

## *Improved Estimates of Site Index Curves Using a Varying-Parameter Model*

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**ABSTRACT.** Current methods for developing site index curves from stem analysis data or from remeasured permanent plots commonly regress height on age (or age and site) using a nonlinear regression model fitted to the pooled observations. While this is a computationally efficient method, it does not satisfactorily account for between-tree differences in individual tree height growth. This paper presents a varying-parameter (linear random regression coefficient) model that is derived by fitting height growth models to each individual tree in the data set. A weighted least squares technique is then employed to combine these individual estimates to form a mean estimate of the parameters of a sigmoid height growth model. These parameters are then used to predict the height development of site trees. An example of the procedure is given using stem analysis data from primarily dominant trees in the young-growth mixed conifer forests of California. FOREST SCI. 31:248-259.

**ADDITIONAL KEY WORDS.** Stem analysis data, sigmoid model, height growth.

HISTORICALLY, development of site index curves has been carried out with either cross-sectional data or stem analysis data (see Monserud 1984). For cross-sectional data, a series of heights and ages for trees comprising a select component of the stand (e.g., dominants or dominants and codominants) are sampled. Either a freehand curve is drawn through the height-over-age plot of the data (see Dunning 1942, Dunning and Reineke 1933, Arvanitis and others 1964) or a mathematical model is fit to the pooled data using least squares techniques (e.g., Brickell 1968). This curve is termed a "guide curve." A series of proportioned curves all having the same shape (anamorphic) are then generated around the mean regression line to describe other site classes. The curves, so generated, are usually sigmoid and are commonly called "site curves."

Most current research utilizes stem analysis data (e.g., Carmean 1972, Krumland and Wensel 1977, Barrett 1978, Monserud 1984) which provides improved estimates of site productivity in part because multiple observations of individual trees comprise a real growth series (Curtis 1964). Simple and complex forms of the Chapman-Richards growth model are often used to model height growth of site trees using pooled stem analysis data (e.g., Carmean 1971, 1972; Monserud and Ek 1976; and Krumland and Wensel 1977). In simplest form, the Chapman-Richards model produces anamorphic site curves (e.g., Lundgren and Dolid 1970). In more complex forms, height is no longer constrained to be proportional to site at a given age and thus polymorphic curves can be generated. Another approach to generation of polymorphic site curves is given by Bailey and Clutter (1974). They assumed that the logarithm of height is a linear function of the inverse of age raised to a constant power. Then by identifying a parameter that influenced

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curve form, and allowing it to be site-specific, they can generate polymorphic site curves.

An inherent drawback in using standard modelling techniques is that the full information available in stem analysis data is not exploited. Usually, a model with a few independent variables is fitted to the pooled observations (either cross-sectional or stem analysis data). A regression model fitted under these circumstances predicts the conditional mean height of the sample given specific values of the explanatory variables (age or age and site). However, if there is significant variation in individual tree growth this approach will yield results different than if coefficients in a growth model are allowed to vary by individual (e.g., Ferguson and Leech's 1978 work with yield functions). Consequently, it should not be assumed that the mean regression line derived from a standard approach represents the height growth development of the average tree. This paper presents an alternative method of analyzing site data by modelling height growth of individual trees. The procedure uses a varying-parameter (random regression coefficient) model derived from weighted least-squares fitting of height growth models to the observations of individual trees over time which produces a height growth curve for the average tree.

#### DATA SOURCES

The study was based on data from a cooperative growth and yield project entitled the Northern California Forest Yield Cooperative (NCFYC) in the mixed conifer region of California. The study combined efforts of twelve private industries and the University of California, Berkeley. In one aspect of this project thirty-one clusters containing 3 one-fifth acre (0.08 ha) plots and eight clusters containing two one-tenth acre (0.04 ha) plots were located in northern California for a stem analysis project (see Fig. 1).

On each plot, four to six dominants (two to three for each of the two most prevalent species in the overstory) were chosen randomly and felled as site index trees for stem analysis. Section rounds (1-2 inches (2.5-5.1 cm) thick) were taken at stump height (1.5 feet (0.46 m)), breast height and subsequent log lengths (16.5 feet (5.03 m) or 20.5 feet (6.25 m)). Additionally, three sections were cut in the nonmerchantable section of the tip. These sections corresponded to the three most recent 5-year height growth intervals. Each section was tagged and photographed. Laboratory analysis to determine age and annual radial growth from the photographs followed a procedure given by Biging and Wensel (1984) in which a digitizer was used to record the Cartesian coordinates of annual ring boundaries from the pith to the outer edge of a section.

