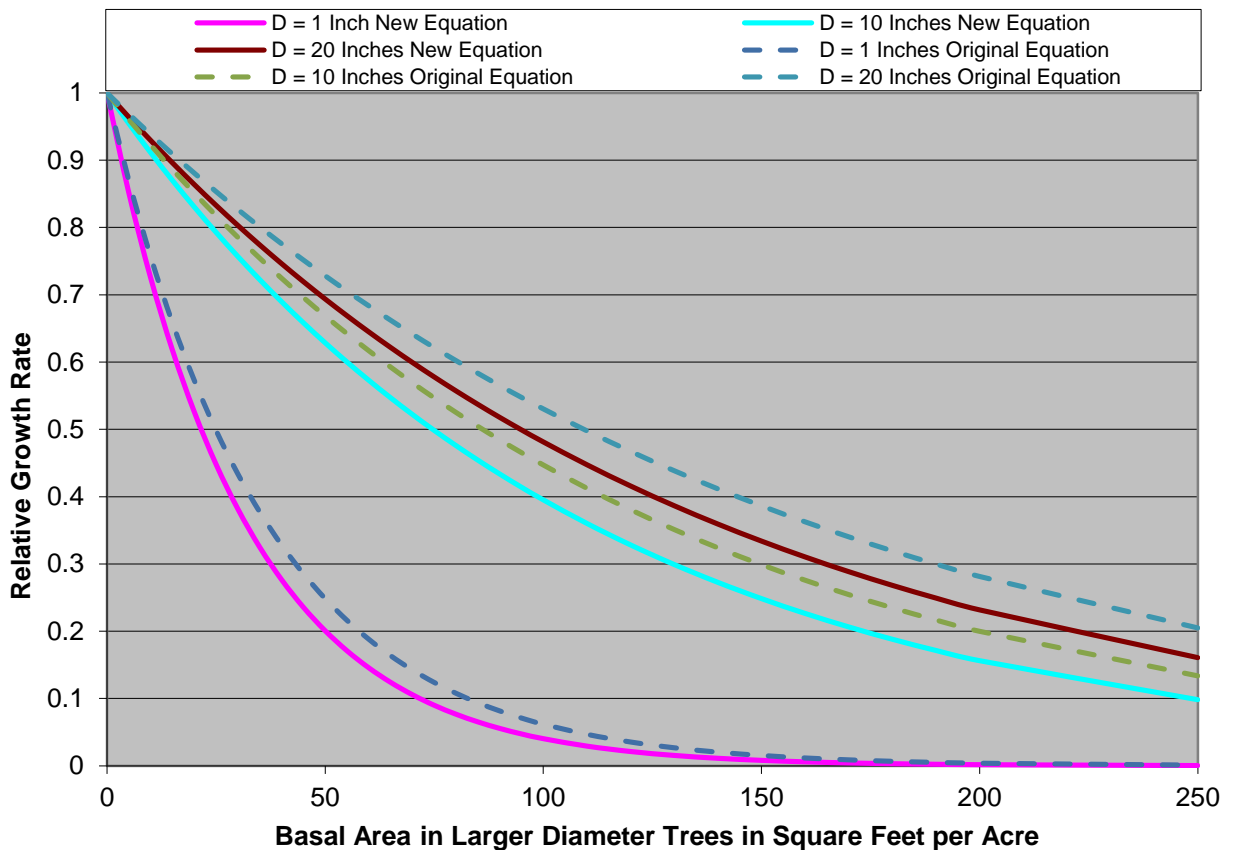
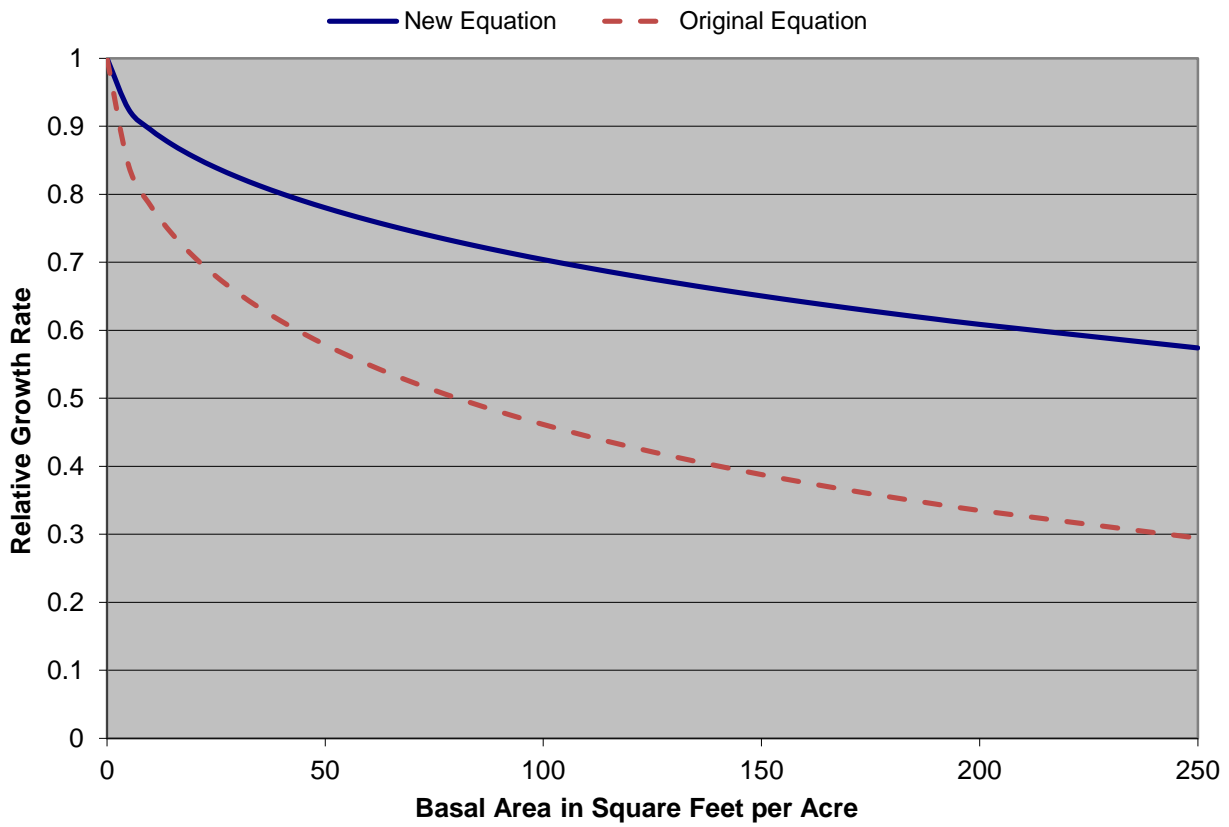


Figure 5.4 Multiplicative modifier for adjusting the predicted maximum ΔD to the measured BA of the plot for both the new parameters and the original parameters in Hann et al. (2011).



A comparison between the original set of parameters and the parameters in Table 5.1 for Equation (5.1) indicates that the largest differences are manifested via the differences in the parameter values that affect Figures 5.1, 5.2, and 5.4. The peak maximum predicted ΔD in Figure 5.1 is smaller for the new set of parameters and, more significantly, the values of ΔD decrease faster for the new set of parameters as DBH increases (Figure 5.1). Surprisingly, the change to 2.8 in X_5 has resulted in a greater impact of X_5 upon diameter increment than the usage of 1.0 (Figure 5.2). Finally, counter acting the decrease in maximum ΔD from the new parameters is the effect of BA upon maximum ΔD and, to a lesser extent, the effect of CR upon maximum ΔD . The b_6 parameter value on BA for the new fit of Equation (5.1) is approximately 1/3 the size as that found in the original equation. As a result, the negative impact of BA upon ΔD is substantially less for the new equation than the original equation.

5.4 Literature Cited

Hann, D.W., A.A. Bluhm, and D.E. Hibbs. 2011. Development and evaluation of the tree-level equations and their combined stand-level behavior in the red alder plantation version of ORGANON. Oregon State University, Department of Forest Engineering, Resources, and Management, Corvallis, Oregon. Forest Biometrics Research Paper 1. 127p.

6.0 Annual Height Increment Equation for Red Alder

The height growth rate (ΔH) equation used in RAP-ORGANON consists of a direct and indirect function of tree and plot attributes (Hann et al. 2011). The tree attributes include total height (H), crown ratio (CR), and crown closure at the tip of the tree (CCH). The plot attribute is site index uncorrected for planting density (SI_{UC}). The combination of H and SI_{UC} are used to determine the tree's growth effective age (GEA) at the start of the growth period (e.g., Hann and Ritchie 1988). H40 at the end of the annual growth period is then predicted for the combination of GEA+1 and SI_{UC} using Equation (3.3). Finally, potential height growth rate (POT ΔH) is calculated as H40 at the end of the growth period minus H at the start of the growth period. The resulting predicted POT ΔH is illustrated in Figure 3.2. The remaining attributes are used to predict a modifier equation that transforms POT ΔH to an estimate of a tree's ΔH .

6.1 Data

A periodic annual increment (PAI) data set was used to model the modifier equation for all control plots. The periodic annual predictor variables were determined for the central year of the growth period using linear interpolation. The particular predictor variables used in this analysis were H, CR, and CCH at the start of the central, annual growth period, POT ΔH for the growth period, and SI_{UC} of the plot. A description of the untreated plots employed to form the modeling data set is found in Table 6.1.

Table 6.1 Descriptive statistics for the central PAI modeling data set used to fit the annual ΔH equations for untreated plantation grown red alder.

Attribute	Mean	Minimum	Maximum	Std. Deviation
Tree Level Attributes: N = 17,122				
H (ft.)	39.65	5.27	100.22	19.20
ΔH (ft.)	2.69	-4.10	10.00	1.78
POT ΔH (ft.)	2.98	0.50	6.77	1.38
CR	0.627	0.065	0.988	0.221
CCH (%)	18.84	0.00	188.19	24.93
Plot Level Attribute: N = 97				
SI_{UC} (ft.)	60.2	33.5	82.3	10.9

6.2 Data Analysis and Results

The general model form from Hann et al. (2011) was used to predict ΔH of red alder growing in plantations. The equation is a product of POT ΔH and a modifier equation (MOD):

$$\Delta H = \text{POT}\Delta H \times \text{MOD} + \varepsilon_{\Delta H} \quad (6.1)$$

Where,

$$\text{MOD} = \Delta H / \text{POT}\Delta H$$

$$\text{MOD} = b_0(e^{b_1+b_2\text{CCH}} + (e^{b_3\text{CCH}^{0.5}} - e^{b_1+b_2\text{CCH}})e^{-(1.0-\text{CR})^2}e^{b_4\text{CCH}^{0.5}}) \quad (6.2)$$

Historically, the parameters and their standard errors were fit using Equation (6.2), which assumes that the variance about Equation (6.1) increases with POT ΔH^2 . However, examination of the variances from the unweighted fit of Equation (6.1) to the weighted fit from Equation (6.2) showed that the variance from Equation (6.1) resulted in residuals that better met the assumption of homogeneity. The resulting unweighted parameters and their standard errors are found in Table 6.2.

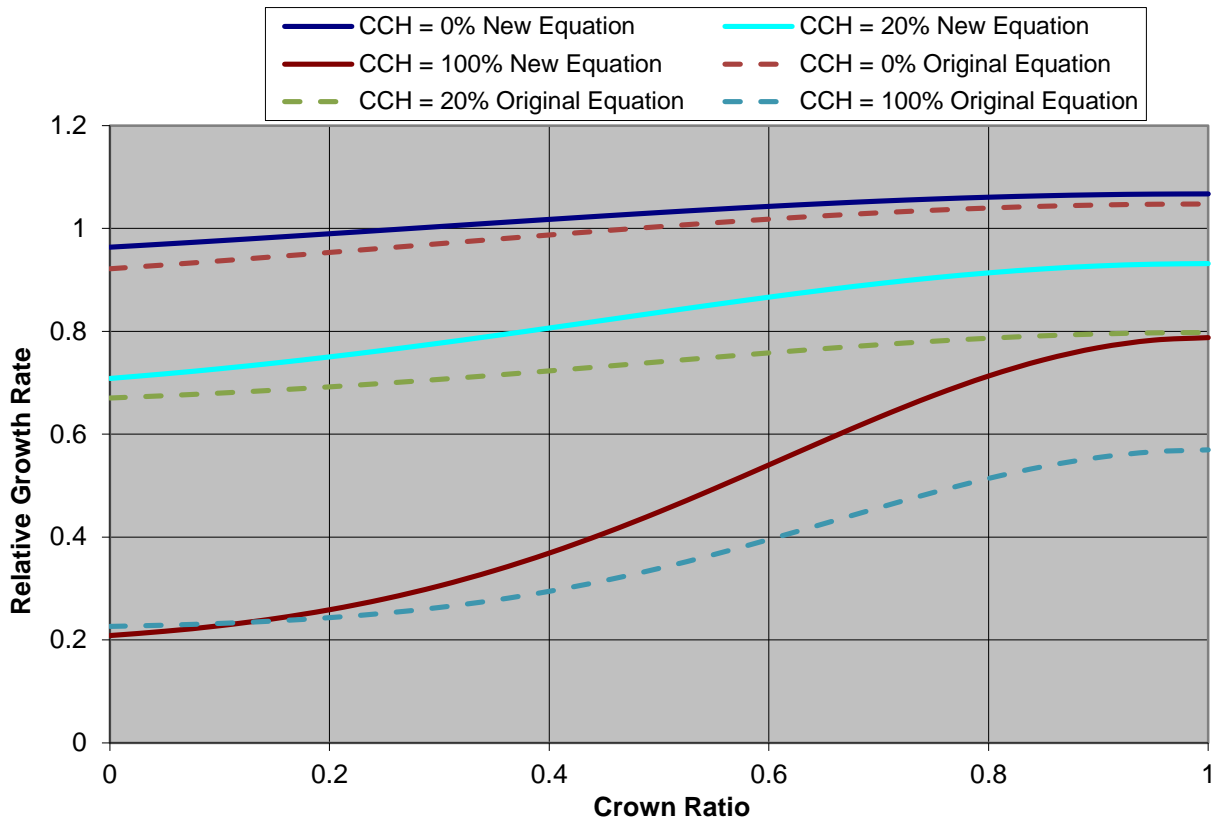
Table 6.2 Parameter estimates and their standard errors for the red alder plantation annual ΔH equation.

Parameter	Estimate	Standard Error
b_0	1.06726645	0.006544451
b_1	-0.166715197	0.04251862
b_2	-0.0157684667	0.001903119
b_3	-0.0303561419	0.002018234
b_4	0.119861797	0.01300643

6.3 Discussion

The new estimates of POT ΔH derived from Equation (3.3) predicts lower values than the equation of Weiskittel et al. (2009) for growth effective ages (GEA) below 6-years old and greater values for GEA of 6-years old or larger (Figure 3.2). A graph of the new modifier Equation (6.1) using the parameters in Table 6.2 versus the original parameters of Hann et al. (2011) can be found in Figure 6.1. Examination of Figure 6.1 shows that the new modifier equation will produce larger values of MOD than the original ΔH of Hann et al. (2011) across almost all of the range of CR and CCH. Combining the resulting predicted new POT ΔH derived from Equation (3.3) with the predicted new modifier Equation (6.1) would produce larger predicted values of ΔH across most of the range of GEA, SI_{UC}, CR, and CCH.

Figure 6.1 Graph of the multiplicative modifier Equation (6.1) plotted across CR for CCH values of 0, 20, and 100 percent for both the new and original equations.



