AN ABSTRACT OF THE THESIS OF

John A. Scrivani for the degree of Doctor of Philosophy in Forest Management presented on August 12, 1985.

Title: Nonlinear Models of Height Growth for Douglas-fir in Southwestern Oregon.

Abstract approved: ______________________________

A review is made of methods which assess the bias and non-normality of parameter estimates and predictions obtained with nonlinear regression. Particular emphasis is placed upon curvature measures of nonlinearity, related measures of parameter and prediction bias, and the effects of reparameterizations. Alternate models of individual tree height growth are compared on the basis of mean square error, intrinsic nonlinearity, parameter effects nonlinearity, and estimated bias. While results are specific to the data examined, some general conclusions are made concerning appropriate models for individual tree height growth. Both the Richards and a Weibull-type growth model are found to adequately describe individual tree height growth, with low levels of intrinsic nonlinearity, and acceptable parameter effects nonlinearity following reparameterization. Some evidence is found for a modification of either the Richards or Weibull model to include an asymptotic linear growth rate when modeling the height growth of some western conifers past the age of 200.

Stem analysis data on Douglas-fir height growth in mixed confier stands located in southwestern Oregon are used to develop a system of dominant height growth and site index prediction. The Weibull model is used successfully to develop a polymorphic height growth prediction equation. A linear model, estimated with site index as the dependent variable, is used to predict site index. A comparision is made of pooled least squares and random coefficient estimation methods. The random coefficient method is found to more closely model the shape of early height growth, but appears to result in more biased predictions and performs very poorly on older height growth, with both the estimation and validation data. Alternative error assumptions are examined with the pooled data method. The best performance in validation is obtained with assumption of independent errors, heteroscedastic across trees.

Nonlinear Models of Height Growth for Douglas-fir in Southwestern Oregon

by

John Scrivani

A THESIS

submitted to

Oregon State University

in partial fulfillment of
the requirements for the
degree of

Doctor of Philosophy

Completed August 12, 1985

Commencement June 1986

APPROVED:

Professor of Forest Management in charge of major

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Date thesis is presented August 12, 1985

Typed by John Scrivani for John Scrivani

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INTRODUCTION

The height growth of dominant and codominant trees in even-aged forest stands is a major component of volume growth. The prediction of future dominant height growth is thus essential to accurate simulation and prediction of future stand growth. Furthermore, the height growth of dominant trees is often used as an index of site productivity, as dominant height growth is relatively independent of stand density. Thus, accurate models of the height and age relationship can be used to estimate site quality.

The height of dominant trees typically follows a sigmoidal pattern with age. This implies that mathematical functions which are capable of assuming a sigmoidal shape are most appropriate for modeling height growth. The most flexible of such functions are generally nonlinear in some or all of their parameters, requiring the use of nonlinear parameter estimation techniques. In using nonlinear estimation methods, many of the desirable properties associated with linear estimation are lost. In finite samples, the parameter estimates and predictions obtained are no longer unbiased nor are they efficient.

The first chapter of this thesis will examine the degree of nonlinearity inherent in modeling individual tree height growth with standard data sets. Alternate models of individual height growth will be compared on the basis of bias and nonlinearity, as well as on the more familar basis of mean square error.

In developing a general model for predicting height growth across a variety of site indices, some simplifying assumptions are required. The simplest assumption is that height growth follows the same general pattern across all site indices. Anamorphic curves which can be scaled up or down to reflect relative levels of site quality can be developed under this assumption. If it is believed that height growth follows different patterns on different site indices, then a polymorphic prediction equation is appropriate. Polymorphic equations can be developed with the "parameter prediction" approach (Clutter, et al 1983). The parameters of a polymorphic equation can be estimated with either a pooled data approach or a "random coefficient" approach (Ferguson and Leech 1978, West 1981, Biging 1985).

Using a model found suitable from the work reported in Chapter I, a polymorphic equation for predicting height growth of Douglas-fir in southwestern

Oregon is developed and presented in Chapter II. The pooled data estimation method is compared to the random coefficient method. The effects of different error assumptions under the pooled approach are also examined. In addition to examining performance on the estimation data, two validation data sets are used to compare models and estimation methods. The results of this validation and a system for predicting site index and height are presented at the end of Chapter II.

CHAPTER I

NONLINEAR REGRESSION DIAGNOSTICS: APPLICATIONS TO INDIVIDUAL TREE HEIGHT GROWTH

Many biological processes are nonlinear in nature. Much emphasis in biometrics is placed on finding mathematical functions which can adequately describe nonlinear growth. In the field of forest biometrics numerous authors, including Grosenbaugh (1965), Prodan (1968), Pienaar and Turnbull (1973), Yang, Kozak and Smith (1978), and Bailey (1980), have examined and applied various nonlinear functions to forest growth processes.

Some of these mathematical functions have been derived from theoretical relationships. Perhaps best known is the Richards function. This function is developed from a hypothesized relationship between anabolic and catabolic metabolism, expressed mathematically bv von Bertalanfy (1951). Richards (1959) generalized von Bertalanfy's model by allowing the hypothesized allometric constant to vary.

Other functions have had more empirical origins. The shape of cumulative growth curves resemble cumulative probability curves. Likewise, growth rate curves resemble in shape probability density curves. It seems logical then to use such mathematical functions to describe growth processes. Most successful have been the Weibull function (Wang, Kozak and Smith, 1978), and the log-logistic function (Monserud, 1984).

Whatever nonlinear function is choosen to represent a growth process, a fitting method is needed to estimate the parameters of the function. The most commonly used method is nonlinear least squares. Most researchers are familar with the many desirable properties of linear least squares estimation. It is commonly assumed that nonlinear least squares estimation has the same set of desirable properties. In fact, similar results are only obtained asymptotically, i.e. in very large samples. For small samples, nonlinear least squares estimators are capable of being significantly biased and inefficient.

NONLINEAR LEAST SQUARES

Suppose that a growth process can be described by a mathematical function $f(x,\beta)$, where x is an explanatory variable such as age, and β is a p-dimensional vector of functional parameters which we wish to estimate. Given n pairs of an observed response and its associated explanatory variable, (y_i, x_i), we may write the model as:

$$y_i = f(x_i, \beta) + e_i \ , \ i = 1,\ldots,n \qquad (1)$$

where e_i is the error associated with the i-th observation.

The nonlinear least squares (NLS) estimate of β is defined as the value of β which minimizes the sum of the squared errors from equation (1). Provided that $f(x_i, \beta)$ is defined and continuous for all possible values of x_i and β, the NLS estimator exists and is unique (Malinvaud, 1970).

If we assume that the errors (the e_i's) about (1) have zero expectation and are independently and identically distributed with a constant variance, σ^2, then Jennrich (1969) and Malinvaud (1970) have shown that the NLS estimator of β is consistent. Furthermore, $s^2 = \sum_{i=1}^{n} e_i^2/(n - p)$ is a consistent estimator of the variance of the errors, σ^2.

To obtain further results we must assume that the first partial derivatives of f(.) with respect to β

exist and are continuous for all possible β and for each x_i . We further assume that the n x p matrix B with elements $\frac{\partial f_i}{\partial \beta_j}$, has full column rank such that the p x p matrix A = B'B is nonsingular. With these additional assumptions the NLS estimator is asymptotically normally distributed with covariance matrix A^{-1} . Furthermore, the NLS estimator can be used to consistently estimate A^{-1}. (See Jennrich, 1969 or Malinvaud, 1970).

Summarizing the results so far, the NLS estimator is consistent and asymptotically normally distributed. That is, for large enough samples, the NLS estimator can be considered unbiased and normally distributed. However, in small samples the NLS estimator is generally biased and non-normally distributed.

If we make an additional assumption that the errors are normally distributed, than the NLS estimator coincides with the maximum likelihood estimator. This assumption assures us that the NLS estimator is asymptotically efficient. However, in small samples the NLS estimator is still to some degree biased and possibly inefficient.

The implications of these results are that for small samples the fitting of nonlinear models to biological growth processes may result in misleading, i.e. biased, estimates of the parameters of interest, and in biased predictions of future growth. Furthermore, any tests of significance or confidence intervals based upon the asymptotic normality of the NLS etimators may be inexact.

The question naturally arises of when are NLS estimators acceptably unbiased and efficient. Fortunately, recent work has given us some diagnostic tools which enable us to assess the degree of bias and nonlinearity associated with particular data and models. To gain some understanding of these diagnostics, it is helpful to have some understanding of the geometry of least squares.

A GEOMETRIC VIEW OF NLS ESTIMATION

The n observations on the dependent variable Y can be thought of as a vector, which we shall term $\underline{y}$, existing in an n-dimensional space. We refer to this n-dimensional space as the sample space. For any acceptable value of the p-dimensional vector , an n-dimensional vector of predicted values is defined by $\underset{\sim}{\eta}(\beta) = f(x;\beta)$. This vector, $\underset{\sim}{\eta}$, also exists in the sample space. As β is varied over all permissable values, $\underset{\sim}{\eta}(\beta)$ traces a p-dimensional surface, which we shall refer to as the solution locus. The least squares estimator of β is associated with the point on the solution locus which is closest to the vector $\underline{y}$. For a fuller treatment of these concepts the reader is referred to Draper and Smith (1981).

Linear least squares can be thought of as a special case of NLS estimation. In this special case the solution locus is a linear subspace, a p-dimensional hyperplane intersecting the origin. The linear least squares estimator of β is easily found by dropping a perpendicular vector from $\underline{y}$ to the solution locus. This is also referred to as projecting $\underline{y}$ onto the solution locus. The well-known solution to the normal equations of linear least squares accomplishes this projection with a single iteration.

A second attribute of the solution locus in the linear case is important, the fact that straight, parallel, and equally spaced lines in the parameter space map into straight, parallel and equally spaced lines on the solution locus. In other words, a uniform grid of β coordinates translates to a uniform grid of $\eta(\beta)$ coordinates. This allows us to use the covariance matrix of β to develop exact confidence intervals for $\eta(\beta)$ as well as for β.

In the general nonlinear case, the solution locus is not a linear subspace but rather a curved surface. No exact analytical technique exists for finding the NLS estimator. Instead, methods which are iterative and approximate must be relied upon. Many of these methods, however, to some extent mimic the linear solution method by using a local linear approximation to the solution locus. For example, in the Gauss-Newton method an initial guess at β is used to approximate the solution locus. The observed vector y is projected onto the linear approximation provided by the initial guess, resulting in a new guess at β. This process is repeated until the value of β converges. Thus the Gauss-Newton method can be thought of as a series of linear regressions.

The local linear approximation to the solution locus is provided by the first term of a Taylor series expansion of $\eta(\beta)$ about $\hat{\beta}_i$, the current guess at

β ,

$$\eta(\beta) \doteq \eta(\hat{\beta}_i) + (\beta - \hat{\beta}_i)' \frac{\partial \eta}{\partial \beta} \qquad (2)$$

where, $\frac{\partial \eta}{\partial \beta}$ is the vector of first partial derivatives of $\eta(\beta)$ with respect to β. This local approximation in effect replaces the solution locus with its tangent plane at $\eta(\hat{\beta}_i)$. Once the NLS estimator of β is found, this same approximation is used to provide a consistent estimate of the covariance matrix of $\hat{\beta}$.

In the special case of linear least squares the local approximation is exact and only a single iteration is required to find the least squares estimator. Furthermore, the covariance matrix of $\hat{\beta}$ is given exactly by $\mathbf{A}^{-1}$. (In the linear case $\mathbf{A}^{-1} = (\mathbf{X}'\mathbf{X})^{-1}$).

It may be intuitively seen that if the local linear approximation is very good at approximating the solution locus, a nonlinear model will behave very much like a linear model. It follows then that a good diagnostic tool would be some measure of how well the local linear approximation mimics the solution locus.

Beale (1960) proposed an empirical measure of the adequacy of the local linear approximation. His method, in the simplest terms, consists of comparing, for a number of points on the solution locus near the NLS estimator, the actual distance between each point and the NLS estimate with the distance estimate provided by the local linear approximation.

Bates and Watts (1980) have criticized Beale's empirical measure on several grounds, proposing instead their own measures, which are based upon concepts of differential geometry. Bates and Watts point out that the local linear approximation implies two assumptions. The first, termed the planar assumption, assumes that the solution locus is a plane in the vicinty of the least squares solution. The second, the uniform coordinate assumption, imposes a uniform coordinate system upon this plane. More specifically, this assumes that straight, parallel, and equally spaced lines in the parameter space map into straight, parallel and equally spaced lines on the solution locus.

Using second partial derivatives of $\eta(\beta)$, Bates and Watts calculate the curvature of the solution locus at the least squares solution. The second partials are first scaled to allow comparison of different models and data sets. The scaling factor used is $s\sqrt{p}$, where s is the standard error and p the number of parameters. This scaling factor is derived from the following formula for the radius of a $(1 - \alpha)$ joint confidence region, $r = s\, p\sqrt{F(p,n-p;\alpha)}$.

Bates and Watts separate out the curvature due to the planar assumption from that due to the uniform coordinate assumption. This is accomplished by a coordinate rotation in the sample space, the details of which can be found in their 1980 paper. Since the solution locus may not be symmetric about the least squares solution, the curvatures may vary in different directions. Thus an iterative method is required to find the maximum curvatures.

The two curvature measures proposed by Bates and Watts are termed *intrinsic non linearity* (IN) and *parameter effects curvature* (PE). The first can be thought of as a measure of the discrepancy between the tangent plane provided by the linear approximation and the true surface of the solution locus. As such, it can be used as a measure of validity for the planar assumption. The second is a measure of the departure of the uniform coordinate system, which is imposed by the linear approximation, from the true coordinate system of the solution locus. It is therefore a measure of validity of the uniform coordinate assumption.

In order to assess the magnitude of their nonlinear curvature measues, Bates and Watts suggest comparing computed values to the value $1/\sqrt{F}$, where F is the $(1-\alpha)$ critical value of the F-distribution with n-p and p degrees of freedom. This correspond to the standardized radius of a $100(1-\alpha)$ per cent joint confidence region. When curvature measures are greater than this value they may be considered "large".

Large values of IN mean that the linear

approximation of the solution locus is poor for a particular combination of model and data. Prediction bias may be high. Interpretation of the parameters is hazardous because of the potential for high parameter bias. Inference procedures based upon the asymptotic normality of the parameter estimates are likely to be very inexact. Remedies for high IN include selection of a less nonlinear model and the collection of new data. Generally more data is better; but certain settings of the independent variables may be more valuable in the reduction of high IN. For example, if the model has inflection points, extreme points, or asymptotes, settings of the independent variables which may be close to these important locations may do more than other points to reduce IN.

If IN is acceptably low, then the PE measure can be examined. If prediction is the sole objective, however, PE can be ignored, as it depends solely on the parametrization. Reparametrization will not change predicted values, nor will it change the IN measure. The PE measure does provide an assessment of how good are the approximate inference procedures based upon asymptotic normality. Acceptable levels of PE imply that the standard asymptotic t-tests and confidence intervals can be used safely. Conversely, unacceptable levels of PE imply these methods are likely to be inexact. Reparameterization may provide a remedy for unacceptable levels of PE, provided IN is acceptably low.

Working with an assumption of normal errors, Box (1971) developed an approximate expression for the bias of NLS parameter estimates. He also developed an approximation for the bias in predictions obtained by NLS methods. He showed that the biases of both predictions and parameters are of an order of magnitude lower than their standard errors. This gives us a practical, and reassuring, upper bound on the bias inherent in NLS estimation.

A general formula for calculating Box's estimate of parameter biases is presented in the Appendix, along with a general formula for estimating prediction bias. Also presented is a formula for estimating the bias of a general nonlinear function of the parameters. This last formula can be useful for obtaining a quick estimate of the effect of a reparametrization.

Ratkowsky (1981) showed that high parameter bias was associated with high PE nonlinearity. In fact, when attempting to reduce PE, parameter bias can be used as a practical guide to parameters which are most in need of reparameterization. He also showed that reparametrization has no impact upon prediction bias; prediction bias remains unchanged after reparameterization, and is solely dependent upon IN.

Bates and Watts (1980) and Ratkowsky (1981) have applied the curvature measures diagnostics to many commonly used nonlinear models and data. They have found that PE is typically higher than IN; with IN commonly well below the acceptable upper limit, and PE often in excess of the acceptable limit. With simulation studies, Ratkowsky has found that parameters often behave in a close to linear manner, even when PE is slightly above the critical value, provided that parameter biases are low. He suggests a estimated bias of one percent of the estimated parameter or less as a rough criterion for a nearly linear parameter.

The two curvature measures of Bates and Watts, IN and PE, and Box's estimation method for biases, can be used along with mean square error and visual assessment of lack of fit to select appropriate nonlinear models. If inference about parameters is an objective, the PE measure and Box's estimate of parameter biases can be used to help select among alternative parameterizations of a selected model.

HEIGHT GROWTH MODELS

The cumulative height growth of dominant trees in even-aged stands shares a characteristic with many biological growth processes; it follows a sigmodial-shaped curve over time. Various mathematical functions have been used to describe such height growth curves. We have used the diagnostics discussed above to help in our selection of appropriate nonlinear functions to describe cumulative height growth over time.

Schumacher (1939) suggested the simple ln(height)/reciprocal of age model, written as

$$H = b_1 \exp(b_2 A^{-1}) \quad , \tag{3}$$

where, H refers to cumulative height at age A.

Piennar and Turnbull (1973) presented the theory behind the Richards (or Chapman-Richards) model, and fitted it to some height growth data as an example of its potential use. This three parameter model may be most simply written as,

$$H = b_1 [1 - \exp(-b_2 A)]^{b_3} \quad . \tag{4}$$

Since their paper, the Richards function has enjoyed widespread use in the forest biometrics field.