Site trees chosen for felling were healthy dominants receiving full light from above and partly from the sides. They had well-developed crowns, but they could be somewhat crowded on the sides. In all-aged stands, site trees needed to extend above the general level of their group, but not necessarily above the general level of the stand to be dominant. Additionally, site trees had minimal past damage to tops and minimal height-growth reduction due to extremes in density. Increment borings were taken to inspect the pattern of past radial growth which provided information on past stand density effects. In cases where no dominants could be found that displayed unsuppressed radial growth, the following types of trees were selected in decreasing preference: codominants showing no signs of suppression, dominants displaying moderate radial suppression or codominants that have undergone moderate radial suppression. There were 198 site trees available for analysis in the mixed conifer forest type. However, eleven trees were dropped from analysis because their breast height ages were less than 40 years. This was done to avoid long extrapolations when estimating site index at reference

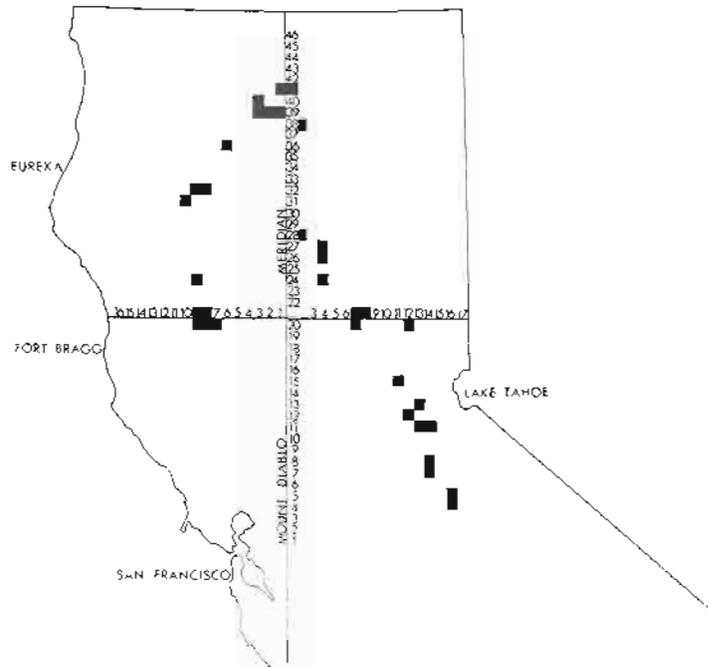


FIGURE 1. Location of stem analysis plots by township.

age 50. This left 187 trees for analysis of which 172 were dominants and 15 were codominants. Of the 172 dominant trees selected, 21 displayed some past radial suppression and of the 15 codominant trees selected, 6 displayed some past radial suppression. Table 1 summarizes the site tree data. For these 187 site trees, there was a total of 1,551 individual measurements of diameter inside bark, age, and height above ground. Thus, there was an average of about 8 measurements per tree.<sup>1</sup>

#### METHODS

*Theoretical Development.*—Most site index studies have utilized either cross-sectional or stem analysis data to predict height as a function of site and age or solely of age (see e.g., Bailey and Clutter 1974, Curtis and others 1974). However, it is unlikely that between-tree differences observed in a sample of stem analysis trees are adequately explained by a simple model with a few independent variables fitted to the pooled observations. In this study, between-tree heterogeneity is treated by using a varying-parameter model in which coefficients of height over age curves for individual trees are treated as random (see Swamy 1970).

These two approaches can lead to different estimates of the parameters of the height growth model. Consider the diagram presented in Figure 2. This figure depicts an idealized representation of the height growth of individual trees over time. Using standard regression techniques the coefficients are considered to be

<sup>1</sup> There were 1,855 original measurements of height above ground and age for the 187 site trees. However, there were 117 missing data points due mainly to film development errors. Additionally, 187 stump cuts were not utilized leaving 1,551 data points.

TABLE 1. Summary statistics for the site tree data base comprised of 187 trees.

