

# **Estimating Site Productivity from Non-Site Trees:**

## **A Site Index Based Approach**

By

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## Estimating Site Productivity from Non-Site Trees: A Site Index Based Approach

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Site index (SI) is an indirect measure of potential site quality that is widely used in the Inland Northwest. However, a serious problem exists in applying site curves in the Inland Northwest due to a shortage of suitable 'site' trees. Site trees are explicitly defined for any given set of site index curves; generally the trees must be dominant or co-dominant and must exhibit characteristics that indicate the tree has been able to grow in height at its potential rate. Due to uneven-aged forest conditions and past selective harvest practices, it can be difficult to find trees that meet the site index criteria. Serious underestimates of SI will arise when non-site trees are used.

The primary objective of this research was to develop models for predicting SI from non-site trees, using tree variables that represent vigor, competition, size, and social status. It was hypothesized that these variables would quantify the degree to which a tree is not a site tree. A secondary objective was to investigate whether a quantitative variable for species tolerance would allow analyses of pooled data in order to increase sample size.

Stem analysis data from site and non-site trees was gathered on 100 sites located throughout NW Montana. Species included ponderosa pine, Douglas-fir, lodgepole pine, and western larch. At each sample site, site and non-site trees were sampled for as many species as were evident on the site. Regression analysis was used to build SI prediction equations for each species, all species combined, and all species combined using a derived tolerance variable.

Results showed that species level models performed the best. These models had standard errors ranging from 5.0' to 7.8' and explained about 80% of the variation in observed SI with no bias. For comparison's sake, soil/site models (no tree attributes used in prediction) typically have standard errors in the 6.25' to 9.0' range, while site index curves typically have standard errors less than 5.0'. While the calculated tolerance variable did not capture the species difference as much as hoped, further investigation of tolerance may prove to be fruitful.

In conclusion reliable models for estimating SI from non-site trees can be constructed using tree and stand variables that represent vigor, competition, social status, and size. Such models will reduce bias and permit SI estimation where site trees are not available.

## Acknowledgements

The journey to earning my masters degree has been a long and difficult path at times. I know that I will miss people that deserve credit, please accept my apologies in advance.

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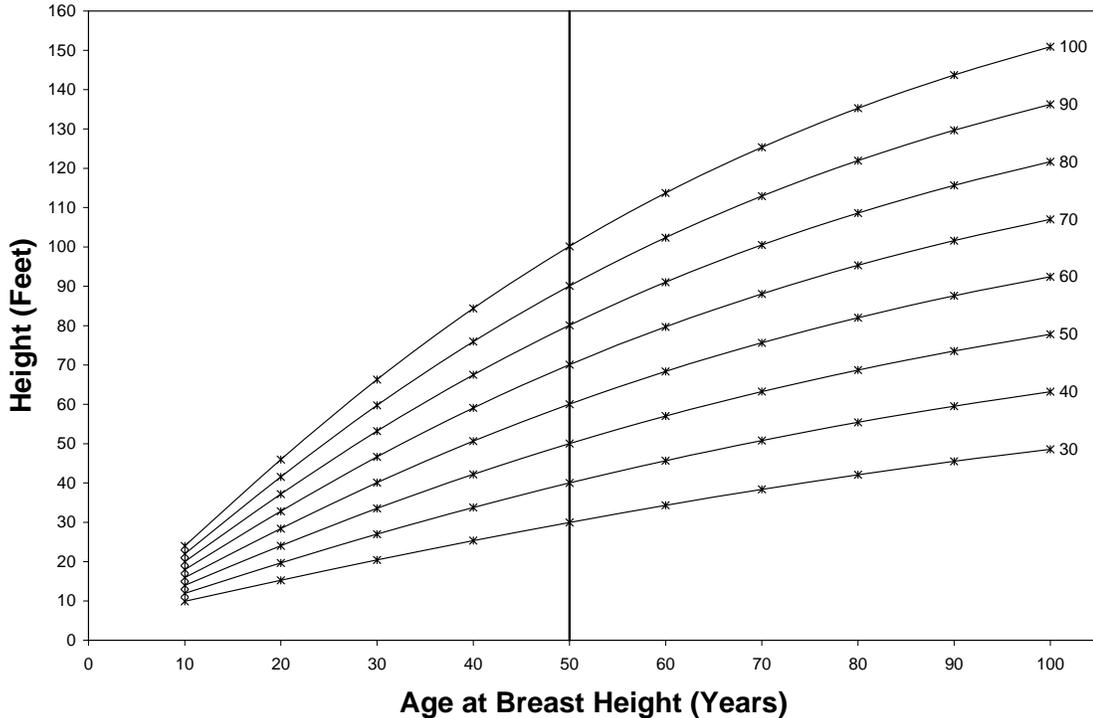
## **Introduction**

For years, estimating potential forest site productivity has plagued both modelers and managers alike. As early as 1913, an article by Raphael Zon entitled *Quality Classes and Forest Types* discussed the need to classify forestland based on silvicultural reasons, not economic. This stirred up a series of papers for nearly the next decade (Roth, 1916; Bates, 1918; Frothingham, 1918 & 1921) and has not been solved to this day. Although Zon had suggested a classification by height and other characteristics, some of the responses to his article didn't necessarily agree, saying that volume on a 'fully stocked acre' should be the index (Frothingham, 1921). The volume per unit area approach, while theoretically preferred, has severe practical problems that preclude field applications. As a consequence, Zon's recommendation to use tree height as a basis for classifying site productivity was widely adopted. The underlying assumption is that volumetric productivity is closely related to height growth rates of dominant trees. This assumption is described in Eichhorn's Law (Eichhorn, 1904), which states that, across levels of site quality; stands with the same top height (dominant tree height) will exhibit the same per unit area volume.

The height-based method of quantifying potential site productivity is known as the Site Index (SI) approach. In this approach, site index curves or site curves are prepared for a species in a particular region. These curves describe the pattern of height development with increasing age and are indexed according to the height achieved at some reference age. For example, Figure 1 illustrates site curves prepared for Douglas-fir in western Montana using a 50-year reference age. The underlying equations allow for prediction of SI given height and age, or alternatively, prediction of height, given SI

and age. See Appendix A for the Milner curve equations used in this paper to predict ponderosa pine (*Pinus ponderosa*), Douglas-fir (*Pseudotsuga menziesii*), western larch (*Larix occidentalis*), and lodgepole pine (*Pinus contorta*) site indices.

**Figure 1.** Douglas-fir Site Index Curves (Milner, 1992)



To use the site curves, height and age data are collected on dominant trees growing on the location of interest. These data are entered into the SI equation ( $SI = f(\text{Height}, \text{Age})$ ) and the height at reference age (SI) is predicted. The problem in the Inland Northwest forests, of northern Idaho, eastern Washington and western Montana, is that you must measure ‘suitable’ site trees.

*A ‘suitable’ site tree is defined as a tree that is 50 to 100 years old. The tree has been free to grow with a good crown (30 %+ ) and regular whorl spacing. There must be no clear sign of insect or disease problems as well as no clear top damage. Upon examining the increment core of the subject tree, there are*

*minimal irregularities only after breast height age 20 years. Additionally, there can be no more than one period of suppression not exceeding five years followed by a release event.*

Finding ‘suitable’ site trees in many western forests is impossible due to uneven-aged conditions and past management practices that have periodically removed the dominant trees. (Stage, 1963) Trees in these conditions cannot be assumed to have been ‘free-to-grow’ in height. Use of these non-site trees or trees that do not meet the criteria of a site tree will always result in underestimates of SI and thus cause bias in growth and yield estimates based on SI. The growth and yield consequences of a bias in SI estimation can be demonstrated by simply running a SI based growth model for the same stand over a period of time with different SI settings as seen in Table 1.

**Table 1. Growth and Yield by Site Index level**

SI	Age @ CMAI	Per Acre Values		
		Board_Net BF/ac	CMAI BF/ac/yr	Board_Net @ 100 yrs
40	130	11547.37	88.83	8329.82
50	110	18025.47	163.87	16251.15
60	100	24057.62	240.58	24057.62
70	90	30614.78	340.16	33057.63
80	90	39946.53	443.85	43140.49
90	80	44415.03	555.19	52713.67
100	70	47571.17	679.59	61918.31
110	60	47850.90	797.52	67121.27
120	50	46461.50	929.23	73306.95
130	50	53924.35	1078.49	79850.88

Values generated from the Forest Projection and Planning System (FPS) version 6.5 yield tables.

SI: Site Index  
 BF: Board foot (12" x 12" x 1")  
 Ac: Acre (43560 ft<sup>2</sup>)

CMAI: Culmination of Mean Annual Increment  
 Board\_Net: Board foot volume net of defect

A 10 foot difference in SI can yield almost ±10 thousand board feet (mbf) per acre difference at 100 years depending on the SI. In a 20-acre stand, then, the estimates

of standing volume would be off by almost  $\pm 200$  mbf. Similar results can be seen in any published SI based yield table.

There are three commonly used approaches to address the problems of using SI. One is to just not use SI as a means of quantifying potential productivity. For example, the north Idaho variant of the United States Forest Service (USFS) Forest Vegetation Simulator (FVS) formerly called Prognosis (Wykoff, 1982) makes no use of SI. Site quality is captured by using site characteristics such as slope, aspect, elevation, and habitat type as predictor variables in growth equations.

A second approach is to develop so called ‘soil/site’ equations for predicting SI from soil and site characteristics alone, without reference to tree attributes (Carnean, 1956). Many forest management organizations use such soil/site equations in areas where suitable site trees are unavailable. However, the precision of SI estimates using soil/site equations is significantly reduced relative to the precision of site curves as seen in Table 2.

**Table 2.** Soil site and site curve standard errors (Milner (1987,1992))

	<b>Site Curves</b>	
	<u>@ 50 years</u>	<u>Soil Site</u>
ponderosa pine	1.2'	9.0'
Douglas-fir	1.5'	6.8'
western larch	1.4'	7.6'
lodgepole pine	1.75'	6.25'

Site Curves @ 50 years as read from graph (Milner 1987)

Standard error at 50 years was used because the error at reference age is the smallest value.

A third less commonly used approach is to modify the site curve system to include reference to tree attributes that differentiate between site trees and non-site trees. For example, Stage (1960) used past radial growth as an additional predictor variable in

his site curve system for interior Douglas-fir. On the other hand, Lynch (1958) used stand density as an additional predictor in his site curve system for ponderosa pine.

The goal of the study described in this paper was to investigate whether an adjustment based on tree attributes can provide adequate SI estimates when using published site curves with height and age (H,A) inputs from non-site trees.

## **Objectives**

*Research Hypothesis I:* Reliable SI estimates can be obtained from ‘non-site trees’ through adjustments based on non-destructive measures of vigor, competition, past growth and other factors.

*Research Hypothesis II:* A variable quantifying tolerance can adequately represent species effects in a pooled analysis of SI relationships across species.

*Primary Objective:* Develop an algorithm for adjusting site index calculated from non-site trees based on non-destructive variables representing competition, tree size, and tree vigor.

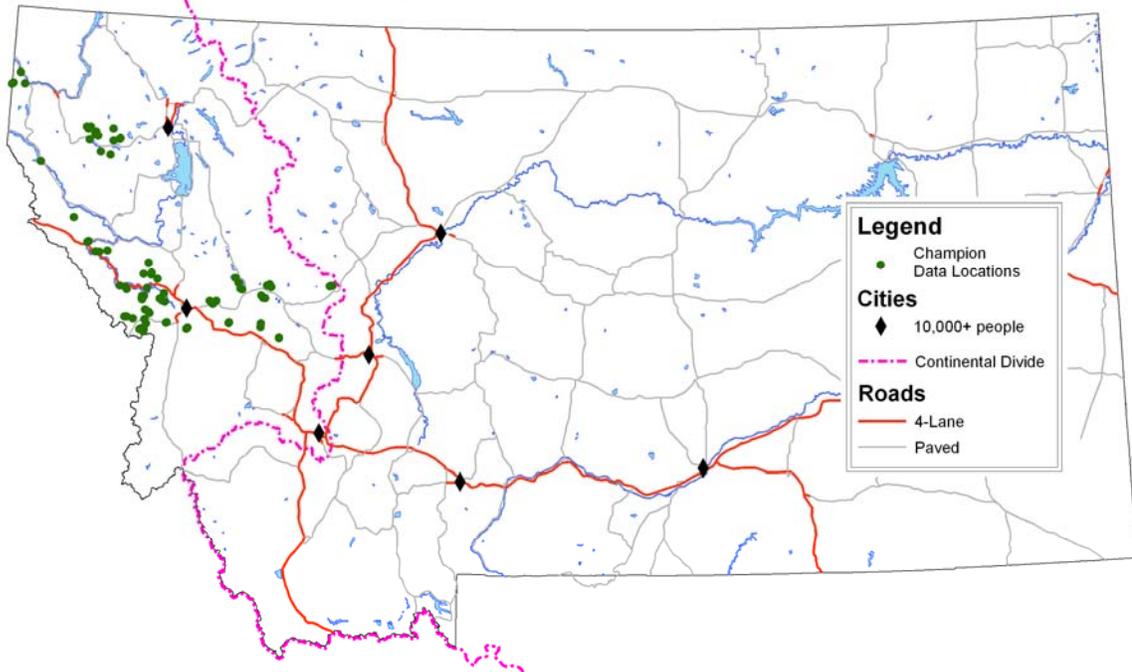
*Secondary Objective:* Investigate the use of a tolerance variable to represent species in a pooled analysis.

## Methods

### Data Description

The data used in this research were collected in 1984 by Kelsey Milner for the Champion International Corporation. The data were originally used to develop site index curves (Milner, 1991) for use on land with suitable site trees, and soil-site equations for estimating site index on land where no suitable site trees existed. The sample locations covered the range of geo-climatic conditions on Champion timberlands in western Montana and are shown in Figure 2.

**Figure 2.** Champion Data Locations in relation to Montana



Species sampled included ponderosa pine, Douglas-fir, western larch, and lodgepole pine. The database is particularly interesting because the original sampling design explicitly reflected a secondary objective of building relationships between site and non-site index trees, but this secondary objective was never pursued.

For each individual species, both site and non-site sample trees were selected from trees existing on a three to five acre area that exhibited uniform slope, aspect, elevation and soils. Sample trees included trees that met all criteria for site index determination (site trees), as well as trees that failed one or more of the criteria (non-site trees) as defined by:

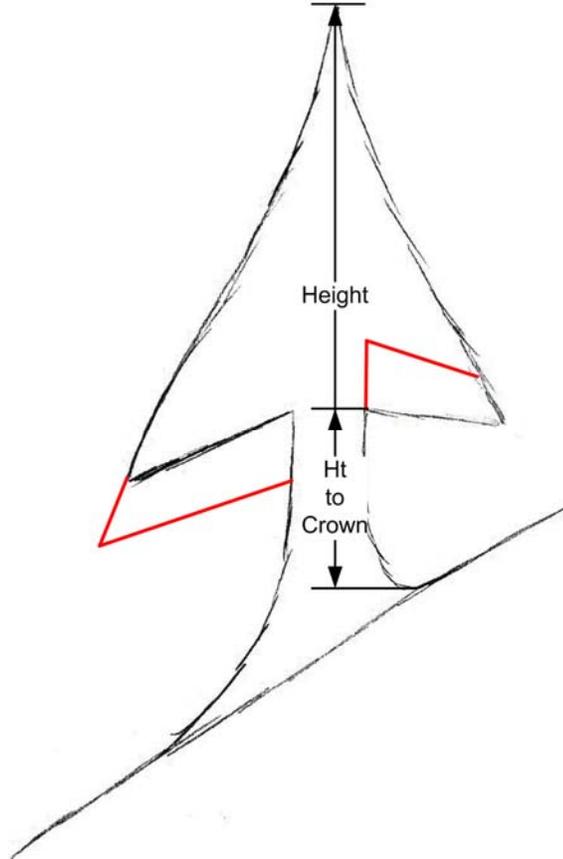
*A 'suitable' site tree is defined as a tree that is 50 to 100 years old. The tree has been free to grow with a good crown (30 %+ ) and regular whorl spacing. There must be no clear sign of insect or disease problems as well as no clear top damage. Upon examining the increment core of the subject tree, there are minimal irregularities only after breast height age 20 years. Additionally, there can be no more than one period of suppression not exceeding five years followed by a release event.*

Each sampling location supported at least one species where a minimum of three site trees could be found in a five acre area of homogeneous geophysical attributes (elevation, aspect, slope, geomorphologic characteristics, etc). Multi-species locations were common. A location was considered to be a multi-species location if on the five acre area there were at least 3 sample trees of another species. Non-site trees were sampled at roughly the same frequency as site trees; the immediate research question involved site trees thus it is not always true that the sampling of site and non-site trees occur at roughly the same frequency at all locations.

