SAMPLING AND MODELING STRATEGIES FOR ESTIMATING INDIVIDUAL TREE BIOMASS

by

SUDIP SHRESTHA

(Under the direction of Bruce E. Borders)

ABSTRACT

Estimating forest biomass is an essential aspect of carbon (C) stock estimation and global carbon balance studies. Biomass sampling strategies and estimation techniques were investigated. The first Chapter is a general discussion on biomass modeling and sampling strategies. In the second Chapter, sampling distributions of randomized branch samples were investigated based on the destructive and intensive measurement of slash pine (*Pinus elliottii*) and red maple (*Acer rubrum*) trees. In this study, biomass estimates for all possible randomized branch sampling (RBS) paths per tree were determined for each sample tree. We found that sampling distributions are more variable for red maple than for slash pine. When tested with all available trees, we found that RBS alone or RBS in combination with importance sampling (IS) procedure are not suitable for estimating biomass at individual tree level. In the third Chapter, additive systems of individual tree biomass equations were developed for both species. We found that more tree size attributes such as, diameter at breast height (Dbh), tree height (Ht) and diameter at the base of live crown provided better prediction of component biomass than using Dbh only or Dbh and Ht in the model. In the Chapter four, we developed an indirect method, which utilizes inside bark volume predicted from a taper function along with density and specific gravity information and crown component information from an explicit biomass prediction model, to estimate biomass.

INDEX WORDS: Randomized branch sampling, Importance sampling, Systems of equations, Taper/volume equation

Sampling and modeling strategies for estimating individual tree biomass

by

Sudip Shrestha

B.Sc., Trivuwan University, 2006
M.Sc., Oklahoma State University, 2010

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Sudip Shrestha

Approved:

Major Professor:	Bruce E. Borders
Committee:	Michael Kane Dehai Zhao Daniel B. Hall

Electronic Version Approved:

Julie Coffield
Dean of the Graduate School
The University of Georgia
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DEDICATION

I dedicate this dissertation to my lovely wife Binita KC, precious son Niket KC Shrestha and my supportive parents.

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Chapter 1

Introduction and literature review

1.1 Introduction

Forest ecosystems are a major part of the global carbon (C) cycle and are capable of storing large amounts of carbon in solid wood, bark, leaf and other organic matter. More than 80% of all terrestrial aboveground C and more than 70% of all soil organic C are stored in forest ecosystems (Jandl et al. 2007). Forests have both favorable and adverse roles in atmospheric CO_2 manipulation. Increases in plant biomass and organic matter accumulation in forests may reduce the total amount of CO_2 in the atmosphere, whereas atmospheric CO_2 content increases due to deforestation, dying and decomposition of trees, and burning of forest areas. Birdsey (1992) stated that because of high metabolic activities, the carbon uptake in young plant communities is higher than the mature old aged plant communities. He further explained that the amount of CO_2 release to the atmosphere depends on the types of forest products created from harvested timber. Forest products, such as furniture, wooden bridges, wood frame houses and other solid wood products, store wood based carbon for long periods (Elliot 1985). However, paper based forest products such as cardboard and various types of paper are used and discarded rapidly, and the carbon they contain is released to the atmosphere relatively quickly (Dewar 1990). Hence, the amount of carbon sequestered in forests and forest products largely depends on the forest characteristics such as growth, death and decomposition as well as the types of products that are produced from harvested trees.

Forest biomass and soils have major roles for temporary and long-term C storage (Gower 2003; Houghton 2005). In forest ecosystems, the largest quantities of aboveground biomass and C storage is found within tree biomass components, such as stem, branches, twigs, and foliage (Santa Regina and Tarazona 2001). Biomass of understory and ground vegetation, as well as of dead and dry woody debris, also provides a significant contribution (e.g. Whittaker and Woodwell 1968, Long and Turner 1975) in carbon storage in forest ecosystems. Apart from aboveground vegetation in forest ecosystems, belowground biomass such as tree root, forest floor, and mineral soil are major components of large C pools (Johnson et al. 2003, Oliver et al. 2004). It is very difficult to get a precise estimate of tree root biomass, hence C storage in tree roots is often neglected or estimated from standard root to shoot ratios (Kurz et al. 1996, Cairns et al. 1997). A study conducted by Zhang et al. (2010) found that soil C comprised of 23.8-29.6% of total forest ecosystem C.

After an absence of about 30 years from scientific research, forest biomass has regained its historical importance (Zianis and Mencuccini 2003). Forest biomass monitoring and evaluation is becoming more important because forest ecosystems play vital roles in regulating global carbon balance, and possibly mitigating global climate change (Tomppo et al. 2010). Estimation of biomass at the tree, stand and regional levels using forest inventory data is an essential component of monitoring carbon storage in forests (Kauppi et al. 1992, Nabuurs et al. 2003).

1.2 Biomass sampling strategies

Forest ecosystems are typically very large and complex. Within a given forested area there may be tens of thousands or even millions of individual trees. Consequently, it is not possible to know the characteristics of these trees with certainty. To obtain estimates of forest characteristics of interest that are comprised of many individual trees (e.g. above ground and below ground biomass and carbon storage) it is necessary to use probability sampling techniques (Shiver and Borders 1996).

Cochran (1977) described that the major benefits of sampling as compared with complete enumeration are that it's less expensive, less time consuming, and likely provides for greater accuracy of measurement. Various sampling theories and sampling procedures (simple random sampling, stratified sampling, sampling probability proportional to size etc.) have been developed. The main objective of such sampling theories is to make sampling more efficient.

During the past five decades, various sampling strategies have been developed and applied in estimating an individual tree's bark, stem, and foliage biomass or other tree characteristics, such as mineral content, bole volume, bole surface area, and bark volume of the bole (e.g. Gregoire et al. 1986, Gregoire et al. 1987, Gregoire et al. 1995, Valentine and Hilton, 1977, Valentine et al. 1984, Valentine et al. 1992, Ozcelik and Eraslan 2011). Providing an efficient and practical method of sampling to estimate biomass allows for testing current biomass models or the development of new models. There are many sampling strategies based on probability theory, specifically for tree characteristics, that have been used in ecological studies (Gregoire and Valnetine 1996). Two of the sampling procedures that have been used to estimate individual tree and component biomass are randomized branch sampling (RBS) and importance sampling (IS) (e.g. Gregoire et al. 1995, Valentine and Hilton 1977, Ozcelik and Eraslan 2012). RBS, a rigorous statistical method based on multistage probability sampling, was first applied applied to determine total number of fruits in a tree (Jessen 1955). Since then the procedure has been used to estimate various attributes of a tree, such as tree component biomass (Good et al. 2001, Williams 1989), stem length and surface area for various tree species (Gregoire and Valentine 1996), as well as aboveground carbon pools and fluxes (Bascietto et al. 2012).

Similarly, RBS with IS or IS alone has been applied to estimate biomass of an individual tree. For example, IS procedure has been employed to estimate stem volume and volume increment (Gregoire et al. 1987), RBS with IS has been used to estimate individual tree biomass (Ozcelik and Eralsan 2012).

Burrows et al. (2000) used ratio sampling to estimate individual tree biomass. Using the ratio sampling scheme, fresh weight of major tree components, including the main-stem, are taken with subsamples to determine the ratio of fresh weight to dry weight. Total dry weight is calculated simply by multiplying the ratio of dry to fresh weight with total fresh weight. Although this method provides close estimates, it requires significant manpower, equipment and cost.

1.3 volume/weight equations

As a precursor to component biomass modeling, there has been a lot of work done in individual tree taper, volume and weight modelling. Aboveground biomass and stem volume are major factors that characterize a forest productivity. For more than a hundred years, volume equations have been developed and used in estimating individual tree and stand volume. Heinrich Cotta was first to introduce the concept of a volume table around 1804 (Clark 1902). A volume table is a table showing average volume of trees, logs or sawtimber for given diameter at breast height (Dbh) alone or Dbh and tree height (Ht) or Dbh, Ht and a measure of stem form or rate of stem taper.

Individual tree volume equations are used to quantify volume of standing trees through the measurement of variables such as Dbh and total or merchantable height (Burkhart 1977). A volume equation developed by Schumacher and Hall (1933) is considered one of the earliest volume equations found in literature (Bi and Hamilton 1998). The form of the Schumacher and Hall equation serves as the basis for many modern day volume equations

$$\text{Volume} = \beta_0 + \beta_1 \text{Dbh}^2\text{Ht} \tag{1.1}$$

Note that the independent variable Dbh^2 time Ht multiplied by a constant has a geometric relationship with the volume contained in solids of various shapes (cylinder, paraboloid, cone, etc.). It has also been determined that equations used to model tree volume are also useful for modeling tree weight (and hence biomass). Traditionally, volume or weight is considered as a function of tree Dbh, Ht and a measure of tree form, and can be expressed as (Clutter et al. 1983)

$$\text{Y} = \text{f}(\text{Dbh}, \text{Ht}, \text{F}) \tag{1.2}$$

where, F is a measure of stem form. The most commonly used measure of stem form is known as a form quotient (Spurr 1052), which is a ratio of upper stem diameter at specified height to tree Dbh.

Following are the commonly used equation forms for individual tree volume and weight estimation (Clutter et al. 1983)

Table 1.1: Commonly used equation forms to estimate individual tree volumes and weights

Name of equation	Equation form
1. Constant form factor	$\text{Volume}=\text{b}_1\ \text{Dbh}^2\text{Ht}$
2. Combined variable	$\text{Volume} = \text{b}_0 + \text{b}_1\text{Dbh}^2\text{Ht}$
3. Generalized combined variable	$\text{Volume} = \text{b}_0 + \text{b}_1\text{Dbh}^2 + \text{b}_2\text{Dbh}^2\text{Ht}$
4. Logarithmic	$\text{Volume} = \text{b}_1\text{Dbh}^{\text{b}_2}\text{Ht}^{\text{b}_3}$
5. Generalized logarithmic	$\text{Volume} = \text{b}_0 + \text{b}_1\text{Dbh}^{\text{b}_2}\text{Ht}^{\text{b}_3}$
6. Honer transformed variable	$\text{Volume} = \text{Dbh}^2/(\text{b}_0 + \text{b}_1\text{H}^{-1})$
7. Form class	$\text{Volume} = \text{b}_0 + \text{b}_1\text{Dbh}^2\text{HtF}$

where, b_0, b_1, b_2 and b_3 are constants and others are as described earlier.

These equations have been used to estimate total-stem cubic-foot volumes and weights and merchantable-stem cubic-foot volumes and weights (Clutter et al. 1983). It is often necessary to estimate merchantable volume or weights to a certain upper stem diameter or height limit. Several volume and weight equations have been developed to estimate merchantable volume (Honer 1964, Burkhart 1977, Brister et al. 1980). These equations use merchantability limit as a predictor of volume hence the merchantable volume is predicted as a percentage of total volume of a tree (Honer 1964, Burkhart 1977)). For example Brister et al. (1980) developed a system of equations (Equation 1.3) that predicts total volume as well as merchantable volume of a tree.

$$\begin{aligned} V_t &= 0.00616 Dbh^{2.05779} Ht^{0.74679} \\ V_m &= V_t(1 - 0.61529 d^{3.66827} Dbh^{-3.47361}) \end{aligned} \tag{1.3}$$

Bryne and Reed (1986) stated that a system of equations to predict total and merchantable volumes to any upper stem diameter would be very useful for forest inventory work. There are two common approaches that allow for stem volume/weight estimates to any upper stem diameter limit: (1) volume ratio equations, and (2) stem taper equations.

Volume ratio equations provide the proportion of merchantable volume to total volume based on variables such as Dbh and an upper-stem diameter. Merchantable volume equations provide prediction of volume to a desired upper stem diameter. An example of a volume ratio equation based on the equation form used by Burkhart (1977) is

$$R = 1 + \beta_1 \frac{D_t^{\beta_2}}{D^{\beta_3}} \tag{1.4}$$

where, $R = \frac{V_m}{V_t}$ which is less than 1.

Equation 1.4 may be fitted using R or merchantable volume as a dependent variable

$$\mathrm{V_m} = \mathrm{V_t}(1 + \beta_1 \frac{\mathrm{D_t}^{\beta_2}}{\mathrm{D}^{\beta_3}}) \tag{1.5}$$

The term “taper” is used to express the decrease in stem diameter with increase in stem height. A taper function is an equation that is used to model stem diameter at any point on a tree starting at the base of the tree and going to the tip of the tree. The integration of a taper function from base to any specified height provides an estimate of merchantable volume to that height (Kozak et al. 1969). In addition, volume ratio equations can be derived from taper equations (Reed and Green 1984).

Most taper functions have the following general form

$$\mathrm{d} = \mathrm{f}(\mathrm{h}, \mathrm{D}, \mathrm{H}, \beta_1, \beta_2, \ldots, \beta_\mathrm{m}) \tag{1.6}$$

where,

d= stem diameter at upper-stem height h

h = height from ground to upper-stem diameter d

D= Dbh

H= total tree height, and

β_1, β_2, …, β_m are parameters to be estimated.

The relatively simple parabolic function with three parameters (Kozak et al. 1969) is an example of a simple taper function

$$\begin{aligned}\frac{\mathrm{d}^2}{\mathrm{D}^2} &= \beta_0 + \beta_1(\frac{\mathrm{h}}{\mathrm{H}}) + \beta_2(\frac{\mathrm{h}^2}{\mathrm{H}^2}) \\ \mathrm{d} &= \mathrm{D}\sqrt{\beta_0 + \beta_1(\frac{\mathrm{h}}{\mathrm{H}}) + \beta_2(\frac{\mathrm{h}^2}{\mathrm{H}^2})} \qquad (1.7)\end{aligned}$$

By using such a simple taper function the whole bole is represented with a single continuous function. If stem shape is more complex than the shape that the function can assume it may not provide an accurate representation of tree taper. Increased accuracy can be achieved by using segmented polynomial taper models that consist of a sequence of grafted sub-models representing different segments along the bole (Martin 1981, Amidon 1984). Max and Burkhart (1976) presented a three segment taper function created by splining three polynomial forms at two join points

$$\begin{aligned} d^2 &= D^2\{\beta_1(\frac{h}{H}-1)+\beta_2(\frac{h^2}{H^2}-1)+\beta_3(\alpha_1-\frac{h}{H})^2 I_1+\beta_4(\alpha_2-\frac{h}{H})^2 I_2\} \\ I_1 &= \begin{cases} 1, & \frac{h}{H} \leq \alpha_1 \\ 0, & \text{otherwise} \end{cases} \\ I_2 &= \begin{cases} 1, & \frac{h}{H} \leq \alpha_2 \\ 0, & \text{otherwise} \end{cases} \end{aligned} \tag{1.8}$$

The parameters α_1 and α_2 are called join points or inflection points and I_1 and I_2 are their associated indicator variables and all other variables are as described above. The indicator variables allow additional polynomial terms to be added in the lower bole.

Other less commonly used taper functions include within-tree variable form (or variable exponent equation), and between-tree variable form.

Ideally, volume and taper equations should be compatible that is the volumes estimated by integration of the taper function are equal to the volumes obtained from total volume or appropriate volume ratio equations (Demaerschalk 1972). As such, the accuracy and precision of volume estimates that are derived from taper equations really depend on the fit of taper equations.

1.4 Biomass Modeling

Biomass modeling is important for quantifying tree, stand and forest biomass. Estimation of forest biomass aids in assessing forest growth, quantifying carbon, and potential for bioenergy production. Various statistical models and methods have been proposed to estimate biomass at local and national scales. Of course, individual tree biomass models are the basic building block for biomass and C estimation at other scales. Individual trees are normally separated into three aboveground components: (i) bole/ main stemwood, (ii) bole/main stembark, and (iii) crown (branches and foliage). Sometimes a fourth component, belowground biomass, which is typically considered stump and major roots within a fixed distance, is considered (Parresol 2001). Recently, considerable research effort has been devoted to estimating biomass of individual trees. Most of this work makes use of the extensive knowledge base that has been accumulated through development of individual tree taper, volume and weight equations. Various individual tree biomass equations have been developed in which biomass components of a tree are related with tree size characteristics, such as diameter at breast height (Dbh), square of Dbh (Dbh^2), total tree height (Ht), product of square of Dbh and Ht, crown width, and crown length (Burkhart and Tome 2012). Biomass modeling in this study focuses on aboveground components, namely stemwood, stembark, total stem, branch, foliage, crown and total biomass.

Historically, there are three forms of equations, which have been used in individual tree biomass modeling (Parresol 1999)

$$y = \beta_0 + \beta_1 x_1 + \ldots + \beta_j x_j + \varepsilon \tag{1.9}$$

$$y = \beta_0 x_1^{\beta_1} x_2^{\beta_2} \ldots x_j^{\beta_j} + \varepsilon \tag{1.10}$$

$$y = \beta_0 x_1^{\beta_1} x_2^{\beta_2} \ldots x_j^{\beta_j} \varepsilon \tag{1.11}$$

where y is tree total or component biomass, x_j is a predictor variable (tree dimension variable), β_s are regression parameters to be estimated and ε is an error term which is identically and independently distributed with $\varepsilon \overset{iid}{\sim} N(0, \sigma^2)$. Equations 1.9, 1.10, and 1.11 are also known as linear additive error, nonlinear additive error and nonlinear multiplicative error equations, respectively.

Equation 1.9 is the simplest form of individual tree biomass estimation equations. This equation can be fitted with multiple linear regression techniques. Whereas, Equation 1.10 can be fitted using nonlinear least squares algorithms. And, Equation 1.11 can be fitted with multiple linear regression techniques after transformation to a linear function of parameters using logarithmic transformation. Equation 1.11 is the most commonly used model form for whole tree and component biomass estimation (Fehrmann and Kleinn 2006, Zianism et al. 2005). As is typical when modeling individuals of different sizes, variance in biomass components typically increase with increasing tree size. Clearly this problem needs to be accounted for with any least squares fitting technique. It often turns out that the increasing variance associated with larger trees is appropriately accounted for using the log transformation of Equation 1.11 (Burkhart and Tome 2012). The logarithmic transformed equation can be written as

$$\ln y = \ln\beta_0 + \beta_1 \ln x_1 + \beta_2 \ln x_2 + \ldots + \beta_j \ln x_j + \ln\varepsilon \tag{1.12}$$

where ln is natural logarithm. Test statistics and confidence intervals from original (model 1.11) and logarithmic transformed models are not directly comparable. It is required to take the antilogarithm of predicted values of lny to get the estimated values of y in arithmetic or untransformed units. However, when we take the antilog of lny we get the median of the skewed arithmetic distribution rather than the mean. To correct bias due to logarithmic transformation the predicted value of response variable i.e. $\hat{y}$ is calculated as

$$\begin{aligned} \hat{y} &= \exp(\hat{\mu} + \hat{\sigma}^2/2) \\ \hat{\sigma}_a^2 &= \exp(2\hat{\sigma}^2 + 2\hat{\mu}) - \exp(\hat{\sigma}^2 + 2\hat{\mu}) \end{aligned} \tag{1.13}$$

where exp is the base of natural logarithm, $\hat{y}$ is the estimated value in arithmetic units, $\hat{\mu} = \widehat{\ln y}$, $\hat{\sigma}^2$ is sample variance of the logarithmic equation, and $\hat{\sigma}_a^2$ is the estimated variance of y in arithmetic units (Flewelling and Pienaar 1981, Yandle and Wiant 1981, Sprugel 1983). It has been determined that logarithmic bias correction factors, i.e. Equation 1.13, sometimes overestimate the true bias (e.g. Madgwick and Satoo 1975, Hepp and Brister 1982). Generalized least squares (GLS) is considered as an alternative to logarithmic transformation for stabilizing error variance and obtaining asymptotically efficient parameter estimates (Burkhart and Tome 2012).

1.5 Additivity of biomass equations

Additivity of biomass is a desirable characteristic for a system of individual tree component biomass equations. That is, the logical constraint that component biomass estimates (stemwood, stembark, branch and foliage) should sum to total aboveground biomass. In addition to this, a system of additive biomass equations when estimated by taking into account the inherent correlation among the biomass components has greater statistical efficiency than separately estimated equations for individual components (Bi et al. 2004).

1.5.1 Additivity of linear biomass equations

As mentioned earlier, it is desirable that the prediction from a total tree biomass equation should equal to the sum of the predictions from individual component estimates. Parresol (1999) proposed three methods that ensure additivity of biomass equations.

1.5.1.1 Procedure 1

Procedure 1 is a simple combination approach in which the total biomass regression function is the sum of separately calculated k components biomass regression functions

$$\begin{aligned}
\hat{y}_1 &= f_1(\mathbf{x}_1^T) \\
\hat{y}_2 &= f_2(\mathbf{x}_2^T) \\
&\vdots \\
\hat{y}_k &= f_2(\mathbf{x}_k^T) \\
\hat{y}_{total} &= \hat{y}_1 + \hat{y}_2 + \ldots + \hat{y}_k
\end{aligned} \tag{1.14}$$

where $\hat{y}_1, \hat{y}_2, \ldots, \hat{y}_k$ are predicted biomass components of an individual tree and $\hat{y}_{total}$ is total predicted biomass for the tree.

Variance of prediction can be given as: $\mathrm{Var}(\hat{y}_{total}) = \sum_i^k \mathrm{Var}(\hat{y}_i) + 2\sum_{i<j}\sum \mathrm{Cov}(\hat{y}_i, \hat{y}_j)$ where $\mathrm{Cov}(\hat{y}_i, \hat{y}_j) = \rho_{y_i,y_j}\sqrt{\mathrm{Var}(\hat{y}_i)\mathrm{Var}(\hat{y}_j)}$ and ρ_{y_i,y_j} is correlation between y_i and y_j.

1.5.1.2 Procedure 2

In *procedure 2*, the same independent variables and the same weight function (if weighed least squares is used) of biomass components and total tree biomass are used. In this procedure, the sum of the regression coefficients of the component equations (the $\mathbf{b}_i$ vectors) serve as the regression coefficients of the total equation.

$$\begin{aligned}
\hat{y}_1 &= (\mathbf{x}^T\mathbf{b}_1) \\
\hat{y}_2 &= (\mathbf{x}^T\mathbf{b}_2) \\
&\vdots \\
\hat{y}_k &= (\mathbf{x}^T\mathbf{b}_k) \\
\hat{y}_{total} &= \mathbf{x}^T[\mathbf{b_1} + \mathbf{b_2} + \ldots + \mathbf{b_k}]
\end{aligned} \tag{1.15}$$

In Equation 1.15, k components $\mathrm{y_i}(\mathrm{i} = 1, 2, \ldots, \mathrm{k})$ are assumed to be independent; i.e. error terms ε_i $(\mathrm{i} = 1, 2, \ldots, \mathrm{k})$ are not correlated to each other. Regression statistics and reliability of estimates can be computed for the total equation (Chiyenda and Kozak 1984). The variance is given as $\mathrm{Var}(\hat{\mathrm{y}}_{\mathrm{total}}) = \sum_{\mathrm{i}=1}^{\mathrm{k}} \mathrm{Var}(\hat{\mathrm{y}}_\mathrm{i})$. The covariance term is dropped out since the k components are assumed to be independent.

1.5.1.3 Procedure 3

In *procedure 3*, generalized least squares (GLS) regression with a dummy variables approach is used to fit the system of equations. This approach accounts for statistical dependencies among the sample data. Sets of regression functions are calculated using GLS such that:

- each component equation has its own independent variables, and the regression function for total tree biomass is calculated as a function of all independent variables that were used in each component regression
- each component equation can have its own weight function; and
- additivity property of biomass is ensured by providing linear restrictions on the regression coefficients that we obtain from fitting each component biomass equation

Cunia and Briggs' (1984, 1985) *procedure 3* is the same as using joint generalized least squares, also known as "seemingly unrelated regression (SUR)". SUR is applicable when we have a set of linear statistical models which are contemporaneously correlated with cross-equation constraints. The system of equations in the framework of SUR with additive biomass can be specified as

$$\begin{aligned} y_1 &= f_1(\mathbf{X}_1) + \varepsilon_1 \\ y_2 &= f_2(\mathbf{X}_2) + \varepsilon_2 \\ &\vdots \\ y_k &= f_3(\mathbf{X}_k) + \varepsilon_1 \\ y_{total} &= f_{total}(\mathbf{X}_1, \mathbf{X}_2, \ldots, \mathbf{X}_k) + \varepsilon_{total} \end{aligned} \tag{1.16}$$

The redundant columns in f_{total} are not included. When linear restrictions in the models and stochastic properties of the error vectors are specified, the structural equations produce a statistical model which provide efficient parameter estimates and reliable prediction intervals.

Procedure 3 is considered as the best approach among the three procedures discussed above for estimating parameters for a system of equations. *Procedure 2* requires the assumption of independence among components on the same tree, which is unrealistic. In *procedure 2* the issue of multicolinearity would be a problem due to use of the same predictor variables in all equations in a system.

1.5.2 ADDITIVITY OF NONLINEAR BIOMASS EQUATIONS

Parresol (2001) provided two procedures for forcing additivity for nonlinear models. The procedures are unique based on how the separate components are aggregated.

1.5.2.1 PROCEDURE 1

In this approach the additivity property is ensured by summing the component regression functions to produce the total biomass function. The equation structure of this procedure is given as

$$\begin{aligned}
\hat{y}_1 &= f_1(\mathbf{X}_1, \mathbf{b}_1) = \\
\hat{y}_2 &= f_2(\mathbf{X}_2, \mathbf{b}_2) = \\
&\vdots \\
\hat{y}_k &= f_k(\mathbf{X}_k, \mathbf{b}_k) = \\
\hat{y}_{total} &= \hat{y}_1 + \hat{y}_2 + \ldots + \hat{y}_k \qquad (1.17)
\end{aligned}$$

1.5.2.2 PROCEDURE 2

Procedure 2 is a nonlinear case of SUR. In this approach, statistical dependencies among sample data are accounted for by using nonlinear joint generalized least squares regression, which is also known as nonlinear seemingly unrelated regressions (NSUR). The NSUR approach originally developed for equation systems used for whole stand growth and yield modelling by Borders (1987) and adapted to individual tree biomass equation systems by Parresol (2001) has the same properties as in *procedure 3* of additivity of linear biomass equation described above. This procedure allows that (i) component regressions have their own independent variables (ii) total tree regression uses all predictors that were used in component regressions (iii) component regression can have their own weight function and (iv) additivity property is satisfied by allowing constraints in regression coefficients. The equation form of NSUR can be written as

$$\begin{aligned}
y_1 &= f_1(X_1, \beta_1) + \varepsilon_1 \\
y_2 &= f_2(X_2, \beta_2) + \varepsilon_2 \\
&\vdots \\
y_k &= f_k(X_k, \beta_k) + \varepsilon_k \\
y_{total} &= f_{total}(X_1, X_2, \ldots, X_c, \beta_1, \beta_2, \ldots, \beta_c) + \varepsilon_{total} \qquad (1.18)
\end{aligned}$$

When stochastic properties of the error vectors are specified in conjunction with coefficient restrictions, the statistical model provides efficient parameter estimates and reliable prediction intervals (Burkhart and Tome 2012). The NSUR procedure accounts for the contemporaneous correlations (correlation among errors in different equations) providing lower variance (Borders 1989, Parresol 2001).

Although many studies have suggested using Dbh only as an independent variable to estimate individual tree component biomass (Ter-Mikaelian and Korzukhin 1997, Clough and Scott 1989), others point out that making use of both Dbh and Ht will improve these estimates at the tree level as well as at larger regional and national scale (Jenkins et al. 2003). Lambert et al. (2005) developed two sets of equations: (i) Dbh based and (ii) Dbh and Ht based systems of equations. Several studies suggested that using height as an additional predictor, does not have significant change in predictive ability than Dbh only based biomass equations (e.g. Ter-Mikaelian and Korzukhin 1997, Johansson 1999, Jenkins et al. 2003). Parresol (1999) found height as a useful variable to predict stem wood, but not for stem bark. Similarly, Lambert et al. (2005) and Bi et al. (2004) found tree height is an important variable for stem component equations, but not for crown component equations. Likewise, Pitt and Bell (2004) and Ter-Mikaelin and Parker (2000) found that use of tree height did not improve the predictive ability of needle and branch biomass models. However, they also found height as an important variable for predicting stem biomass.

