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Individual tree basal-area growth parameter estimates for four models

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Abstract

Four sigmoid growth models are fit to basal-area data derived from increment cores and disks taken at breast height from oak trees. Models are rated on their ability to fit growth data from five datasets that are obtained from 10 locations along a longitudinal gradient across the states of Delaware, Pennsylvania, West Virginia, and Ohio in the USA. We examine and compare the estimated parameters for the four models across a range of sample sites and tree ages. We then examine the differences among these models. The Chapman–Richards model is recognized as the best regarding minimum Mean Square Error (MSE) and gives reasonable estimates of maximum basal-area growth for old-age trees. The Weibull model is shown to be the poorest in terms of ability to fit the data. The apparent reason for this lack of fit is discussed. The Richards model ranked third in terms of meeting the MSE criteria but did best in terms of meeting the SAS stop criteria. The von Bertalanffy model is shown to have problems meeting the stop criteria of the SAS non-linear fit algorithm but ranks second in terms of samples meeting the MSE criteria. The von Bertalanffy model also tends to underestimate the long-term maximum value or asymptote of basal area over time.

Keywords: Individual tree basal-area growth; Goodness-of-fit; Parameter estimation; Non-linear model

1. Introduction

The Mid-Atlantic region of the United States contains a mixture of forest types. The forest stands are usually quite diverse in canopy composition and contain from 5 to 20 or more different tree species. A forest growth and yield model that includes the ability to examine the effects of a major forest defoliator, the gypsy moth, *Lymantria dispar*, was developed (Colbert and Sheehan, 1995) to permit analysis of forest management practices. The forest growth portion of this model is an extension of a forest gap simulator. Gap type forest growth simulation modeling has been used for many years. Botkin et al. (1972) produced the first forest gap simulator, JABOWA. There have been a number of similar models (FORET, Shugart, 1984;

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ZELIG, Urban, 1993; FORESKA, Linder et al., 1997) that expand the ecological interactions, range, and uses of this original form. All of these models use a fixed quadratic diameter–height relationship for each species and a basal-area growth model that starts with an optimal or maximum possible basal-area growth rate. That rate is defined as a ratio of fourth and second order polynomials in D, the tree diameter. Investigations of this model form using parameters proposed in the literature have demonstrated weaknesses (Colbert et al., 2003). It was recognized that new formulations are required to provide reasonable growth predictions.

Sigmoid growth models were identified that would provide improved ability to estimate future tree growth and yield as functions of age (Colbert et al., 2002). Analyses of four forest tree basal-area growth models were carried out using data from the states of Delaware (DE), Pennsylvania (PA), West Virginia (WV), and Ohio (OH). We published additional work examining these models and provided additional background on the base models and their use in forest management in the northeastern United States (Colbert et al., 2003). In those earlier studies, the models were fit under a specific biological constraint on the asymptote or upper bound for total basal area. The asymptotic maximum value of total basal area was constrained to be less than or equal to 8.0 m^2, yet the models did not always produce asymptotic estimates of long-term basal-area growth that seem realistic. Those unrealistic estimates may be due to the fact that the maximum number of years of basal-area data per tree was less than 145 years. Here we have relaxed that constraint by removing the maximum basal-area boundary condition because we have expanded the datasets to include 44 samples from older white oak trees with ages from 180 to 379 years. This permits us to examine whether or not our earlier concerns were justified. Using the relaxed boundary conditions, all models were refit to all of the original data as well as to these 44 additional older samples.

Here we propose alternative model forms that can more adequately track tree basal-area growth throughout the life of a tree. In the following analysis, we fit individual tree data in order to examine the range of parameter values among tree species across the sites and stand conditions that are represented in this portion of their full ecological range.

2. Methods

Forest growing conditions in the Mid-Atlantic Region of the United States are quite variable, with continental climate and annual rainfall from 50 to 180+ cm but generally in the range of 100–130 cm in the areas where managed forests are most prevalent. Rainfall is generally well distributed throughout the year. The forests we studied are considered mixed mesophytic and consisted of oak-dominated, mixed oak-hickory, or oak-maple forest types. Study site elevations range from just 2–10 m above sea level on the coastal plains of DE to 400–600 m above sea level in the forests of central PA and north central WV. In OH, stands were located on the Dorr Run Management Unit, Athens District of the Wayne National Forest that has 210–320 m elevation. Here, old-age white oak data have been added to data used in earlier studies (Colbert et al., 2002, 2003). These new samples were taken from Collins Woods, Belmont County, OH; Wright Woods, Washington County, PA; Watter Smith State Park, Harrison County, WV; Horner Woods, Lewis County, WV; and the Murphy Tract, Ritchie County, WV (Rentch, 2001).

