ABSTRACT

SMITH, BENJAMIN CHRISTIAN. Modeling the Diameter Distribution in Juvenile Loblolly Pine (Pinus taeda L.) from Diverse Genetic Provenances Under Deficient and Optimum Nutrition Regimes. (Under the direction of Dr. Bronson P. Bullock.)

The ability to predict diameter distributions is an important tool for the forest manager; by accurately predicting the diameter distribution, the manager may make better-informed decisions regarding the silvicultural treatments for a stand. This study compares the suitability of the gamma, lognormal, and two-parameter Weibull distributions for modeling diameter distributions in juvenile loblolly pine from ages 5 to 11. The two-parameter Weibull distribution was found to be the most appropriate distribution as determined by the Anderson-Darling goodness-of-fit statistic. The study also determined the most suitable method for estimating distributional parameters from stand level characteristics (e.g. mean basal area, relative spacing, quadratic mean diameter, and age). Methods tested were a parameter prediction method (PPM), a parameter recovery method (PRM), and a percentiles-based method (PCT). Comparisons were made from ages 5 to 10 using a modification of the Reynolds error index, weighted by basal area. Final parameter estimation equations were developed for juvenile loblolly pine over ages 5 to 11.

The parameter recovery method of parameter estimation proved to be most appropriate for modeling these data. Although the PPM had a slightly lower Reynolds error index than the PRM, the shape parameter was predicted within a very narrow range about the mean, while the distribution of shape parameters recovered by the PRM was much closer to the empirical distribution. In addition, the PRM required fewer inputs into the model, and as such was more desirable for modeling purposes. An application of the PRM was presented to demonstrate the construction of stand tables from the estimated parameters.
The relationships among the maximum likelihood fitted parameters of the two-parameter Weibull distribution and the treatment effects due to fertilization, genetic provenances, and open-pollinated genetic families were also examined. Both the scale and shape parameters differed significantly between the non-fertilized control treatment and the optimally fertilized treatment. No significant differences were observed in the shape parameters between genetic provenances, but significant differences did exist in the younger ages between provenances in the scale parameters.

Family means tended to increase over time for the scale parameter, and family mean rankings were relatively stable within and across fertilization treatments. The shape parameter family mean rankings were less stable over time than the scale parameter ranks, with the means tending to increase in the non-fertilized treatment and decrease in the fertilized treatment, reflecting the differences in stand development. Year to year rank changes were more minor than long-term family mean rankings.
Modeling the Diameter Distribution in Juvenile Loblolly Pine (Pinus taeda L.) from Diverse Genetic Provenances Under Deficient and Optimum Nutrition Regimes

by
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A thesis submitted to the Graduate Faculty of North Carolina State University in partial fulfillment of the requirements for the Degree of Master of Science in Forestry

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BIOGRAPHY

Benjamin Christian Smith was born in 1978 in Stevens Point, WI. He received a Bachelor of Arts in Biology with departmental honors from Albion College in Albion, Michigan under the direction of Dr. J. Dan Skean in 2000. He moved to Indianapolis, Indiana in 2001 and married Sarah Andrews in July 2001. The couple moved to Raleigh, North Carolina in 2003 where Ben began his graduate studies at North Carolina State University.
Acknowledgements

I would like to thank my committee chair, Dr. Bronson Bullock, for his guidance and support with my research. He is to be commended for his patience helping me with SAS coding. I would also like to thank the other members of my committee, Drs. Steve McKeand and Heather Cheshire for their insight and advice. Thanks are also due to the NCSU Cooperative Tree Improvement Program and Forest Nutrition Cooperative for allowing me to use the SETRES-2 study site. I also appreciate the graduate students who assisted me with measurements. I especially want to thank John Adams and Josh Sherrill for their friendship and encouragement in graduate school.

Finally, I owe my wife Sarah a debt of gratitude for all she has done for me. She provided endless encouragement in my pursuit of graduate studies; I could not have done this without her. She has always been there for me when I needed her most, and been the most supportive person in my life. There can be no doubt she loves me for enduring this process.
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DIAMETER DISTRIBUTIONS

Introduction

Diameter distributions have been utilized for many years to model forest growth and yield. The value of the diameter distribution in growth and yield modeling lies in its ability to predict frequency by size class from stand level measurements that do not inherently contain this information. Stand tables may be constructed from the diameter distribution, aiding in forest management decisions.

One common method for modeling the diameter distribution is to fit a distribution function based upon available data. Historically, a variety of functions have been fitted, including the Beta (Clutter and Bennett 1965; Lenhart and Clutter 1971; Maltamo et al. 1995; Cao 1997), Log-normal (Nanang 1998), Johnson’s Sb (Hafley and Schreuder 1977; Rennolls and Wang 2005; Newberry and Burk 1985; Zhang et al. 2003), Johnson’s Su (Zhou and McTague 1996), and the Weibull (Bailey and Dell 1973; Rennolls et al. 1985; Shifley and Lentz 1985; Brooks et al. 1992; Cao 2004).

Since its introduction for modeling diameter distributions (Bailey and Dell 1973), the Weibull function has become the most widely used function for that purpose. One of the original reasons for selection of the Weibull function is the ease with which the required calculations could be made (Bailey and Dell 1973). This has become a minor consideration with the improvement of computing systems and statistical software packages, but it is still in favor due to its flexibility in assuming a wide range of unimodal distribution shapes including positive or negative skewness. In addition, the calculations needed to create a stand table from a given set of parameters may be carried out on an ordinary scientific
calculator capable of performing exponential computations; a decided advantage when considering the end use of diameter distribution models for forest managers.

Various approaches have been utilized to estimate the parameters that define a diameter distribution of best fit. In general, the techniques fall into one of three general categories: parameter prediction methods (PPM); parameter recovery methods (PRM); and percentile prediction methods (PCT). For an example of a system of parameter prediction equations, see Feduccia et al. (1979), where the parameters of the three-parameter Weibull are predicted as a function of dominant height, trees surviving, and age since planting.

Very few diameter distribution modeling efforts have focused on juvenile stands (see Bullock and Burkhart (2005), Liu and Burkhart (1993)). These models have not specifically accounted for the effects of fertilization on early growth. In addition, the planting of genetically improved loblolly pine seedlings has become widespread in the southeastern United States, with a large portion of the over 1 billion loblolly pine seedlings planted annually being genetically improved seedlings (McKeand et al. 2003). Estimates of volume gain due to the use of improved stock range from 10 to 30 percent (McKeand et al. 2003). Given the magnitude of the changes due to tree breeding, the impact of including family or seed source information in diameter distribution models has been under-reported. Janssen and Sprinz (1987) compared improved and unimproved stands using parameter prediction with the beta distribution, and found shapes and peaks for the distributions to be different; the average maximum diameter was greater in the improved stands. They expressed a need to repeat the study using the Weibull and Johnson’s $S_b$ distributions, but no reports of those results were found.
**Data and Materials**

The data for this study were collected at the SouthEastern Tree Research and Education Site-2 (SETRES-2), situated adjacent to the original SETRES research site (see Albaugh et al. 1998). The SETRES-2 study site is in the Sandhills of North Carolina in Scotland County (Figure 1). Soil at the site is a Wakulla series-sand to a depth of over 43 meters. It is a siliceous, thermic Psammentic Hapludult soil, and is very infertile. The site is excessively drained, having a two meter profile water holding capacity of 12-14 centimeters. The 30 year mean annual rainfall is 1200 millimeters, although extended periods of drought can occur during the growing season (Albaugh et al. 1998). The 30 year mean annual temperature is 17°C, with a mean winter temperature of 9°C and mean summer temperature of 26°C (see McKeand et al. 2000 for site details).

The SETRES-2 study was established by the Cooperative Tree Improvement Program at North Carolina State University as a genotype by environment interaction (GxE) trial. The study is a split-split-plot design of two silvicultural treatments, fertilized and non-fertilized (control), and two genetic provenances (each with five open-pollinated loblolly pine families). The study is divided into nine blocks, with two main treatment plots per block, each containing two provenance sub-plots, and five family sub-sub-plots nested within each provenance plot. Provenance and family plot location were randomly assigned. Figure 2 illustrates the layout of a single block. 100 trees were planted in each family plot with a rectangular spacing of 1.5 m by 2.1 m (3075 TPH), for a total of 18,000 measurement trees. A tenth block was established; but due to incomplete planting and destructive sampling, it has since been excluded from measurement.
Figure 1. Natural range of loblolly pine (Little 1971, shaded region) showing location of SETRES-2 study, Atlantic Coastal Plain (ACP) provenance, and Lost Pines Texas (LPT) provenance seed source locations in the southeastern United States.
Figure 2. Example layout of one block, showing fertilization treatment, provenance sub-plots, and family sub-sub-plots.
The genetic component of the study consists of two genetic provenances, each with five open-pollinated families, making the individuals within families half-siblings. The provenances are from very different regions; one from the Atlantic Coastal Plain (ACP) and the other from the “Lost Pines” area of Texas (LPT) (McKeand et al. 2000). The “Lost Pines” are an isolated population in central Texas at the western extreme of the range of loblolly pine (Figure 1). Plantations from the LPT seed source have been previously established in one study on sites with mean annual rainfall levels ranging from 84 centimeters to 132 centimeters (van Buijtenen 1978). The Atlantic Coastal Plain source is generally a fast-growing, fusiform rust (caused by *Cronartium quercuum* (Berk) Miyabe ex Shirai f. sp. *fusiforme*) susceptible provenance, while the Lost Pines Texas source is a slower growing, drought-hardy, and more fusiform rust-resistant provenance, as is typical of coastal and western sources, respectively (Sierra-Lucero et al. 2000). The families selected were average to slightly above average growth performers (McKeand et al. 2000).