Each sample tree was measured for total height (HT) from the base of the uphill side of the tree to the tip of the leader. Height to base of live balanced crown

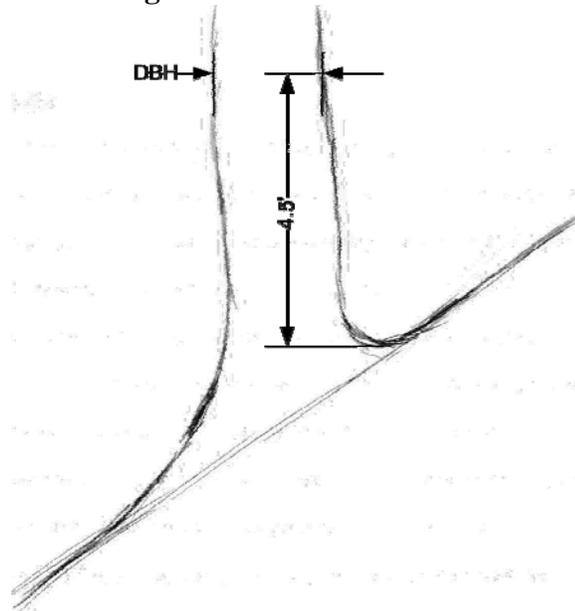
(CRWN) was measured from the base of the tree on the uphill side and as can be seen in Figure 3. The determination of balanced live crown is demonstrated in Figure 3 by the original crown base drawn in red and the visually balanced crown base shown sketched in black. To balance the crown it is necessary for the person measuring the crown to visualize lower limbs being moved to fill in the side of the crown that is not as low. Crown ratio (CR) is then calculated by subtracting CRWN from HT and dividing by HT.

**Figure 3.** Measurement of height and base of live balanced crown



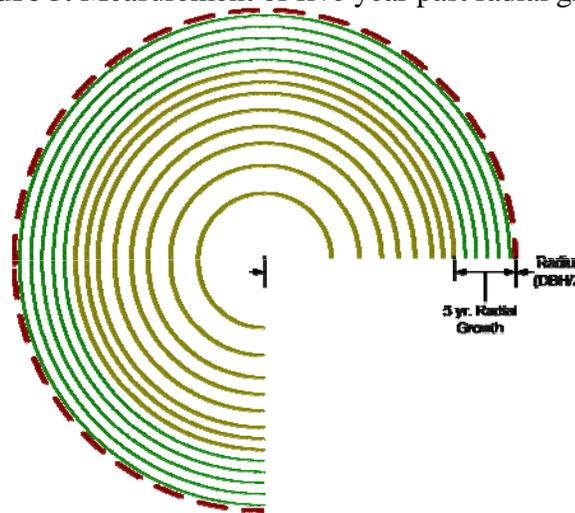
Diameter breast height (DBH) was measured at four and a half feet above ground on the uphill side of the tree as shown in Figure 4.

**Figure 4.** Measurement of DBH



Five year past radial growth was measured in 20ths of an inch from tree cookies cut from sample trees at breast height (Figure 5). For the purpose of this data set these measurements were then converted to inches.

**Figure 5.** Measurement of five year past radial growth

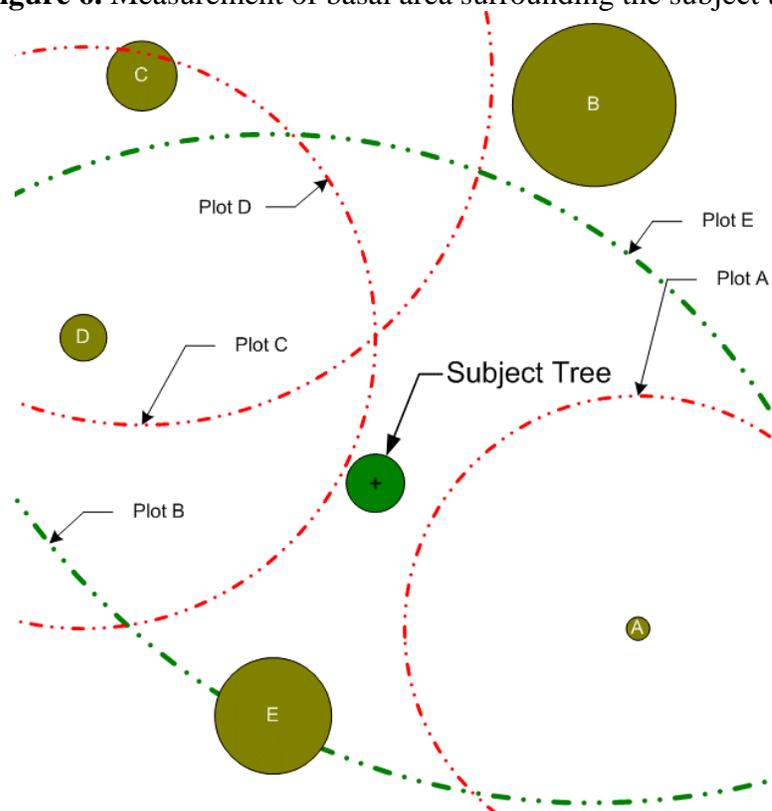


A variable radius prism plot with a basal area factor (BAF) of 10 square feet of basal area per acre was used to calculate the basal area per acre (BA/acre) surrounding each tree. Therefore, each 'count' tree found with a basal area sweep using a 10 BAF will

represent 10 square feet of basal area per acre of competition to the subject tree.

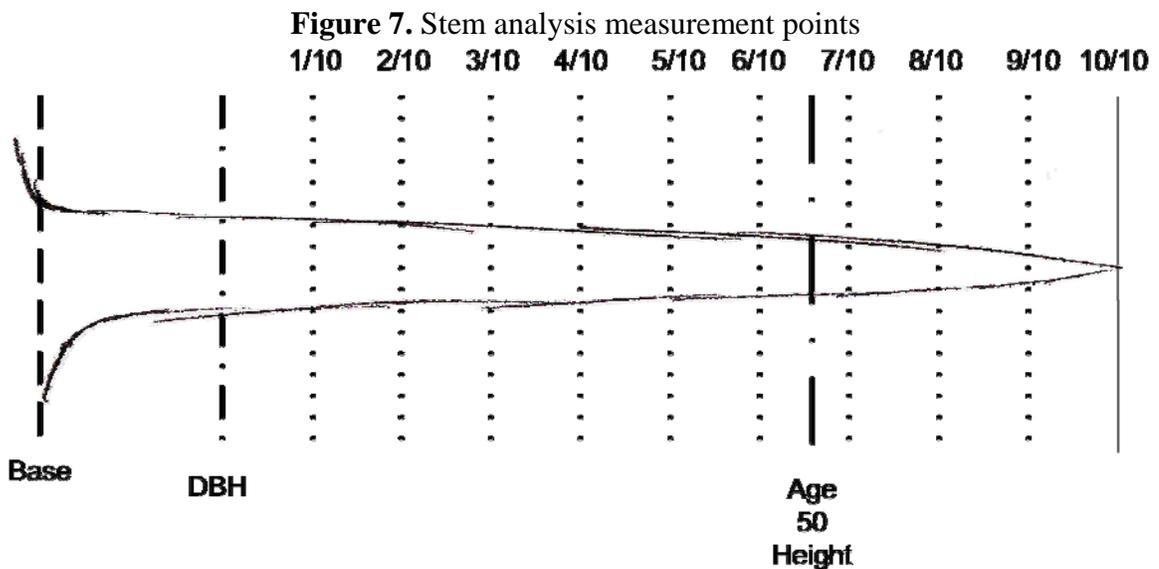
Figure 6 shows that individual trees have their own plot and larger trees have larger plots. Since the individual trees have their own plot, it was a matter of the subject tree falling onto the 'count' tree's plot. The example shows a basal area of 20 square feet per acre of competition because only 2 trees have a plot that overlaps the sample tree's stem. In Figure 6, the trees indicated by labels A, C, and D do not overlap the pith or core of the subject tree as indicated by the red circles surrounding those trees. The larger green circles that indicate the plots of trees E and B overlap the subject tree.

**Figure 6.** Measurement of basal area surrounding the subject tree



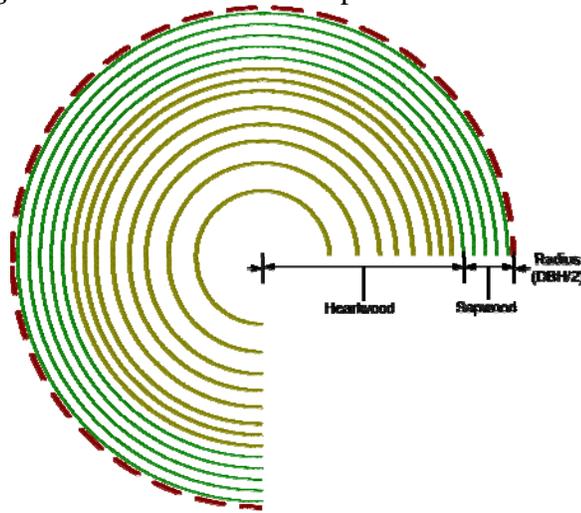
Each tree was felled and cut into 10 equal sections. There was also a cut at the base and breast height and at 50 year height (rings at 50 year height = breast height age - 50) for the tree's 'true' site index, thus resulting in a maximum of 13 measurements on

the stem (Figure 7). Total height at breast height age of 50 years (SI) was obtained via stem analysis for each felled tree. In the example below, age 50 may not have occurred between measurement 6/10 and 7/10 as indicated. The location of age 50 is not at a fixed location and was only placed at that location for the purposes of illustration. Although full stem analysis was performed at all cut locations on the stem, the only ones used in this analysis were the cookies cut at DBH, from which the measurement was obtained.



Sapwood and heartwood areas were measured on the disk or cookie that had been removed at breast height (Figure 8). The measurements from the cookie included, but were not limited to, a ring count for total age, radial measurement of five-year past radial growth, and bark thickness.

**Figure 8.** Measurement of Sapwood and Heartwood



Thus, the database contains observations of past growth, levels of competition, diameter, height, crown ratio, vigor and SI for both site and non-site trees.

Table 3 is a summary of tree attributes by species and site tree type; it shows the Calculated SI, DBH, HT and crown ratio against the minimum, mean ( $\bar{x}$ ), maximum and standard deviation ( $S_x$ ) of the sample values. Table 3 shows what the tree attribute ranges must be within in order to yield reasonable and reliable results from these models, no testing or fitting of the models occurred outside these ranges. Sample tree values that do not fall within these ranges cannot be expected to yield reliable results with these models.

**Table 3. Tree Level Attributes Summarized**

Site Tree	n	C_SI (ft)				DBH (in)				Height (ft)				Crown Ratio (%)			
		min	$\bar{x}$	max	$S_x$	min	$\bar{x}$	max	$S_x$	min	$\bar{x}$	max	$S_x$	min	$\bar{x}$	max	$S_x$
<b>ponderosa pine</b>																	
All	98	31.7	60.6	89.5	12.4	7.0	15.7	22.4	3.7	35.4	76.2	109.6	16.0	3.7	55.3	81.4	13.8
NS	17	31.7	54.2	68.6	9.9	7.0	10.9	16.6	3.2	35.4	63.5	84.2	12.7	3.7	43.0	60.5	14.0
S	81	38.4	61.9	89.5	12.5	10.3	16.7	22.4	2.9	49.9	78.9	109.6	15.4	33.3	57.9	81.4	12.4
<b>Douglas-fir</b>																	
All	160	24.4	56.3	97.4	13.7	4.5	14.2	25.8	3.9	30.7	69.3	105.6	15.4	32.7	61.7	95.5	14.3
NS	32	24.5	49.6	85.5	14.8	4.5	10.1	14.0	2.5	30.7	57.3	84.2	12.7	32.7	56.0	85.3	12.6
S	128	24.4	58.0	97.4	13.0	7.7	15.2	25.8	3.6	34.8	72.4	105.6	14.6	33.9	63.1	95.5	14.4
<b>western larch</b>																	
All	108	42.8	69.1	103.6	11.8	5.6	13.4	20.5	3.1	44.0	84.2	116.8	14.0	27.0	50.0	73.0	10.6
NS	18	42.8	61.9	82.1	12.8	5.6	9.5	14.6	2.6	44.0	70.8	91.8	15.9	27.0	43.8	73.0	11.8
S	90	54.0	70.5	103.6	11.2	9.6	14.2	20.5	2.6	65.0	86.9	116.8	12.0	27.3	51.3	72.7	9.9
<b>lodgepole pine</b>																	
All	155	22.3	57.9	89.3	12.8	4.2	10.9	19.2	3.0	28.7	70.5	106.4	15.2	18.4	48.8	90.6	15.9
NS	43	22.3	52.2	81.8	12.2	4.2	8.5	15.6	2.7	28.7	62.9	96.3	14.2	18.4	44.0	79.9	14.6
S	112	27.9	60.1	89.3	12.5	7.4	11.8	19.2	2.5	40.9	73.4	106.4	14.6	23.6	50.7	90.6	16.0

Site Tree Codes: All: all sample trees together  
 NS: Non-site trees only  
 S: Site trees only

DBH: Diameter at breast height  
 C\_SI: Calculated SI  
 n: Number of trees  
 $\bar{x}$ : Sample mean  
 $S_x$ : Sample standard deviation

Table 4 summarizes species and site tree type by physiographic attributes (elevation, aspect, slope and precipitation), and provides the physiographic limitations of the data set.

**Table 4. Physiographic Attributes Summarized**

Site Tree	Locs	n	Aspect (count)				Elevation (100 ft)			Slope (%)			Precip (cm)		
			North	East	South	West	min	$\bar{x}$	max	min	$\bar{x}$	max	min	$\bar{x}$	max
<b>ponderosa pine</b>															
ALL	37	98	19	9	58	12	24	39	57	0	13	33	15	26	50
NS	9	17	1	0	16	0	24	37	57	2	14	27	19	30	40
S	28	81	18	9	42	12	28	40	57	0	13	33	15	26	50
<b>Douglas-fir</b>															
ALL	60	160	29	24	56	51	24	47	66	1	20	42	16	30	55
NS	16	32	6	4	16	6	24	50	66	1	21	33	16	34	40
S	44	128	23	20	40	45	24	46	66	1	20	42	16	29	55
<b>western larch</b>															
ALL	44	108	42	17	36	13	24	43	59	1	16	33	15	37	60
NS	12	18	5	3	10	0	24	44	59	1	12	28	17	43	60
S	32	90	37	14	26	13	24	43	59	1	17	33	15	35	60
<b>lodgepole pine</b>															
ALL	59	155	35	41	61	18	20	50	64	0	15	31	15	38	60
NS	20	43	7	14	17	5	24	53	64	3	15	31	17	40	60
S	39	112	28	27	44	13	20	48	64	0	15	31	15	37	60

Site Tree Codes:

All: all sample trees together  
 NS: Non-site trees only  
 S: Site trees only

Locs: number of sample locations

n: Number of trees  
 $\bar{x}$ : Sample mean

Cardinal directions in degrees corrected for declination:

North: 315° - 45°                      East: 45° - 135°  
 South: 135° - 225°                      West: 225° - 315°

## Data Analysis

### Independent Variables

Over 100 variables were measured directly or calculated for each tree (Appendix B). The variables represent alternative ways to quantify competition, tree vigor, social status, and past performance; all factors known to influence tree growth.

In order to select the most effective model, one must explore what factors may influence the measurement of site index. As a quick review, traditional Site Index is based on height and age. Since age is based on the constant of time; height is the variable that will be addressed in this study. What variables may affect height growth? Based on the types of variables available, the following general model form seems reasonable:

$$\begin{array}{l} MSI \\ (Mean\ Site\ Index) \\ SI\_D \\ (Site\ Index\ Difference) \\ SI\_R = \\ (Site\ Index\ Ratio) \end{array} = f(Competition, Vigor, Tree\ Status, Growth\ Rate)$$

The following procedures were followed to evaluate each independent variable:

1. Formulate alternative variables to represent the growth factors of Competition, Vigor, Tree Status and Growth Rate.
2. Graph each independent variable against site index and other variables of interest from the measured trees.
3. Evaluate a correlation matrix of independent variables across all species combined to find independent variables that are highly correlated with the dependent variables.