A total of 234 radial growth-increment samples were used. The data were obtained from southern red oak (*Quercus falcata* Michx. var *falcata*) and white oak (*Quercus alba* L.) from the coastal plain in central and southern DE; northern red oak (*Quercus rubra* L.) from the Ridge-and-Valley province of central PA; northern red oak on the Coopers Rock State Forest in north central WV; northern red oak from OH; and white oak from five old-growth sites described above. Table 1 provides the type, number, and species of samples used in this study. All samples were taken at breast height, 137 cm. Increment cores were taken with 4.3 mm borers and disk samples were taken from felled trees. We attempted to take core samples to the tree pith, the location at age zero, but trees displayed sufficient radial growth variability around the circumference that it was not possible to obtain samples to pith on all trees. When necessary, we used a concentric-circle ruler to estimate tree radius and age at the inner most ring to provide initial starting values for basal area and age. We used a minimum of two samples per tree to crosscheck these estimates. Annual basal-area values were created assuming uniform circular growth around the circumference of the

Table 1
Basal-area tree growth data source counts by location, type, and tree species

Location	Type	Species	Number
DE	IC[a]	Q.f.	24
	IC	Q.a.	32
PA	IC	Q.r.	26
WVD	Disk	Q.r.	21
Log Grade (LG)	IC	Q.r.	60
OH	IC	Q.r.	27
Old age	IC	Q.a.	44

Abbreviations: Q.f., southern red oak (*Q. falcata*); Q.a., white oak (*Q. alba*); Q.r., northern red oak (*Q. rubra*).
[a] Increment core sample; disks samples taken at breast height from felled trees.

tree at breast height. Annual radial increments were accumulated to obtain radius and the estimated basal area at age data.

The four-parameter models selected for this study have been shown to be adequate for modeling sigmoid growth with sufficient flexibility and good statistical properties (Draper and Smith, 1981; Schnute, 1981; Myers, 1986; Vanclay, 1994). Fekedulegn et al. (1999) describe the non-linear sigmoid growth models that are used here. They present these as well as five other models that are less flexible. Three do not have the required sigmoid form. They discuss the data requirements for fitting such models. They suggest that without data that covers the full range of early juvenile growth, adolescent, mature, and senescent stages, parameter estimates may be non-significant. Here we have basal-area data that starts at or very near the first year of growth at breast height for each tree sampled. Adding the old-growth white oak samples has provided additional data range to examine the full range of life stages. The models were fit to basal-area data derived from the annual radial increment samples and estimates of inner radius and age. The models selected all have a similar general shape under the parameter restrictions described below. We chose these particular four models because they are flexible in their ability to model growth. These forms permit us to model growth that is not symmetric but exhibits and early accelerated growth period following establishment, then a peak followed by a gradual slowing of rate through maturity and a decline into senescence. These forms have been used in modeling forest tree growth and particularly tree basal-area growth for many years (Pienaar and Turnbull, 1973).

The non-linear models fit were the following:

Chapman–Richards (Turnbull, 1963),

$$\omega(t) = \beta_0(1 - \beta_1 \exp(-\beta_2 t))^{1/(1-\beta_3)} + \varepsilon \quad (1)$$

Richards (1959, Pienaar and Turnbull 1973),

$$\omega(t) = \frac{\beta_0}{(1 + \beta_1 \exp(-\beta_2 t))^{1/\beta_3}} + \varepsilon \quad (2)$$

von Bertalanffy (1957),

$$\omega(t) = (\beta_0^{1-\beta_3} - \beta_1 \exp(-\beta_2 t))^{1/(1-\beta_3)} + \varepsilon \quad (3)$$

Weibull (Ratkowsky, 1983),

$$\omega(t) = \beta_0 - \beta_1 \exp(-\beta_2 t^{\beta_3}) + \varepsilon \quad (4)$$

In all model formulations, $\omega(t)$ represents basal area at age t, β_0 represents the asymptote, $\omega(t)$, as $t \to +\infty$. Other parameters are model specific. Fekedulegn et al. (1999) define the mathematical and biological interpretation of the parameters β_0, β_1, β_2, and β_3 all of which have consistent meaning in the four models. β_1 is the biological constant. β_2 is the parameter that governs the rate at which the asymptote, β_0, is approached. β_3 is the allometric constant. Exponential (exp) is the base of the natural logarithm and ε is the residual or error term. To obtain the desired sigmoid form, there are restrictions on the parameters. All parameters are assumed to be positive ($\beta_0, \beta_1, \beta_2, \beta_3 > 0$) for all models; in Eq. (1) $\beta_1 < 1$; in both Eqs. (1) and (3), $\beta_3 < 1$; and in Eq. (4) $\beta_1 < \beta_0$.

The Marquardt (1963) method in the NLIN Procedure (SAS, 1999, 2000) was used to estimate the parameters for each model and basal-area series, supplying the partial derivatives (Fekedulegn et al., 1999). We first used initial conditions estimated for each sample data series as described in Fekedulegn et al. (1999), to fit each sample. From these outputs we obtained estimates of the range of possible parameter values. Using the range of these fitted values for each parameter, we created an initial search grid (Table 2) for the parameters of each model. Utilizing the SAS Macro language, we created a collection of SAS programs that permit each model to be fit to all data

Table 2
Initial search grid for model parameters (L: lower bound; U: upper bound; S: step size)

Model	β_0	β_1	β_2	β_3
Richard				
L	0.101	10^{-4}	10^{-3}	5×10^{-5}
U	5.0	0.1	0.3	2.0
S	0.6	10^{-2}	0.03	0.2
Weibull				
L	0.2	10^{-2}	10^{-4}	0.1
U	5.0	4.9	10^{-3}	4.5
S	0.6	0.59	2×10^{-4}	0.5
Chapman–Richards				
L	1.01	10^{-4}	10^{-3}	10^{-2}
U	5.0	0.99998	0.1	0.99
S	0.6	0.15	0.015	0.15
von Bertalanffy				
L	0.2	0.36	0.002	0.36
U	5.0	1.04	0.022	0.80
S	0.4	0.05	0.003	0.03

efficiently and store all tabular and graphic outputs as well as build summary datasets for use in further analyses.