Variable	Mean	Standard deviation	Minimum	Maximum
Dbh (in)	21.5	5.4	9.4	35.5
Ht (ft)	101.1	20.3	39.4	148.9
Site index at age 50 (ft)	80.2	20.3	35.0	130.5

constant between individuals. The regression line resulting from the ordinary least squares estimates of the parameters (OLS) predicts the conditional mean height of the sample given specific values of the explanatory variable (in this example age). However, if the coefficients are thought to vary by individual and a varying-parameter model is employed then the resultant estimate of the parameters will produce a different regression line than that produced by OLS.

To specify the varying-parameter (random coefficient regression) Model [1] consider  $N$  individual trees having  $T$  observations each. Model [1] is then given as follows:

Let  $Y_{ij}$  = the  $j^{\text{th}}$  observation of height on the  $i^{\text{th}}$  site tree, and  $X_{ij}$  =  $j^{\text{th}}$  observation of age on the  $i^{\text{th}}$  site tree. Then

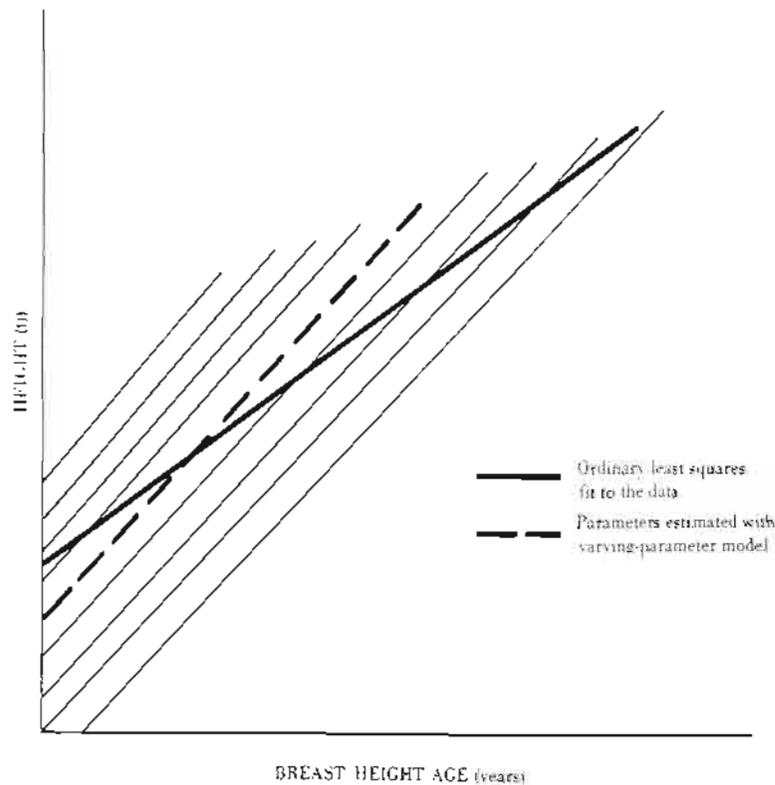


FIGURE 2. Comparison of the regression surfaces derived from a varying-parameter model and a standard regression fit to pooled data.

$$Y_{ij} = X_{ij}\beta_i + e_{ij}^{2,3} \quad [1]$$

where  $i = 1, \dots, N$  and  $j = 1, \dots, T$ .

Assume further that the  $e_{ij}$ 's are all independent with mean zero and variance  $\sigma_i^2$ . Thus the error is assumed to have constant variance for an individual tree, but may vary between trees. For Model [1], the betas ( $\beta_i$ ) are assumed independent with mean  $\beta$  and variance  $\delta^2$ . Assume  $\beta_i = \beta + \delta_i$ , where  $\delta_i$  is a random element with expectation zero, variance  $\delta^2$ , and that it is independent of the error terms ( $e_{ij}$ ). Under these assumptions, we can write Model [1] as

$$Y_{ij} = X_{ij}\beta + \delta_i X_{ij} + e_{ij} \quad [2]$$

Let  $D_{ij} = \delta_i X_{ij} + e_{ij}$ , then

$$Y_{ij} = X_{ij}\beta + D_{ij} \quad [3]$$

Where the  $\text{Var}(D_{ij}) = \delta^2 X_{ij}^2 + \sigma_i^2$  and

$$\begin{aligned} \text{Cov}(D_{ij}, D_{ik}) &= \text{Cov}(\delta_i X_{ij} + e_{ij}, \delta_i X_{ik} + e_{ik}) \\ &= \delta^2 X_{ij} X_{ik} \end{aligned}$$