6.4 Literature Cited

- Hann, D.W., A.A. Bluhm, and D.E. Hibbs. 2011. Development and evaluation of the tree-level equations and their combined stand-level behavior in the red alder plantation version of ORGANON. Oregon State University, Department of Forest Engineering, Resources, and Management, Corvallis, Oregon. Forest Biometrics Research Paper 1. 127p.
- Hann, D.W. and M.W. Ritchie. 1989. Height growth rate of Douglas-fir: a comparison of model forms. *Forest Science*: 34: 165-175.
- Weiskittel, A.R., D.W. Hann, D.E. Hibbs, T.Y. Lam, and A.A. Bluhm. 2009. Modeling top height growth of red alder plantations. *Forest Ecology and Management* 258: 323-331.

7.0 Maximum Size-Density Trajectory for Red Alder

The maximum size-density trajectory is used as an option in RAP-ORGANON to restrict stand development in a manner that keeps the stand on or below the maximum size-density trajectory as it develops over time (Hann and Wang 1990, Hann et al. 2003). In the original RAP-ORGANON analysis (Hann et al. 2011), the data sets used did not have trees and stands old enough to adequately develop a maximum size-density trajectory for red alder plantations. As a result, it was decided to use the trajectory developed by Puettmann et al. (1993) in the original RAP-ORGANON. The objective of this analysis was to determine if it is now possible to develop a maximum size-density trajectory for the HSC's red alder plantation data set, and, if the data is adequate, to develop a maximum size-density trajectory for red alder plantations.

7.1 Data

The HSC initially established 28 installations that included four blocks of control plots with initial targeted planting densities of 100, 230, 525, and 1200 trees per acre (the plots were denoted as plots 201, 202, 204, and 208, respectively). Substantial tree damage rendered five of the installations of no use for modeling the maximum size-density trajectory, and four additional plots on the remaining 23 installations were also excluded from the dataset due to damage. This resulted in 541 measurements on 88 plots available for modeling the maximum size-density trajectory.

The maximum size-density trajectory used in ORGANON incorporates three variables: (1) the quadratic mean diameter on the i^{th} plot for the j^{th} measurement since the start of mortality ($QMD_{i,j}$), (2) the number of trees per acre taller than 4.5-feet on the i^{th} plot for the j^{th} measurement since the start of mortality ($N_{i,j}$), and (3) the maximum number of trees per acre taller than 4.5-feet on the i^{th} plot for the measurement just prior to the start of mortality ($N_{i,0}$). The mean, standard deviation, minimum and maximum values of $QMD_{i,j}$ and $N_{i,j}$ for each control plot planting density and for the total data are found in Table 7.1. The mean, standard deviation, minimum and maximum values of $N_{0,j}$ for each control plot planting density and for the total data are found in Table 7.2. Modeling the maximum size-density trajectory is sensitive to the range in SDI values available, therefore the mean, standard deviation, minimum and maximum SDI values at the first and last measurements for each control plot planting density are found in Table 7.3 for both the four types of control plot planting density and for the total data set.

Table 7.1. Description of the measurement-level data used to model the maximum size-density trajectory, by type of plot and all plots.

Variable	Mean	Standard Deviation	Minimum	Maximum
Type 201 Plots, N = 74				
QMD _{i,j}	7.3	3.2	0.7	11.9
N _{i,j}	123.2	35.8	72.0	249.0
Type 202 Plots, N = 107				
QMD _{i,j}	6.3	2.6	0.5	9.5
N _{i,j}	275.8	45.6	150.0	375.0
Type 204 Plots, N = 119				
QMD _{i,j}	4.9	1.8	0.7	8.7
N _{i,j}	547.9	94.8	294.0	870.0
Type 208 Plots, N = 136				
QMD _{i,j}	1.7	0.6	1.0	3.0
N _{i,j}	974.0	246.9	402.0	1515.0
All Plots, N = 436				
QMD _{i,j}	5.0	2.3	0.5	11.9
N _{i,j}	542.0	357.3	72.0	1515.0

Table 7.2. Description of the plot-level data used to model the maximum size-density trajectory, by type of plot and all plots.

Variable	Mean	Standard Deviation	Minimum	Maximum
Type 201 Plots, N = 18				
N _{0,j}	130.5	42.1	76.0	249.0
Type 202 Plots, N = 23				
N _{0,j}	289.7	45.4	195.0	375.0
Type 204 Plots, N = 24				
N _{0,j}	596.5	90.7	390.0	870.0
Type 208 Plots, N = 25				
N _{0,j}	1130.4	207.6	570.0	1515.0
All Plots, N = 90				
N _{0,j}	573.2	403.2	76.0	1515.0

7.2 Data Analysis and Results

The following is the maximum size-density trajectory equation used in previous editions of ORGANON:

$$\ln(\text{QMD}_{i,j}) = a_1 - a_2 \cdot \ln(N_{i,j}) - (a_1 \cdot a_4) \cdot (N_{i,0}/N_{i,j})^{-a_3} \quad (7.1)$$

Puettmann et al. (1993) discovered that the a_2 parameter in Equation (7.1) for red alder differed significantly from the value of 0.62305 found by Reineke (1933). Therefore, the following model form was used to test whether this finding was still true for the current HSC modeling data set:

$$\ln(\text{QMD}_{i,j}) = a_1 - (0.62305 + a_5) \cdot \ln(N_{i,j}) - (a_1 \cdot a_4) \cdot (N_{i,0}/N_{i,j})^{-a_3} \quad (7.2)$$

A fit of Equation (7.2) to the entire HSC data found that a_5 was significantly different from zero. However, restricting the modeling data set to those type of plots most likely to be on the maximum size-density line (i.e., the 204 and 208 plots) resulted in a_5 not being significantly different from zero. Therefore, Reineke's (1933) value for a_2 (i.e., 0.62305) was judged to be appropriate for characterizing the maximum size-density trajectory of HSC red alder plantations.

The a_4 parameter of Equations (1) and (2) assume that the values of N_0 fall on a line that parallels the maximum size-density line (Smith and Hann 1984). Smith and Hann (1984) also developed the following formulation in order to test whether this line was indeed parallel to the maximum size-density line:

$$\ln(\text{QMD}_{i,j}) = a_1 - 0.62305 \cdot \ln(N_{i,j}) - (a_1 \cdot a_4 - 0.62305 \cdot a_6 \cdot N_{i,0}) \cdot (N_{i,0}/N_{i,j})^{-a_3} \quad (7.3)$$

A fit to the combined 204 and 208 plot types showed that a_6 was not significantly different from zero. Therefore, the values of N_0 do fall on a line that parallels the maximum size-density line.

The resulting model form from these two evaluations is:

$$\ln(\text{QMD}_{i,j}) = a_1 - 0.62305 \cdot \ln(N_{i,j}) - (a_1 \cdot a_4) \cdot (N_{i,0}/N_{i,j})^{-a_3} \quad (7.4)$$

Equation (7.4) provided biased predictions when the antilog of it is used to predict $\text{QMD}_{i,j}$ and to estimate maximum SDI (e.g., Flewelling and Pienaar, 1981). To avoid this problem, the final parameter estimates and their standard errors were estimated using the following model form:

$$\text{QMD}_{i,j} = \text{EXP}[a_1 - 0.62305 \cdot \ln(N_{i,j}) - (a_1 \cdot a_4) \cdot (N_{i,0}/N_{i,j})^{-a_3}] \quad (7.5)$$

This model form was then fit to the four types of plots in the HSC data set. The resulting parameter estimates of Equation (7.5), their standard errors, their t-statistics and the probabilities that the parameter estimates are zero (P-values) are found in Table 7.4.

Table 7.4. Parameter estimates, standard errors, t-statistics and probabilities that the parameter estimates are zero (P-values) for Equation (7.5) fit to the modeling data for the 201 plots, the 202 plots, the 204 plots, and the 208 plots.

Parameter	Estimate	Standard Error	T-Statistic	P-Value
201 Plots (Number of Observations = 74)				
a ₁	4.9262268	0.0	1.0E+030	0.00001
a ₃	1550.63763	0.0	1.0E+030	0.00001
a ₄	0.132926179	0.0	1.0E+030	0.00001
202 Plots (Number of Observations = 107)				
a ₁	5.35620819	0.04858003	110.26	0.00001
a ₃	114.034768	45.7043	2.50	0.01417
a ₄	0.132813042	0.02728812	4.87	0.00001
204 Plots (Number of Observations = 119)				
a ₁	5.66130652	0.02568016	220.45	0.00001
a ₃	68.7336818	19.85658	3.46	0.00075
a ₄	0.113496088	0.01373943	8.26	0.00001
Plots 208 (Number of Observations = 136)				
a ₁	5.79738631	0.01554907	372.84	0.00001
a ₃	21.9130313	2.951404	7.42	0.00001
a ₄	0.126847247	0.008616897	14.72	0.00001

Examination of Table 7.4 shows that a₁ increases, a₃ decreases and a₄ remains fairly stable as the N_{i,0} values associated with the four types of plots increases. Table 7.5 contains the adjusted coefficient of determination (R_a²) and the predicted maximum SDI calculated for those fits using the following equation:

$$\text{Maximum SDI} = \text{EXP}\{[a_1 - \ln(10)]/0.62305\} \quad (7.6)$$

Table 7.5. The adjusted coefficient of determination (R_a²) and the predicted maximum SDI resulting from fitting Equation (7.5) to the modeling data for the 201 plots, the 202 plots, the 204 plots, and the 208 plots.

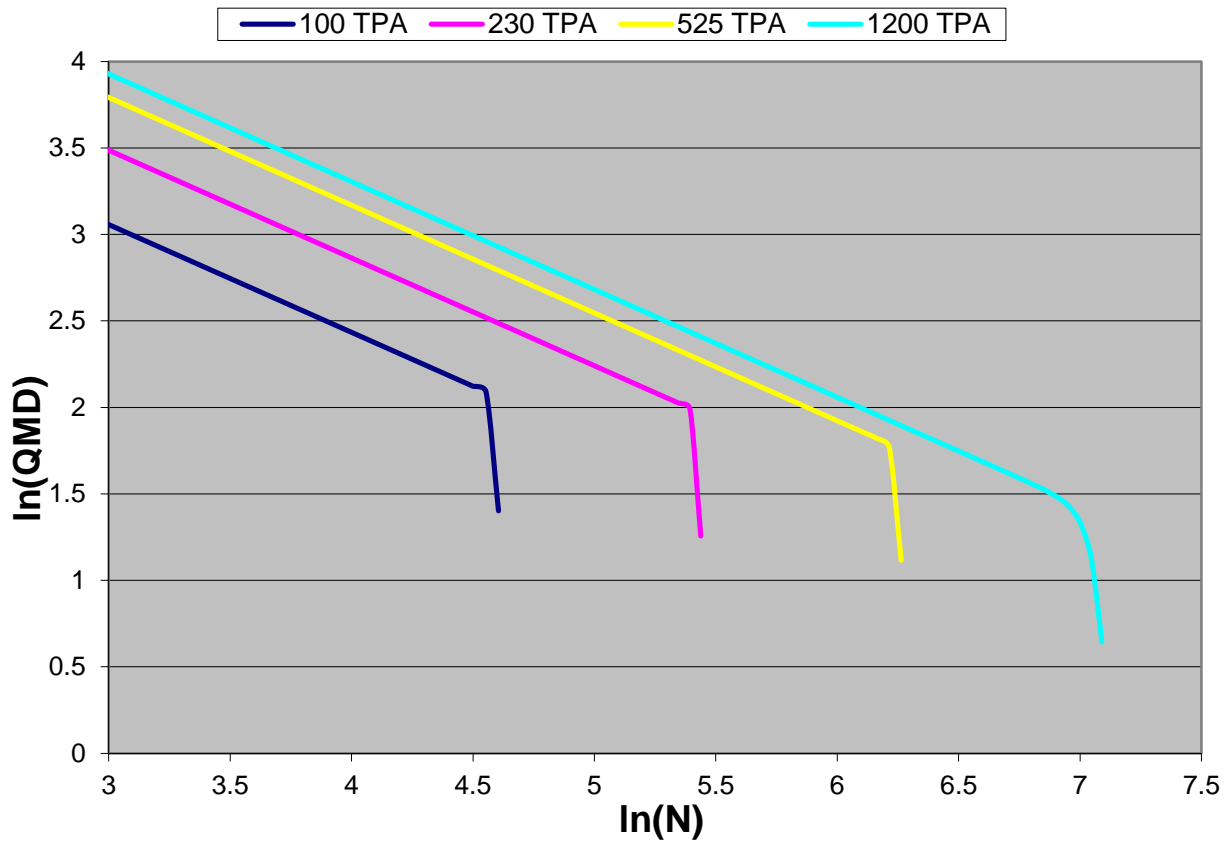
Type of Plot	R _a ²	Maximum SDI
201	0.0507	67.4
202	0.1584	134.4
204	0.5641	219.4
208	0.8619	272.9

The data in Table 7.5 shows that both the fit to the data, as represented by the value of R_a², and the size of the maximum SDI increase as the N_{i,0} values associated with the four types of plots increases.

A graph of the four size-density trajectories using the sets of parameters found in Table 7.4 and also using N_{i,0} values of 100, 230, 525, and 1,200 TPA, respectively, for the plot 201, plot 202, plot 204 and plot 208 trajectories are found in Figure 7.1. Of the four size-density trajectories in Figure 7.1, only the trajectory for the 208 plots (i.e., the 1,200 TPA plots) exhibits the expected smooth transition to the maximum size-density line. The abrupt change to the predicted

maximum size-density line of the other three plot types indicates that their data sets are still insufficient for estimating the parameters of Equation 7.5.

Figure 7.1. The predicted maximum size-density trajectories using $N_{i,0}$ values of 100, 230, 525, and 1,200 trees per acre that result from the application of Equation (7.5) and the four sets of parameters arising from the fits to the 201, 202, 204 and 208 plots found in Table 7.4.



Further insight can be obtained by graphing, in the natural log-log space, the basic modeling data for each type of plot (Figure 7.2).

Figure 7.2. The modeling data used to parameterize Equation 7.5 (i.e., the results found in Tables 7.4 and 7.5) to each of the four types of plots graphed in natural log-log space. The maximum size-density line from the fit of Equation 7.5 to the 208 plot data is included for comparison purposes.