To assess the predictive power of each model, we truncated the data set by removing the last (most recent) 15 years growth and refit the model to the truncated dataset. This allowed us to examine both the differences in estimated parameter values as series length changed and allowed us to test each model's ability to project the data forward for prediction of future basal area. Using 234 basal-area series, the 4 models and 2 series lengths (full and truncated), we made 1872 runs of the NLIN Procedure.

To test for convergence, the NLIN Procedure uses the relative offset measure of Bates and Watts (1981)

$$\sqrt{\frac{r'X(X'X)^{-1}X'r}{\mathrm{LOSS}^j}} < c \tag{5}$$

where r is the residual vector and X is the Jacobian matrix, $X = (\partial F/\partial\beta)$ for $Y = F(\beta, t) + \varepsilon$; the LOSS function is the sum of squared errors (SSE), with $c = 10^{-6}$. This is a measure of the relative change of the residual and not a measure of goodness-of-fit. We first examined both the statistical results of individual fits and graphically reviewed each fitted curve and residuals to develop criteria for accepting or rejecting individual cases. We found that the SAS stop criteria did not always provide reasonable parameter estimates. We spent considerable time examining the range of possible starting values. We considered a broader and denser range of starting values but found that this did not improve the final results. In extreme instances, with SAS showing convergence, the fitted curve was essentially a constant modal value and the distribution of fit residuals consequently was quite large.

To further judge the quality of model fits and parameter estimates, we used the MSE of the fitted models and de-emphasized the SAS convergence criteria. We extended our SAS macro language program to calculate the MSE associated with each fitted curve. We examined the number of samples where the SAS convergence criteria were met and used MSE to test for differences among models. We explored parameter interactions and consistency of fits among sites and between species. We examined the interactions among parameter estimates within models because the biological interpretation for β_0 is the same for all models. This parameter is the maximum potential basal area as the tree's growth levels off in old age. We examined the values of B_0, the estimates of β_0, among models.

The fact that MSE and β_0 were not normally distributed required us to use non-parametric tests. We used the Wilcoxon (Kruskal–Wallis) test for location and a one-way Chi-Square analysis on the Ansari–Bradley scores for dispersion (Gibbons and

Chakraborti, 1992). We examined for differences among models and among data sets as well as between truncated and non-truncated series and between those that did and did not meet the SAS criteria.

3. Results

In this study, as in earlier studies, we used the SAS NLIN Procedure. We initially tested the different convergence methods available and found that the Marquardt method outperformed the alternatives. Earlier we used the SAS NLIN convergence criteria to retain final parameter estimates. After detailed examination, we found some fits where the convergence criteria had been met but the MSE was large or graphical examination showed an extremely poor fit. After careful review of all individual fits, both graphically and statistically, it was recognized that the MSE was a better indicator of the fitted model's performance. Fig. 1 is a histogram of MSE for all fits. We found high quality results (MSE $< 10^{-4}$) in 92% of the 1872 cases. We chose to use just those results with MSE below 10^{-4}, dropping 156 sample fits (129 that did not satisfy the SAS NLIN convergence criteria and 27 that did) and leaving 1716 for further analysis.

Table 3
Proportion of fits that meet the MSE goodness-of-fit criteria vs. the SAS stopping criteria

Model	SAS (%)[a]	Non-SAS[a]	Total[b]
Chapman–Richards	71 (327)	29 (134)	99 (461)
Richards	92 (400)	8 (33)	93 (433)
von Bertalanffy	47 (211)	53 (238)	96 (449)
Weibull	75 (280)	25 (93)	80 (373)

Counts are shown in parentheses.
[a] Percentages in the column are with respect to counts in last column.
[b] Percentages are relative to total number of fits performed (468).

3.1. Convergence

The MSE criteria were met most often by fits to the Chapman–Richards model, followed by the von Bertalanffy, Richards, and finally the Weibull model (Table 3). The following discussion will concern only those fits where MSE was less than 10^{-4}. Among those 1716 fits that met our MSE convergence criteria, the Richards model met the SAS NLIN convergence criteria most often and the von Bertalanffy least often (Table 3). The SAS convergence criteria suggest that the Richards model performed best, followed by the Weibull model. However, we will later provide