1.6 OBJECTIVES

The broad objective of this study was to determine appropriate sampling strategies and modeling approaches to estimate individual tree and component biomass. Specifically, in Chapter 2, we evaluated sampling distribution of randomized branch samples and utilized RBS and combination of RBS and IS to estimate tree total biomass. In Chapter 3, additive biomass models for red maple and slash pine were developed. This procedure is also known as direct approach of estimating biomass. Two data sets, one from a UGA study and the other from previous studies (Legacy data) were utilized separately, to develop system of equations for both species. The UGA system of equations was tested against the legacy data and vice-versa for both species. Finally, in Chapter 4, we utilized revised versions of the compatible taper and volume model developed by Fang et al. (2000), to estimate tree and component biomass.

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CHAPTER 2

SAMPLING STRATEGIES FOR ESTIMATING INDIVIDUAL TREE TOTAL BIOMASS (WOOD AND FOLIAGE) : RANDOMIZED BRANCH SAMPLING WITH AND WITHOUT IMPORTANCE SAMPLING

2.1 INTRODUCTION

Estimating forest biomass is an essential aspect of carbon (C) stock estimation and global carbon balance studies. Forest ecosystems store about 80% of all above-ground and 40% of all below-ground terrestrial organic carbon (IPCC 2001). Study of forest biomass is important in the study of ecosystem productivity, energy and nutrient flows, standing tree carbon and the effect of forestland dynamics on the global carbon cycle (Parresol 1999). Many techniques have been applied for sampling and subsampling trees for biomass estimation. Selection of sampling technique is controlled by many factors, for example, size of sampling area, accuracy required, availability of time, money and manpower, tree species and tree attributes of interest.

Commonly, sampling methods known as nondestructive and destructive sampling are used for measuring sample tree biomass. A nondestructive method does not require tree felling for estimating tree biomass (Montes et al. 2000). This method is generally applied when the species of interest are rare and cannot be destructively sampled (Brown 1997, Montes et al. 2000). Destructive sampling requires sample tree felling and direct measurement of various characteristics such as stem and crown weight.

Direct measurement of individual trees and their components is the most accurate method of quantifying above-ground tree biomass. However, direct measurement of stem, foliage, and bark biomass is tedious, laborious and very costly. As a result simple allometric equations are used to estimate total tree or component biomass. Fitted allometric equations are useful in estimation and prediction of characteristics such as total tree, stem, foliage, bark , and root biomass. However, fitted allometric equations are data dependent. Equations fitted to data of one particular area or region may not work well for other geographic regions (Gregoire et al. 1995). Hence sampling strategies, such as randomized branch sampling (RBS), and importance sampling (IS), that do not require regression equations to estimate biomass may be useful for biomass estimation across various site conditions.

As discussed above, direct measurement of whole tree and tree component biomass is cumbersome and time consuming therefore, sub-samples are often collected and used to quantify fresh weight, dry weight, and volume of individual trees and tree components (Montes et al. 2000). Selection of sub-samples varies with sample design. Example sample designs that have been applied to select the sample are simple random sampling, systematic sampling, and stratified random sampling (Temesgen et al. 2010). These sampling designs are considered as simple approaches as they require only easily measured information such as counting and identifying branches (Temesgen et al. 2010). Other examples of sampling designs, which use sampling protocols that require detailed auxiliary information about the branch characteristics (Temesgen et al. 2010) are randomized branch sampling (RBS), importance sampling (IS) and probability proportional to size (PPS) sampling.

This chapter provides insight into RBS and RBS in conjunction with IS sampling strategies. The purpose of these methods is to reduce the amount of work required to estimate total tree biomass by selecting and obtaining detailed data for a portion of the tree rather for the entire tree. The objectives of this study are to: (i) obtain tree biomass estimates for all possible RBS paths for sample trees for which we have direct measurement of total tree biomass (ii) investigate the sampling distribution of RBS estimates using all possible combination of different numbers of paths (iii) investigate the number of RBS paths required to obtain reliable and unbiased estimates of wood and foliage weight and its variance by species and (v) implement and evaluate the efficacy of RBS in combination with IS to estimate individual tree biomass. Unlike previous studies, this study uses a larger number of sample tree data to evaluate these methods.

2.2 Materials and Methods

2.2.1 Randomized branch sampling (RBS)

Randomized branch sampling (RBS), a special type of multistage probability sampling, was first introduced by Jessen (1955) to quantify number of fruits on a tree. RBS has been used to estimate different characteristics of individual trees or any other type of branch bearing plants. The major objective in applying RBS is to determine a total quantity for a tree or a branch. RBS, as well as other sampling methods, such as importance sampling (IS) (Gregoire et al. 1986, 1987, 1995), Centroid sampling (Wood et al. 1990) and a combination of these methods (Williams and Wiant, 1998), use a conditional probability sampling scheme for tree and branch populations using easily available individual tree attributes such as branch diameter and branch length, to develop unbiased and efficient estimates (Bascietto et al. 2012). The sampling scheme in RBS is design-unbiased, meaning the average estimated value from all possible samples is equal to the population parameter (Gregoire et al. 1995). RBS is easily extended from individual tree level to stand-level, in which selection of sample trees is done with unequal probability (Gove et al. 2002, Snowdon et al. 2002).

Valentine and Hilton (1977) applied RBS to determine biomass, surface area and number of leaves on Quercus species. The sampling scheme was carried out in two stages. In the first stage, the total number of leaf clusters was determined on the selected branch. In the second stage, average number of leaves, average dry weight, and average surface area per cluster were estimated from systematically selected clusters. Finally, by combining the estimates from the two stages, tree level estimates of total number of leaves, leaf dry mass, and leaf surface area were calculated.

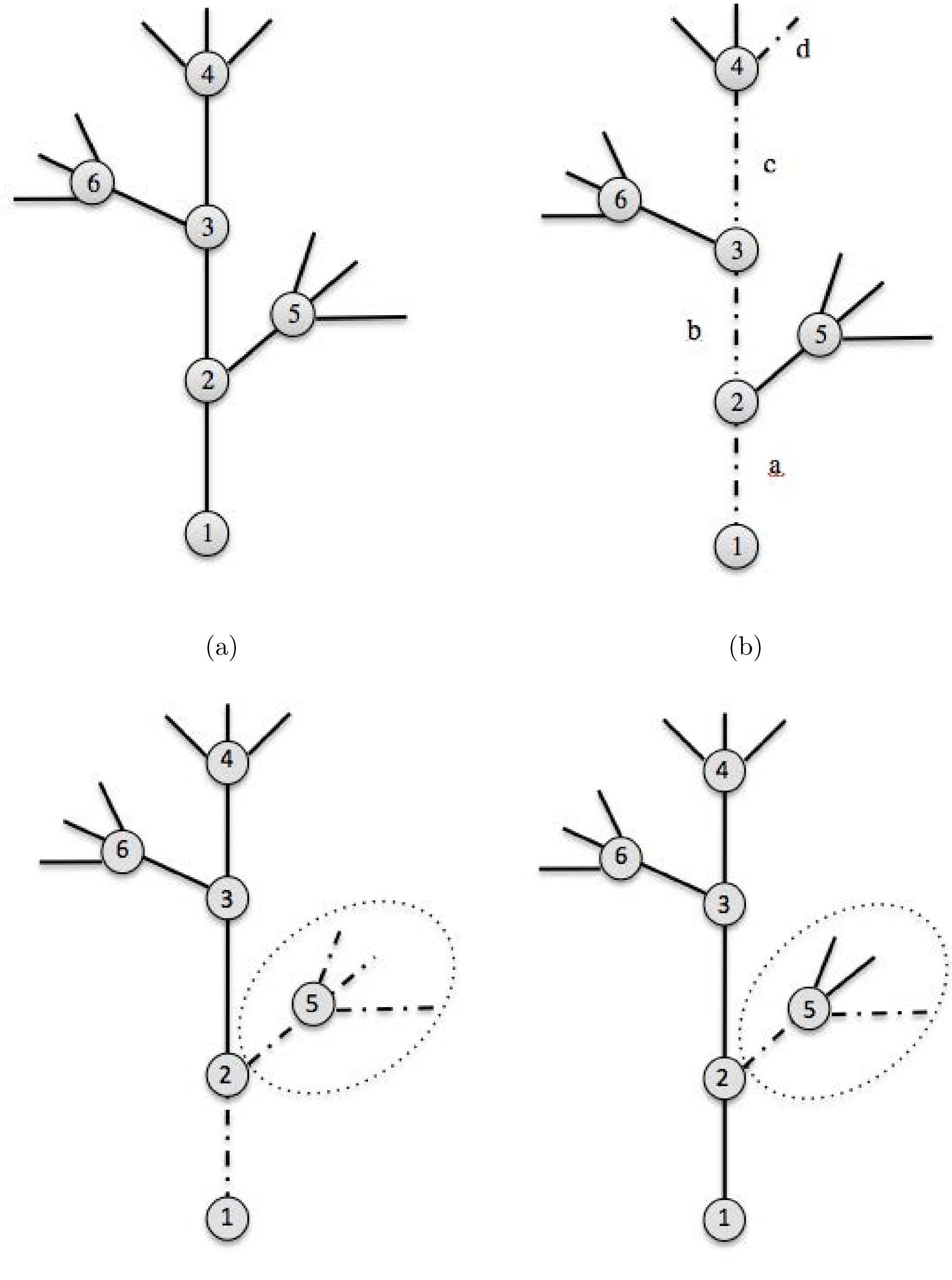
Valentine et al. (1984) used RBS and importance sampling (IS) to determine individual tree aboveground biomass, woody volume, and mineral content. For both RBS and IS techniques, they used selection probability proportional to estimated size. They further discussed that RBS and IS can be employed separately or combined together in such a way that measurements taken on a single disk would be sufficient to estimate the aboveground woody components of a tree. They performed a field test of RBS and IS with eight trees from a mixed oak stand. One to four paths on a tree were selected where a path was terminated when a 5 cm or smaller diameter was reached. For the purpose of IS they used only one disk per path. Sampling error from their field test ranged from 5.6 to 14.4% of the actual green weights of the trees and the overall sampling error from all the trees was relatively small (4.9 %).

Gregoire et al. (1995) proposed a variety of sampling methods including RBS to estimate foliage and other attributes of individual trees. Bascietto et al. (2012) used RBS for direct assessment of the aboveground carbon pools, fluxes and plant surface areas in three European forests. They pointed out that RBS is less time-consuming than other traditional sampling schemes because it requires fewer sample branches to achieve the target precision levels.

2.2.1.1 Terms used in RBS

Commonly used terminology in RBS include ‘branch’, ‘branch segment’ or simply ‘segment’, ‘object branch’, and ‘path’. A ‘branch’ is known as the entire system that develops from a single bud (later or terminal) whereas a ‘branch segment’ is a part of branch between two consecutive nodes. Node is considered a point from where branches arise. All side branches including segments of the main stem are considered as a branch for the purpose of RBS. An ‘object branch’ is considered as a branch (or tree) for which we need an estimate of the quantity of some attribute or characteristic. The ‘path’ is a sequence of connected branch segments or internodes. The total number of possible paths in a tree is actually the total number of terminal shoots. The path is a sample that results from a RBS scheme.

Figure 2.1, a modified form of Valentine (2002), (a) shows 9 possible paths from the butt of the main stem (node 1) to a terminal shoot. The numbered circles are the nodes. There are 6 nodes and 14 branch segments in total. Figure 2.1 (b) shows one possible path (dotted lines) with 4 branch segments (a, b, c, d) selected. Any node can be selected as a final node of RBS. In Figure 2.1 (c) , node 2 is considered as the final node and the entire component of the branch emanating from the node 2 is considered as the terminal segment of the path. RBS can be started from the butt of any branch. For example, Figure 2.1 (d) shows that the RBS is started from node 2. In such case estimates obtained is of the entire branch, not the entire tree.



(a) (b)

(c) (d)

Figure 2.1: Tree diagram with branch segments, nodes, and a possible path in RBS.

2.2.1.2 RBS PROCEDURE-PATH SELECTION

For the purpose of RBS, a tree comprises two distinct elements, segments and decision nodes. RBS sampling procedure starts from the butt of the basal segment object branch, which is also known as the first node of the path. The basal segment is considered as the first segment of the path. The first segment is the part of branch between first node (butt) and second node (the first whorl of live branches). Similarly, the second segment of the path extends from second node to third node, and so on for other segments. The last (n^{th}) segment of the path extends from the nth node (last node) to the terminal bud. This last segment is the same as branch (Valentine et al. 1984). The total number of terminal branches in a tree, in fact, represents the number of possible paths within that tree.

Using RBS, selection of a path is made in such a way that resultant segments of the path comprise a probability sample of an entire branch or tree. As described above, the starting point of the path is the butt of the first segment of the path. By convention, the probability of selection of the first segment of the path is denoted by q_1 and equals to one. The first segment is followed acropetally to the second node. To determine a path, a selection probability is assigned to each branch arising from the second node and one of the branches is chosen randomly with probability proportional to this probability. The randomly selected branch on the second node has selection probability denoted as q_2. The selected branch fixes the second segment of the path (Valentine et al. 1984). After the selection of the branch at the second node, we follow the second segment to a third node where a selection probability is assigned to each branch emanating from the third node and one is selected with probability proportional to this probability. The selection probability of the randomly selected branch at the third node is denoted as q_3. The selection of this branch fixes the third segment of the path. This procedure is repeated until a terminal shoot is selected at the final R^{th} node with selection probability q_R.

Ozcelik and Eraslan (2012) also explained a RBS path selection procedure in which a main stem is selected as a first branch at each node. And the remaining branches emanating from the node are considered in a clockwise direction around the node, first choosing the branch arising from the node on the left side of the main stem, facing towards the top of the tree. The selection probability of each branch is computed and compared with the previously drawn uniform (0,1) random number. Beginning with main stem, if the selection probability of the main stem is greater than or equal to the random number, the path continues along the main stem up to a main-stem diameter of less than or equal to 5 cm (Williams 1989). If the selection probability of the main stem is found to be less than the random number, the selection probability of the second branch at the same node is added to the selection probability of the first branch at the node. If this sum is greater than the random number, then the second branch is chosen for sampling and measurement is done. If the sum of selection probabilities of the first and second branch is smaller than the random number, the selection probability of the third branch is added, and the process is continued until the selection probability is greater than the random number and a branch is selected at a node. If one of the branches at a node is chosen, the path is stopped with the selection of that branch. This selected branch is flagged and labeled and the process of selecting a second path started (Williams 1989).

Gregoire and Valentine (1996) discussed that we do not necessarily need to select the butt of the main stem as the starting point of a path and terminus of a path as a terminal shoot. The starting point of a path, for example, can be a butt of a first-order branch and terminus can be a terminal shoot. In this case, using RBS we get the estimate of quantity of interest only for the entire first order branch rather than for the entire tree. Or, paths may extend from the butt of the main stem to a high-order branch, in which case the entire high-order branch is considered as the terminal segment of the path.

2.2.1.3 RBS PROCEDURE-SELECTION PROBABILITIES

Gregoire and Valentine (2008) described the selection probabilities assigned to branches emanating from nodes as conditional probabilities because the branch selection at the node is conditioned upon the path reaching the node from which the branch arises. The unconditional probability of selection of the $\mathrm{r^{th}}$ (r=1,2, . . . , R) branch segment included in the path is given by

$$\begin{aligned} \mathrm{Q_r} &= \mathrm{q_1 \times q_2 \times \cdots \times q_r} \\ &= \prod_{\mathrm{k=1}}^{\mathrm{r}} \mathrm{q_k} \end{aligned} \tag{2.1}$$

where; $\mathrm{Q_r}$ is the unconditional selection probability for the $\mathrm{r^{th}}$ segment of the path and $\mathrm{q_r}$ is the selection probability of the selected branch at the $\mathrm{r^{th}}$ node. Here R is the number of segments in the path.

In general, the conditional selection probability of the $\mathrm{r^{th}}$ segment of an $\mathrm{i^{th}}$ path can be denoted by $\mathrm{q_{ir}}$. Then, the unconditional selection probability for the $\mathrm{r^{th}}$ segment of the $\mathrm{i^{th}}$ path can be written as

$$\mathrm{Q_{ir}} = \prod_{\mathrm{k=1}}^{\mathrm{r}} \mathrm{q_{ik}}, \quad \mathrm{r} = 1, 2, 3, \ldots, \mathrm{R} \tag{2.2}$$

An important aspect to note in RBS is, for each node, the sum of the selection probabilities assigned to branches emanating from the nodes equals one. Assignment of selection probabilities is based on what is being estimated.

Jessen (1955) provided three methods of calculating selection probabilities; namely “probabilities equal”, “probabilities proportional to number”, and “probabilities proportional to area”. In the “probabilities equal” method (also known as a uniform random selection of a branch), all potential sample branches are identified and numbered prior to sampling. Out of all the potential sample branches, a previously determined number of branches are randomly selected with equal probability. With this scheme Jessen (1955) first, averaged the number of oranges in the selected branches and secondly, this averaged value was multiplied by the total number of branches in the tree to obtain the total number of oranges in the tree. This selection method requires identifying and counting all the branches in a tree, which sometime are difficult and laborious tasks. Jessen (1955) proposed RBS, which does not require a complete enumeration of branches in a tree, with this first method of calculating selection probabilities. This procedure of selecting branches uses equal probabilities, where the unconditional probability of selecting any given terminal branch i is given as

$$\mathrm{Q_i} = \frac{1}{\mathrm{M}} \tag{2.3}$$

where M is number of terminal branches.

The second method was "probabilities proportional to number", where the numbers of branches arising from a particular node are the basis for deriving conditional selection probabilities. For example, if we count 5 branches emanating from a given node, the conditional selection probability for each branch is $\frac{1}{5}$. The unconditional selection probability for the terminal branch, which is the product of the conditional probabilities at all R nodes within a path, can be written as Equation 2.1. This method of selecting branches provides unequal unconditional selection probabilities for the M terminal branches.

The third method provided by Jessen (1955) was "probabilities proportional to area", where he used the square of circumference of each branch directly above the forking to obtain the branch selection probabilities. Similar to the second method, the product of all probabilities within a path provides the unconditional branch selection probability. The conditional probabilities in this sampling scheme are derived as

$$\mathrm{q_r} = \frac{\mathrm{c_r^2}}{\sum_{\mathrm{k=1}}^{\mathrm{n_r}} \mathrm{c_k^2}} \tag{2.4}$$

where,

$\mathrm{c_r}$ = circumference of branch of the $\mathrm{r^{th}}$ segment in a RBS path,

c_k = branch circumferences of the n_r segments emanating from node r

-c_r is also one of the c_k.

Jessen (1955) found the “probability proportional to area” selection method as the best method because it produced the least variability in estimates among all three methods.

Higher precision estimates can be obtained by choosing conditional selection probabilities proportional to the quantities of interest borne by the respective branches from a decision node (Gregoire et al. 1995). Valentine (2002) discussed the ideal selection probability of a b^{th} of B branches at a particular node should equal $\frac{X_b}{\sum_{i=1}^{B} X_i}$, where X_b (b=1,2,. . . , B) is the quantity of interest that we want to estimate (e.g. biomass) borne by branch b. In general, however, it is difficult to discern the quantity of interest, otherwise, we would not be taking a sample (Valentine 2002). It would be wise to choose tree attributes such as branch diameter (D), branch length (L), power of these (e.g. D^u, L^v) , or product (eg. $D^u * L^v$) which are highly correlated with the quantity of interest (Valentine 2002). Here, powers u and v are numbers such as 2, 3. RBS results in unbiased estimates regardless whatever power is used, however , it is recommended to use a value that is biologically justifiable and produces precise estimates (Pearce and Holland 1957).

Valentine et al. (1984) described if, for example, we want to quantify woody biomass, wood volume, or total biomass of an individual tree, the ideal probability of selection assigned to each branch should be equal to the fraction of total woody biomass, wood volume or total biomass, respectively, beyond the node and contained in the branch. Similarly, if our main objective is to estimate foliar biomass, the ideal selection probability assigned to each branch should be equal to the fraction of the total biomass of foliage beyond the node and attached to the branch.

Valentine et al.(1984) suggested using selection probabilities proportional to the product of squared branch diameter and branch length to estimate woody biomass, woody volume or total biomass of a tree. The product of squared branch diameter and branch length is related to the volumes and weights of the branches. For a particular node, the probability of selection p can be expressed as $\mathrm{p} = \frac{\mathrm{D_i^2 L_i}}{\sum_{\mathrm{i=1}}^{\mathrm{n}} \mathrm{D_i^2 L_i}}$, where, D and L are diameter at the branch base and length for a branch, respectively and i is from 1 to n branches at the node. Some other alternatives for assigning selection probabilities are subjective probabilities proportional to ocular estimates of woody biomass or volume, use of probability proportional the cube of diameter etc.

While estimating biomass of foliage, a pipe model theory developed by Shinozaki and others (1964) can be applied to assign a selection probability (Valentine et al. 1984). The pipe model theory suggests that the branch foliage is related to squared diameter of the branch. Therefore, for a particular node, a selection probability for each branch can be assigned as the reciprocal of its own squared diameter and the sum of the squared diameters for all the branches arising from the node. The probability of selection can be expressed as $\mathrm{p} = \frac{\mathrm{D_i^2}}{\sum_{\mathrm{i=1}}^{\mathrm{n}} \mathrm{D_i^2}}$, where D and i are as described above.

2.2.1.4 RBS estimation

Once a RBS path has been fully determined, the tree attributes of interest are measured on each of the selected segments within the path (Gregoire and Valentine 2008). Let $\mathrm{y_r}$ be the quantity of a characteristic of interest (e.g. biomass) measured on the $\mathrm{r^{th}}$ branch segment of a path, an unbiased estimator of the total amount of the characteristic of interest, say Φ, of all branches arising from the first node of the path is given by

$$\begin{aligned} \hat{\Phi} &= \frac{\mathrm{y_1}}{\mathrm{Q_1}} + \frac{\mathrm{y_2}}{\mathrm{Q_2}} +, \ldots, + \frac{\mathrm{y_R}}{\mathrm{Q_R}} \\ &= \sum_{\mathrm{r=1}}^{\mathrm{R}} \frac{\mathrm{y_r}}{\mathrm{Q_r}} \end{aligned} \tag{2.5}$$

where, r= 1,2,. . . ,R branch segments at a node and $\mathrm{Q_r}$ is as in Equation 2.1. Here, $\mathrm{Q_1}$=$\mathrm{q_1}$=1, $\mathrm{Q_2}$=$\mathrm{q_1} \times \mathrm{q_2}$, $\mathrm{Q_3}$=$\mathrm{q_1} \times \mathrm{q_2} \times \mathrm{q_3}$ and so on.

As described above, it is necessary to select more than one path in order to get the variance of the estimator (Gregoire and Valentine 2008). Suppose $\hat{\Phi}_i$ is the estimate from path i for $i = 1, 2, \ldots, m$ paths within a tree, where $\hat{\Phi}_i$ is calculated using Equation 2.5 for i^{th} path, then an unbiased estimator of the tree level total for the variable of interest is:

$$\hat{\hat{\Phi}} = \frac{\hat{\Phi}_1 + \hat{\Phi}_2 +, \ldots, + \hat{\Phi}_m}{m} = \frac{1}{m} \sum_{i=1}^{m} \hat{\Phi}_i \tag{2.6}$$

and an unbiased estimate of variance of $\hat{\hat{\Phi}}$ is given by

$$\mathrm{Var}(\hat{\hat{\Phi}}) = \frac{1}{m(m-1)} \sum_{i=1}^{m} (\hat{\Phi}_i - \hat{\hat{\Phi}})^2 \tag{2.7}$$

provided $m \geq 2$.

When more than one path is selected per tree, the number of segments in one path may be different from number of segments in another path. Hence, the conditional and unconditional probabilities of selection of the segments may also vary by path (Gregoire and Valentine 1996). We sometimes write q_{ri} and Q_{ri}, respectively, to denote conditional and unconditional probabilities of selection of the r^{th} segment in the i^{th} path.

Gregoire and Valentine (1996) suggested excluding the measurement of small epicormic branches or spur shoots when selecting paths, otherwise the variance of $\hat{\hat{\Phi}}$ will be inflated unnecessarily. To avoid bias resulting from excluding small branches in the selection of a path, its characteristic of interest is considered part of the characteristic from the branch segment to which it is associated.

2.2.2 IMPORTANCE SAMPLING (IS)

Valentine et al. (1984) were first to apply importance sampling in forestry. IS, which is a continuous analogue of sampling discrete units with probability proportional to size (pps), is based upon a Monte Carlo integration technique. This sampling technique allows for estimation of tree biomass by selecting disks which results in unbiased estimates and also reduces work by eliminating need to section and weigh the heavy segments of a path. In fact, a single disk can be selected and weighed for each path (Valentine et al. 1984).

In IS, the stem diameter of the tree is measured at various points along the path from the butt (first node) to a point where the tip is cut. Measurements such as diameter, distance from the butt, and the path segment number are recorded. We can calculate a quantity proportional to the inflated cross-sectional area of the stem at each measured diameter as

$$\mathrm{A}(\mathrm{L_s}) = \frac{\mathrm{D}(\mathrm{L_s})^2}{\mathrm{Q_k}} \tag{2.8}$$

where, $\mathrm{D}(\mathrm{L_s})$ is the stem diameter on the segment of the path at a distance $\mathrm{L_s}$ from the butt and k is used to denote the path segment in which $\mathrm{L_s}$ occurs. To calculate the quantity proportional to the inflated woody volume of the path, the following equation is used

$$\mathrm{V}(\lambda) = \int_0^{\lambda} \mathrm{S}(\mathrm{L})\mathrm{dL} \tag{2.9}$$

In calculating inflated woody volume of the path, an interpolation S(L) is fitted to values of $\mathrm{A}(\mathrm{L_s})$ and is integrated over the length λ.

An exact location, say ϑ, on the path to cut a disk is selected at random with probability proportional to S(L). The point, ϑ is selected such that $\mathrm{V}(\vartheta) = \mathrm{uV}(\lambda)$, where u is a randomly generated number from a uniform distribution (0,1). In the next step, the disk is cut at $\mathrm{L} = \vartheta$ and the fresh weight per unit thickness of the disk cut, say $\mathrm{B}(\vartheta)$, is determined. Equation 2.10 is used to determine inflated weight per unit thickness of the disk

$$\mathrm{B}^*(\vartheta) = \frac{\mathrm{B}(\vartheta)}{\mathrm{Q_k}} \tag{2.10}$$

where, k is an index to represent the path segment in which ϑ occurs. Finally, the estimate of the inflated weight of the path and the actual woody weight of the tree is calculated as

$$\widehat{\mathrm{W}} = \frac{\mathrm{B}^*\vartheta \times \mathrm{V}(\lambda)}{\mathrm{S}(\vartheta)} \tag{2.11}$$

If cross-sectional area at ϑ is entered in Equations 2.10 and 2.11, we will get an unbiased estimate of the woody volume of the tree (Valentine et al. 1984). Similarly, the estimation of weight of other quantities of interest for the tree can be accomplished by obtaining the measurement of appropriate weight per unit length at an exact point, ϑ, and using Equations 2.10 and 2.11.

The estimated total weight of a tree, $\hat{b}$, which includes inflated weight of the terminal branch and inflated weights of all remaining small shoots and foliage associated with the path is given as

$$\hat{b} = \widehat{W} + \frac{b_j}{Q_j} + \sum_{k=1}^{j-1} \frac{e_k}{Q_k} \tag{2.12}$$

where b_j is weight of the terminal branch j and e_k is the weight of the small shoots and foliage associated with the k^{th} segment of the path (Valentine et al. 1984).