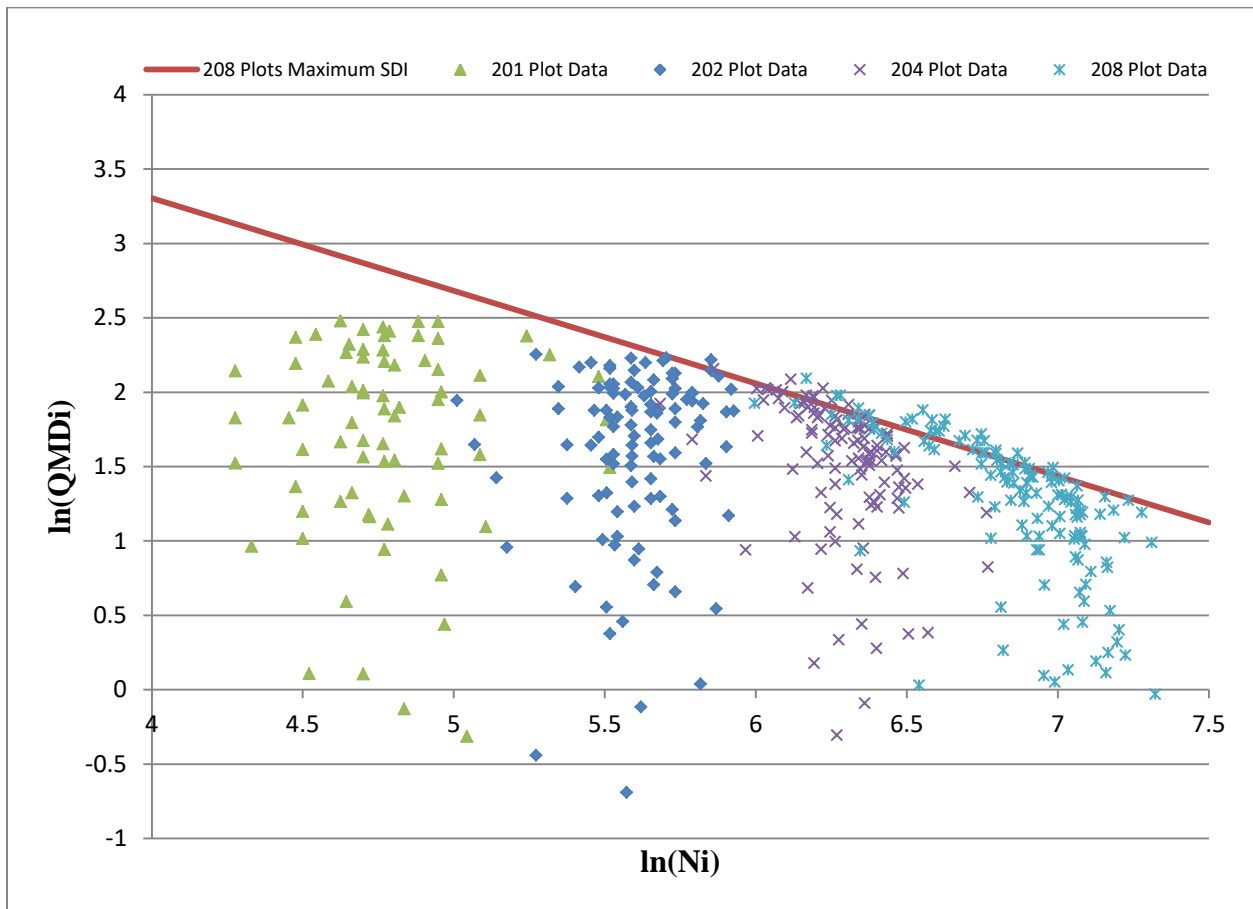
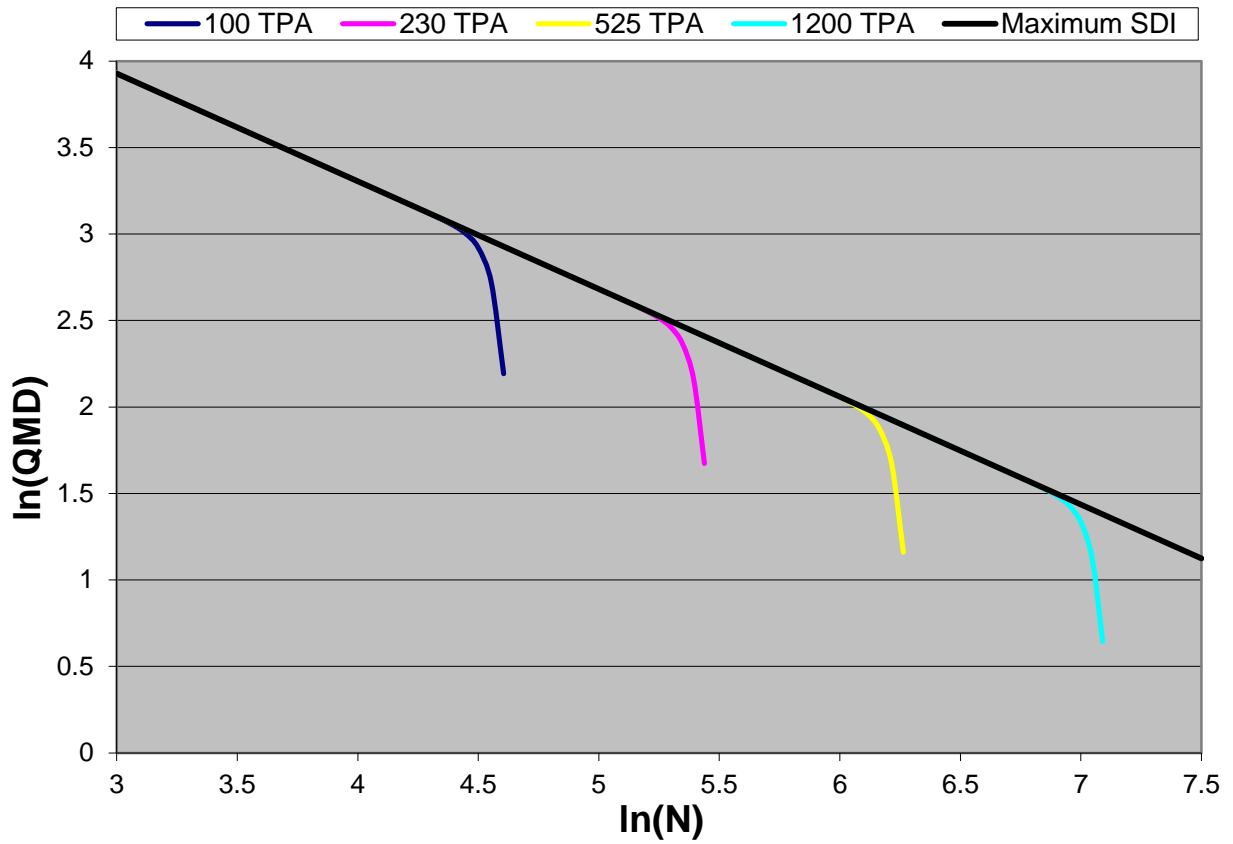


Figure 7.2 shows that a substantial part of the plot 208 data is clearly tracking along its maximum size-density line, while the plot 204 data has begun to fall on the maximum size-density line. The figure also shows that all of the plot 201 data have not reached the maximum size-density line, while only three observations of the plot 202 data has reached the maximum size-density line. Therefore, the plot 201 and plot 202 data are inadequate for estimating the parameters of Equation 7.5.

All of these results reveal that only the plot 208 data has developed enough for it to have reached the maximum size-density trajectory. The resulting maximum SDI of 272.9 for the plot 208 data is very close to the value of 273.2 found by Hibbs and Carlton (1989). A graph of the final maximum size-density trajectory can be found in Figure 7.3.

Figure 7.3. The predicted maximum size-density trajectories using $N_{i,0}$ values of 100, 230, 525, and 1,200 trees per acre that result from the application of Equation (7.5) and those parameters resulting from the fit to just the 208 plots found Table 7.4.



7.3 Discussion

The original RAP-ORGANON analysis was unable to estimate the maximum size-density trajectory because the data had not yet approached the maximum size-density line. As a result, the original RAP-ORGANON used the maximum size-density trajectory of Puettmann et al. (1993), which had a slope for the maximum line that differed significantly from the slope of Reineke (1933).

In the roughly 10 years since that work, the HSC 208 plots have developed enough so that it is now possible to estimate the maximum size-density trajectory using this restricted data set. Evaluation of the fit to the restricted data set found that the slope of the maximum line was not significantly different from the slope of Reineke (1933). Further evaluation found that the start of mortality occurred on a line that paralleled the maximum size-density line. Equation (7.5) was the result of fitting the maximum size-density trajectory to the restricted data set using the Reineke (1933) slope and the assumption that the start of mortality paralleled the maximum size density line. The remaining three parameters were different from zero at a high level of significance (Table 7.4). Equation (7.5) explained 86.19 percent of the variation in $QMD_{i,j}$ beyond what is explained by a mean value of $QMD_{i,j}$.

The most notable feature of the size density trajectory depicted by Equation (7.5) and its parameters in Table 7.3 is the large value of a_3 (i.e., 21.9130313). Previous fits of either Equation (7.1) or Equation (7.4) found the following values for a_3 : 3.92 for red alder stands (Puettmann et al. 1993) and 14.40 for Douglas-fir (*Pseudotsuga menziesii*) plantations (Hann et al. 2003).

Counteracting the large size of a_3 is the large size of a_4 . As examples, a_4 was 0.07 for red alder stands (Puettmann et al. 1993) and 0.05 for Douglas-fir plantations (Hann et al. 2003). The parameter a_4 is related to the value of relative density at which competition mortality (RDCM) is predicted to start in the stand by the following equation:

$$RDCM = EXP(-a_4 \times a_1 / a_2) \quad (7.7)$$

In previous studies, RDCM calculated from Equation (7.7) was 0.52 for red alder stands (Puettmann et al. 1993) and 0.60 for Douglas-fir plantations (Hann et al. 2003). In this study, RDMC was 0.31. This small value indicates that competition induced mortality starts earlier in stand development. The fact that a_3 is relatively large and a_4 is also relative small for the current red alder study produces the effect that early mortality, when relative densities of the stand starts to exceed RDCM, will have low predicted rates of mortality in that phase of stand development, and the mortality rate will only become substantial when the relative density of the stand gets large. Stands with relative densities below RDCM will exhibit no competition induced mortality, resulting in a vertical component of the size-density trajectory below that relative density. Therefore, the early, low mortality rate of red alder (with a nearly vertical line) will exhibit similar size-density trajectories to those species with later, larger mortality rate as long as a_3 for those other species is smaller than that found for red alder in this study.

7.4 Literature Cited

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8.0 Annual Tree-Level Survival Rate Equation for Red Alder

The survival rate equation predicts the annual probability of survival (PS) for a specified sample tree. This equation is then used to predict the mortality rate (PM) via the relationship of $PM = (1.0 - PS)$. PM is then used in RAP-ORGANON to reduce each sample tree's expansion factor (EF) over time. The variable sizes of the growth periods lengths (LEN) in the modeling data sets required that the parameters be estimated using the following formulation (Flewelling and Monserud 2002) in order to standardize them to annual predictions:

$$PS = \left[1.0 + e^Z \right]^{-LEN} \quad (8.1)$$

Where,

Z = The logistic link function (Flewelling and Monserud 2002)

Once the parameters of the variables in Z have been determined in Equation (8.1), then PM can be predicted by:

$$PM = \left[1.0 + e^{-Z} \right]^{-LEN} \quad (8.2)$$

The need to use Equation (8.1) to estimate the parameters in the Z-function is due to the fact that survival is a Markov process which allows the usage of LEN as an exponential in Equation (8.1), while mortality is not a Markov process. In other words, a tree can die only once in a given growth period but a tree can survive for multiple growth periods (Flewelling and Monserud 2002). It should be noted that the only difference between Equation (8.1) and Equation (8.2) is that Equation (8.1) has a positive sign on the Z-function and Equation (8.2) has a negative sign. In this formulation, the parameters estimated using Equation (8.1) can be used in Equation (8.2) without any changes.

The previous RAP-ORGANON PS equation used both tree and plot attributes as predictor variables. The tree attributes used in the prior analysis included:

1. A dichotomous Survival variable (SURV) indicating whether the tree survived over the growth period (SURV = 1 if tree survived over the growth period and SURV = 0 if tree died within the growth period).
2. Diameter at breast height (D).
3. Crown ratio (CR = $1.0 - HCB/H$, in which HCB = height to crown base and H = tree height).
4. Predicted crown ratio using the original procedure ($PCR_1 = 1.0 - PHCB_1/PH_1$, in which $PHCB_1$ = original predicted HCB₁ and PH_1 = original predicted H) using Equations (2.1) and (4.1) and the parameters found in Tables 2.2 and 4.3 of Hann et al. (2011). In the original analysis, both Equations (2.1) and (4.1) were calibrated to the measured values of H and HCB on each plot/measurement combination in the modeling data set.
5. A dichotomous CR variable indicating whether the tree had a measured CR ($I_{CR} = 1$ if CR is measured, = 0 if not).
6. Basal area per acre in larger diameter trees (BAL). The plot/measurement combination attribute used in the previous analysis was basal area per acre (BA).

The plot attributes used in the previous analysis included:

1. Site index [this study uses red alder site index corrected for planting density, SI_C , using Equations (3.2) and (3.4), in combination]
2. Length of growth period in years (LEN).
3. The expansion factor (EF) of all sample trees on a plot.
4. Basal area per acre (BA).

The method used previously for calculating PCR_1 assumed that ORGANON would be used to dub PH_1 and $PHCB_1$. However, many users of ORGANON preferred to use their own dubbing routines. These alternative dubbing procedures can introduce bias to predicted PS if the alternative dubbing procedures for the estimation of PCR differs from those used to create PS_1 for the modeling data set, effectively introducing measurement error to the prediction process.

Another problem with the original approach of using CR when measured and PCR_1 when CR isn't measured also arises from the fact that input data sets used to run ORGANON often do not differentiate between the two. Therefore, the improvement in prediction of PS_1 found when the model using both CR and PCR_1 was parameterized cannot be realized in application.

The following method for calculating PCR (i.e., PCR_2) was developed in this analysis to avoid these problems. This process consisted of calculating HCB_2 using Equation (4.1) and the parameters in Table 4.3 and calculating H_2 using Equations (2.2) and the parameters in Table 2.3 for all trees on the plot/measurement combinations (Equation 2.2 has been found to explain more variation than Equation 2.1 when applied to plantations). Furthermore, the estimates of HCB_2 and H_2 were not calibrated to measured values on the plot/measurement combination. Finally, the resulting values of PCR_2 are used for all trees on the plot/measurement combinations, thus eliminating the need to keep track of which trees have values of CR versus PCR. A final check of PCR_2 was done by fitting the following equation to the 35,394 trees in the dataset with measured values of CR:

$$CR = a_0 + a_1 \times PCR_2 \quad (8.3)$$

An initial fit of Equation (8.3) to the data found that a_0 was not significantly different from zero for $P = 0.01$. Equation (8.3) was then refit fixing a_0 to zero. The resulting value of a_1 was 0.995300182, which was statistically significant from one but the difference was judged by the authors to be of no practical difference from one. The adjusted coefficient of determination (R_a) was 0.8369.

The objective of this analysis was to develop a new PS/PM equation that can replace the original one developed by Hann et al. (2011) for RAP-ORGANON. To achieve this objective, the following variables (defined above) were calculated:

1. SURV
2. D
3. BAL
4. PCR_2
5. BA
6. LEN
7. SI_C

8. EF

8.1 Data

The modeling data set was created from the control plot data. The attributes used to create the predictor variables were those measured at the start of each variable length growth period. Growth periods longer than 11-years were eliminated from the modeling data set. A description of the calculated predictor variables used in the modeling data set is found in Table 8.1.

Table 8.1 Descriptive statistics for the data set used to fit and evaluate the annual PM equations for plantation grown red alder.