Yang, Kozack and Smith (1978) presented a Weibull-type function as a flexible growth curve. They compared their Weibull-type curve to other functions on a fit to height growth data. The three parameter Weibull-type curve may be written as,

$$H = b_1 [1 - \exp(-b_2 A^{b_3})] . \qquad (5)$$

Bailey (1980) proposed the use of a generalized Weibull function, which includes, as special cases, both the Weibull and Richards functions. This four parameter model may be written as:

$$H = b_1 [1 - \exp(-b_2 A^{b_3})]^{b_4} . \qquad (6)$$

Monserud (1984) has recently used a log-logistic function to describe height growth. The function is a reparameterization of a function proposed by Prodan (1968). It is also equivalent to a model proposed by Morgan, Mercer and Flodin (1975) for a nutritional model. It is similar to a polynomial approximation to the Prodan model, suggested by Prodan and used by King (1968) for a height growth and site index model. The model obviously has many parameterizations, a simple one being,

$$H = b_1 / [1 + \exp(b_2 + b_3 \ln(A))] . \qquad (7)$$

Two other models are often used in biological growth applications, the Gompertz and the logistic. The Gompertz model is given by,

$$H = b_1 \exp[-\exp(b_2 - b_3 A)] \ . \qquad (8)$$

The logistic may be written as,

$$H = b_1 / [1 + \exp(b_2 - b_3 A)] \ . \qquad (9)$$

Both the Gompertz and the logistic have the undesirable property, at least when tree height is the dependent variable, of not being constrained to go through the origin. Bailey (1980) correctly stated that the Gompertz and logisitic can be forced to go through the origin by reparameterization. However, simply setting b = 0, as Bailey suggested, will not accomplish this. One way which will, however, is by rewritting (8) and (9) with only two parameters as follows:

$$H = \exp[b_1 - \exp(\ln b_1 - b_2 A)] - 1 \ , \qquad (8a)$$

$$H = b_1 / [1 + \exp(\ln(b_1 - 1) - b_2 A)] - 1. \qquad (9a)$$

A SIMPLE EXAMPLE

Data on the height growth of a dominant Douglas-fir tree growing on a medium-high site in southwest Oregon was used as an example of the use of nonlinear regression diagnostics. The data was collected by stem analysis of a felled tree. The tree was sectioned at the stump, breast height, and thereafter at 2.56 m intervals up the stem. At each section age and the height to the section were recorded. Figure I.1 presents the pattern of cumulative height growth over age.

The seven models mentioned above, the Schumacher, Richards, Weibull, generalized Weibull, log-logistic, Gompertz and logistic models, were all fit with NLS estimation to the data. Figures I.2-I.10 present the fitted height growth curves. The nonlinearity measures of Bates and Watts were calculated for each model. Table I.1 presents the results of these computations.

The four parameter generalized Weibull (6) appears superior in terms of mean square error (s^2 = 1.741), followed closely by (5), the three parameter Weibull (s^2 = 2.311). The Richards (4), log-logistic (7), and three parameter Gompertz (8) followed in order, and had mean square errors of roughly the same order of magnitude. The three parameter logistic (9) and Schumacher's model

(1) fitted poorly, with mean square errors of 40.6 and 61.8. The constrained versions of the Gompertz (8a) and logistic (9a) fitted worst of all, with mean square errors of 165.3 and 757.6.

From the values of mean square error associated with each model and the visual evidence presented in figures I.2-I.10, we concluded that the only models flexible enough to describe Douglas-fir height growth were the Richards, Weibull, generalized Weibull and log-logistic.

The acceptable values of the curvature measures (for a 95 per cent confidence interval) with this sample size are .2696 for a 2-parameter model, .2853 for a 3-parameter model, and .2953 for a 4-parameter model. From Table I.1 it is apparent that all models have acceptable IN, with the notable exception of the generalized Weibull. Thus for all models except the generalized Weibull, the solution locus is close to linear in the vicinity of the least squares solution. The 3-parameter Weibull is most nearly linear, followed closely by the Richards.

The 4-parameter generalized Weibull appears to be severely overparameterized. Further evidence for this conclusion is provided by the asymptotic t-statistics for the parameters of this model; two of the four are not significantly different from zero.

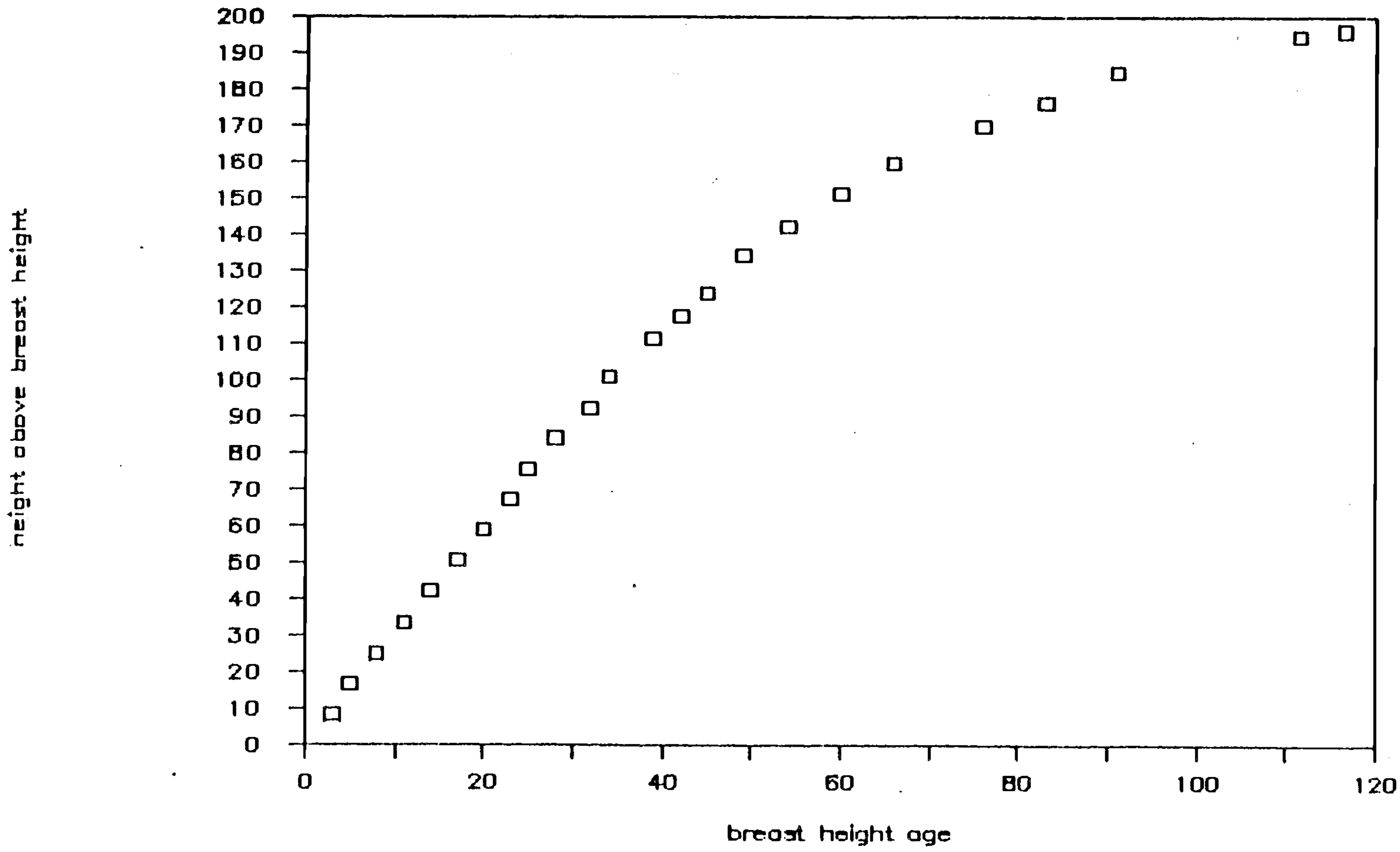

Figure I.1. Height growth of a dominant Douglas-fir.

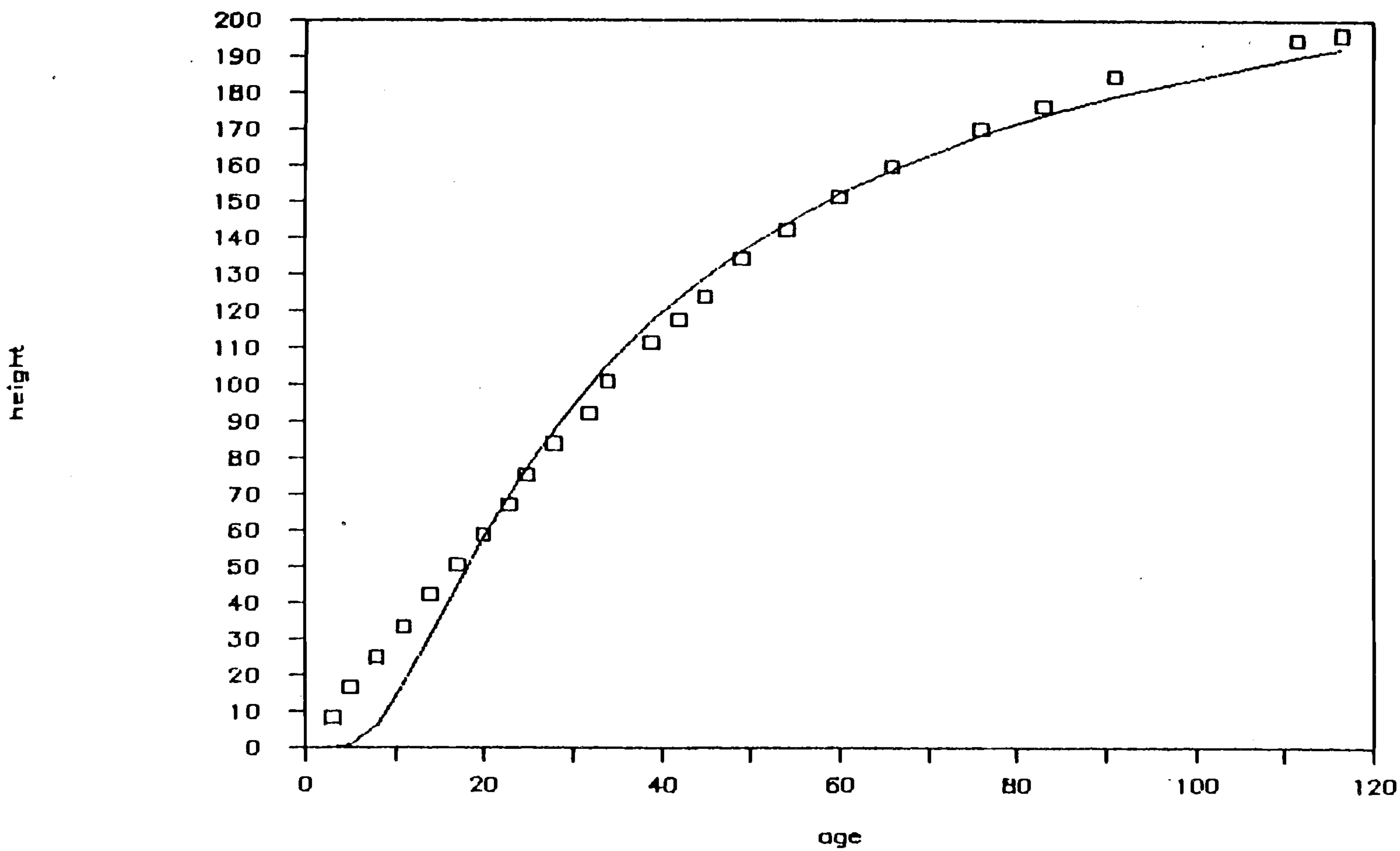

Figure I.2. Schumacher height growth model.

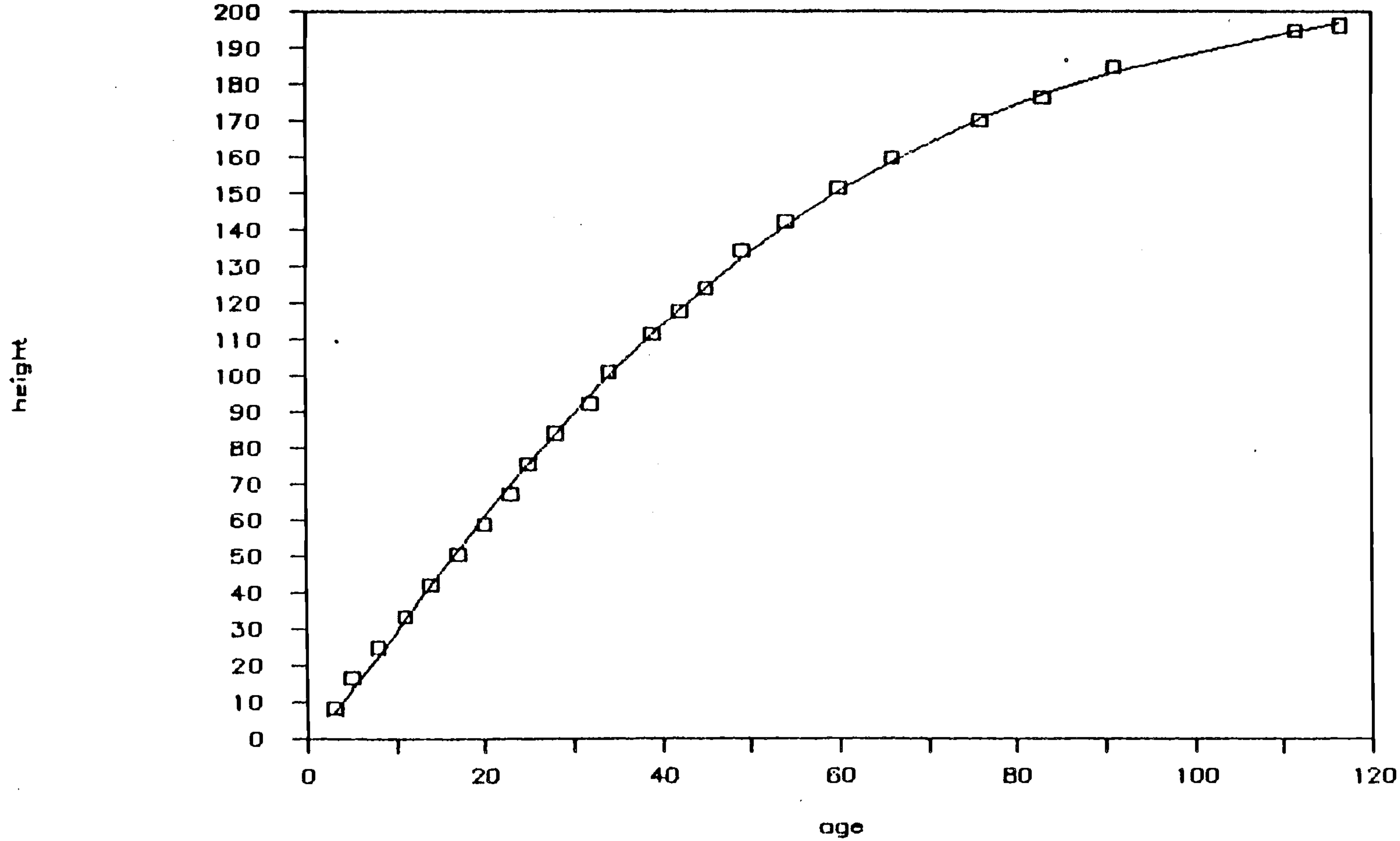

Figure I.3. Weibull height growth model.

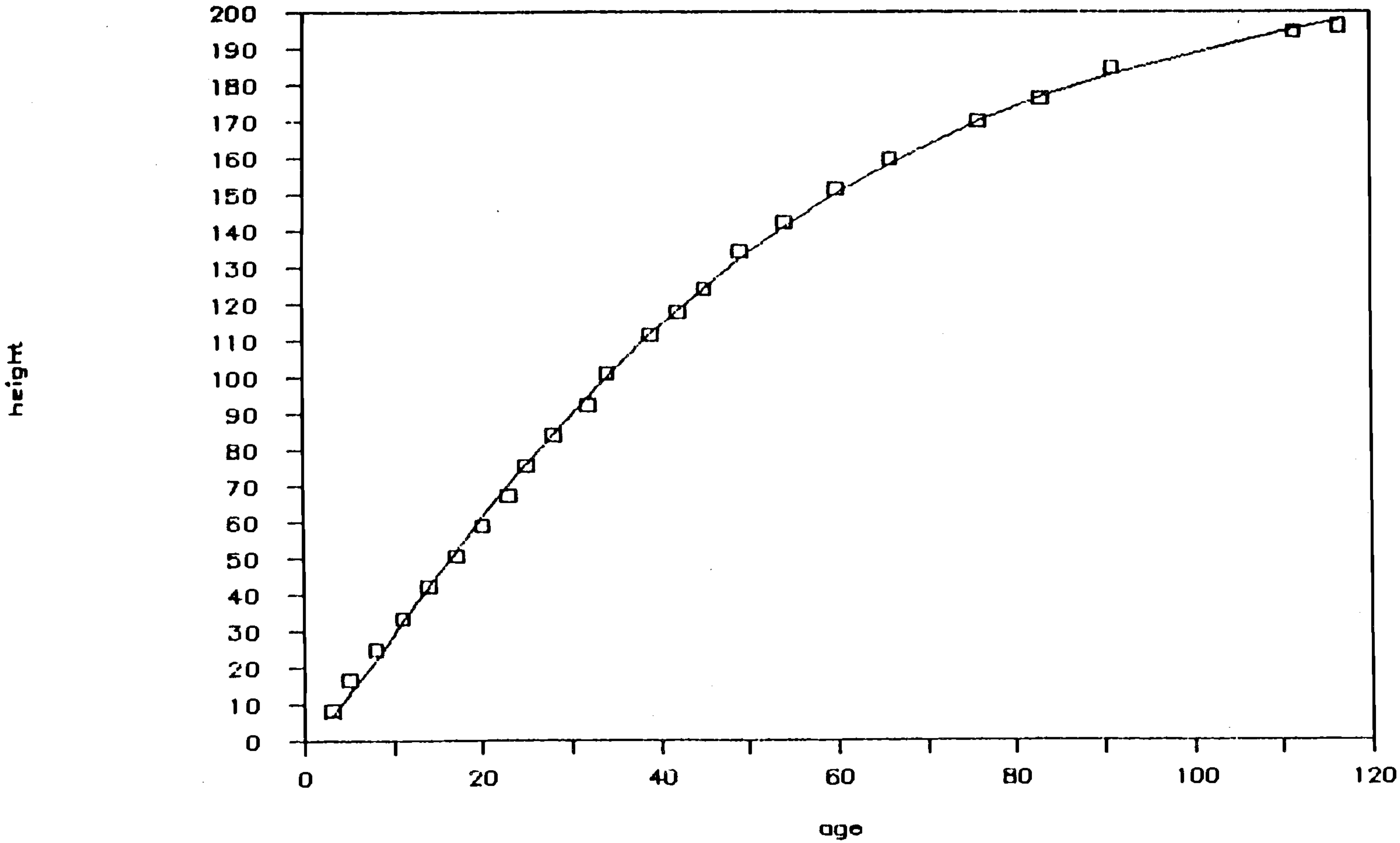

Figure I.4. Richards height growth model.