There are  $\{1/2[P(P+1)] + N + NP\}$  parameters to estimate with  $NT$  observations.<sup>4</sup> The parameters to estimate include the variance of the  $e_{ij}$ 's ( $\sigma_1^2, \dots, \sigma_N^2$ ), the betas ( $\beta_1, \dots, \beta_N$ ), and the elements of the variance-covariance matrix of the betas ( $\delta^2$ ). Under this formulation the disturbances ( $D_{ij}$ ) are heteroskedastic and vary by tree (recall  $\text{var}(D_{ij}) = \delta^2 X_{ij}^2 + \sigma_i^2$ ). Maddala (1977) states that if we estimate Model [3] by ordinary least squares (OLS) the estimate of the betas will be consistent, but not efficient. To obtain an efficient estimate of  $\beta$  we can employ generalized least squares (GLS). The GLS estimate of  $\beta$  is given by Swamy (1970):

$$\hat{\beta} = \left[ \sum_{i=1}^N X_i' (\sigma_i^2 I + \delta^2 X_i X_i')^{-1} X_i \right]^{-1} \left[ \sum_{i=1}^N X_i' (\sigma_i^2 I + \delta^2 X_i X_i')^{-1} Y_i \right] \quad [4]$$

where  $X_i'$  is the vector of observations ( $X_{i1}, X_{i2}, \dots, X_{iT}$ ) on the  $i^{\text{th}}$  tree and  $I$  is a  $(T \times T)$  identity matrix. We can rewrite equation [4] as

$$\hat{\beta} = \sum_{i=1}^N W_i \hat{\beta}_i \quad \text{where } W_i = \frac{1/[\delta^2 + \sigma_i^2/(X_i' X_i)]}{\sum_{k=1}^N \{1/[\delta^2 + \sigma_k^2/(X_k' X_k)]\}} \quad [5]$$

and  $\hat{\beta}_i$  is the OLS estimate of the parameter for an individual tree. The variance of the estimate of the betas is given as

$$\text{Var}(\hat{\beta}_i) = \sigma_i^2 / X_i' X_i$$

The estimator given in [5] is the weighted average of the betas with the weights ( $W_i$ ) inversely proportional to the variance-covariance matrix of the coefficients. In the special case where the variance of the betas ( $\sigma_i^2 / X_i' X_i$ ) is the same for all  $i$ , then the estimate of  $\beta$  would not change with  $\delta^2$ . That is, the estimate of  $\beta$  obtained with the varying-parameter (random coefficient regression) model would be identical to that obtained when the coefficients are not random.

<sup>2</sup> The model is derived from Swamy (1970). Swamy's notation is retained with some adaptations from Maddala (1977).

<sup>3</sup> The formulation presented is for one independent variable, but can readily be expanded to higher dimensions.

<sup>4</sup> The number of parameters to be estimated for the regression model presented is  $P = 1$ , but in general  $P$  may be any positive integer value.

When  $\delta^2$  and  $\sigma_i^2$  ( $i = 1, \dots, N$ ) are unknown we need to estimate these parameters. Maddala (1977) suggests the following estimators:

$$\hat{\sigma}_i^2 = \frac{1}{T} e_i' e_i$$

$$\hat{\delta}^2 = \frac{1}{N} \sum \hat{\beta}_i^2 - \left( \frac{1}{N} \sum \hat{\beta}_i \right)^2.$$

*Height Growth Model.*—Carmean (1971, 1972), Monserud and Ek (1976), Krumland and Wensel (1977), and others have successfully applied the Chapman-Richards function, or a modification of it, to height growth data for site trees. The basic form of the model is

$$H = b_0 S (1 - e^{-b_1 t})^{b_2}. \quad [6]$$

If time ( $t$ ) is changed from total age to breast height age then when  $t = 0$  (at breast height) height is 4.5 feet. Thus a model reflecting height growth from breast height is given as

$$H = 4.5 + b_0 S (1 - e^{-b_1 t})^{b_2} \quad [7]$$

where

- $H$  = height above ground in feet
- $t$  = breast height age in years
- $S$  = site index = height at breast height age of 50 years.