Valentine et al. (1984) interpolated $A(L_s)$ with a segmented linear function to get the values between the measurements at various distances such as L_1, L_2,...,L_t. In this case $L_1=0$ at the butt and $L_t=\lambda$, which is the total length. An integration to get a value of V(L) is done piece by piece using Smalian's formula also known as the trapezoidal rule over the two successive lengths such as between L_1 and L_2, L_2 and L_3,and so on,to get the value of Δ $V(L_r)$ as

$$\Delta V(L_r) = \frac{[A(L_{r+1}) + A(L_r)] \times (L_{r+1} - L_r)}{2} \tag{2.13}$$

where, r=1,2,..., $t-1$, next the value up to $V(L_{s+1})$ can be obtained summing $\Delta V(L)$ from 1 to s. This can be written as

$$V(L_{s+1}) = \sum_{r=1}^{s} \Delta(L_r) \tag{2.14}$$

where, s=1,2,...,$t-1$. We can select a segment in which the disk is to be cut by finding z such that $V(L_z) < u \times V(\lambda) < V(L_{z+1})$ and the value of ϑ, an exact location to cut the disk, is obtained as

$$\vartheta = L_z + \frac{-b + \sqrt{b^2 - 4ac}}{2a} \tag{2.15}$$

where, a, b and c are calculated as

$a = \frac{[A(L_{z+1}) - A(L_z)]}{(L_{z+1} - L_z)}$

$b = 2A(L_z)$

$c = -2[u \times V(\lambda) - V(L_z)]$ The value of interpolation function, $S(\vartheta)$, at the point of disk cut (ϑ) is computed as

$$S(\vartheta) = A(L_z) + a(\vartheta - L_z) \tag{2.16}$$

More than one disk can be selected and cut per path. Equation 2.11 is used to get the separate estimate for the total quantity of interest of a tree for each path. When more than one disk is cut, the final combined estimate of the total quantity of interest is obtained by averaging the estimates from using various disks. Valentine et al. (1984) suggested using more than one path, each with a single disk rather than using a single path with more than one disk. The later being less efficient.

To estimate dry weights or dry biomass of the woody stem of a tree, the disk selected and cut from the path is oven-dried and weighed. Dry weight of foliage and small shoots are calculated separately and added to the dry weight of woody stem to obtain total weight of the tree.

2.2.3 DATA

This study is a part of a national effort on estimating tree biomass. Experts from academia, forest industry, US Forest Service Forest Inventory and Analysis program (FIA) are working collaboratively to develop nationally consistent forest volume, biomass and carbon models. These models are developed at individual tree level by component (bark, bole, branch, foliage, etc.) and species. Our study includes trees from southern part of the U.S., specifically from Georgia and Florida. In this study, we selected red maple (*Acer rubrun*) and slash pine (*Pinus elliottii*). The architecture of these two species is quite different. Slash pine, a softwood tree species, has more regular tree structure than red maple, a hardwood tree species. The crown structure of these species is also known as excurrent and deliquescent for slash pine and red maple, respectively. In general, regular tree crown are characterized by paths with approximately equal length and is expected to provide RBS estimates with smaller variance. On the other hand, an irregular tree crown comprises paths having unequal lengths providing large variance of the estimates.

2.2.3.1 Sample tree selection

Spatial location such as state, county , latitude, longitude, topographic information (slope, aspect, elevation) and other stand characteristics were recorded for each sampled tree. Individual trees were selected based on wide variation in tree form, specific gravity, size, geographic location, as well as many other factors that are related to biomass and carbon content. Red maple and slash pine data were used to test sampling strategies and construct models for predicting individual tree and tree component biomass. Thirty eight sample trees from slash pine and 14 from red maple were felled and measured. Trees in this study were destructively sampled and intensively measured.

Pertinent tree stem measurements for biomass calculation and modeling include total green weight of each branch with foliage (0.1 lb), branch diameter (0.1 inch), total green weight of stem (0.1 lb), stem disk diameter (0.1 inch), and weight (0.1 lb), diameter at breast height (Dbh) (0.1 inch), total tree height (0.1 foot), height to live crown (0.1 foot), diameter outside bark at ground line, stump height, 2.75 feet, 4.5 feet, 8 feet and then every 4 feet up the stem (0.1 inch).

2.2.3.2 Branch measurement

Branch number was assigned to each first order branch with diameter >0.5 inch starting from base of a tree. If the first order branch contains very large second order branches then the second order branch was measured treating it as a smaller first order branch. For each branch, height above ground (0.1 foot), diameter at the base (0.1 inch), length (0.1 foot) were measured. Green weight of branch with foliage was also measured for all branches in a tree. As a foliage sub-sample, approximately 35 individual leaves excluding twigs were removed from the branch and were placed in a zip lock bag and stored in a cooler until transfer to the lab. Green weight of sub-sampled foliage was measured. In addition, branch with foliage (excluding foliage sub-sample) was weighed. All small twigs from the branch were clipped and the small twigs and leaves off of the twig were placed in a paper bag for drying. Branches were cut into pieces and placed in a paper bag and weighed to the nearest gram. The foliage sub-sample, branch, and twigs were dried in 105° C until the weight stabilized. These measurements of branch including sub-sample measurements were used to calculate total green weight of branch and green weight of foliage for each branch in a tree.

For N branches on a tree, total green weight of branch and foliage at a tree level was calculated as

$$\mathrm{T_{GBF}} = \sum_{\mathrm{i}=1}^{\mathrm{N}} \mathrm{G_{BF_i}} \tag{2.17}$$

where $\mathrm{T_{GBF}}$ is total green of weight branch and foliage , $\mathrm{G_{BF_i}}$is green weight of branch and foliage for branch $\mathrm{i} = 1, 2, \ldots, \mathrm{N}$.

For n sub-sample branches on a tree, green weight of foliage and green weight of branch were calculated as

$$\begin{aligned}\hat{\mathrm{G}}_{\mathrm{F_i}} &= \mathrm{D_{F_i}}\left(\frac{\mathrm{G_{FSS_i}}}{\mathrm{D_{FSS_i}}}\right) \quad \text{and} \\ \hat{\mathrm{G}}_{\mathrm{B_i}} &= \mathrm{G_{BF_i}} - \hat{\mathrm{G}}_{\mathrm{F_i}} \end{aligned} \tag{2.18}$$

where $\hat{\mathrm{G}}_{\mathrm{F_i}}$ and $\hat{\mathrm{G}}_{\mathrm{B_i}}$ are total estimated green weight of branch and green weight of foliage for branch i, respectively. $\mathrm{G_{FSS_i}}$ and $\mathrm{D_{FSS_i}}$ are green and dry weight of foliage sub-sample of branch i, respectively. $\mathrm{D_{F_i}}$ is dry weight of foliage of a branch i and $\mathrm{G_{BF_i}}$ is green weight of wood and foliage of a branch i. There are i = 1, 2, …, n sub-sample branches on a tree.

For the branches that were not sub-sampled, we have the following information available:

G_{BF_i} = green weight of branch and foliage for branch i

B_{D_i} = basal diameter (0.1 inch) of branch i

B_{L_i} = length (0.1 foot) of branch i

We also have this information available for all sub-sampled branches in addition to D_{B_i} and D_{F_i}.

To obtain the estimated value of D_{B_i} (Dry branch), D_{F_i} (Dry foliage), G_{B_i} (Green branch) and G_{F_i} (Green foliage) for non-sub-sample branches we used the ratios: $\frac{D_{B_i}}{G_{BF_i}}$, $\frac{D_{F_i}}{G_{BF_i}}$, $\frac{G_{B_i}}{G_{BF_i}}$, $\frac{G_{F_i}}{G_{BF_i}}$, respectively. We also used weighted ratio for the branches with high variation in diameter at base and length. For example, to calculate the green weight of a branch (without foliage) we used the following ratio

$\text{WR}=\frac{\sum_{i=1}^{n}(\frac{G_{B_i}}{G_{BF_i}})(D_i^2 L_i)}{\sum_{i=1}^{n}(D_i^2 L_i)}$ and

$\hat{G_{B_j}} = G_{BF_j} \times (\text{WR})$ where, WR is the weighted ratio, $\hat{G_{B_j}}$ is estimated green weight of branch j, G_{BF_j} is green weight of branch j with foliage, D and L are diameter at base and length of branch, respectively, and others are as described above.

2.2.3.3 MAIN STEM BOLT, DISK AND BARK MEASUREMENT

Trees were felled at 0.5 foot from the ground level. The stem was then sectioned at 4.5 ft, 8 ft and every 8 ft. up the bole to a minimum dob of 4 inches. Each section was weighed. A disk was removed from the base of each bolt. All disks were weighed green with and without bark, had diameter measured with and without bark and then debarked disks were soaked until saturation. Saturated disk volume was determined using water displacement and then disks were dried at 105° C until weight change stopped. Additionally, a sample of bark from each disk was selected, weighed green, saturated and had its volume determined using water displacement and finally dried to constant weight at 105° C.

2.2.3.4 TREE VOLUME AND WEIGHT CALCULATIONS

Total tree volume was calculated using a combination of Newtown's, Smalian's and conic formula. Measured diameters at the lower and upper end of each bolt (main stem section) were used to calculate the bolt volume. Newton's formula was used to calculate the volume of a stem from base the breast height (4.5 ft) measurement point, whereas the cone formula was used to calculate volume of last stem section assuming it has the shape of a cone and Smalian's formula was used to calculate volume of stem taper measurements from 4.5 feet to the minimum 4-inch dob top using the taper measurements at 4.5, 8, 12 and every 4 feet up the stem. The total tree volume was then obtained by summing the volumes of the component bolts.

Newton's formula is

$$\mathrm{V} = \frac{\mathrm{A_l} + 4\mathrm{A_m} + \mathrm{A_s}}{6} \times \mathrm{L} \tag{2.19}$$

Cone formula is

$$\mathrm{V} = \frac{\mathrm{A}}{3} \times \mathrm{L} \tag{2.20}$$

Smalian's formula is

$$\mathrm{V} = \frac{\mathrm{A_l} + \mathrm{A_s}}{2} \times \mathrm{L} \tag{2.21}$$

where,

V = bolt volume (ft^3)

$\mathrm{A_l}$ = cross sectional area at large end (ft^2)

$\mathrm{A_s}$ = cross sectional area at small end (ft^2)

$\mathrm{A_m}$ = cross sectional area at mid-point (ft^2)

L = bolt length (ft)

A = cross sectional area (ft^2)

Total green bolt weight outside bark was calculated by simply summing the weight of component bolts which were measured in the field using a platform scale. Total green bolt weight can also be calculated using Equation 2.22. To calculate bolt weights inside bark, sample disk (inside bark) data that include disk diameter inside bark and disk weight inside bark, were used.

The green weight of a bolt (with bark) can also be calculated as

$$\mathrm{W_g} = \frac{\mathrm{L(A_l D_{gu} + 2A_l D_{gl} + 2A_u D_{gu} + A_u D_{gl})}}{6} \tag{2.22}$$

and, dry weight of bolt (without bark) is obtained as

$$\mathrm{W_d} = \frac{\mathrm{L(A'_l D_{du} + 2A'_l D_{dl} + 2A'_u D_{du} + A'_u D_{dl})}}{6} \tag{2.23}$$

where,

$\mathrm{W_g}$ = bolt green weight

$\mathrm{A_l}$ = cross-sectional area of wood with bark at the lower end of the bolt

$\mathrm{A_u}$ = cross-sectional area of wood with bark at the upper end of the bolt

$\mathrm{D_{gl}}$ = green-weight density at the lower end of the bolt

$\mathrm{D_{gu}}$ = green-weight density at the upper end of the bolt

L = bolt length

$\mathrm{W_d}$ = bolt dry weight

$\mathrm{A'_l}$ =cross-sectional area of wood without bark at the lower end of the bolt

$\mathrm{A'_u}$ =cross-sectional area of wood without bark at the upper end of the bolt

D_{dl} = dry-weight density at the lower end of the bolt

D_{du} = dry-weight density at the upper end of the bolt

Green-weight density (D_g) and dry-weight density (D_d) can be calculated as

$$D_g = \frac{\text{Green weight of wood and bark}}{\text{Green volume with bark}} \tag{2.24}$$

and

$$D_d = \frac{\text{Oven} - \text{dry weight of wood only}}{\text{Green volume without bark}} \tag{2.25}$$

Equations 2.22 and 2.23 are derived by integrating over the length of the bolt. Assuming that both cross-sectional area and weight density vary in linear fashion along the bolt (Clutter et al. 1983).

We used green volume with bark as a denominator for calculating dry-weight density which was used in calculating dry weight of wood only. Similarly, the green volume with bark was used in calculating stem green weight inside bark.

2.2.3.5 Sample data for RBS

The detailed data available for each destructively sampled tree allows us to evaluate the use of RBS and RBS in combination with IS to develop estimates of tree biomass. Table 2.1 provides an example of variables that were used in the RBS procedure. Clearly, red maple tree structure is quite different from slash pine and it exhibits much more variation from tree to tree than does slash pine. Consequently, RBS and IS study is carried out separately for these two distinctly different tree species.

Table 2.1: Sample data structure for RBS estimation

Tree no.	Species code	Node (k) no.	Branch no.	Face	Diameter (inch)	Length (ft)	Wt (lbs)	Height to node
11	111	1	1	5	6.60	29.20	185.11	0.00
11	111	2	1	5	3.40	3.00	14.53	29.20
11	111	2	2	3	0.70	7.40	1.37	29.20
11	111	3	1	5	3.30	3.30	14.02	32.20
11	111	3	2	4	0.90	7.60	1.16	32.20
11	111	3	3	3	0.50	3.90	0.34	32.20
11	111	3	4	2	0.70	4.40	0.52	32.20
11	111	4	1	5	2.95	2.10	7.22	35.50
11	111	4	2	4	1.30	8.60	3.03	35.50
11	111	4	3	2	0.60	6.00	0.88	35.50
11	111	5	1	5	2.68	3.43	9.24	37.60
11	111	5	2	3	0.80	5.30	1.14	37.60
11	111	5	3	2	0.70	5.90	1.19	37.60
11	111	6	1	5	2.00	12.47	10.57	41.03
11	111	6	2	3	0.50	2.50	0.20	41.03
11	111	6	3	3	0.80	5.70	2.06	41.03
11	111	6	4	1	1.00	6.00	2.40	41.03

2.2.4 EVALUATION

With the detailed destructively sampled tree data, it is possible to know total tree biomass using direct measurement. Furthermore, it is also possible to estimate total tree biomass for all possible paths using RBS. This allows us to develop empirical sampling distributions for the RBS procedure for use in individual tree biomass estimation. All possible paths in each tree were determined and estimates from these paths were obtained. We obtained RBS estimates of total tree biomass for all possible combinations of one path, two paths, three paths, four paths and five paths. The total number of possible combinations of one path for a given tree is equal to the number of first order branches plus one (for main-stem). Total number of possible combinations of two paths, three paths, four paths and five paths was determined using combinatoric formula as

$$\mathrm{nC_r} = \frac{\mathrm{n!}}{\mathrm{r!(n-r)!}} \tag{2.26}$$

where n is number of first order branches and r (r=1,2,3,4,5) is a possible path.

Estimated green weight of wood and foliage from all possible combinations resulted in the empirical sampling distribution for RBS using a given number of paths. Actual tree biomass (obtained via direct measurement) was then related to the characteristics of this sampling distribution. Bias was calculated as the difference of mean of the sampling distribution for each number of paths used and actual measured tree biomass. Standard error of the empirical sampling distribution is easily determined as the square root of variance of estimates from all available combinations of a given number of paths. Standard error is a measure of the dispersion of the distribution of all samples. Mean absolute percentage error (MAPE), commonly used in time series analysis was also used to evaluate estimation from RBS using different sampling paths (Equation 2.27).

$$\mathrm{MAPE} = 1/\mathrm{n}\sum_{\mathrm{i=1}}^{\mathrm{n}} |\frac{\mathrm{w_i} - \hat{\mathrm{w}}_\mathrm{i}}{\hat{\mathrm{w}}_\mathrm{i}}| \tag{2.27}$$

where n is number of possible combinations of a path, $\mathrm{w_i}$ is actual weight of a tree from using $\mathrm{i^{th}}$ path and $\hat{\mathrm{w}}_\mathrm{i}$ is estimated tree weight.

As an another measure, RBS precision was assessed using relative standard error (RSE) using Equation 2.30 as described in Chirici et al. (2013). Using the data , it was possible to obtain the selection probability $\mathrm{Q_{iR}}$ and the corresponding estimate $\hat{\Phi}_\mathrm{i}$ for each of the M possible paths for each tree. Here, Q_{iR} is defined as the joint probability of selecting all R segments in the i^{th} path. Number of segments (R) may vary by path, however, for M possible paths with unique terminal segments, we can get $\sum_{p=1}^{M} Q_{iR} = 1$. The variance of $\hat{\Phi}$ can be calculated using

$$\mathrm{var}(\hat{\Phi}) = \sum_{i=1}^{M} \{\hat{\Phi}_i - E(\hat{\Phi})\}^2 Q_{iR} \tag{2.28}$$

Not surprisingly, with increase in number of paths, the variance of $\hat{\hat{\Phi}}_m$ decreases i.e.

$$\mathrm{var}(\hat{\hat{\Phi}}_m) = \frac{\mathrm{var}(\hat{\Phi})}{m} \tag{2.29}$$

where m is the number of RBS paths.

Similarly, the relative standard error (RSE) of $\hat{\hat{\Phi}}_m$ decreases with increase in m as shown by

$$RSE_m = \frac{\sqrt{\mathrm{var}(\hat{\Phi})/m}}{\Phi} \times 100 \tag{2.30}$$

where Φ is the actual weight of wood and foliage of a tree.

2.3 Results and discussion

2.3.1 Sampling distributions of RBS estimates

The shape of the sampling distribution of average estimated biomass for red maple changes dramatically from one path to two path sampling and approaches a normal distribution as number of paths increase further from three to five (Figures 2.2, 2.3, and 2.4). Empirical sampling distribution of average estimated biomass of a small red maple (tree 48 with Dbh 4.8 inch) resulting from use of one, two, three, four, and five paths is presented in Figure 2.2. There are 20, 190, 1140, 4845 and 15504 samples resulting from use of one, two, three, four, and five paths, respectively. The sampling distribution of the average estimated biomass is approximately normal after three paths. As expected, that the spread of the sampling distribution of average estimated biomass decreases with increase in number of paths. For an average size red maple (tree 43 with Dbh 9.1 inch) the sampling distribution is approaching normal only after four paths and for a large size red maple (tree 41 with Dbh 14.7 inch) we may require more than five paths to obtain an approximate normal sampling distribution.

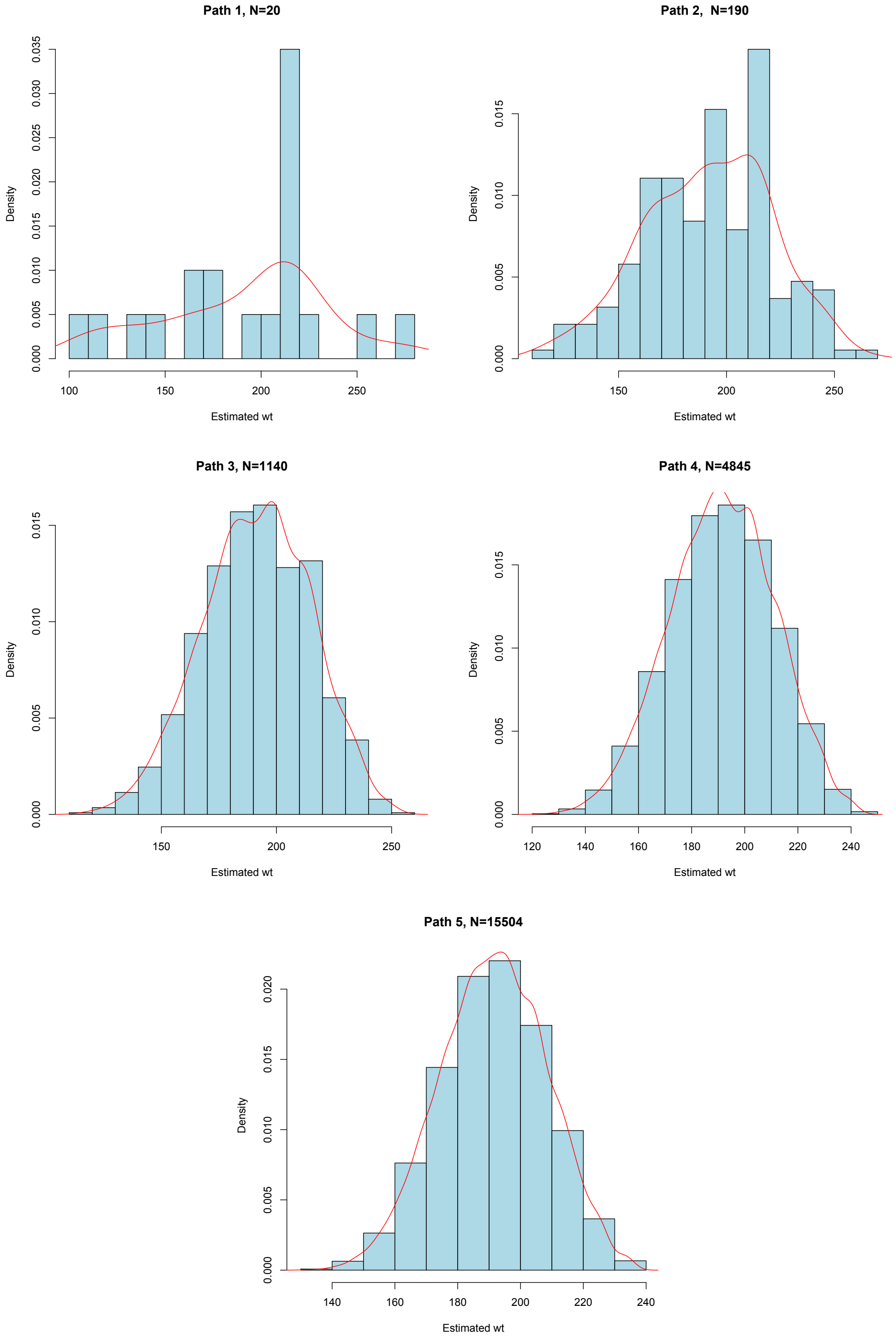
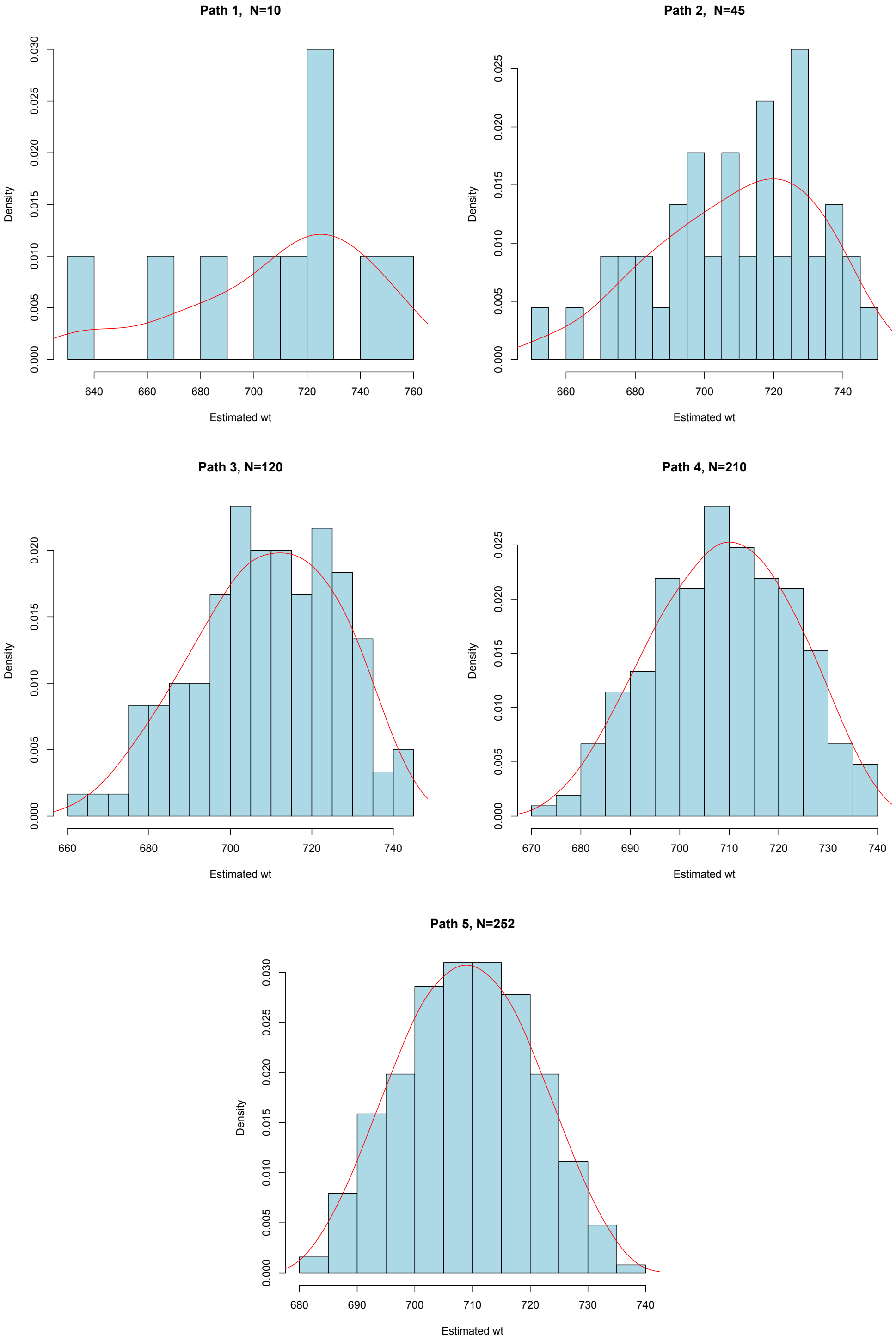


Figure 2.2: Sampling distribution of mean estimated biomass of small red maple tree by path


Path 1, N=10

Path 2, N=45

Path 3, N=120

Path 4, N=210

Path 5, N=252

Figure 2.3: Sampling distribution of mean estimated biomass of average red maple tree by path

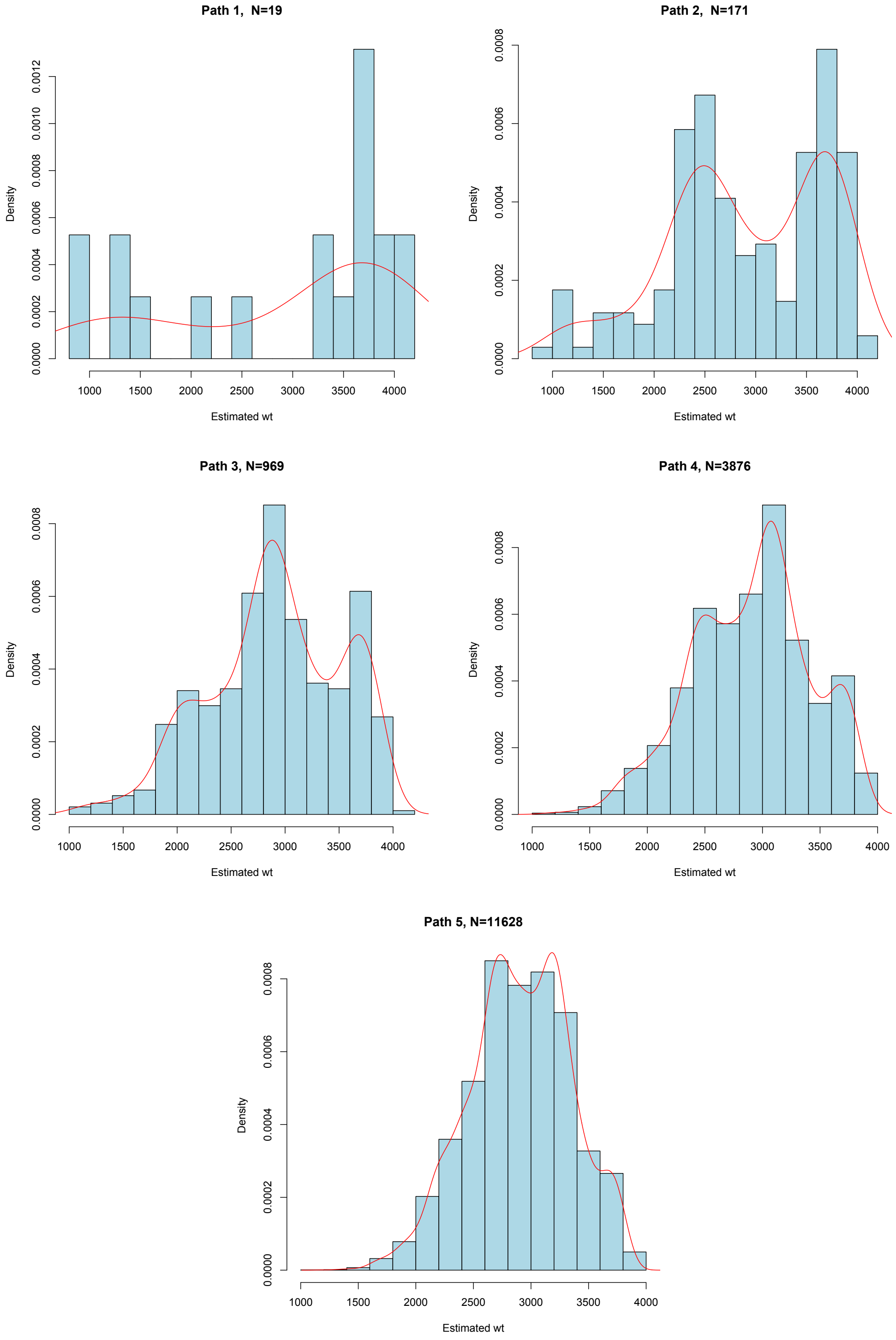


Figure 2.4: Sampling distribution of mean estimated biomass of large red maple tree by path

For a small slash pine (tree 6 with Dbh 5.6 inch) the shape of the sampling distribution is approaching normal after three paths (Figure 2.5). But, for an average size slash pine (tree 18 with Dbh 7.8 inch) (Figure 2.6) and large size slash pine (tree 35 with Dbh 10.1 inch) (Figure 2.7) the sampling distribution is approximately normal after two paths. This indicates, for slash pine, regardless of tree size the sampling distribution is approaching to normal on or after two paths. For all size trees, the spread of distribution is decreasing with increase in number of paths.