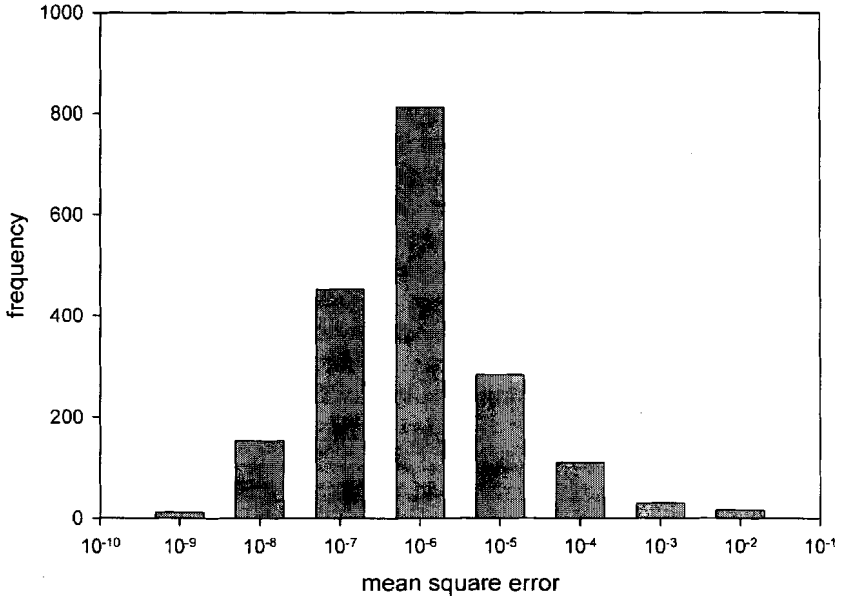

Fig. 1. Mean Square Error (MSE) histogram for all 1872 non-linear fit cases (models × series × truncations).

Table 4
Adequacy of MSE criteria among data sets; the percentage of cases that met the MSE $< 10^{-4}$ criteria

Model	802	812	LG	OH	PA	OA	WV
Chapman–Richards (%)	100	100	99	100	100	93	100
Richards (%)	80	100	93	94	96	95	88
von Bertalanffy (%)	100	100	98	98	100	82	100
Weibull (%)	100	92	96	98	100	3	100

Data set: 802 = DE, *Q. alba*; 812 = DE, *Q. falcata*; LG = WV-LG; OA = old-age *Q. alba*; WV = WV disk samples.

additional evidence concerning the weaknesses of these two model formulations. Looking at the 498 cases where the SAS convergence criteria were not met but our MSE criteria was met (MSE $< 10^{-4}$), we found that the better the initial estimate, the smaller the MSE.

The numbers of acceptable fits for each model was consistent across datasets except that the Weibull model performed poorly when fit to the old-age white oak samples (Table 4). Among datasets, the Chapman–Richards model most consistently produced MSE $< 10^{-4}$.

3.2. MSE

Average MSE was smaller for those fits done using the Chapman–Richards (0.520×10^{-5}) and von Bertalanffy (0.547×10^{-5}) models, followed by the Weibull (0.779×10^{-5}) and Richards (0.938×10^{-5}) models. The variation among MSE values was large for all models; standard deviations followed the same rank order as means but were almost twice mean values. This large skew precluded tests dependent upon normal distributions. MSE showed highly significant location differences among models ($P < 0.0001$), but did not show significant dispersion differences. In general, MSE varied considerably among data sources yet could be summarized into three distinct groups. The first of these groups is the longer old-age white oak samples which had the greatest MSE value (1.926×10^{-5}); the second consisted of the southern red oak from Delaware (0.859×10^{-5}), the Delaware white oak (0.784×10^{-5}), the WV Log Grade study samples (0.459×10^{-5}), and OH (0.437×10^{-5}) that tended to have intermediate values. The PA dataset (0.198×10^{-5}) was grouped with the WV disk data (0.121×10^{-5}) and had the smallest average MSE. These differences were highly significant in both location and dispersion ($P < 0.0001$). While the old-growth white oak samples tended to have the highest MSE, these data were tightly grouped, showing dispersion similar to that of the PA increment core and WV disk data. The OH northern red oak, the DE white oak, and the WV increment core samples had the highest variability in MSE values.

MSE was lower (location difference significance level: $P < 0.0001$) among the truncated series but there was no significant difference in dispersion between the truncated and full series. On average, those series that met the SAS/Marquardt convergence criteria had MSE about half that of those that did not; differences were significant in location (location difference significance level: $P = 0.01$) and highly significant in dispersion ($P < 0.0001$). The Weibull model did poorest as measured by the number of series fits meeting our convergence criteria. Yet, when it did fit, the average MSE was smallest among those series that both met the SAS convergence criteria and had MSE $< 10^{-4}$.

3.3. B_0

The long-term behavior of each model is determined by B_0. Environmental factors such as release from competition can produce short-term spurts in basal-area growth. A number of samples showed this type of increasing basal-area growth in the period just prior to the collection of growth data. The estimation procedure tended to project this growth forward (location differences significance level: $P < 0.0001$). These produce extreme values of B_0 in 18% of the fits. Ignoring these extreme values (basal area $> 10\,m^2$ or radius $> 1.78\,m$), we find that B_0 averages $0.718\,m^2$ overall; $0.809\,m^2$ for the Chapman–Richards model; $0.589\,m^2$ for the Richards model; $0.914\,m^2$ for the von Bertalanffy model; and $0.607\,m^2$ for the Weibull model. The Weibull and von Bertalanffy models showed the greatest spread in predicted values for

B_0 while the Chapman–Richards model performed best (dispersion differences significance level: $P < 0.0001$). These estimates for the long-term maximum potential basal-area values are quite reasonable for mature oak in this region of the northeast USA.

The differences among datasets are more pronounced. Tests indicate highly significant location and dispersion differences among datasets ($P < 0.0001$). The overall average is $0.718\,m^2$, but the average for the old-growth white oak samples is $2.36\,m^2$, while the young coastal white oak samples from DE averaged $0.242\,m^2$. Average B_0 values were also low in the southern red oak of DE and northern red oak of PA, while most realistic for the northern red oak samples of WV ($0.877\,m^2$) and OH ($0.726\,m^2$). The old-age white oak samples showed the smallest dispersion among B_0 values followed by the PA increment core data and the WV disk data, while the OH northern red oak showed the largest. All models and datasets produced some extremely large estimates of β_0. While there was no location difference between the full and truncated series, the truncated series did show significantly less dispersion ($P < 0.0001$). Those series that converged under the SAS criteria produced smaller values of B_0 ($P < 0.0001$) while those that did not converge tended to be less scattered ($P < 0.0001$).