Arvanitis and others (1964) indicate breast height age to be more useful than total age since it is easier to determine breast height age. Since early height growth is affected by nonsite factors such as brush competition and animal browsing, total age is a poorer choice for an independent variable than is breast height age (Husch 1956). Thus breast height age was used in this study.

If the coefficients in Model [7] are allowed to vary for each individual tree and site is allowed to have a power, then

$$H_i = 4.5 + b_{0i} (S_i^{b_{3i}}) (1 - e^{-b_{1i} t})^{b_{2i}} \quad i = 1, \dots, N. \quad [8]$$

Model [8] can then be viewed as a nonlinear counterpart to a linear random regression coefficient (varying-parameter) model as stated in [2]. We need not impose the restriction that there be an equal number of observations for each individual ( $T$ ). However,  $T_i$  should be large enough to reliably estimate the parameters of the model and the residual variance ( $\sigma_i^2$ ). For the data described above there were, on the average, eight observations per tree available for use in estimation. Attempts to estimate the four parameters in Model [8] were not always successful owing to the frequent nonconvergence of the estimates of the asymptote parameter when using a nonlinear regression routine. This frequently happens because young trees in the sample provide too little information for estimating the upper asymptote. Additionally, estimating the four parameters in Model [8] leaves too few degrees of freedom for reliable estimation of  $\sigma_i^2$ . Thus, an attempt was made to linearize the estimation process to ensure estimability of the parameters and increase the degrees of freedom available for estimating  $\sigma_i^2$ . This was accomplished by reducing the number of parameters in the model to be estimated. Model [8] was rewritten as

$$H_i = 4.5 + b_{0i} S_i^{c_i} (1 - e^{-a_i t})^{b_i} \quad [9]$$

$$\text{or } \ln \left[ \frac{H_i - 4.5}{S_i^{c_i}} \right] = \ln(b_{0i}) + b_i \ln(1 - e^{-a_i t}) \quad [10]$$

where  $c_1$  and  $c_2$  are constants set before estimating the parameters  $b_{0i}$  and  $b_{1i}$ . The values of  $c_1$  and  $c_2$  were set to 0.89 and 0.024, respectively. Krumland and Wensel (1977) found  $c_1$  to be 0.68 for young-growth redwoods of California. In a preliminary study, Model [9] was fit to a subset of the data ( $n = 63$  ponderosa pine trees) and the average computed  $c_1$  value was 0.89 (S.E. = 0.06) and thus was set at 0.89. This differs from Krumland and Wensel's results in part due to species differences, but also because of significant differences in estimation techniques. In another study, Model [7] was fit to each species in the data base on an individual tree basis. The average  $b_1$  coefficient ( $c_2$  in Model [10]) varied from 0.028 for Douglas-fir to 0.020 for ponderosa pine. The average across all species was 0.024. Hence,  $c_2$  was set to 0.024. The parameters  $c_1$  and  $c_2$  were set to prescribed values to ensure estimability of the parameters by linearization of Model [9] to the form of Model [10] and to allow sufficient degrees of freedom for reliable estimation on an individual tree basis of the residual variation. The performance of Model [10] (see Table 4) will be discussed in the next section.

#### MODEL FITTING

*Determining Site Index for Individual Trees ( $S_i$ ).*—One of two methods was employed to determine individual tree height at breast height age 50 (denoted  $S_i$ ). If the tree was older than 50 years at breast height, Lagrange polynomials were used to assess height at age 50 (see e.g., Burden and others 1979). For trees between 40 and 50 years in age at breast height, a variation of Model [9] was employed since site index is unknown for these trees and thus is not available as an independent variable. The model used was

$$H_i = 4.5 + b_{0i}(1 - e^{-c_2 t})^{b_{1i}} \quad [11]$$

where  $H_i$  = height of the  $i^{\text{th}}$  tree at age  $t$ .  $b_{0i}$  and  $b_{1i}$  are regression coefficients for the  $i^{\text{th}}$  tree, and  $c_2$  is a constant equal to 0.024 (see Model [10]). This model can be transformed to allow linear estimation of the parameters as

$$\ln[H_i - 4.5] = \ln(b_{0i}) + b_{1i} \ln(1 - e^{-c_2 t}). \quad [12]$$

Site index is then estimated by substituting  $t = 50$  into equation [11] and solving for  $H_i$ .