4. Use variables of interest to conduct a stepwise regression for all dependent variables, by species.
5. Track independent variables that remain in the reverse stepwise regression for all species and all dependent variables.
6. Evaluate independent variables for reasonableness of sign and magnitude with biological processes and graph as necessary to determine variables of most importance.

### Dependent variables

Three alternative dependent variables were evaluated for use in modeling the adjustment of SI calculations from non-site trees.

1. MSI        A direct prediction of site index which is defined as the mean SI (MSI) of the several SI sample trees at a location.
2. SI\_D        The difference between MSI and the calculated SI (C\_SI) of an individual tree ( $SI\_D = MSI - C\_SI$ ). Where C\_SI is the SI calculated using Milner's (1991) SI curves and an individual tree's total height and age at breast height.
3. SI\_R.        The ratio of MSI to SI\_C of an individual tree ( $SI\_R = MSI / C\_SI$ ).

### Modeling

#### Species Level Modeling

For each species, a site index adjustment model was built for each of the three dependent variables. The data from both site and non-site trees were combined for the regressions. The steps were as follows:

1. Ordinary least squares (OLS), which is a form of multiple linear stepwise regression, was coupled with graphical displays and used to screen potential independent variables for the adjustment models for each species.
2. OLS regression analysis was used to construct prediction models for SI adjustment, by species, for each dependent variable. Final variables were selected on the basis of statistical significance, logical signs on coefficients, and biological reasonableness. An example would be if the basal area of competition was used in the regression. If the sign demonstrated that the site index needed less adjustment with greater levels of competition, this would be incorrect since it is moving away from being an open grown tree as required by the definition of a site tree.
3. The fit of the SI adjustment models to non-site and site trees was then evaluated separately. The actual mean SI (MSI) was regressed on the individual tree predicted SI and generated a new model. The predicted SI was obtained by applying the SI adjustment model to an individual tree. Bias was indicated by  $\beta_0$  not equal to 0, and/or  $\beta_1$  not equal to 1. This approach was used because a perfect fit should yield a slope ( $\beta_0$ ) of 1 and an intercept ( $\beta_1$ ) of 0 with an equation of  $MSI = \beta_0 + \beta_1 * \text{Predicted SI}$ . Precision was indicated by the standard error (SE) of the regression with an acceptable range of no more than two standard errors difference in the  $\beta_x$ .  $R^2$  was interpreted as the proportion of the variability in the sample explained by the model.

4. The final model for each species was selected on the basis of overall statistical fit, biological reasonableness, and fit to site tree and non-site tree sub-categories. The final models contained independent variables common to all four species. While not all variables were significant for all species, they were included in the model for the sake of comparison.

#### Across Species Modeling

Combined species approaches were used to increase the number of observations (n) and expand the distribution. Individual species sample sizes are relatively small and resulting models are sensitive to artifacts of these distributions. The thought was that a more robust model might result by modeling across species, so long as species differences were not too great (i.e., a tree is a tree no matter what species with minimal species difference). Tests were conducted to determine if this benefit out-weighed the error due to lack-of-fit for a given species.

#### *Modeling with All Species Pooled*

In the first approach, the data were pooled and an OLS multiple linear regression model was built based on variables most highly correlated with SI and on biologically reasonable independent variables from the individual species analysis. The resulting model provided a base-line set of fit statistics and performance for a model that does not recognize species. Subsequent approaches, which attempt to quantify a species level effect or difference through tree attributes, can be evaluated against the all species pooled model of fit statistics.

The performance of the model for site and non-site trees was assessed by regression of the MSI on the predicted SI. This was obtained by applying the adjustment model to individual trees of each group. Standard errors, F-statistics, and  $R^2$ 's for each group were then compared to those from alternative approaches.

#### *Modeling with Dummy Variables*

The next step was to take the best variables from the individual species model and add a dummy binary variable for all species but one. These dummy variable coefficients represented the intercept adjustment for each species. The OLS requirement for minimal collinearity forces one of the binary variables to be left out of the regression. The species that was consistently left out of all models was Douglas-fir. Therefore, the base model or the model with a value of 0 for all the species variables would represent the model for Douglas-fir. The use of Douglas-fir as a default species was done to maintain a standard set of variables in the models.

As with the first approach, the performance of the model for site and non-site trees was assessed by the regression of the actual SI (MSI) on the predicted SI. The predicted SI was obtained by applying the adjustment model to individual trees of each group. Standard errors, F-statistics, and  $R^2$ 's for each group were then compared to those from alternative approaches.

### *Modeling with Tolerance*

A tolerance variable was developed to use as a replacement for species and was incorporated into the best variables found in the individual species model.

### **Calculating Species Tolerance Variables**

To investigate if all tree data could be used simultaneously for a regression in the site calculation methods, many factors were used to simulate species differences without using ‘dummy’ variables. One such method was the use of tolerance.

In 1911 Raphael Zon and Henry Graves published an article called *Light in Relation to Tree Growth*. This article details the methods that were used to classify species into tolerance categories. However, some researchers did not agree that light was the driving factor. In response, Frederick Baker published *A Revised Tolerance Table* (1949) in which the real modification was the addition of more merchantable species of trees. Along this same theme, Dr. James D. Arney used these 'tolerance tables' in the early 1990's to determine regeneration in the Forest Projection and Planning System (FPS). (Arney et al, 2004)

The approach that Arney used was based on stem mapped permanent plot data. Since FPS is an individual tree, distance dependent model, tree level data could be used to calculate competition. Part of the calibration of this model was to look at the crown ratio for a tree with a competition level of 300 competitive stress index (CSI) (Arney, 1978). A level of 300 was chosen as it has been determined to approximate the beginning of the zone of imminent mortality in some species of conifers. Although Arney's approach was based on real tree data and some intuition, the following approach attempts to recreate that using published equations. (Arney et al, 2004)

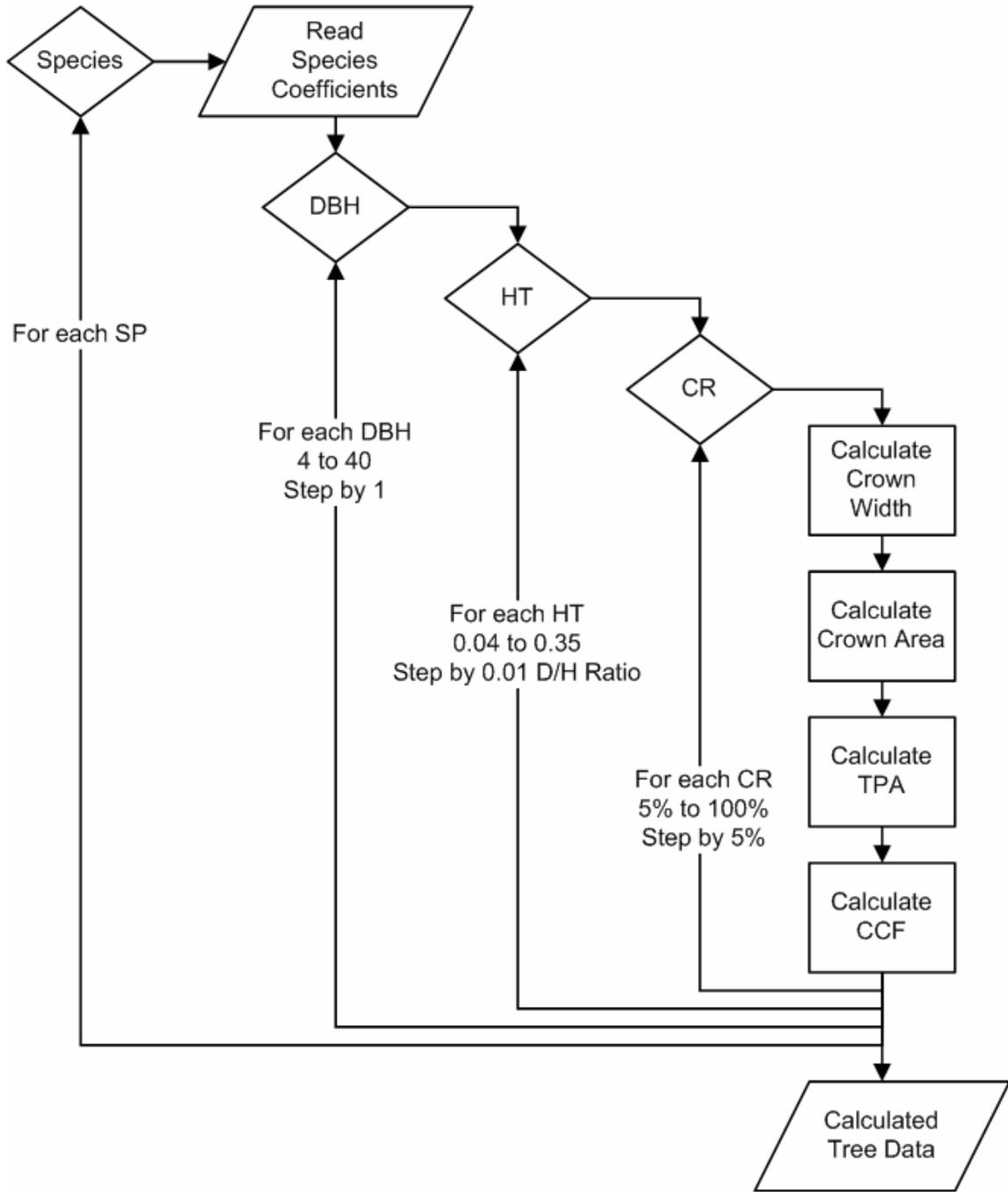
To apply Arney's (2004) methods, tree data must first be generated. Trees were generated using Melinda Moeur's (1981) crown width equations (Appendix C) and the Prognosis crown competition factor (CCF) (Wykoff et al, 1982) (Appendix D), which may be substituted for CSI in equations. The substitution of CCF and CSI can be done for the purposes of the estimation a tolerance variable as they are similar measures of competition. CCF is a stand level measure of competition and CSI is an individual tree measure of competition. Since the simulations assume a uniformly spaced plantation of trees, the CCF and CSI values should be identical. The ranges listed in Table 5 were implemented in the generation of tree data to maintain reasonable tree dimensions.

**Table 5. Tolerance Attribute Limits**

<u>Category</u>	<u>Value</u>	<u>Description</u>
Species	PP	ponderosa pine
	DF	Douglas-fir
	WL	western larch
	LP	lodgepole pine
DBH	4" – 40"	Step by 1 Diameters used to limit the range of possible diameters for this calculation.
DBH/HT	0.04 – 0.35	Step by 0.01 Ratios used to limit the range of possible heights for a given diameter to keep trees realistic in form. These values have been found to be a reasonable rule of thumb in the Inland Northwest forests. These values have been converted from the metric values ranging from .3 (DBH <sub>cm</sub> /HT <sub>m</sub> ) to 3.0 (DBH <sub>cm</sub> /HT <sub>m</sub> ) with 1.0+ being an open-grown tree. (Arney, 2003)
CR	5% – 100%	Step by 5% Values needed to generate the full range of crown ratios for a later regression.

While observing the above limitations, a large set of nested loops are used to calculate a crown width based on  $f(\text{Species}, \text{DBH}, \text{HT}, \text{CR})$  for the current iteration (Figure 9). Once a crown width has been calculated for the specified 'tree', the crown area is calculated using  $\text{Area} = \pi * r^2$ . The number of trees per acre (TPA) can then be calculated for the tree by  $\text{TPA} = \text{Acre}_{43560\text{sqft}} / \text{Crown Area}$ . Once the crown area is known the Prognosis CCF function can be used to calculate the CCF for the TPA of trees with specified sizes. An iteration of the values occurs until all values have been cycled through. Figure 9 depicts the process used to generate the data.

**Figure 9.** Tolerance Tree Data Generation Flowchart



Generated data were graphed, with the Prognosis CCF on the X axis and the crown ratio (CR) on the Y axis. A requested 'fit' line was placed on the graph by species, which then reported the 'fit' equation for the data points. A 300 CCF was then entered into the equation and the calculated CR for that level of competition was determined.

## Results and Discussion

### Data Analysis

#### *Selection of Independent Variables*

**Table 6.** Independent Variables defined

<b><u>Variable Name</u></b>	<b><u>Variable Description</u></b>
BAComp	Basal area in square feet of competition estimated using a 10-BAF prism which represents 10 sqft/ac of basal area per 'in' tree
D6	Diameter in feet (12" DBH would be a 12 foot radius) plus 6 feet.
LCLSap	Log(crown length in feet * sapwood basal area in square feet)
CRWN	Height in feet to base of live crown
CR	Crown ratio which is the balanced live crown length divided by the total tree height, expressed in percent.
V1	Diameter growth in square feet divided by sapwood basal area in square feet
V2	Sapwood basal area in square feet divided by total basal area in square feet
V3	Basal area growth in square feet divided by sapwood basal area in square feet
SiteTree	a binary representation of whether the tree was a Site(1) or Non-Site(0) tree
BAGRPerDIB	5-year Basal Area Growth in square feet per Diameter Inside Bark in inches
HG	Height Growth in feet
RADG	5-year Radial Growth in inches
BAGR	5-year Basal Area Growth in square feet
SP1	a binary variable to represent all ponderosa pine trees
SP2	a binary variable to represent all Douglas-fir trees
SP3	a binary variable to represent all western larch trees
SP5	a binary variable to represent all lodgepole pine trees
Toler	Calculated Tolerance
C_SI	Calculated site index in feet
HT	Height in feet
Age	Age in years
HEART	Radius of heartwood in inches
DOB	Diameter outside bark in inches at 4.5 feet above ground
DIB	Diameter inside bark in inches at 4.5 feet above ground
TBA	Total basal area in square feet
HRTBA	Heartwood basal area in square feet
SAPBA	Sapwood basal area in square feet
BDIA	Base of tree diameter in inches or the diameter at the ground
BBA	Base of tree basal area in square feet or the cross-sectional area at the ground

In Table 7 the variables are categorized by what they best represent whether it is competition, vigor tree status, growth rate, species and other.

**Table 7.** Independent Variables Categorized

<u>Competition</u>	<u>Vigor</u>	<u>Tree Status</u>	<u>Growth Rate</u>	<u>Species</u>	<u>Other</u>
BAComp	CR	SiteTree	BAGR	SP1	Age
D6	CRWN		BAGRPerDIB	SP2	BBA
	LCLSap		HG	SP3	BDIA
	V1		RADG	SP5	C_SI
	V2			Toler	DIB
	V3				DOB
					HEART
					HRTBA
					HT
					SAPBA
					TBA

Table grouped then sorted by variable name

After categorizing the variables, a correlation matrix using all tree data was evaluated to determine which variables best correct for the tree site index to the MSI. Correlations of selected independent variables with dependent variables are reported in Table 8.

**Table 8.** All Trees Selected Independent Variable Correlation Matrix

	<u>SI R</u>	<u>SI D</u>	<u>MSI</u>
Age	-0.2164	-0.2607 <sup>15</sup>	-0.2740 <sup>15</sup>
BAComp	0.4689 <sup>1</sup>	0.4426 <sup>1</sup>	0.0420
BAGR	-0.3154 <sup>12</sup>	-0.2960 <sup>10</sup>	0.2968 <sup>10</sup>
BAGRPerDIB	-0.3020 <sup>13</sup>	-0.2795 <sup>13</sup>	0.2611 <sup>16</sup>
BBA	-0.3230 <sup>11</sup>	-0.2955 <sup>11</sup>	0.3200 <sup>9</sup>
BDIA	-0.3849 <sup>6</sup>	-0.3429 <sup>5</sup>	0.3376 <sup>7</sup>
C_SI	-0.3477 <sup>8</sup>	-0.2945 <sup>12</sup>	0.8725 <sup>1</sup>
CR	-0.1138	-0.1209	-0.1846
CRWN	-0.1381	-0.1064	0.5052 <sup>3</sup>
D6	0.1499	0.1606	0.2923 <sup>12</sup>
DIB	-0.3901 <sup>4</sup>	-0.3483 <sup>4</sup>	0.3419 <sup>6</sup>
DOB	-0.3691 <sup>7</sup>	-0.3320 <sup>7</sup>	0.3518 <sup>5</sup>
HEART	-0.2459	-0.2074	0.2954 <sup>11</sup>
HG	-0.3927 <sup>3</sup>	-0.3669 <sup>3</sup>	0.4241 <sup>4</sup>
HRTBA	-0.1958	-0.1676	0.2833 <sup>14</sup>
HT	-0.3888 <sup>5</sup>	-0.3379 <sup>6</sup>	0.7014 <sup>2</sup>
LCLSap	-0.4206 <sup>2</sup>	-0.3725 <sup>2</sup>	0.2834 <sup>13</sup>
RADG	-0.2983 <sup>14</sup>	-0.2762 <sup>14</sup>	0.2586 <sup>17</sup>
SAPBA	-0.2596 <sup>15</sup>	-0.2492	0.1734
SiteTree	-0.3242 <sup>10</sup>	-0.3093 <sup>8</sup>	0.0150
TBA	-0.3291 <sup>9</sup>	-0.3019 <sup>9</sup>	0.3244 <sup>8</sup>
V1	0.2057	0.1698	0.0122
V2	0.0043	-0.0070	-0.1105
V3	-0.0542	-0.0444	0.1991

Table sorted by variable name where the y of  $x^y$  is the sorted correlation absolute value ranking down to a minimum correlation value of 0.25. The rank value of 1 represents the most highly correlated value progressing to less correlated values as the rank number of the selected independent variables increases.