The environmental (silvicultural treatment) component of the study is comprised of two levels of nutrition: non-fertilized (control) and optimally fertilized. Fertilizer was applied to the optimally fertilized treatment annually at the rates shown in Table 1. Application rates were prescribed each year as indicated from foliage samples collected during the dormant seasons.

Prior to the study establishment, the site contained a 10-year-old loblolly pine plantation that was manually cleared. The selected source seed was greenhouse sown in containers (160cc RL Super Cells) in June of 1993, and field planted in November of 1993 (McKeand et al. 2000). Buffer rows were planted with bare-root seedlings in early 1994, but suffered near total mortality due to a period of drought in the spring of 1994. The buffer
Table 1. Fertilizer applied through age 10 (lbs/acre) to fertilized treatment plots.

<table>
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<th>Year</th>
<th>Fertilizer</th>
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<td>1995</td>
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*Micros 0.5 B, 2.0 Cu, 5.0 Fe, 5.0 Mn, 2.0 Zn

**1.2 B
rows were replanted the next winter with bare-root loblolly seedlings. Herbicide weed control was applied to all plots after the first growing season.

Height measurements were made on every tree at planting and at ages 1, 2, 3, 4, 5, 6, 8, and 10. Diameter at breast height (DBH) (1.37 m above ground) measurements were tallied with the height measurements at all ages after age 2, once the stems attained breast height. Additionally, diameter measurements were collected for the interior 64 trees (due to adjacency effect concerns) of each family plot at age 11. Measurements were taken during the dormant season, in either winter or early spring. Height was measured with height poles to the nearest centimeter at younger ages, and with Haglöf Vertex III hypsometers to the nearest decimeter at later ages. Diameter was measured with diameter tapes to the nearest millimeter.

Due to the size of the trees relative to the buffer distance between treatment plots, as well as the smaller size of the younger buffer trees, potentially inducing edge effects, only measurements from the interior 64 trees were used for this study. Individuals forked below breast height were not measured for DBH and were excluded from analysis. In addition, dead trees were excluded from the analysis. Consideration was given to excluding defective trees such as those forked above breast height, but since those individuals still affect stand competition dynamics, they were included in the analysis. In order to avoid truncating the distribution and biasing results upward, analysis was begun at the age where nearly all stems had achieved breast height.

**Methods**

The initial step in the modeling process was the selection of a family of distributions. The primary selection factor was the ability of a family of distributions to adequately fit the
empirical diameter distributions (the distributions formed by the observed diameters) over the range of the dataset. For even-aged, single species stands, this requires a distributional function that can accommodate unimodal distributions with varying degrees of skewness. The Gamma, Log-normal, and two-parameter Weibull families of functions were fitted to each plot at each measured age. Plots consisted of the diameters from each family, treatment, block, and age combination, for a total of 900 plots (10 families x 2 treatments x 9 blocks x 5 ages). The distributional fit was accomplished with the CAPABILITY procedure in SAS (SAS Institute Inc. 1999) using maximum likelihood estimators for the parameters, with the Newton-Raphson approximation for the maximum likelihood estimator used for the shape parameters of the Gamma and two-parameter Weibull. The distributional fit was evaluated by the Anderson-Darling (A-D) goodness-of-fit (GOF) statistic. The second distribution selection factor, ease of estimation and use, was harder to quantify. Preference was given to functions requiring simpler computations to estimate the parameters and construct a stand table from the estimated parameters.

After fitting the distribution to the datasets, a parameter estimation technique needed to be chosen. This required the construction of models from each type of parameter estimation method. Appropriate stand-level variables had to be calculated prior to model development based on individual-tree-level measurements. A number of variable sets have been previously utilized in parameter estimation, including age, mean height of dominants and co-dominants, site index, stand density, arithmetic mean diameter, quadratic mean diameter, surviving trees per acre, average total height of the 10 tallest trees, and mean diameter (Lenhart 1988; Liu et al. 2004; Rennolls et al. 1985). Dominant/co-dominant
height, $H_{\text{dom/co-dom}}$, was estimated as the mean of the individual heights greater than the plot mean height, as shown in Equation (1).

$$H_{\text{dom/co-dom}} = \frac{\sum_{i=1}^{n} (x_i > \bar{x})}{n}$$  \hspace{1cm} (1)

where $x_i$ is the height of the $i^{th}$ individual, $\bar{x}$ is the mean plot height, and $n$ is the number of individuals with height greater than plot mean height.

Calculation of per area stand level measures such as trees per hectare (TPH) presents a difficulty. Plot areas are a constant 0.02081 ha, simply the area occupied by 64 planting locations in a 1.5 m x 2.1 m spacing. However, choosing which individuals should be considered for calculations is not clear. For example, trees forked below breast height were not included in calculations for basal area per hectare (the sum of all cross-sectional areas at breast height in one hectare), as diameter measurements were not recorded for those individuals. When considered from the perspective of modeling stand dynamics, forked trees play a role in competition, and ignoring those individuals will result in a lower basal area per unit area than is actually present in the stand. From the standpoint of merchantability, inclusion of forked trees will yield a basal area per unit area that is higher than should be expected for operational decisions. This difference could be considered trivial if forking patterns are consistent across all treatments, but if any genetic basis for forking exists, if treatments such as fertilization impact the incidence of forking, or especially if any genotype by environment interaction exists, ignoring the problem could seriously impact the results.

One possible way to deal with this dilemma is to calculate the plot area as a function of the number of trees considered in the analysis, since a fixed spacing exists. By using the area occupied by the included number of trees as the divisor for a variable such as basal area
per hectare, an upper threshold for the estimate can be established. The estimate obtained by ignoring the problematic trees over the fixed total area can be treated as the lower threshold for the estimate, since inclusion of any additional individuals will only increase the estimate. For this study, TPH was estimated using the fixed area, as shown in Equation (2). This gives an estimate of the total number of stems per unit area, not just merchantable stems.

$$TPH = \frac{n}{Area} \tag{2}$$

where $n$ is the number of trees measured in the plot at that age, and $Area$ is the area of the plot in hectares (1.5 m x 2.1 m x 64 trees = 0.2081028096 ha). Equation (3) was used to estimate relative spacing (RS), which is a measure of stand density relative to stand dominant/co-dominant height (Avery and Burkhart 2002).

$$RS = \sqrt{\left(\frac{10000}{TPH}\right)} \tag{3}$$

Mean basal area, $\overline{BA}$, was calculated as the mean of the cross-sectional areas (m$^2$) at breast height corresponding to the measured diameters of the trees in a plot. Quadratic mean diameter, $\overline{D}_q$, was calculated as the diameter (cm) of a tree with the mean basal area (m$^2$) at breast height of trees in a plot, as shown in Equation (4) (Avery and Burkhart 2002).

$$\overline{D}_q = 2\sqrt{\frac{10000 \times \overline{BA}}{\pi}} \tag{4}$$

In addition to the stand level variables, the diameter corresponding to a specified percentile of the distribution of diameters, in one-percent increments from 0 to 100 percent, was computed for each of the plots. These variables are denoted for the $i^{th}$ percentile as $D_i$, e.g. the value of the diameter greater than 25 percent of the observed diameters would be $D_{25}$. 


After the generation of stand level variables, each of the stand level independent variables were plotted against the scale and shape parameters of the fitted diameter distribution to examine relationships between the variables and to highlight any non-linear trends in the data that required a linearizing transformation. Natural log and square root transformations were applied to variables as necessary to establish a linear relationship. Plots of the natural logs of the $i^{th}$ percentile of the diameter distribution against stand level variables were also examined. The equation used for the cumulative distribution function (c.d.f.) of the two-parameter Weibull function is shown in Equation (5).

$$F(x) = 1 - \exp\left[-\left(\frac{x}{b}\right)^c\right] \quad \text{for } x \geq 0, b > 0, c > 0$$ (5)

where $F(x)$ is the proportion of the distribution less than $x$, $x$ is the diameter, $b$ is the scale parameter, and $c$ is the shape parameter. Equation (6) gives the probability density function (p.d.f.) of the two-parameter Weibull function.

$$F(x) = \frac{c}{b} \left(\frac{x}{b}\right)^{c-1} \exp\left[-\left(\frac{x}{b}\right)^c\right] \quad \text{for } x \geq 0, b > 0, c > 0$$ (6)

where all variables are as previously defined.