3.4. Model fits: histograms and selected parameter interaction graphs

For each model, we tested for interactions between MSE and parameter values to look for possible

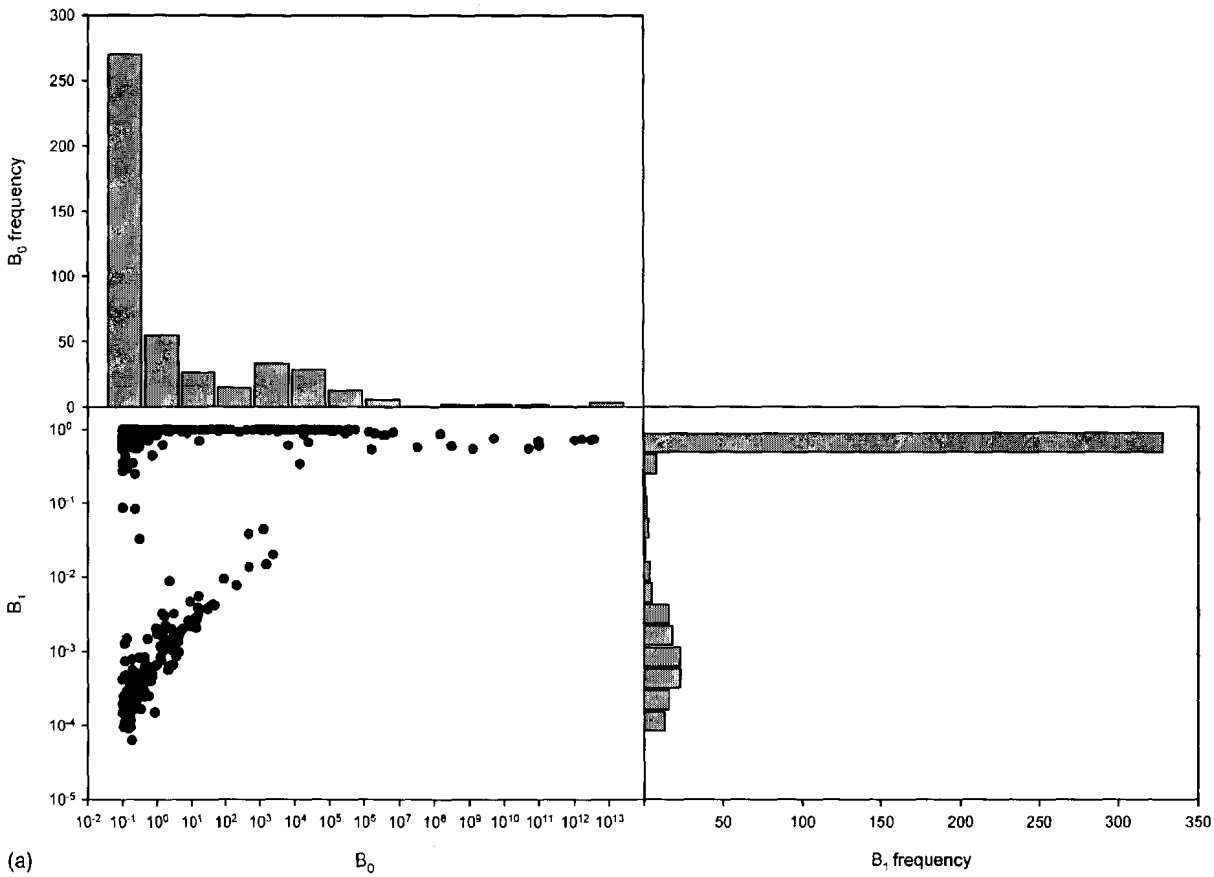

Fig. 2. The distribution and interaction of the parameters of the Chapman–Richards model: (a) histograms of parameters B_0 and B_1 and the scatter plot B_0–B_1; (b) histograms of parameters B_2 and B_3 and the scatter plot B_2–B_3; (c) the scatter plots B_1–B_3, B_0–B_3, B_1–B_2, and B_0–B_2, showing the distributions and lack of significant interaction between these parameters.