The independent variables were then placed in an OLS multiple linear reverse stepwise regression. This minimized the residuals of the specified dependent variables against candidate independent variables, with the desired outcome being the fewest number of variables remaining in the final regression. Results of the stepwise regression indicating variables remaining in the regression and species by dependent variable can be found in Table 9.

**Table 9. Stepwise Regression Variable Results**

	PP			DF			WL			LP		
	<u>SI</u>	<u>R</u>	<u>MSI</u>									
Age		*	*	*	*		*	*	*	*	*	*
BAComp				*	*	*	*	*	*		*	*
BAGRPerDIB	*	*	*	*	*	*				*		
BBA				*	*	*			*			
C_SI			*			*			*			*
CR							*					
CRWN	*	*	*	*	*	*		*				
D6	*						*	*				
DOB	*	*	*		*	*				*	*	*
HEART	*	*	*		*	*	*	*				
HG	*	*	*	*	*	*	*	*	*	*	*	*
HRTBA					*	*	*	*	*	*	*	*
HT	*	*		*	*	*			*			*
LCL Sap	*	*	*	*	*	*	*	*	*	*	*	*
RADG				*	*	*			*		*	*
SiteTree	*	*	*						*			
TBA				*	*	*	*		*	*	*	*
V1				*	*	*	*	*	*	*	*	*
V2	*	*	*		*	*		*	*			
V3							*	*	*	*	*	*

\*: variable was remaining in the final step of the stepwise regression.

Stepwise regression results are further summarized in Table 10, which reports the number of times a variable comes in across species and dependent variables.

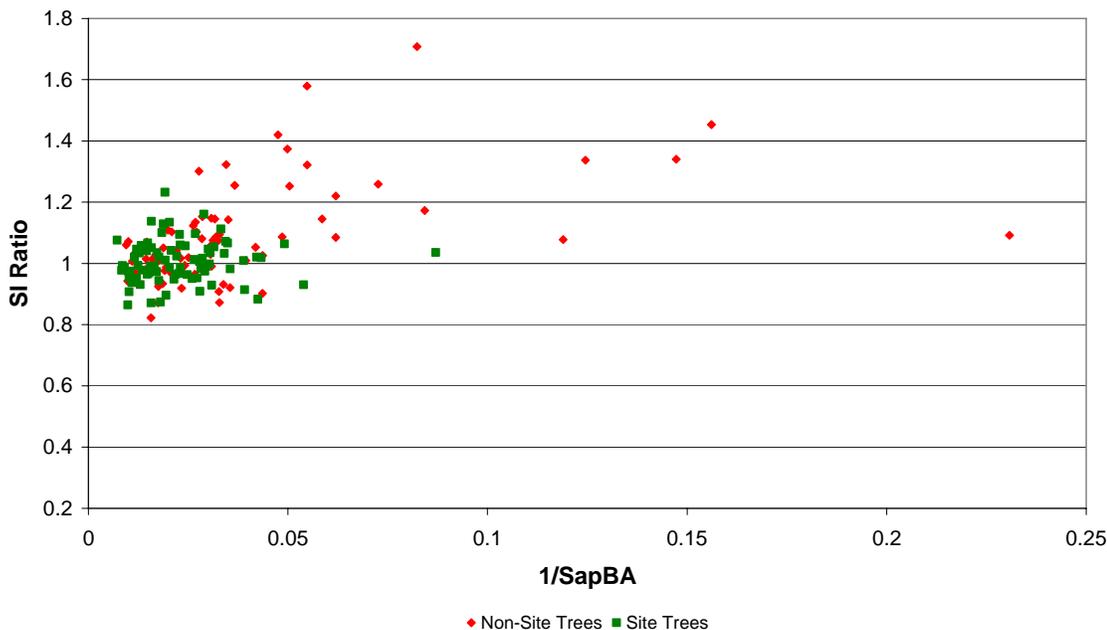
**Table 10.** Stepwise Regression Summary

<u>Variable</u>	<u>Count</u>	<u>Variable</u>	<u>Count</u>
HG	12	HEART	7
LCLSap	12	HT	7
Age	10	V2	7
V1	9	RADG	6
BAComp	8	V3	6
DOB	8	BBA	4
HRTBA	8	C_SI	4
TBA	8	SiteTree	4
BAGRPerDIB	7	D6	3
CRWN	7	CR	1

Table sorted by number of times a value remained in the stepwise regression series

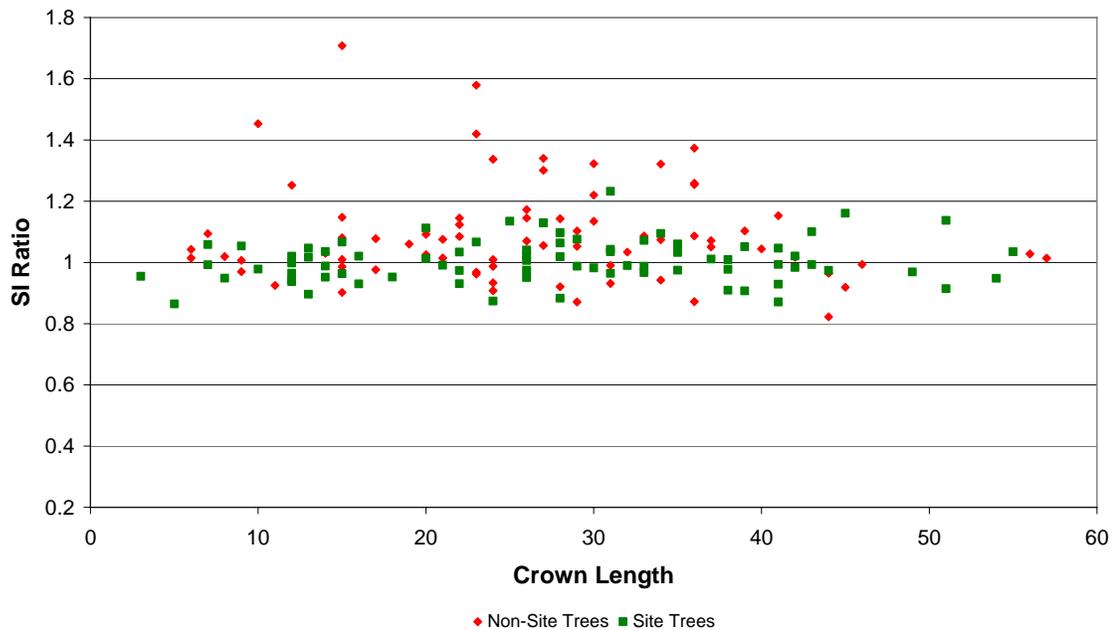
The combined results from Table 7 - Table 10 provide the basis for determining what variables to use. Some of the initial attempts to screen variables exposed artifacts of the data. For example, Figure 10 demonstrates that a variable like 1/SapBA shows a clear trend across all levels of site index, but doesn't differentiate between site and non-site trees.

**Figure 10.** SI\_R vs. 1/SapBA Trend Example



While in Figure 11 you can see no clear pattern evolving from the scatter of data.

**Figure 11. SI\_R vs. Crown Length Lack of Trend Example**



The variables Age, BAComp, BAGRPerDIB, BBA, C\_SI, CR, CRWN, D6, DOB, HEART, HG, HRTBA, HT, RADG and TBA occur across all levels of site index. Thus, the use of these variables must be carefully evaluated. Another consideration is that a variable like height growth (HG) is a destructive measure and was not considered for the model, as non-destructive means were preferred. While the procedures for data collection were stringent, the calculated variable of DBH in feet + 6 feet ('D+6') as a measure of competition was not complete throughout the dataset and therefore was not used. BAComp was complete throughout the dataset and was used as a measure of competition.

After examining the available independent variables, four were chosen for their ability to represent Competition, Vigor, Tree Status and Growth Rate. Only four were selected to minimize the number of coefficients due to the small dataset and concerns about over fitting the data. The variables chosen were:

*Competition:* BAComp

*Vigor:* LCLSap

*Tree Status:* SiteTree

*Growth Rate:* BAGRPerDIB

These four variables were used throughout the analysis to keep the model simple and directly comparable. While not all of these variables are significant for all models, they did appear to be the best variables available to represent the factors of interest.

## Modeling

### **Species Level Model**

Final prediction models for SI adjustment, by species, were constructed for each dependent variable and used as a general statistical baseline. This was done because an individual species model should explain the most variation for each species and make the best fit model. The results of those regressions can be found in Table 11.

After some initial regressions, the MSI model was consistently found to perform as badly if not worse than the sample standard deviation. The model was then modified for MSI to include C\_SI, since all the other models accounted for calculated site index in some way. By adding C\_SI to the MSI model, the model performed as well as the other models and the associated R<sup>2</sup> and standard error values improved greatly.

Initial examination of the  $\beta$  coefficients showed that WL and LP both had a change of sign associated with BAGRPerDIB (Table 11). This would indicate that for a greater 5 year basal area growth per diameter inside bark dimension, greater site index adjustment would be necessary. This is illogical as site trees should require less correction. This issue was never resolved. It may be due to the relatively small samples sizes for WL and LP and this may be an artifact of the data or result from a few outliers heavily skewing the results.

**Table 11.** Individual Species Model Statistics and Variable Estimates

	PP			DF		
	<u>SI_R</u>	<u>SI_D</u>	<u>MSI</u>	<u>SI_R</u>	<u>SI_D</u>	<u>MSI</u>
SE	0.099	5.063	5.082	0.101	5.047	5.015
R <sup>2</sup>	0.574	0.554	0.823	0.408	0.363	0.867
Intercept	1.4881 <sup>3</sup>	22.624 <sup>3</sup>	22.0901 <sup>3</sup>	1.0539 <sup>3</sup>	2.0635	0.4387
BAComp	0.0	0.0014	0.0008	0.0005 <sup>3</sup>	0.0254 <sup>3</sup>	0.023 <sup>3</sup>
BAGRPerDIB	-12.6284 <sup>1</sup>	-829.0721 <sup>2</sup>	-825.1353 <sup>2</sup>	-5.6925	-331.4578	-345.9852
LCLSap	-0.0986 <sup>3</sup>	-4.145 <sup>3</sup>	-4.5369 <sup>3</sup>	-0.0181	-0.4672	-1.3109
SiteTree	-0.0283	-1.5741	-1.5705	-0.0187	-0.9821	-1.041
C_SI			1.0325 <sup>3</sup>			1.0744 <sup>3</sup>

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	WL			LP		
	<u>SI_R</u>	<u>SI_D</u>	<u>MSI</u>	<u>SI_R</u>	<u>SI_D</u>	<u>MSI</u>
SE	0.109	6.897	6.498	0.091	4.614	4.594
R <sup>2</sup>	0.295	0.227	0.672	0.291	0.254	0.849
Intercept	1.0586 <sup>3</sup>	0.8736	11.3829 <sup>2</sup>	1.1003 <sup>3</sup>	3.6852 <sup>1</sup>	5.7338 <sup>2</sup>
BAComp	0.0004 <sup>3</sup>	0.0235 <sup>3</sup>	0.0309 <sup>3</sup>	0.0001	0.0089 <sup>1</sup>	0.0098 <sup>1</sup>
BAGRPerDIB	9.2554 <sup>1</sup>	551.3306	583.8963 <sup>1</sup>	11.3387 <sup>1</sup>	416.0266	399.3712
LCLSap	-0.0646 <sup>3</sup>	-2.8818 <sup>1</sup>	-0.2139	-0.0548 <sup>3</sup>	-2.1745 <sup>3</sup>	-1.6603 <sup>1</sup>
SiteTree	-0.0303	-1.8643	-1.7516	-0.0404 <sup>1</sup>	-2.0169 <sup>1</sup>	-1.9913 <sup>1</sup>
C_SI			0.7425 <sup>3</sup>			0.9427 <sup>3</sup>

<sup>3</sup>: Significance of < 0.001

<sup>2</sup>: Significance of 0.001 to 0.01

<sup>1</sup>: Significance of 0.01 to 0.05

R<sup>2</sup>: Percent variation explained by the model

SE: Standard Error of the regression

*Residual Analysis in SI Units*

The initial regression statistics seen in Table 11 are all in the original units of the regression. This means that standard errors of the regressions will represent the standard error of the ratio for the SI\_R model and the standard error of the difference for SI\_D model. To compare values, each individual model was then applied to all trees to predict SI for every tree in the data set. Predicted SI was then regressed against the MSI values in the form of:

$$MSI = \beta_0 + \beta_1 * Predicted_{SI}$$

The resulting statistics allow the comparison of all models in the common units of SI feet (Table 12).

**Table 12.** Individual Species Model Residual Statistics

	<b>PP</b>			<b>DF</b>		
	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>
<b>Non-Site Trees</b>						
SE <sub>F<sub>feet</sub></sub>	5.980	5.613	5.605	5.615	5.788	5.750
R <sup>2</sup>	0.767	0.795	0.795	0.846	0.837	0.839
β <sub>0</sub>	2.088	-2.727	-1.072	-0.324	-4.488 <sup>1</sup>	-1.806
β <sub>1</sub>	0.963	1.044	1.017	1.005	1.077 <sup>1</sup>	1.031
<b>Site Trees</b>						
SE <sub>F<sub>feet</sub></sub>	4.723	4.445	4.449	4.342	4.096	4.101
R <sup>2</sup>	0.832	0.852	0.851	0.888	0.901	0.900
β <sub>0</sub>	-1.652	-0.802	0.952	0.043	-0.818	1.696
β <sub>1</sub>	1.030	1.013	0.985	1.001	1.014	0.971

	<b>WL</b>			<b>LP</b>		
	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>
<b>Non-Site Trees</b>						
SE <sub>F<sub>feet</sub></sub>	7.779	7.592	7.570	5.050	5.013	5.012
R <sup>2</sup>	0.554	0.576	0.578	0.816	0.819	0.819
β <sub>0</sub>	22.084 <sup>2</sup>	18.210 <sup>2</sup>	7.484 <sup>1</sup>	5.158 <sup>1</sup>	3.743 <sup>1</sup>	1.447
β <sub>1</sub>	0.679 <sup>2</sup>	0.742 <sup>2</sup>	0.894 <sup>1</sup>	0.907	0.936 <sup>1</sup>	0.975
<b>Site Trees</b>						
SE <sub>F<sub>feet</sub></sub>	5.854	5.488	5.187	4.167	4.023	3.998
R <sup>2</sup>	0.710	0.745	0.772	0.872	0.881	0.882
β <sub>0</sub>	5.664 <sup>1</sup>	6.467 <sup>1</sup>	-7.937 <sup>1</sup>	-0.258	1.235	-1.708
β <sub>1</sub>	0.918 <sup>1</sup>	0.906 <sup>1</sup>	1.115 <sup>1</sup>	1.006	0.979	1.029

β value without marking is within one standard deviation of desired β value

<sup>1</sup>: one to two standard deviations from desired β value

<sup>2</sup>: > two standard deviations from desired β value

R<sup>2</sup>: Percent variation explained by the model

SE<sub>F<sub>feet</sub></sub>: Regression Standard Error

All models appear to perform similarly, both in terms of species and dependent variables (Table 12). The standard errors and R<sup>2</sup> for site trees range from about 4' to 4.5' and .83 to .90, respectively. These ranges

do not include the western larch results. The western larch models had standard errors nearly a foot greater as well as lower  $R^2$ 's. While it is important that results from site trees used in this process must remain reasonable, the non-site tree results provide the real basis for comparison. Non-site trees have standard errors ranging from nearly 5' to 6' and  $R^2$ 's ranging from 0.75 to 0.85, while western larch standard errors range from 7.5 to 7.9 and  $R^2$ 's from .55 to .60.