*Parameter Estimation Methods*

Three distinct methods of parameter estimation for the distribution were applied to determine the best method for modeling juvenile stand development. The first was parameter prediction (PPM), which involves using regression equations to directly predict the distributional parameters from stand-level variables. The second method applied was a parameter recovery technique (PRM), where selected log-transformed percentile values of the diameter distribution predicted by regression were used to solve expressions equating
moments of the diameter distribution to the shape and scale parameters. The third method tested was a percentiles method (PCT), in which regression-predicted percentiles of the diameter distribution were directly equated to the parameters.

**Parameter Prediction Method (PPM)**

A number of variable combinations and transformations were tested. Due to the simultaneous estimation of two correlated models, seemingly unrelated regression (SUR) techniques were utilized to estimate the regression parameters of these models (Bullock and Burkhart 2005). All models tested involved direct prediction of the two distribution parameters from stand level variables. The models were all linear, and forward selection was utilized in the evaluation for inclusion of variables. A variety of indicator variables were tested to assess whether the inclusion of class variables would result in significant improvement in the model. These included indicators for genetic provenance, genetic families, and silvicultural treatment. In addition, interactions between variables were tested for significance in the model building process. The target set of equations was the most parsimonious model that sufficiently accounted for the variation in the diameter distribution shape and scale parameters.

**Parameter Recovery Method (PRM)**

Several variations of the parameter recovery method were tested to determine the best model. Parameter recovery methods have been used successfully for the Weibull family of functions for the diameter distribution (e.g. Rennolls et al. 1985). The initial step in each was the creation of models to predict two selected percentiles from the empirical diameter distribution. The general form of the regression equations utilized in this research is shown in Equation (7).
\[
\ln(D_p) = \beta_0 + \beta_1 \ln(\bar{BA}) + \beta_2 \ln(Age) + \varepsilon
\]  

(7)

where \( D_p \) is the \( p^{th} \) percentile of the diameter distribution, \( \bar{BA} \) is the mean basal area of the stand, \( \text{Age} \) is the age of the stand in years, and \( \varepsilon \) is the error term. Parameters for a system of two equations of this form utilizing two different percentiles of the diameter distribution were estimated using seemingly unrelated regression techniques. The predicted diameters and selected values of \( p \) were used to recover the shape parameter, \( c \), using Equation (8).

\[
\hat{c} = \frac{\ln \left( \frac{\ln(1-p_i)}{\ln(1-p_j)} \right)}{\ln(D_{\hat{p}_i}) - \ln(D_{\hat{p}_j})}
\]

(8)

where \( \hat{c} \) is the recovered two-parameter Weibull shape parameter, and \( \hat{D}_{\hat{p}_i} \) is the diameter of the \( p_i \) percentile of the diameter distribution. The results from Equation (8) were then substituted in Equation (9) to recover the scale parameter, \( b \).

\[
\hat{b} = \sqrt{\frac{(\bar{D}_{q})^2}{\Gamma(1+2/\hat{c})}}
\]

(9)

where \( \hat{b} \) is the recovered Weibull scale parameter, \( \hat{c} \) is the recovered Weibull shape parameter from Equation (8), \( \bar{D}_{q} \) is the quadratic mean diameter in cm, and \( \Gamma(\cdot) \) is the gamma function.

In addition to using the second moment (quadratic mean diameter) of the diameter distribution as in Equation (9) to recover the scale parameter, the first moment (mean diameter) was also used to determine whether any improvement in the model would result. The method of determining the scale parameter using the first moment is shown in Equation (10).
\[ \hat{b} = \frac{D}{\Gamma(1+1/\hat{c})} \]  

Equations (9) and (10) are derived from the moment generating function shown in Equation (11).

\[ M_k = b^k \Gamma(1+k/c) \]  

where \( M_k \) is the \( k^{th} \) moment.

**Percentiles Method (PCT)**

Given the need to integrate the gamma function to use the previous set of equations, a method was also tested that eliminated the use of either Equation (9) or (10). By setting \( x=b \) in Equation (5), the c.d.f. of the two-parameter Weibull distribution can be solved to determine the percentile of the distribution which is identical to the scale parameter. This proof is shown in Equation (12).

\[
F(x) = \left[ 1 - \left( \frac{b}{x} \right)^c \right] \\
= \left[ 1 - (1)^c \right] \\
= \left[ 1 - 1 \right] \\
= 1 - 0.36788 \\
= 0.63212
\]  

(12)

Therefore, the diameter value below which 63.212 percent of the individuals occur will correspond to the scale parameter of the Weibull distribution. Murthy et al. (2004) suggests that an appropriate combination of percentiles to use in determining the parameters of the Weibull distribution is the 63.212 and 31 percentiles. By using Equation (7) to predict these two percentiles, the calculation to determine the scale parameter is given by Equation (13).

\[ \hat{b} = \exp \left[ \ln \left( \hat{D}_{63.212} \right) \right] \]  

(13)
When the 63.212 percentile is used, Equation (8) simplifies to Equation (14) since

\[ \ln(1 - 0.63212) = -1. \]

\[
\hat{c} = \frac{\ln \left( -\ln \left( 1 - p_j \right) \right)}{\ln \left( \hat{D}_{63,212} \right) - \ln \left( \hat{D}_{p_j} \right)}
\]

(14)

and the shape parameter is obtained from Equation (15).

\[
\hat{c} = \frac{\ln \left( 1 - 0.63212 \right)}{\ln \left( 1 - 0.31 \right)} \left( \frac{\ln \left( \hat{D}_{63,212} \right) - \ln \left( \hat{D}_{31} \right)}{\ln \left( \hat{D}_{63,212} \right) - \ln \left( \hat{D}_{31} \right)} \right)
\]

(15)

\[ = \frac{0.99138006}{\ln \left( \hat{D}_{63,212} \right) - \ln \left( \hat{D}_{31} \right)} \]

Assessing model fit

There are several approaches to assessing the fit of the estimated parameters. One way is to compare the distribution defined by the estimated parameters to the empirical diameter distribution. Another method is to compare the estimated distribution to the MLE fitted distribution. A third way is to directly compare the estimated and MLE fitted parameters. By comparing the estimated and fitted parameters directly, the interaction of the parameters is not accounted for in defining the diameter distribution.

In this research, model fit was evaluated using a modification of the Reynolds error index. This error index was preferred to \( R^2 \) as a measure of fit as it compares the predicted diameter distribution to the empirical diameter distribution, as opposed to comparing only the predicted parameters to the fitted parameters. As proposed by Reynolds et al. (1988), the error index is shown in Equation (16).
where \( e = \text{Reynolds error index}, \ N \) is the number of trees per unit area, \( w(x) \) is a “weight” associated with a tree of diameter \( x \), \( \hat{F}(x) \) is the c.d.f. of diameters on a plot predicted by the model, and \( F^*(x) \) is the empirical c.d.f. of observed diameters on the plot. Using basal area as the weight, the error index for this study is given by:

\[
e = N \sum_{j=1}^{k} w(x_j) \left| \hat{F}(x_j) - F^*(x_j) \right|
\]

where \((x_j)\) is the centerpoint of the \( j \)th d-class, \( \hat{F}(x_j) \) is the proportion of the distribution predicted in the \( j \)th d-class, \( F^*(x_j) \) is the proportion of the distribution observed in the \( j \)th d-class, and \( w(x_j) \) is the basal area of a tree of diameter \( x_j \). One cm d-classes were used in the calculation of the error index, with the classes centered about the half-cm values, in order to avoid a d-class of different width near zero. Hence, the first d-class is the interval from zero to one, and the diameter used in calculating the basal area for the weight function was 0.5 cm.

**Results and Discussion**

Table 2 shows the percentage of surviving individuals attaining breast height by each measurement age. At age 3, 82.49 percent of individuals over all treatments had reached at least 1.37 m in height, but within the control LPT treatment, an insufficient proportion of individuals, 63.29 percent, had passed the breast height threshold to form a meaningful empirical diameter distribution. At age 4, this proportion was 89.16 percent in the control LPT treatment, and still less than desirable for modeling the diameter distribution. At age 5, 96.16 percent of individuals in those same plots were at or above breast height, and suitable
Table 2. Percent of individuals attaining breast height by age, treatment, and provenance.