Attribute	Mean	Minimum	Maximum	Std. Deviation
Tree Attributes: N = 100,082				
D (in.)	3.752057	0.09	15.87	2.385799
BAL (ft. ² /ac.)	36.77775	0.00	170.497	34.02759
PCR ₂	0.5837029	0.108117	0.99613	0.222924
Plot/Measurement Attributes: N = 569				
BA (ft. ² /ac.)	53.64789	0.071	170.726	43.82147
LEN (years)	3.690685	1	11	1.422629
Plot Attributes: N = 97				
SI _C (ft.)	64.8	39.1	84.2	11.3
EF (#/Ac.)	2.819485	2.00	4.00	0.4197702

8.2 Data Analysis and Results

Because the sample trees have unequal sampling probabilities caused by the use of different plot sizes in the modeling data sets, each observation in Equation (8.1) was weighted by EF. Eight alternative Z-functions were evaluated to determine which best characterized PM:

$$Z=b_0 + b_1D + b_2BAL + b_3SI_C + b_4BA \quad (Z.1)$$

$$Z=b_0 + b_1D + b_2PCR_2 + b_3BAL + b_4SI_C \quad (Z.2)$$

$$Z=b_0 + b_1D^{1/2} + b_2BAL + b_3SI_C + b_4BA \quad (Z.3)$$

$$Z=b_0 + b_1D^{1/2} + b_2PCR_2 + b_3BAL + b_4SI_C \quad (Z.4)$$

$$Z=b_0 + b_1D^2 + b_2BAL + b_3SI_C + b_4BA \quad (Z.5)$$

$$Z=b_0 + b_1D^2 + b_2PCR_2 + b_3BAL + b_4SI_C \quad (Z.6)$$

$$Z=b_0 + b_1D + b_2D^2 + b_3BAL + b_4SI_C + b_5BA \quad (Z.7)$$

$$Z=b_0 + b_1D + b_2D^2 + b_3PCR_2 + b_4BAL + b_5SI_C \quad (Z.8)$$

There are four sets of two basic Z-Functions. For example Z-function (Z.1) does not use either CR or PCR₂ but, instead, it includes BA. Z-function (Z.2) uses PCR₂ but not BA and it has been commonly used (with different alternative formulations of CR and PCR) in various versions of ORGANON, including the original edition of RAP-ORGANON. What differs between the four sets is the form of D used in the Z-Function. The first two Z-Functions use D, the second set D^{1/2}, the third set D², and the final set D and D².

The inclusion of both D and D² allows the resulting PM equation to first decrease with an increase in D and then to increase for large, older trees. The decline in mortality with increasing D is consistent when trees and stands are relatively youthful, but, as a tree matures into old age, the probability of mortality should begin to increase with age or size (Buchman et al. 1983, Harcombe 1987, Monserud and Sterba 1999), thereby producing a U-shaped mortality curve. To mimic this behavior in their older stands, Hann and Hanus (2001) added D and D² to their PS/PM Z-function.

The regression coefficients of the eight Z-Functions inserted into Equation (8.2) were estimated using the maximum likelihood estimation procedures of SAS (e.g., Hann and Hanus 2001, Hann et al. 2006). Flewelling and Monserud (2002) suggested that the predictor variables used in a model annualizing the prediction of mortality rate should be calculated at the center of the growth period. One of the data sets they used in their evaluations was the control plot data for unthinned Stand Management Cooperative (SMC) plots. They reported that using predictor variables at the center of the growth period fit for this data set performed worse than the fit that used predictor variables at the start of the variable length growth period data. When I examined their parameters I found more change in the parameters between those two fits than between the other fitting methods they examined. Furthermore, all of the mortality trees in the HSC data set did not have measurements of D, H, or HCB at the end of their growth periods, making the calculation of predictor variables at the center of the growth period for those trees problematic. Therefore, it was decided to use predictor variables measured at the start of each measurement period when fitting Equation (8.2).

The resulting fits were evaluated using a relative χ^2 goodness of fit statistic. The first step in determining the relative χ^2 goodness of fit statistic was to calculate the standard χ^2 goodness of fit statistic for predictions of the number of trees surviving per year from each of the eight equations across classes of the following four tree and stand attributes: D, BAL, SI_C, and BA. Predicted number of trees surviving per year was calculated by inserting Z-Functions (Z.1) to (Z.8) into Equation (8.1) and multiplying the resulting PS by EF/PLEN. In addition, the standard Chi-square value was also calculated across classes of the predicted PS for each of the eight models of interest. The resulting standard χ^2 goodness of fit statistics are found in Table 8.2.

Table 8.2. Predicted PS Chi-Square statistics across classes of D, BA, BAL, SI_C for eight alternative Z-Functions.

Z-Function	D	BA	BAL	SI _C
Z.1	24.36	23.42	29.72	20.82
Z.2	25.97	23.28	28.02	21.10
Z.3	42.20	42.99	45.90	27.00
Z.4	43.86	39.62	40.53	27.10
Z.5	30.95	17.31	23.31	15.13
Z.6	32.68	18.00	20.09	15.87
Z.7	29.00	37.89	43.04	25.98
Z.8	31.47	35.02	39.40	26.15

The comparison of the calculated χ^2 goodness of fit statistics in Table 8.2 to expected χ^2 values from the χ^2 table indicated that Z-functions (Z.1), (Z.2) (Z.5), and (Z.6) produced predicted values of PS that demonstrated no lack of fit across all four predictor variables at P=0.05 and P=0.01. For Z-function (Z.3), the statistics in Table 8.2 indicated lack of fit for all four variables at P=0.01, while Z-function (Z.4) showed lack of fit across D^{1/2} and SI_C at P=0.01. For Z-function (Z.7), the statistics in Table 8.2 indicated lack of fit for SI_C and BAL at P=0.01, while Z-function (Z.8) showed lack of fit across SI_C at P=0.01. Based upon these results, Z-functions (Z.1), (Z.2) (Z.5), and (Z.6) were retained for further evaluation.

The decision on whether to use D in Z-functions (Z.1) and (Z.2), or D² in Z-functions (Z.5), and (Z.6) was made based upon the size of calculated χ^2 goodness of fit statistics in Table 8.2 for the predictor variable constructed using D. Examination of Table 8.2 shows that both Z-functions (Z.1) and (Z.2) had smaller values for the χ^2 goodness of fit statistics associated with using D instead of D². Therefore, Z-functions (Z.1) and (Z.2) were chosen for further analysis. Their parameter estimates and associate standard errors are found in Table 8.3.

Table 8.3. Parameter estimates and their standard errors for Z-Functions (Z.1) and (Z.2).

Parameter	Estimate	Standard Error
Z-Function (Z.1)		
b ₀	-4.409350098	0.048950804
b ₁	-0.840245936	0.011330728
b ₂	0.03142376506	0.00071422845
b ₃	0.01228331619	0.00083453287
b ₄	0.01612003767	0.00085918136
Z-Function (Z.2)		
b ₀	-2.637550602	0.067732869
b ₁	-0.734393478	0.007048828
b ₂	-3.656630241	0.10648708
b ₃	0.02570721811	0.0005831662
b ₄	0.0297357805	0.00101031849

Based on this primary evaluation, it was decided to further evaluate how well Z-Functions (Z.1) or (Z.2) inserted into Equation (8.1) would predict the change in TPA, BA, quadratic mean diameter (QMD), stand density index (SDI), average diameter of the 40 largest diameter trees per acre (D40), average height of the 40 largest diameter trees per acre (H40), total stem cubic foot volume per acre (TSCFV), and the mean crown ratio (MCR) over time when used with HCB Equation (4.1) that was fit to just the undamaged trees to predict Δ HCB, Δ D Equation (5.1), and Δ H Equation (6.1). The evaluation was done using tree lists from those installations in the modeling data set with the smallest, midrange, and largest values of SI (40.1-feet, 63.5-feet, and 82.3-feet, respectively), and then making projections of TPA, BA, QMD, SDI, D40, H40, TSCFV, and MCR from age four to age 50 using both alternative Z-Functions. These eight variables were calculated using all living trees at the start of the first annual growth period and then at the end of each of the 50 subsequent annual growth periods for the four targeted planting densities installed on each installation (e.g. 100, 230, 525, and 1200 trees per acre). The runs were made without using the ORGANON option of limiting QMD to be no higher than the maximum size-density trajectory defined by Equation (7.5) and without using the tripling option. This analysis resulted in a total of 32 graphs for evaluation.

The expected biological behaviors of these stand-level attributes over stand age are discussed in Weiskittel et al. (2011). This evaluation examined the reasonableness of the shape of the relationships and not necessarily the reasonableness of the quantitative values of the predictions, though this latter validation process can also be useful. For the sake of parsimony, only the graphs of those stand attributes judged to be unreasonable in behavior are illustrated below.

The result of this evaluation found questionable behavior for only the graph of SDI across age for the installation with the highest value of SI and the plot with the highest PDEN value in the evaluation data set. This questionable behavior was found for both Z-Function (Z-1) and Z-Function (Z-2). Figure 8.1 shows the SDI relationship for the installation with a SI value of 82.3 feet using Z-Function (Z-1). Figure 8.2 shows the SDI relationship for the installation with a SI value of 82.3 feet using Z-Function (Z-2).

Figure 8.1. SDI predicted using Z-Function (Z.1) and with the limit on maximum size-density turned off, for four plots with different initial target planting densities (PDEN) plotted over stand age from seed for the installation with a SI of 82.3 feet.

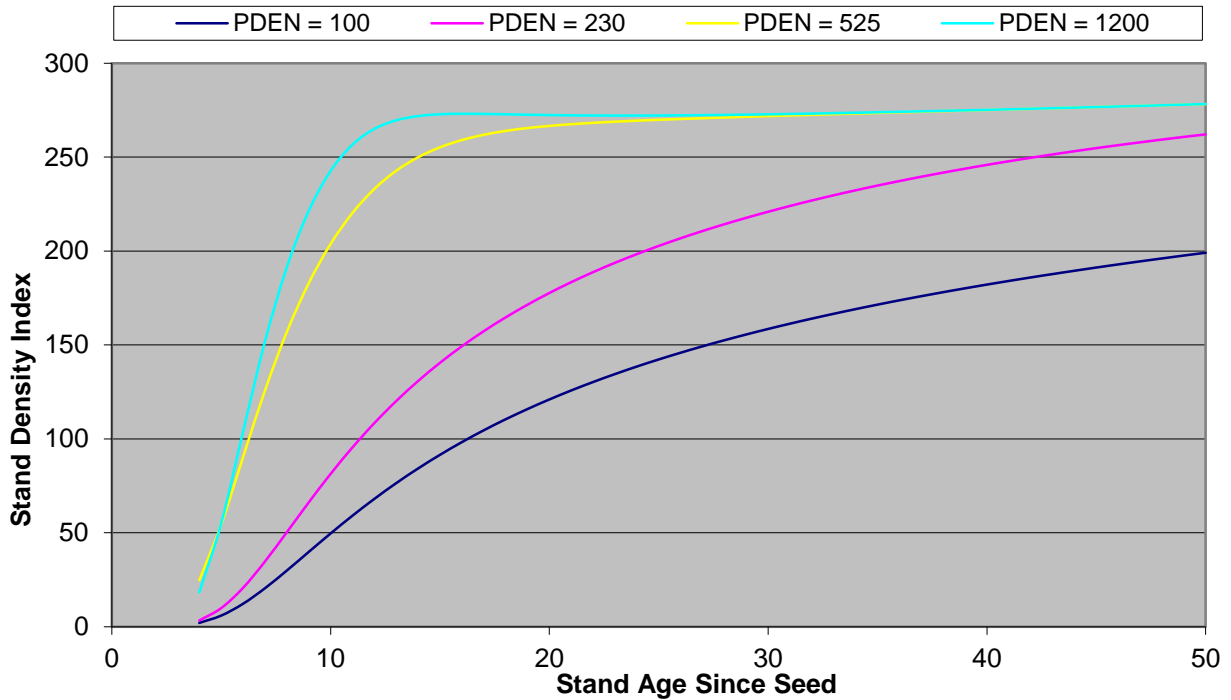
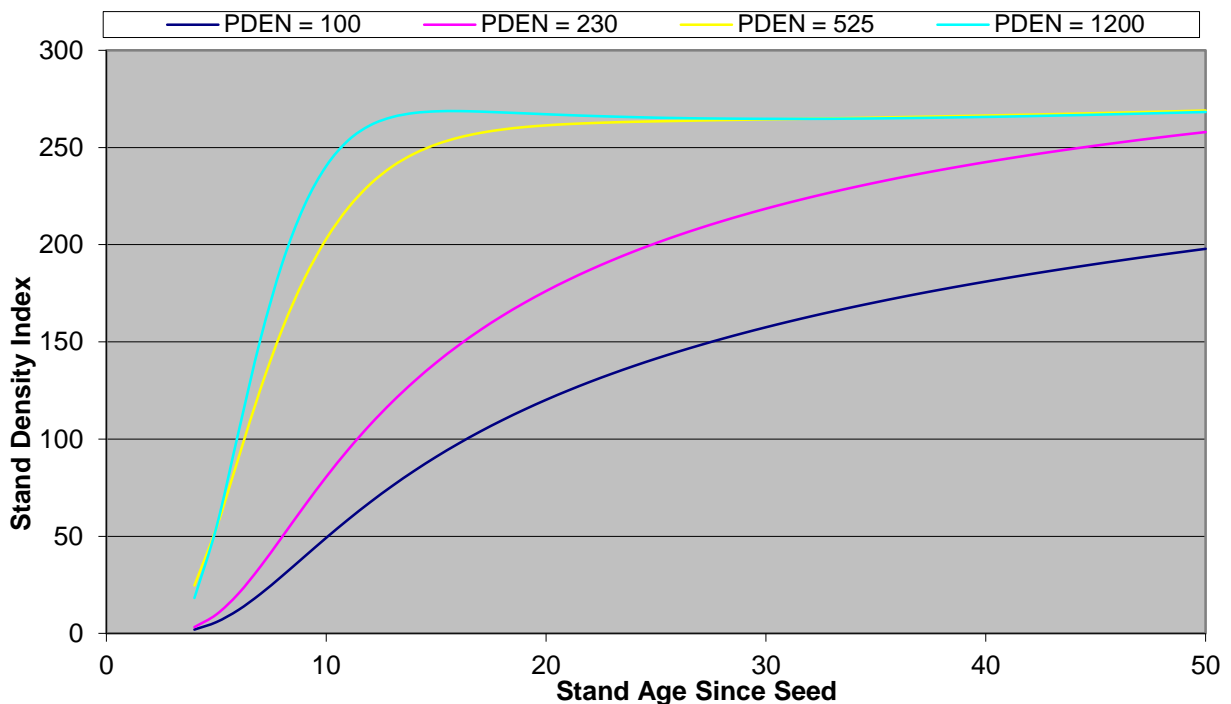


Figure 8.2. SDI predicted using Z-Function (Z.2) and with the limit on maximum size-density turned off, for four plots with different initial target planting densities (PDEN) plotted over stand age from seed for the installation with a SI of 82.3 feet.



Both figures Figure 8.1 and 8.2 shows a dip in predicted SDI for the highest value of PDEN, which does not meet expected behavior. The size of dip for the projection using Z-Function (Z.1) was 0.35% and occurs between ages 16 and 33 years. The size of the dip for the projection using Z-Function (Z.2) was 1.48% and starts at age 16 but has not recovered by end of the projection at age 50 years. Furthermore, the size of the projected SDI values at age 50 years was 278.3 for the projection using Z-Function (Z.1) and 268.3 for the projection using Z-Function (Z.2), which are 2.00% greater than and 1.69% less than the maximum SDI value (e.g., 272.9) predicted by the maximum size-density trajectory Equation (7.5) that was fitted to the 208 type plots (1,200 trees per acre plots). It must be remembered that these projections were made without using the ORGANON option of constraining predicted SDI to be no larger than 272.9. These close agreements indicate that the four dynamic equations in RAP-ORGANON are working well together when making stand level projections.