Comparison to alternative methods of calculating SI from sites with limited or no site trees, such as the soil site equation reported (Table 2), ponderosa pine, Douglas-fir and lodgepole pine models perform better across all dependent variables by approximately 3' for PP, 1' for DF and 1.2' for LP, respectively. Further comparison shows that a soil site equation performs as well as site index correction for WL.

Evaluating bias by the use of  $\beta_0 < 0$  and  $\beta_1 < 1$  shows minimal bias in the models, with the exception of WL which consistently demonstrated bias with standard errors 1 to 2+ larger than the given  $\beta$ 's expected value. Lodgepole pine models exhibited some tendency of bias, but estimates are still within 2 standard errors or 98% likelihood of the expected  $\beta$  values.

*Across Species Modeling*

**All Species Pooled Model**

A set of final prediction models was constructed using pooled data for the SI adjustment and for each dependent variable, yielding the results in the original units of the regression (Table 13).

**Table 13.** All Species Regression Statistics

	<u>SI R</u>	<u>SI D</u>	<u>MSI</u>
SE	0.107	5.754	5.674
R <sup>2</sup>	0.287	0.246	0.809
Intercept	1.08181 <sup>3</sup>	3.15839 <sup>2</sup>	6.49177 <sup>3</sup>
BAComp	0.00033 <sup>3</sup>	0.01707 <sup>3</sup>	0.01815 <sup>3</sup>
BAGRPerDIB	-0.5576	-57.070	26.9451
LCLSap	-0.0314 <sup>3</sup>	-1.2590 <sup>3</sup>	-0.8018 <sup>1</sup>
SiteTree	-0.0367 <sup>3</sup>	-1.9123 <sup>3</sup>	-1.7878 <sup>3</sup>
C_SI			0.91420 <sup>3</sup>

<sup>3</sup>: Significance of < 0.001

<sup>2</sup>: Significance of 0.001 to 0.01

<sup>1</sup>: Significance of 0.01 to 0.05

R<sup>2</sup>: Percent variation explained by the model

SE: Standard error of the regression

*Residual Analysis in SI Units*

To compare the values for each individual model, the models were applied to all trees to predict SI for every tree in the data set (Table 13). Predicted SI's were then regressed against the MSI values in the form of:

$$MSI = \beta_0 + \beta_1 * Predicted_{SI}$$

The resulting statistics found in Table 14 allow comparison of all models in the common units of SI feet.

**Table 14.** All Species Regression Residual Statistics

	<b>PP</b>			<b>DF</b>		
	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>
	<b>Non-Site Trees</b>					
SE <sub>F<sub>feet</sub></sub>	6.997	6.915	7.097	5.900	5.975	6.031
R <sup>2</sup>	0.681	0.688	0.672	0.830	0.826	0.823
β <sub>0</sub>	10.925 <sup>1</sup>	10.136 <sup>1</sup>	6.439 <sup>1</sup>	0.537	-3.309	-7.929 <sup>2</sup>
β <sub>1</sub>	0.861 <sup>1</sup>	0.872 <sup>1</sup>	0.926	1.001	1.071 <sup>1</sup>	1.144 <sup>2</sup>
	<b>Site Trees</b>					
SE <sub>F<sub>feet</sub></sub>	4.831	4.739	4.883	4.151	4.043	4.094
β <sup>2</sup>	0.825	0.831	0.821	0.898	0.903	0.901
β <sub>0</sub>	5.163 <sup>1</sup>	7.365 <sup>2</sup>	3.094	-1.538	-0.616	-5.011 <sup>2</sup>
β <sub>1</sub>	0.948	0.901 <sup>1</sup>	0.962	1.045 <sup>1</sup>	1.031	1.101 <sup>2</sup>

	<b>WL</b>			<b>LP</b>		
	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>
	<b>Non-Site Trees</b>					
SE <sub>F<sub>feet</sub></sub>	7.913	7.830	7.792	5.161	5.131	5.121
R <sup>2</sup>	0.539	0.549	0.553	0.808	0.810	0.811
β <sub>0</sub>	22.396 <sup>2</sup>	18.331 <sup>2</sup>	14.876 <sup>2</sup>	6.705 <sup>2</sup>	3.917 <sup>1</sup>	-0.036
β <sub>1</sub>	0.659 <sup>2</sup>	0.731 <sup>2</sup>	0.789 <sup>2</sup>	0.858 <sup>2</sup>	0.911 <sup>1</sup>	0.978
	<b>Site Trees</b>					
SE <sub>F<sub>feet</sub></sub>	5.744	5.541	5.428	4.104	4.041	4.066
β <sup>2</sup>	0.721	0.740	0.751	0.876	0.880	0.878
β <sub>0</sub>	5.000 <sup>1</sup>	4.791 <sup>1</sup>	0.303	0.024	0.895	-3.669
β <sub>1</sub>	0.907 <sup>1</sup>	0.916 <sup>1</sup>	0.990	0.981 <sup>2</sup>	0.969	1.044

β value without marking is within one standard deviation of desired β value

<sup>1</sup>: one to two standard deviations from desired β value

<sup>2</sup>: > two standard deviations from desired β value

R<sup>2</sup>: Percent variation explained by the model

SE<sub>F<sub>feet</sub></sub>: Regression Standard Error

While the assumption is that an individual species model is the best and that a model using all data with no species difference would perform the worst. In comparison to the individual species models the all species models have higher SE's and lower R<sup>2</sup>'s, though differences

are not great. Site tree SE's range from approximately 4' to 5' and  $R^2$ 's from .82 to .90. Western larch models once again performed the worst, with SE's of 5.5 to 5.75 and  $R^2$ 's of 0.72 to 0.75. Comparing differences between the individual species models and the pooled data for site trees, there is a maximum loss of only 0.5' and a minimum loss of about 0.1' in SE's. For the non-site tree results, SE's range from 5.1' to 7' and  $R^2$ 's of 0.68 to 0.85; with WL SE's ranging from 7.7' to 7.9' and  $R^2$ 's of about 0.55. In comparison to the individual species models, there is a maximum of 1.3' to a minimum of 0.1' difference in standard errors.

All-species models do not differ greatly from the individual species model, which means they still out perform soil site equations by at least a foot of SI. However, a soil site equation would be slightly better (less than .5') for WL.

A comparison of bias estimates among models suggests that more all-species model forms show bias. For example, the DF MSI model and the LP SI\_R model show bias tending to exceed 2 SE's.

### Dummy Variable Model

The final prediction models for SI adjustment, including the dummy variables representing species difference for each dependent variable, are reported in the original models units in Table 15.

**Table 15.** Dummy Variable Regression Statistics

	<u>SI R</u>	<u>SI D</u>	<u>MSI</u>
SE	0.103	5.602	5.588
R <sup>2</sup>	0.344	0.29	0.815
Intercept	1.14901 <sup>3</sup>	6.29184 <sup>3</sup>	7.60307 <sup>3</sup>
BAComp	0.00028 <sup>3</sup>	0.01508 <sup>3</sup>	0.01614 <sup>3</sup>
BAGRPerDIB	-0.4487	-75.932	-69.638
LCLSap	-0.0511 <sup>3</sup>	-2.0385 <sup>3</sup>	-1.5469 <sup>2</sup>
SiteTree	-0.0309 <sup>2</sup>	-1.6682 <sup>2</sup>	-1.6551 <sup>2</sup>
C_SI			0.95147 <sup>3</sup>
SP1	0.05146 <sup>3</sup>	1.77656 <sup>1</sup>	1.47357
SP3	-0.0416 <sup>2</sup>	-2.1311 <sup>2</sup>	-1.3867
SP5	-0.0394 <sup>2</sup>	-2.2032 <sup>3</sup>	-2.0482 <sup>2</sup>

<sup>3</sup>: Significance of < 0.001

<sup>2</sup>: Significance of 0.001 to 0.01

<sup>1</sup>: Significance of 0.01 to 0.05

R<sup>2</sup>: Percent variation explained by the model

SE: Sample Standard Error

#### *Residual Analysis in SI Units*

The adjustment models were then applied to each sample tree.

The adjusted SI was then compared to actual MSI for each model by regressing MSI on Adjusted SI. Results for the dummy variable models show both non-site trees and site trees have slightly larger standard errors than with the individual tree models (Table 16).

**Table 16.** Dummy Variable Regression Residual Statistics

	<b>PP</b>			<b>DF</b>		
	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>
	<b>Non-Site Trees</b>					
SE <sub>Feet</sub>	6.807	6.693	6.796	5.799	5.873	5.889
R <sup>2</sup>	0.698	0.708	0.699	0.836	0.832	0.831
β <sub>0</sub>	8.759 <sup>1</sup>	6.208 <sup>1</sup>	4.557	-1.467	-6.574 <sup>1</sup>	-8.816 <sup>2</sup>
β <sub>1</sub>	0.860 <sup>1</sup>	0.909 <sup>1</sup>	0.936	1.024	1.110 <sup>1</sup>	1.148 <sup>2</sup>
	<b>Site Trees</b>					
SE <sub>Feet</sub>	4.676	4.633	4.698	4.278	4.085	4.064
R <sup>2</sup>	0.836	0.839	0.834	0.892	0.901	0.902
β <sub>0</sub>	3.251	4.231 <sup>1</sup>	2.121	-3.563 <sup>1</sup>	-3.317 <sup>1</sup>	-5.473 <sup>2</sup>
β <sub>1</sub>	0.937 <sup>1</sup>	0.924 <sup>1</sup>	0.958	1.066 <sup>1</sup>	1.060 <sup>1</sup>	1.097 <sup>2</sup>

	<b>WL</b>			<b>LP</b>		
	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>
	<b>Non-Site Trees</b>					
SE <sub>Feet</sub>	7.975	7.825	7.807	5.283	5.178	5.156
R <sup>2</sup>	0.532	0.549	0.551	0.799	0.807	0.809
β <sub>0</sub>	21.603 <sup>2</sup>	18.009 <sup>2</sup>	15.913 <sup>2</sup>	4.766 <sup>1</sup>	3.295 <sup>1</sup>	1.415
β <sub>1</sub>	0.686 <sup>2</sup>	0.746 <sup>2</sup>	0.776 <sup>2</sup>	0.910 <sup>2</sup>	0.940 <sup>1</sup>	0.972
	<b>Site Trees</b>					
SE <sub>Feet</sub>	6.078	5.691	5.618	4.275	4.108	4.084
R <sup>2</sup>	0.688	0.726	0.733	0.865	0.876	0.877
β <sub>0</sub>	4.157	4.956 <sup>1</sup>	2.197	-1.460	1.085	-1.311
β <sub>1</sub>	0.940	0.926 <sup>1</sup>	0.966	1.033	0.987	1.027

β value without marking is within one standard deviation of desired β value

<sup>1</sup>: one to two standard deviations from desired β value

<sup>2</sup>: > two standard deviations from desired β value

R<sup>2</sup>: Percent variation explained by the model

SE<sub>Feet</sub>: Regression Standard Error

The dummy variable models have site tree SE's ranging from 4.0' to 4.7', while the SE for non-site trees ranges from approximately 5.2' to 6.8'. R<sup>2</sup>'s of site and non-site trees range from .83 to .90 and .70 to .80, respectively. The SE's of WL non-site trees range from 7.8' to

8.0' with  $R^2$ 's of .5. Western larch site trees have SE's ranging from 5.6' to 6.0', with  $R^2$ 's of 0.70. PP, DF and even WL to a lesser degree, benefit from the use of dummy variables as a means of differentiating species attributes, but show only a slight improvement to the all species pooled regression. The LP models, however, become slightly worse than the all species pooled regression. While the desired effect of using dummy variables was to improve on the individual species model, no such improvement in non-site tree values occurred over the individual tree models.

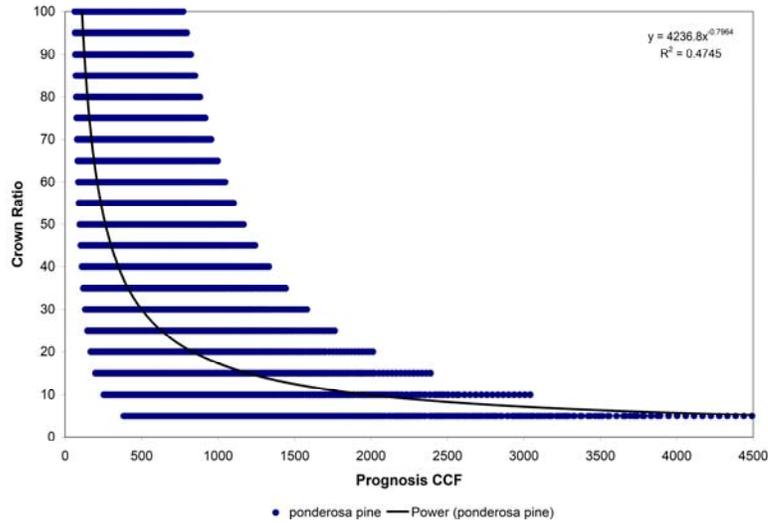
With no improvement on the individual species model, there is little that can be learned from the comparison of the soil site equation with the dummy variable model. The dummy model still performs better, with the exception of WL, than the soil site equation with minor improvements over the all species model. There was negligible change in bias with this model form in comparison to the all species model.

## Tolerance Model

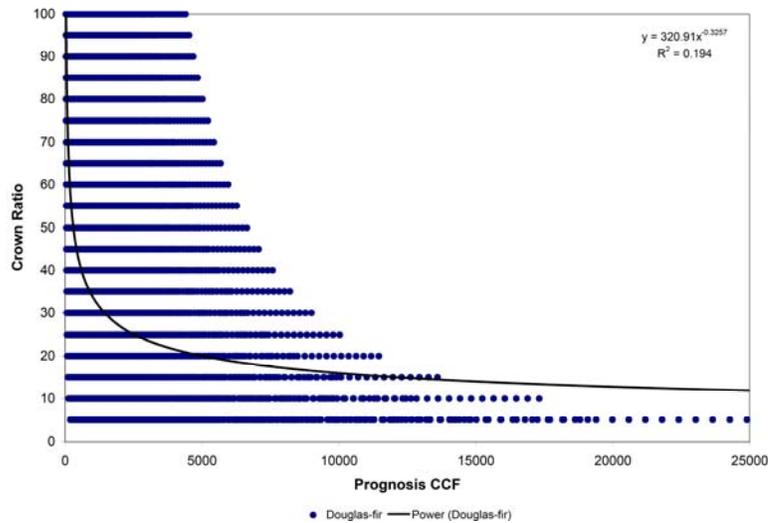
### Calculation of the Species Tolerance Variable

Nearly 23,000 trees per species were generated based on predefined attributes ranges. The crown ratio and CCF results of these generated trees were then graphed and had a fit line regressed through the data as seen in Figure 12, Figure 13, Figure 14 and Figure 15.

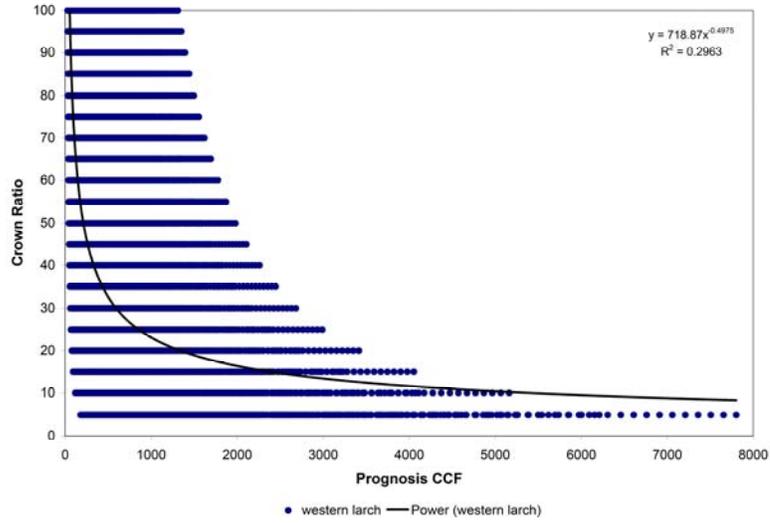
**Figure 12. Ponderosa Pine Tolerance Model**



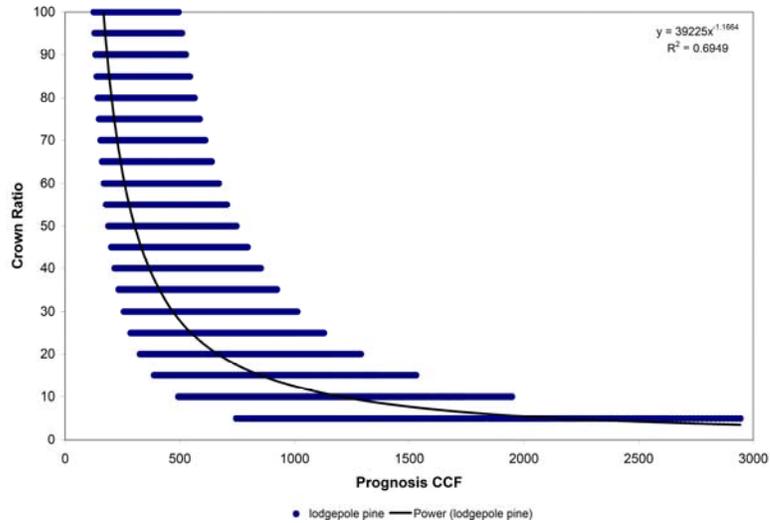
**Figure 13. Douglas-fir Tolerance Model**



**Figure 14. Western Larch Tolerance Model**



**Figure 15. Lodgepole Pine Tolerance Model**



Coefficients for the regression model ( $CR = \beta_0 * CCF^{\beta_1}$ ) for each species are displayed in Table 17.