<table>
<thead>
<tr>
<th>Age</th>
<th>Treatment</th>
<th>Provenance</th>
<th>Percent greater than breast height</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>Control</td>
<td>ACP</td>
<td>69.16</td>
</tr>
<tr>
<td>3</td>
<td>Control</td>
<td>LPT</td>
<td>63.29</td>
</tr>
<tr>
<td>3</td>
<td>Fertilized</td>
<td>ACP</td>
<td>98.93</td>
</tr>
<tr>
<td>3</td>
<td>Fertilized</td>
<td>LPT</td>
<td>98.97</td>
</tr>
<tr>
<td>4</td>
<td>Control</td>
<td>ACP</td>
<td>92.07</td>
</tr>
<tr>
<td>4</td>
<td>Control</td>
<td>LPT</td>
<td>89.16</td>
</tr>
<tr>
<td>4</td>
<td>Fertilized</td>
<td>ACP</td>
<td>99.73</td>
</tr>
<tr>
<td>4</td>
<td>Fertilized</td>
<td>LPT</td>
<td>99.93</td>
</tr>
<tr>
<td>5</td>
<td>Control</td>
<td>ACP</td>
<td>97.57</td>
</tr>
<tr>
<td>5</td>
<td>Control</td>
<td>LPT</td>
<td>96.16</td>
</tr>
<tr>
<td>5</td>
<td>Fertilized</td>
<td>ACP</td>
<td>99.96</td>
</tr>
<tr>
<td>5</td>
<td>Fertilized</td>
<td>LPT</td>
<td>99.96</td>
</tr>
</tbody>
</table>
for empirical diameter distributions. As expected, the fertilized plots had a greater proportion of individuals reaching breast height at younger ages. The dramatic effect of fertilization on height growth can be easily observed even at age 3 by the differences in percentages between the fertilization treatments; less than 70 percent in the control and greater than 98 percent in the fertilized treatment. Based on these results, diameter distribution modeling was begun at age 5.

In addition to the necessity of a sufficient percentage of individuals in a plot being represented in the diameter sample, a large sample was necessary to produce a reasonable empirical diameter distribution. In this study, over ages 5 to 11, the minimum plot size observed was 42 individuals of a possible 64, and the maximum number of individuals observed was 64. The mean number of observations per plot was 57.65 trees, with a standard deviation of 3.53 trees. The number of observations per plot could be biased due to the exclusion of trees forked below breast height, but in this study the effect should be minimal, since at age 10, trees forked below breast height accounted for only 0.66% of the measurement trees (0.47% in control and 0.85% in fertilized plots).

The mean of plot mean diameters, based on 90 plot means per fertilization treatment, ranged from 3.8 cm (age 5 control) to 13.3 cm (age 11 fertilized). Means of plot mean height and quadratic mean diameter were also lowest in the age 5 control plots, and highest for height in the age 10 fertilized plots (height was not measured for age 11), and quadratic mean diameter was highest in the age 11 fertilized plots. These results are summarized in Table 3. Note that at each age, the variability of plot means is greater in the control treatment than in the fertilized treatment.
Table 3. Averages of 90 plot means for diameter at breast height, total stem height, and quadratic mean diameter, by age and fertilization treatment. Height was not measured at age 11.

<table>
<thead>
<tr>
<th>Age</th>
<th>Fertilization Treatment</th>
<th>DBH (cm)</th>
<th>Height (m)</th>
<th>Quadratic Mean Diameter (cm)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Mean</td>
<td>Standard Deviation</td>
<td>Mean</td>
</tr>
<tr>
<td>5</td>
<td>Control</td>
<td>3.82</td>
<td>0.70</td>
<td>3.09</td>
</tr>
<tr>
<td>5</td>
<td>Fertilized</td>
<td>7.12</td>
<td>0.52</td>
<td>4.71</td>
</tr>
<tr>
<td>6</td>
<td>Control</td>
<td>5.04</td>
<td>0.82</td>
<td>3.67</td>
</tr>
<tr>
<td>6</td>
<td>Fertilized</td>
<td>8.98</td>
<td>0.56</td>
<td>5.80</td>
</tr>
<tr>
<td>8</td>
<td>Control</td>
<td>6.70</td>
<td>0.92</td>
<td>4.88</td>
</tr>
<tr>
<td>8</td>
<td>Fertilized</td>
<td>11.05</td>
<td>0.58</td>
<td>8.22</td>
</tr>
<tr>
<td>10</td>
<td>Control</td>
<td>8.08</td>
<td>1.06</td>
<td>6.32</td>
</tr>
<tr>
<td>10</td>
<td>Fertilized</td>
<td>12.62</td>
<td>0.68</td>
<td>10.64</td>
</tr>
<tr>
<td>11</td>
<td>Control</td>
<td>8.65</td>
<td>1.07</td>
<td>-</td>
</tr>
<tr>
<td>11</td>
<td>Fertilized</td>
<td>13.26</td>
<td>0.66</td>
<td>-</td>
</tr>
</tbody>
</table>
The Anderson-Darling goodness-of-fit statistics for each of the tested distributions are shown in Table 4. At age 10, the gamma function adequately fit 37.2 percent of plots, the lognormal fit 24.4 percent of plots, while the two-parameter Weibull fit 76.1 percent of the study plots. The Weibull family of distributions provided the best fit for these data. When choosing between the two-parameter and three-parameter Weibull function, the two-parameter Weibull distribution was preferred because of the reduction in stand information required to estimate the distribution parameters (Eriksson and Sallnäs 1987). The three-parameter Weibull has been used in a number of studies, but the location parameter has typically been estimated as a proportion of the minimum predicted diameter. The parameter recovery system presented by Lenhart (1988) set the location parameter equal to the predicted minimum diameter, and Cao (2004) predicted the location parameter as one-half the predicted minimum diameter for the maximum likelihood estimator (MLE) regression and cumulative distribution function (c.d.f.) regression techniques. In light of the young ages of the stands being modeled, inclusion of minimum diameter information, which is typically very close to zero, might not add much to the accuracy of the models and would require the use of additional stand level information for estimating the distributional parameters. As shown in Equations (18) and (19), the two-parameter Weibull p.d.f. is equivalent to setting the location parameter, \( a \), of the three-parameter Weibull p.d.f. equal to zero; hence the trade-offs for inclusion of the location parameter are not justified in this situation.

\[
f(x) = \frac{c}{b} \left( \frac{x-a}{b} \right)^{c-1} \exp \left[ - \left( \frac{x-a}{b} \right)^c \right] \quad \text{for } a \leq x \leq \infty, b > 0, c > 0
\]  

(18)
Table 4. Anderson-Darling goodness-of-fit statistic means and percent of plots adequately fit by the distribution function (alpha level = 0.15).

<table>
<thead>
<tr>
<th>Function</th>
<th>Age</th>
<th>Mean Anderson-Darling statistic</th>
<th>Mean p-value</th>
<th>Percent plots fit</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gamma</td>
<td>5</td>
<td>1.2969</td>
<td>0.0836</td>
<td>20.00</td>
</tr>
<tr>
<td>Gamma</td>
<td>6</td>
<td>1.1360</td>
<td>0.1047</td>
<td>27.78</td>
</tr>
<tr>
<td>Gamma</td>
<td>8</td>
<td>1.0286</td>
<td>0.1147</td>
<td>31.67</td>
</tr>
<tr>
<td>Gamma</td>
<td>10</td>
<td>0.9354</td>
<td>0.1373</td>
<td>37.22</td>
</tr>
<tr>
<td>Gamma</td>
<td>11</td>
<td>0.99028</td>
<td>0.1399</td>
<td>36.67</td>
</tr>
<tr>
<td>Lognormal</td>
<td>5</td>
<td>1.8496</td>
<td>0.0520</td>
<td>10.56</td>
</tr>
<tr>
<td>Lognormal</td>
<td>6</td>
<td>1.6024</td>
<td>0.0759</td>
<td>17.22</td>
</tr>
<tr>
<td>Lognormal</td>
<td>8</td>
<td>1.4237</td>
<td>0.0808</td>
<td>18.33</td>
</tr>
<tr>
<td>Lognormal</td>
<td>10</td>
<td>1.3199</td>
<td>0.1065</td>
<td>24.44</td>
</tr>
<tr>
<td>Lognormal</td>
<td>11</td>
<td>1.2618</td>
<td>0.1018</td>
<td>21.67</td>
</tr>
<tr>
<td>Two-parameter Weibull</td>
<td>5</td>
<td>0.5973</td>
<td>0.1632</td>
<td>58.89</td>
</tr>
<tr>
<td>Two-parameter Weibull</td>
<td>6</td>
<td>0.5428</td>
<td>0.1752</td>
<td>65.56</td>
</tr>
<tr>
<td>Two-parameter Weibull</td>
<td>8</td>
<td>0.4783</td>
<td>0.1874</td>
<td>71.11</td>
</tr>
<tr>
<td>Two-parameter Weibull</td>
<td>10</td>
<td>0.4586</td>
<td>0.1974</td>
<td>76.11</td>
</tr>
<tr>
<td>Two-parameter Weibull</td>
<td>11</td>
<td>0.4628</td>
<td>0.1965</td>
<td>74.44</td>
</tr>
</tbody>
</table>
\[ f(x) = \frac{c}{b} \left( \frac{x-0}{b} \right)^{c-1} \exp \left[ -\left( \frac{x-0}{b} \right)^c \right] \]

\[ f(x) = \frac{c}{b} \left( \frac{x}{b} \right)^{c-1} \exp \left[ -\left( \frac{x}{b} \right)^c \right] \text{ for } x \geq 0, b > 0, c > 0 \]  

where \( a \) is the location parameter, \( b \) is the scale parameter, \( c \) is the shape parameter, and \( x \) is a specified diameter.

The two-parameter Weibull function was also preferred to the gamma and lognormal functions computationally due to the ease of parameter estimation calculations, as well as the simplicity of application, which does not require integration to obtain proportions of the distribution.