8.3 Discussion

A comparison of Z-Function (Z.1) to Z-Function (Z.2) indicates that the two provide very similar predictions of stand development out to age 50. There are two elements that lead me to favor Z-Function (Z.1) over Z-Function (Z.2). First, the usage of BA instead of PCR_2 , which uses two prediction equations to calculate, is more straight-forward to calculate and understand as a predictor variable, and its implementation would require fewer changes to the ORGANON FORTRAN code for implementing the new PS and associated PM equation. Second, the dip in predicted SDI for the 1200 TPA plot on the installation with the largest value of SI is smaller and of more limited duration for Z-Function (Z.1) than Z-Function (Z.2). My experience with modeling PS/PM using the southwest Oregon modeling data set, which measured H and HCB on every tree, showed that CR is an important tree attribute for characterizing PS/PM. It is unfortunate that the HSC chose to subsample both H and HCB.

Due to the difference in the predictor variables between the previous Z-Function in Hann et al. (2011) the new Z-Function (Z.1), it was not possible to create graphs in which both equations are presented for comparison purposes. Therefore, Figures 8.3 through 8.7 are presented for only the new Z-Function (Z.1). Figure 8.3 shows annual predicted PM values for a simulated open grown tree, in which BAL is set to zero and BA is set to one, plotted across D and for SI of 30, 60, and 90 feet. Figures 8.4 through 8.6 shows annual predicted PM plotted across relative BAL (defined as BAL/BA) for BA values of 20, 60, 100 and 140 ft² when SI has been fixed to 60 feet and D fixed to the three values of 1.0, 6.0, and 11.0 inches. It should be noted that the scale of the Y-axis changes between Figures 8.4, 8.5, and 8.6.

Figure 8.3. Predicted annual probability of mortality (PM) for an open grown tree (i.e., BA = 1.0 and BAL = 0.0) plotted across D and for SI of 30, 60, and 90 feet.

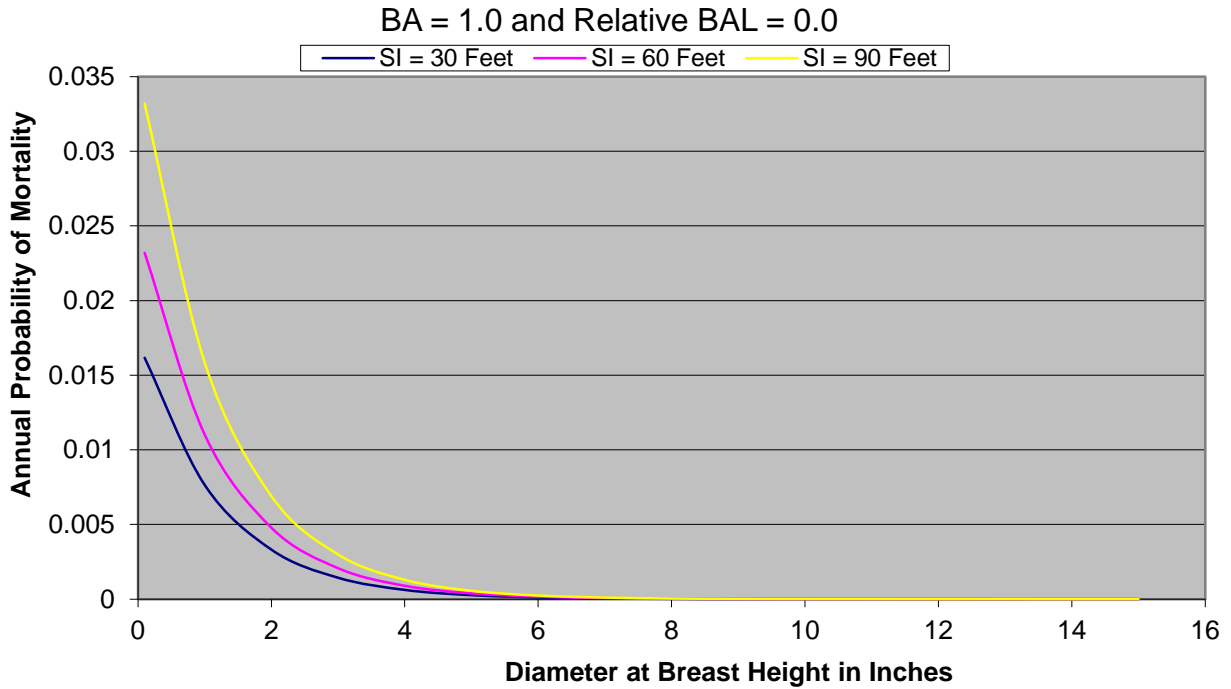


Figure 8.4 Predicted annual probability of mortality (PM) plotted across relative BAL for BA values of 20, 60, 100, 140 ft² per acre and with D = 1.0 inches and SI = 60 feet equation.

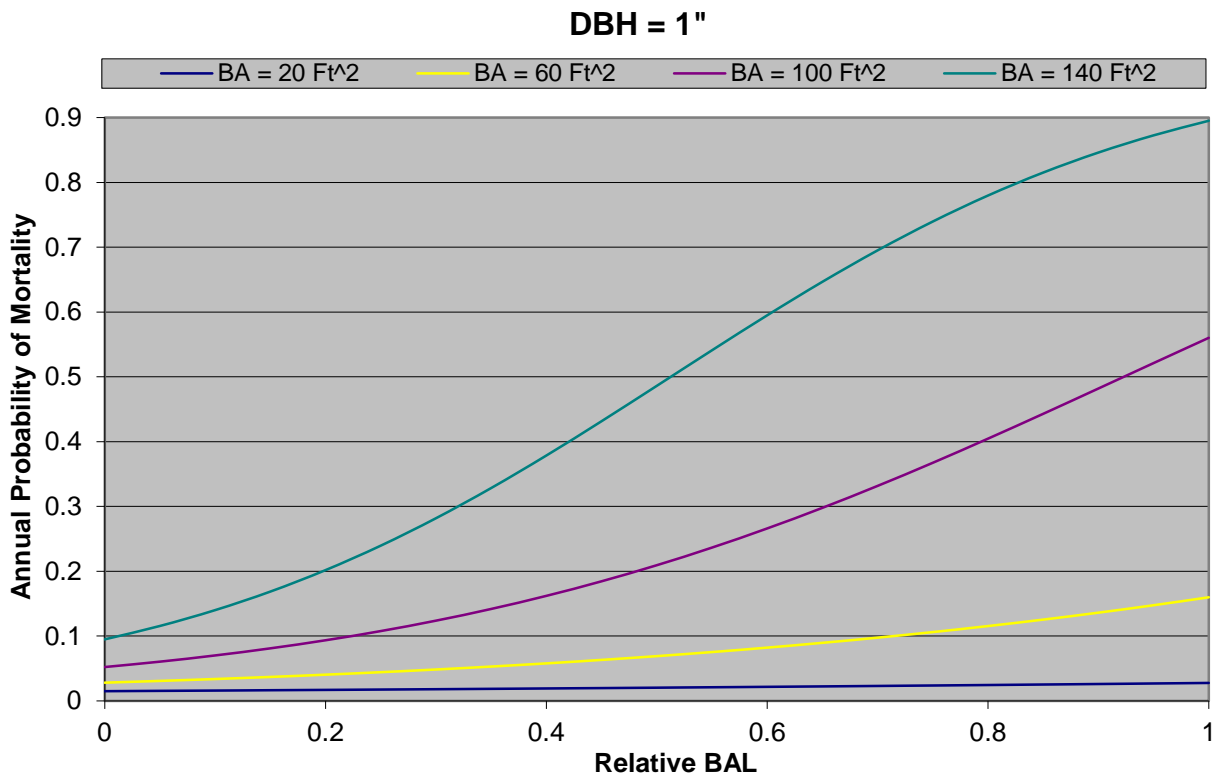


Figure 8.5 Predicted annual probability of mortality (PM) plotted across relative BAL for BA values of 20, 60, 100,140 ft² per acre and with D = 6.0 inches and SI = 60 feet.

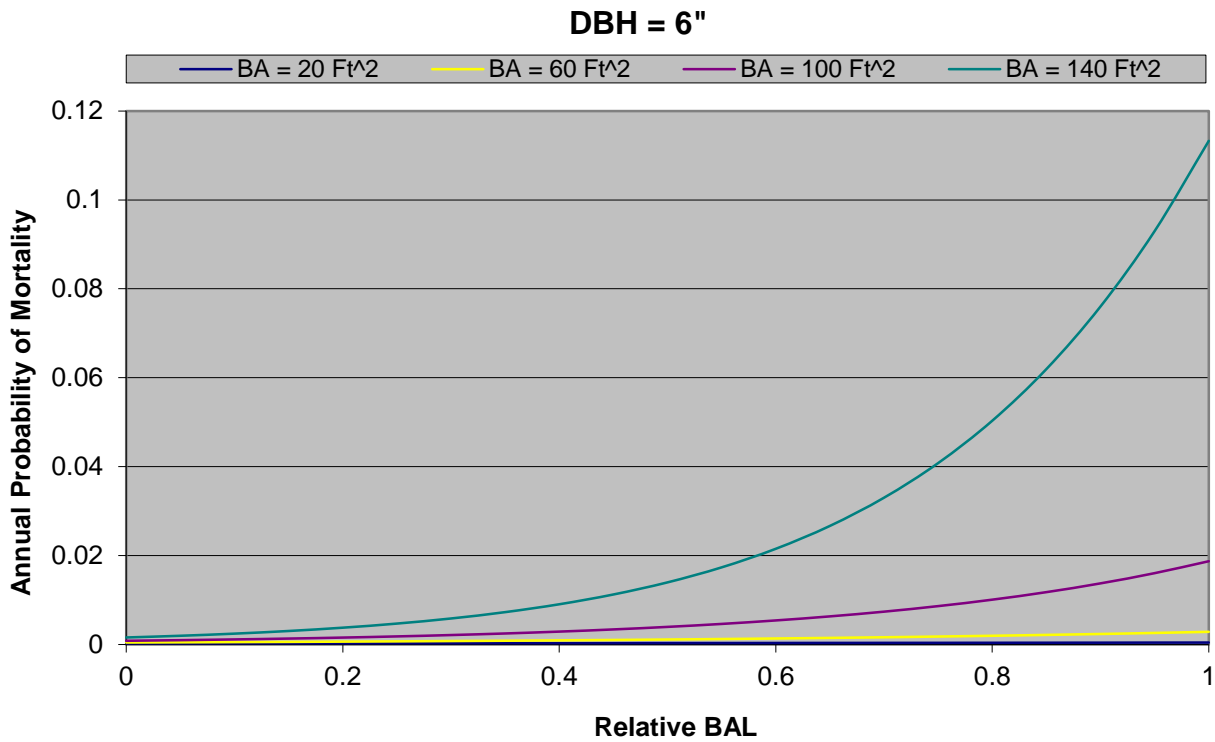
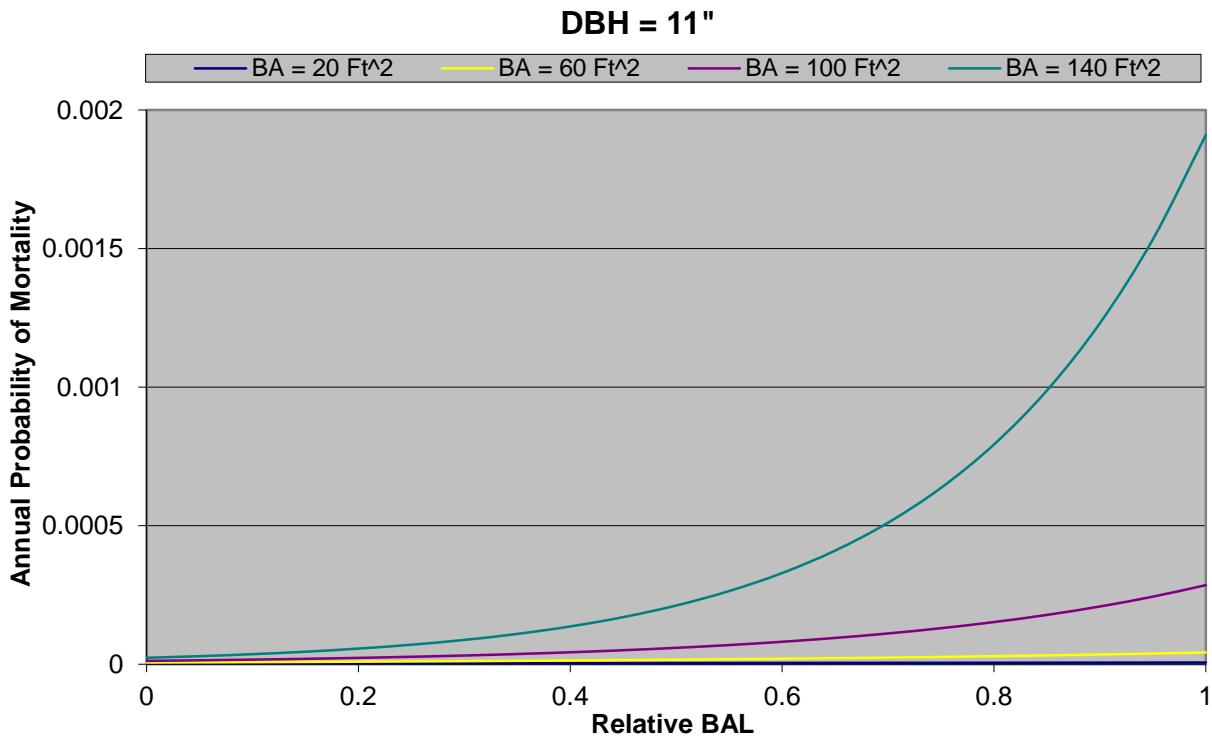


Figure 8.6. Predicted annual probability of mortality (PM) plotted across relative BAL for BA values of 20, 60, 100,140 ft² per acre and with D = 11.0 inches and SI = 60 feet.



Examination of Figure 8.3 indicates that the new Z-Function (Z.1) predict PM of near zero when D approaches 11.0 inches for simulated open grown trees. Examination of Figures 8.4 through 8.6 shows that PM increases both with increasing relative BAL and increasing BA, and that it

decreases with increasing D . All of these behaviors meet expected behavior from a tree-level PM equation.

These results show that the continued remeasurement of the HSC installations has greatly improved the ability to predict probability (PM) (and the maximum size-density trajectory). However, one would expect PM to first decline (as shown in the new PM equation) and then increase over D (Hann and Hanus 2001). As with Hann et al. (2011), incorporation of this behavior into the PS model was attempted by incorporating D^2 into Z-Function (Z.1) but this resulted in a lack of fit for SI_C and BAL at $P=0.01$. Therefore, the PS/PM modeling data set is still too young to display the expected U-shaped behavior expected over D . As before, it is still critical to continue to remeasure the red alder installations in order to ultimately address this issue.

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9.0 Residual Equations for the Red Alder Annual Diameter Increment and Height Increment Equations

RAP-ORGANON has an option of record tripling in order to increase variability into the user's input tree list. This pseudo random feature is particularly useful for small tree lists (Stage 1973). Rap-ORGANON triples the tree list first based upon diameter increment and then upon height increment resulting in a nine times increase in the length of the tree list at the end of each growth cycle. Tripling continues until the expanded tree list reaches the maximum length of 2000 records. If a tripling of every tree record would increase the tree list above 2000 records, then tripling every other tree record is used but only if that alternative strategy would keep the resulting expanded tree list below 2000.