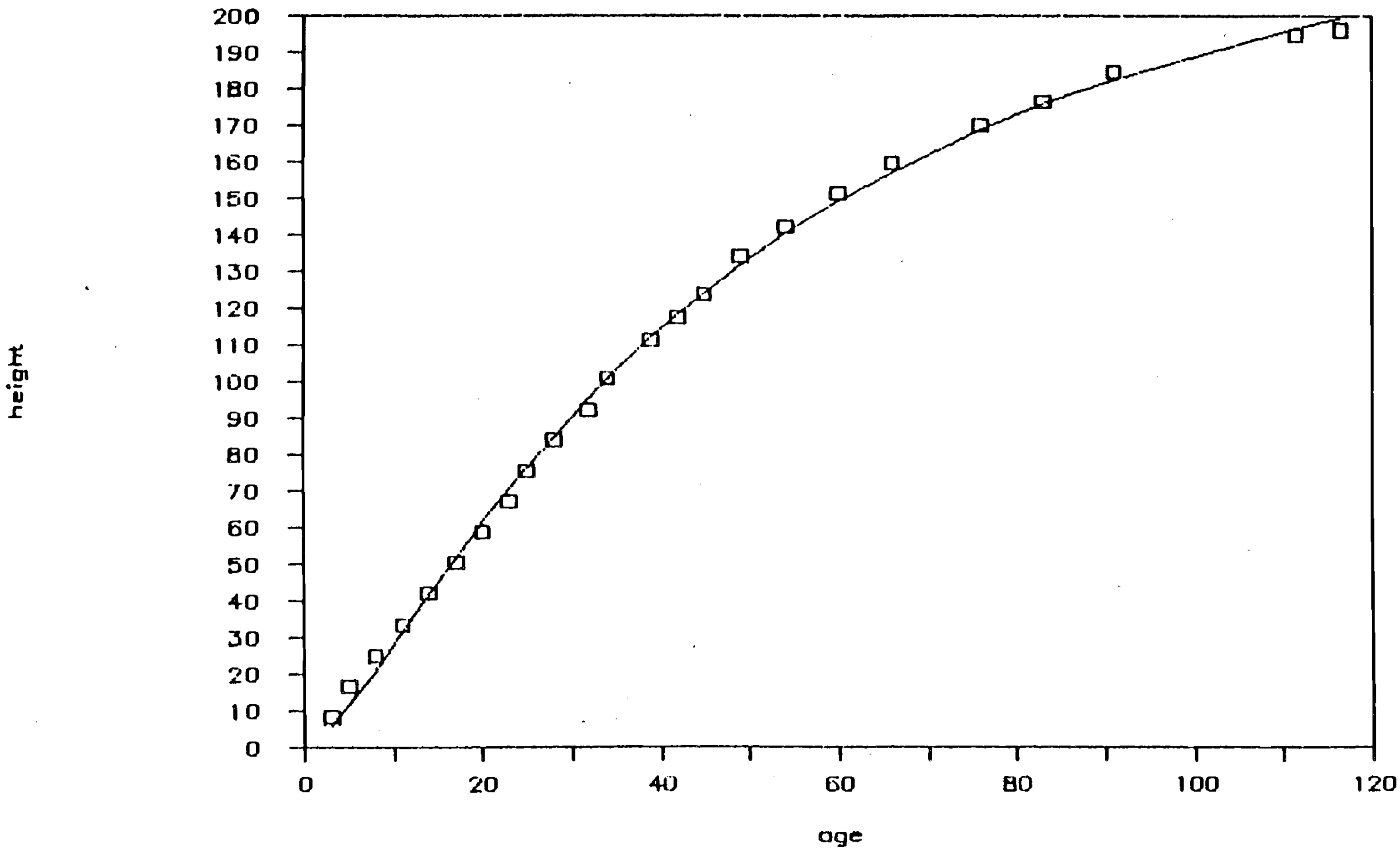

Figure I.5. Log-logistic height growth model.

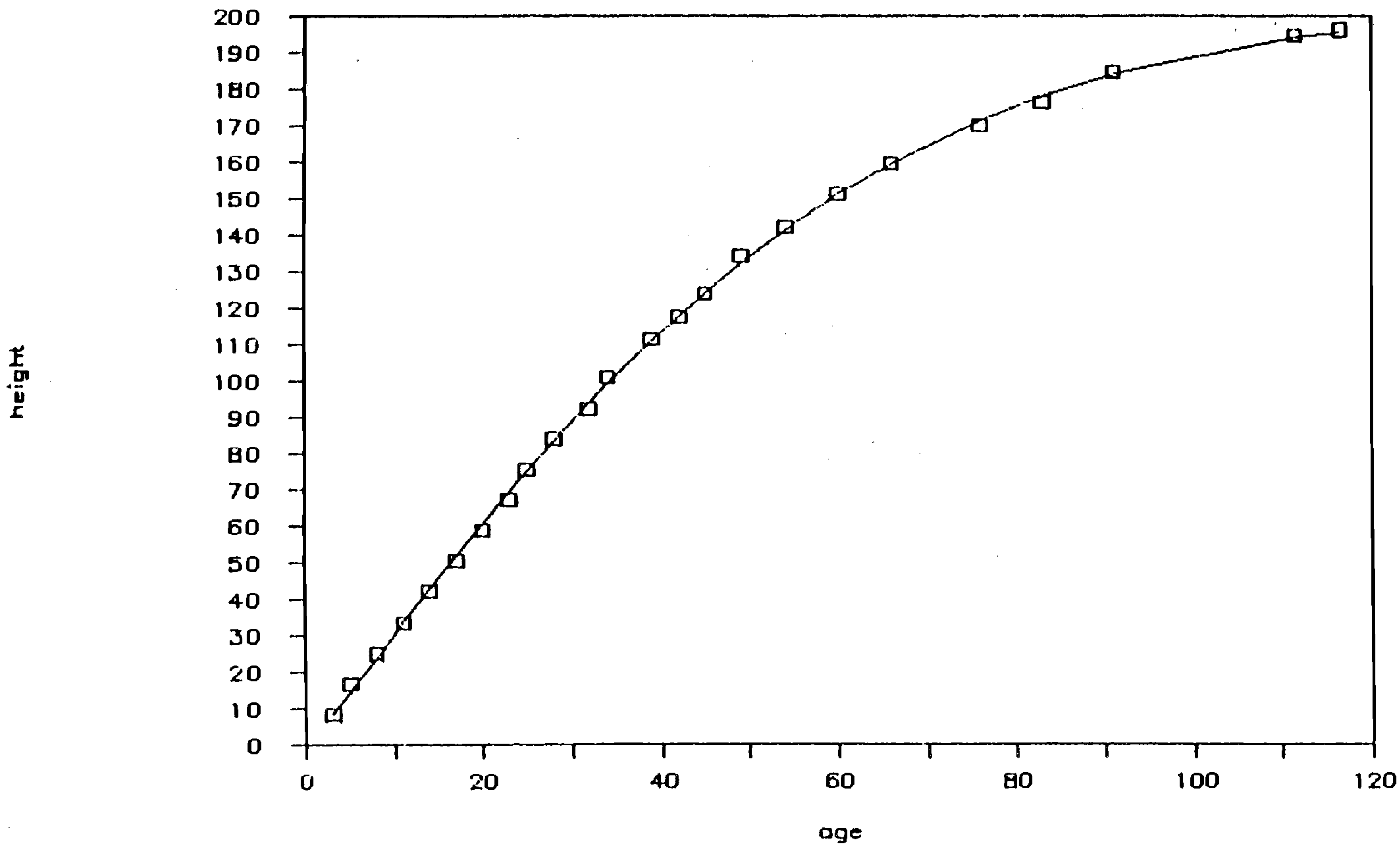

Figure I.6. Generalized Weibull height growth model.

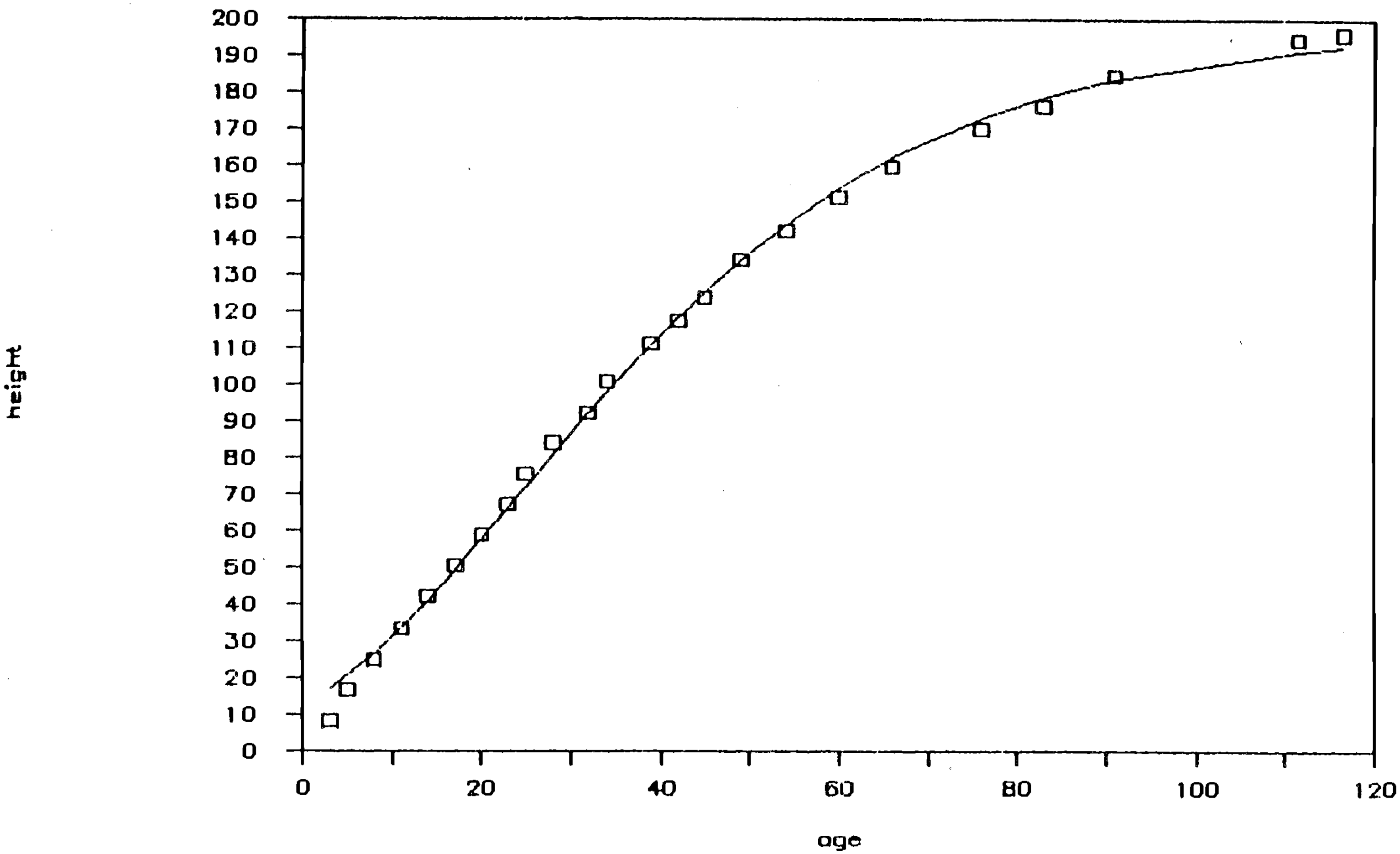

Figure I.7. Gompertz height-growth model.

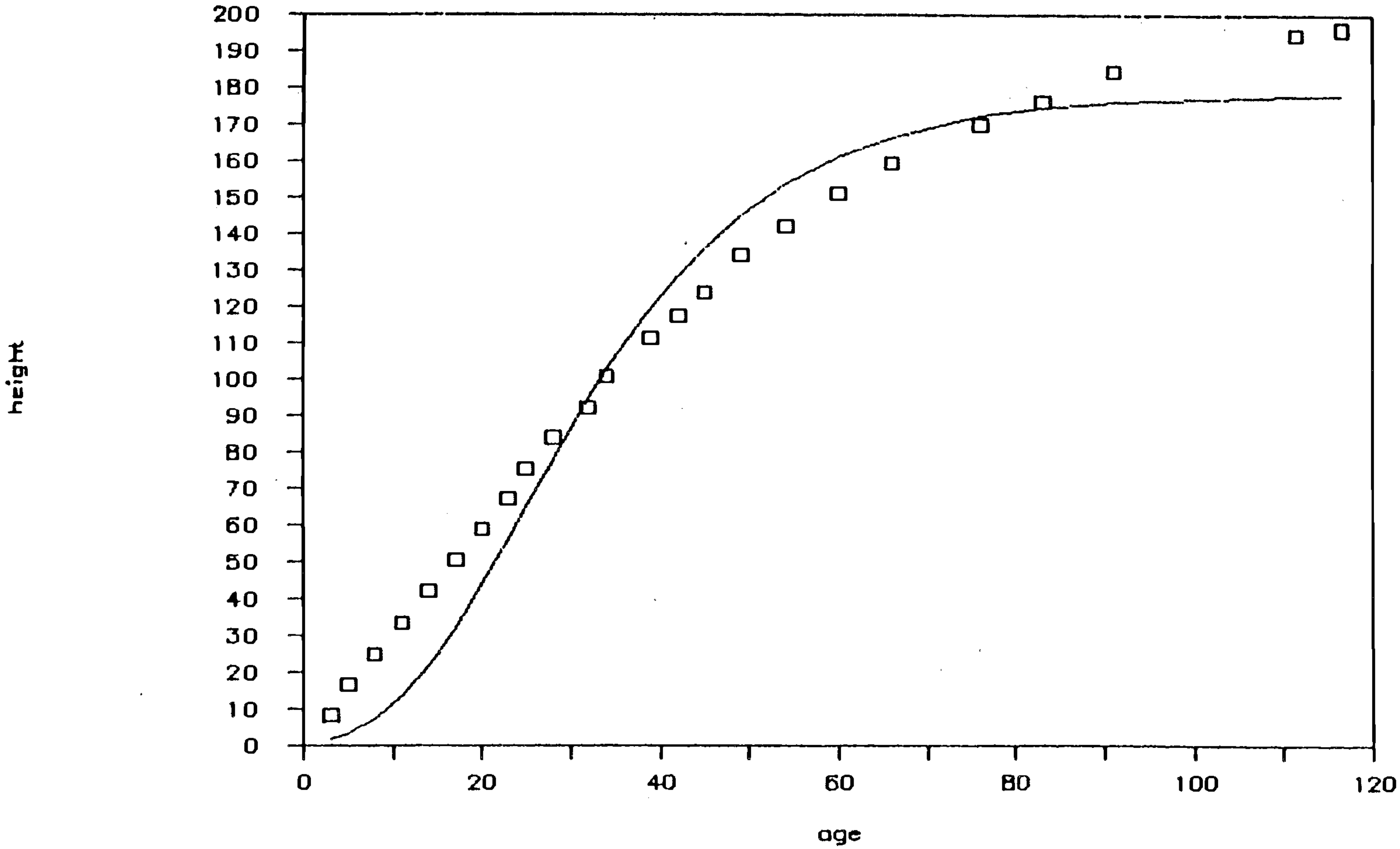

Figure I.8. Constrained Gompertz height growth model.