The percentages of plots adequately fit by the two-parameter Weibull are partitioned by age, fertilization treatment, and provenance in Table 5 and Table 6. These results are also shown graphically in Figure 3, Figure 4, and Figure 5. Notice that in general the goodness-of-fit increases over time. The effects on fit due to fertilization treatment and provenance are not clear.

Following selection of the two-parameter Weibull as the most appropriate family of distributions, the parameters fit to the empirical distributions by maximum likelihood estimation were observed over time. As Figure 6 illustrates, the scale parameter is increasing in a nearly linear trend over time, with a relatively constant variance and with parallel slopes, but differing intercepts, between the control and fertilized treatments.

The shape parameter shown in Figure 7, in contrast to the scale parameter, shows very little trend over time, with a relatively constant variance, and a linear relationship with a slope very close to zero. The implication of this is that any attempt to predict the shape
**Table 5.** Percentage of empirical diameter distributions adequately fit by the two-parameter Weibull distribution function, by age, provenance, and fertilization treatment.

<table>
<thead>
<tr>
<th>Age</th>
<th>Provenance</th>
<th>Control</th>
<th>Fertilized</th>
</tr>
</thead>
<tbody>
<tr>
<td>5</td>
<td>ACP</td>
<td>55.6</td>
<td>53.3</td>
</tr>
<tr>
<td>5</td>
<td>LPT</td>
<td>51.1</td>
<td>75.6</td>
</tr>
<tr>
<td>6</td>
<td>ACP</td>
<td>75.6</td>
<td>53.3</td>
</tr>
<tr>
<td>6</td>
<td>LPT</td>
<td>62.2</td>
<td>71.1</td>
</tr>
<tr>
<td>8</td>
<td>ACP</td>
<td>73.3</td>
<td>60.0</td>
</tr>
<tr>
<td>8</td>
<td>LPT</td>
<td>75.6</td>
<td>75.6</td>
</tr>
<tr>
<td>10</td>
<td>ACP</td>
<td>68.9</td>
<td>82.2</td>
</tr>
<tr>
<td>10</td>
<td>LPT</td>
<td>75.6</td>
<td>77.8</td>
</tr>
<tr>
<td>11</td>
<td>ACP</td>
<td>66.7</td>
<td>75.6</td>
</tr>
<tr>
<td>11</td>
<td>LPT</td>
<td>73.3</td>
<td>82.2</td>
</tr>
</tbody>
</table>

**Table 6.** Percentage of empirical diameter distributions adequately fit by the two-parameter Weibull distribution function, by age and fertilization treatment.

<table>
<thead>
<tr>
<th>Age</th>
<th>Control</th>
<th>Fertilized</th>
</tr>
</thead>
<tbody>
<tr>
<td>5</td>
<td>53.3</td>
<td>64.4</td>
</tr>
<tr>
<td>6</td>
<td>68.9</td>
<td>62.2</td>
</tr>
<tr>
<td>8</td>
<td>74.4</td>
<td>67.8</td>
</tr>
<tr>
<td>10</td>
<td>72.2</td>
<td>80.0</td>
</tr>
<tr>
<td>11</td>
<td>70.0</td>
<td>78.9</td>
</tr>
</tbody>
</table>
Figure 3. Percentage of empirical diameter distributions adequately fit by the two-parameter Weibull distribution function over age (all plots).
Figure 4. Percentage of empirical diameter distributions adequately fit by the two-parameter Weibull distribution function over age, by fertilization treatment.
Figure 5. Percentage of empirical diameter distributions adequately fit by the two-parameter Weibull distribution function over age, by fertilization treatment and provenance combination.
Figure 6. Scale parameter of the MLE fitted two-parameter Weibull diameter distribution over time, by fertilization treatment.
Figure 7. Shape parameter of the MLE fitted two-parameter Weibull diameter distribution over time, by fertilization treatment.
parameter at any age will require variables that explain the variability within that age.

Effective modeling of the diameter distribution required a thorough understanding of the explanatory variables that could be used in the models. Figure 8 shows the trend of relative spacing over time, which decreases steadily over time, as should be expected. Variability within treatment of relative spacing is much lower in the fertilized treatment than in the control treatment. The relative spacing in the fertilized plots appears to be approaching the lower limit for relative spacing in loblolly pine (Lemin and Burkhart 1983).

Additional explanatory variable plots over time were also examined to determine the usefulness of transformations. Figure 9 indicates the relationship between the 95th percentile of the empirical diameter distribution and age is linear, but the variance increases over time. The natural log transformation applied to both variables as shown in Figure 10 does very little to change the linear relationship, but does stabilize the variance over time. Similarly, in Figure 11, the variance is increasing slightly over time in the control treatment. In this case, the natural log transformation of Figure 12 results in a fairly linear trend, but results in non-constant variance for the control plots over time.

In addition to understanding the behavior of variables over time, it is also necessary to explore the manner in which the variables interact with each other. Figure 13 shows the two-parameter Weibull MLE fitted scale parameter over plot mean basal area, which is clearly curvilinear. Most of the curvature occurs in the control treatment, with the fertilized treatment having a more linear trend. However, when the square-root transformation is applied to the mean basal area, both fertilization treatments become linear with only a very slight difference in the slopes of the treatments, as shown in Figure 14. The close relationship indicates that the square-root transformed basal area
Figure 8. Trend of relative spacing over time, by fertilization treatment.
Figure 9. Diameter of the 95\textsuperscript{th} percentile of empirical diameter distribution over age, by fertilization treatment.
**Figure 10.** Natural log transformed diameter of the 95th percentile of empirical diameter distribution over natural log transformed age, by fertilization treatment.
Figure 11. Diameter of the 25th percentile of empirical diameter distribution over age, by fertilization treatment.
Figure 12. Natural log transformed diameter of the 25th percentile of empirical diameter distribution over natural log transformed age, by fertilization treatment.
Figure 13. Scale parameter of the MLE fitted two-parameter Weibull diameter distribution over mean basal area, by fertilization treatment.
Figure 14. Scale parameter of the MLE fitted two-parameter Weibull diameter distribution over square-root transformed mean basal area, by fertilization treatment.
should be a very good predictor for the scale parameter, and illustrates part of the reason that scale has historically been modeled with very good precision.

A curvilinear trend very similar to that observed between the MLE fitted scale parameter and mean basal area was also observed between the 95th and 25th percentiles of the empirical distribution and mean basal area, although the variability is much greater (Figure 15 and Figure 16). A natural log transformation of both the percentiles and the mean basal area effectively linearized the relationship, with only slight differences in slopes between fertilization treatments, as shown in Figure 17 and Figure 18.

The systems of equations used for comparison with the Reynolds error index are shown in Equations (20) through (30). Equations were fitted using ages 5, 6, 8, and 10; age 11 data was excluded since only diameters were available for that age, thus not providing the height information required for the parameter prediction method. Equations (20) and (21) show the shape and scale prediction equations, respectively, from the PPM.

\[
\hat{c} = 7.08377 + 4.90044(Fert) - 7.97094(RS) - 0.34313(Fert)(Age)
\]  
\[
\hat{b} = -0.01393 + 119.02733\left(\overline{BA}\right)^{1/2}
\]

where \(\hat{c}\) is the estimated Weibull shape parameter, RS is the relative spacing as defined in Equation (3), Fert is an indicator variable for fertilization (0 if non-fertilized, 1 if fertilized), Age is the stand age in years, and \(\overline{BA}\) is the mean basal area, in square meters.

The parameter recovery equations utilizing the second moment of the distribution include Equations (22) and (23), the prediction equations for the natural log of the 25th and 95th percentiles of the distribution, as well as Equation (24) for recovering the shape parameter and Equation (25) for recovering the scale parameter.
Figure 15. Diameter of the 95\textsuperscript{th} percentile of the empirical diameter distribution over plot mean basal area, by fertilization treatment.
Figure 16. Diameter of the 25th percentile of the empirical diameter distribution over mean basal area, by fertilization treatment.
Figure 17. Natural log transformed diameter of the 95th percentile of the empirical diameter distribution over natural log transformed mean basal area, by fertilization treatment.
Figure 18. Natural log transformed diameter of the 25\textsuperscript{th} percentile of the empirical diameter distribution over natural log transformed mean basal area, by fertilization treatment.
\begin{align*}
\ln(\hat{D}_{25}) &= 6.00492 + 0.69558 \ln(\overline{BA}) - 0.22289 \ln(\text{Age}) \quad (22) \\
\ln(\hat{D}_{95}) &= 3.81682 + 0.35309 \ln(\overline{BA}) + 0.20260 \ln(\text{Age}) \quad (23) \\
\hat{c} &= \frac{2.34309}{\ln(\hat{D}_{95}) - \ln(\hat{D}_{25})} \quad (24) \\
\hat{b} &= \sqrt{\frac{\left(\overline{D}_q\right)^2}{\Gamma\left(1 + 2/\hat{c}\right)}} \quad (25)
\end{align*}

where all variables are as defined previously.