**Table 17. Tolerance Coefficient Results**

	$\beta_0$	$\beta_1$	$R^2$
ponderosa pine	4236.8	-0.7964	0.47
Douglas-fir	320.91	-0.3257	0.19
western larch	718.87	-0.4975	0.29
lodgepole pine	39225	-1.1664	0.69

Calculated individual species tolerance variables at a CCF of 300 are displayed in Table 18, along with FPS tolerance values for comparison.

**Table 18. Tolerance Species Calculation Results**

<u>Code</u>	<u>Species</u>	<u>FPS</u>	<u>CalcTol</u>	<u>FPSToler</u>
1	ponderosa pine	PP	0.4510	0.30
2	Douglas-fir	DF	0.5007	0.40
3	western larch	WL	0.4210	0.25
5	lodgepole pine	LP	0.5061	0.30

While there do appear to be species differences, the comparison of differences lies outside the scope of this report, since the use of tolerance and not tolerance itself was being investigated to explain species differences.

Statistics for the final tolerance prediction models for SI adjustment, by dependent variable, are shown in Table 19.

**Table 19. Tolerance Regression Statistics**

	<u>SI R</u>	<u>SI D</u>	<u>MSI</u>
SE	0.107	5.752	5.652
R <sup>2</sup>	0.289	0.248	0.811
Intercept	1.1202 <sup>3</sup>	5.0073 <sup>2</sup>	10.5955 <sup>3</sup>
BAComp	0.0003 <sup>3</sup>	0.0171 <sup>3</sup>	0.0183 <sup>3</sup>
BAGRPerDIB	-1.8733	-120.3915	-84.9288
LCLSap	-0.0296 <sup>3</sup>	-1.1727 <sup>2</sup>	-0.5665
SiteTree	-0.0369 <sup>3</sup>	-1.9188 <sup>3</sup>	-1.7824 <sup>3</sup>
C_SI			0.9018 <sup>3</sup>
Toler	-0.0956	-4.6009	-9.0119 <sup>1</sup>

<sup>3</sup>: Significance of < 0.001  
<sup>2</sup>: Significance of 0.001 to 0.01  
<sup>1</sup>: Significance of 0.01 to 0.05

R<sup>2</sup>: Percent variation explained by the model  
 SE: Sample Standard Error

*Residual Analysis in SI Units*

The tolerance model is applied to each sample tree yielding the predicted SI value. The MSI value is then regressed against the predicted SI so that the regression statistics can be compared to the other models. Results for non-site trees and site trees are shown in Table 20.

**Table 20.** Tolerance Regression Residual Statistics

	<b>PP</b>			<b>DF</b>		
	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>
<b>Non-Site Trees</b>						
SE <sub>Fect</sub>	6.994	6.920	7.072	5.899	5.977	6.015
R <sup>2</sup>	0.681	0.688	0.674	0.830	0.826	0.823
β <sub>0</sub>	10.915 <sup>1</sup>	10.183 <sup>1</sup>	5.612	0.521	-3.317	-8.404 <sup>2</sup>
β <sub>1</sub>	0.861 <sup>1</sup>	0.872 <sup>1</sup>	0.935	1.002	1.070 <sup>1</sup>	1.157 <sup>2</sup>
<b>Site Trees</b>						
SE <sub>Fect</sub>	4.829	4.743	4.867	4.150	4.045	4.077
R <sup>2</sup>	0.825	0.831	0.822	0.898	0.903	0.902
β <sub>0</sub>	5.145 <sup>1</sup>	7.410 <sup>2</sup>	2.198	-1.550	-0.630	-5.411 <sup>2</sup>
β <sub>1</sub>	0.948	0.900 <sup>1</sup>	0.973	1.046 <sup>1</sup>	1.030	1.112 <sup>2</sup>

	<b>WL</b>			<b>LP</b>		
	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>	<b><u>SI R</u></b>	<b><u>SI D</u></b>	<b><u>MSI</u></b>
<b>Non-Site Trees</b>						
SE <sub>Fect</sub>	7.915	7.829	7.795	5.163	5.129	5.136
R <sup>2</sup>	0.539	0.549	0.553	0.808	0.811	0.810
β <sub>0</sub>	22.400 <sup>2</sup>	18.374 <sup>2</sup>	14.105 <sup>2</sup>	6.708 <sup>2</sup>	3.885 <sup>1</sup>	-0.198
β <sub>1</sub>	0.659 <sup>2</sup>	0.731 <sup>2</sup>	0.795 <sup>2</sup>	0.858 <sup>2</sup>	0.912 <sup>1</sup>	0.984
<b>Site Trees</b>						
SE <sub>Fect</sub>	5.747	5.537	5.448	4.104	4.042	4.067
R <sup>2</sup>	0.721	0.741	0.749	0.876	0.880	0.878
β <sub>0</sub>	5.005 <sup>1</sup>	4.834 <sup>1</sup>	-0.597	0.021	0.869	-3.958 <sup>1</sup>
β <sub>1</sub>	0.907 <sup>1</sup>	0.916 <sup>1</sup>	0.998	0.981 <sup>2</sup>	0.969	1.053 <sup>1</sup>

β value without marking is within one standard deviation of desired β value

<sup>1</sup>: one to two standard deviations from desired β value

<sup>2</sup>: > two standard deviations from desired β value

R<sup>2</sup>: Percent variation explained by the model

SE<sub>Fect</sub>: Regression Standard Error

Standard error values for the tolerance-adjusted regression models range from 5.1' to 7.9' and 4.0' to 5.7' for non-site and site trees, respectively, while R<sup>2</sup>'s range from .65 to .85 and from .80 to .90 for non-site and site trees, respectively. The western larch model performs similarly to the other species models. In a comparison to the

all species model, there is an average improvement of only 0.01' of SE using the tolerance value.

Due to the slight differences between the tolerance model and the all species model the same recommendations would hold true.

The tolerance model has reduced the potential bias associated with the WL site tree model within an acceptable range, and has removed bias from the LP site tree results.

## Conclusions

Results showed that there was little difference between the chosen dependent variables of MSI, SI\_D and SI\_R modeling approaches, and that no one model form performed consistently better than another. While all of the models developed throughout this project significantly improve upon the sample error terms and consistently beat a soil site equation by at least a foot for species other than WL, these models are not intended to and cannot replace the proper measurement of site trees used with appropriate site curves. These models may prove to be less costly than developing a soil site equation given there are site and non-site trees available, and should provide equivalent if not better site quality prediction. The results tend to demonstrate that these approaches would result in a more accurate estimation of productivity and lead to increased accuracy of future modeling.

While the individual species models performed best, with the highest  $R^2$  and the lowest SE, there was a degradation (>1' of SI) of results using the pooled models. The pooled models demonstrated that there is a species difference that we were unable to account for. Further investigations will be needed to find an appropriate explanation for species differences. With the consistent lack of performance coming from WL models, pooled on a larger dataset (minus WL) would be suggested.

Although, the use of tolerance provided little improvement in this analysis, the use of tolerance should still be considered for other analyses, particularly in sensitivity analyses to determine if 300 CSI is an appropriate level to use. Specifically sampling crown ratio from stem mapped plots to determine if the relationship of CSI to CR that has been modeled is similar to what would occur in all aged stands should be conducted.

After these questions have been addressed a reexamination may be warranted based on the findings.

Even with the lofty goal of finding a universal correction model using factors like tolerance, the individual species models perform well enough to demonstrate that estimating site productivity from non-site trees is possible and can reduce the population SE rate by half. With a 1' difference in SI yielding a modeled difference of  $\pm 1$  mbf volume at CMAI, this approach appears to improve results enough to be considered a viable alternative. However, further investigation is warranted given that no dataset was available to validate these results.

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## Appendix A: Milner 1991 Site Equations

### Site Index Equations:

ponderosa pine

$$SI = 59.6 + \left( 4.787 + (0.012544 * A) - (1.141 * \ln A) + \frac{11.4}{A^2} \right) * \left( H - 4.5 - 121.4 * \left( 1 - e^{(-0.01756 * A)} \right)^{1.483} \right)$$

Douglas-fir

$$SI = 57.3 + \left( 7.06 + (0.02275 * A) - (1.858 * \ln A) + \frac{5.496}{A^2} \right) * \left( H - 4.5 - 114.6 * \left( 1 - e^{(-0.01462 * A)} \right)^{1.179} \right)$$

western larch

$$SI = 69.0 + \left( -0.8019 + (17.06 / A) + (0.4268 * \ln A) - 0.00009635 * A^2 \right) * \left( H - 4.5 - 127.8 * \left( 1 - e^{(-0.01655 * A)} \right)^{1.196} \right)$$

lodgepole pine

$$SI = 59.6 + \left( 1.055 - (0.006344 * A) + \frac{14.82}{A} - \frac{5.212}{A^2} \right) * \left( H - 4.5 - 96.93 * \left( 1 - e^{(-0.01955 * A)} \right)^{1.216} \right)$$

### Height Growth Equations:

ponderosa pine

$$H = 4.5 + \left( 121.4 * \left( 1 - e^{(-0.01756 * A)} \right)^{1.483} \right) + \left( 1.189 * \left( 1 - e^{(-0.05799 * A)} \right)^{2.63} \right) * (SI - 59.6)$$

Douglas-fir

$$H = 4.5 + \left( 114.6 * \left( 1 - e^{(-0.01462 * A)} \right)^{1.179} \right) + \left( 1.703 * \left( 1 - e^{(-0.02214 * A)} \right)^{1.321} \right) * (SI - 57.3)$$

western larch

$$H = 4.5 + \left( 127.8 * \left( 1 - e^{(-0.01655 * A)} \right)^{1.196} \right) + \left( 1.289 * \left( 1 - e^{(-0.03211 * A)} \right)^{1.047} \right) * (SI - 69.0)$$

lodgepole pine

$$H = 4.5 + \left( 96.93 * \left( 1 - e^{(-0.01955 * A)} \right)^{1.216} \right) + \left( 1.410 * \left( 1 - e^{(-0.02656 * A)} \right)^{1.297} \right) * (SI - 59.6)$$

Appendix B: **Full List of Measured and Derived Values**

<b><u>Table</u></b>	<b><u>Column</u></b>	<b><u>Description</u></b>
841xydata	ASP30	30m Aspect
	ECOREG_L3	L3 Eco Region
	ECOREG_L4	L4 Eco Region
	ELE30	30m Elevation Data
	HEAT1000	1000m Heat Data
	NLCD92	National Land Cover Designation
	PCP1000	1000m Precipitation Data
	POINTS_ID	Unique ID
	RAD1000	1000m Solar Radiation Data
	SLP30	30m Slope Data
	X_COORD	Montana State Plane X
	Y_COORD	Montana State Plane Y
CLASS	Code	Class Number
	Comment	Comment for Class
	Label	Class Name
	Max	Maximum Class Number Value
	Min	Minimum Class Number Value
LIBRSPP	Form	Life form, 10 = grass, 20 = brush, 30 = woody, 40 = tree
	Region	FPS Region code
	Site	Site index ratio to reference species (Form = 40)
	Species	Species code
	SpGr	Specific gravity
	SPName	Local Species Name
	Toler	Tolerance ranking
Location	1_4	PLSS Quarter Section
	1_4-1_4	PLSS Quarter Quarter Section
	OwnShp	CIC Ownership
	PltNo	Plot Number
	Rng	PLSS Range
	Sec	PLSS Section
	Twn	PLSS Township
Masters_Final	BAComp	Basal Area Competition
	BAGRPerBADIB	Basal Area Growth / Basal Area Diameter Inside Bark
	C_SI	Calculated Site Index
	LCLSap	Log (Crown length * Sap Wood Basal Area)
	MSI	Mean Site Index
	OwnShp	CIC Ownership
	PltNo	Plot Number
	SI_D	Site Index Difference
	SI_R	Site Index Ratio
	SiteTree	Site Tree Designation
	SP	Species
	TrNo	Tree Number
	Montana	E_W
N_S		PLSS Township N/S
RANGE		PLSS Range

<u>Table</u>	<u>Column</u>	<u>Description</u>	
OwnShp	SECTION_	PLSS Section	
	TOWN	PLSS Township	
	XCord	Montana State Plane X	
	YCord	Montana State Plane Y	
	Owner Ship Code	CIC Ownership Districts	
	Ownership Name	Ownership Description	
SP	CalcTol	Calculated Tolerance	
	Code	841 Species Codes	
	FPS	FPS Species Code	
	MMb0	Melinda Moeur Crown Width Equation B0	
	MMb1_D	Melinda Moeur Crown Width Equation B1 - Diameter	
	MMb2_H	Melinda Moeur Crown Width Equation B2 - Height	
	MMb3_CL	Melinda Moeur Crown Width Equation B3 - Crown Length	
	ProgA0	Prognosis CCF Equation A0	
	ProgA1	Prognosis CCF Equation A1	
	ProgA2	Prognosis CCF Equation A2	
	ProgB0	Prognosis CCF Equation B0	
	ProgB1	Prognosis CCF Equation B1	
	Species	Species Name	
	Toler	FPS Tolerance Value	
	TableDesc	Column	Column Name
		Constraints	Data Constraints
Data_Type		Data Type	
Default		Default Value	
Description		Description	
Possn		Position in table	
Table		Table Name	
TAPHEAD		Crn	% live crown
TAPTREE	Age	Age at measurement point	
	Bark	Double bark thickness	
	Dob	Diameter outside bark	
	Height	Total height to measurement	
	Msmt	Measurement number	
	Type1	Ash	Ash Cap Depth (Inches)
Asp		Aspect (Azimuth - True)	
BdRck		Depth to bedrock	
Cly1		Clay Horizon 1 (%)	
Cly2		Clay Horizon 2 (%)	
Cly3		Clay Horizon 3 (%)	
Dpth1		Horizon 1 Thickness (Inches)	
Dpth2		Horizon 2 Thickness (inches)	
Dpth3		Horizon 3 Thickness (inches)	
Elev		Elevation (100 Feet)	
Frgs1		Course Fragments (%)	
Frgs2		Course Fragments (%)	
Frgs3		Course Fragments (%)	
GMT		Geomorphic type	
Hab		Habitat Type	
Hzn1		NE Horizon Inclination (degrees)	