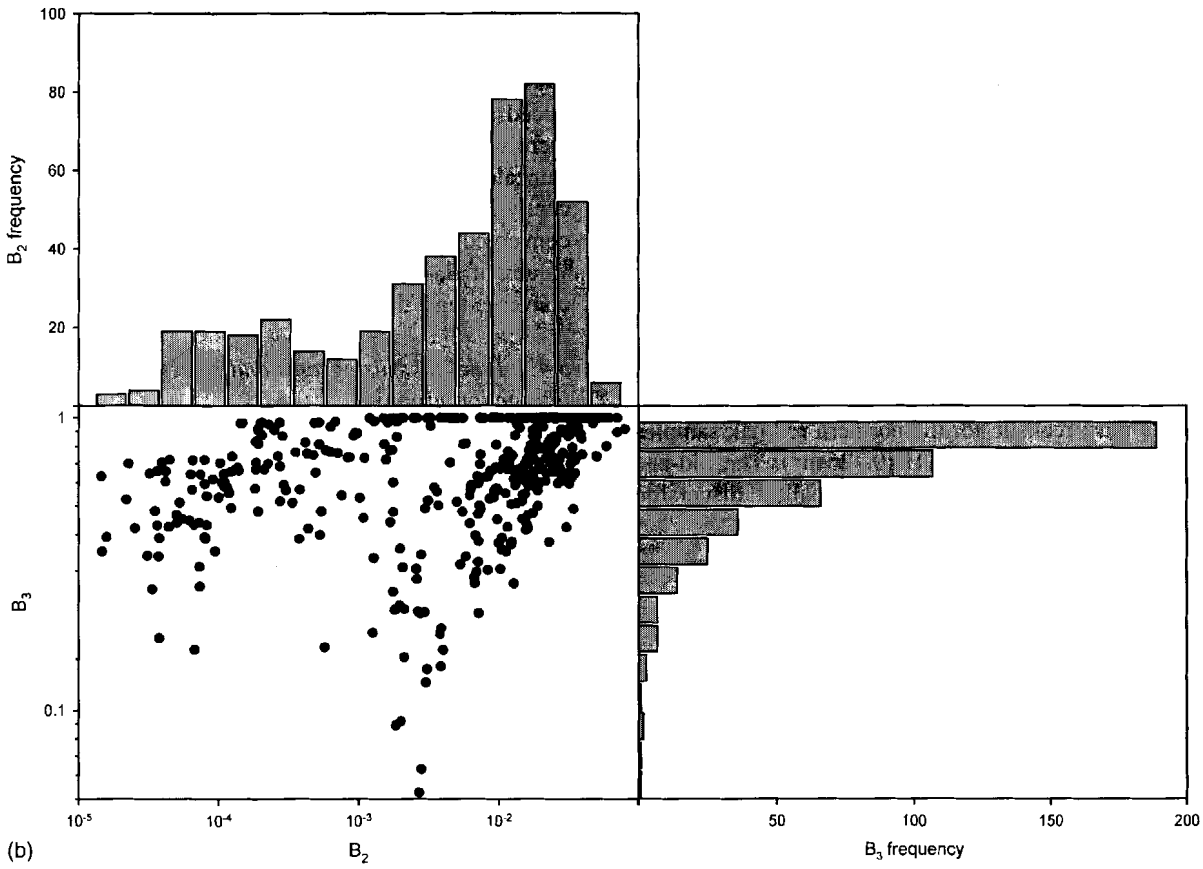

Fig. 2. (*Continued*)

relationships between quality of fit and range of parameters but found no significant interactions. We examined each model's estimated long-term basal-area maximum, B_0 (the estimate of the asymptotic behavior parameter, β_0). Longer data series imply larger values of B_0, i.e., fits of data from young (age < 100) trees tend to underestimate B_0 but there was no significant difference in B_0 between full and truncated series. The von Bertalanffy model fits tend to have the most underestimated asymptotic behavior of basal-area growth. Chapman–Richards model fits tend to provide significantly higher estimates of B_0 than the other three models. These estimates compare well to field experience. Fig. 2 provides both the distribution of estimates of each parameter and graphic displays of the interactions between parameters for the Chapman–Richards model.

A strong dependence occurs between values of B_0 and B_1 in the Weibull model (Fig. 3). B_1 can be predicted from B_0 as follows: $B_1 = 0.999796B_0 - 0.000557$ ($R^2 = 0.999999$). This strong interaction is evidence that this four-parameter Weibull model is inappropriate for estimating these types of data and could be replaced with a three-parameter model with essentially no loss in fit. The tendency of the Weibull formulation not to fit the longer series (Table 4) is additional reason to reject this model. The fact that there is a very highly significant linear relationship between B_0 and B_1 for the Weibull model does suggest over parameterization of the model.

The Richards model showed a significant non-linear interaction between B_1 and B_3 (Fig. 4). For $B_1 < 1$, the relationship to B_3 is nearly linear; then for $B_1 > 1$,