*Estimating  $b_{0i}$  and  $b_{1i}$ .*—A linear regression routine was used to estimate  $\ln(b_{0i})$  and  $b_{1i}$  ( $i = 1, \dots, N$ ) of Model [10]. The  $2 \times 2$  variance-covariance matrix of the parameters was calculated as  $\text{Var}(\hat{\beta}) = \hat{\sigma}^2(X'X)^{-1}$ . An example is presented in Table 2.

*Inverting the Variance-Covariance Matrix.*—Recall that

$$\hat{\beta} = \sum_{i=1}^N W_i \hat{\beta}_i \text{ where } W_i \text{ is defined by equation [5]}$$

with  $\hat{\sigma}_i^2$  replacing  $\sigma_i^2$  and  $\hat{\delta}^2$  replacing  $\delta^2$ . This change of notation emphasizes that the parameters are unknown and need to be estimated from the sample data.

$$\begin{aligned} \text{Let } Q_i &= \hat{\delta}^2 + \hat{\sigma}_i^2/(X_i'X_i) \\ &= \hat{\delta}^2 + \text{estimated variance-covariance of the estimated parameters of} \\ &\quad \text{the } i^{\text{th}} \text{ cross-sectional unit (tree).} \end{aligned}$$

Then

$$\hat{W}_i = \frac{Q_i^{-1}}{\sum_{k=1}^N Q_k^{-1}}$$

TABLE 2. Parameter estimates for Model [10] for selected trees.

Cluster-plot- tree-species	ln( $b_0$ )	$b_1$	$\widehat{\text{Var}}(\beta)$		
			$b_0$	$b_1$	
2-1-47-PP	0.875	1.940	0.002502	0.004087	$b_0$
			004087	.010129	$b_1$
2-3-25-WF	1.268	2.473	.000274	.000665	$b_0$
			.000665	.001669	$b_1$
3-1-503-WF	1.005	1.586	.000221	.000260	$b_0$
			.000260	.000385	$b_1$

$Q_i$  is a 2 by 2 matrix and we only need its inverse to form  $\hat{W}_i$ . The algorithm for calculating a 2 by 2 inverse is well known.

RESULTS

To examine whether there was significant variation in the parameters for individual trees and, thus, whether a varying parameter model approach is required, the hypothesis of equality of coefficients between trees was tested. The test statistic for homogeneity of coefficients ( $H_0$ ) is given as (Swamy 1970)

$$H_0 = \sum_{i=1}^N \frac{(b_i - \beta)' X_i' X_i (b_i - \beta)}{\hat{\sigma}_i^2}$$

where  $b_i$  are coefficients estimated by ordinary least squares (OLS) for an individual tree and  $\beta$  is the generalized least squares estimator (GLS) given in [5]. (Refer to footnote 4 concerning formulation of this statistic in higher dimensions.) The asymptotic distribution of the  $H_0/P(N - 1)$  statistic can be approximated by an  $F$  distribution having  $P(N - 1)$  and  $N(T - P)$  degrees of freedom. For this comparison a  $T$  value of 8 was used. The computed value of  $H_0/P(N - 1)$  was 152.7. This value is considerably above the 5 percent value of  $F$  with 372 and 1.122 degrees of freedom. Therefore, we cannot conclude that the coefficients are homogeneous across trees and thus, a varying parameter model approach is warranted.

The results of the GLS parameter estimation based on individual trees and the OLS parameters estimated from the pooled data are given in Table 3. To compare the results of the two estimation techniques, the hypothesis of equality of coefficients between methods was tested (see Swamy 1970 for the test statistic). This hypothesis was rejected at  $\alpha = 0.05$ . Thus it is evident that there are substantive differences in the values of the coefficients between the two estimation techniques. Figure 3 shows the differences in site curves (with all species combined) due to

TABLE 3. GLS and OLS estimates of the betas.