Performing tripling requires models for predicting the means for the lower 1/3 and upper 1/3 residuals of annual diameter increment or annual height increment. These annual residual equations were developed using the annual central PAI control plot data sets and associated parameter estimates developed for both equations. The residuals for the middle 1/3 of the residuals is formed by summing together the predictions from the lower and upper 1/3 residuals equations.

9.1 Data Analysis and Results

For diameter increment, the model form for the residual models was:

$$\Delta DRES_{i,j} = MWRES_i \cdot P\Delta D_j^{0.5} \quad (10.1)$$

Where,

$\Delta DRES_{i,j}$ = The i^{th} type of annual diameter increment residual for the j^{th} tree

$MWRES_i$ = Mean weighted annual residual for the i^{th} type of residual

$P\Delta D_j$ = The predicted diameter increment for the j^{th} tree

$i = 1$ if a lower 1/3 residual and 2 if an upper 1/3 residual

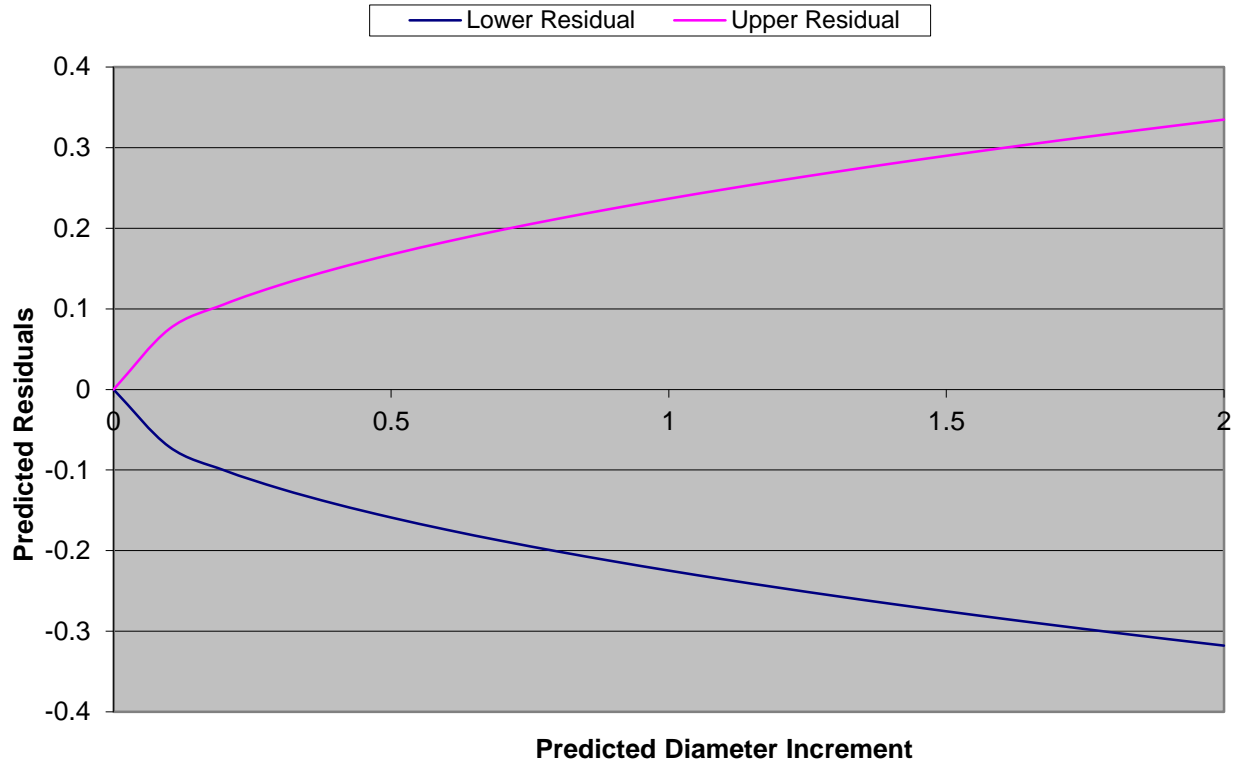
The resulting values of $MWRES_i$ for Equation (10.1) are found in Table 10.1. A graph of the predicted upper and lower 1/3 residual models for the ΔD model fit using the weighted summation procedure is found in Figure 10.1.

Table 9.1 Red alder mean weighted residuals and their standard errors for the lower 1/3 of the ΔD residuals ($MWRES_1$) and the upper 1/3 of the ΔD residuals ($MWRES_2$).

Type of Residual	Mean	Standard Error
$MWRES_1$	-0.22472060	0.06243074
$MWRES_2$	+0.23666874	0.07796166

Figure 9.1 Predicted upper and lower 1/3 residual models for the plantation red alder diameter increment (ΔD) plotted over predicted diameter increment ($P\Delta D$).

Red Alder Weighted Center PAI Diameter Increment Model



For the height increment equation, the model form for the residual models was:

$$\Delta HRES_{i,j} = b_{0,i} + b_{1,i} \cdot P\Delta H_j + b_{2,i} \cdot P\Delta H_j^2 \quad (9.2)$$

Where,

- $\Delta HRES_{i,j}$ = The i^{th} type of annual height increment residual for the j^{th} tree
- $b_{k,i}$ = The k^{th} parameter for the i^{th} type of residual
- $P\Delta H_j$ = The predicted height increment for the j^{th} tree
- $i = 1$ for the lower 1/3 residuals and 2 for the upper 1/3 residuals

The values of $b_{k,i}$ for Equation (9.2) were determined using ordinary least squares regression. While all of the parameters were determined to be statistically different from zero because of the large sample size, only a few of the parameters made a practical difference in explaining the behavior of Equation (9.2). To illustrate, Figure 9.2 shows the upper 1/3 of the residuals plotted across $P\Delta H$ with both linear and quadratic trend lines and associated value of coefficient of determinations (R^2). Figure 9.3 shows the same for the lower 1/3 residuals.

Figure 9.2. The upper 1/3 of the residuals plotted across PΔH with linear and quadratic trend lines and their associated R² values.

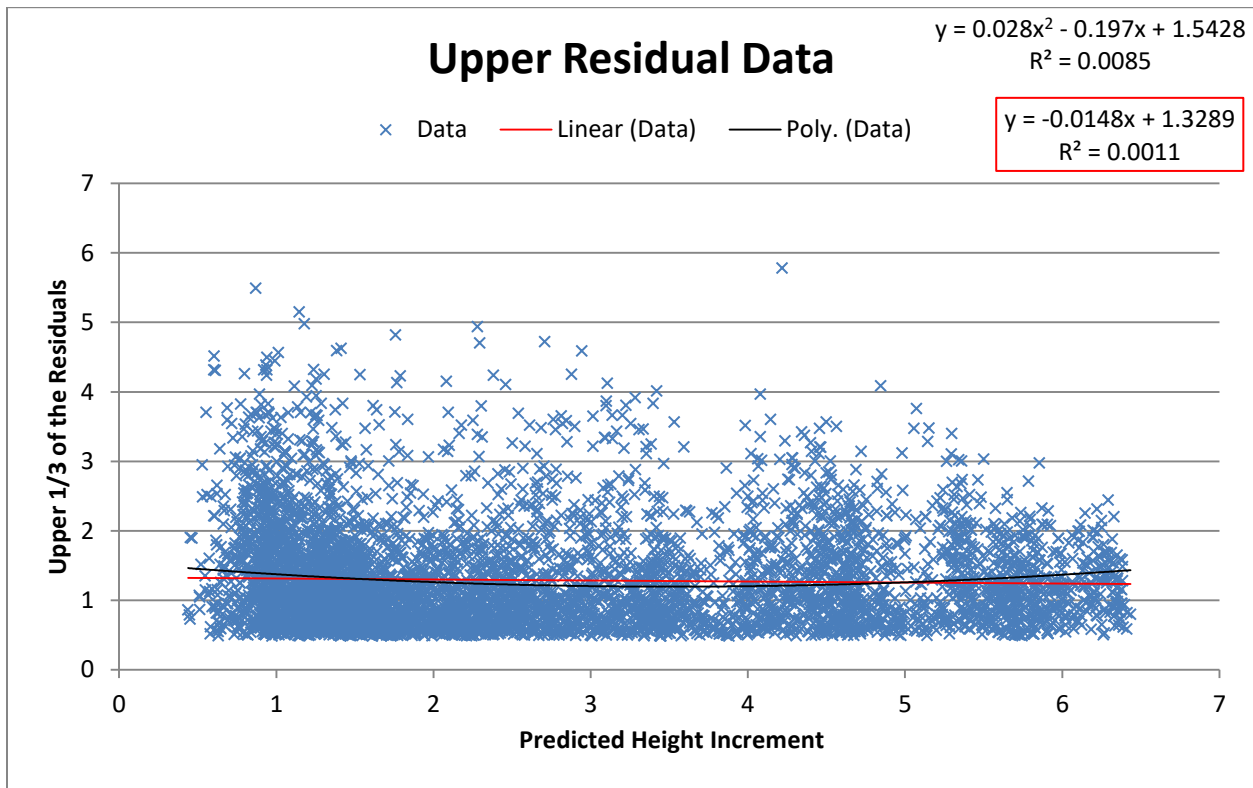
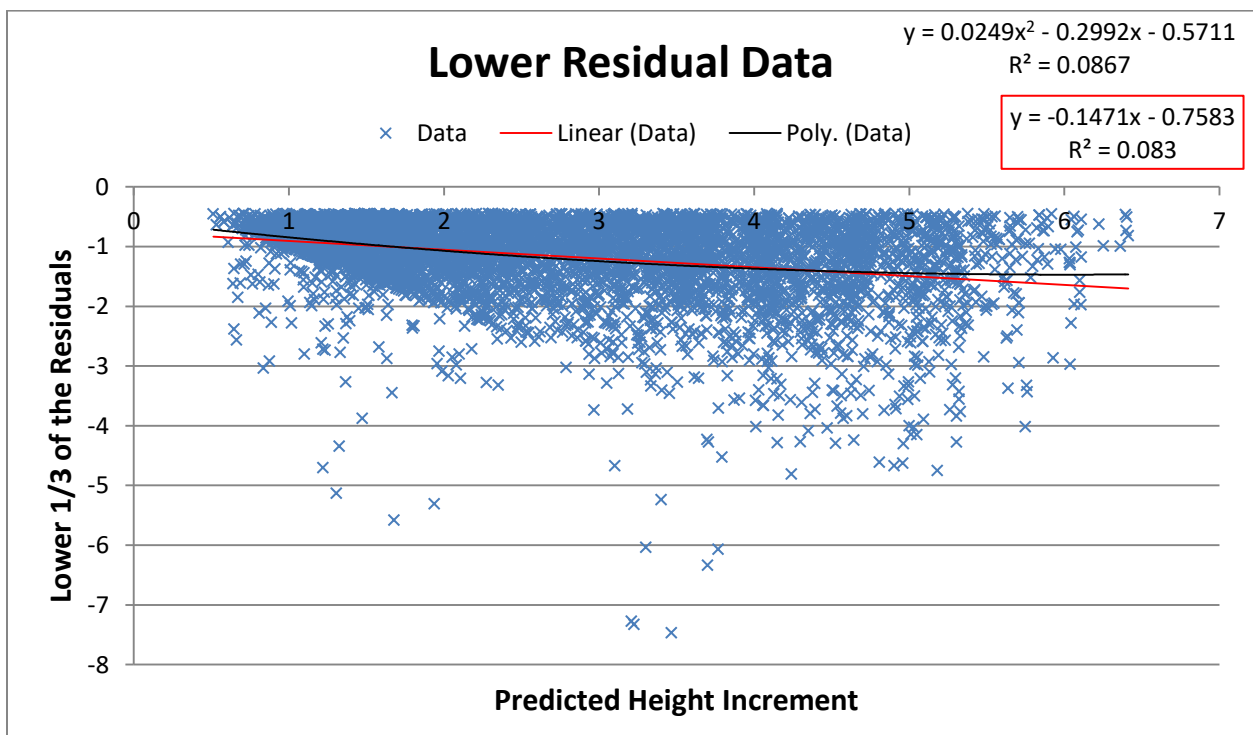


Figure 9.3. The lower 1/3 of the residuals plotted across PΔH with linear and quadratic trend lines and their associated R² values.



For the upper 1/3 residual model, application of the quadratic model form resulted in a R^2 value of only 0.0085, while the linear model form had a R^2 value of just 0.0011 (Figure 9.2). Neither of these values provided convincing evidence that a model more complicated than a simple mean was justified for characterizing the relationship between the upper 1/3 of the residuals and $P\Delta H$. Therefore, only parameter $b_{0,2}$ was used in this relationship.

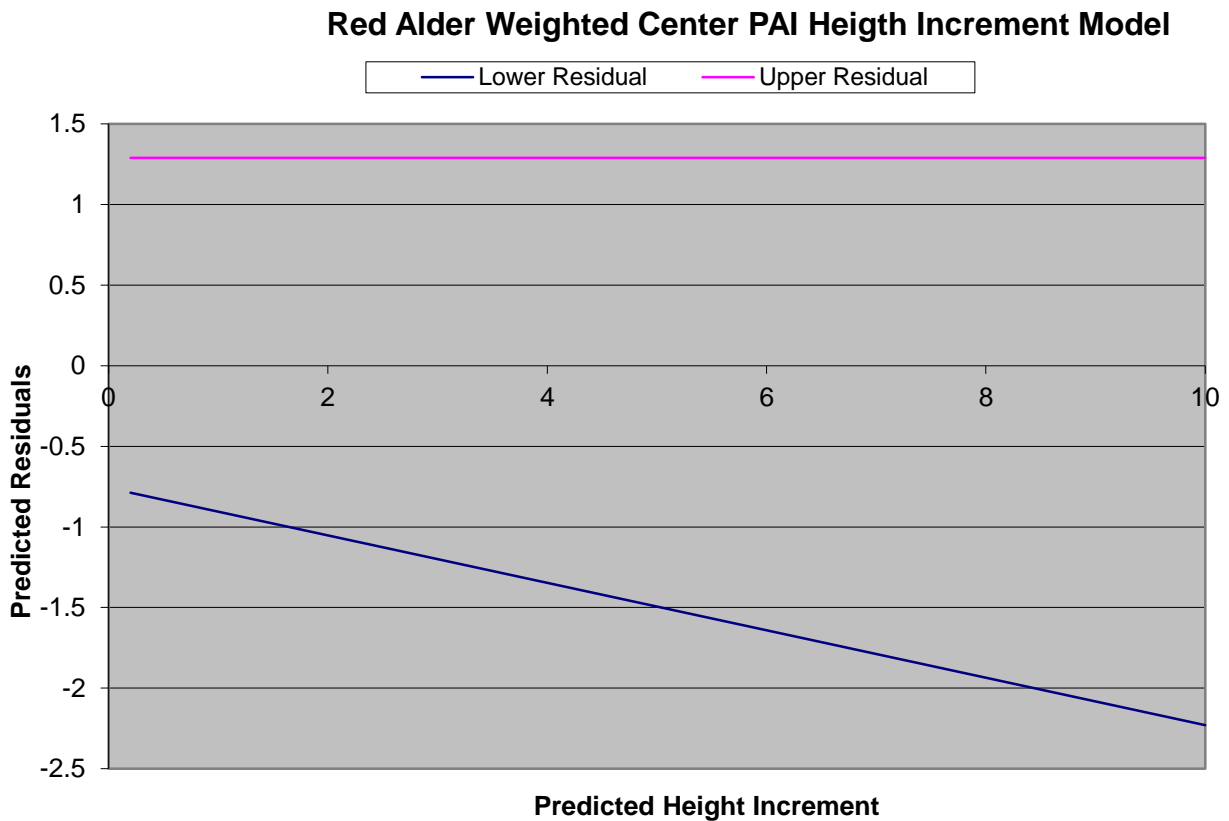
For the lower 1/3 residual model, application of the quadratic model form resulted in a R^2 value of 0.0867, while the linear model form had a R^2 value of 0.0830 (Figure 9.3). The small difference in the R^2 between the quadratic and linear model forms resulted in the decision that only parameters $b_{0,1}$ and $b_{0,2}$ were needed to characterize the relationship between the upper 1/3 of the residuals and $P\Delta H$.