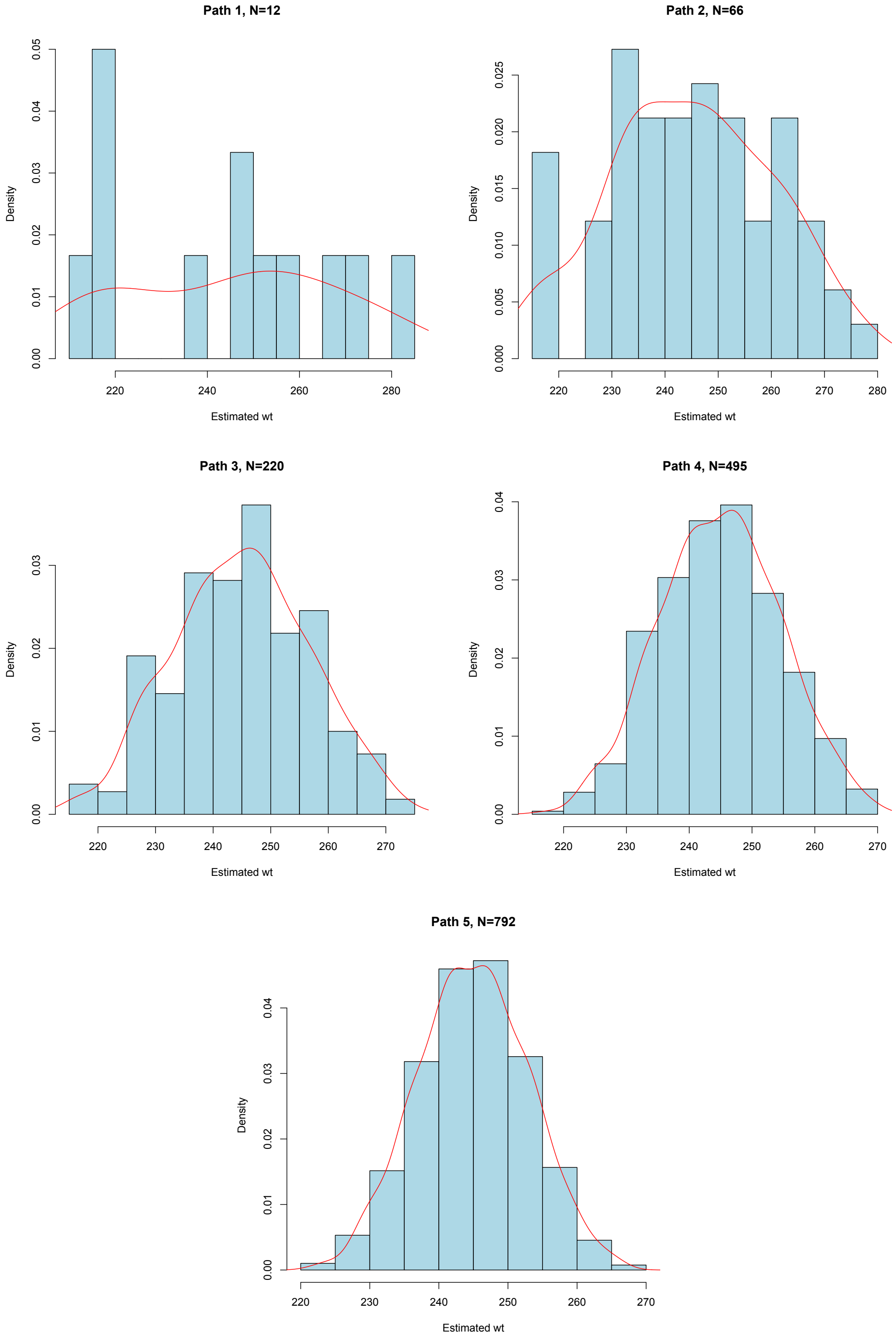


Figure 2.5: Sampling distribution of mean estimated biomass of small slash pine tree by path

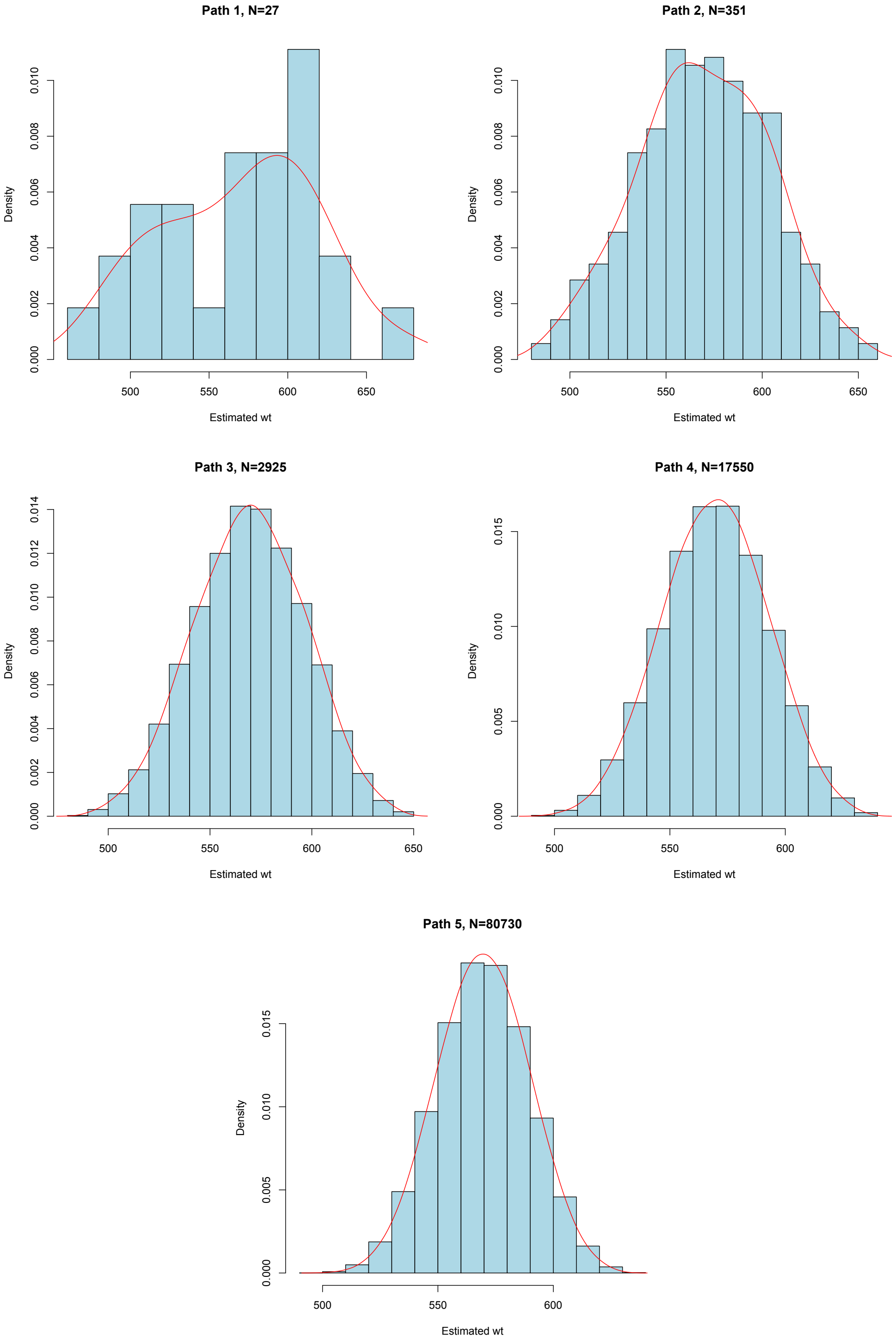


Figure 2.6: Sampling distribution of mean estimated biomass of average slash pine tree by path

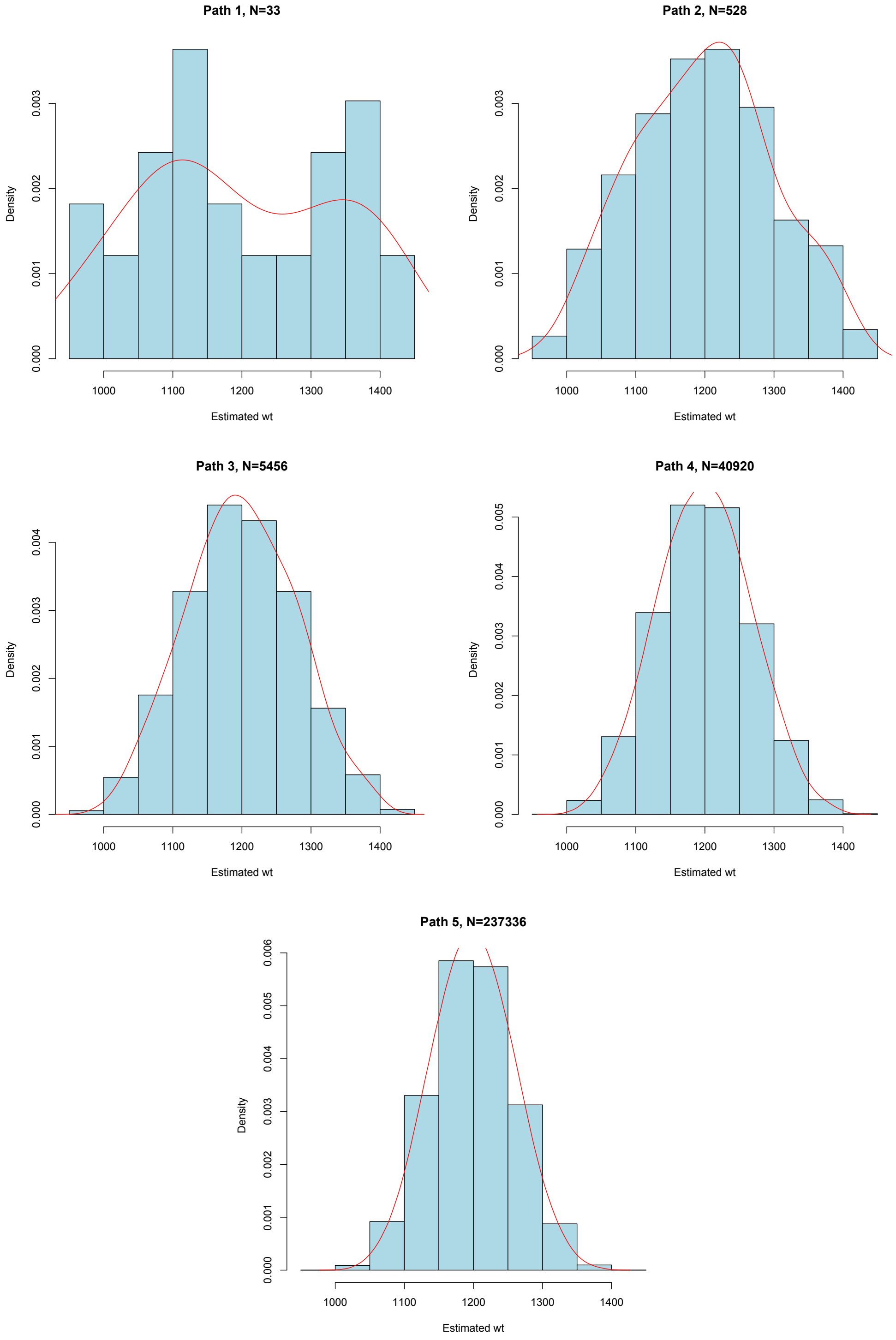


Figure 2.7: Sampling distribution of mean estimated biomass of large slash pine tree by path

Sampling distribution of biomass estimates for all slash pine and red maple trees by Dbh (small to large) and number of RBS paths is presented in Appendix A and B, respectively.

Table 2.2 and 2.3 present empirical sampling distribution characteristics for small, average and large size trees resulting from use of one, two, three, four and five paths, for red maple and slash pine, respectively. For example, for a small size red maple (tree 48) there are 20 possible paths from using one path sampling. Actual weight of the tree is 201.85 lbs, whereas the mean estimated weight which was obtained by averaging estimates from all 20 possible paths is 191.41 lbs. Clearly, the empirical sampling distribution indicates a bias of approximately 10 lbs for this tree. The mean estimated weight remained unchanged by paths. This is because the mean estimated weight was derived by averaging the estimated weights from all possible paths.

Regardless of tree size, the standard error (Std. err.) of estimates is smaller for larger number of paths (total paths) (Table 2.2). Standard error decreased from 43.74 to 16.94 from one to five paths for tree 48. If we were to choose one RBS path, for tree 48, our estimated biomass would range from 109.80 to 275.90 lbs, where the actual biomass is 201.85 lbs. Whereas, choosing five paths would produce an estimate between 131.40 lbs to 237.90 lbs. This range is narrower than the range from choosing one path, which implies more sample paths result in estimates that have a higher probability of being closer to the actual value. As expected, the range of estimated biomass decreased with increase in number of paths. For example, the range of estimates is 166.1 (275.90-109.80), 151.8 (263.2-111.4), 132.1 (250.3-118.2), 118 (242.1-124.1), 106.5 lbs (237.9-131.4) using one, two, three, four, and five paths, respectively for tree 48. Similarly, the range of estimates is decreasing with increase in sample paths for average (43) and larger (41) size trees.

Similar results are found for slash pine (Table 2.3).

Table 2.2: RBS empirical sampling distribution characteristics by Dbh and combinations of path for small, average and larger red maple trees

Tree id	Species code	Dbh (inch)	Path	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Std. err.	Min. est. wt. (lbs)	Max. est. wt (lbs)
48	316	4.80	1	20	201.85	191.41	43.74	109.80	275.90
48	316	4.80	2	190	201.85	191.41	29.42	111.40	263.20
48	316	4.80	3	1140	201.85	191.41	23.92	118.20	250.30
48	316	4.80	4	4845	201.85	191.41	19.56	124.10	242.10
48	316	4.80	5	15504	201.85	191.41	16.94	131.40	237.90
43	316	9.10	1	10	708.05	708.93	36.04	635.80	752.60
43	316	9.10	2	45	708.05	708.93	23.05	652.50	749.10
43	316	9.10	3	120	708.05	708.93	17.48	664.10	742.60
43	316	9.10	4	210	708.05	708.93	13.99	674.20	739.20
43	316	9.10	5	252	708.05	708.93	11.42	682.10	735.80
41	316	14.70	1	19	3106.75	2904.68	1156.03	852.90	4131.00
41	316	14.70	2	171	3106.75	2904.68	775.49	871.40	4088.00
41	316	14.70	3	969	3106.75	2904.68	612.80	1021.00	4021.00
41	316	14.70	4	3876	3106.75	2904.68	513.65	1115.00	3980.00
41	316	14.70	5	11628	3106.75	2904.68	443.80	1193.00	3939.00

Table 2.3: RBS empirical sampling distribution characteristics by Dbh and combinations of path for small, average and larger slash pine trees

Tree id	Species code	Dbh (inch)	Path	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Std. err.	Min. est. wt. (lbs)	Max. est. wt (lbs)
6	111	5.60	1	12	275.55	244.95	23.31	214.00	282.00
6	111	5.60	2	66	275.55	244.95	15.16	215.90	277.10
6	111	5.60	3	220	275.55	244.95	11.68	216.90	274.00
6	111	5.60	4	495	275.55	244.95	9.53	217.40	269.90
6	111	5.60	5	792	275.55	244.95	7.97	221.90	266.50
18	111	7.80	1	27	586.52	569.52	49.80	475.30	673.60
18	111	7.80	2	351	586.52	569.52	33.93	484.50	654.50
18	111	7.80	3	2925	586.52	569.52	27.11	489.50	646.90
18	111	7.80	4	17550	586.52	569.52	22.98	493.40	639.90
18	111	7.80	5	80730	586.52	569.52	20.10	496.60	635.00
35	111	10.10	1	33	1189.04	1198.98	146.77	955.60	1447.00
35	111	10.10	2	528	1189.04	1198.98	100.68	960.20	1437.00
35	111	10.10	3	5456	1189.04	1198.98	80.80	963.30	1425.00
35	111	10.10	4	40920	1189.04	1198.98	68.79	979.50	1418.00
35	111	10.10	5	237336	1189.04	1198.98	60.46	990.70	1413.00

For all trees, RBS empirical sampling distribution characteristics by individual tree for RBS estimates resulting from use of one path, two paths, three paths, four paths and five paths are shown in Appendix C. In general, the sampling distribution characteristics in tables in the Appendix C suggest that standard error and MAPE values decrease substantially with increasing number of paths. Similarly, the range of estimates is smaller for larger number of paths. This indicate that the samples comprised of more paths reduces variation among samples. It is interesting to note that for individual trees, RBS (for any number of paths considered) shows a bias for estimating total tree biomass.

As expected, sampling distribution variation (standard error) is larger for larger trees. Further, red maple shows higher variation among samples than does slash pine, likely due to the irregular crown structure of red maple (Figures 2.8, and 2.9).

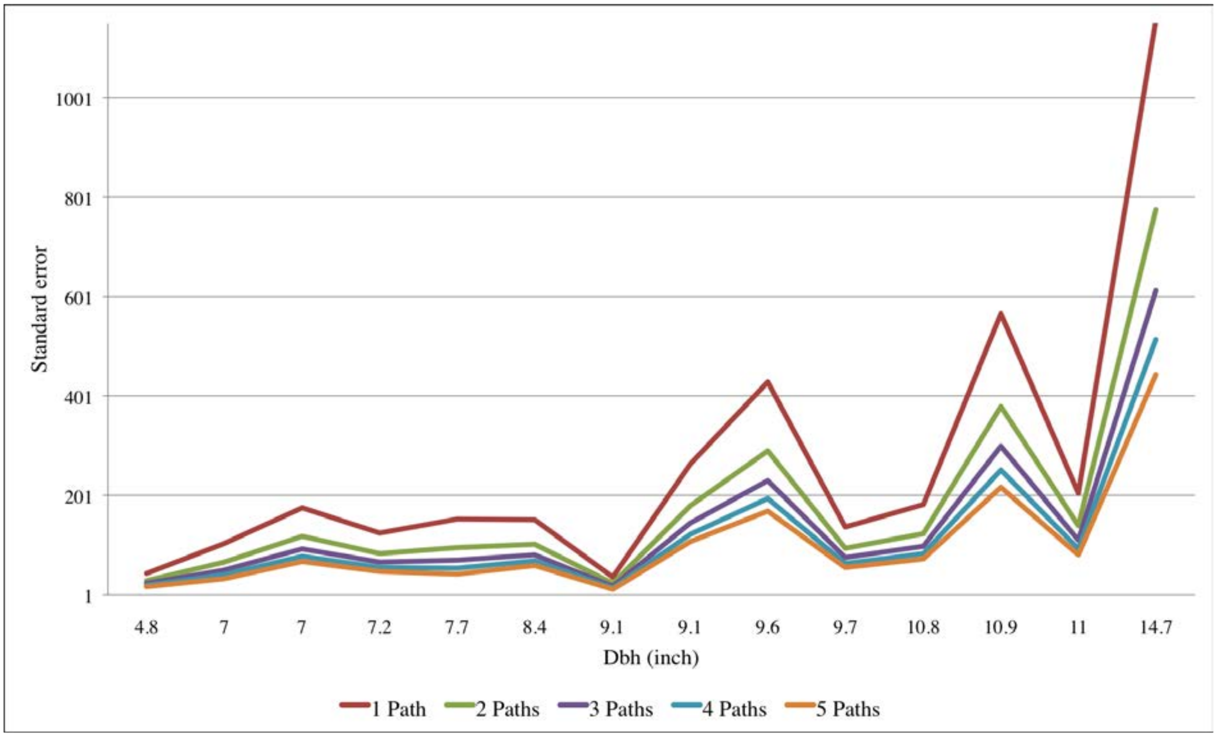


Figure 2.8: Standard error of sampling distribution by Dbh and path for red maple

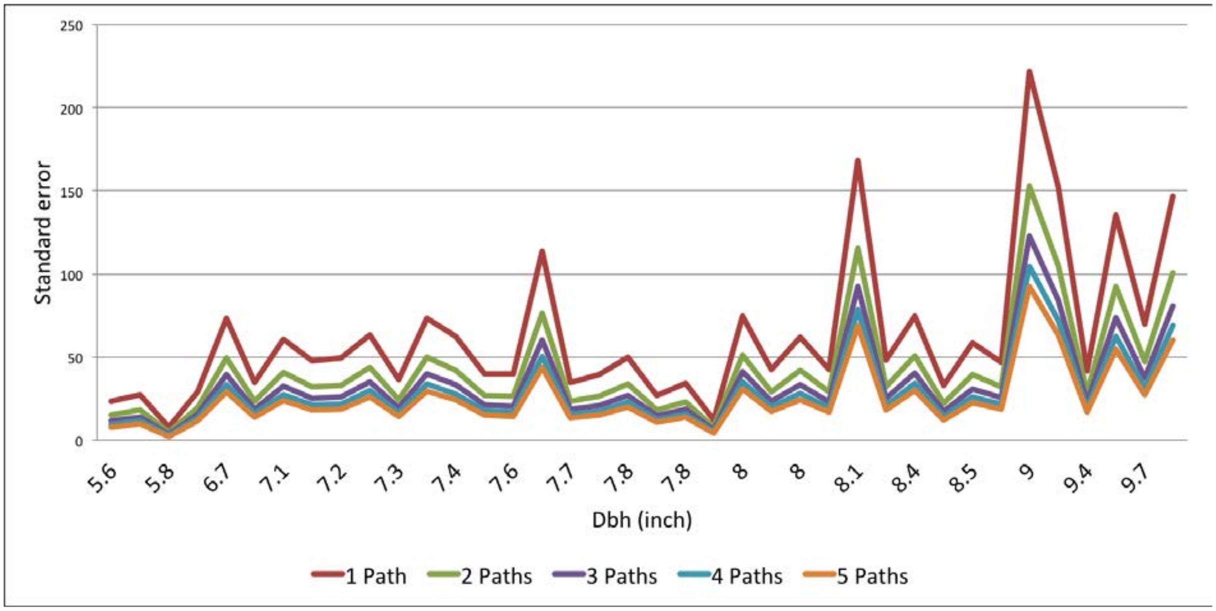


Figure 2.9: Standard error of sampling distribution by Dbh and path for slash pine

Moreover, when comparing these two species, average standard error of estimates, MAPE values, and RSE are higher for red maple than slash pine (Figures 2.10, 2.11, and 2.12) . In fact, the average standard error of estimates for red maple is more than four times and MAPE and RSE are more than two times larger than for slash pine for all paths considered. Tables for standard error, MAPE and RSE by species and path are given in Appendix D.

The reduction in average standard error, for slash pine, is about 20 lbs increasing from one to two path RBS, 9 lbs from two to three, 5 lbs from three to four and 4 lbs from four to five paths. For red maple, the change in average standard error is about 88 lbs from one to two paths, 38 lbs from two to three, 23 lbs from three to four and 16 lbs from four to five paths.

The change in average MAPE, for slash pine, is about 2% choosing from one to two paths, 1% from two to three , 0.5% from three to four and 0.3% from four to five paths. For red maple, the change in average MAPE is about 5% from one to two paths, 2% from two to three, 1% from three to four and 1% from four to five paths.

The change in average RSE, for slash pine, is about 2% increasing from one to two path RBS, 1% from two to three, 1% from three to four and 0.5% from four to five paths. For red maple, the change in average RSE is about 6% from one to two paths, 3% from two to three, 2% from three to four and 1% from four to five paths.

The change in average standard error (Figure 2.10), MAPE (Figure 2.11) and RSE (Figure 2.12) is minimal after two paths for slash pine and after three paths for red maple. This suggests that choosing from two to three paths for slash pine and three to four paths for red maple, we do not gain much accuracy in estimates. Hence, the results suggest that at least two path RBS should be used for slash pine and at least three path RBS should be used for red maple.

The RSE of wood and foliage estimates with number of paths used on the same tree is given in Table 2.14, Appendix E.