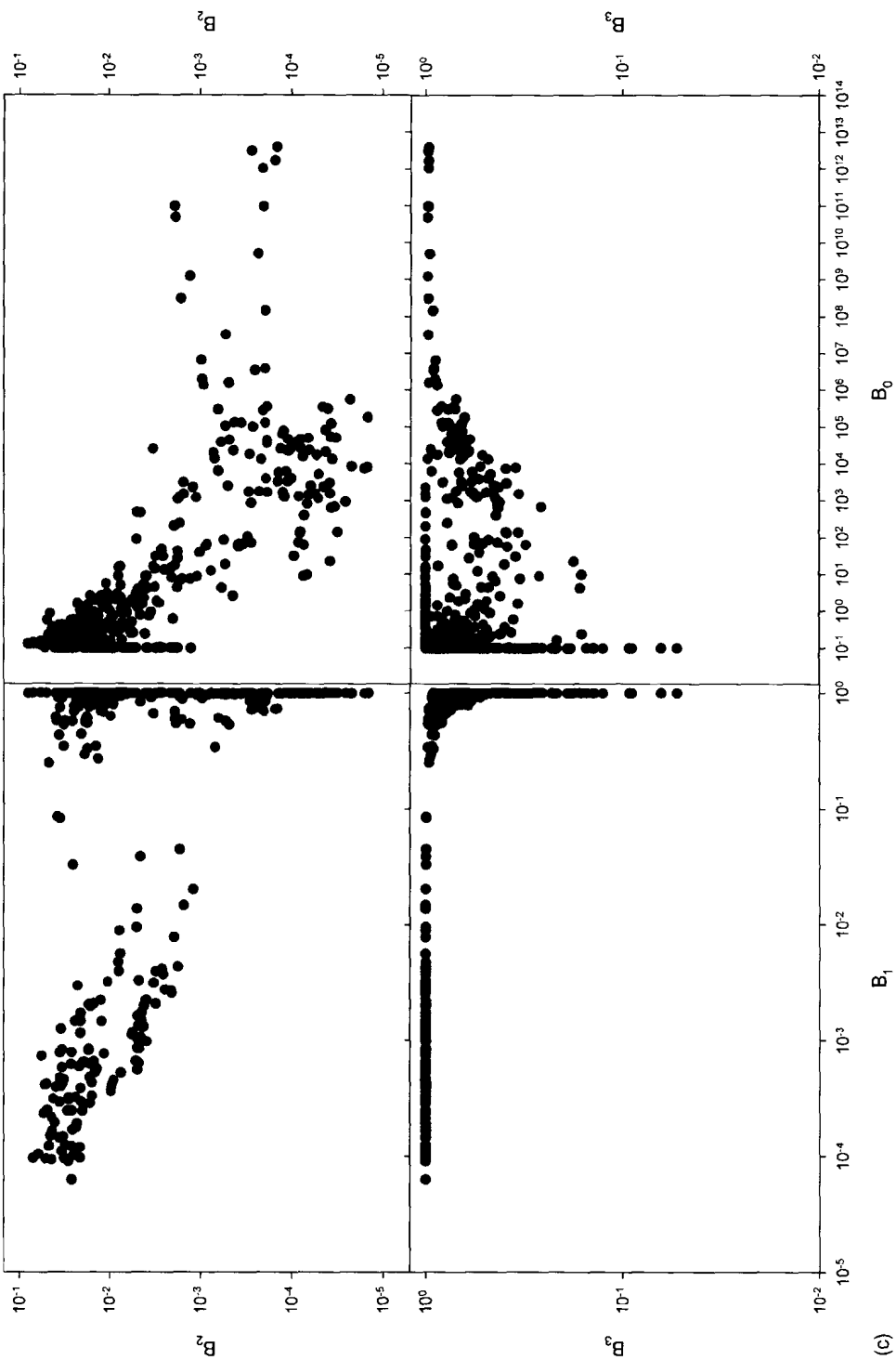

Fig. 2. (*Continued*).

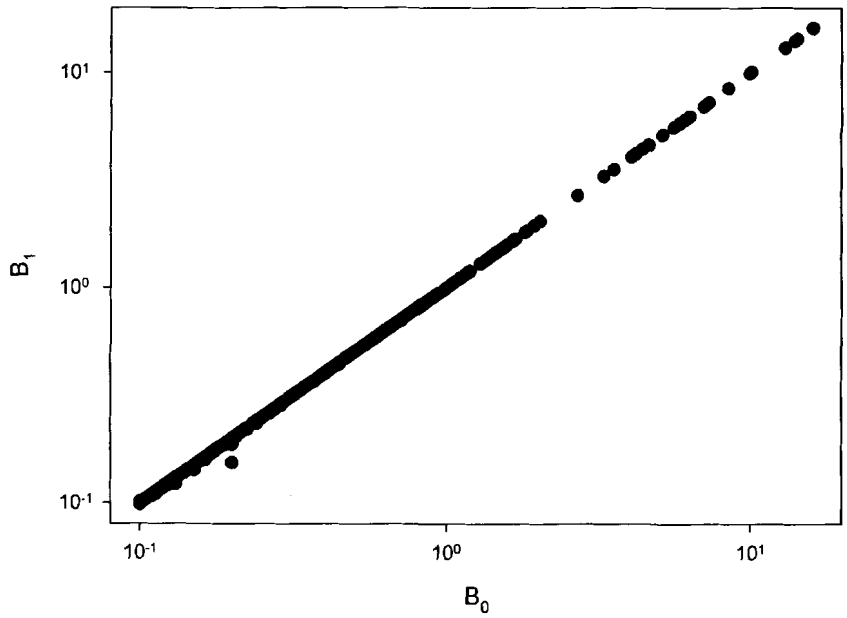

Fig. 3. Interaction between the B_0 and B_1 parameter estimates on a log-log scale for the Weibull model.