<u>Table</u>	<u>Column</u>	<u>Description</u>
	Hzn2	E Horizon Inclination (degrees)
	Hzn3	SE Horizon Inclination (degrees)
	Hzn4	S Horizon Inclination (degrees)
	Hzn5	SW Horizon Inclination (degrees)
	Hzn6	W Horizon Inclination (degrees)
	Hzn7	NW Horizon Inclination (degrees)
	Ownshp	Ownership (Champion Districts CF-Clarkfork PV-Pleasant Valey HE-Hellgate PO-Potomac LI-Lincoln)
	PltNo	Plot Number
	PM	Parent Material
	Precip	Precipitation (Mean Inches per year)
	React1	Limestone PH Reaction (1/0)
	React2	Limestone PH Reaction (1/0)
	React3	Limestone PH Reaction (1/0)
	Slp	Slope (Degrees)
	Slt1	Silt Horizon 1 (%)
	Slt2	Silt Horizon 2 (%)
	Slt3	Silt Horizon 3 (%)
	Snd1	Sand Horizon 1 (%)
	Snd2	Sand Horizon 2 (%)
	Snd3	Sand Horizon 3 (%)
Type2	BAF	# of in trees on a 20 BAF plot with subject tree as center
	CRWN	TH to base of Crown ( ft)
	D6	Basal area on D+6 plot (sqft)
	DIB1	Diameter Inside Bark @ Ground (average of 2 measurements @ right angles)
	DIB2	Diameter Inside Bark @ Breast Height (average of 2 measurements @ right angles)
	DOB1	Diameter Outside Bark @ Ground (average of 2 measurements @ right angles)
	DOB2	Diameter Outside Bark @ Breast Height (average of 2 measurements @ right angles)
	HEART	Heartwood Diameter (in)
	HG	Height Growth (ft)
	HT	Height (ft)
	OwnShp	Ownership
	PltNo	Plot Number
	RADG	Radial Growth (1/20 in)
	Rng1	Ring count @ ground
	Rng2	Ring count @ Breast Height
	SI	Site Index (height @ age 50 physically measured)
	SP	Species (1 - PP 2- DF 3-WL 5-LP 4-ES 6-AF)
	TrNo	Tree Number
Type3	BAF	# of in trees on a 20 BAF plot with subject tree as center
	CRWN	TH to base of Crown ( ft)
	D6	Basal area on D+6 plot (sqft)
	DIB1	Diameter Inside Bark @ Ground (average of 2 measurements @ right angles)
	DIB2	Diameter Inside Bark @ Breast Height (average of 2 measurements @ right angles)
	DIB3	Diameter Inside Bark @ 3/10 Tree Height (average of 2 measurements @ right angles)

<u>Table</u>	<u>Column</u>	<u>Description</u>
	DIB4	Diameter Inside Bark @ 4/10 Tree Height (average of 2 measurements @ right angles)
	DOB1	Diameter Outside Bark @ Ground (average of 2 measurements @ right angles)
	DOB2	Diameter Inside Bark @ Breast Height (average of 2 measurements @ right angles)
	DOB3	Diameter Outside Bark @ 3/10 Tree Height (average of 2 measurements @ right angles)
	DOB4	Diameter Outside Bark @ 4/10 Tree Height (average of 2 measurements @ right angles)
	HEART	Heartwood Diameter (in)
	HG	Height Growth (ft)
	HT	Height (ft)
	OwnShp	Ownership
	PltNo	Plot Number
	RADG	Radial Growth (1/20 in)
	Rng1	Ring Count @ Ground
	Rng2	Ring count @ Breast Height
	RNG3	Ring count @ 3/10 Tree Height
	RNG4	Ring Count @ 4/10 Tree Height
	SI	Site Index (height @ age 50 physically measured)
	SP	Species (1 - PP 2- DF 3-WL 5-LP 4-ES 6-AF)
	TrNo	Tree Number
Type4	DIB10	Diameter Inside Bark @ 10/10 Tree Height (average of 2 measurements @ right angles)
	DIB11	Diameter Inside Bark @ 11/10 Tree Height (average of 2 measurements @ right angles)
	DIB5	Diameter Inside Bark @ 5/10 Tree Height (average of 2 measurements @ right angles)
	DIB6	Diameter Inside Bark @ 6/10 Tree Height (average of 2 measurements @ right angles)
	DIB7	Diameter Inside Bark @ 7/10 Tree Height (average of 2 measurements @ right angles)
	DIB8	Diameter Inside Bark @ 8/10 Tree Height (average of 2 measurements @ right angles)
	DIB9	Diameter Inside Bark @ 9/10 Tree Height (average of 2 measurements @ right angles)
	DOB10	Diameter Outside Bark @ 10/10 Tree Height (average of 2 measurements @ right angles)
	DOB11	Diameter Outside Bark @ 11/10 Tree Height (average of 2 measurements @ right angles)
	DOB5	Diameter Outside Bark @ 5/10 Tree Height (average of 2 measurements @ right angles)
	DOB6	Diameter Outside Bark @ 6/10 Tree Height (average of 2 measurements @ right angles)
	DOB7	Diameter Outside Bark @ 7/10 Tree Height (average of 2 measurements @ right angles)
	DOB8	Diameter Outside Bark @ 8/10 Tree Height (average of 2 measurements @ right angles)
	DOB9	Diameter Outside Bark @ 9/10 Tree Height (average of 2 measurements @ right angles)
	OwnShp	Ownership
	PltNo	Plot Number
	RNG10	Ring Count @ 10/10 Tree Height

<u>Table</u>	<u>Column</u>	<u>Description</u>	
Type5	RNG11	Ring Count @ 11/10 Tree Height	
	RNG5	Ring Count @ 5/10 Tree Height	
	RNG6	Ring Count @ 6/10 Tree Height	
	RNG7	Ring Count @ 7/10 Tree Height	
	RNG8	Ring Count @ 8/10 Tree Height	
	RNG9	Ring Count @ 9/10 Tree Height	
	SP	Species	
	TrNo	Tree Number	
	Crwn	Height to live crown (ft)	
	D6	Basal area on D+6 plot (sqft)	
	DIB2	Diameter Outside Bark @ Breast Height	
DOB2	Diameter Inside Bark @ Breast Height		
Heart	Heartwood Diameter (in)		
HG	Height Growth		
HT	Tot Height (ft)		
OwnShp	Ownership		
PltNo	Plot Number		
RadG	Radial Growth (1/20 in)		
Rng2	Ring Count @ Breast Height		
SP	Species		
TrNo	Tree Number		
Type6	Age10	Age @ 9/10 Total Height	
	Age11	Age @ 10/10 Total Height	
	Age2	Age @ Breast Height	
	Age3	Age @ 2/10 Total Height	
	Age4	Age @ 3/10 Total Height	
	Age5	Age @ 4/10 Total Height	
	Age6	Age @ 5/10 Total Height	
	Age7	Age @ 6/10 Total Height	
	Age8	Age @ 7/10 Total Height	
	Age9	Age @ 8/10 Total Height	
	Dia10	Diameter @ 9/10 Total height (Inches)	
	Dia11	Diameter @ 10/10 Total height (Inches)	
	Dia2	Diameter @ Breast Height (Inches)	
	Dia3	Diameter @ 2/10 Total height (Inches)	
	Dia4	Diameter @ 3/10 Total height (Inches)	
	Dia5	Diameter @ 4/10 Total height (Inches)	
	Dia6	Diameter @ 5/10 Total height (Inches)	
	Dia7	Diameter @ 6/10 Total height (Inches)	
	Dia8	Diameter @ 7/10 Total height (Inches)	
	Dia9	Diameter @ 8/10 Total height (Inches)	
	OwnShp	Ownership	
	PltNo	Plot Number	
	SP	Species	
	TrNo	Tree Number	
	TypeSpecs	End	Character End Possn
		Name	Column Name
		Start	Character Start Possn
Type		Data Type Number	
Vigr	Area	area of D+6 (acres)	
	BAComp	BA / Ac	

<u>Table</u>	<u>Column</u>	<u>Description</u>
	BAGR	basal area growth
	BBA	beginning BA
	BDIA	beginning dia
	CR	Crown Ratio
	DG	Diameter growth
	DIB	DIB
	DOB	DOB
	HG	Height Growth
	HRTBA	heartwood basal area (in)
	OwnShp	Ownership
	PltNo	Plot Number
	Radius	radius of D+6 plot
	SAPBA	Sapwood Basal area (in)
	SI	height @ age 50
	SP	Species
	TBA	total basal area inside bark (in)
	TrNo	Tree Number
	V1	diameter growth / unit sap wood area (sapwood to total)
	V2	sapwood per tree basal area
	V3	basal area growth per unit sapwood
Zeide	AGE1	Age Point 1
	AGE2	Age Point 2
	C1	Cut Point Number 1
	C2	Cut Point Number 2
	HT1	Height Point 1
	HT2	Height Point 2
	OwnShp	CIC Ownership
	PltNo	Plot Number
	TrNo	Tree Number
	Z_Number	Zeide Number
	Z_SI	Zeide Site Index

Appendix C: Melinda Moeur 1981 Crown Width Equations

For all trees greater than 3.5 inches DBH

$$\ln(CW) = \beta_0 + \beta_1 * \ln(D) + \beta_2 * \ln(HT) + \beta_3 * \ln(CL)$$

Where:

$\beta_0$ : Y-intercept	CW: Crown width in feet
$\beta_1$ : Diameter coefficient	D: Diameter breast height in inches
$\beta_2$ : Height coefficient	HT: Tree height in feet
$\beta_3$ : Crown length coefficient	CL: Crown length in feet

Subset of only  $\beta$ 's used in this study:

$$\beta_1 = 1.08137$$

$$\beta_3 = 0.29786$$

	$\beta_0$	$\beta_2$
ponderosa pine	1.62325	-0.68098
Douglas-fir	3.02271	-1.00486
western larch	2.31359	-0.80919
lodgepole pine	1.06804	-0.55987

Appendix D: Prognosis 1982 Crown Competition Factor equations

For trees < 10 inches DBH

$$CCF = TPA * \beta_0 * DBH^{\beta_1}$$

Where:

$\beta_0$ : Intercept	CCF: Crown competition factor
$\beta_1$ : Diameter exponent	TPA: Trees per acre
	DBH: Diameter breast height

Subset of only  $\beta$ 's used in this study:

	$\beta_0$	$\beta_1$
ponderosa pine	0.00781	1.7680
Douglas-fir	0.01730	1.5571
western larch	0.00724	1.8182
lodgepole pine	0.00919	1.7600

For trees  $\geq$  10 inches DBH

$$CCF = TPA * (\alpha_0 + (\alpha_1 * DBH) + (\alpha_2 * DBH^2))$$

Where:

$\alpha_0$ : Intercept	CCF: Crown competition factor
$\alpha_1$ : Diameter coefficient	TPA: Trees per acre
$\alpha_2$ : Diameter squared coefficient	DBH: Diameter breast height

Subset of only  $\alpha$ 's used in this study:

	$\alpha_0$	$\alpha_1$	$\alpha_2$
ponderosa pine	0.03	0.0180	0.00281
Douglas-fir	0.11	0.0333	0.00259
western larch	0.02	0.0148	0.00338
lodgepole pine	0.02	0.0168	0.00325

## Appendix E: Ordinary Least Squares - Multiple Linear Regression Assumptions

### Assumption 1: Linear in parameters

The model can be represented in a linear fashion such as:

$$y = \beta_0 + \beta_1x_1 + \beta_2x_2 + \dots + \beta_nx_n + u$$

### Assumption 2: Random Sampling

Data has been collected in a random manor and is able to properly represent the population without known bias.

### Assumption 3: No perfect collinearity

There is variation in the independent variables values and none of the independent variables have a strong linear relationship to each other.

### Assumption 4: Zero conditional mean

The expected value of the unexplained variable ( $u$ ) is equal to zero if the model truly explains the population.

### Assumption 5: Homoskedasticity

The variance of the unexplained variable ( $u$ ) remains constant across all levels of the independent variables.

### Assumption 6: Normality

The error term of the population ( $u$ ) is normally distributed throughout the range of independent variables so that there is a mean of zero and a variance of  $\sigma^2$ .

## Appendix F: Source Code - VBA - Tolerance

```
Public Function CCFLoop()  
  
Dim SPP, DBH, HT, CR, TPA, CCF, CW, CA, CA100, ProgCCF  
Dim MMb0, MMb1, MMb2, MMb3  
Dim ProgB0, ProgB1, Proga0, Proga1, Proga2  
Dim Acre  
Acre = 43560  
  
Dim LoopSPP, LoopDBH, LoopHT, LoopCR  
  
For LoopSPP = 1 To 5 Step 1  
    MMb0 = DLookup("MMb0", "SP", "Code = " & LoopSPP)  
    MMb1 = DLookup("MMb1_D", "SP", "Code = " & LoopSPP)  
    MMb2 = DLookup("MMb2_H", "SP", "Code = " & LoopSPP)  
    MMb3 = DLookup("MMb3_CL", "SP", "Code = " & LoopSPP)  
    ProgB0 = DLookup("ProgB0", "SP", "Code = " & LoopSPP)  
    ProgB1 = DLookup("ProgB1", "SP", "Code = " & LoopSPP)  
    Proga0 = DLookup("Proga0", "SP", "Code = " & LoopSPP)  
    Proga1 = DLookup("Proga1", "SP", "Code = " & LoopSPP)  
    Proga2 = DLookup("Proga2", "SP", "Code = " & LoopSPP)  
    For LoopDBH = 4 To 40 Step 1  
        For LoopHT = 0.04 To 0.35 Step 0.01  
            For LoopCR = 100 To 5 Step -5  
                CW = Exp(MMb0 + MMb1 * Log(LoopDBH) + MMb2 *_  
                    Log(LoopDBH / LoopHT) + MMb3 * Log((LoopDBH / LoopHT)_  
                        * (LoopCR / 100)))  
                CA = 3.14159265359879 * (CW / 2) ^ 2  
                TPA = Acre / CA  
                If LoopCR = 100 Then CA100 = CA  
                CCF = Round(100 * CA100 * TPA / Acre, 2)  
                If LoopDBH < 10 Then  
                    ProgCCF = TPA * ProgB0 * LoopDBH ^ ProgB1  
                Else  
                    ProgCCF = TPA * (Proga0 + Proga1 * LoopDBH + Proga2_  
                        * LoopDBH ^ 2)  
                End If  
                DoCmd.RunSQL ("INSERT INTO ToleranceCalc ( Species,_  
                    DBH, HT, CR, TPA, CCF, CA, CA100, CW, ProgCCF )_  
                    Values (" & LoopSPP & ", " & LoopDBH & ", " &_  
                    LoopDBH / LoopHT & ", " & LoopCR & ", " & TPA & ", " &_  
                    CCF & ", " & CA & ", " & CA100 & ", " & CW & ", " &_  
                    ProgCCF & ")")  
            Next LoopCR  
        Next LoopHT  
    Next LoopDBH  
Next LoopSPP  
  
End Function
```

## Appendix G: Source Code - VBA - Milner (1992) Site Curves

```
Public Function SI_Calc(Species As String, Height As Integer, _
    Age As Integer) As Double

    Select Case Species
        Case "PP", 1
            SI_Calc = 59.6 + (4.787 + 0.012544 * Age - 1.141 * _
                Log(Age) + 11.44 / Age ^ 2) * (Height - 4.5 - 121.4 * _
                (1 - Exp(-0.01756 * Age)) ^ 1.483)
        Case "DF", 2
            SI_Calc = 57.3 + (7.06 + 0.02275 * Age - 1.858 * _
                Log(Age) + 5.496 / Age ^ 2) * (Height - 4.5 - 114.6 * _
                (1 - Exp(-0.01462 * Age)) ^ 1.179)
        Case "WL", 3
            SI_Calc = 69 + (-0.8019 + 17.06 / Age + 0.4268 * _
                Log(Age) - 0.00009635 * Age ^ 2) * (Height - 4.5 - _
                127.8 * (1 - Exp(-0.0165 * Age)) ^ 1.196)
        Case "LP", 5
            SI_Calc = 59.6 + (1.055 - 0.006344 * Age + 14.82 / Age - _
                5.212 / Age ^ 2) * (Height - 4.5 - 96.93 * (1 - _
                Exp(-0.01955 * Age)) ^ 1.216)
        Case Else
            SI_Calc = -255
    End Select

    SI_Calc = Round(SI_Calc, 2)

End Function
```

Appendix H: Source Code - R - Entire Statistical Run

```
#####  
##                                                                                               ##  
##           Measuring Site Productivity from Subordinate Trees:                               ##  
##                   A Site Index Based Approach                                             ##  
##                                                                                               ##  
##                   By Charles Edward Vopicka                                              ##  
##                                                                                               ##  
##                   Masters Student (9/2004 - 5/2006)                                       ##  
##                   College of Forestry and Conservation                                     ##  
##                                                                                               ##  
#####  
  
#####  
##                   Open database and read Table for data                                   ##  
#####  
  
library(RODBC)  
con <- odbcConnectAccess("y:/841_dat.mdb")  
Trees <- sqlQuery(con, 'Select * From Masters_Final')  
  
#####  
##                   Set dummy variables for species                                       ##  
#####  
  
#for(i in 1:length(Trees$Type)){ Trees$SiteTree[i] <- if( Trees$Type[i] == 5) 0 else 1}
```

```

#####
##                               Create Variables to test or use                               ##
#####

OrgData <- Trees
  con <- odbcConnectAccess("y:/841_dat.mdb")
  Bias = "R_Bias"
  Coef = "R_Coef"
  Org  = "R_Original"
  CorMatrix = "R_Step_Cor_Out"
  StepOut = "R_Step_Out"
  sqlDrop(con,Bias,errors=FALSE)
  sqlDrop(con,Coef,errors=FALSE)
  sqlDrop(con,CorMatrix,errors=FALSE)
  sqlDrop(con,StepOut,errors=FALSE)

#####
##                               Create Correlation Matrix                               ##
#####

CorData <- sqlQuery(con, 'Select * From R_Step_IN')
sqlSave(con,data.frame(cor(CorData)),tablename = "R_Step_Cor_Out",append = FALSE, rownames=TRUE)