Item	All species combined	Estimation procedure
ln( $\beta_0$ )	1.055	GLS
$\beta_1$	1.732	
ln( $\beta_0$ )	0.954	OLS
$\beta_1$	1.457	
$N$	187	

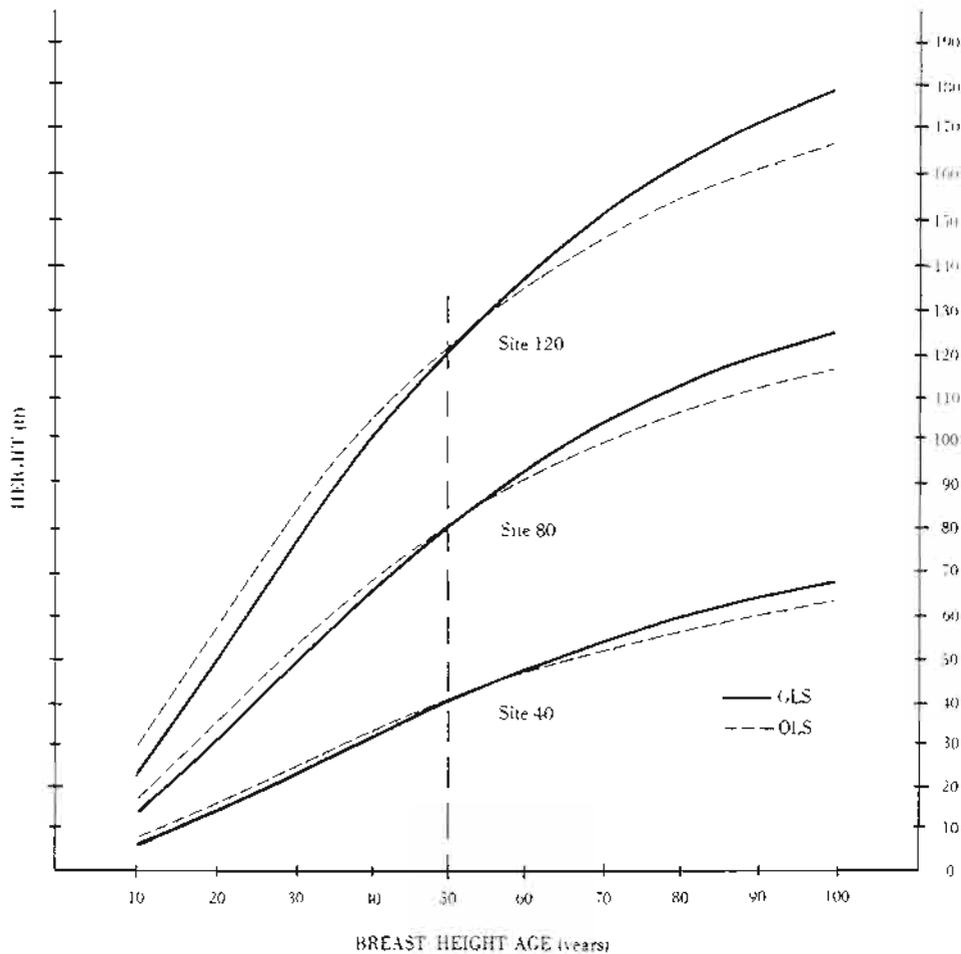


FIGURE 3. Site index curves estimated by GLS and OLS techniques.

the two estimation techniques.<sup>5</sup> That is, the GLS estimate for the asymptote ( $b_0$ ) was higher than its OLS counterpart, producing higher levels of growth past age 50. In addition, the rate and shape parameter ( $b_1$ ) estimated by GLS was larger than when estimated by OLS. The net effect of these trends is to increase the slope of the curves. These differences would have an effect on growth and yield estimation, particularly on sites of at least 80 feet at breast height age 50, in that the GLS-estimated curves show significantly higher potential height growth beyond age 50 than do their OLS counterparts. In a simulation or inventory update, the height growth of trees experiencing little or moderate competition would likely be underestimated by the traditional OLS curves with resulting underestimates of volume productivity. This is because growth and yield simulators frequently utilize site curves in estimating height growth potential and induce reductions based upon the level of competition effecting individual trees (e.g., Daniels and others 1979, Monserud 1975, Krumland 1982, Mitchell 1975). In a related study, Ferguson and Leech (1978) compared OLS and GLS estimates of parameters of

<sup>5</sup> For the figures presented, the curves have been adjusted to go through site index at age 50. This adjustment was accomplished by setting  $t = 50$  and  $h = S$  and solving for the parameter  $b_1$ . However, the basic relationships are unchanged by this adjustment.