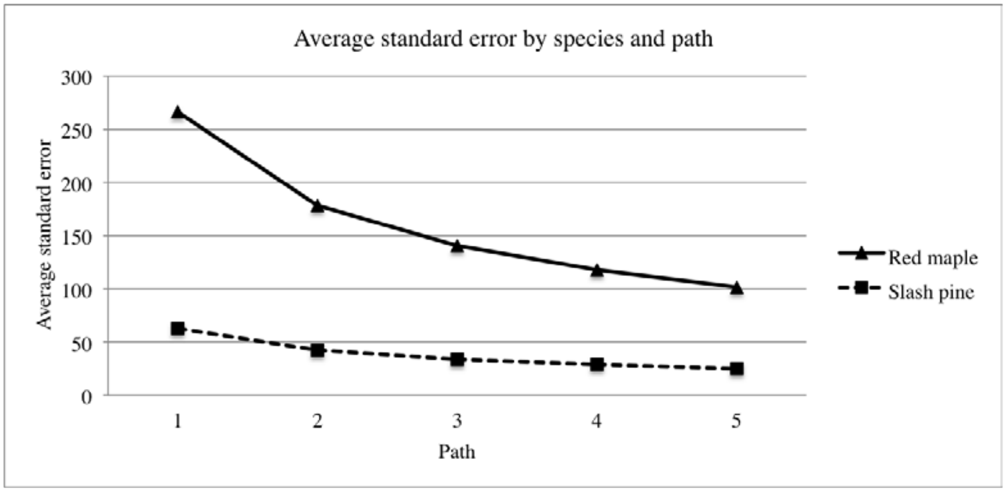


Figure 2.10: Average standard error of estimates by species and path combinations

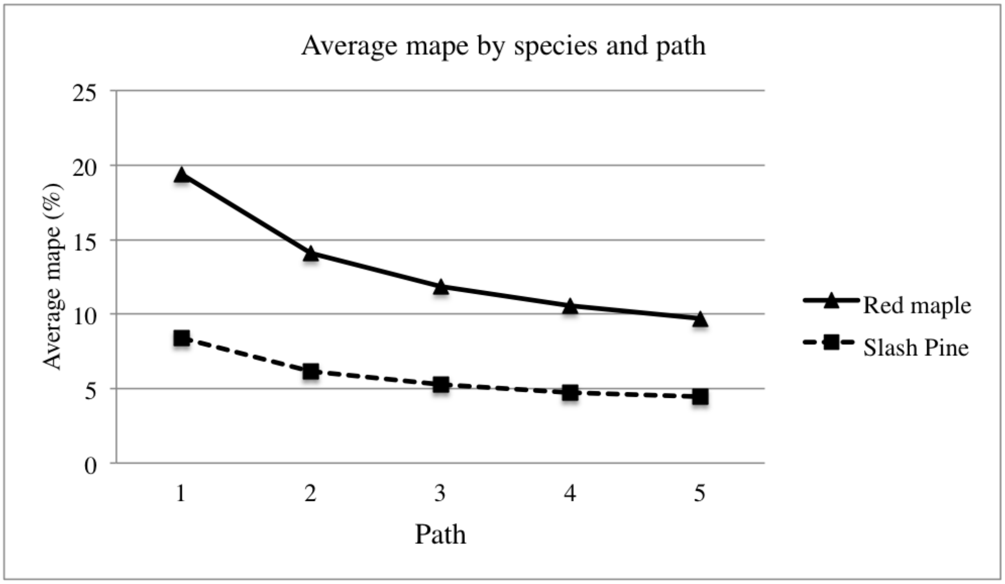


Figure 2.11: Average mape (%) by species and path combinations

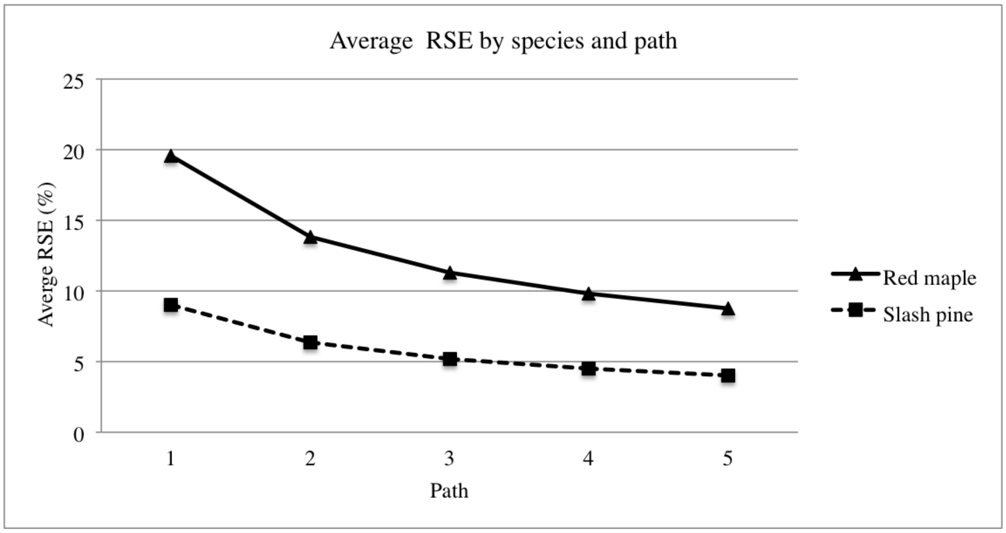


Figure 2.12: Relative standard error (%) by species and path combinations

Tree structure, branchiness, and stem form play significant roles in estimating precision (Chirici et al. 2013) of tree biomass estimates. Slash pine has a more regular tree structure than red maple. Red maple with an irregular tree crown comprises paths having unequal lengths providing large variance of the estimates due to high unconditional selection probabilities of the paths (Chirici et al. 2013). The results in this study support the findings from Chirici et al. (2013) in that slash pine shows less variation in sampling distributions than red maple.

2.3.2 APPLICATION OF RBS AND COMBINATION OF RBS AND IS TO TOTAL TREE BIOMASS

Based on study of RBS sampling distributions, it is clear that at least two paths should be used to estimate above ground biomass for slash pine and at least three paths should be used for red maple. When it is not possible to weigh entire sections of stem and/or branches, importance sampling (IS) has been suggested as a viable alternative for weight and biomass estimation. To evaluate the utility of IS in this context, we compare RBS estimates with RBS/IS estimates for both slash and red maple. Based on our work above, we use two RBS paths for slash pine and three RBS paths for red maple.

2.3.3 A NUMERICAL EXAMPLE OF RBS AND IS USING D^2L AS SELECTION PROBABILITY

A numerical example to illustrate use of RBS with IS is presented below. RBS is applied exactly as previously described above. First, dead branch material is removed and weighted separately. The RBS procedure starts from the base of the tree where diameter at base of the stem (Branch “a”) is 6.60 inches and length and weight are 29.20 ft and 185.11 lbs, respectively. The base of the stem is defined as node 1 from where we proceed to the second node and measure branch b and c. Two branches of which the first one i.e. b is stem and second branch c is branch, are emanating from the second node. Diameter and length of b are 3.40 inch and 3.00 ft, respectively. Branch c has diameter of 0.70 inch and length of 7.40 ft.

Selection probability (q_k) for b is calculated as $\frac{3.40^2 \times 3.00}{3.40^2 \times 3.00 + 0.70^2 \times 7.4} = 0.905$ and for c is 1-0.905 = 0.095. Selection probability of branch b (0.905) is greater than a randomly drawn uniform(0,1) number u=0.222, therefore branch b is selected and followed to node 3. There are 4 branches including stem emanating from node 3. Selection probabilities for these branches are calculated as described above. These are 0.794, 0.136, 0.022 and 0.048 for branches d, e, f, and g, respectively. Since the selection probability of branch d = 0.794 is greater than a random number u=0.270 (drawn for this node),branch d is selected and the path followed to node 4. There are 3 branches emanating from node 4. Selection probability of branch h= 0.523 is less than the random number u=0.800 hence the branch h is not selected. Now, the selection probabilities of branch h and i are added and compared to the random number. Cumulative selection probabilities (q_{ksum}) are shown by node in Table 2.4. Sum of the selection probabilities of branches h and i is 0.523+0.415=0.938 and is greater than the random number, 0.80, hence the second branch i is selected with a selection probability q_3= 0.415. At this point the RBS path is ended and branch i is cut off and weighed. The weight of branch and foliage of branch i is 3.03 lbs and the unconditional probability of reaching branch i is calculated using Equation 2.1 as $Q_4 = 1 \times 0.905 \times 0.794 \times 0.415 = 0.299$. The inflated weight of branch i is calculated as $Wt/Q_4 = 3.03/0.299 = 10.15$ lbs. Total estimated weight of branch and foliage of the tree can be calculated using Equation 2.5. Hence the total estimated weight of the tree for this path is $185.11/1 + 14.53/0.905 + 14.02/0.719 + 3.03/0.299 = 230.81$ lbs. Adding the dead branch the total weight is $230.81+1.5 = 232.31$ lbs.

Table 2.4: Data for Randomized Branch Sampling

Node	Branch	Branch name	Face	D (inch)	LBr (ft)	Wt (lbs)	D^2L	$\sum D^2L$	q_k	q_{ksum}	u	Selected branch	Q_k	Inflated wt (lbs)
1	1	a	5	6.60	29.20	185.11	1271.952	1271.952	1.000	1.000	0.198	Yes	1.000	185.11
2	1	b	5	3.40	3.00	14.53	34.680	38.306	0.905	0.905	0.222	Yes	0.905	16.05
2	2	c	3	0.70	7.40	1.37	3.626	38.306	0.095	1.000	0.222			
3	1	d	5	3.30	3.30	14.02	35.846	45.133	0.794	0.794	0.270	Yes	0.719	19.50
3	2	e	4	0.90	7.60	1.16	6.156	45.133	0.136	0.931	0.270			
3	3	f	3	0.50	3.90	0.34	0.975	45.133	0.022	0.952	0.270			
3	4	g	2	0.70	4.40	0.52	2.156	45.133	0.048	1.000	0.270			
4	1	h	5	2.95	2.10	7.22	18.301	34.995	0.523	0.523	0.800			
4	2	i	4	1.30	8.60	3.03	14.534	34.995	0.415	0.938	0.800	Yes	0.299	10.15
4	3	j	2	0.60	6.00	0.88	2.160	34.995	0.062	1.000	0.800			
5	1	k	5	2.68	3.43	9.24	24.729	31.012	0.797	0.797	0.185			
5	2	l	3	0.80	5.30	1.14	3.392	31.012	0.109	0.907	0.185			
5	3	m	2	0.70	5.90	1.19	2.891	31.012	0.093	1.000	0.185			
6	1	n	5	2.00	12.47	10.57	49.867	60.140	0.829	0.829	0.536			
6	2	o	3	0.50	2.50	0.20	0.625	60.140	0.010	0.840	0.536			
6	3	p	3	0.80	5.70	2.06	3.648	60.140	0.061	0.900	0.536			
6	4	q	1	1.00	6.00	2.40	6.000	60.140	0.100	1.000	0.536			

Note: Calculation may not be exact due to rounding effect

After selecting a path using RBS, IS can be conducted using measurement of diameter at numerous points along the path. Table 2.5 shows the data such as stem height (distance from the butt), diameter at base of the stem, node number and Q_k based on the path selected from RBS for this tree. Equations 2.8, 2.13, and 2.14 are used to calculate A(L), ΔV(L) and V(L), respectively.

Basically, IS using a RBS path uses the following steps:

- Find a stem section where a disk is to be cut
- Find an exact disk cut position (ϑ) in the section
- Cut the disk, weigh it and calculate its inflated weight

- Calculate the entire weight of the tree

The stem section or location to cut the sample disk is determined using the product of a uniform(0,1) random number and V(λ). In our case the product of random number u =0.53 and V(λ)=760.04 is 402.8212 which is between 347.8575 and 436.5775 (refer to V(L) column in Table 2.5). Hence the stem section to cut the disk is between L5 = 12 and L6 =16. Now, the exact disk cut position (ϑ) is determined by solving Equation 2.15 where

a = (19.36-25)/(16-12) = -1.41

b = 2 × 25 = 50

c = -2 × (0.53 × 760.04-347.86) = -109.92

which produces ϑ = 14.35.

Therefore the sample disk is cut at 14.35 ft above the base of the tree. The width of the disk cut is 0.1 ft and the overbark green weight at this position is 0.83127 lbs. The weight per unit of thickness i.e. B(ϑ) is 0.83127/0.1 =8.3127 lbs/ft and this is also the inflated weight per unit of thickness because Q_k=1 at this disk cut position (see Node column in Table 2.5). Using Equation 2.16, S(ϑ) can be calculated as

$S(\vartheta) = 25 - 1.41*(14.35-12) = 21.68 \text{ ft}^2$.

The calculated value of S(ϑ) is also used in Equation 2.11 to estimate the woody weight of the tree from node 1 to the point where branch is severed as

$\widehat{W} = (8.312 \times 760.0367)/21.67965 = 291.422$ lbs.

And, Green weight of the entire tree is estimated using Equation 2.12. Hence the total green weight of entire tree is given by

$\hat{b} = 291.42 + 10.15 + 1.57 = 303.14$ lbs.

In summary, the total estimated green weight of the tree is 232.31 lbs from RBS and 303.14 lbs from IS whereas the actual tree weight is 266.33 lbs. In this case, RBS underestimated the total weight whereas IS overestimated.

Table 2.5: Data for Importance sampling

Length index	Stem height (ft)	D (inch)	Node	Q_k	A(L)	ΔV(L)	V(L)
L1	0.50	6.60	1	1.000	43.56	0.00	0.00
L2	2.50	5.60	1	1.000	31.36	74.92	74.92
L3	4.50	5.60	1	1.000	31.36	62.72	137.64
L4	8.00	5.30	1	1.000	28.09	104.04	241.68
L5	12.00	5.00	1	1.000	25.00	106.18	347.86
L6	16.00	4.40	1	1.000	19.36	88.72	436.58
L7	17.50	4.50	1	1.000	20.25	29.71	466.29
L8	20.00	4.20	1	1.000	17.64	47.36	513.65
L9	24.00	3.90	1	1.000	15.21	65.70	579.35
L10	28.00	3.40	1	1.000	11.56	53.54	632.89
L11	29.20	3.40	2	0.905	12.77	14.60	647.48
L12	31.20	3.40	2	0.905	12.77	25.54	673.02
L13	32.20	3.30	3	0.719	15.11	13.94	686.96
λ	35.50	2.95	4	0.299	29.18	73.08	760.04

We used RBS and RBS/IS to calculate individual tree biomass. Fit statistics such as root mean square error (RMSE) as well as percent error were calculated to evaluate the methods (Table 2.15). Percent error was calculated by $\frac{\text{RMSE}}{\text{Actual weight}} \times 100$.

When using RBS alone, the sampling error varied from 0.35 to 37.58% for slash pine and 1.47 to 72.33 % for red maple (Table 2.15 in Appendix F). For combination of RBS and IS, sampling error for slash pine varied from 12.19 to 87.47 % and for red maple from 7.13 to 108.63% (Table 2.16 in Appendix F). As expected, results indicate that RBS alone provided more precise estimates compared to RBS and IS. Valentine et al. (1984) found sampling error ranging from 4.9 to 14.4% when they tested their RBS and IS sampling procedure for estimating total fresh above-ground biomass of 6 different hardwood species. In their tested tree, the number of paths varied from 1 - 4. They found total sampling error to be 4.9%. The within individual tree variation for hardwood (red maple) in our data is much larger compared with the variation found in Valentine et al. (1984). They tested RBS and IS on a single tree for 6 different species. Our work involves more trees hence the sources of variability might be due to different size, foliage content among selected branches and structure of trees. However, the sampling error for total biomass of across all red maple trees tested in this study was smaller (2.52%) than that found for the total biomass of hardwood trees they tested (4.9%). In another study, William (1989) found sampling error per tree ranging from 5.3 to 28.9% with a total sampling error of 3.3% when they used two or three RBS paths and IS to estimate Loblolly pine biomass. Similarly, Ozcelik (2012) used RBS and IS to estimate individual tree biomass in their study where they found sampling error ranging from 2.51 to 22.63% with the total of 2.65%.

Unlike results from Ozcelik (2012), it is observed that the combination of RBS and IS generally overestimated the total biomass of the tree (Figures 2.13, 2.14). Both figures show that estimates from RBS alone are closer to actual values than estimates from using combination of RBS and IS. The higher sampling error associated with using RBS and IS in combination than RBS alone is not very surprising given that only a single small disk is weighed when using IS.

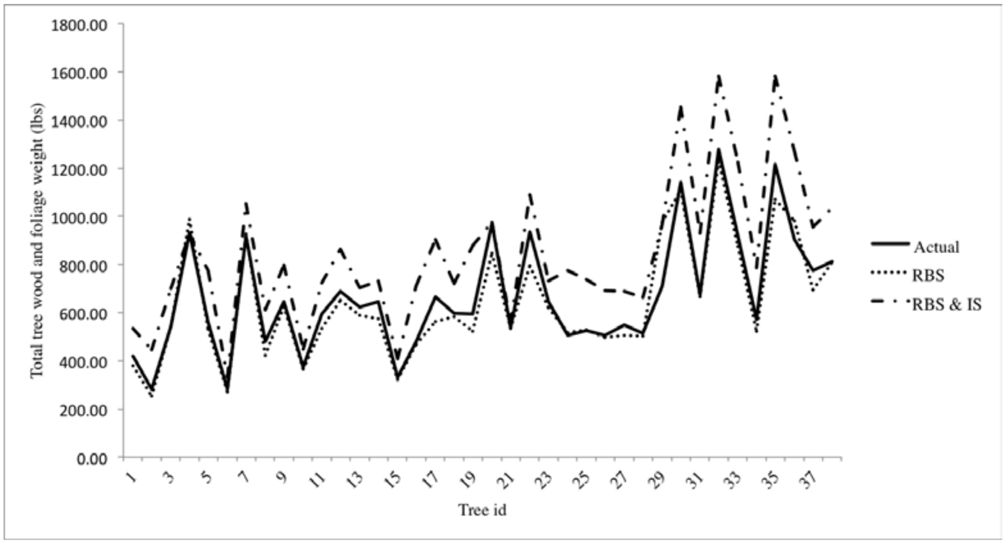


Figure 2.13: Actual and estimated wood and foliage from RBS and IS for slash pine

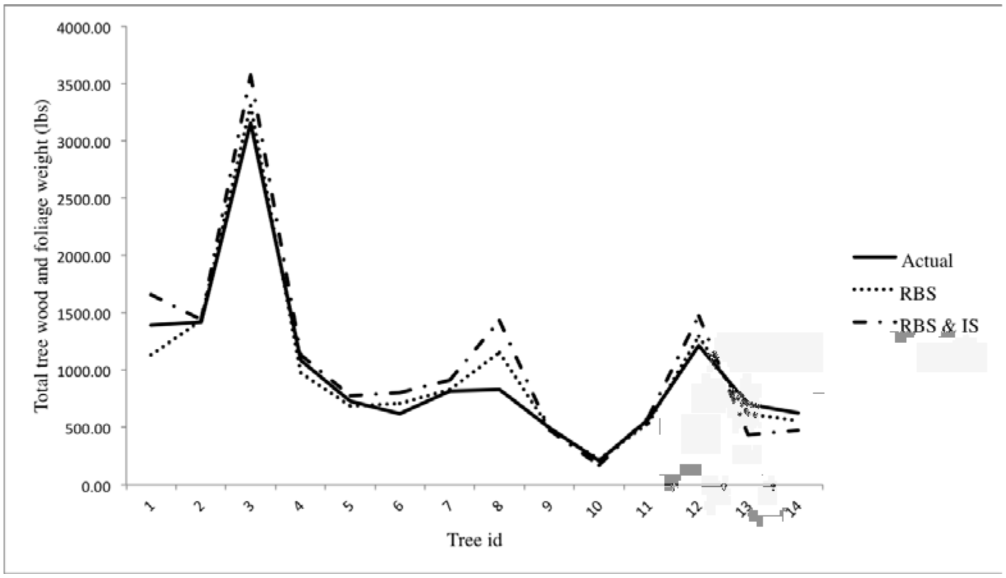


Figure 2.14: Actual and estimated wood and foliage from RBS and IS for red maple

Although, the sampling error per tree in this study shows a wide range , the total sampling error in both RBS and combination of RBS and IS are smaller than the total sampling error found in similar studies. Consequently, we can not recommend use of RBS alone or RBS in combination with IS when obtaining data to model individual tree biomass. However, for estimating biomass for larger populations using a large sample of trees RBS and RBS with IS may be viable.

2.4 Conclusion

In this study we simulated estimates of wood and foliage weight from all possible RBS paths for each tree. Data from 52 individual trees consisting of 38 slash pine and 14 red maple trees were used to simulate RBS. The use of all possible RBS paths in each tree allowed us to develop empirical sampling distributions for the RBS procedure. We generated sampling distributions of estimates using one, two, three, four and five possible paths for each tree. For these sampling distributions we determined standard error, mean absolute prediction error, and relative standard error.

The shape of the sampling distribution of average estimated biomass is quite irregular for one path RBS and becomes more normal as the number of paths increase. For red maple (irregular tree structure), the approach toward normality required more RBS paths for larger trees. But, for slash pine (regular tree structure), sampling distribution changed from irregular shape for a single RBS path to a more normal shape for two or more RBS paths.

Chirici et al. (2013) suggests using multiple RBS paths to obtain reliable estimates of tree biomass. Our results support this conclusion in that for both slash pine and red maple it was necessary to use at least two RBS paths to have sampling distributions that were approaching normal and were capable of providing a nearly unbiased estimate of tree biomass. However, it should be noted that many empirical sampling distributions do not in fact produce unbiased biomass estimates as indicated by their mean value differing from the observed tree biomass value. Further, the variation among estimates as measured by the range of estimates, standard error of the sampling distribution and MAPE clearly indicate that for a given instance of an RBS sample it is likely that the estimate can be quite different than the actual biomass of a given tree. This indicates that RBS sampling should not be used to generate data for modeling individual tree biomass using allometric modelling techniques. In fact, RBS may only be useful when obtaining a relatively large number of trees from a given population for the purpose of estimating the total biomass of all trees in the population via a sub-sampling approach.

Using RBS in combination with IS adds variation to sampling distributions and further diminishes the utility of resulting information for the modeling of individual tree biomass relationships. It may be possible to make use of RBS in combination with IS if large numbers of sample trees are obtained in a probability sampling process. However, we recommend that RBS be used without IS if at all possible.

2.5 References

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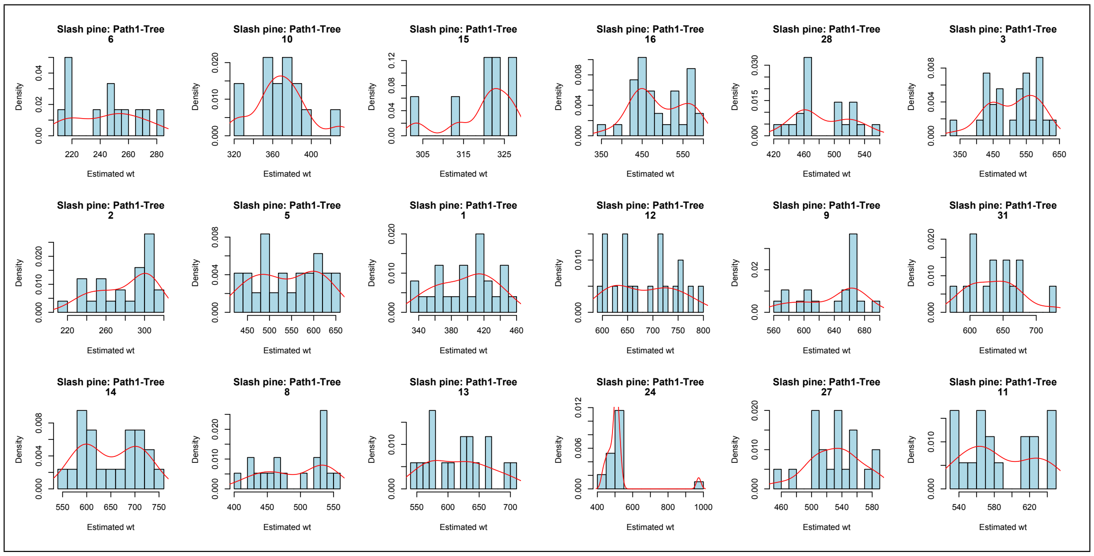
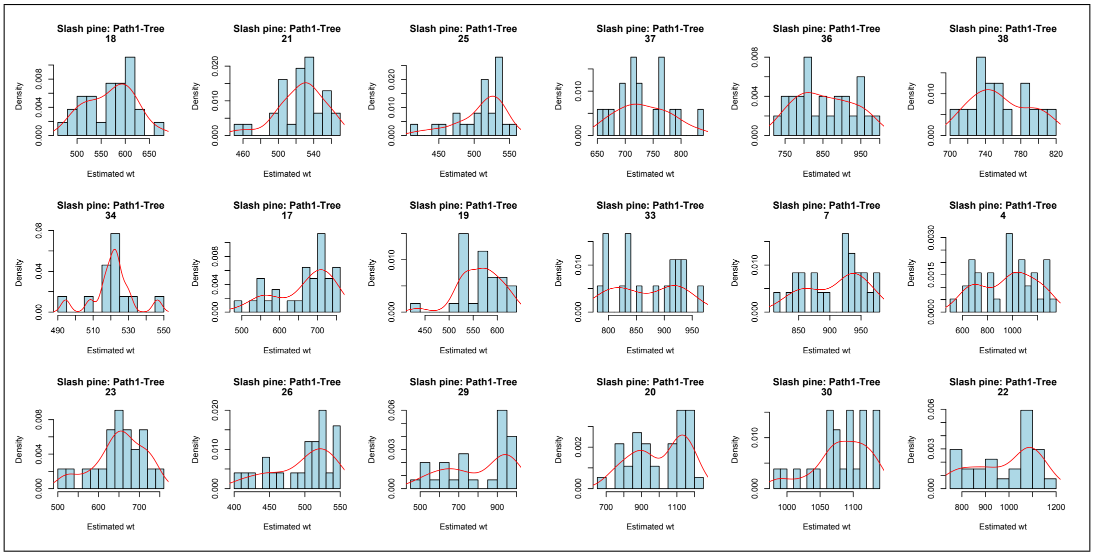
2.6 Appendix A: Sampling distribution of biomass estimates for slash pine by Dbh size and path





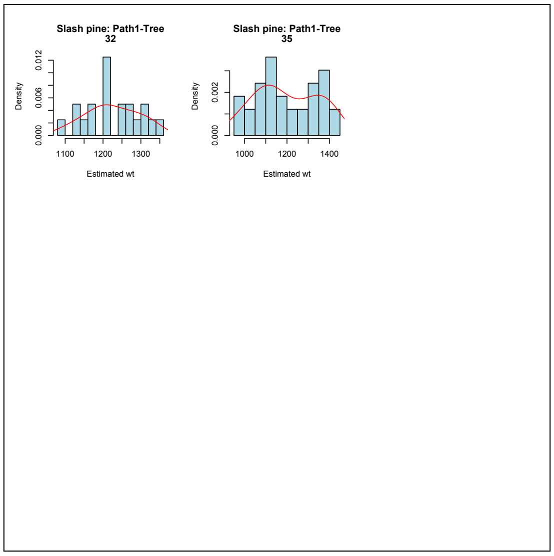
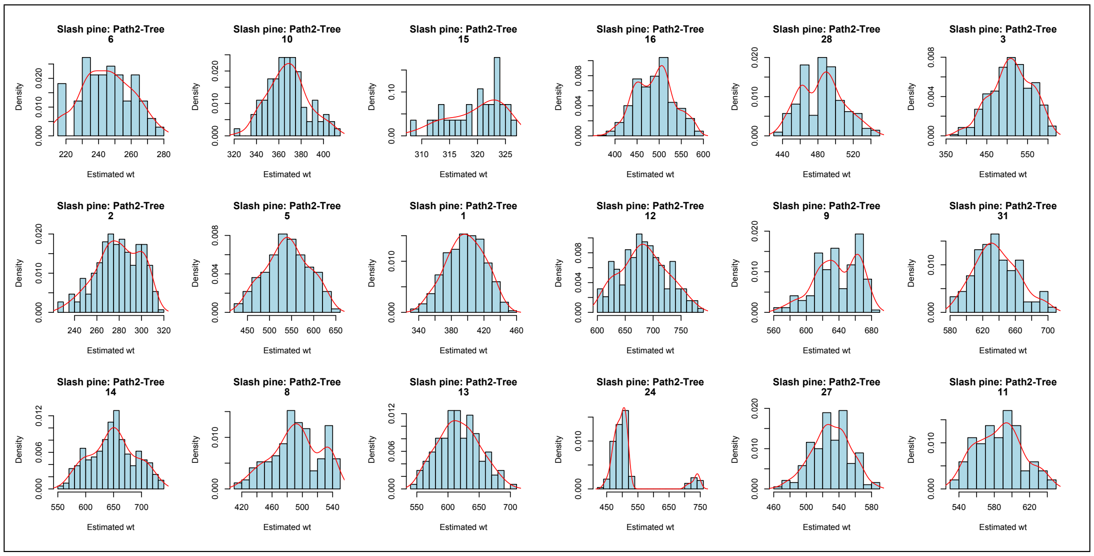
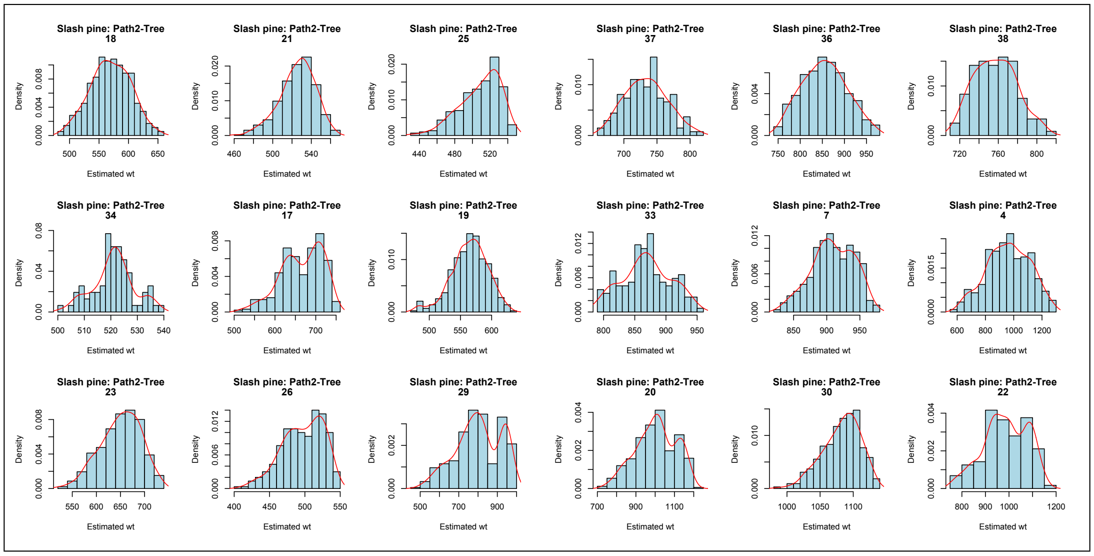