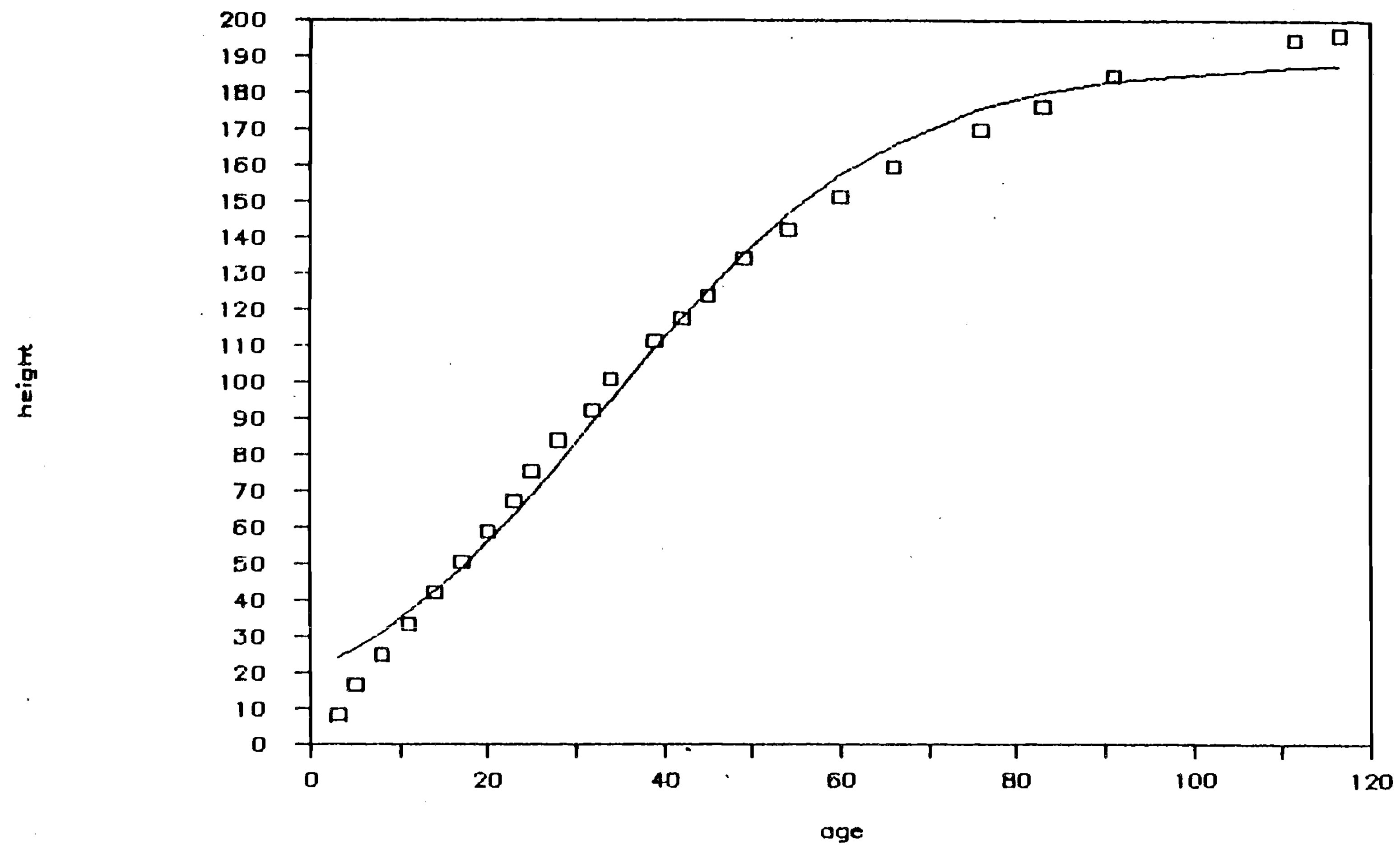

Figure I.9. Logistic height growth model.

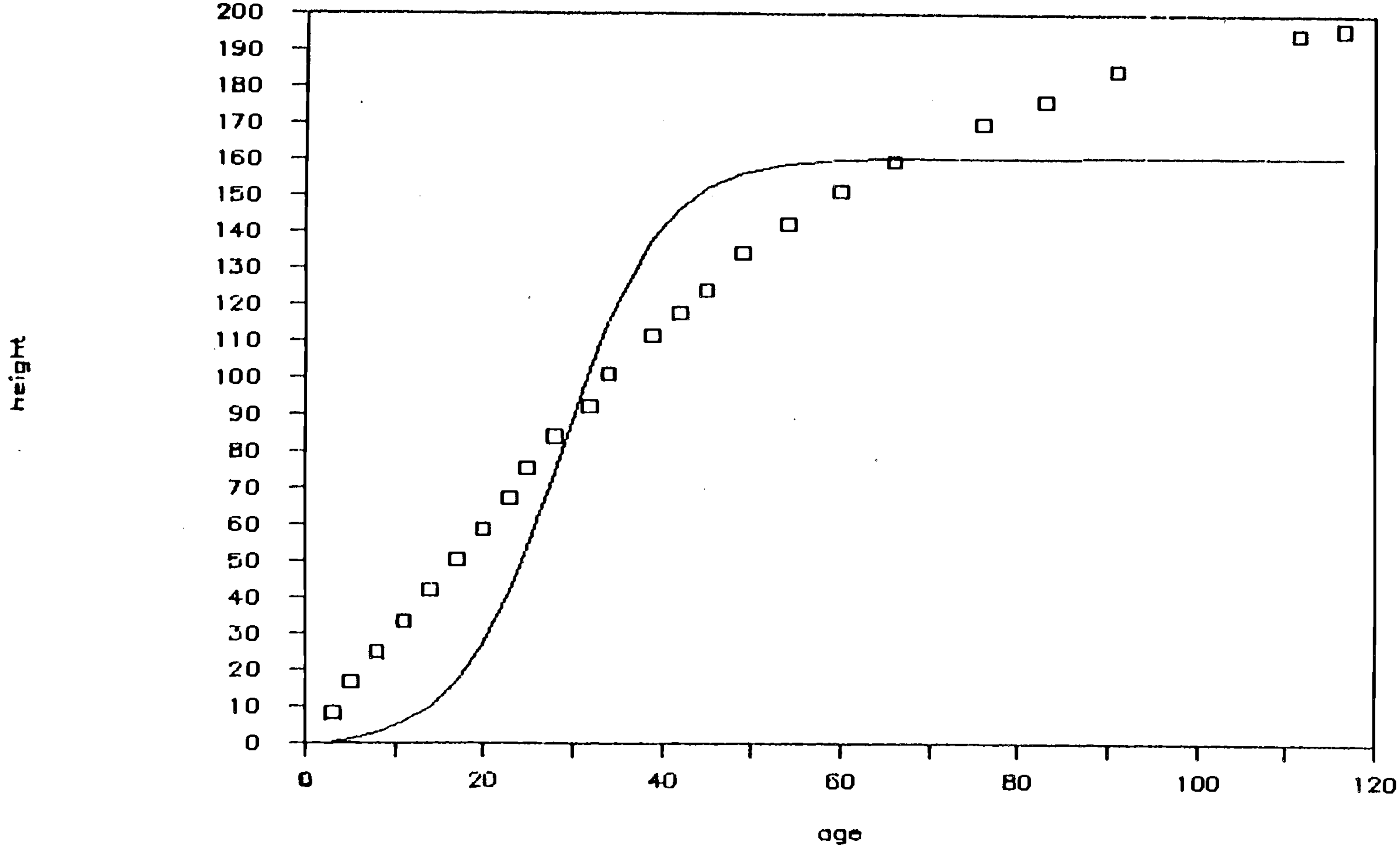

Figure I.10. Constrained logistic height growth model.

Table I.1. Parameters, mean square errors and diagnostics for the nine nonlinear models fitted to the example data.

	Model								
	(3)	(4)	(5)	(6)	(7)	(8)	(8a)	(9)	(9a)
b0	246.7	215.7	209.8	202.6	259.4	197.5	5.191	188.7	161.7
b1	-20.04	.0234	.0096	.0015	5.213	.0400	.0659	2.105	.1764
b2	-	1.281	1.192	1.160	1.348	1.013	-	.0621	-
b3	-	-	-	.6645	-	-	-	-	-
mean square error	61.85	3.151	2.311	1.741	5.610	9.601	165.3	40.58	576.0
IN	.0432	.0188	.0162	5.456	.0864	.0324		.0833	
PE	.0608	.3793	.9014	383.6	83.86	.2007		.2754	
PE^2	.0518	.3036	.2022	-		.1691		.2422	

Table I.2. Estimated percentage biases for the parameters of three selected models fitted to the example data.

Model	PE[2]	b0	b1	b2
		percentage bias[1]		
Weibull (5)	.9014	.0311	.0633	.0633
Richards (4)	.3793	.0346	.0235	.0488
Log-logistic (7)	83.86	-9.888	-.2470	-.1524
Reparameterized models				
Weibull (5a)	.2022	.0048	.0126	.0633
Richards (4a)	.3036	.0051	.0235	.0488
Log-logistic (7a)	2.281	.0106	-.2470	-.1524

[1] Estimated with Box's procedure
[2] Parameter effects nonlinearity

We have found similar rapid rises in IN due to adding an additional parameter to an already well-fitting model form in other data sets and with other nonlinear models. Apparently, IN is very useful in identifying overparameterized models.

The PE measures are larger than their acceptable levels for every model except the Gompertz and the Schumacher. This suggests that the other models are in need of reparameterization if parameter inference or interpretation are objectives.

At this point, we decided to restrict further attention to three models, the Richards, Weibull, and log-logistic. These three fit reasonably well, as measured by mean square error; all three pass through the origin as desired; and, all three have acceptable levels of IN. At this point, if prediction had been our sole objective, we could have stopped and choosen among these three. However, we continued by examining possible reparameterizations for each of these models, with the hope of finding new parameterizations with lower PE. Such parametrizations would be more useful in providing interpretable parameters; they would also allow us to use inference procedures based upon asymptotic normality with greater confidence.

In order to get some idea of which parameters are contributing most to the PE nonlinearity, we examined

Box's estimates of the parameter biases for each of the three models. These biases are presented in Table I.2.

Percentage bias is very high for the first parameter in the log-logistic. The first parameter in each model can be interpretated as the asymptotic limit on height. You will note from Table I.1 that the log-logistic has a significantly higher value for this parameter estimate than either the Richards or Weibull. You may also note from figure I.5 that the log-logistic exhibits some lack of fit as the tree approaches its asymptotic height. All this suggests a reparameterization with a different scale for the asymptote parameter. We tried the following parameterization,

$$H = e^{b_1} / [1 + \exp(b_2 + b_3 \ln(A)] . \qquad (7a)$$

In other words we replaced b_1 with $\ln(b_1)$. This parameterization gave us a PE value of 2.828, a significant reduction from the previous value of 83.86, but still not acceptable. However, the percentage bias for the asymptote was reduced from -9.884 to 0.0106.

The Weibull model had a PE value of .9014 for parametrization (5). The percentage parameter biases were all below one, but were higher for the asymptote (the first parameter) and the rate parameter (second parameter). The following parameterization, which replaces the first and second parameters from (5) with their logarithms, was tried.

$$H = e^{b_1} [1 - \exp(-e^{-b_2} A^{b_3})] . \quad (5a)$$

This parameterization resulted in a PE value of .2022, which is below the acceptable level of .2853. The percentage biases for the two altered parameters were also reduced. We concluded that the parameters from (5a) are very close to being normally distributed.

The original Richards parameterization had the lowest PE value of the three original parametrizations. The estimated percentage parameter biases were all below one percent. However, since the changing first and second parameters to a logarithmic scale improved the Weibull model, this was also tried for the Richards. The result was an increase in the estimated bias of the second (rate) parameter, and an increase in PE to .8873. Thus, we settled on the following reparameterization of the Richards,

$$H = e^{b_1} [1 - \exp(-b_2 A)]^{b_3} . \quad (4a)$$

This parameterization resulted in a slight decrease in PE, from 0.3793 to 0.3036, and a decrease in percentage estimated bias for the first parameter. The PE value however remains slightly above the acceptable value.

We drew the following conclusions on the choice between the three models. For this particular data for a single tree, the Weibull parametrization (5a) was superior on four criteria; lowest mean square error, lowest IN, lowest PE, and lowest parameter biases. The first two criteria implied that the Weibull would provide the best predictions. The second two criteria implied that the parameters from (5a) were most nearly normal of all the parameterizations examined.

The Richards model was a close second on all four criteria. This implied that for a similar data set the Richards might prove superior to the Weibull on one or more of these criteria.

The log-logistic model was inferior to both the Weibull and Richards on all four criteria. Perhaps most significant was the much poorer performance of the log-logistic on the PE and parameter bias criteria. We concluded that the log-logistic provided the least interpretable parameters, and provided the most difficulties in applying standard inference procedures.

Generalizing these conclusions beyond this particular data may be hazardous. In order to obtain more general empirical conclusions, we applied these analysis methods to the observed height growth from many more trees.

RESULTS WITH MANY TREES

We applied the nonlinear regression diagnostics discussed above to five additional data sets. Two of these data sets were collected for the Forestry Intensified Research (FIR) Growth and Yield Project in the second-growth mixed conifer stands of southwest Oregon. The first of these consisted of stem analysis data for 89 site quality, dominant Douglas-fir trees. The other was similar data for 40 site-quality, dominant ponderosa pines.

The third and fourth data sets were contributed by Joe Means of the USFS's Pacific Northwest Forest and Range Experiment Station. The third data set consisted of stem analysis data for 6 dominant Douglas-fir trees from high elevation, old-growth sites in the Oregon Cascades. The fourth data set was similar data for 4 dominant mountain hemlock trees, also from high elevation sites in the Oregon Cascades.

The fifth, and final, set consisted of stem analysis data on a single spruce tree from Austria, and was obtained from Prodan (1968), who attributed the original data to Guttenberg (1915). This data set has been used as an example by both Pienaar and Turnbull (1973) and Yang, et al. (1978).

Table I.3 presents weighted averages of mean square error, IN and PE for each of these data sets. The individual values of each statistic for each tree were weighted by the number of observations per tree.

In the largest of the data sets, the 89 Douglas-fir trees from southwest Oregon, the Weibull model (5a) was superior in terms of mean square error and PE. However, the Richards model performed nearly as well by those two measures and had slightly lower IN. All three models fit reasonably well and had acceptable IN. None of the three had acceptable PE values.

The ponderosa pine data from the same region had more problems with parameter effects nonlinearity. While all three models had acceptable levels of IN, PE was high in each case. No clearcut choice among the three models was apparent. The log-logistic proved superior in terms of mean square error, although the Richards and Weibull models fitted nearly as well. The Richards had the lowest IN, but once again all three models were very close. The Weibull had the lowest PE value.

The spruce tree data is best fit by the log-logistic model, in terms of mean square error. However, the Richards model has the lowest values for IN and PE.

The two sets of data from the high elevation, old-growth stands had similar results. The log-logistic

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Table I.3. Weigthed averages for mean square error, IN and PE for the five data sets.

data	model	mean square error	IN	PE
		(feet)		
Douglas-fir	(5a)	1.5265	.0217	.7345
SW Oregon	(4a)	1.5379	.0184	1.631
89 trees	(7a)	1.5513	.0539	2.931
Ponderosa pine	(5a)	1.9361	.0215	2.344
SW Oregon	(4a)	1.8527	.0151	10.00
40 trees	(7a)	1.8224	.0365	7.971
		(meters)		
Douglas-fir	(5a)	.82442	.0374	.3970
Oregon Cascades	(4a)	1.8527	.0411	.4126
6 trees	(7a)	1.8224	.1015	2.987
Mountain hemlock	(5a)	.53897	.0494	.2713
Oregon Cascades	(4a)	.43527	.0464	.5769
4 trees	(7a)	.31711	.6772	18.93
Spruce	(5a)	.31327	.0427	.4704
Austria	(4a)	.16114	.0347	.3533
1 tree	(7a)	.09065	.1734	4.335

model proved best in terms of mean square error, but had relatively high levels of IN and PE. In fact, the log-logistic fit to the mountain hemlock data was the only fit which had unaccepatble IN for an entire data set. The Weibull and Richards models were considerably better in terms of the curvature measures.

The trees in these two data sets ranged in age from just over 200 years to just over 400 years old. Examination of plots of height over age for these trees indicate that height growth does not decline indefinitely, but instead appears to maintain a constant, although slow, rate at advanced ages. The slow approach to an asymptote which is characteristic of the log-logistic best approximates this, which may account for that model's superior fit to this data.

The three sigmodial-shaped models used here can be modified to represent an asymptotic constant growth rate. The Richards can be reparameterized as

$$H = e^{b_1} [1 - \exp(-b_2 A)]^{b_3} + b_4 A , \qquad (4b)$$

the Weibull as

$$H = e^{b_1} [1 - \exp(-e^{-b_2} A^{b_3})] + b_4 A , \qquad (5b)$$

and the log-logistic as

$$H = e^{b_1} / [1 + \exp(b_2 + b_3 \ln(A)] + b_4 A . \qquad (7b)$$

These 4-parameter models were fit to those data sets in which trees older than 200 years were measured. Table I.4 presents the results of these fits. For the Douglas-fir data the addition of a linear asymptotic growth rate significantly improved the fit. It did so with some loss in linearity, raising both the IN and the PE measures. However, IN was still acceptable for the Weibull and Richards models, and the parameter biases for these two models wera all below one percent. The high nonlinearity of the log-logistic model was aggravated with the addition of a fourth parameter; IN was raised above the acceptable level and the already high PE was further increased.