The resulting parameter estimates and their standard errors for Equation (9.2) are found in Table 9.2. A graph of the predicted upper and lower 1/3 residual models for the ΔH model fit using the weighted summation procedure is found in Figure 9.4.

Table 9.2 Red alder parameter estimates and their standard errors for predicting the lower 1/3 of the annual ΔH residuals ($b_{k,1}$) and the upper 1/3 of the annual ΔH residuals ($b_{k,2}$).

Parameter	Parameter Estimate	Standard Error
$b_{0,1}$	-0.758330552	0.01987981
$b_{1,1}$	-0.147113628	0.006475338
$b_{2,1}$		NA
$b_{0,2}$	+1.28899463	0.009617207
$b_{1,2}$	0.0	NA
$b_{2,2}$	0.0	NA

Figure 9.4 Predicted upper 1/3 and lower 1/3 residual models for the plantation red alder height increment (ΔH) model plotted over predicted height increment ($P\Delta H$).



9.3 Discussion

The residual models for diameter increment follow the same trends as found in previous versions of ORGANON. The absolute values of the diameter increment residual equations monotonically increase as $P\Delta D$ increases and the inequity of the $MWRES_i$ values indicate a slight, positive skewness.

In the original analysis (Hann et al. 2011), the absolute value of the height increment residual equations first increased, peaked, and then declined as $P\Delta H$ increased, with the peaks occurring within the range of $P\Delta H$ found in the data set. In this reanalysis, the behavior of the upper 1/3 residuals were found to be constant across $P\Delta H$, while the lower 1/3 residuals linearly declined as $P\Delta H$ increased. These changes have resulted in residual equations that better characterize the relationships between the residuals and $P\Delta H$ (Figures 9.3 and 9.4).

9.4 Literature Cited

Hann, D.W., A.A. Bluhm, and D.E. Hibbs. 2011. Development and evaluation of the tree-level equations and their combined stand-level behavior in the red alder plantation version of ORGANON. Oregon State University, Department of Forest Engineering, Resources, and Management, Corvallis, Oregon. Forest Biometrics Research Paper 1. 127p.

Stage, A.R. 1973. PROGNOSIS model for stand development. USDA Forest Service, Intermountain Forest and Range Experiment Station, Ogden, Utah. Research Paper INT 138. 32p.

10.0 Effects of Thinning upon Red Alder Diameter Increment, Height Increment, and Mortality Rate Equations

A properly applied thinning that does not damage the residual trees will increase the diameter increment of the residual trees because of the increased availability of moisture, nutrients, and light (Oliver and Larson, 1996, Tappeiner et al., 2007). Thinning may increase, decrease, or maintain the height increment of the residual trees depending upon tree species, crown class, age, and density of the stand before thinning (Oliver and Larson, 1996, Tappeiner et al., 2007). The increase in growing space from thinning will lead to an increase in crown width, a reduction in crown recession, and an increase in crown length if height increment is still significant (Oliver and Larson, 1996, Tappeiner et al., 2007). Moreover, the improvement of the light environment will increase foliage density within the crown (Oliver and Larson, 1996, Tappeiner et al., 2007). Finally, a properly applied thinning should reduce the probability of mortality for the residual trees. How quickly these responses will be manifested in the residual trees will depend upon stand structure and tree species, crown size, and crown class of the trees before thinning, with the duration of thinning responses extending well beyond crown closure (Oliver and Larson, 1996).

Tree-level models, such as RAP-ORGANON, that incorporate one- and two-sided measures of competition and a measure of crown size into their equations for untreated stands will inherently produce an indirect thinning response that is sensitive to both the intensity and the type of thinning. Intensity of thinning is reflected in the size of reduction in the competition measures, and type of thinning is reflected in the relative reduction in the two measures of competition often expressed in tree level models. For example, thinning from below will reduce just the two-sided measure of competition, while thinning from above will reduce both resulting in larger predicted responses from thinning from above than thinning from below. Furthermore, use of crown size variables in the prediction equations will also provide differential response due to type of thinning if the understory trees have smaller crowns than the overstory trees. On the other hand, smaller size trees can be predicted to have larger potential increments, particularly if a potential times modifier approach is used for the basic untreated equation.

These predicted thinning responses may not fully characterize the actual thinning response. Thinning modifiers can be important in tree level models because: (1) crown density often increases after thinning, (2) damaged trees, which can reduce diameter increment (Hann and Hanus, 2002a) and height increment (Hann and Hanus, 2002b), are often removed in thinning and, as a result, the population is modified, (3) thinning shock can occur after treatment, (4) thinning can increase the susceptibility of the residual stand to damaging agents such as wind and snow, and (5) the dynamics of diameter increment, height increment, and crown recession can accelerate after thinning. The last possibility is of particular concern if the measurement intervals used to collect the modeling data are particularly long resulting in larger changes in those attributes over the growth period than would be predicted by the untreated equations.

The RAP-ORGANON model includes equations for predicting the development of untreated stands. Furthermore, all of the dynamic equations incorporate measures of competition. Therefore, the RAP-ORGANON equations developed using untreated data will predict a response to thinnings because of the reduction in competition. Whether or not this predicted behavior is adequate to characterize the effects of thinning depends upon the species; the type, timing, and intensity of thinning; and the particular dynamic equation being examined. Hann et al. (2003) found that ORGANON's predicted thinning response from the untreated diameter

increment and height increment equations of Douglas-fir and western hemlock were inadequate for characterizing the full response to thinning. They did find that the untreated mortality rate equations for both species adequately characterized the mortality rate after thinning. These results were for five-year growth periods in which the predictor variables were measured at the start of the growth period. Therefore, any large thinning induced changes to the dynamics of how the untreated trees' predictor variables (such as height to crown base) change over the growth period might not be adequately reflected in those start of growth period values for thinned trees. However, such problems might be reduced or eliminated with shorter growth periods.

In developing the original RAP-ORGANON, Hann et al (2011) used an annual rather than a five-year growth period. However, that analysis could not find a need for thinning modifiers for their ΔD , HCB, and PM equations.

Hann et al. (2003) found that the direct effects of thinning could be adequately characterized by stand level predictor variable of proportion of the basal area removed in the thinning (PREM) and the number of years since the thinning (YT). For the diameter increment (ΔD) and height increment (ΔH) equations the multiplicative thinning modifier (TMOD) took the general form:

$$TMOD_{j,k} = 1.0 + b_1(PREM_{j,k})^{L_1} e^{b_2(YT_{j,k})^{L_2}} \quad (10.1)$$

Where,

L_1 = Alternative whole numbers for the ΔD TMOD equation and estimated b_3 for the ΔH TMOD equation.

L_2 = Alternative whole numbers for both the ΔD TMOD and ΔH TMOD equations.

Hann et al. (2003) reported that the modifier predicted a direct effect increase in diameter increment and a direct effect decrease in height increment after thinning for both conifer species. Most of the effect was gone after 10 years for both the diameter increment and height increment equations.

While the modifier equation could be fit to individual tree data, the fact that the predictor variables use only stand level attributes would result in inflated number of degrees of freedom and, therefore, under estimated variances of the resulting parameters. Therefore, the red alder thinning analyses used stand level data sets to estimate the parameters and standard errors of the parameters.

For the ΔD and ΔH equations, the basic relationship to be estimated from the treatment plot data is:

$$TI_{i,j,k} = (TMOD_{j,k}) (UI_{i,j,k})$$

Where,

$TI_{i,j,k}$ = Measured thinning increment for tree i, plot j, and measurement k.

$TMOD_{j,k}$ = Thinning modifier value for plot j and measurement k.

$UI_{i,j,k}$ = Adjusted and calibrated untreated increment prediction for tree i, plot j, and measurement k.

If $TMOD_{j,k}$ is one for a given plot and measurement, then $UI_{i,j,k}$ is adequate for predicting the response to thinning. However, if $TMOD_{j,k}$ varies across values of PREM and YT, then the $TMOD_{j,k}$ values can be used to develop an appropriate modifier equation.

10.1 Data

10.1.1 ΔD Thinning Modifier and ΔH Thinning Modifier Data Sets

The following describes the steps taken to develop the ΔD modifier and ΔH modifier data sets:

1. Untreated Equation (5.1) for ΔD and Equation (6.1) for ΔH were applied to the thinned data in order to provide the indirect estimate of the effect of thinning. For both ΔD and ΔH , the untreated equations were either uncalibrated or calibrated to the data collected on each thinned plot before application of the thinning. For the resulting calibrated data, the calibration factors were computed using the data from just the last growth period before treatment. Hann and Hanus (2002a), Hann et al. (2003), and Hann et al. (2011) found that this type of calibration could reduce the variation caused by between plot differences in the ΔD or ΔH . Weighted simple linear regression through the origin was used to calculate these plot level calibrations.
2. Both the plot level uncalibrated and calibrated untreated equations were then used to predict the post treatment increments (i.e., $UI_{i,j,k}$) for all trees and all growth periods for each of the treated plots.
3. The values of $TI_{i,j,k}$ and $UI_{i,j,k}$ were then used to calculate $TMOD_{j,k}$ using the following equation and the same weights ($w_{i,j,k}$) used to estimate the parameters of the untreated equations ($w_{i,j,k} = P\Delta D^{-0.5}$ for ΔD and $w_{i,j,k} = 1.0$ for ΔH):

$$TMOD_{j,k} = \frac{\sum_{i=1}^{KNT_{j,k}} (w_{i,j,k})(UI_{i,j,k})(TI_{i,j,k})}{\sum_{i=1}^{KNT_{j,k}} (w_{i,j,k})(UI_{i,j,k})^2} \quad (10.2)$$

Where,

$KNT_{j,k}$ = The number of sample trees for plot j and measurement k.

4. The resulting values of $TMOD_{j,k}$ from Equation (10.2) are the response variables used in developing the $TMOD$ prediction equations. The consequent ΔD data set for fitting Equation (10.1) is described in Table 10.1 and the consequent ΔH data set for fitting Equation (10.1) is described in Table 10.2.

Table 10.1 Descriptive statistics for the plantation grown red alder thinning data set used to fit the annual ΔD thinning modifier equation.

Attribute	Mean	Minimum	Maximum	Std. Deviation
Plot/Measurement Level Attributes: N = 319				
TMOD $_{\Delta D}$ Uncalibrated	1.110274	0.243724	2.01831	0.2796988
TMOD $_{\Delta D}$ Calibrated	1.040618	0.255445	1.819702	0.2671003
PREM	0.5911307	0.291185	0.856418	0.1424948
YT (yrs.)	6.819749	0.0	20.0	5.451295
KNT	35.721	2.0	67.0	8.895651

Table 10.2 Descriptive statistics for the plantation grown red alder thinning data set used to fit the annual ΔH thinning modifier equation.

Attribute	Mean	Minimum	Maximum	Std. Deviation
Plot/Measurement Level Attributes: N = 319				
TMOD $_{\Delta H}$ Uncalibrated	0.8643635	-0.325725	2.855696	0.4156529
TMOD $_{\Delta H}$ Calibrated	0.861262	-0.309865	2.485861	0.4132734
PREM	0.5911307	0.291185	0.856418	0.1424948
YT (yrs.)	6.819749	0.0	20.0	5.451295
KNT	35.721	2.0	67.0	8.895651

10.1.2 PS & PM Thinning Modifier Data Set

A completely different approach was used to form the annual probability of survival (PS) thinning modifier data sets. The survival analysis was complicated by the fact that a multiplicative modifier equation would not work with the logistic model form used to characterize tree survival rate. Therefore, the following approach was used to form the plot level thinning effects response variable.

First, the measured proportion of all trees on thinned plot “j” and measurement “k” surviving over the growth period (PPST $_{\bullet,j,k}$) was calculated by:

$$PPST_{\bullet,j,k} = \frac{\sum_{i=1}^{KNT_{j,k}} (I_{i,j,k} \cdot EXPAN_{i,j,k})}{\sum_{i=1}^{KNT_{j,k}} EXPAN_{i,j,k}}$$

Where,

- $I_{i,j,k}$ = Survival indicator variable for jth tree on the ith thinned plot and kth measurement
- = 1.0 if the tree survived in the growth period
- = 0.0 if not

The measured proportion of all trees on thinned plot “i” surviving annually (PST $_{\bullet,j,k}$) was then calculated by:

$$PST_{\bullet,j,k} = (PPST_{\bullet,j,k})^{1/LEN}$$

Where,

LEN = Length of growth period in years

Finally, the response variable consisting of measured proportion of all trees on thinned plot “i” dying annually (PMT_{•,j,k}) was calculated by:

$$PMT_{\bullet,j,k} = 1.0 - PST_{\bullet,j,k}$$

Given the measured response variable for each plot, the model form used in the thinned stand mortality analysis was created in the following manner. First, the proportion of all trees on a thinned plot surviving annually as predicted from the untreated plot Equation (8.1) using Z-Function (Z1), PSC_{•,j,k}, was calculated by:

$$PSC_{\bullet,j,k} = \frac{\sum_{i=1}^{KNT_{j,k}} (PSC_{i,j,k} \cdot EXPAN_{i,j,k})}{\sum_{i=1}^{KNT_{j,k}} EXPAN_{i,j,k}}$$

Where,

PSC_{i,j,k} = Predicted annual probability of survival for tree “i” on thinned plot “j” and measurement “k” from the previously estimated untreated Equation (8.1) using Z-Function (Z.1).

The predicted annual proportion of mortality for all trees on thinned plot “j” and measurement “k” (PSC_{•,j,k}) was then calculated by:

$$PMC_{\bullet,j,k} = 1.0 - PSC_{\bullet,j,k}$$

Given that PMC_{•,j,k} and PSC_{•,j,k} are known, the next step was to algebraically solve the following expression of the logistic equation for $e^{-ZC_{\bullet,j,k}}$:

$$PSC_{\bullet,j,k} = \frac{1.0}{1.0 + e^{ZC_{\bullet,j,k}}}$$

The resulting solution was:

$$e^{ZC_{\bullet,j,k}} = (PMC_{\bullet,j,k}) / (PSC_{\bullet,j,k})$$

The resulting plot level equation used for modeling the effect of thinning upon predicted survival rate was:

$$PST_{\bullet,j,k} = \frac{1.0}{1.0 + e^{ZC_{\bullet,j,k} b_0 + b_1 (PREM_{j,k})^{L_1} e^{b_2 (YT_{j,k})^{L_2}}} + \varepsilon_{j,k}$$

Another expression of the same equation would be:

$$PST_{j,k} = \frac{1.0}{1.0 + e^{(ZC_{j,k} + b_0 + b_1(PREM_{j,k})^{L_1} e^{b_2(YT_{j,k})^{L_2}})}} + \varepsilon_{j,k} \quad \text{Equation (10.3)}$$

If there is no thinning effect upon plot level rate of mortality, then $b_0 = b_1 = 0.0$ and:

$$PST_{j,k} = PSC_{j,k} + \varepsilon_{j,k}$$

The resulting $PST_{j,k}$ data set for fitting Equation (10.3) with the basic predictor variables using crown ratio predictor variables but not a basal area predictor variable is described in Table 10.3, and the resulting $PMT_{j,k}$ data set for fitting Equation (10.3) with the basic predictor variables that use basal area but not crown ratio predictor variables is described in Table 10.4.