The parameter recovery method incorporating the first moment of the distribution is identical to the previous method in Equations (22) through (24), but replaces Equation (25) with Equation (26), which is derived from the first moment.

\begin{align*}
\hat{b} &= \frac{\overline{D}}{\Gamma\left(1 + 1/\hat{c}\right)} \quad (26)
\end{align*}

The percentiles method was tested using parameters estimated from Equations (27) to (30).

\begin{align*}
\ln(\hat{D}_{63}) &= 4.63220 + 0.48112 \ln(\overline{BA}) + 0.02482 \ln(\text{Age}) \quad (27) \\
\ln(\hat{D}_{31}) &= 5.68063 + 0.64533 \ln(\overline{BA}) - 0.16679 \ln(\text{Age}) \quad (28) \\
\hat{b} &= \exp\left[\ln(\hat{D}_{63})\right] \quad (29) \\
\hat{c} &= \frac{\ln\left[\frac{-1}{\ln(1 - 0.31)}\right]}{\ln(\hat{D}_{63}) - \ln(\hat{D}_{31})} \quad (30)
\end{align*}
Results from the Reynolds error index are shown in Table 7. Due to the nature of the statistic, the application of the Reynolds error index can result in highly variable magnitudes of the statistic depending upon the size of the diameter interval, or bin width. A narrower interval will produce a larger statistic compared to a statistic based upon a wider interval. Also, some error is inherent in the statistic, as the empirical distribution is restricted to whole numbers of trees in a bin of given width, while the estimated distribution is computed from proportions of the area under the curve within an interval. Parameter prediction was the best estimator of the parameters, followed by parameter recovery with the 95th and 25th percentiles using the second moment of the diameter distribution (quadratic mean diameter).

All the methods of modeling tested reveal difficulties in modeling the shape parameter for the Weibull distribution in the fertilized stands. Parameter prediction compresses the range of the shape parameter in the fertilized stands, modeling the parameter as the mean. This can be seen in Table 8, where the mean of the MLE fitted shape parameter is 7.450 and standard deviation 1.065 for the fertilized plots, and the mean of the predicted shape parameter from PPM is 7.365 and standard deviation 0.196 for the fertilized plots. The drastic reduction in variation strongly indicates a mean model. The plot of the PPM shape parameter over the MLE shape parameter in Figure 19 also indicates the presence of a mean model for the shape parameter of fertilized plots.

Much of the reason for this difficulty of parameter prediction in modeling the shape parameter may be explained by the variables used for prediction. The fertilization indicator variable can simply shift the regression line upward for the fertilized stands, and does not impact the slope of the line. The fertilization-age interaction variable changes the slope of the regression line downward for fertilized stands. Relative spacing, the best predictor of the
Table 7. Comparison of Reynolds error index to MLE fitted parameter error, in m$^2$/ha of basal area classified in wrong 1 cm d-class.

<table>
<thead>
<tr>
<th>Parameter estimation method</th>
<th>Mean Reynolds error index, m$^2$/hectare misclassified</th>
</tr>
</thead>
<tbody>
<tr>
<td>MLE fitted parameters</td>
<td>4.136</td>
</tr>
<tr>
<td>PPM</td>
<td>4.512</td>
</tr>
<tr>
<td>PRM, 95$^{th}$ and 25$^{th}$ percentiles, 2$^{nd}$ moment</td>
<td>4.795</td>
</tr>
<tr>
<td>PRM, 95$^{th}$ and 25$^{th}$ percentiles, 1$^{st}$ moment</td>
<td>4.899</td>
</tr>
<tr>
<td>PCT, 63$^{rd}$ and 31$^{st}$ percentiles</td>
<td>5.008</td>
</tr>
</tbody>
</table>

Table 8. Comparison of MLE fitted shape parameters to estimated parameters for fertilized plots through age 10. The PCT and PRM (1$^{st}$ moment) methods were not included as they were previously eliminated.

<table>
<thead>
<tr>
<th>Method</th>
<th>Mean</th>
<th>Standard Dev.</th>
<th>Minimum</th>
<th>Maximum</th>
</tr>
</thead>
<tbody>
<tr>
<td>MLE Fitted</td>
<td>7.450</td>
<td>1.065</td>
<td>5.132</td>
<td>11.615</td>
</tr>
<tr>
<td>PPM</td>
<td>7.365</td>
<td>0.196</td>
<td>6.886</td>
<td>7.971</td>
</tr>
<tr>
<td>PRM (2$^{nd}$ moment)</td>
<td>7.768</td>
<td>1.401</td>
<td>4.529</td>
<td>12.058</td>
</tr>
</tbody>
</table>
Figure 19. Plot of shape parameter from MLE fitted two-parameter Weibull diameter distribution versus shape parameter from parameter prediction method (PPM). A simple linear regression model is presented for each treatment to aid in trend visualization.
shape parameter other than fertilization treatment, does not account for variation within the fertilized treatment. An examination of Figure 20 shows there is a strong trend between relative spacing and the shape parameter in the non-fertilized plots, but virtually no trend in the fertilized plots. Figure 21 clearly shows that although relative spacing is very strongly negatively correlated with age (decreases with an increase in age) in the fertilized plots, there is virtually no relationship between relative spacing and the shape parameter at a given age.

The parameter recovery model, in contrast to the parameter prediction model, slightly inflates the range of the shape parameter. This suggested the possibility of modeling the fertilized and non-fertilized stands separately, but efforts to this end proved unsuccessful in improving the model significantly. Figure 8 indicates that the non-fertilized stands seem to be at an earlier stage of stand development, as relative spacing is still decreasing in the non-fertilized plots at age 10 while the fertilized stands are beginning to reach the asymptote for relative spacing in loblolly pine. Note again the difference in the variance of the two treatments; the fertilized stands are much less variable than the non-fertilized, and the non-fertilized are also slightly decreasing in variance over time (Figure 8).

The plot of PRM estimated versus MLE fitted shape parameter in Figure 22 shows that in the fertilized treatments, the shape parameter tends to be under-predicted by the parameter recovery method. Perhaps the most convincing evidence for preference of the PRM over the PPM is seen in Figure 23, where the distribution of the PPM shape parameter estimates is very narrow and very different from the distribution of MLE fitted shape parameter estimates from the empirical distributions. On the other hand, the distribution of the PRM shape parameter estimates is quite similar to the MLE fitted shape parameter
Figure 20. Relative spacing over the shape parameter from the MLE fitted two-parameter Weibull diameter distribution, by fertilization treatment. A simple linear regression model is presented for each treatment to aid in trend visualization.
Figure 21. Relative spacing over the two-parameter Weibull MLE fitted shape parameter, by age, for fertilized plots only. A simple linear regression model is presented for each age to aid in trend visualization.
Figure 22. Shape parameter of the diameter distribution generated by PRM over the shape parameter of the MLE fitted two-parameter Weibull diameter distribution, by fertilization treatment. Lines were fitted by simple linear regression for each fertilization treatment.
Figure 23. Distributions of the MLE fitted, PPM, and PRM shape parameters within the fertilized treatment.
distribution. Also, as evidenced by Figure 24, the PRM estimates of the scale parameter are very nearly identical to the MLE fitted scale parameter estimates.

After selection of the PRM as the preferred method, the final parameter recovery equations developed utilizing measurements from age 5 to age 11 are shown in Equations (31) through (34). The coefficients here differ from Equations (22) and (23) due to the inclusion of age 11 data, since no height information is used in this system of equations.

\[
\ln(\hat{D}_{25}) = 5.89988 + 0.68360 \ln(\bar{BA}) - 0.20221 \ln(Age) \tag{31}
\]

\[
\ln(\hat{D}_{95}) = 3.87163 + 0.35889 \ln(\bar{BA}) + 0.19035 \ln(Age) \tag{32}
\]

\[
\hat{c} = \frac{2.34309}{\ln(\hat{D}_{95}) - \ln(\hat{D}_{25})} \tag{33}
\]

\[
\hat{b} = \sqrt{\frac{(\hat{D}_q)^2}{\Gamma(1 + 2 / \hat{c})}} \tag{34}
\]

The application of these equations is discussed in the following section.

**Application**

The greatest usefulness in applying estimated diameter distributions comes from the ability to create stand tables, thereby providing information about tree frequency by size class. Utilizing the parameter recovery method, a stand table may be created from an even-aged stand of known age, mean basal area, and the number of trees per hectare. These stand-level parameters may be estimated with far greater ease in terms of sampling effort (i.e. time and monetary cost) than would be required to construct an empirical distribution.

Supplied with the stand parameters listed previously, the stand table may be generated. For this example an eight year old stand with a mean tree basal area of 0.0038 m²
Figure 24. Recovered scale parameter over MLE fitted scale parameter, by fertilization treatment.
and a density of 2100 trees per hectare will be considered. The desired diameter size class width is 2 cm.