Figure 2.15: Sampling distribution by Dbh size resulting from using 1 path





Slash pine: Path2-Tree 18

Slash pine: Path2-Tree 21

Slash pine: Path2-Tree 25

Slash pine: Path2-Tree 37

Slash pine: Path2-Tree 36

Slash pine: Path2-Tree 38

Slash pine: Path2-Tree 34

Slash pine: Path2-Tree 17

Slash pine: Path2-Tree 19

Slash pine: Path2-Tree 33

Slash pine: Path2-Tree 7

Slash pine: Path2-Tree 4

Slash pine: Path2-Tree 23

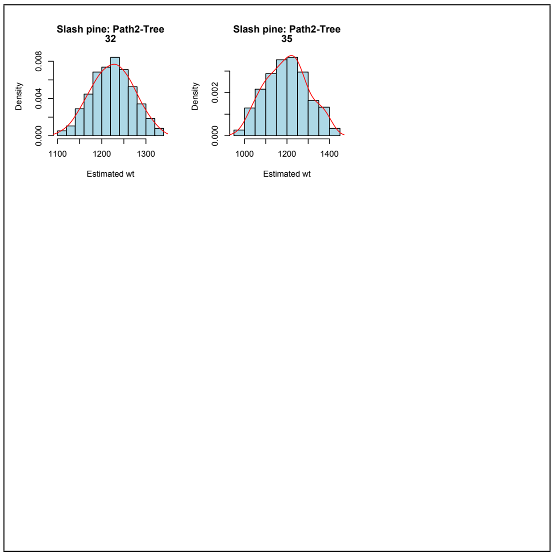
Slash pine: Path2-Tree 26

Slash pine: Path2-Tree 29

Slash pine: Path2-Tree 20

Slash pine: Path2-Tree 30

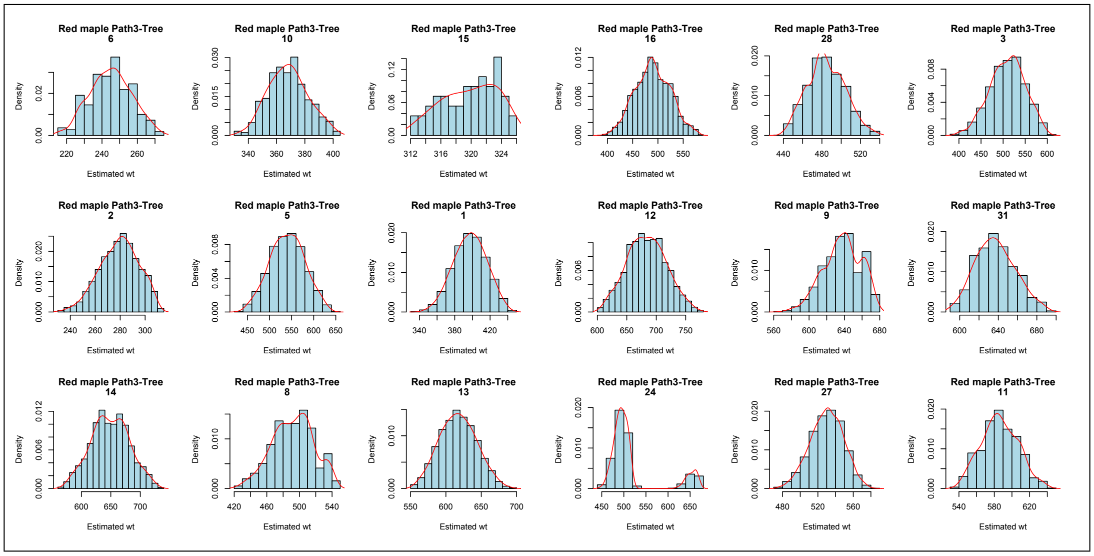
Slash pine: Path2-Tree 22

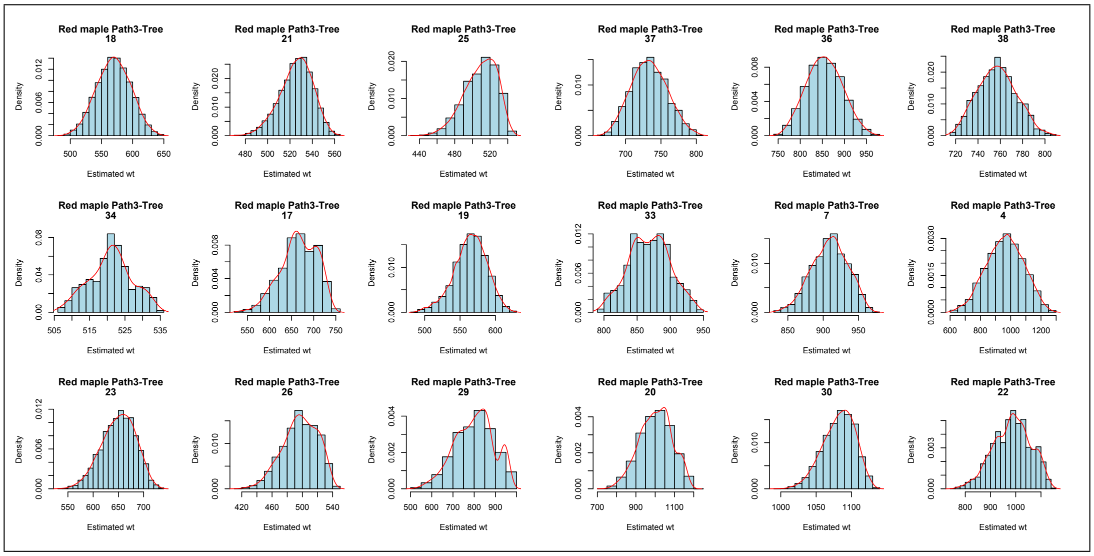


Slash pine: Path2-Tree 32

Slash pine: Path2-Tree 35

Figure 2.16: Sampling distribution by Dbh size resulting from using 2 path


Red maple Path3-Tree 6
Red maple Path3-Tree 10
Red maple Path3-Tree 15
Red maple Path3-Tree 16
Red maple Path3-Tree 28
Red maple Path3-Tree 3
Red maple Path3-Tree 2
Red maple Path3-Tree 5
Red maple Path3-Tree 1
Red maple Path3-Tree 12
Red maple Path3-Tree 9
Red maple Path3-Tree 31
Red maple Path3-Tree 14
Red maple Path3-Tree 8
Red maple Path3-Tree 13
Red maple Path3-Tree 24
Red maple Path3-Tree 27
Red maple Path3-Tree 11
Density
Estimated wt


Red maple Path3-Tree 18
Red maple Path3-Tree 21
Red maple Path3-Tree 25
Red maple Path3-Tree 37
Red maple Path3-Tree 36
Red maple Path3-Tree 38
Red maple Path3-Tree 34
Red maple Path3-Tree 17
Red maple Path3-Tree 19
Red maple Path3-Tree 33
Red maple Path3-Tree 7
Red maple Path3-Tree 4
Red maple Path3-Tree 23
Red maple Path3-Tree 26
Red maple Path3-Tree 29
Red maple Path3-Tree 20
Red maple Path3-Tree 30
Red maple Path3-Tree 22
Density
Estimated wt

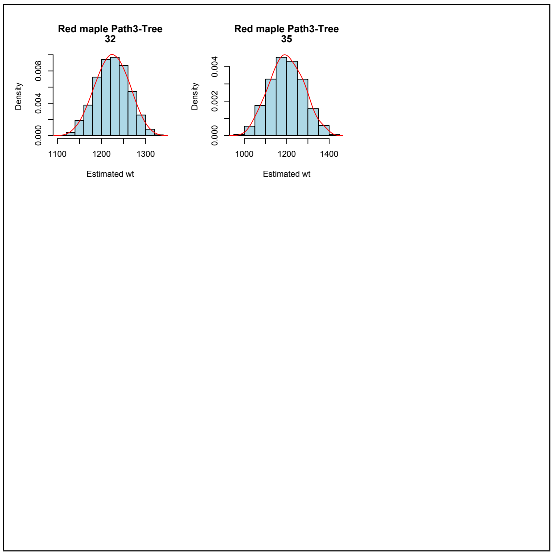
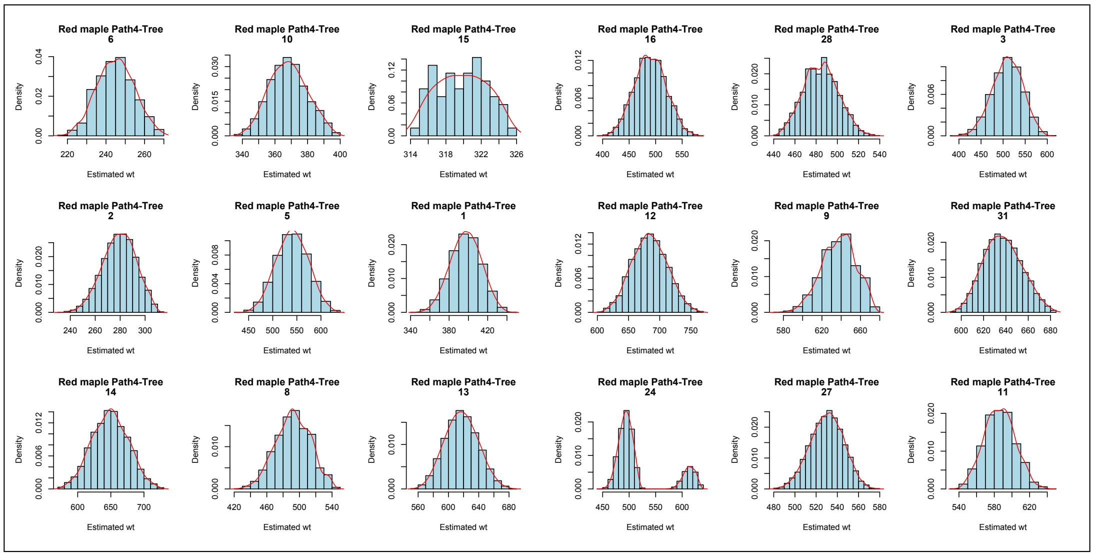
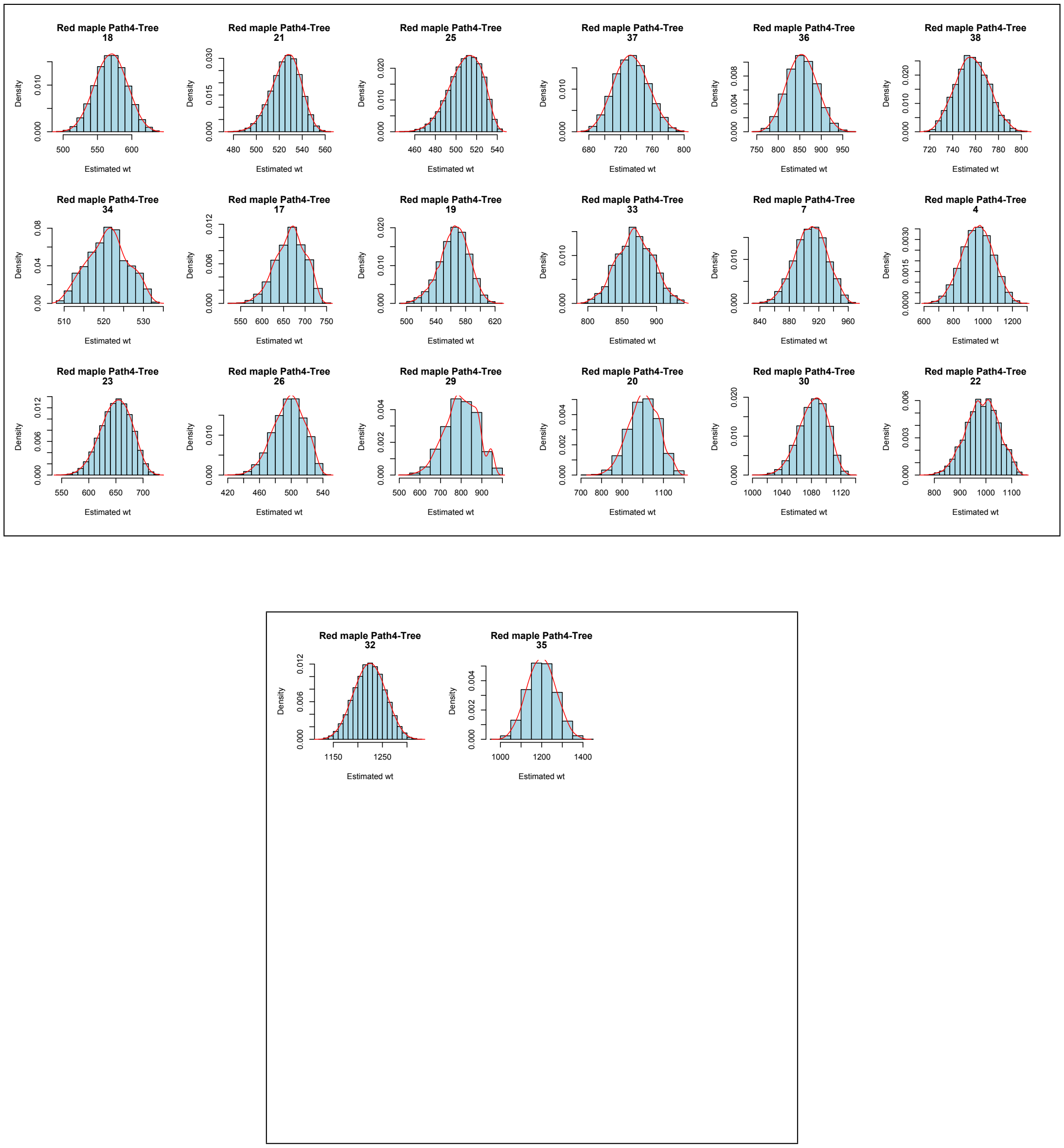


Figure 2.17: Sampling distribution by Dbh size resulting from using 3 path





Red maple Path4-Tree 18

Red maple Path4-Tree 21

Red maple Path4-Tree 25

Red maple Path4-Tree 37

Red maple Path4-Tree 36

Red maple Path4-Tree 38

Red maple Path4-Tree 34

Red maple Path4-Tree 17

Red maple Path4-Tree 19

Red maple Path4-Tree 33

Red maple Path4-Tree 7

Red maple Path4-Tree 4

Red maple Path4-Tree 23

Red maple Path4-Tree 26

Red maple Path4-Tree 29

Red maple Path4-Tree 20

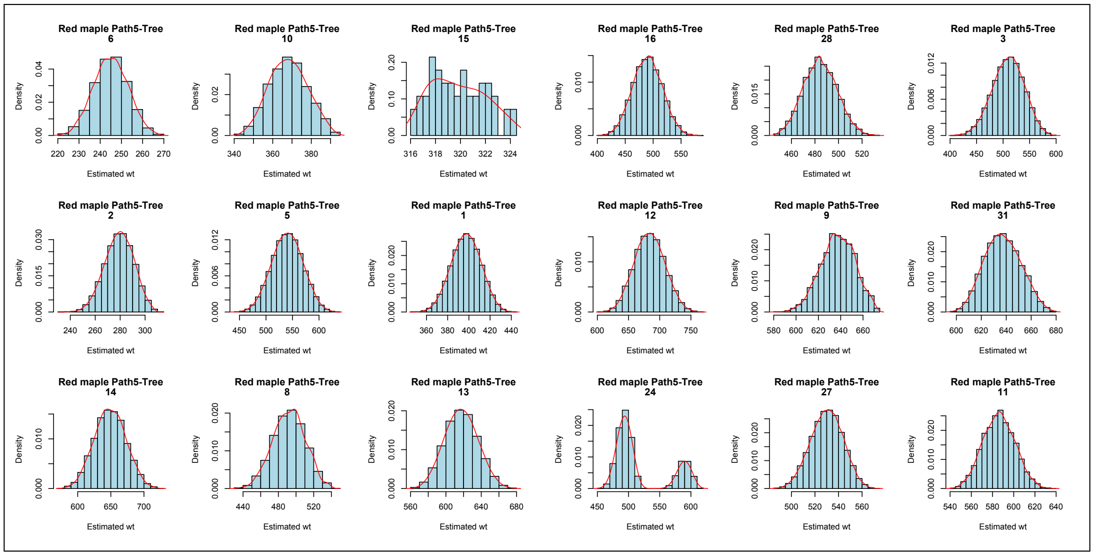
Red maple Path4-Tree 30

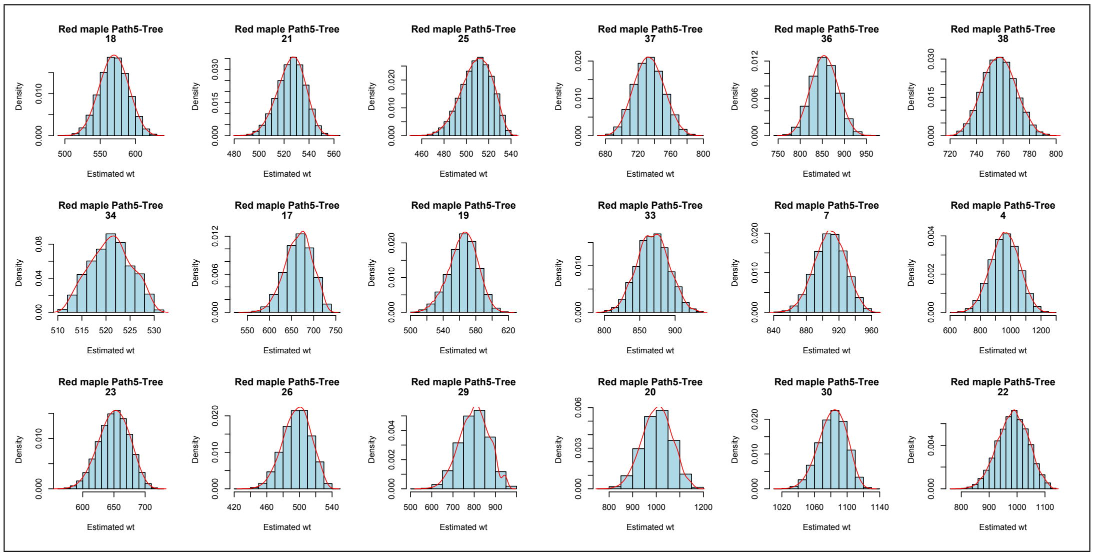
Red maple Path4-Tree 22

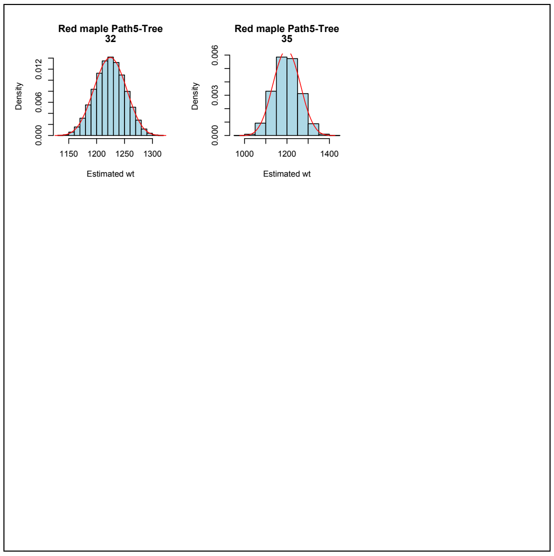
Red maple Path4-Tree 32

Red maple Path4-Tree 35

Figure 2.18: Sampling distribution by Dbh size resulting from using 4 path


Red maple Path5-Tree 6
Red maple Path5-Tree 10
Red maple Path5-Tree 15
Red maple Path5-Tree 16
Red maple Path5-Tree 28
Red maple Path5-Tree 3
Red maple Path5-Tree 2
Red maple Path5-Tree 5
Red maple Path5-Tree 1
Red maple Path5-Tree 12
Red maple Path5-Tree 9
Red maple Path5-Tree 31
Red maple Path5-Tree 14
Red maple Path5-Tree 8
Red maple Path5-Tree 13
Red maple Path5-Tree 24
Red maple Path5-Tree 27
Red maple Path5-Tree 11
Density
Estimated wt


Red maple Path5-Tree 18
Red maple Path5-Tree 21
Red maple Path5-Tree 25
Red maple Path5-Tree 37
Red maple Path5-Tree 36
Red maple Path5-Tree 38
Red maple Path5-Tree 34
Red maple Path5-Tree 17
Red maple Path5-Tree 19
Red maple Path5-Tree 33
Red maple Path5-Tree 7
Red maple Path5-Tree 4
Red maple Path5-Tree 23
Red maple Path5-Tree 26
Red maple Path5-Tree 29
Red maple Path5-Tree 20
Red maple Path5-Tree 30
Red maple Path5-Tree 22
Density
Estimated wt