Table 10.3 Descriptive statistics for the plantation grown red alder thinning data set used to fit the PS thinning modifier equation.

Attribute	Mean	Minimum	Maximum	Std. Deviation
Plot/Measurement Level Attributes: N = 310				
PPST	0.9962389	0.9242282	1.0	0.007211241
PPSC	0.9965866	0.9849647	0.9999292	0.002494912
PREM	0.5926535	0.291185	0.856418	0.142386
YT (yrs.)	5.256966	0.0	18.0	4.993061
LEN (yrs.)	3.996904	1.0	9.0	1.415308
KNT	80.11765	30.0	124.0	18.12787

10.2 Data Analysis, Results, and Discussion

10.2.1 Diameter Increment Equation

The values of $KNT_{j,k}$ used to calculate the mean responses from Equation (10.2) ranged from 2.0 to 67.0 (Table 10.1). Therefore, it was decided to give more weight in the parameter estimating process to those observations with higher values of $KNT_{j,k}$ by multiplying both sides of Equation (10.1) by $KNT_{j,k}$:

$$(TMOD_{j,k}) \times KNT_{i,j} = (1.0 + b_1(PREM_{j,k})^{L_1} e^{b_2(YT_{j,k})^{L_2}}) \times KNT_{i,j} \quad (10.4)$$

Equation (10.4) was fit to the ΔD $TMOD_{j,k}$ uncalibrated and ΔD $TMOD_{j,k}$ calibrated data sets using nonlinear regression and four combinations of L_1 set to 0.5 or 3 and L_2 set to 1 or 2. The resulting values of b_2 were not significantly different from zero for all eight equations. This was the same result found in the original analysis (Hann et al. 2011).

The one and two sided competition predictor variables (e.g., BAL and BA) and HCB used to estimate the crown ratio predictor variable in the untreated plot ΔD equation can result in an increase in predicted ΔD after thinning. For those trees in the stand experiencing a reduction in the size of the tree's one-sided predictor variable, BAL, due to thinning will experience an increase in the size of predicted ΔD . A reduction in the size of the two-sided competition predictor variable, BA, due to thinning will cause an increase in the size of predicted ΔD for all residual trees in the stand. Finally, thinning will cause the HCB equation to predict a reduction predicted crown recession and, as a result will increase the value of CR over time for the residual trees, which will also result in an increase in predicted ΔD .

The results of this analysis indicate that a thinning modifier to the untreated plot ΔD equation is unnecessary for red alder growing in plantations. Therefore, RAP-ORGANON will predict an unmodified increase to ΔD after thinning. This finding agrees with those of Hibbs et al. (1989) and Hibbs et al. (1995) who also reported an increase in ΔD after thinning red alder.

10.2.2 Height Increment Equation

Equation (10.4) was fit to the ΔH TMOD_{j,k} uncalibrated and ΔH TMOD_{j,k} calibrated data sets using nonlinear regression. A comparison of the results using both the uncalibrated data to the calibrated data indicated that calibration did not improve the ability of the untreated ΔH equation to predict ΔH of the thinned data. Therefore, the analysis used the ΔH TMOD_{j,k} uncalibrated data. The resulting parameter estimates, their standard errors, t-statistics, and associated P-values are found in Table 10.4.

Table 10.4 Parameter estimates, their standard errors, their t-statistics, and the probability that the parameter estimates are zero (P-Value) for Equation 10.4 fit to the plantation grown red alder annual ΔH thinning modifier equation.

Parameter	Estimate	Standard Error	t-statistic	P-Value
b ₁	-0.722761907	0.08872884	-8.15	0.00001
b ₂	-0.224900434	0.05442178	-4.13	0.00005

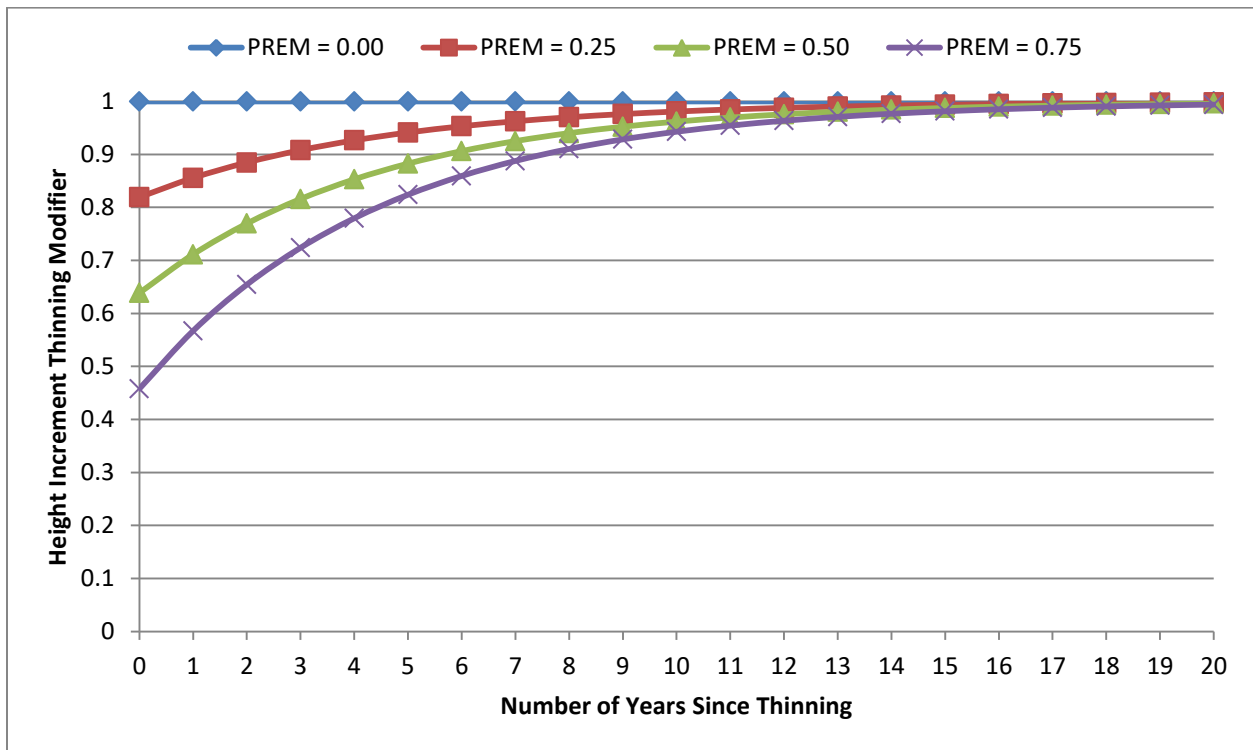
An examination of the parameter estimates, their standard errors, and associated t-statistics and P-values (Table 10.4) indicated that both of the parameters are significantly different from 0.0 at $\alpha = 0.01$.

The one sided competition predictor variable (e.g., CCH) and HCB used to estimate the crown ratio predictor variable in the untreated plot ΔH equation can result in an increase in predicted ΔH after thinning. For those trees in the stand experiencing a reduction in the size of the tree's one-sided predictor variable due to thinning will experience an increase in the size of predicted ΔH . Finally, thinning will cause the HCB equation to predict a reduction predicted crown recession and, as a result will increase the value of CR over time for the residual trees, which will also result in an increase in predicted ΔH .

A graph of the ΔH modifier (ΔH TMOD_{j,k}) showed that there was a substantial reduction in predicted ΔH immediately after thinning resulting from the indirect effect, with the size of the

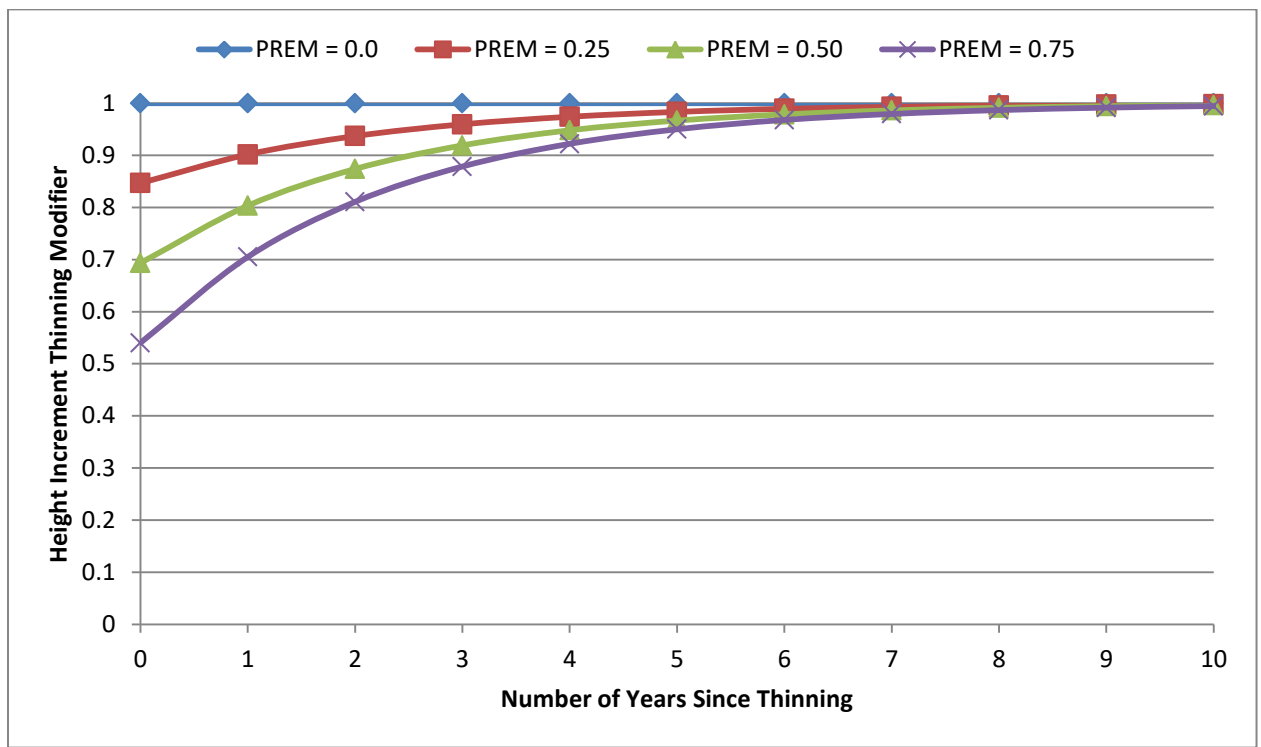
reduction being related to the proportion of the basal area removed in thinning (Figure 10.1). Also shown is that the reduction was basically gone after fifteen years. Therefore, the indirect effect of thinning caused an increase in predicted ΔH while the direct effect of thinning, as expressed by the ΔH $TMOD_{j,k}$ multiplicative modifier, causes a reduction in predicted ΔH resulting from the indirect effect. The result is that the combined indirect and direct effects might produce a prediction of ΔH which is larger or smaller than that which would have been predicted if the plot had not been thinned.

Figure 10.1. Height increment thinning modifier for red alder plantations plotted across the number of years since thinning for three levels of the proportion of the basal area removed (PREM) in thinning.



The original RAP-ORGANON analysis of Hann et al. (2011) also found a significant ΔH thinning modifier. However, the size of the reduction from this modifier (Figure 10.2) is smaller and approaches the value of one more rapidly than the new modifier equation.

Figure 10.2. The Hann et al. (2011) height increment thinning modifier for red alder plantations plotted across the number of years since thinning for three levels of the proportion of the basal area removed (PREM) in thinning.



Weiskittel et al. (2009) and Chapter 2 of this reanalysis both found that the dominant height increment of red alder was significantly less on low density plots. The reduction in ΔH immediately after thinning in red alder has also been reported by Hibbs et al. (1989). They found that five year ΔH rates immediately after thinning had been reduced by 47% for the crop trees on the mechanical thinned treatment, and Hibbs et al. (1995) reported that the reduction was gone 10 years after the thinning. Hann et al. (2003) also found that thinning resulted in decreased ΔH after treatment for both Douglas-fir and western hemlock. They also reported that the effect of thinning was basically gone after ten years.

10.2.3 Probability of Survival Equation

Equation (10.3) was fit to the $PST_{\bullet,j,k}$ data using iteratively reweighted nonlinear regression and eight combinations of the parameters in which L_1 was set to values of $\frac{1}{2}$ and 1 and L_2 was set to 1, 2, 3, and 4. The weight (WT) used was:

$$WT = KNT_{i,j}^2 / [(P\hat{S}T_{\bullet,i,j})(1.0 - P\hat{S}T_{\bullet,i,j})]$$

The resulting parameter estimates, their standard errors, t-statistics, and associated P-values for all eight combinations of L_1 and L_2 showed none of combinations produced estimates of b_0 or b_2 that were significantly different from zero at $\alpha = 0.5$ (data not shown).

The maximum likelihood ratio test, commonly called the G-statistic for this application, was then used to test whether the inclusion of the thinning transformation explained a significant amount of additional variation. The G-statistic uses the difference in deviance between Equation (10.3) with just the intercept term, b_0 , of the thinning modifier component of the equation and the full Equation (10.3) and is calculated by:

$$G = -2.0[DIFF1 + DIFF2]$$

Where,

$$DIFF1 = \sum_{j=1}^{n_j} \sum_{k=1}^{n_k} PST_{\bullet,j,k} \ln(PST\hat{R}_{j,k}) - \sum_{j=1}^{n_j} \sum_{k=1}^{n_k} PST_{\bullet,j,k} \ln(PST\hat{F}_{j,k})$$

$$DIFF2 = \sum_{j=1}^{n_j} \sum_{k=1}^{n_k} PMT_{\bullet,j,k} \ln(PMT\hat{R}_{j,k}) - \sum_{j=1}^{n_j} \sum_{k=1}^{n_k} PMT_{\bullet,j,k} \ln(PMT\hat{F}_{j,k})$$

$PSTR_{i,j}$ = Predicted probability of survival using the reduced model

$PSTF_{i,j}$ = Predicted probability of survival using the full model

$PMTR_{i,j}$ = Predicted probability of mortality using the reduced model

$PMTF_{i,j}$ = Predicted probability of mortality using the full model

The G-statistic is chi-squared distributed with two degrees of freedom. A G-statistic value above the critical chi-square value indicates the full model is significantly improved over the reduced model with just an intercept.

None of the eight combinations of L_1 and L_2 produced G-statistics which were above the critical chi-square value of 5.99 for $\alpha = 0.5$. Therefore, the introduction of the thinning modifier to the untreated PS/PM Equation (8.1) did not explain a significant amount of additional variation. These findings replicate the previous finds of Hann et al. (2011).

The one-sided competition predictor variable (e.g., BAL) and the two sided competition predictor variable (e.g., BA) in the untreated plot PS equation using Z-Function (Z.1) will predict a reduction in predicted PS after thinning. The results of this analysis indicate that a thinning modifier to the untreated plot PS equation is unnecessary for red alder growing in plantations. Therefore, RAP-ORGANON will predict an unmodified reduction to PS after thinning. This finding agrees with those of Hibbs et al. (1989) and Hibbs et al. (1995) who also reported an increase to PS after thinning red alder.

10.3 Literature Cited

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