```

```

#####
##                               Create Functions                               ##
#####

DB.Coeff <- function(Title,Form,SP,Table,Model) {
  sqlSave(con,data.frame(Title=Title,Form=Form,SP=SP,summary(Model)[["coefficients"]]),tablename =
Table,append = TRUE, rownames="Coef")

  SE <- round(summary(Model)[["sigma"]],3)
  R2   <- round(summary(Model)[["r.squared"]],3)

  sqlSave(con,data.frame(Title=Title,Form=Form,SP=SP,SE=SE,R2=R2),tablename = Org,append = TRUE,
rownames=FALSE)
}

DB.Bias <- function(Title,Form,SP,Type,Data) {
  SE <- round(summary(lm(MSI ~ Predicted,data=Data))[["sigma"]],3)
  R2  <- round(summary(lm(MSI ~ Predicted,data=Data))[["r.squared"]],3)
  B0  <- round(summary(lm(MSI ~ Predicted,data=Data))[["coefficients"]][["(Intercept)","Estimate"]],3)
  SE0 <- round(abs((0 - round(summary(lm(MSI ~
Predicted,data=Data))[["coefficients"]][["(Intercept)","Estimate"]],3))/summary(lm(MSI ~
Predicted,data=Data))[["coefficients"]][["(Intercept)","Std. Error"]],3)
  B1  <- round(summary(lm(MSI ~ Predicted,data=Data))[["coefficients"]][["Predicted","Estimate"]],3)
  SE1 <- round(abs((1 - round(summary(lm(MSI ~
Predicted,data=Data))[["coefficients"]][["Predicted","Estimate"]],3))/summary(lm(MSI ~
Predicted,data=Data))[["coefficients"]][["Predicted","Std. Error"]],3)
  sqlSave(con,data.frame(Title=Title,Form=Form,SP=SP,Type=Type,SE=SE,R2=R2,B0=B0,SE0=SE0,B1=B1,SE1=SE1),ta
blename = Bias,append = TRUE, rownames=FALSE)
}

# by(Trees,Trees$SP,function(Trees){sd(Trees$C_SI)})

```

```

#####
##                               species Stepwise Regressions                               ##
#####

Title    <- "Stepwise"

by(CorData,CorData$SP,function(CorData){

#####
##  SI_R                               ##
#####

Form      <- "SI Ratio"
SP        <- mean(CorData$SP)
Type     <- "ALL"

CorData$TestSI <- CorData$MSI / CorData$C_SI

Original.model <- step(lm(TestSI ~ BAComp + LCLSap + SiteTree + BAGRPerDIB + HT + CRWN + D6 + HG + HEART
+ RADG + Age + DOB + DIB + CR + TBA + HRTBA + SAPBA + BDIA + BBA + BAGR + V1 + V2 + V3,data=CorData))

DB.Coeff(Title,Form,SP,StepOut,Original.model)

#####
##  SI_D                               ##
#####

Form      <- "SI Diff"
SP        <- mean(CorData$SP)
Type     <- "ALL"

CorData$TestSI <- CorData$MSI - CorData$C_SI

Original.model <- step(lm(TestSI ~ BAComp + LCLSap + SiteTree + BAGRPerDIB + HT + CRWN + D6 + HG + HEART
+ RADG + Age + DOB + DIB + CR + TBA + HRTBA + SAPBA + BDIA + BBA + BAGR + V1 + V2 + V3,data=CorData))

DB.Coeff(Title,Form,SP,StepOut,Original.model)

```

```

#####
##  MSI          ##
#####

Form      <- "MSI"
SP        <- mean(CorData$SP)
Type      <- "ALL"

CorData$TestSI <- CorData$MSI

Original.model <- step(lm(TestSI ~ C_SI + BAComp + LCLSap + SiteTree + BAGRPerDIB + HT + CRWN + D6 + HG
+ HEART + RADG + Age + DOB + DIB + CR + TBA + HRTBA + SAPBA + BDIA + BBA + BAGR + V1 + V2 +
V3,data=CorData))

DB.Coef(Title,Form,SP,StepOut,Original.model)

})

```

```

#####
##                               species Regressions                               ##
#####

by(OrgData,OrgData$SP,function(Trees){

  #####
  ##  SI_R                          ##
  #####

  Title    <- "Individual Species Model"
  Form     <- "SI Ratio"
  SP       <- mean(Trees$SP)
  Type     <- "ALL"

  Trees$TestSI <- Trees$MSI / Trees$C_SI

  Original.model <- lm(TestSI ~ BAComp + LCLSap + SiteTree + BAGRPerDIB,data=Trees)

  Trees$Predicted <- predict(Original.model)

  DB.Coeff(Title,Form,SP,Coef,Original.model)

  #-----#

  Trees$Predicted <- Trees$Predicted * Trees$C_SI

  DB.Bias(Title,Form,SP,Type,Trees)

  #-----#

  by(Trees,Trees$SiteTree,function(Data){
    DB.Bias(Title,Form,SP,mean(Data$SiteTree),Data)
  })
})

```

```

#####
##  SI_D      ##
#####

Title      <- "Individual Species Model"
Form       <- "SI Diff"
SP         <- mean(Trees$SP)
Type       <- "ALL"

Trees$TestSI <- Trees$MSI - Trees$C_SI

Original.model <- lm(TestSI ~ BAComp + LCLSap + SiteTree + BAGRPerDIB,data=Trees)

Trees$Predicted <- predict(Original.model)

DB.Coeff(Title,Form,SP,Coef,Original.model)

#-----#

Trees$Predicted <- Trees$Predicted + Trees$C_SI

DB.Bias(Title,Form,SP,Type,Trees)

#-----#

by(Trees,Trees$SiteTree,function(Data){
  DB.Bias(Title,Form,SP,mean(Data$SiteTree),Data)
})

```

```

#####
##  MSI      ##
#####

Title      <- "Individual Species Model"
Form       <- "MSI"
SP         <- mean(Trees$SP)
Type       <- "ALL"

Trees$TestSI <- Trees$MSI

Original.model <- lm(TestSI ~ BAComp + LCLSap + SiteTree + BAGRPerDIB + C_SI,data=Trees)

Trees$Predicted <- predict(Original.model)

DB.Coeff(Title,Form,SP,Coef,Original.model)

#-----#

Trees$Predicted <- Trees$Predicted

DB.Bias(Title,Form,SP,Type,Trees)

#-----#

by(Trees,Trees$SiteTree,function(Data){
  DB.Bias(Title,Form,SP,mean(Data$SiteTree),Data)
})
})

```

```

#####
##                               all data regressions                               ##
#####

#####
##  SI_R                          ##
#####

Title    <- "All Species Regression"
Form     <- "SI Ratio"
SP       <- 0
Type     <- "ALL"

Trees$TestSI <- Trees$MSI / Trees$C_SI
Original.model <- lm(TestSI ~ BAComp + LCLSap + SiteTree + BAGRPerDIB,data=Trees)
Trees$Predicted <- predict(Original.model)
DB.Coeff(Title,Form,SP,Coef,Original.model)

#-----#

Trees$Predicted <- Trees$Predicted * Trees$C_SI
DB.Bias(Title,Form,SP,Type,Trees)

#-----#

by(Trees,Trees$SiteTree,function(Data){
  DB.Bias(Title,Form,SP,mean(Data$SiteTree),Data)
})

#-----#

by(Trees,Trees$SP,function(Trees){
  DB.Bias(Title,Form,mean(Trees$SP),Type,Trees)
  by(Trees,Trees$SiteTree,function(Data){
    DB.Bias(Title,Form,mean(Data$SP),mean(Data$SiteTree),Data)
  })
})

})

```

```

#####
##  SI_D          ##
#####

Title    <- "All Species Regression"
Form     <- "SI Diff"
SP       <- 0
Type     <- "ALL"

Trees$TestSI <- Trees$MSI - Trees$C_SI
Original.model <- lm(TestSI ~ BAComp + LCLSap + SiteTree + BAGRPerDIB,data=Trees)
Trees$Predicted <- predict(Original.model)
  DB.Coeff(Title,Form,SP,Coef,Original.model)

#-----#

Trees$Predicted <- Trees$Predicted + Trees$C_SI
  DB.Bias(Title,Form,SP,Type,Trees)

#-----#

  by(Trees,Trees$SiteTree,function(Data){
    DB.Bias(Title,Form,SP,mean(Data$SiteTree),Data)
  })

#-----#

by(Trees,Trees$SP,function(Trees){
  DB.Bias(Title,Form,mean(Trees$SP),Type,Trees)
  by(Trees,Trees$SiteTree,function(Data){
    DB.Bias(Title,Form,mean(Data$SP),mean(Data$SiteTree),Data)
  })
})

```

```

#####
## MSI ##
#####

Title <- "All Species Regression"
Form <- "MSI"
SP <- 0
Type <- "ALL"

Trees$TestSI <- Trees$MSI
Original.model <- lm(TestSI ~ BAComp + LCLSap + SiteTree + BAGRPerDIB + C_SI,data=Trees)
Trees$Predicted <- predict(Original.model)
DB.Coeff(Title,Form,SP,Coef,Original.model)

#-----#

Trees$Predicted <- Trees$Predicted
DB.Bias(Title,Form,SP,Type,Trees)

#-----#

by(Trees,Trees$SiteTree,function(Data){
  DB.Bias(Title,Form,SP,mean(Data$SiteTree),Data)
})

#-----#

by(Trees,Trees$SP,function(Trees){
  DB.Bias(Title,Form,mean(Trees$SP),Type,Trees)
  by(Trees,Trees$SiteTree,function(Data){
    DB.Bias(Title,Form,mean(Data$SP),mean(Data$SiteTree),Data)
  })
})
})

```

```

#####
##                               Toler Regression                               ##
#####

#####
## SI_R                           ##
#####

Title    <- "Tolerance Regression"
Form     <- "SI Ratio"
SP       <- 0
Type     <- "ALL"

Trees$TestSI <- Trees$MSI / Trees$C_SI
Original.model <- lm(TestSI ~ BAComp + LCLSap + SiteTree + BAGRPerDIB + Toler,data=Trees)
Trees$Predicted <- predict(Original.model)
DB.Coeff(Title,Form,SP,Coef,Original.model)

#-----#

Trees$Predicted <- Trees$Predicted * Trees$C_SI
DB.Bias(Title,Form,SP,Type,Trees)

#-----#

by(Trees,Trees$SiteTree,function(Data){
  DB.Bias(Title,Form,SP,mean(Data$SiteTree),Data)
})

#-----#

by(Trees,Trees$SP,function(Trees){
  DB.Bias(Title,Form,mean(Trees$SP),Type,Trees)
  by(Trees,Trees$SiteTree,function(Data){
    DB.Bias(Title,Form,mean(Data$SP),mean(Data$SiteTree),Data)
  })
})

```

```

#####
##  SI_D          ##
#####

Title      <- "Tolerance Regression"
Form       <- "SI Diff"
SP         <- 0
Type      <- "ALL"

Trees$TestSI <- Trees$MSI - Trees$C_SI
Original.model <- lm(TestSI ~ BAComp + LCLSap + SiteTree + BAGRPerDIB + Toler,data=Trees)
Trees$Predicted <- predict(Original.model)
  DB.Coeff(Title,Form,SP,Coef,Original.model)

#-----#

Trees$Predicted <- Trees$Predicted + Trees$C_SI
  DB.Bias(Title,Form,SP,Type,Trees)

#-----#

  by(Trees,Trees$SiteTree,function(Data){
    DB.Bias(Title,Form,SP,mean(Data$SiteTree),Data)
  })

#-----#

by(Trees,Trees$SP,function(Trees){
  DB.Bias(Title,Form,mean(Trees$SP),Type,Trees)
  by(Trees,Trees$SiteTree,function(Data){
    DB.Bias(Title,Form,mean(Data$SP),mean(Data$SiteTree),Data)
  })
})

```

```

#####
##  MSI      ##
#####

  Title      <- "Tolerance Regression"
  Form       <- "MSI"
  SP        <- 0
  Type      <- "ALL"

Trees$TestSI <- Trees$MSI
Original.model <- lm(TestSI ~ BAComp + LCLSap + SiteTree + BAGRPerDIB + C_SI + Toler,data=Trees)
Trees$Predicted <- predict(Original.model)
  DB.Coeff(Title,Form,SP,Coef,Original.model)

#-----#

Trees$Predicted <- Trees$Predicted
  DB.Bias(Title,Form,SP,Type,Trees)

#-----#

  by(Trees,Trees$SiteTree,function(Data){
    DB.Bias(Title,Form,SP,mean(Data$SiteTree),Data)
  })

#-----#

by(Trees,Trees$SP,function(Trees){
  DB.Bias(Title,Form,mean(Trees$SP),Type,Trees)
  by(Trees,Trees$SiteTree,function(Data){
    DB.Bias(Title,Form,mean(Data$SP),mean(Data$SiteTree),Data)
  })
})

```

```

#####
##                               Dummy vars                               ##
#####

#####
## SI_R                          ##
#####

Title    <- "Dummy Variable Regression"
Form     <- "SI Ratio"
SP       <- 0
Type     <- "ALL"

Trees$TestSI <- Trees$MSI / Trees$C_SI
Original.model <- lm(TestSI ~ BAComp + LCLSap + SiteTree + BAGRPerDIB + SP1 + SP3 + SP5,data=Trees)
Trees$Predicted <- predict(Original.model)
DB.Coeff(Title,Form,SP,Coef,Original.model)

#-----#

Trees$Predicted <- Trees$Predicted * Trees$C_SI
DB.Bias(Title,Form,SP,Type,Trees)

#-----#

by(Trees,Trees$SiteTree,function(Data){
  DB.Bias(Title,Form,SP,mean(Data$SiteTree),Data)
})

#-----#

by(Trees,Trees$SP,function(Trees){
  DB.Bias(Title,Form,mean(Trees$SP),Type,Trees)
  by(Trees,Trees$SiteTree,function(Data){
    DB.Bias(Title,Form,mean(Data$SP),mean(Data$SiteTree),Data)
  })
})

```

```

#####
##  SI_D      ##
#####

Title      <- "Dummy Variable Regression"
Form       <- "SI Diff"
SP         <- 0
Type      <- "ALL"

Trees$TestSI <- Trees$MSI - Trees$C_SI
Original.model <- lm(TestSI ~ BAComp + LCLSap + SiteTree + BAGRPerDIB + SP1 + SP3 + SP5,data=Trees)
Trees$Predicted <- predict(Original.model)
  DB.Coeff(Title,Form,SP,Coef,Original.model)

#-----#

Trees$Predicted <- Trees$Predicted + Trees$C_SI
  DB.Bias(Title,Form,SP,Type,Trees)

#-----#

  by(Trees,Trees$SiteTree,function(Data){
    DB.Bias(Title,Form,SP,mean(Data$SiteTree),Data)
  })

#-----#

by(Trees,Trees$SP,function(Trees){
  DB.Bias(Title,Form,mean(Trees$SP),Type,Trees)

  by(Trees,Trees$SiteTree,function(Data){
    DB.Bias(Title,Form,mean(Data$SP),mean(Data$SiteTree),Data)
  })
})

```

```

#####
##  MSI      ##
#####

Title    <- "Dummy Variable Regression"
Form     <- "MSI"
SP       <- 0
Type     <- "ALL"

Trees$TestSI <- Trees$MSI
Original.model <- lm(TestSI ~ BAComp + LCLSap + SiteTree + BAGRPerDIB + C_SI + SP1 + SP3 + SP5,data=Trees)
Trees$Predicted <- predict(Original.model)
  DB.Coeff(Title,Form,SP,Coef,Original.model)

#-----#

Trees$Predicted <- Trees$Predicted
  DB.Bias(Title,Form,SP,Type,Trees)

#-----#

  by(Trees,Trees$SiteTree,function(Data){
    DB.Bias(Title,Form,SP,mean(Data$SiteTree),Data)
  })

#-----#

by(Trees,Trees$SP,function(Trees){
  DB.Bias(Title,Form,mean(Trees$SP),Type,Trees)
  by(Trees,Trees$SiteTree,function(Data){
    DB.Bias(Title,Form,mean(Data$SP),mean(Data$SiteTree),Data)
  })
})

close(con)

```