Red maple Path5-Tree 32

Red maple Path5-Tree 35

Figure 2.19: Sampling distribution by Dbh size resulting from using 5 path

2.7 Appendix B: Sampling distribution of biomass estimates for red maple by Dbh size and path

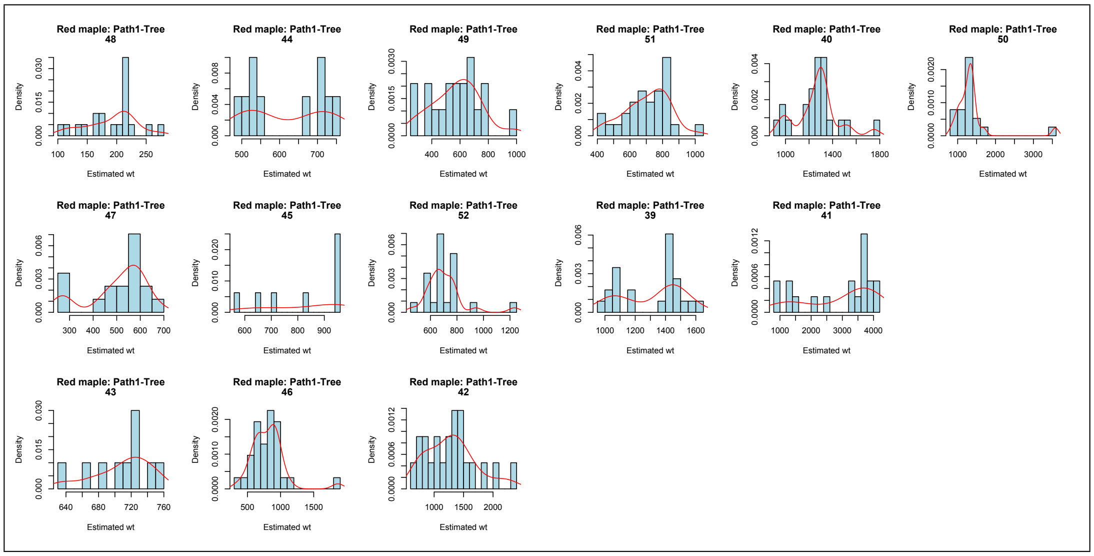


Figure 2.20: Sampling distribution by Dbh size resulting from using 1 path

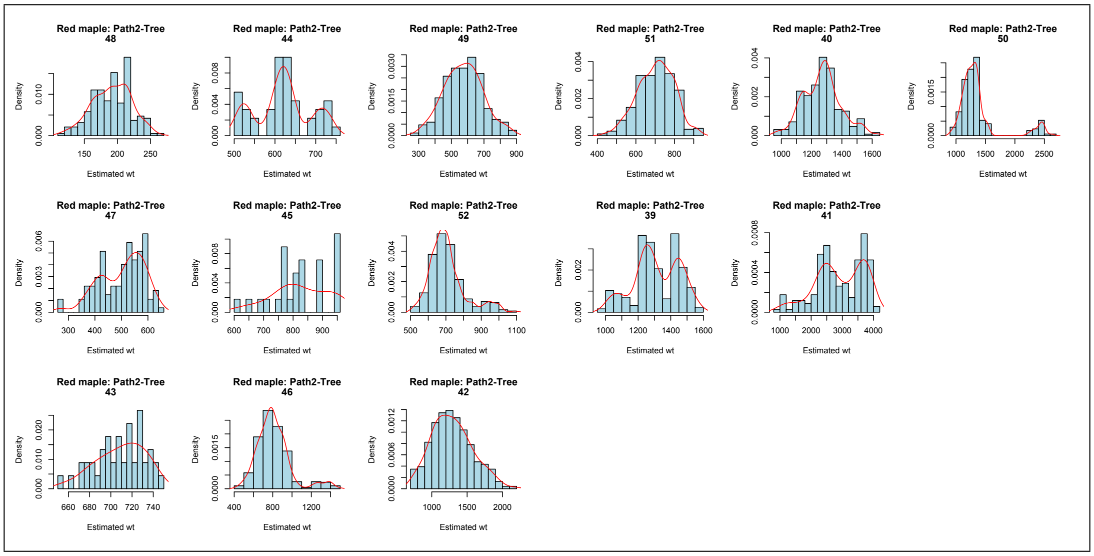


Figure 2.21: Sampling distribution by Dbh size resulting from using 2 path

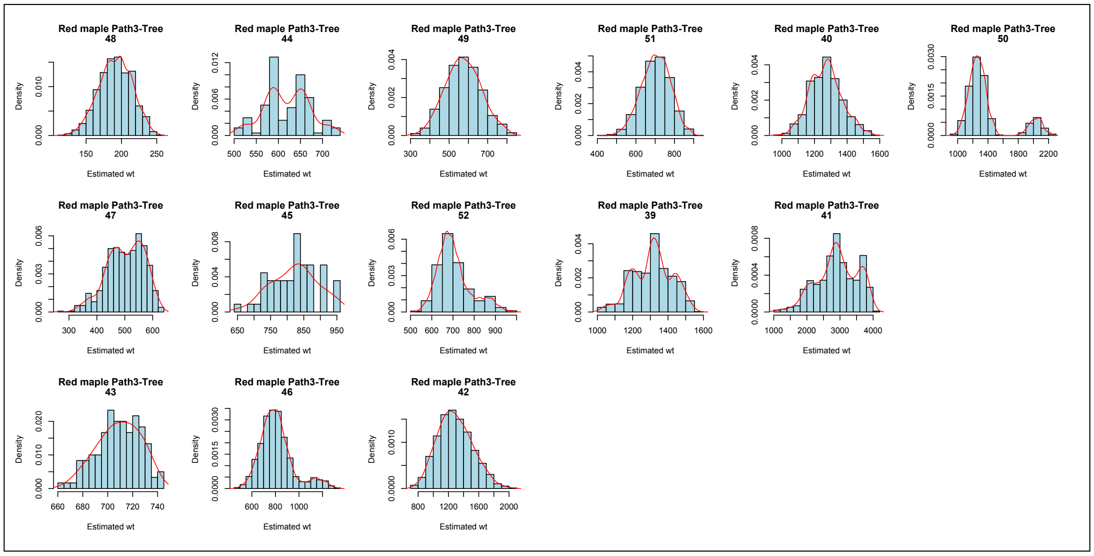


Figure 2.22: Sampling distribution by Dbh size resulting from using 3 path

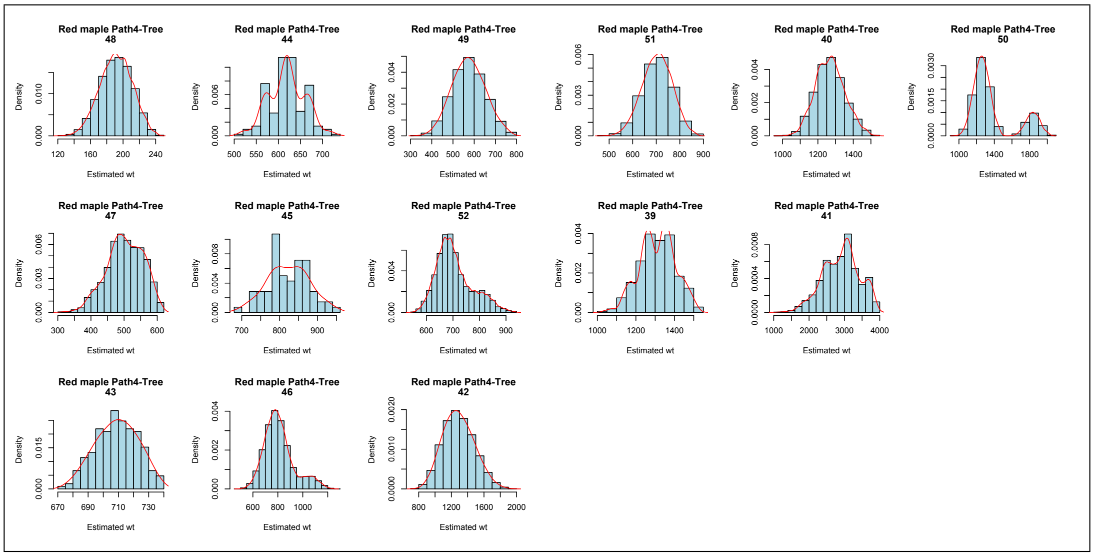


Figure 2.23: Sampling distribution by Dbh size resulting from using 4 path

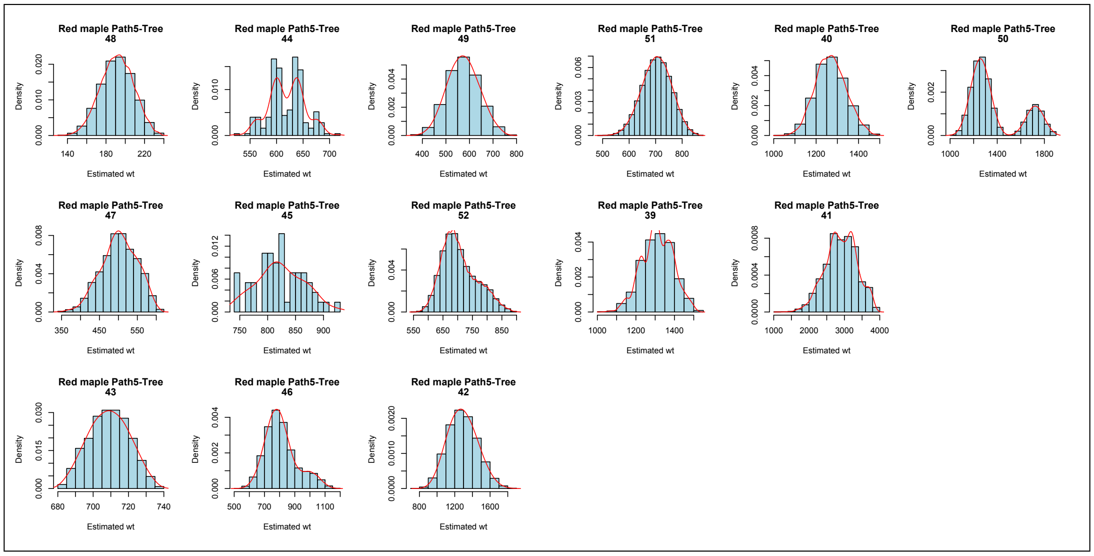


Figure 2.24: Sampling distribution by Dbh size resulting from using 5 path

2.8 APPENDIX C: RBS SAMPLING DISTRIBUTION CHRACTERISTICS

Table 2.6: RBS empirical sampling distribution characteristics by individual tree for RBS estimates resulting from use of one path

Tree id	Species Code	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Bias	Std. err.	MAPE (%)	Min. est. wt. (lbs)	Max. est. wt (lbs)
1	111	25	410.46	397.30	13.16	34.79	7.16	333.8	455.40
2	111	25	275.53	279.15	3.62	28.99	9.28	218.4	318.90
3	111	27	528.34	509.63	18.70	73.55	11.74	338.1	620.30
4	111	38	911.27	961.77	50.50	221.63	21.73	549.2	1316.00
5	111	24	544.90	540.19	4.71	73.16	11.80	420.4	658.10
6	111	12	275.55	244.95	30.59	23.31	11.49	214.0	282.00
7	111	24	903.44	909.07	5.63	47.06	4.63	816.7	975.30
8	111	19	469.01	492.01	23.00	47.61	9.52	405.7	550.60
9	111	19	632.04	637.29	5.25	39.85	5.69	560.3	690.20
10	111	14	366.04	368.17	2.14	27.34	5.45	320.3	429.40
11	111	18	582.68	586.13	3.45	39.39	5.76	530.2	645.10
12	111	20	673.39	683.71	10.32	62.47	8.15	600.0	795.60
13	111	17	611.04	617.33	6.29	49.60	6.89	540.7	704.30
14	111	21	632.43	648.91	16.48	60.71	8.56	548.5	749.10
15	111	8	323.06	319.83	3.23	7.88	1.65	303.4	327.30
16	111	34	470.68	489.68	19.01	63.53	11.46	354.8	586.60
17	111	31	651.24	665.64	14.40	74.86	10.22	491.1	755.20
18	111	27	586.53	569.52	17.01	49.80	7.06	475.3	673.60
19	111	30	582.64	564.58	18.06	42.54	6.11	435.4	636.40
20	111	37	948.65	1003.17	54.52	152.42	14.86	695.8	1221.00
21	111	31	524.44	525.61	1.17	26.84	3.88	451.0	569.40

Table 2.6 – continued from previous page

Tree id	Species Code	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Bias	Std. err.	MAPE (%)	Min. est. wt. (lbs)	Max. est. wt. (lbs)
22	111	27	913.61	985.16	71.55	135.49	14.62	750.3	1184.00
23	111	22	631.83	650.22	18.39	62.07	8.24	519.7	741.30
24	111	19	493.66	518.17	24.52	113.74	9.55	430.4	973.50
25	111	25	514.80	509.00	5.80	34.14	4.88	418.7	557.90
26	111	25	493.78	496.91	3.12	42.67	7.29	405.3	546.70
27	111	20	536.97	530.01	6.97	34.87	5.05	450.5	586.20
28	111	21	502.54	484.47	18.07	36.30	6.90	424.6	554.50
29	111	30	696.69	800.19	103.50	168.63	24.60	467.8	992.00
30	111	26	1117.50	1082.19	35.32	41.72	3.63	981.8	1137.00
31	111	14	660.09	637.18	22.91	40.11	5.50	576.3	726.90
32	111	20	1254.02	1224.04	29.97	70.03	4.93	1088.0	1343.00
33	111	18	901.00	868.61	32.39	58.79	6.04	789.6	964.30
34	111	13	557.36	520.97	36.38	11.97	6.53	494.4	546.40
35	111	33	1189.04	1198.98	9.94	146.77	10.57	955.6	1447.00
36	111	25	884.49	854.85	29.65	74.76	7.63	736.2	989.60
37	111	17	757.57	733.52	24.05	47.98	5.80	659.7	830.70
38	111	16	793.60	757.12	36.48	33.04	5.18	709.4	813.10
39	316	23	1362.28	1311.78	50.50	205.26	12.79	983.8	1634.00
40	316	23	1388.34	1269.33	119.00	182.70	12.44	934.9	1751.00
41	316	19	3106.75	2904.68	202.07	1156.03	30.84	852.9	4131.00
42	316	22	1064.34	1289.52	225.18	428.62	35.00	641.3	2309.00
43	316	10	708.05	708.93	0.89	36.04	3.95	635.8	752.60
44	316	10	606.20	619.19	12.99	103.65	15.73	496.9	746.60

Table 2.6 – continued from previous page

Tree id	Species Code	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Bias	Std. err.	MAPE (%)	Min. est. wt. (lbs)	Max. est. wt. (lbs)
45	316	8	802.51	822.78	20.28	152.81	16.75	579.4	952.80
46	316	31	814.10	810.05	4.05	263.05	22.01	357.0	1865.00
47	316	17	489.38	502.09	12.71	125.48	20.67	263.2	673.50
48	316	20	201.85	191.41	10.43	43.74	16.77	109.8	275.90
49	316	19	562.47	573.86	11.40	176.12	24.03	262.9	979.00
50	316	19	1179.81	1378.87	199.06	566.06	24.72	851.5	3579.00
51	316	29	684.54	703.49	18.95	136.96	16.51	426.6	1004.00
52	316	23	612.65	705.89	93.25	150.95	19.17	462.5	1234.00

Table 2.7: RBS empirical sampling distribution characteristics by individual tree for RBS estimates resulting from use of two paths

Tree id	Species Code	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Bias	Std. err.	MAPE (%)	Min est. wt. (lbs)	Max est. wt. (lbs)
1	111	300	410.46	397.30	13.16	23.63	5.32	336.8	450.9
2	111	300	275.53	279.15	3.62	19.70	5.99	226.4	315.8
3	111	351	528.34	509.63	18.70	50.11	8.12	371.0	612.5
4	111	703	911.27	961.77	50.50	152.64	14.46	583.9	1299.0
5	111	276	544.90	540.19	4.71	49.62	7.42	426.5	650.5
6	111	66	275.55	244.95	30.59	15.16	11.12	215.9	277.1
7	111	276	903.44	909.07	5.63	31.91	2.94	826.8	975.0
8	111	171	469.01	492.01	23.00	31.94	6.98	417.0	549.1
9	111	171	632.04	637.29	5.25	26.73	3.58	565.2	684.3
10	111	91	366.04	368.17	2.14	18.00	3.90	324.8	412.8
11	111	153	582.68	586.13	3.45	26.35	3.77	532.6	644.5
12	111	190	673.39	683.71	10.32	42.02	5.20	601.2	785.0
13	111	136	611.04	617.33	6.29	33.07	4.46	548.0	700.5
14	111	210	632.43	648.91	16.48	40.93	5.70	557.5	737.9
15	111	28	323.06	319.83	3.23	4.91	1.33	308.6	326.9
16	111	561	470.68	489.68	19.01	43.62	8.30	372.3	586.0
17	111	465	651.24	665.64	14.40	51.25	6.89	514.8	754.6
18	111	351	586.53	569.52	17.01	33.93	5.22	484.5	654.5
19	111	435	582.64	564.58	18.06	29.09	4.57	471.3	631.6
20	111	666	948.65	1003.17	54.52	104.90	10.29	723.9	1208.0
21	111	465	524.44	525.61	1.17	18.38	2.80	460.2	567.3
22	111	351	913.61	985.16	71.55	92.32	10.61	755.4	1160.0

Table 2.7 – continued from previous page

Tree id	Species Code	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Bias	Std. err.	MAPE (%)	Min. est. wt. (lbs)	Max. est. wt. (lbs)
23	111	231	631.83	650.22	18.39	41.94	6.04	521.1	737.1
24	111	171	493.66	518.17	24.52	76.30	7.98	437.3	752.5
25	111	300	514.80	509.00	5.80	23.20	3.62	430.2	549.2
26	111	300	493.78	496.91	3.12	28.99	4.95	409.9	546.7
27	111	190	536.97	530.01	6.97	23.45	3.65	464.5	584.1
28	111	210	502.54	484.47	18.07	24.48	5.02	431.6	545.8
29	111	435	696.69	800.19	103.50	115.33	18.77	497.3	990.6
30	111	325	1117.50	1082.19	35.32	28.39	3.29	986.7	1136.0
31	111	91	660.09	637.18	22.91	26.40	4.44	585.9	701.8
32	111	190	1254.02	1224.04	29.97	47.10	3.60	1108.0	1334.0
33	111	153	901.00	868.61	32.39	39.32	4.69	790.4	950.5
34	111	78	557.36	520.97	36.38	7.84	6.53	501.3	538.4
35	111	528	1189.04	1198.98	9.94	100.68	6.96	960.2	1437.0
36	111	300	884.49	854.85	29.65	50.79	5.43	740.9	978.6
37	111	136	757.57	733.52	24.05	31.99	4.35	663.5	813.1
38	111	120	793.60	757.12	36.48	21.95	4.72	710.9	810.4
39	316	253	1362.28	1311.78	50.50	138.96	9.14	995.3	1592.0
40	316	253	1388.34	1269.33	119.00	123.69	10.42	962.8	1648.0
41	316	171	3106.75	2904.68	202.07	775.49	21.71	871.4	4088.0
42	316	231	1064.34	1289.52	225.18	289.60	26.85	702.3	2198.0
43	316	45	708.05	708.93	0.89	23.05	2.67	652.5	749.1
44	316	45	606.20	619.19	12.99	66.29	8.62	500.1	742.8
45	316	28	802.51	822.78	20.28	95.30	9.61	616.4	952.1

Table 2.7 – continued from previous page

Tree id	Species Code	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Bias	Std. err.	MAPE (%)	Min. est. wt. (lbs)	Max. est. wt. (lbs)
46	316	465	814.10	810.05	4.05	180.10	15.80	418.9	1497.0
47	316	136	489.38	502.09	12.71	83.65	14.87	265.7	640.7
48	316	190	201.85	191.41	10.43	29.42	12.42	111.4	263.2
49	316	171	562.47	573.86	11.40	118.15	16.93	273.8	868.6
50	316	171	1179.81	1378.87	199.06	379.73	20.44	923.1	2628.0
51	316	406	684.54	703.49	18.95	93.56	11.41	435.4	934.3
52	316	253	612.65	705.89	93.25	102.19	16.64	513.1	1089.0

Table 2.8: RBS empirical sampling distribution characteristics by individual tree for RBS estimates resulting from use of three paths

Tree id	Species Code	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Bias	Std. err.	MAPE (%)	Min. est. wt. (lbs)	Max. est. wt. (lbs)
1	111	2300	410.46	397.30	13.16	18.85	4.51	339.7	447.5
2	111	2300	275.53	279.15	3.62	15.71	4.80	230.7	313.6
3	111	2925	528.34	509.63	18.70	40.04	6.65	388.3	607.2
4	111	8436	911.27	961.77	50.50	122.81	11.88	601.8	1292.0
5	111	2024	544.90	540.19	4.71	39.52	5.94	431.1	643.6
6	111	220	275.55	244.95	30.59	11.68	11.10	216.9	274.0
7	111	2024	903.44	909.07	5.63	25.42	2.35	834.1	972.7
8	111	969	469.01	492.01	23.00	25.24	6.02	421.0	545.3
9	111	969	632.04	637.29	5.25	21.12	2.82	569.3	679.4
10	111	364	366.04	368.17	2.14	14.01	3.11	333.8	403.9
11	111	816	582.68	586.13	3.45	20.77	2.91	533.9	643.8
12	111	1140	673.39	683.71	10.32	33.27	4.18	603.7	775.1
13	111	680	611.04	617.33	6.29	26.01	3.54	554.5	690.1
14	111	1330	632.43	648.91	16.48	32.46	4.64	567.3	733.0
15	111	56	323.06	319.83	3.23	3.63	1.18	312.4	325.7
16	111	5984	470.68	489.68	19.01	35.02	6.85	388.9	583.2
17	111	4495	651.24	665.64	14.40	41.08	5.50	525.0	754.1
18	111	2925	586.53	569.52	17.01	27.11	4.40	489.5	646.9
19	111	4060	582.64	564.58	18.06	23.30	3.99	489.5	628.5
20	111	7770	948.65	1003.17	54.52	84.36	8.70	738.2	1203.0
21	111	4495	524.44	525.61	1.17	14.73	2.27	471.1	564.7
22	111	2925	913.61	985.16	71.55	73.77	9.41	758.1	1147.0

Table 2.8 – continued from previous page

Tree id	Species Code	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Bias	Std. err.	MAPE (%)	Min. est. wt. (lbs)	Max. est. wt. (lbs)
23	111	1540	631.83	650.22	18.39	33.31	4.98	535.7	730.9
24	111	969	493.66	518.17	24.52	60.29	7.20	443.4	677.8
25	111	2300	514.80	509.00	5.80	18.50	2.96	438.0	546.1
26	111	2300	493.78	496.91	3.12	23.11	3.86	416.3	546.0
27	111	1140	536.97	530.01	6.97	18.57	2.95	476.9	582.6
28	111	1330	502.54	484.47	18.07	19.41	4.38	436.5	539.9
29	111	4060	696.69	800.19	103.50	92.38	16.81	513.9	985.9
30	111	2600	1117.50	1082.19	35.32	22.66	3.20	997.3	1135.0
31	111	364	660.09	637.18	22.91	20.55	3.95	591.0	691.4
32	111	1140	1254.02	1224.04	29.97	37.29	3.10	1117.0	1326.0
33	111	816	901.00	868.61	32.39	31.01	4.12	791.4	944.3
34	111	286	557.36	520.97	36.38	6.07	6.53	506.0	534.9
35	111	5456	1189.04	1198.98	9.94	80.80	5.55	963.3	1425.0
36	111	2300	884.49	854.85	29.65	40.50	4.64	744.5	971.6
37	111	680	757.57	733.52	24.05	25.16	3.81	668.0	804.8
38	111	560	793.60	757.12	36.48	17.21	4.62	715.0	806.0
39	316	1771	1362.28	1311.78	50.50	110.54	7.15	1001.0	1568.0
40	316	1771	1388.34	1269.33	119.00	98.39	9.50	972.1	1594.0
41	316	969	3106.75	2904.68	202.07	612.80	16.73	1021.0	4021.0
42	316	1540	1064.34	1289.52	225.18	230.05	24.27	723.4	2066.0
43	316	120	708.05	708.93	0.89	17.48	2.04	664.1	742.6
44	316	120	606.20	619.19	12.99	50.28	7.02	511.4	733.3
45	316	56	802.51	822.78	20.28	70.38	7.50	650.3	950.9

Table 2.8 – continued from previous page

Tree id	Species Code	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Bias	Std. err.	MAPE (%)	Min. est. wt. (lbs)	Max. est. wt. (lbs)
46	316	4495	814.10	810.05	4.05	144.35	13.19	463.5	1337.0
47	316	680	489.38	502.09	12.71	65.79	11.43	270.2	628.9
48	316	1140	201.85	191.41	10.43	23.29	10.10	118.2	250.3
49	316	969	562.47	573.86	11.40	93.36	13.42	310.8	830.5
50	316	969	1179.81	1378.87	199.06	300.06	18.91	947.8	2232.0
51	316	3654	684.54	703.49	18.95	74.89	9.15	446.1	900.2
52	316	1771	612.65	705.89	93.25	81.29	15.86	536.9	985.4

Table 2.9: RBS empirical sampling distribution characteristics by individual tree for RBS estimates resulting from use of four paths

Tree id	Species Code	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Bias	Std. err.	MAPE (%)	Min. est. wt. (lbs)	Max. est. wt. (lbs)
1	111	12650	410.46	397.30	13.16	15.94	4.08	344.6	445.7
2	111	12650	275.53	279.15	3.62	13.29	4.07	232.8	312.2
3	111	17550	528.34	509.63	18.70	33.94	5.86	398.3	604.0
4	111	73815	911.27	961.77	50.50	104.82	10.36	613.9	1283.0
5	111	10626	544.90	540.19	4.71	33.39	5.00	435.0	638.1
6	111	495	275.55	244.95	30.59	9.53	11.10	217.4	269.9
7	111	10626	903.44	909.07	5.63	21.48	2.00	838.0	968.6
8	111	3876	469.01	492.01	23.00	21.16	5.58	425.2	543.5
9	111	3876	632.04	637.29	5.25	17.70	2.40	574.9	675.5
10	111	1001	366.04	368.17	2.14	11.56	2.60	338.6	398.9
11	111	3060	582.68	586.13	3.45	17.37	2.46	537.9	640.0
12	111	4845	673.39	683.71	10.32	27.94	3.56	605.0	769.4
13	111	2380	611.04	617.33	6.29	21.69	2.98	558.5	684.6
14	111	5985	632.43	648.91	16.48	27.31	4.09	572.5	728.6
15	111	70	323.06	319.83	3.23	2.80	1.09	314.5	325.1
16	111	46376	470.68	489.68	19.01	29.84	6.07	398.2	581.5
17	111	31465	651.24	665.64	14.40	34.93	4.78	532.9	751.8
18	111	17550	586.53	569.52	17.01	22.98	3.95	493.4	639.9
19	111	27405	582.64	564.58	18.06	19.80	3.68	498.7	624.8
20	111	66045	948.65	1003.17	54.52	71.97	7.83	748.0	1196.0
21	111	31465	524.44	525.61	1.17	12.52	1.94	476.5	563.0
22	111	17550	913.61	985.16	71.55	62.53	8.79	766.2	1141.0

Table 2.9 – continued from previous page

Tree id	Species Code	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Bias	Std. err.	MAPE (%)	Min. est. wt. (lbs)	Max. est. wt. (lbs)
23	111	7315	631.83	650.22	18.39	28.07	4.38	548.7	727.7
24	111	3876	493.66	518.17	24.52	50.54	6.73	448.6	637.6
25	111	12650	514.80	509.00	5.80	15.65	2.56	447.6	543.8
26	111	12650	493.78	496.91	3.12	19.55	3.27	424.0	544.8
27	111	4845	536.97	530.01	6.97	15.59	2.54	483.4	576.2
28	111	5985	502.54	484.47	18.07	16.33	4.07	442.3	536.9
29	111	27405	696.69	800.19	103.50	78.50	15.97	522.6	983.5
30	111	14950	1117.50	1082.19	35.32	19.19	3.17	1007.0	1134.0
31	111	1001	660.09	637.18	22.91	16.96	3.70	593.5	683.6
32	111	4845	1254.02	1224.04	29.97	31.32	2.84	1127.0	1321.0
33	111	3060	901.00	868.61	32.39	25.93	3.87	792.0	939.2
34	111	715	557.36	520.97	36.38	4.99	6.53	509.0	532.2
35	111	40920	1189.04	1198.98	9.94	68.79	4.72	979.5	1418.0
36	111	12650	884.49	854.85	29.65	34.26	4.21	752.1	966.9
37	111	2380	757.57	733.52	24.05	20.99	3.54	674.1	795.9
38	111	1820	793.60	757.12	36.48	14.31	4.60	719.3	801.7
39	316	8855	1362.28	1311.78	50.50	93.29	6.19	1014.0	1548.0
40	316	8855	1388.34	1269.33	119.00	83.03	9.05	987.9	1540.0
41	316	3876	3106.75	2904.68	202.07	513.65	14.01	1115.0	3980.0
42	316	7315	1064.34	1289.52	225.18	193.86	22.93	747.0	1961.0
43	316	210	708.05	708.93	0.89	13.99	1.62	674.2	739.2
44	316	210	606.20	619.19	12.99	40.24	5.60	517.6	725.6
45	316	70	802.51	822.78	20.28	54.42	5.85	695.8	949.7

Table 2.9 – continued from previous page

Tree id	Species Code	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Bias	Std. err.	MAPE (%)	Min. est. wt. (lbs)	Max. est. wt. (lbs)
46	316	31465	814.10	810.05	4.05	122.75	11.56	487.2	1253.0
47	316	2380	489.38	502.09	12.71	54.87	9.40	309.8	619.6
48	316	4845	201.85	191.41	10.43	19.56	8.80	124.1	242.1
49	316	3876	562.47	573.86	11.40	78.25	11.31	332.3	798.5
50	316	3876	1179.81	1378.87	199.06	251.51	18.11	977.1	2026.0
51	316	23751	684.54	703.49	18.95	63.59	7.85	464.6	882.4
52	316	8855	612.65	705.89	93.25	68.60	15.50	549.3	932.0

Table 2.10: RBS empirical sampling distribution characteristics by individual tree for RBS estimates resulting from use of five paths

Tree id	Species Code	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Bias	Std. err.	MAPE (%)	Min. est. wt. (lbs)	Max. est. wt. (lbs)
1	111	53130	410.46	397.30	13.16	13.92	3.82	348.1	443.1
2	111	53130	275.53	279.15	3.62	11.60	3.58	234.5	310.7
3	111	80730	528.34	509.63	18.70	29.69	5.31	405.9	599.7
4	111	501942	911.27	961.77	50.50	92.36	9.37	623.2	1278.0
5	111	42504	544.90	540.19	4.71	29.11	4.36	442.0	633.3
6	111	792	275.55	244.95	30.59	7.97	11.10	221.9	266.5
7	111	42504	903.44	909.07	5.63	18.72	1.75	841.2	965.0
8	111	11628	469.01	492.01	23.00	18.28	5.31	430.1	542.0
9	111	11628	632.04	637.29	5.25	15.30	2.08	581.1	673.2
10	111	2002	366.04	368.17	2.14	9.80	2.23	342.0	394.3
11	111	8568	582.68	586.13	3.45	14.97	2.12	541.6	636.2
12	111	15504	673.39	683.71	10.32	24.20	3.14	608.0	764.8
13	111	6188	611.04	617.33	6.29	18.64	2.59	562.1	677.6
14	111	20349	632.43	648.91	16.48	23.70	3.70	576.3	724.0
15	111	56	323.06	319.83	3.23	2.18	1.04	316.3	324.3
16	111	278256	470.68	489.68	19.01	26.24	5.57	404.1	580.5
17	111	169911	651.24	665.64	14.40	30.66	4.27	537.9	748.4
18	111	80730	586.53	569.52	17.01	20.10	3.66	496.6	635.0
19	111	142506	582.64	564.58	18.06	17.37	3.49	504.6	622.6
20	111	435897	948.65	1003.17	54.52	63.39	7.27	756.7	1191.0
21	111	169911	524.44	525.61	1.17	10.99	1.70	482.0	561.1
22	111	80730	913.61	985.16	71.55	54.70	8.42	776.5	1133.0