TABLE I.4 Weighted averages for mean square error, IN and PE for the three old-growth data sets fitted with linear asymptotic growth.

data	model	mean square error (meters)	IN	PE
Douglas-fir	(5b)	.25904	.1138	.5909
Oregon Cascades	(4b)	.22698	.0893	.9574
6 trees	(7b)	.21372	.3557	10.81
Mountain hemlock	(5b)	.13528	.2898	2.935
Oregon Cascades	(4b)	.16988	.1861	12.23
4 trees	(7b)	.15080	10.66	305.9
Spruce	(5b)	.07414	.1393	.6393
Austria	(4b)	.00847	.0358	.5395
1 tree	(7b)	.00817	.5471	11.68

CONCLUSIONS

Of all the models examined, the Richards, Weibull and log-logistic seem to be the best fitting models for height growth data. None of these three appear to be consistently superior to the others for all height growth data. While the Weibull model has the lowest mean square error for the second growth Douglas-fir data, the log-logistic has the lowest mean square error in all the remaining data sets. However, the Richards is in every case a close second.

The log-logistic exhibits relatively high intrinsic nonlinearity, reaching unacceptable levels with some data. The Richards and Weibull models are consistently better in terms of IN, maintaining acceptable levels for all the data we examined.

The Weibull parameterization (5a) appears best in terms of parameter effects nonlinearity, consistently outperforming the best parameterizations of the Richards and log-logistic. If parameter inference or interpretation are objectives, the Weibull may be preferred on this basis. While the Richards often has unacceptable levels of PE, its parameter biases generally remain under one percent, indicating that approximate inference methods may be used with caution. The log-logistic has severe parameter effects nonlinearity, with parameter biases often above one percent. The parameters of the log-logistic should be interpretated only with extreme caution.

CHAPTER II

POLYMORPHIC HEIGHT GROWTH AND SITE INDEX MODELS FOR DOUGLAS-FIR IN SOUTHWESTERN OREGON

Height growth of even-aged stands is a major component of their volume growth. Also, since height growth is relatively independent of stand density, height growth can be used as a measure of site productivity. Site index, defined as the average height of the dominant trees in an even-aged stand at a selected base age, is the common term for such a measure.

Equations for predicting height growth and site index have been a major concern to forest biometricians. Early efforts (e.g. Bruce 1926, Osborne and Schumacher 1935.) used single measurements of height and age from many stands. Such cross-sectional data were used to fit a general "guide curve", i.e. an estimate of the general height growth pattern, which could then be scaled up or down to reflect differences in site index. Site index was estimated by solving the general guide curve equation for site index. The resulting equations were termed anamorphic since they exhibited the same shape for all site indices.

Most recent height growth and site index efforts have utilized stem analysis data, which provides real growth series data, i.e multiple observations of height and age from individual trees. Curtis (1964) presents the many advantages of using stem analysis data, the prime one being a greater ability to model polymorphic height growth patterns. The resulting predictions of height growth follow different patterns for different site indices, an attribute thought more representative of the true height growth behavior.

A standard practice in estimating polymorphic height growth models has been to pool stem analysis data and use the pooled data to estimate a single equation capable of polymorphism across site indices (e.g. Curtis et al 1974, Monserud and Ek 1976, Krumland and Wensel 1977, and Monserud 1984).

An alternative approach is to fit seperate height growth models to individual trees (or a group of trees from the same sample plot) and then predict the parameters of the resulting growth models from site index. King (1966) used such an approach in developing site index curves for Douglas-fir in the Pacific Northwest. This approach may be termed a random coefficients (RC) approach (Swamy 1970). Biging (1985) used a RC procedure to estimate height growth curves for mixed conifer stands in northern California. Ferguson and Leech (1978) and West (1981) have used a a two-stage RC method to predict yields, diameter growth and mortality. A RC approach is believed to be capable of better modeling differences in growth trends, or mortality trends, across sites.

The major objective of this study was to develop a Douglas-fir height growth and site index model for use in the mixed conifer stands of southwestern Oregon. In developing such a model we compared the performance of pooled estimation procedures to the performance of RC estimation procedures. This comparision was performed on the data used to develop both models, and, on two validation data sets.

DATA

Data for this study was collected by the Southwest Oregon Growth and Yield Project, a cooperative study on the growth of mixed conifer stands in southwestern Oregon. As part of this project, one or two dominant Douglas-fir trees were felled in each of 246 sample stands. Potential site index trees were selected from among these by elimination of any trees with evidence of past top damage or height growth suppression. 126 Douglas-fir trees were so selected. Stem analysis was conducted on each potential site tree; with sectioning at stump height (1.0 ft (.3048 m)), breast height (4.5 ft (1.37 m)), and at 8.4 ft (2.56 m) intervals thereafter up the stem. Age of each section was determined by ring counts, providing an observation of tree height and age for each section. Stem analysis revealed past top damage or height suprression on 23 potential site trees, leaving 103 quality site trees. Of these, 14 were under the breast height age of 50 years, leaving 89 trees as old or older than the selected base age of 50.

On all the felled dominants the most recent full five-year height growth was identified by whorl count and measured to the nearest tenth-foot (3.048 cm). The whorl count was confirmed by a ring count on a section made directly below the fifth whorl from the tree tip.

Thus, at least two observations of height and age were available on 404 dominant Douglas-fir trees.

The height growth data described above was divided into three groups; a set of growth series observations of height and age on the 89 selected site index trees which were above the breast height age of 50, a set of five year height growth observations on 404 dominant trees, and a set of growth series observations on 14 site quality trees which fell below 50 years in breast height age. The first data set was used to develop height growth and site index prediction equations. The second two data sets were used as validation data sets.

All data were transformed to height above breast height (total height - 4.5 ft) and breast height age. Further reference to height and age shall mean height above breast height and breast height age.

ANALYSIS

Height growth model. The Weibull-type function described in Chapter I was taken as the general form for height growth. The results from Chapter I indicate that the Weibull model is an acceptable choice for individual tree height growth. When fit individually to the 89 site quality trees, the Weibull had the lowest overall mean square error, and the lowest parameter effects nonlinearity of the three models examined. It had acceptably low intrinsic nonlinearity for all 89 trees.

For an individual tree model, the Weibull model has three parameters, one which may be consider as the asymptotic limit of growth, another which may be thought of as a growth rate parameter, and a third which may be thought of as a shape parameter. This distinction between the second and third parameters is somewhat arbitrary, as they jointly determined both the shape and rate of growth.

A general height growth model, polymorphic with respect to site index, can be created by expressing two or more of the parameters of the Weibull-type model as functions of site index. In its most general form, with all three parameters expressed as functions of site index, this may be written as,

$$H = f_1(S)[1 - \exp(-f_2(S)A^{f_3(S)})]$$

where, H is height above breast height, S is site index, and A is breast height age.

Other authors (e.g. Payandeh 1974, Monserud and Ek 1976, Carmean and Hahn 1981, Krumland and Wensel 1977) have used a similar approach with the Richards model and the following functional relationships,

$$f_1(S) = a_1 S^{a_2}$$
$$f_2(S) = a_3$$
$$f_3(S) = a_4 S^{a_5}$$

These authors have used a constant rate parameter and have expressed the asymptote and the shape parameters as functions of site index. Other combinations are possible, but apparently have not been examined. The most general form we examined used the functions f_1 and f_3 as expressed above, but replaced the constant rate parameter, f_2, with the following function,

$$f_2 = \exp(a_3 + a_6 \ln S)$$

This general model form has six parameters in a complex nonlinear form. We expected some difficulty in obtaining nonlinear least squares estimates with pooled data. Initials attempts to estimate the six parameter model confirmed this. The parameters of the asymptote function, f_1, seemed to be the most unstable. This led us to develop a method of constraining the model and reducing the dimensionality of the estimation problem.

Estimates of site index for each of the 89 site trees were obtained by using the individual fits of the Weibull model to predict height at age 50, the selected base age. The 3 parameter individual tree height growth model can be reduced to two parameters by constraining the curve to go through the estimated site index at age 50. The model may be written,

$$H = S[1 - \exp(-b_2 A^{b_3})] / [1-\exp(-b_2 50^{b_3})] .$$

One or both of the two parameters of this constrained model may be expressed as functions of site index in order to create a polymorphic height growth model.

Results from Chapter I indicate that reparametrization can facilitate nonlinear parameter estimation. We found the most success with the following parameterizations of five models. An unconstrained 6 parameter model,

$$H = e^{b_1 + b_2 \ln S}[1-\exp(-\exp(b_3 + b_4 \ln S + b_5 S^{b_6} \ln A))] \quad (1)$$

an unconstrained 5 parameter model,

$$H = e^{b_1 + b_2 \ln S}[1-\exp(-\exp(b_3 + b_4 \ln S + b_5 \ln A))] \quad (2)$$

a constrained 4 parameter model,

$$H = S \frac{1-\exp(-\exp(b_3 + b_4 \ln S + b_5 S^{b_6} \ln A))}{1-\exp(-\exp(b_3 + b_4 \ln S + b_5 S^{b_6} \ln A))} \tag{3}$$

a constrained 3 parameter model, with the rate parameter expressed as a function of site index,

$$H = S \frac{1-\exp(-\exp(b_3 + b_4 \ln S + b_5 \ln A))}{1-\exp(-\exp(b_3 + b_4 \ln S + b_5 \ln A))} \tag{4}$$

and a constrained 3 parameter model, with the shape parameter expressed as a function of site index,

$$H = S \frac{1-\exp(-\exp(b_3 + b_5 S^{b_6} \ln A))}{1-\exp(-\exp(b_3 + b_5 S^{b_6} \ln A))} \tag{5}$$

Estimation Methods. Models (1)-(5) can be estimated either with pooled stem analysis data or by a random coefficient (RC) approach. The pooled data approach assumes that the parameters of the height growth model are nonrandom functions of site index. The RC approach procedes with the assumption that the height growth model parameters are random functions of site index.

The pooled data approach combines all observations into a single nonlinear squared error minimization (non-linear least squares) problem. We shall refer to this approach as pooled least squares (PLS). The estimation method finds the parameter estimates which result in the lowest sum of squared errors between predicted height and observed height. If we wish to make probability statements about the parameter estimates of the predictions, we must make assumptions about the distributions of the errors about the model.

The simplest, but most restrictive, set of assumptions we can make is that the errors about the model are independently and identically distributed, with zero mean and constant variance. With this set of assumptions the parameters and predictions are consistent and asymptotically normally distributed, even with a nonlinear model (Jennrich 1969, Malinvaud 1966). We shall term estimates obtained under these assumptions as the PLS1 estimates. This assumption ignores the likely correlation among errors from the same tree, and the possibility of nonconstant variance across trees.

A second set of assumptions recognizes the second of these two problems. Errors are assumed to be independent and identically distributed within a tree, but the variance of the errors is allowed to vary among trees. Kmenta (1971) presents a consistent two-stage estimation method under these assumptions for linear models, which by analogy can be extended to nonlinear models using techniques described in Bard (1974). The mean square errors from the individual tree model fits to each tree are used as estimates of the true variance about the model for each tree. This method of estimating individual tree error is independent of the lack of fit of the general model. The inverses of these estimated variances are used as weights in a weighted nonlinear least squares estimation. Estimates obtained under these assumptions we shall term PLS2 estimates.

A third set of assumptions go a step further and recognize the likely serial correlation among errors within a tree. By assuming a first-order serial correlation scheme, with a correlation coefficient which is constant across trees, we can consistently estimate the correlation coefficient by techniques outline in Kmenta (1971), and use a nonlinear estimation method as presented by Bard (1974). The errors from the individual tree fits are used to estimate the first-order serial correlation coefficient. Estimates obtained under this set of assumptions we shall term PLS3 estimates.

Curtis (1974) procceded under a different set of assumptions when fitting pooled stem analysis data. He ignored serial correlation within a tree, but assummed nonconstant variance across ages (implying that within a tree the error had nonconstant variance, but that variance is constant across trees for a given age). A similar set of assumptions was used by Monserud (1984) with the addition of a first-order serial correlation scheme, assuming a constant first-order correlation coefficient across trees. For our study we identified a fourth set of assumptions, similar to Curtis (1974), which allowed for nonconstant variance across ages. An iterative estimation procedure was used. Errors from the PLS1 fit were used to estimate error variance for 5-year age classes. The inverses of these estimated variances were used as weights in weighted nonlinear least squares. We repeated this process with the errors resulting from the second fit, and so on, until convergence of the age class weights were obtained. (The convergence criteria used was 10   , after Monserud, 1984). We shall refer to estimates obtained under this set of assumptions as PLS4 estimates. The estimation method used with this set of assumptions does not seperate out the lack of fit error of the general model from the estimated age class variances.

The random coefficients approach proceeds from the assumption that the height growth model itself is random, varying from tree to tree. A two-stage estimation methods is called for under this premise. The first stage involves fitting individual height growth models to each tree. The second stage involves prediction of the individual tree model coefficients by site index.

The RC approach is thought to account better for intertree variability. With pooled estimates, the prediction for a given age and site index is of the conditional mean height of the pooled sample. With RC estimates, the corresponding prediction is the height at the given age on the height growth curve predicted for the given site index. These predictions are not necessarily the same. As explained by Biging (1985), with linear models pooled estimation methods tend to result in flatter (i.e., regressed towards the mean) regression lines than do the average regression lines estimated by a random coefficients approach. It is not known if a similar effect can be expected with nonlinear models.

Biging (1985) applied a RC approach to height growth using linear model techniques developed by Swamy (1970). In order to apply the linear methods it was necessary to linearize the nonlinear height growth model (the Richards model in this case) by presetting two coefficients. Swamy's (1970) method also requires that the second-stage coefficients appear in the first-stage model which is fit to each tree. The second-stage RC estimates are obtained as a weighted average of the first-stage coefficients. This further limits the flexibility of the Swamy method.

A more flexible approach was presented by Ferguson and Leech (1978), with refinements contributed by Davis and West (1981). In this approach the second-stage coefficients need not appear in the first-stage model which is fit to each tree. The second-stage of estimation is a system of regressions on the first-stage coefficients. As pointed out by Ferguson and Leech, the second-stage estimation is exactly analogous to the "seemingly unrelated regression" estimation problem presented by Zellner (1962). A generalized least squares (GLS) estimation procedure is considered most appropriate for such estimation problems. We shall refer to the Ferguson and Leech approach as RC-GLS.

Ferguson and Leech (1978) developed their procedures using linear models. In the problem faced here, the first-stage model is nonlinear in form. The second-stage model, however, is linear. In the Ferguson and Leech approach, the linear least squares estimates of the first-stage coefficients and their covariances are used in the second stage. In our problem we used nonlinear least squares estimates of the first-stage coefficients and their covariances. These nonlinear estimates are consistent, but not necessarily unbiased nor efficient, even with the assumption of normal errors. However, they are maximum likelihood estimates under the assumption of normal errors. The good performance of the Weibull model, in terms of the nonlinear curvature measure discussed in Chapter I, help justify our reliance upon these nonlinear estimates. The exact distribution of the estimated variances obtained with RC-GLS techniques is not known, as pointed out by Davis and West (1981), even for the purely linear case.

The RC-GLS estimation proceeds on the assumption that the first-stage coefficients are correlated within each tree's model and that each tree has its own error variance. If we make a further assumption, which may not be tenable, that the first-stage coefficients are uncorrelated and have constant variances, we may use ordinary least squares estimation technques to predict the first-stage coefficients. We shall refer to such estimates as RC-OLS estimates.

Evaluation of Estimation Methods. The prime objective of this study is to provide a system which gives "good" predictions of future height growth. A secondary objective is to provide "good" estimates of site quality via a site index prediction system. We defined "good" as predictions and estimates which are nearly unbiased and have relatively low variances over the ages 50 to 150 and for site indices ranging from 50 to 130.

We are not particularly interested in making probability statements about the parameters in our model. However, we would like the parameter estimates to be robust, i.e. to be relatively constant under differing sets of statistical assumptions. The six estimation methods described above differ because each seeks to obtain efficient estimates of the model parameters under different assumptions. Furthermore, the RC approach is thought to model more effectively polymorphism across site index which may be partly obscured with pooled estimation methods.

With a single data set it is not possible to determine which set of assumptions are most appropriate for modeling tree height growth across site indices. In fact, since not every possible set of assumptions about the model errors was examined, it is possible that another estimation method based upon a different set of assumption is most appropriate.

With these considerations in mind we decided to examine the performance of each estimation method on three data sets. The first data set is the stem analysis data from the 89 site trees which were over 50 years of age. This was the data on which each estimation method was applied. On this data we examined mean overall bias, and bias in each 5-year age class and 10 foot site index class. Variances of the prediction errors for each model were examined similarly, but are not directly comparable across models due to the differing assumptions about the error variance.

The other two data sets are validation data sets, i.e. these data were not used to estimate the model parameters. The first was the 5-year height growth data for 404 dominant Douglas-fir trees. The begining height and age were used to estimate site index, and this estimated site index and end of growing period age were used to predict end of growing period height. The differences between this predicted and the observed end of growing period heights were examined for bias and variance over age and site index classes.

The second validation data set consisted of the stem analysis data from the 14 site quality trees which where under 50 years of age. Two approaches where taken to validate the height growth model on this data. To validate as best as possible just the height growth prediction component of the system, the final age and height observation of each tree was used to estimate site index for each tree. The height growth curve predicted for that site index was then used to predict height at each observed age. The differences from observed height were then examined for bias and variance in 5 year age classes. The second approach was designed to assess the overall performance of the combined site index and height growth prediction system. The first height and age observation over the age of 15 was used to estimate site index, and the curve associated with this predicted site index used to predict height at each observed age. The differences with observed heights were also examined for bias and variance in 5 year age classes.

Site Index Models. Heger (1968) and Curtis (1974) suggested that for a given age site index could be adequately described by a simple linear regression on height. With the data of this study, initial plots of site index over height for each five year period exhibited some nonlinearities, particularly at young ages. These plots suggested the following model,

$$\ln(S/H) = b_1 + b_2 \ln(H)$$

where, S = site index (height above breast height at breast height age 50), H = height (ft) above breast height, and b_1 , b_2 are coefficients which vary with age.