TABLE 4. Sum of squared differences between predicted and actual heights summed over 187 individual site trees using the GLS and OLS parameter estimates of the untransformed Model [9] and the GLS estimates of Model [7] estimated with nonlinear regression techniques (NLIN).

Item	Model [9], linear parameter estimates, all species combined		Model [7], nonlinear parameter estimates, all species combined.
	GLS	OLS	GLS
Total residual sum of squares	106,538	131,453	120,259

a yield function. Although not discussed, their model predictions for cubic meter yields using the GLS estimates of the parameters were also higher (3–6 percent) than their OLS counterparts over a wide range of sites and ages.

It is not surprising that these approaches lead to different parameter estimates owing to the fundamental difference in parameter estimation techniques. For these two approaches to lead to equivalent results, the random elements ( $\delta_i$ ) must be equivalent across individuals. That is, the growth form of the individual trees must be equivalent. Sullivan and Reynolds (1976) have discussed the properties of the OLS estimators while using time series data. The OLS estimates of the parameters are unbiased even in the presence of correlated data. However, the OLS parameters are unbiased in estimating the regression line that predicts the conditional mean height of the sample given specific values of the explanatory variables. This regression line is not equal to the height growth curve of the average tree if the random elements vary by individual. Hence, the traditional OLS regression estimates of cross-sectional data lead to estimation of a different regression line. Thus a more accurate estimate of the mean height growth curve should be obtained with the GLS procedure presented in which a varying-parameter model is fitted to each individual tree in the data set.

To assess the performance of the GLS estimates of the parameters, Model [9] was used to predict height over age of all 187 individual site trees.<sup>6</sup> The sum of squared differences of predicted versus actual heights was calculated for each tree in the data base and summed using the GLS and OLS estimates of the coefficients. The results are presented in Table 4.<sup>7</sup> The sum of squared differences of predicted versus actual heights was considerably lower when using the GLS estimates of the parameters of Model [9] than when using the OLS estimates. It is also interesting to note that using Model [10] (or equivalently Model [9]), which was a linearization of the sigmoidal model, was superior in residual variation when judged against the GLS estimates of a nonlinear equation (Model [7]). Thus, there appears to have been no resultant loss in predictive power incurred by setting parameters to specific values to allow linearization of the sigmoid model.<sup>8</sup>

<sup>6</sup> The residual sum of squares using the OLS estimates of the parameters would be less than when using the GLS estimates for Model [10]. However, in the untransformed metric this relationship may not hold.

<sup>7</sup> For the tabled values presented, the curves have been constrained to go through site index at age 50 (see footnote 5).

<sup>8</sup> The values presented in Table 4 for Model [7] are not directly comparable to those of Model [9] owing to the frequent nonconvergence of the asymptote for young trees when estimating parameters of Model [7]. Thus, fewer trees were utilized in estimating the coefficients of Model [7] than of Model [9].

## CONCLUSIONS

Two methods of estimating the parameters of site index curves were investigated. Commonly, pooled stem analysis data are used to develop a regression equation describing height as a function of age and site (or age). The OLS estimates of the parameters, so computed, may provide different estimates of the height growth development of the average tree than if a varying-parameter model is employed. Thus, an alternative approach was presented that utilizes the full information inherent in stem analysis data for individual trees. The procedure used a varying-parameter (random regression coefficient) model derived from weighted least-squares fitting of height growth models to the observations of individual trees over time.

An example was presented for primarily dominant trees in the mixed conifer forest of California. For the sigmoid model tested, the varying-parameter model predicted higher asymptotic growth than its OLS counterpart estimated using pooled data. The corresponding measures of model fit for the untransformed Model [9] (residual sum of squared differences between predicted and actual on individual trees) showed that the GLS technique fitted the stem analysis data well. This approach should prove useful in modelling many growth processes provided the growth series is of sufficient length to accurately estimate the parameters of the hypothesized model as well as estimate residual variance on an individual tree basis.

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