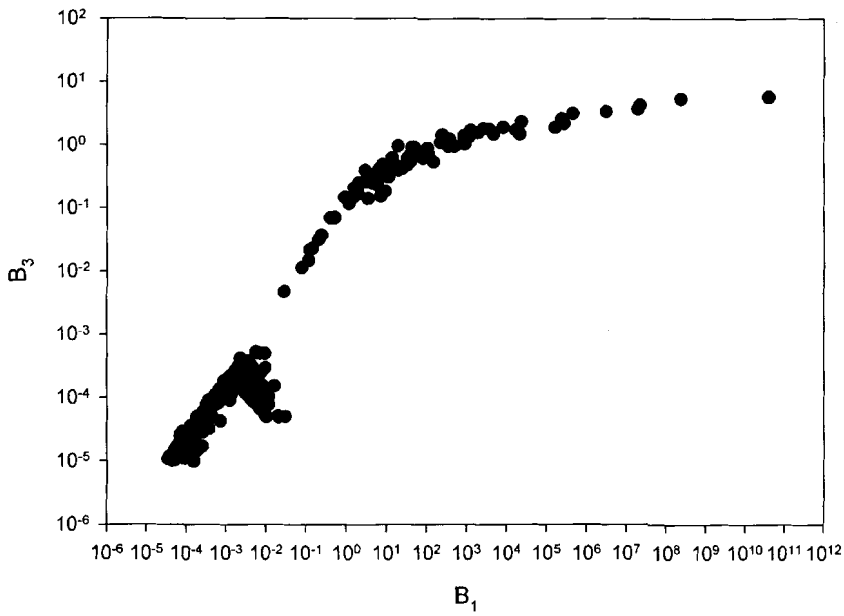

Fig. 4. Interaction between parameters B_1 and B_3 of the Richards model on a log-log scale.

B_3 tends to show asymptotic behavior, staying below 10 as B_1 covers several orders of magnitude. There are no other model parameters that have strong interactions.

4. Discussion

We found convergence to be quite sensitive to the starting values. There were cases where the SAS

convergence criteria were met but the resulting model was essentially constant ($\hat{\omega} = c$, i.e., a horizontal line). In this study, using the iterative NLIN Procedure, starting values were obtained through the coverage of the initial search grid. Considerable effort was given to develop an adequate grid. It was found that careful development of a well-designed grid (e.g., Table 2) is critical to good results. A less dense initial search grid was first used and we found that the procedure did not converge for a very large proportion of the samples across all models. We found the choice of limits and mesh size to have a pronounced effect on the number of converging series and the quality of the fit (smaller MSE values). It should also be noted that since the procedure used did not permit the inclusion of non-constant constraints (boundary conditions) among parameters, when fitting to the von Bertalanffy model, the procedure did not make use of early growth data. It is sufficient that the condition ${\beta_0}^{1-\beta_3} > \beta_1$ be met for $\hat{\omega}$ to be positive for all t. When this condition is not met (for small t), $\hat{\omega}$ will remain undefined, and the associated data are ignored during the fitting procedure.

We chose 10^{-4} as the MSE cut-off point rather than using a more widely accepted 80/20 rule because we found no obvious bias as the additional 12% of the data were included. The relative distribution of "good" fits is consistent across datasets and models.

While improvement can be made to obtain SAS convergence, results obtained on samples that did not converge under the SAS NLIN criteria often appear to be quite adequate and represent the data well throughout their range. We examined pairs of samples from the same tree when SAS did not converge for a particular model form. We found that the distribution of errors about the fitted curve where SAS did not converge are often no worse and sometimes better than another sample from the same tree where SAS converged. The ability to find an adequate fit does not appear to be associated with the starting point (basal area at age) of the data series. As expected, MSE was generally smaller where the series converged under the SAS criteria. However, those series that did not converge under the SAS criteria showed significantly less dispersion, indicating that the fits were much more consistent across models and between the full and truncated series.

By adding the old-age white oak samples we have been able to examine differences among these model forms when fit to the two age groups. The old-age samples showed the highest MSE and the largest B_0 estimates but they also produced the least dispersed B_0 values and second lowest dispersion in MSE values among data sets. While the large asymptotic values may not appear biologically reasonable, these data indicate that trees can continue to show substantial basal-area growth rates at older ages.

As described, there were only two cases where there were strong dependences found among the parameter estimates for each model. Strong dependence indicates that the model can be replaced with a more parsimonious model that takes advantage of the dependence. But in this study we found that the Richards model had the highest and most dispersed MSE values, indicating lack of fit. The Weibull model met our convergence criteria least often, showed the most dispersion in B_0 values, and the second highest B_0 estimates. The von Bertalanffy fits lead to an extremely dispersed set of B_0 estimates, many far above what is biologically reasonable. Because the form of the von Bertalanffy model also leads to difficulty in fitting for small basal-area or early age data, we do not recommend this model for use in estimating and predicting future basal-area growth.

The significant differences in the dispersion of B_0 estimates across data sets and across series lengths shows the Chapman–Richards model to be most consistent. The Chapman–Richards model produces a range of B_0 estimates that also appear to be the most reasonable biologically. After review of all results, we find the Chapman–Richards model to be the best choice to replace the quadratic equation form used as the base growth equation in forest gap type models.

Colbert et al. (2002) discuss the bias that arrives from the quadratic height–diameter relationship and the ratio of polynomial functions of diameter that are used in the growth equations of gap models. All the models considered here are of forms that permit more flexible growth functions. The Chapman–Richards model, as fit to data in this study, does not exhibit any such biases in growth trajectory. The quality of fits to basal-area data demonstrates the strength of this formulation for these species across the Mid-Atlantic Region of the United States. The flexibility of the Chapman–Richards model can be seen in its wide use in forest growth modeling and predictions (Larocque,

1998; Smith et al., 1992; Somers and Farrar, 1991; Peng et al., 2001). There has been extensive use of the Chapman–Richards model in height–age modeling and site index development. As computing power has increased, it has become possible to utilize more detailed and robust models for analyzing forest tree and stand dynamics. The models we have analyzed can be utilized within simulation systems to more accurately reflect the growth history and probable future growth of individual trees within forest stands.

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