The first step in the process is to apply Equations (31) and (32) to predict the natural logs of the 25th and 95th percentiles of the distribution as shown in Equations (35) and (36) for the given stand parameters.

\[
\ln(\hat{D}_{25}) = 5.89988 + 0.68360 \ln(0.0038) - 0.20221 \ln(8) \\
= 1.66986 \text{ cm}
\]

\[
\ln(\hat{D}_{95}) = 3.87163 + 0.35889 \ln(0.0038) + 0.19035 \ln(8) \\
= 2.26745 \text{ cm}
\]

The quadratic mean diameter of 6.96 cm is calculated from the mean basal area as given in Equation (37).

\[
\overline{D}_q = 2\sqrt{\frac{(10000 * BA)}{\pi}}
\]

These values are substituted into Equation (33) to estimate the shape parameter, as shown in Equation (38).

\[
\hat{c} = \frac{2.34309}{2.26745 - 1.66986} \\
= 3.92090
\]

The estimated shape parameter is subsequently substituted into Equation (34) to estimate the scale parameter, given in Equation.
Figure 25. Plot of the two-parameter Weibull p.d.f. using parameter recovery method (PRM) ($\hat{b} = 7.39172$, $\hat{c} = 3.92090$) for an 8 year old stand with a mean basal area 0.0038 m$^2$ and 2100 TPH.
\[ \hat{b} = \sqrt{\frac{(6.96)^2}{\Gamma(1+2/3.92090)}} \]
\[ = \sqrt{\frac{(6.96)^2}{0.88660}} \]
\[ = 7.39172 \]  

(39)

The p.d.f. for the two-parameter Weibull defined by the recovered parameters is shown in Figure 25.

The c.d.f. of the two-parameter Weibull distribution (Equation (5)), enables calculation of the percentage of the distribution less than a specified diameter. By calculating the percentages for the upper and lower bounds of a size class, the percentage within the size class may be obtained by taking the difference between the two. Using the distribution parameters estimated previously, this process is shown for the 9 cm diameter class (8 to 10 cm) in Equations (40) to (42).

\[ F(10) = 1 - \exp \left[ -\left( \frac{10}{7.38727} \right)^{3.92093} \right] \]
\[ = 0.96231 \]  

(40)

\[ F(8) = 1 - \exp \left[ -\left( \frac{8}{7.38727} \right)^{3.92093} \right] \]
\[ = 0.74506 \]  

(41)

\[ F(10) - F(8) = 0.96231 - 0.74506 \]
\[ = 0.21725 \]  

(42)

After conducting these calculations for each size class until nearly the 100th percentile of the distribution is reached, part of Table 9 can be constructed, showing the proportion of the distribution falling within each size class.
Given the number of trees per hectare, the number of trees in each size class per hectare is obtained by multiplying each proportion in Table 9 by the total number of trees per hectare, as shown in Equation (43). The resulting stand table is shown in Table 9.

\[
TPH_9 = 0.21725(2100)
= 456.2
\]  

(43)

The histogram created from the stand table, as shown in Figure 26, verifies the results of the calculations when compared to the p.d.f. in Figure 25.

**Conclusions**

In choosing a family of distributions to model diameters in juvenile pine, the results very clearly indicated that the two-parameter Weibull distribution is best suited for the task when compared to the other families considered by this study. None of the other distribution functions are as flexible at fitting a variety of shapes, as well as very easy to work with. Parameter prediction and parameter recovery techniques for distribution parameter estimation performed similarly in this study as measured by the Reynolds error index weighted by basal area. Although parameter prediction gave an overall mean error index slightly lower than parameter recovery, it is recommended that the recovery method be preferred in most instances. The first consideration is the ability of the parameter recovery method to reasonably account for the variation in the empirical parameters. The scale parameter is easily characterized by either method, as has been the case in numerous other research studies. The major modeling difficulty is with the shape parameter, which has also been fitted with less accuracy in previous work.

The fundamental difference in modeling the shape parameter is demonstrated by the mean and standard deviation of the estimated shape parameters. The parameter prediction
Table 9. Stand table for an 8 year old stand with a mean basal area 0.0038 m² and 2100 TPH.

<table>
<thead>
<tr>
<th>Diameter class (2 cm interval)</th>
<th>Proportion within diameter class</th>
<th>Number of trees in diameter class (TPH = 2100)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.00594</td>
<td>12.5</td>
</tr>
<tr>
<td>3</td>
<td>0.08034</td>
<td>168.7</td>
</tr>
<tr>
<td>5</td>
<td>0.27122</td>
<td>569.6</td>
</tr>
<tr>
<td>7</td>
<td>0.38756</td>
<td>813.9</td>
</tr>
<tr>
<td>9</td>
<td>0.21725</td>
<td>456.2</td>
</tr>
<tr>
<td>11</td>
<td>0.03646</td>
<td>76.6</td>
</tr>
<tr>
<td>13</td>
<td>0.00123</td>
<td>2.6</td>
</tr>
</tbody>
</table>
Figure 26. Histogram of diameters generated from stand table for an 8 year old stand with a mean basal area 0.0038 m² and 2100 TPH.
model is essentially a mean model for the fertilized treatments, as there is very little variability in the predictions, as was evidenced by the very low standard deviation compared to the MLE fitted shape parameters. In contrast, the recovered shape parameters are similar in dispersion to the MLE fitted parameters, although the mean and standard deviation are slightly higher than the MLE fitted parameters. Of note as well is the change in rank of methods between the fertilization treatments; the parameter recovery method performs slightly better in the non-fertilized plots.

Parameter recovery is also preferred due to the reduced number of stand-level variables required to apply the method. No height data is required, saving considerable time and money on stand measurements. In addition, knowledge of the historical silvicultural management of the stand is not needed, as this variability is captured by the basal area variable. In this study, use of genetic information was not significant in modeling the parameters of the diameter distribution. It should be noted, however, that the genetic families included in the study are typical to slightly above average performers for growth, and as such do not exhibit a great deal of variation among families in terms of basal area.
TREATMENT DIFFERENCES IN THE DIAMETER DISTRIBUTION

Introduction

Forest management of loblolly pine in the last 50 years has changed drastically. Plantation management in particular has shifted toward a more intensive level. As the nutritional requirements of loblolly pine are better understood, forest land managers are taking a more active role in managing available nutrients and ameliorating nutrient deficiencies. Given this, there is a need to understand the impact of changing silvicultural practices on forest growth and yield (Fox et al. 2007). Many studies have been undertaken to explain the effects of intensive silviculture on loblolly pine growth (see Albaugh et al. 2004, Jokela et al. 2004, Hynynen et al. 1998, and others).

In addition to improved silviculture, genetic tree improvement has forever changed plantation forestry in the Southeast United States. Through the advantageous deployment of seed sources, gains in yield may be realized by simply moving certain genetic stock (Lambeth et al. 2005, Schmidtling 2001). Inappropriate movement of seed sources, however, may result in poor growth, poor survival, and even catastrophic losses. On top of gains made from seed source movement, even greater gains have been made through intensive breeding efforts (Byram et al. 2005). As with silvicultural changes, the use of genetically improved planting stock requires an assessment of changes to forest modeling techniques (Buford and Burkhart 1987).

Loblolly pine breeding programs in the Southeast typically involve selection of superior genotypes for breeding from juvenile progeny tests. As a result, relative rankings are utilized, and lack of rank changes over time is highly desirable. Ideally, families selected for the highest growth rates as juveniles are also the highest yielding families at rotation age.
Previous research has shown that families do not change rank with respect to growth traits in loblolly pine (McKeand et al. 1997). Intensity of response to factors such as site quality or silvicultural treatments may vary, but ranks are unchanged.

This study examined the impact of an intensive fertilization regime and the use of varied genetic material on the parameters of the diameter distribution as characterized by the two-parameter Weibull distribution in plantation grown loblolly pine. Tests for statistically significant differences between mean distributional parameters of the fertilization and genetic provenance treatments were conducted, and family mean ranks within and across fertilization treatments were characterized.

**Data and Methods**

The data utilized in this study are from the SETRES-2 study site in Scotland County, North Carolina. The study, established in 1993, is a genetics by environment interaction study in the Sandhills of North Carolina. The experimental design is a split-split plot, with fertilization, genetic provenance, and genetic family treatments. See Chapter 1 for a more complete description of the study design and layout.

Maximum likelihood estimates of the two-parameter Weibull distribution were fitted to the empirical diameter distribution for each family plot within each block for each measured age. Comparisons among the MLE fitted parameters examined the three treatment effects: fertilization, genetic provenance, and genetic family. To compare the effect of the fertilization treatment at a single age, individual family plot parameters at that age were averaged across families and provenances. Tukey’s Honest Significant Difference (HSD) and Duncan’s Multiple Range Test (MRT) were applied to the resulting means to determine the presence of any significant differences. Provenance effects for each age were evaluated.
similarly, averaging all the family plots within each provenance and across fertilization treatments. Differences between provenance means were then also compared with Tukey’s HSD and Duncan’s MRT. Graphs of family mean distribution parameter values by age, within and across fertilization treatments, were examined for consistency of rank over time.