The individual tree fits to the simple Weibull height growth model were used to obtain estimates of each tree's height at age 5 and for every five years therafter up to the age of the tree, or age 100, whichever was less. Individual regressions using the above model were fit to each of the five year heights. Plots of b_1 and b_2 over age showed two curvilinear trends with age, with both parameters passing near or through zero at age 50. This suggested that both parameters be modeled by a linear and a quadratic term of age, giving the following model,

$$S = a_1(A-50) + a_2(A-50)^2 + a_3(A-50)\ln H + a_4(A-50)^2 \ln H \,. \qquad (6)$$

This model has the desirable property of predicting ln(S/H) = 0, i.e. S=H, at age 50. It was fit to the actual height and age observations, rather than the predicted 5 year interval heights, in order to avoid any possible bias arising from a lack of fit of the Weibull height growth model.

Computational Methods. Linear regressions, which were used in developing the site index model, were performed with the BMDP statistical analysis program, IBM-PC version. Nonlinear regressions were computed with our own FORTRAN implementation of the Marquardt algorithm, compiled and run on a IBM-PC/XT in double precision.

RC-GLS estimation was accomplished with our own FORTRAN implementation of the algorithm outlined by Ferguson and Leech (1978) and modified by West (1981). The program was checked by using the example presented by Ferguson and Leech. Our program produced the same estimates reported by West (1981).

Microcomputer graphics programs were used extensively in screenings of data and the assessment of model forms and fits. The assessment of error bias and variance on the validation data sets were accomplished with FORTRAN programs written specifically for these purposes.

RESULTS

Height growth - pooled estimation versus random coefficients. Models (1) and (3) could not be estimated with pooled nonlinear least squares. Using many sets of starting values, the Marquardt algorithm was allowed to iterate up to 150 times, but the convergence criteria (10^{-5}) were never met.

The random coefficients methods did, however, produce estimates for all five models. The RC-GLS estimates which may be preferred on theoretical grounds over the RC-OLS estimates, always produced a lower prediction mean square error than the RC-OLS estimates. (Prediction mean square errors were computed by using the RC estimates to predict height for each age and site index pair, and summing the squared differences from predicted and observed height, and dividing by the number of observations.)

PLS1 estimates, as well as RC estimates, were obtained for the 5-parameter model (2), and both of the 3-parameter constrained models. The pooled estimates, when obtainable, resulted in a considerably lower mean square prediction error than the RC-GLS estimates for the same model.

Greater success was found in fitting the constrained models. PLS estimates were obtained for models (4) and (5), but not for model (3). RC-OLS and

RC-GLS estimates were obtained for all three models. Once again, where PLS estimates were obtainable they had lower mean square prediction error when compared to the best RC estimates for the same model. The mean square errors for all the PLS1, RC-OLS and RC-GLS estimates are presented in Table II.1. The parameter estimates for the same models are presented in Table II.2.

The lowest mean squared prediction error was obtained by the PLS estimates for model (4), the constrained model with the rate parameter expressed as a function of site index. The best RC estimates, in terms of mean squared prediction error, were the GLS estimates for the constrained model (3).

Figures II.1-II.3 present the predicted height growth curves for site indices 65, 95 and 125, for the PLS1, RC-OLS and RC-GLS estimates of model (4). The PLS1 estimates appear to exhibit a greater degree of polymorphism, with considerable flatter curves for low site indices than for high site indices. The RC curves generally have a lower asymptote for the same site index than the PLS1. Closer examination of predictions for younger ages revealed that the RC predictions follow a more curved pattern at ages below 50 than do the PLS1 predictions. The higher values of the shape parameter for the RC models, evident in Table II.2, confirm this greater curvature.

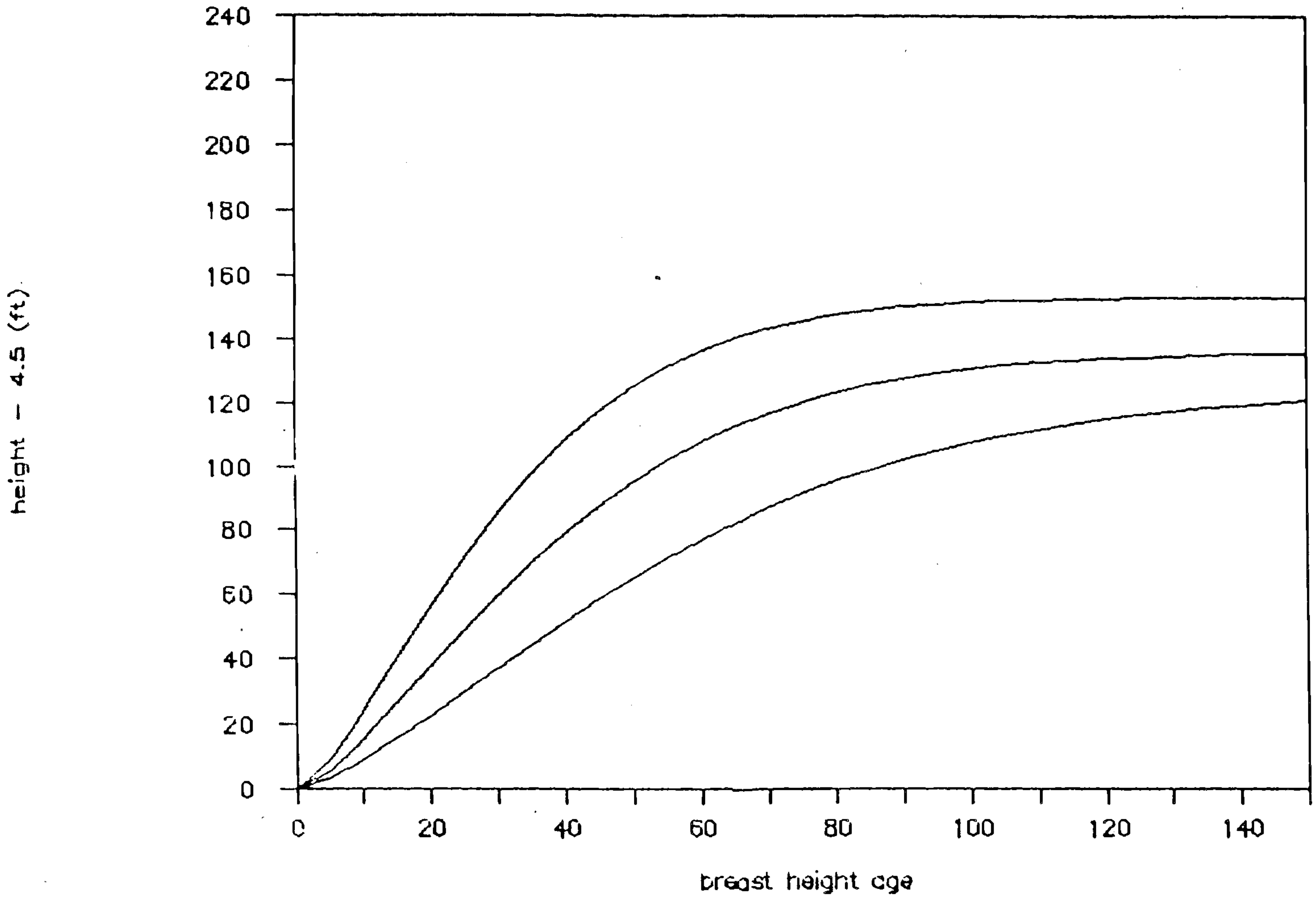

Figure II.1 Model (4): RC-OLS estimates

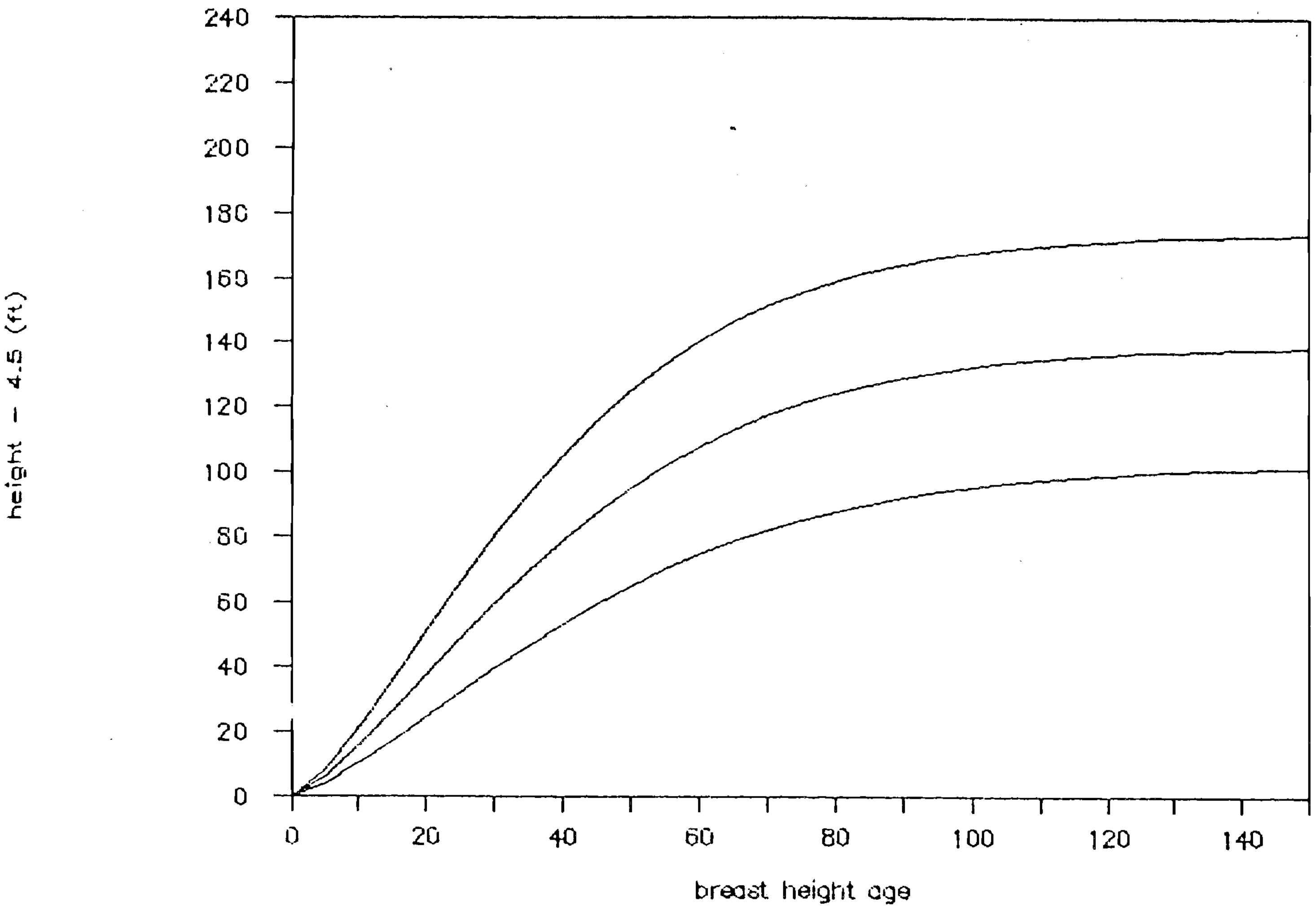

Figure II.2 Model (4): RC-GLS estimates

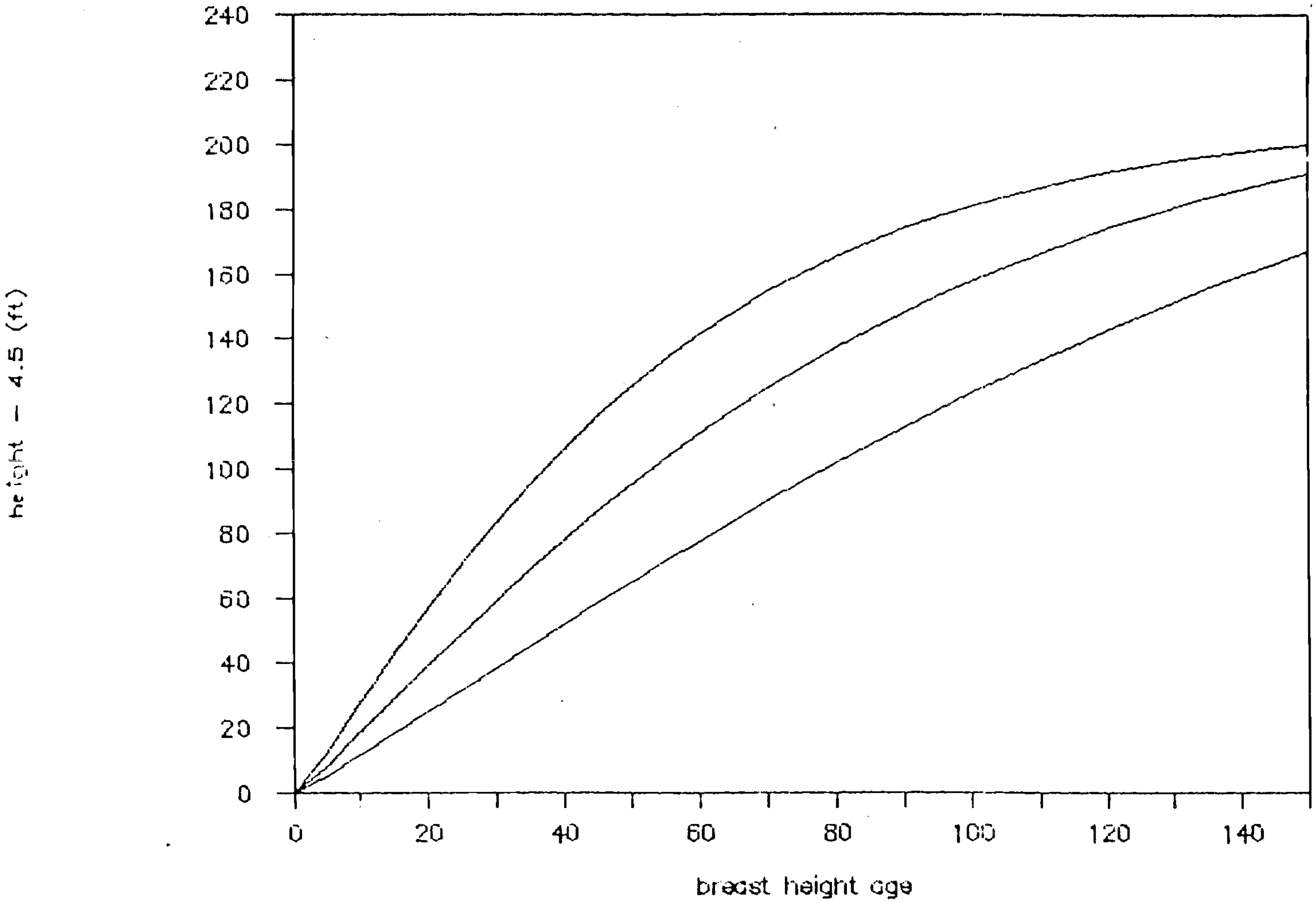

Figure II.3 Model (4): PLS1 estimates

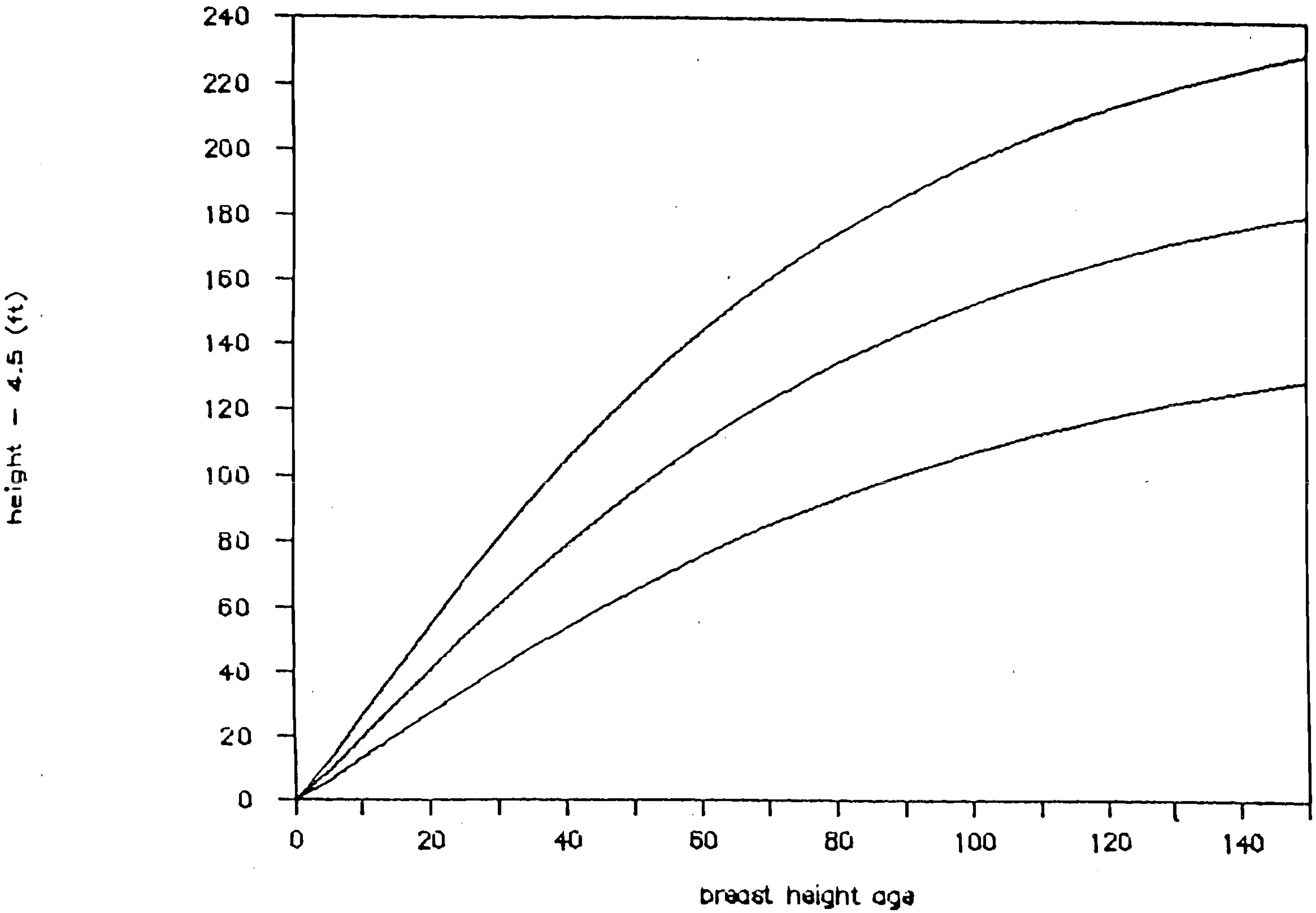

Figure II.4 Model (4): PLS2 estimates

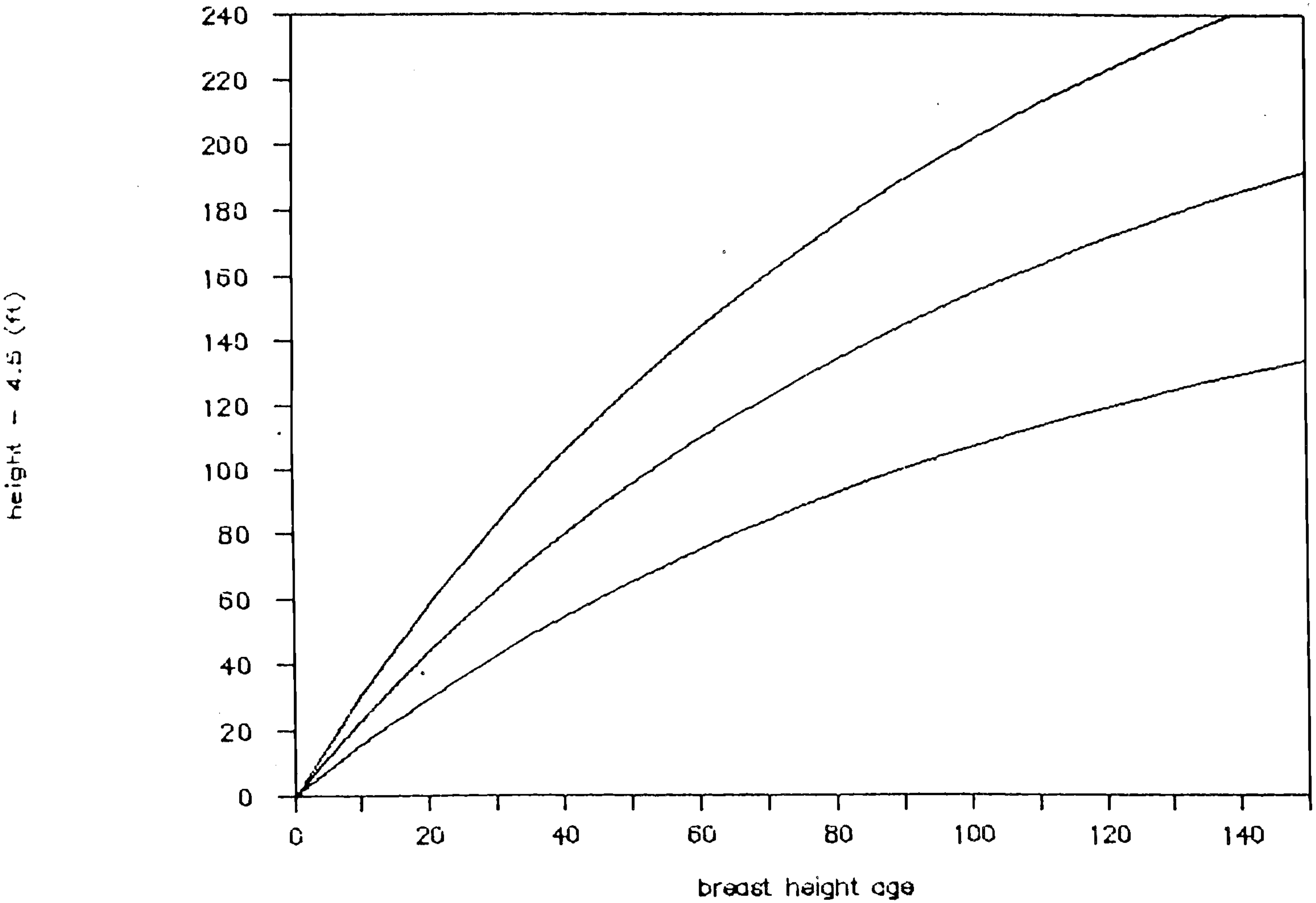

Figure II.5 Model (4): PLS3 estimates

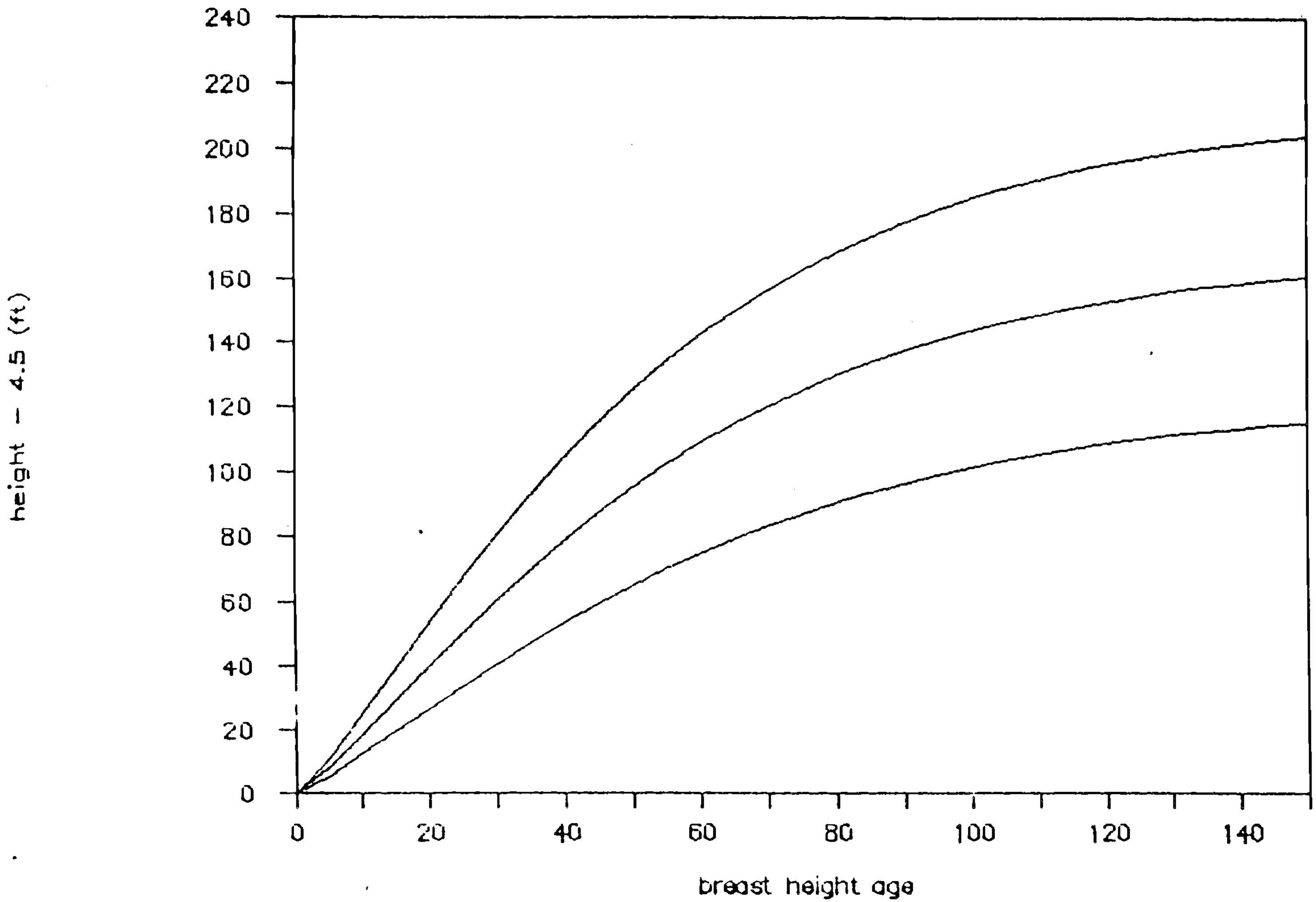

Figure II.6 Model (4): PLS4 estimates

Table II.1 Mean square errors for five height growth models (estimation data).

	Estimation method		
	PLS1	RC-OLS	RC-GLS
Model			
(1)	-	64.37	60.21
(2)	22.12	76.11	73.20
(3)	-	58.97	50.20
(4)	21.40	72.12	63.08
(5)	23.36	69.12	51.45

Table II.2 Parameter estimates for five height growth models (parameter variances in paranthesis).

	Parameter 1	2	3	4	5	6
Model (1)						
RC-OLS	.4036	.9958	-11.58	1.345	1.556	-.2633
	(.5887)	(.1297)	(1.786)	(.3936)	(.5143)	(.1133)
RC-GLS	.5977	.9548	-10.74	1.171	1.315	-.2124
	(.5718)	(.1259)	(1.728)	(.3801)	(.4660)	(.1024)
Model (2)						
PLS1	6.063	-.1439	-12.22	1.571	1.146	-
	(.0389)	(.0017)	(.0613)	(.0029)	(.0001)	
RC-OLS	.4036	.9958	-11.58	1.345	1.447	-
	(.5887)	(.1297)	(1.786)	(.3936)	(.0004)	
RC-GLS	1.185	.8255	-7.043	.3585	1.424	-
	(.2764)	(.0134)	(1.285)	(.0622)	(.0003)	
Model (3)						
RC-OLS	-	-	-11.17	1.261	1.457	-.2437
			(3.141)	(.1525)	(.1318)	(.0064)
RC-GLS	-	-	-10.83	1.193	1.371	-.2260
			(3.105)	(.1459)	(.1066)	(.0051)
Model (4)						
PLS1	-	-	-13.31	1.806	1.148	-
			(.0708)	(.0034)	(.00004)	
RC-OLS	-	-	-11.17	1.261	1.433	-
			(3.141)	(.1525)	(.0003)	
RC-GLS	-	-	-6.961	.3450	1.414	-
			(1.231)	(.0596)	(.0003)	
Model (5)						
PLS1	-	-	-5.065	-	1.154	-.4569
			(.0002)		(.0002)	(.0003)
RC-OLS	-	-	-5.445	-	3.061	-.3590
			(.0043)		(.2601)	(.0126)
RC-GLS	-	-	-5.392	-	1.611	-.0436
			(.0041)		(.1046)	(.0005)

Subjectively, it appeared that the shape of the RC curves were closer to the shape we observed in individual tree plots below the age of 50. However, examination of bias and variance across ages and site indices for the RC models revealed that these models performed poorly at ages over 50, with high negative bias (underprediction) and high variance.

Many of the site index trees had only a few height/age observations past the age of 50. We theorized that the individual fits which resulted in the first-stage coefficients adequately modeled the early stages of height growth, but that there was insufficient data in the later years for the height growth pattern past 50 years to be adequately described by the first stage coefficients.

The pooled estimation method, represented by the PLS1 estimates, appears more capable of modeling after age 50 height growth patterns.

<u>Height growth - different error assumptions with pooled data</u>. Estimates for the best pooled model, model (4), where obtained under the four sets of error assumptions outlined above; the PLS1 estimates assummed completely independent errors with constant variance, the PLS2 estimates assumed independent errors, heteroscedastic across tree, the PLS3 estimates assumed first-order serial correlation within a tree, heteroscedastic across

plots, and the PLS4 estimates assumed independent errors, heteroscedastic across ages.

Since each set of estimates were obtained by minimizing a differently weighted sum of squared errors, the mean square errors are not directly comparable. However, the parameter estimates can be compared for robustness to different error assumptions. Table II.3 presents the parameter estimates and their estimated standard errors for each of the four sets of parameters.

The estimated standard errors under the four error assumptions did not follow any pattern which might be expected from theory. When the assumption of constant variance is violated, ordinary least squares estimates (such as the PLS1 estimates) are expected to result in biased estimation of parameter variances. Generalized least squares methods, such as PLS2, PLS3 and PLS4, are expected to give better estimates of these variances. In the linear case, under heteroscedasticity, whether this bias is negative or positive depends upon the sign of the correlation between the square of the independent variable and the variance of each observation (Kmenta 1971). If the assumption of independence is violated with positive serial correlation, as would be expected with height growth, the variances of the parameters are

Table II.3 Parmeter estimates for model (4) under four pooled error assumptions (parameter variances in paranthesis).

Error assumption	Parameter 3	Parameter 4	Parameter 5
PLS1	-13.306 (.07078)	1.806 (.00339)	1.148 (.00004)
PLS2	-6.217 (.01734)	.2812 (.00089)	1.144 (.00005)
PLS3	-5.449 (.01376)	.1752 (.00104)	.9913 (.00008)
PLS4	-6.092 (.00408)	.2485 (.00018)	1.223 (.00005)

underestimated by ordinary least squares estimation (Kmenta 1971). Since we did not know the true nature of the error distribution, we could not predict any specific underestimation or overestimation of parameters variances. However, with a likely positive correlation among errors within each tree, and a possible increasing variance with age, an underestimation of variance seemed more likely. Contrary to this expectation, the generalized least squares estimation methods resulted in slightly lower estimated variances for most of the parameter estimates.

The PLS1 estimates for the first two parameters (the parameters of the function predicting the rate parameter) are considerably different from the estimates obtained by the other three methods. The two parameters are highly correlated, with estimated correlations of -.98 or greater under each of the four error assumptions, a fact which might exaggerate minor differences. However, these differences did result in perceptibly different predicted height growth curves, as can be seen in figures II.4 through II.6. The major differences occur after age 50. Under 50 years of age, the major difference was exhibited by the PLS3 curve, which had no inflection point (due to an estimated shape parameter less than unity).

<u>Site index estimation</u>. The site index model (6) fit

reasonably well to the stem analysis data. All four parameters appeared highly significant. Regression lines for selected ages are presented in figure II.7. The estimated function was examined for bias and variance across age and site index classes. Mean error was between -1 and 1 for all age classes between 20 and 85 years. In this same range, the standard error of estimate ranged from 1.18 to 7.53 feet (.360-2.30 m). The overall stand error of estimate was 6.56 feet (2.00 m).

The fit of model (6) was compared to two other models; a simplified version of (6) in which the squared (age - 50) terms were removed, and the empirical model form used by Monserud (1984). The Monserud model is the following linear regression for site index,

$$S = b_1 + b_2 (\ln A) + b_3 A \ln A + b_4 H + b_5 H/A \quad .$$

The overall standard error of estimates were 7.42 ft (2.26 m) for the simplified version of model (6), and 6.80 ft (2.07 m) for Monserud's model. The simplified version of model (6) was considerably more biased at younger and older ages than the quadratic version. Monserud' model had only slightly higher bias at younger and older ages, but was not constrained to predict

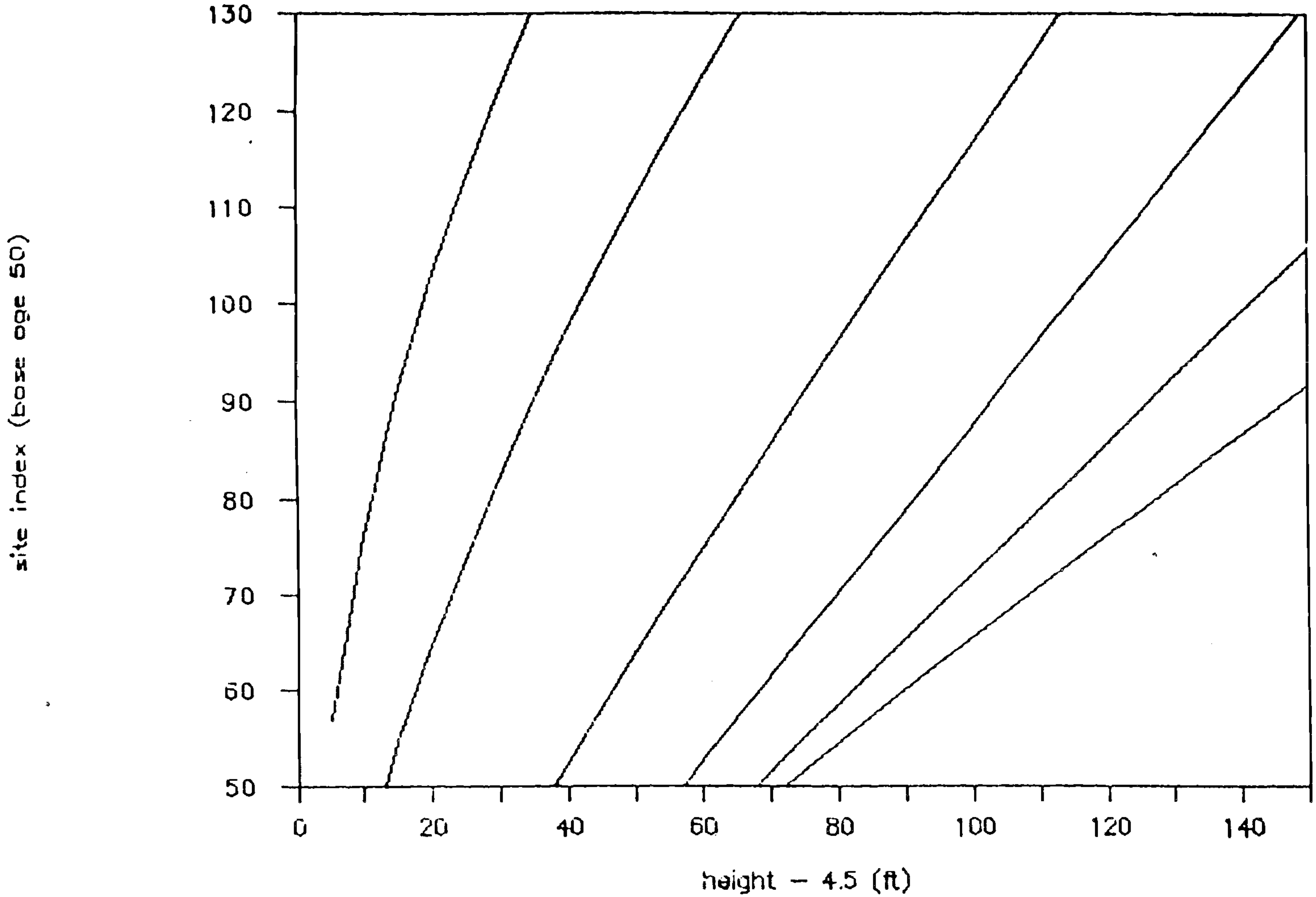

Figure II.7 Site index prediction curves for ages 10, 20, 40, 40, 80 and 100.