**Results**

Over all ages, the means of both the scale \((b)\) and shape \((c)\) parameters from the two-parameter Weibull were significantly different between fertilization treatments at an alpha level of 0.05 (Table 10). In contrast, only the scale parameter was significantly different between provenances, and only at ages five, six, and eight. Within fertilization treatments, only the scale parameter significantly differed, primarily in the non-fertilized treatment. A comparison of the differences in the mean diameter distribution p.d.f.s at age 11, as sorted by fertilization treatment and provenance, is shown in Figure 27. The largest effect on the distribution was clearly fertilization, with the fertilized treatments having a much higher mean, and this was reflected by the significant differences between the parameter means. Only minor differences were observed between the provenances within a fertilization treatment. With the exception of the left tails of the distributions, there was very little difference among the distributions with regard to shape. The statistical differences observed among the parameters may have been due in part to the use of the two-parameter Weibull to characterize the empirical distribution, which is a special case of the three-parameter Weibull distribution with the location parameter fixed at zero. Shifting the fertilized treatment distributions an appropriate number of units to the left would have resulted in nearly identical distributions between fertilization treatments.
Table 10. Significant differences in the parameter means for the two-parameter Weibull distribution by fertilization, provenance, and provenance within fertilization treatment using Tukey’s Honest Significant Difference ($\alpha = 0.05$).

<table>
<thead>
<tr>
<th>Age</th>
<th>Fertilization</th>
<th>Provenance</th>
<th>Provenance within fertilization</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$b$ (scale parameter)</td>
<td>$c$ (shape parameter)</td>
<td>$b$ (scale parameter)</td>
</tr>
<tr>
<td>5</td>
<td>S</td>
<td>S</td>
<td>S</td>
</tr>
<tr>
<td>6</td>
<td>S</td>
<td>S</td>
<td>S</td>
</tr>
<tr>
<td>8</td>
<td>S</td>
<td>S</td>
<td>S</td>
</tr>
<tr>
<td>10</td>
<td>S</td>
<td>S</td>
<td>NS</td>
</tr>
<tr>
<td>11</td>
<td>S</td>
<td>S</td>
<td>NS</td>
</tr>
</tbody>
</table>
Figure 27. Two-parameter Weibull diameter distribution p.d.f. of provenance-fertilization combinations at age 11 (ACP fertilized: $\hat{b}=14.1542$, $\hat{c}=6.9023$; LPT fertilized: $\hat{b}=14.1699$, $\hat{c}=7.1157$; ACP control: $\hat{b}=9.6896$, $\hat{c}=4.6397$; LPT control: $\hat{b}=9.2575$, $\hat{c}=4.4332$).
In general, family mean parameter rankings were quite stable over time for both parameters, as shown in Figure 28 through Figure 33 (see also Appendix 1). Relationships among the scale parameters in the control treatment as shown in Figure 28 remained relatively constant over the range of ages observed. Differences among families were less pronounced at age five, but families began to differentiate at age six, and ranks from age six on were very constant. Similar patterns were observed in the fertilized treatment (Figure 29) and averaged over treatments (Figure 30).

The mean shape parameter ranks within the control treatment were less constant over time, with a total of four rank changes, but were more constant over the short term, with no more than two rank changes between one measurement period and the next (two changes from age six to age eight, Figure 31). In the fertilized plots, the mean shape parameter tended to decrease over time (Figure 32), as opposed to the increasing trend observed in the control plots. Numerous rank changes also occurred over the observation period. When averaged over the fertilization treatments, the general trend in the mean shape parameter was again upward, but four rank changes occurred between ages five and 11 with no more than two rank changes between consecutive measurement periods (Figure 33).

Family mean rankings for both the scale and shape parameters typically had two rank changes within the provenance, with at least one rank change occurring within all provenance-fertilization treatment combinations. See Appendix 1 for rankings within each provenance within and across fertilization treatments. Ranks of mean parameters within provenance and across fertilization treatments are presented in Appendix 2, as well as significant differences between family mean parameters as detected by Duncan’s MRT.
Figure 28. Mean scale parameters over time by family in the control treatment. Families are ordered by value, low to high, of the scale parameter at age 5 for the control treatment.
Figure 29. Mean scale parameters over time by family in the fertilized treatment. Families are ordered by value, low to high, of the scale parameter at age 5 for the fertilized treatment.
Figure 30. Mean scale parameters over time by family over both treatments. Families are ordered by value, low to high, of the scale parameter at age 5.
Figure 31. Mean shape parameters over time by family in the control treatment. Families are ordered by value, low to high, of the shape parameter at age 5 for the control treatment.
Figure 32, Mean shape parameters over time by family in the fertilized treatment. Families are ordered by value, low to high, of the shape parameter at age 5 for the fertilized treatment.
Figure 33. Mean shape parameters over time by family over both fertilization treatments. Families are ordered by value, low to high, of the shape parameter at age 5.
Conclusions

Significant differences were present in the mean scale and shape parameters between fertilization treatments, averaged across provenances. This difference appeared to be due mainly to a shift to the right of the distribution due to fertilization. With the use of the two-parameter Weibull for fitting the empirical distribution, which constrains the location parameter of the Weibull distribution to zero, this shift forces a longer left tail on the distribution. Use of the three-parameter Weibull for fitting might result in a lack of significant differences in the scale and shape parameters between fertilization treatments, but would likely result in significantly different estimates of the location parameter.

The presence of significant differences of the scale parameter observed in the younger ages between provenances may have been due in part to the lack of variability in the stands, resulting in a test of significance more sensitive to minor differences. As the stands matured, growth differences between the provenances and fertilization treatments contributed to greater variability in the scale parameter, resulting in a test with less sensitivity to small differences.

The slightly more stable rankings and increasing trend in the scale parameter as compared to the shape parameter is not surprising. With the left tail of the distribution constrained to zero, as the stand matures and the mean diameter and maximum diameters increase, the scale parameter is forced to increase to fit the empirical distribution. Additionally, the scale parameter is very highly correlated with stand growth traits, which also vary predictably with age. The shape parameter was not linearly related to growth, and therefore age; so as the stand matures the shape parameter began to decrease. This was evidenced in the fertilized treatments, where the shape parameter tended to decrease with
time. Therefore, when growth rate differences exist among genetic families, stages of stand development will also differ at a given age, resulting in rank changes in the shape parameter.

When the two-parameter Weibull distribution is used to characterize the diameter distribution in loblolly pine, significant differences in the distribution parameters should be expected from fertilization effects. Further research with the three-parameter Weibull may restrict those differences to the location parameter. Among genetic families, family mean rankings over time may be expected to be relatively stable, especially as the stand develops and growth differences among families are more differentiated. Family mean rankings of the shape parameter should be expected to be far less stable, as the shape parameter is not linearly related to growth.
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APPENDIX 1: Within provenance two-parameter Weibull distribution family mean parameter rankings within and over fertilization treatments
Figure 34. Mean shape parameters over time of ACP families in the control treatment. Families are ordered by value, low to high, of the shape parameter at age 5 for the control treatment.
Figure 35. Mean shape parameters over time of ACP families in the control treatment. Families are ordered by value, low to high, of the shape parameter at age 5 for the control treatment.
Figure 36. Mean shape parameters over time of LPT families in the control treatment. Families are ordered by value, low to high, of the shape parameter at age 5 for the control treatment.
Figure 37. Mean shape parameters over time of LPT families in the fertilized treatment. Families are ordered by value, low to high, of the shape parameter at age 5 for the fertilized treatment.
Figure 38. Mean scale parameters over time of ACP families in the control treatment. Families are ordered by value, low to high, of the scale parameter at age 5 for the control treatment.
Figure 39. Mean scale parameters over time of ACP families in the fertilized treatment. Families are ordered by value, low to high, of the scale parameter at age 5 for the fertilized treatment.
Figure 40. Mean scale parameters over time of ACP families over both treatments. Families are ordered by value, low to high, of the scale parameter at age 5.
Figure 41. Mean scale parameters over time of LPT families in the control treatment. Families are ordered by value, low to high, of the scale parameter at age 5 for the control treatment.
Figure 42. Mean scale parameters over time of LPT families in the fertilized treatment. Families are ordered by value, low to high, of the scale parameter at age 5 for the fertilized treatment.
Figure 43. Mean scale parameters over time of LPT families over both treatments. Families are ordered by value, low to high, of the scale parameter at age 5.
**Figure 44.** Mean shape parameters over time of ACP families over both treatments. Families are ordered by value, low to high, of the shape parameter at age 5.
Figure 45. Mean shape parameters over time of LPT families over both treatments. Families are ordered by value, low to high, of the shape parameter at age 5.
APPENDIX 2: Within-provenance rankings and significant differences in the two-parameter Weibull distribution parameters
Table 11. ACP family mean rankings (descending) of the shape parameter, with line denoting families not significantly different (Duncan’s MRT, $\alpha = 0.05$).

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Table 12. ACP family mean rankings (descending) of the scale parameter, with line denoting families not significantly different (Duncan’s MRT, $\alpha = 0.05$).

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Table 13. LPT family mean rankings (descending) of the shape parameter, with line denoting families not significantly different (Duncan’s MRT, $\alpha = 0.05$).

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Table 14. LPT family mean rankings (descending) of the scale parameter, with line denoting families not significantly different (Duncan’s MRT, $\alpha = 0.05$).

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