Table II.4 Parameter estimates and fit statistics for site index prediction model (6).

parameter	coeficient estimate	standard error
a_1	-.0521778	.0018171
a_2	.000715141	.0000356
a_3	.00797252	.0003944
a_4	-.000133377	.0000064

mean square error = .005539

Relative mean square residual = .00938

Adjusted R-square = .99062

actual height for site index at age 50. We decided to use model (6) for prediction of site index. The parameter estimates and goodness of fit statistics for this model are presented in Table II.4.

Validation - 5-year dominant height growth data. We validated eight models on the 5-year height growth data for dominant Douglas-firs; the four sets of pooled estimates for model (4), the two sets of RC estimates for model (3), and the two set of RC estimates for model (4). Table II.5 presents the resulting mean errors and mean square errors for each model. These are presented for the entire data, and for two subdivisions of the data, those trees under age 50 and those over age 50 (at the begining of the growth period).

The PLS3 estimates performed best on the overall data, followed closely by the PLS2 estimates. Both of these models had lower mean square errors on this validation data than then they had on the estimation data, despite the fact that site index was estimated for the validation data. The PLS1 estimates, while producing a higher validation mean square error than the PLS2 and PLS3 estimates, had only a slightly higher mean square error than on the estimation data. The PLS4 estimates gave the worst overall performance of the pooled estimation technqiues on this validation data.

The RC estimates were all significantly higher in overall validation mean square error than the pooled estimates. This was primarily due to very poor performance on the over 50 validation data, with both severe underprediction and higher variance. Of the pooled estimates, PLS3 and PLS2 were best on the over 50 data.

Validation results for the data under 50 were less clear. The PLS1 estimates had the lowest variance and mean square error, but the largest bias (underprediction) of all the pooled estimates. The RC estimates all had larger mean square errors than the pooled estimates, largely due to higher biases (underprediction).

Validation - young site trees. Validation on the stem analysis data was performed with two estimates of site index; an estimate obtained from the last age and height observation on a tree (assumed to be the best prediction available), and, by an estimate obatined from the first age and height observation after age 15 (assumed to be a less reliable estimate). Using the first estimate attempts to eliminate as much as possible the error in site index estimation, and thereby isolating to some degree the error of the height growth model. With the second estimate we attempted to measure the combined error involved in using a joint site index and height growth prediction system.

Table II.6 presents the results using the first (better) estimate of site index. With this validation data the RC estimates outperform the pooled estimates in both bias and mean square error. The RC estimates are very close in performance among themselves, with the 4-parameter model (3) doing only slightly better than the 3-parameter model (4). Surprisingly, the RC-GLS estimates performed no better than the RC-OLS estimates, in fact, slightly worse.

The pooled estimates have both higher prediction error variance and higher bias, with a mean overprediction of between 1.87 and 4.91 ft (.570-1.50 m). Among the pooled estimates, the PLS1 estimates were best and the PLS4 estimates were worst.

Table II.7 presents the results obtained using the second, and presumably poorer estimate of site index. With these estimates of site index the RC estimates no longer outperform the pooled estimates in mean square error, largely due a high positive bias. The variance of the prediction errors is lower with the RC estimates, suggesting that the RC curves follow the shape of height growth better, but are consistently underpredicting. The patterns of bias over age for the pooled estimates suggest that their curves are flatter but higher, resulting in less total underprediction.

It is difficult to draw strong conclusions from

Table II.5 Validation results of eight selected models on the 5-year dominant height growth data, overall and by two age classes.

	mean error ages			mean square error ages		
	0-50	50+	total	0-50	50+	total
Model (3)						
RC-OLS	2.71	7.81	6.32	11.98	178.1	124.0
RC-GLS	2.24	8.75	6.23	8.75	177.2	121.2
Model (4)						
PLS1	1.45	-2.52	-1.36	4.89	41.6	27.6
PLS2	1.31	.88	1.01	6.61	12.3	11.3
PLS3	-.76	.32	.45	5.04	9.6	8.5
PLS4	1.17	4.12	3.26	5.91	58.1	41.1
RC-OLS	2.16	5.89	4.80	8.31	129.8	99.6
RC-GLS	2.36	7.54	6.02	10.19	162.8	112.5

Table II.6 Validation results for eight selected models on the under age 50 stem analysis data, using each tree's last height/age observation to estimate site index.

	mean error	variance	mean square error
Model (3)			
RC-OLS	-.449	6.261	6.462
RC-GLS	-.576	6.254	6.586
Model (4)			
PLS1	-1.868	7.239	10.729
PLS2	-2.338	7.764	13.229
PLS3	-4.908	11.732	35.825
PLS4	-2.238	6.964	11.974
RC-OLS	-.774	6.255	6.855
RC-GLS	-.531	6.610	6.892

Table II.7 Validation results for eight selected models on the under age 50 stem analysis data, using each tree's first height/age observation after age 15 to estimate site index.

	mean error	variance	mean square error
Model (3)			
RC-OLS	2.975	9.084	17.937
RC-GLS	2.850	9.211	17.335
Model (4)			
PLS1	2.340	13.027	18.501
PLS2	1.448	13.027	16.050
PLS3	-.760	20.080	20.657
PLS4	1.352	12.704	14.532
RC-OLS	2.963	9.325	18.105
RC-GLS	2.726	9.630	17.067

this small validation data set, but the results suggest that there may be an underprediction of site index using young site quality trees that was not evident in the estimation data set. The 15-20 year old height observations in the estimation data set were actual tree heights anywhere from 30 to 115 years ago. The observations from the young validation data set were actual tree heights anywhere from 5 to 30 years ago. The young stands may well have had different origins and are exhibiting a different height growth pattern.

Comparing the validation results with the results for the estimation data for the same age range we found that the variance of the prediction errors were lower on the validation data. However, the biases were generally larger with the validation data. The mean square errors, which combines variance and squared bias, for the validation data were close in magnitude to the mean square errors for the pooled estimates on the estimation data. Thus, in mean square error terms all of the models performed as well or better than expected, although there is some evidence of bias.

CONCLUSIONS

The following conclusions can be drawn about the performances of the different estimation methods on the estimation and validation data.

1. The RC estimation methods do appear to better model the shape of height growth under the age of 50 than do the pooled estimation methods. However, the RC approach appears to result in predictions with greater bias (underprediction) than do the pooled estimation methods. Furthermore, the RC models do very poorly in predicting height growth past 50 years of age. This may be due to the relatively few trees in the estimation data with a significant number of observations past age 80.
2. Due to the very poor performance of the RC methods past age 50 we can not recommend their use, at least with nonlinear models such as the Richards, Weibull and log-logistic, and with stem analysis data that does not include a significant portion of data in the upper end of the range for which predictions are desired.
3. While the pooled estimation methods perform better overall than the RC methods, they do appear to predict a flatter height growth curve at early ages than observed with individual trees. However, the pooled methods perform significantly better in the older ages, suggesting that such methods are more responsive to sparse data at the margins of the data.

4. The pooled estimation approach did not appear to be very robust to different error assumptions. The estimated height growth curves had different shapes, particularly at later ages, depending upon the error assumptions. The PLS1 curve, estimated under the assumption of independent and constant variance errors, had the most distinctively different shape.

5. Validation of all models on the dominant five-year height data showed the pooled estimates to be superior to the RC estimates, both under and over 50 years of age. Among the pooled estimates, the PLS2 and PLS3 estimates, both of which assumed nonconstant variance across trees, performed the best. The PLS3 estimates , which further assume a first-order serial correlation structure, performed slightly better than the PLS2 estimates. However, the height growth curves predicted with the PLS3 estimates do not have an inflection point, which is inconsistent with the observed pattern of height growth on individual trees.

6. Validation of all the models on the young stem analysis data produced different results. Using the best available estimates of site index, the RC models performed better than the pooled models. All models tended to overestimate height to some degree. The RC models appear to model the shape of the observed height growth curves better. Using poorer estimates of site

index (obtained with younger age and height observations) the difference between the pooled and RC models tended to disappear, suggesting that the flatter shape of the pooled curves tends to compensate for site index estimation errors. The small size of the young stem analysis validation data makes strong conclusions difficult to make. The observed mean square error on this validation data was higher than that observed on the other validation data set, but still of roughly the same order of magnitude as the mean square error of the estimation data.

7. For a general purpose height growth and site index estimation we recommend model (6), (found on page 65), for the prediction of site index and the PLS2 estimates for the predcition of height growth. The PLS2 estimates performed reasonably well on both validation data sets, and had both a general form, and a polymorphic response across site index, which appeared intuitively reasonable. However, we cannot conclude from this single data set that this error assumption is always most appropriate when modeling dominant tree height growth.

8. In modeling height growth and site index we are forced to deal with complex nonlinear estimation problems and the probable violation of many of the assumptions of normal least squares theory. We have

tried to use, as much as possible, consistent estimation methods. We have examined estimation procedures under alternative error assumptions, with the objective of testing the robustness of our models. We have found that the estimates are not strongly robust to varying error assumptions. This finding underscores the value of validation.

SUMMARY AND CONCLUSIONS

Numerous nonlinear models for individual tree height growth were examined on two bases, accuracy of prediction, and the degree of nonlinear curvature. The Richards, Weibull and log-logistic models were found to provide very accurate predictions. Both the Richards and Weibull were found to have acceptable levels of nonlinearity, and thus provided close to unbiased predictions. The degree to which the parameter estimates of the Richards and Weibull models approach being normally distributed was improved upon by reparameterization. The Richards model tended to have a slightly lower intrinsic nonlinearity, while the Weibull model had better values of parameter effects nonlinearity, implying a more nearly normal distribution for its parameter estimates. Both the Richards and Weibull models had considerably better curvature measures than the log-logistic.

The Weibull model was sucessfully used to develop a polymorphic, site index based, height growth prediction model from stem analysis data. Two general methods of estimation were compared, pooled data estimation and a random coeffiecients approach. While the pooled data methods tended to flatten the predicted height growth curves, their predictions were less biased and more accurate, particulary for older ages.

Within the pooled estimation method, several alternate error assumptions were examined. The shape of the predicted height growth curves was found to be not very robust, particularly at extremes of the data (i.e. high and low site indices, older ages). The most success on validation data sets was found with an assumption of independent, heteroscedastic across trees. An estimate of individual tree error variance was obtained from individual tree model fits, which is somewhat independent of the general model's lack of fit.

In conclusion, the Weibull and Richards models were found to be the best models of those examined for modeling individual tree height growth. In modeling polymorphic height growth across site indices, pooled data estimation methods performed better than random coeficient methods, although the latter appeared to model the shape of early height growth more accurately, but at a cost of higher bias. Pooled estimation methods were found to be not very robust to alternate error assumptions, emphasizing the need for validation.

BIBLIOGRAPHY

Bates, D. M. and D. G. Watts. 1980. Relative curvature measures of nonlinearity. J R Stat Soc, Ser B 42:1-25.

Bailey, R. L. 1980. The potential of Weibull-type functions as flexible growth curves: a discussion. Can J For Res 10:117-118.

Bard, Y. 1974. Nonlinear parameter estimation. Academic Press, New York. 337 p.

Beale, E. M. L. 1960. Confidence regions in nonlinear regression. J R Stat Soc, Ser B, 22:41-76.

Bertalanffy, L. von. 1951. Theoretische Biologie. (Band II). Franke, Bern. 403 p.

Biging, G. S. 1985. Improved estimates of site index curves using a varying-parameter model. For Sci 31:248-259.

Box, M. J. 1971. Bias in nonlinear estimation. J R Stat Soc, Ser B, 33:171-201.

Bruce, D. 1926. A method of preparing timber-yield tables. J Agric Res 32:543-557.

Carmean, W. H. 1972. Site index curves for upland oaks in the Central States. For Sci 18:109-120.

Carmean, W. H. and J. T. Hahn. 1978. Revised site index curves for balsam fir and white spruce in the Lake States. USDA Forest Serv Res Pap NC-160, 16 p. North Central Forest Exp Stn, St Paul, Minn.

Curtis, R. O. 1964. A stem analysis approach to site index curves. For Sci 10:241-256.

Curtis, R. O., D. J. DeMars and F. R. Herman. 1974. Which dependent variable in site index-height-age regressions? For Sci 20:74-87.

Dahms, W. G. 1963. Correction for a possible bias in developing site index curves from sectioned tree data. J Forestry 61:25-27.

Davis, A. W. and P. W. West. 1981. Remarks on "Generalized least squares estimation of yield functions" by I. S. Ferguson and J. W. Leech. For Sci 27:233-239.

Draper, N . R. and H. Smith. 1981. Applied Regression Analysis. John Wiley and Sons, New York. 709 p.

Ferguson, I. S. and J. W. Leech. 1978. Generalized least-squares estimation of yield functions. For Sci 24:27-42.

Grosenbaugh, L. R. 1965. Generalizations and reparameterizations of some sigmoid and other nonlinear functions. Biometrics 21:708-714.

Guttenberg, R. von. 1915. Wachstum und Ertrag der Fichte im Hochgebirge. Wien und Leipzig. 153 p.

Heger, L. 1968. A method of constructing site index curves from stem analysis. For Chron 44:11-15.

Jennrich, R. I. 1969. Asymptotic properties of nonlinear least squares estimators. The Annals of Mathematical Statistics 40:663-643.

King, J. E. 1966. Site index curves for Douglas-fir in the Pacific Northwest. Weyerhaeuser Forestry Paper No. 8, Centralia, Washington. 49 p.

Kmenta, J. 1971. Elements of econometrics. Macmillan Publ Co, New York. 655 p.

Krumland, B. and L. C. Wensel. 1977. Procedures for estimating redwood and Douglas-fir site indexes in the north coastal region of California. Univ Calif, Berkeley, Co-op redwood yield res proj, Res Note 5, 10p.

Malinvaud, E. 1970. The consistency of nonlinear regressions. The Annals of Mathematical Statistics 41:956-969.

Monserud, R. A. 1984. Height growth and site index curves for inland Douglas-fir based on stem analysis data and forest habitat type. For Sci 30:943-970.

Monserud, R. A. and A. R. Ek. 1976. Site index curves and eqautions for several northern hardwood forest species. Univ Wisconsin-Madison, Coll Agric and Life Sci, Res Bull R2772, 9 p.

Morgan, P. H., L. P. Mercer and N. W. Flodin. 1975. General model for nutritional responses of higher organisms. Proc Nat Acad Sci, U.S.A. 72:4327-4331.

Osborne, J. B. and F. X. Schumacher. 1935. The construction of normal-yield and stand tables for even-aged timber stands. J Agric Res 51:547-563.

Payandeh, B. 1974. Nonlinear site index equations for several major Canadian timber species. For Chron 50:194-196.

Pienaar, L. V. and K. J. Turnbull. 1973. The Chapman-Richards generalization of von Bertalanffy's growth model for basal area growth and yield in even-aged stands. For Sci 19:2-22.

Prodan, M. 1968. Forest Biometrics. Pergamon Press, Oxford.

Ratkowsky, D. 1983. Nonlinear regression modeling. Marcel Dekker, New York.

Richards, F. J. 1959. A flexible growth function for empirical use. J Exp Bot 10:290-300.

Schumacher, F. X. 1939. A new growth curve and its application to timber-yield studies. Forestry 37:819-820.

Swamy, P. A. V. B. 1970. Efficient inference in a random coefficient regression model. Econometrics 38:311-323.

Weibull, W. 1951. A statistical distribution function of wide applicablity. J Appl Mech 18:293-296.

West, P. W. 1981. Simulation of diameter growth and mortality in regrowth eucalypt forest in southern Tasmania. For Sci 27:603-616.

Yang, R.C., A. Kozak and J. H. G. Smith. 1978. The potential of Weibull-type functions as flexible growth curves. Can J For Res 8:424-431.

Zellner, A. 1962. An efficient method for estimating seemingly unrelated regressions and tests for aggregation bias. J Am Statist Assoc 57:348-368.