Table 2.10 – continued from previous page

Tree id	Species Code	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Bias	Std. err.	MAPE (%)	Min. est. wt. (lbs)	Max. est. wt. (lbs)
23	111	26334	631.83	650.22	18.39	24.40	3.98	560.5	724.9
24	111	11628	493.66	518.17	24.52	43.66	6.40	453.5	612.5
25	111	53130	514.80	509.00	5.80	13.66	2.28	453.4	542.3
26	111	53130	493.78	496.91	3.12	17.07	2.86	428.7	543.3
27	111	15504	536.97	530.01	6.97	13.50	2.27	487.3	572.2
28	111	20349	502.54	484.47	18.07	14.17	3.88	445.9	534.0
29	111	142506	696.69	800.19	103.50	68.84	15.50	536.5	978.4
30	111	65780	1117.50	1082.19	35.32	16.77	3.16	1015.0	1131.0
31	111	2002	660.09	637.18	22.91	14.39	3.57	596.6	677.9
32	111	15504	1254.02	1224.04	29.97	27.12	2.68	1136.0	1313.0
33	111	8568	901.00	868.61	32.39	22.35	3.75	797.9	935.4
34	111	1287	557.36	520.97	36.38	4.20	6.53	510.8	530.6
35	111	237336	1189.04	1198.98	9.94	60.46	4.15	990.7	1413.0
36	111	53130	884.49	854.85	29.65	29.90	3.94	757.2	962.2
37	111	6188	757.57	733.52	24.05	18.03	3.38	678.9	790.3
38	111	4368	793.60	757.12	36.48	12.25	4.60	722.1	798.9
39	316	33649	1362.28	1311.78	50.50	81.21	5.64	1027.0	1530.0
40	316	33649	1388.34	1269.33	119.00	72.28	8.81	1023.0	1498.0
41	316	11628	3106.75	2904.68	202.07	443.80	12.51	1193.0	3939.0
42	316	26334	1064.34	1289.52	225.18	168.50	22.19	770.4	1886.0
43	316	252	708.05	708.93	0.89	11.42	1.33	682.1	735.8
44	316	252	606.20	619.19	12.99	32.84	4.64	523.8	714.6
45	316	56	802.51	822.78	20.28	42.23	4.64	745.9	926.3

Table 2.10 – continued from previous page

Tree id	Species Code	Total paths	Actual wt. (lbs)	Mean est. wt. (lbs)	Bias	Std. err.	MAPE (%)	Min. est. wt. (lbs)	Max. est. wt. (lbs)
46	316	169911	814.10	810.05	4.05	107.74	10.37	502.3	1192.0
47	316	6188	489.38	502.09	12.71	47.15	8.11	341.5	613.8
48	316	15504	201.85	191.41	10.43	16.94	7.93	131.4	237.1
49	316	11628	562.47	573.86	11.40	67.61	9.83	354.8	773.9
50	316	11628	1179.81	1378.87	199.06	217.31	17.62	1007.0	1898.0
51	316	118755	684.54	703.49	18.95	55.72	6.95	485.5	871.3
52	316	33649	612.65	705.89	93.25	59.72	15.34	557.0	898.2

2.9 Appendix D: Standard error and MAPE by species and path

Table 2.11: Standard error by species and path

Species Code	Path combination	Minimum	Mean	Maximum	Range
111	1	7.88	63.17	221.60	213.72
111	2	4.91	42.85	152.60	147.69
111	3	3.63	34.12	122.80	119.17
111	4	2.81	28.83	104.80	102.00
111	5	2.18	25.12	92.36	90.18
316	1	36.04	266.20	1156.00	1119.96
316	2	23.05	178.50	775.50	752.45
316	3	17.48	140.90	612.80	595.32
316	4	13.99	118.00	513.60	499.61
316	5	11.42	101.70	443.80	432.38

Table 2.12: Mape(%) by species and path

Species Code	Path combination	Minimum	Mean	Maximum	Range
111	1	1.65	8.42	24.60	22.95
111	2	1.33	6.13	18.77	17.44
111	3	1.18	5.25	16.81	15.63
111	4	1.09	4.76	15.97	14.88
111	5	1.04	4.44	15.50	14.46
316	1	3.95	19.38	35.00	31.05
316	2	2.67	14.11	26.85	24.18
316	3	2.04	11.88	24.27	22.23
316	4	1.63	10.55	22.93	21.31
316	5	1.33	9.71	22.19	20.86

Table 2.13: RSE (%) by species and path

Species Code	Path combination	Minimum	Mean	Maximum	Range
111	1	1.88	8.99	24.68	22.81
111	2	1.33	6.36	17.45	16.12
111	3	1.08	5.19	14.25	13.17
111	4	0.94	4.50	12.34	11.40
111	5	0.84	4.02	11.04	10.20
316	1	4.99	19.57	29.50	24.51
316	2	3.53	13.84	20.86	17.33
316	3	2.88	11.30	17.03	14.15
316	4	2.49	9.79	14.75	12.26
316	5	2.23	8.75	13.19	10.96

2.10 Appendix E: Relative standard error (RSE) of estimates

Table 2.14: Relative standard error (in percent) of wood and foliage estimates with number of paths (replications) used on the same tree

			RBS paths (replications)				
Tree id	Species Code	Actual weight (lbs)	1	2	3	4	5
1	111	410.46	8.66	6.12	5.00	4.33	3.87
2	111	275.53	10.16	7.18	5.87	5.08	4.54
3	111	528.34	13.44	9.50	7.76	6.72	6.01
4	111	911.27	24.68	17.45	14.25	12.34	11.04
5	111	544.90	12.60	8.91	7.27	6.30	5.63
6	111	275.55	7.20	5.09	4.16	3.60	3.22
7	111	903.44	5.16	3.65	2.98	2.58	2.31
8	111	469.01	8.97	6.34	5.18	4.48	4.01
9	111	632.04	6.19	4.38	3.57	3.10	2.77
10	111	366.04	6.32	4.47	3.65	3.16	2.83
11	111	582.68	6.41	4.53	3.70	3.21	2.87
12	111	673.39	7.93	5.61	4.58	3.96	3.55
13	111	611.04	7.75	5.48	4.48	3.88	3.47
14	111	632.43	8.30	5.87	4.79	4.15	3.71
15	111	323.06	2.40	1.70	1.39	1.20	1.07
16	111	470.68	12.40	8.77	7.16	6.20	5.55
17	111	651.24	12.53	8.86	7.23	6.26	5.60
18	111	586.53	6.45	4.56	3.72	3.23	2.89
19	111	582.64	8.40	5.94	4.85	4.20	3.76
20	111	948.65	15.09	10.67	8.71	7.55	6.75

Table 2.14 – continued from previous page

			RBS paths (replications)				
Tree id	Species Code	Actual weight (lbs)	1	2	3	4	5
21	111	524.44	6.91	4.89	3.99	3.46	3.09
22	111	913.61	14.08	9.96	8.13	7.04	6.30
23	111	631.83	11.74	8.30	6.78	5.87	5.25
24	111	493.66	12.36	8.74	7.14	6.18	5.53
25	111	514.80	7.23	5.11	4.17	3.61	3.23
26	111	493.78	9.22	6.52	5.32	4.61	4.12
27	111	536.97	6.35	4.49	3.66	3.17	2.84
28	111	502.54	7.35	5.20	4.24	3.68	3.29
29	111	696.69	22.41	15.84	12.94	11.20	10.02
30	111	1117.50	4.25	3.01	2.45	2.13	1.90
31	111	660.09	5.24	3.70	3.02	2.62	2.34
32	111	1254.02	5.19	3.67	2.99	2.59	2.32
33	111	901.00	6.03	4.26	3.48	3.01	2.69
34	111	557.36	1.87	1.33	1.08	0.94	0.84
35	111	1189.04	12.41	8.77	7.16	6.20	5.55
36	111	884.49	8.02	5.67	4.63	4.01	3.59
37	111	757.57	5.73	4.05	3.31	2.86	2.56
38	111	793.60	4.18	2.95	2.41	2.09	1.87
39	316	1362.28	12.90	9.12	7.45	6.45	5.77
40	316	1388.34	9.69	6.85	5.59	4.84	4.33
41	316	3106.75	25.74	18.20	14.86	12.87	11.51
42	316	1064.34	27.96	19.77	16.14	13.98	12.50
43	316	708.05	4.99	3.53	2.88	2.49	2.23

Table 2.14 – continued from previous page

			RBS paths (replications)				
Tree id	Species Code	Actual weight (lbs)	1	2	3	4	5
44	316	606.20	17.04	12.05	9.84	8.52	7.62
45	316	802.51	14.72	10.41	8.50	7.36	6.58
46	316	814.10	27.93	19.75	16.13	13.97	12.49
47	316	489.38	29.50	20.86	17.03	14.75	13.19
48	316	201.85	25.11	17.75	14.50	12.55	11.23
49	316	562.47	24.32	17.20	14.04	12.16	10.88
50	316	1179.81	19.30	13.65	11.14	9.65	8.63
51	316	684.54	18.63	13.17	10.76	9.31	8.33
52	316	612.65	16.20	11.46	9.36	8.10	7.25
Average		738.18	11.84	8.38	6.84	5.92	5.30

2.11 APPENDIX F: TOTAL ABOOVEGROUND BIOMASS USING RBS AND RBS WITH IS

Table 2.15: Total aboveground biomass using RBS

Tree id	Species Code	Number of paths	Actual weight (lbs)	Estimated weight (lbs)	RMSE	Percent error
1	111	2	420.62	378.20	61.40	14.60
2	111	2	281.49	253.10	31.17	11.07
3	111	2	541.41	541.62	6.67	1.23
4	111	2	931.90	985.85	178.99	19.21
5	111	2	558.68	531.62	54.87	9.82
6	111	2	281.78	269.42	12.36	4.39
7	111	2	918.70	926.98	50.25	5.47
8	111	2	478.70	423.31	57.67	12.05
9	111	2	646.12	625.18	38.18	5.91
10	111	2	373.15	365.64	12.84	3.44
11	111	2	595.46	533.39	62.11	10.43
12	111	2	688.90	650.46	61.50	8.93
13	111	2	623.95	589.10	37.11	5.95
14	111	2	647.12	572.91	77.28	11.94
15	111	2	330.35	323.60	6.92	2.10
16	111	2	480.21	469.28	26.18	5.45
17	111	2	664.83	562.15	102.68	15.44
18	111	2	597.43	583.11	19.25	3.22
19	111	2	594.98	522.40	73.72	12.39
20	111	2	968.36	845.70	131.57	13.59
21	111	2	535.75	532.73	8.12	1.52
22	111	2	935.28	793.99	144.01	15.40

Table 2.15 – continued from previous page

Tree id	Species Code	Number of paths	Actual weight (lbs)	Estimated weight (lbs)	RMSE	Percent error
23	111	2	645.32	618.86	102.63	15.90
24	111	2	505.16	518.23	13.07	2.59
25	111	2	525.96	528.17	9.18	1.75
26	111	2	504.33	495.55	45.86	9.09
27	111	2	547.94	506.54	41.42	7.56
28	111	2	514.41	501.23	39.32	7.64
29	111	2	708.95	974.17	266.39	37.58
30	111	2	1142.31	1106.10	45.84	4.01
31	111	2	674.73	667.22	63.34	9.39
32	111	2	1280.20	1233.34	51.39	4.01
33	111	2	919.29	875.18	63.08	6.86
34	111	2	570.17	522.21	48.01	8.42
35	111	2	1215.50	1069.72	176.98	14.56
36	111	2	903.71	980.15	77.23	8.55
37	111	2	775.16	695.21	80.01	10.32
38	111	2	811.57	810.45	2.85	0.35
39	316	3	1391.96	1130.00	274.96	19.75
40	316	3	1419.66	1431.34	93.07	6.56
41	316	3	3161.20	3307.34	146.34	4.63
42	316	3	1086.92	974.65	187.52	17.25
43	316	3	726.68	689.95	54.06	7.44
44	316	3	619.12	706.53	92.80	14.99
45	316	3	820.35	832.42	12.07	1.47
46	316	3	830.96	1156.63	601.04	72.33

Table 2.15 – continued from previous page

Tree id	Species Code	Number of paths	Actual weight (lbs)	Estimated weight (lbs)	RMSE	Percent error
47	316	3	497.78	487.56	159.14	31.97
48	316	3	205.65	222.70	60.61	29.47
49	316	3	572.33	537.82	69.95	12.22
50	316	3	1212.29	1297.44	295.14	24.35
51	316	3	701.25	620.28	199.75	28.48
52	316	3	624.17	560.68	152.72	24.47
Total			**39210.21**	**38337.41**	**149.04**	**0.38**

Table 2.16: Total aboveground biomass using RBS and IS

Tree id	Species Code	Number of paths	Actual weight (lbs)	Estimated weight (lbs)	RMSE	Percent error
1	111	2	420.62	534.84	114.92	27.32
2	111	2	281.49	444.81	167.65	59.56
3	111	2	541.41	700.86	159.59	29.48
4	111	2	931.90	926.50	273.20	29.32
5	111	2	558.68	773.61	216.99	38.84
6	111	2	281.78	330.23	48.44	17.19
7	111	2	918.70	1052.96	137.55	14.97
8	111	2	478.70	612.30	134.14	28.02
9	111	2	646.12	797.73	171.86	26.60
10	111	2	373.15	449.63	78.98	21.16
11	111	2	595.46	723.37	128.60	21.60
12	111	2	688.90	862.53	175.42	25.46
13	111	2	623.95	703.81	80.20	12.85
14	111	2	647.12	732.24	86.92	13.43
15	111	2	330.35	406.76	76.51	23.16
16	111	2	480.21	711.25	232.05	48.32
17	111	2	664.83	902.92	238.10	35.81
18	111	2	597.43	720.70	123.92	20.74
19	111	2	594.98	876.47	364.47	61.26
20	111	2	968.36	975.10	118.05	12.19
21	111	2	535.75	558.31	468.60	87.47
22	111	2	935.28	1090.47	156.12	16.69
23	111	2	645.32	732.56	128.76	19.95

Table 2.16 – continued from previous page

Tree id	Species Code	Number of paths	Actual weight (lbs)	Estimated weight (lbs)	RMSE	Percent error
24	111	2	505.16	773.85	268.69	53.19
25	111	2	525.96	736.76	210.92	40.10
26	111	2	504.33	690.84	188.51	37.38
27	111	2	547.94	688.14	140.21	25.59
28	111	2	514.41	663.59	154.57	30.05
29	111	2	708.95	965.14	450.30	63.52
30	111	2	1142.31	1452.38	310.37	27.17
31	111	2	674.73	929.32	267.44	39.64
32	111	2	1280.20	1582.57	302.39	23.62
33	111	2	919.29	1223.42	317.55	34.54
34	111	2	570.17	787.50	219.32	38.47
35	111	2	1215.50	1583.93	368.90	30.35
36	111	2	903.71	1270.18	367.13	40.63
37	111	2	775.16	956.32	181.25	23.38
38	111	2	811.57	1035.95	224.43	27.65
39	316	3	1391.96	1656.51	395.63	28.42
40	316	3	1419.66	1439.68	101.18	7.13
41	316	3	3161.20	3574.23	416.61	13.18
42	316	3	1086.92	1130.77	115.96	10.67
43	316	3	726.68	773.86	60.61	8.34
44	316	3	619.12	803.30	186.02	30.05
45	316	3	820.35	912.50	92.15	11.23
46	316	3	830.96	1437.00	902.69	108.63
47	316	3	497.78	473.21	205.53	41.29

Table 2.16 – continued from previous page

Tree id	Species Code	Number of paths	Actual weight (lbs)	Estimated weight (lbs)	RMSE	Percent error
48	316	3	205.65	170.63	99.62	48.44
49	316	3	572.33	589.74	46.66	8.15
50	316	3	1212.29	1472.43	423.41	34.93
51	316	3	701.25	435.76	475.87	67.86
52	316	3	624.17	475.28	203.98	32.68
Total			**39210.21**	**47304.74**	**279.24**	**0.71**

Chapter 3

ADDITIVE EXPLICIT INDIVIDUAL TREE BIOMASS PREDICTION FUNCTIONS FOR RED MAPLE AND SLASH PINE

3.1 Introduction

Forests are a major part of global the carbon (C) cycle and forest management practices can influence the concentration of the greenhouse gases such as CO_2, in the atmosphere (Houghton and Woodwell 1989). Forest ecosystems store large amounts of carbon in solid wood and other organic matter. Studies have shown that management activities such as afforestation, fertilization, and prescribed burning have increased the amount of C residing in forests (Tans et al. 1990, Cias et al. 1995, Pacala et al. 2001). Over the past four decades, various studies on forest biomass have been conducted to better understand timber production potential, ecosystem productivity, energy and nutrient flow, and forestland contribution to the global carbon cycle (Zeide 1987; Waring and Running 1998; Parresol 1999). Researchers have focused on carbon (C) stocks in forests because forest ecosystems are the main terrestrial sinks for C (Murias et al. 2006).

Recently, interest in estimating individual tree and stand biomass has increased due to increased concern about using biomass for fuel, energy and carbon sequestration around the world. Quantification of forest biomass is important in evaluating the total carbon stock and fluxes in forests (Brown 1997, Navar 2009), amount of energy available from forests as an alternative source to fossil fuels (Richardson et al. 2002), as well as other goods and services from forests. Zianis and Mencuccini (2003) point out that forest biomass is a crucial factor for several ecological and eco-physiological models. Appropriate modeling strategies are necessary to obtain reliable estimates of forest biomass. Individual tree biomass equations , based on dendrometric tree measurements, underpin estimates of aboveground biomass components (bole wood, foliage, and branches) and total tree biomass.

The most common method used in estimating individual tree and stand biomass is by application of allometric equations (Brown et al. 1989, Chave et al. 2001, 2003, Navar 2009). Functions, for example Equation 3.1, that calibrate relationship between plant biomass and one or more tree size variates (eg. stem diameter or height) are sometimes called allometric relationships (West 2009). A classic and widely used allometric equation of nonlinear form is

$$\mathrm{Y} = \alpha \mathrm{Dbh}^{\beta} \tag{3.1}$$

Tree biomass component Y is estimated based on an easily measured variable such as diameter at breast height (Dbh). In Equation 3.1 α and β are scalar coefficients which are typically estimated using least square techniques with appropriate data.

Many researchers use the logarithmic form of the Equation 3.1 (Martin et al. 1998) i.e. the regression parameters $\ln_e\alpha$ (or $\log_{10}\alpha$) and β are estimated using linear regression applied to the logarithm of biomass and Dbh values.

In general, biomass regression models are constructed for total aboveground biomass, and tree components such as stem wood, stem bark, crown (branches and foliage), foliage, stump and roots. Separate equations (univariate models) for each of the components have been used to estimate and predict biomass. Often, models for each of the components is fitted separately and parameters are estimated by ordinary least squares (OLS) (e.g. Brenneman et al. 1978, Bridge 1979, Freedman et al. 1982, Ker 1984). A fundamental assumption in OLS is the error terms of various component models are independent to each other. However, tree biomass components are not independent of one another and hence it is likely that error components of various prediction functions are, in fact, not independent but are correlated with one another.

Zellner (1962) developed the seemingly unrelated regression (SUR) estimator which accounts for contemporaneous correlations (group of equations that share a common error structure and have non-zero covariance is known to have contemporaneous correlations) among error components for individual equations within the system of equations of interest. In SUR, parameters of the system of equations involved are estimated simultaneously.

Equation 3.2 presents a typical SUR system in linear form (Borders 1989)

$$\begin{aligned} \mathrm{Y}_1 &= \beta_{10} + \beta_{11}\mathrm{X}_1 + \beta_{12}\mathrm{X}_2 + \varepsilon_1, \varepsilon_1 \sim \mathrm{N}(0, \sigma_1^2) \\ \mathrm{Y}_2 &= \beta_{20} + \beta_{21}\mathrm{X}_3 + \beta_{22}\mathrm{X}_4 + \varepsilon_2, \varepsilon_2 \sim \mathrm{N}(0, \sigma_2^2) \\ \mathrm{Y}_3 &= \beta_{30} + \beta_{31}\mathrm{X}_5 + \beta_{32}\mathrm{X}_6 + \varepsilon_3, \varepsilon_3 \sim \mathrm{N}(0, \sigma_3^2) \end{aligned} \tag{3.2}$$

In Equation 3.2, no analytical relationships exists between equations. When the covariance term i.e. $\mathrm{cov}(\varepsilon_i, \varepsilon_j) = 0$ then no relationship exist between between i and j. But, in the case of correlated error components i.e. some $\mathrm{cov}(\varepsilon_i, \varepsilon_j) \neq 0$, the equations are considered to be dependent on one another which is also known as presence of cross-equation correlations. In such case, Borders (1989) suggested Zellner's (1962) three-step fitting procedure to estimate the parameters associated with the equations.

Additivity of biomass is an important property in tree level biomass modeling. When modeling total tree and biomass components, we expect that predicted total tree biomass should equal the sum of the predicted biomass of components. This additivity can be guaranteed using SUR (Parresol 1999, 2001).

In this study, our main objective is to develop additive biomass models for slash pine and red maple. In addition, we compare systems of equations developed using Dbh only, Dbh and total tree height, Dbh, total tree height and diameter at the base of live crown as independent variables, for both species. Finally, biomass predictions from the component ratio method (CRM; Heath et al. 2009, Woodall et al. 2010), which is the biomass estimation approach used by the USDA Forest Service Forest Inventory and Analysis program (FIA), is compared with the prediction from the fitted systems of equations.

3.2 MATERIALS AND METHODS

3.2.1 DATA

Two data sets were used separately, to develop systems of individual tree biomass equations for red maple and slash pine species. The first data, UGA data, consisted of 38 slash pine and 13 red maple trees. Trees in this study were destructively sampled and intensively measured. Pertinent measurements for biomass calculation and modeling include diameter at breast height (Dbh) (0.1 inch), total tree height (0.1 foot), height to live crown (0.1 foot), diameter outside bark at ground line, stump height, 2.75 feet, 4.5 feet, 8 feet and then every 4 feet up the stem (0.1 inch). The stem was then sectioned at 4.5 feet, 8 feet and every 8 feet up the bole until a minimum dob of 4 inches. Each section was weighed. A disk was removed from the base of each bolt. All disks were weighted green with and without bark, had diameter measured with and without bark and then debarked disks were soaked until saturation. Saturated disk volume was determined using water displacement and then disks were dried at 105° C until weight change stopped. Additionally, a sample of bark from each disk was selected, weighed green, saturated and had its volume determined using water displacement and finally dried to constant weight at 105° C. All first order stem branches were measured for diameter at the base of the branch, branch length and weighed with foliage. Foliage was then removed and weighed separately or a subsample of foliage was taken. On some trees all branches and foliage was dried to constant weight at 105° C. Some trees had a representative sample of branches and foliage dried to constant weight at 105° C. These measurements on branch including sub-sample measurements were used to calculate total green weight of branch and foliage, separately for each branch in a tree.

For N branches on a tree, total green weight of branch and foliage at a tree level was calculated as

$$T_{GBF} = \sum_{i=1}^{N} G_{BF_i} \tag{3.3}$$

where T_{GBF} is total green of weight branch and foliage , $G_{BF_i}$is green weight of branch and foliage for branch $i = 1, 2, \ldots, N$.

For n sub-sample branches on a tree, green weight of foliage and green weight of branch were calculated as

$$\begin{aligned} \hat{G}_{F_i} &= D_{F_i}\left(\frac{G_{FSS_i}}{D_{FSS_i}}\right) \quad \text{and} \\ \hat{G}_{B_i} &= G_{BF_i} - \hat{G}_{F_i} \end{aligned} \tag{3.4}$$

where $\hat{G}_{F_i}$ and $\hat{G}_{B_i}$ are total estimated green weight of branch and green weight of foliage of branch i, respectively. G_{FSS_i} and D_{FSS_i} are green and dry weight of foliage sub-sample of branch i, respectively. D_{F_i} is dry weight of foliage of a branch i and G_{BF_i} is green weight of wood and foliage of a branch i. There are i = 1, 2, …, n sub-sample branches on a tree.

For the branches that were not sub-sampled, we have the following information available:

G_{BF_i} = green weight of branch and foliage for branch i

B_{D_i} = basal diameter (0.1 inch) of branch i

B_{L_i} = length (0.1 foot) of branch i

We also have this information available for all sub-sampled branches in addition to D_{B_i} and D_{F_i}. To obtain the estimated values of D_{B_i} (Dry branch), D_{F_i} (Dry foliage), G_{B_i} (Green branch) and G_{F_i} (Green foliage) for non-subsample branches we used the ratios: $\frac{D_{B_i}}{G_{BF_i}}$, $\frac{D_{F_i}}{G_{BF_i}}$, $\frac{G_{B_i}}{G_{BF_i}}$, $\frac{G_{F_i}}{G_{BF_i}}$, respectively. For trees with large variation in branch size, we calculated the green weight of a branch (without foliage) using weighted ratio:

$WR=\frac{\sum_{i=1}^{n}(\frac{G_{B_i}}{G_{BF_i}})(D_i^2L_i)}{\sum_{i=1}^{n}(D_i^2L_i)}$ and

$\hat{\mathrm{G}}_{\mathrm{B_i}} = \mathrm{G}_{\mathrm{BF_i}} \times (\mathrm{WR})$ where, WR is the weighted ratio, D and L are diameter at base and length of branch, respectively, and others are as described above.

Sample tree characteristics for two species available for biomass modeling work from UGA study are presented in Table 3.1 . Thirteen red maple trees ranging in Dbh from about 5 to 11 inches and ranging in Ht from about 39 to 74 ft, and 38 slash pine trees ranging in Dbh from about 6 to 10 inches and ranging in Ht from about 44 to 82 ft were used for biomass modeling work. Number of trees by one inch Dbh class for red maple and slash pine are presented in Figures 3.1 and 3.2, respectively.

Table 3.1: Sample tree characteristics for UGA data available for biomass modeling

		Dbh (inch)			Tree height (ft)		
Species	No. of trees	min	mean	max	min	mean	max
Red maple	13	4.8	8.6	11	38.7	57.2	73.6
Slash pine	38	5.60	7.80	10.10	44.30	60.2	81.6

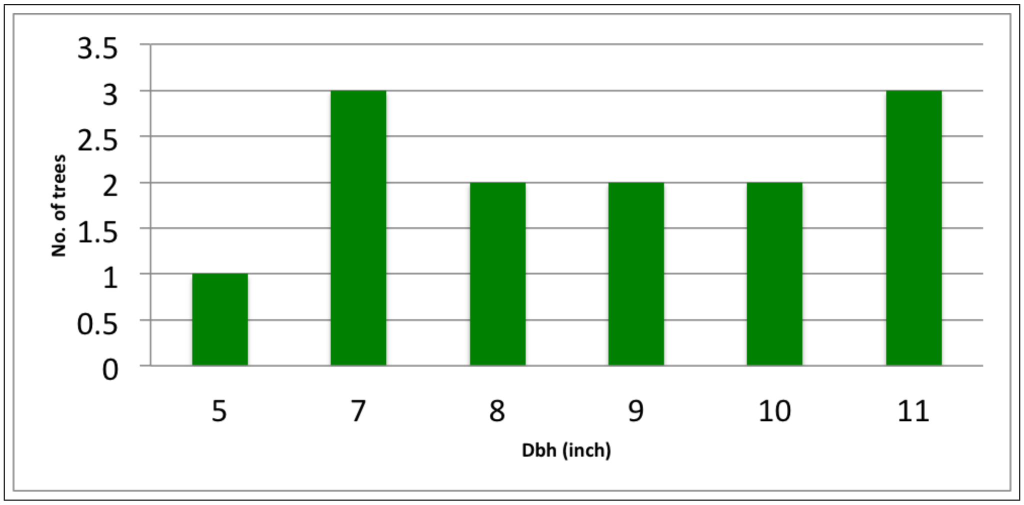


Figure 3.1: Data distribution by 1 inch Dbh class for red maple - UGA data

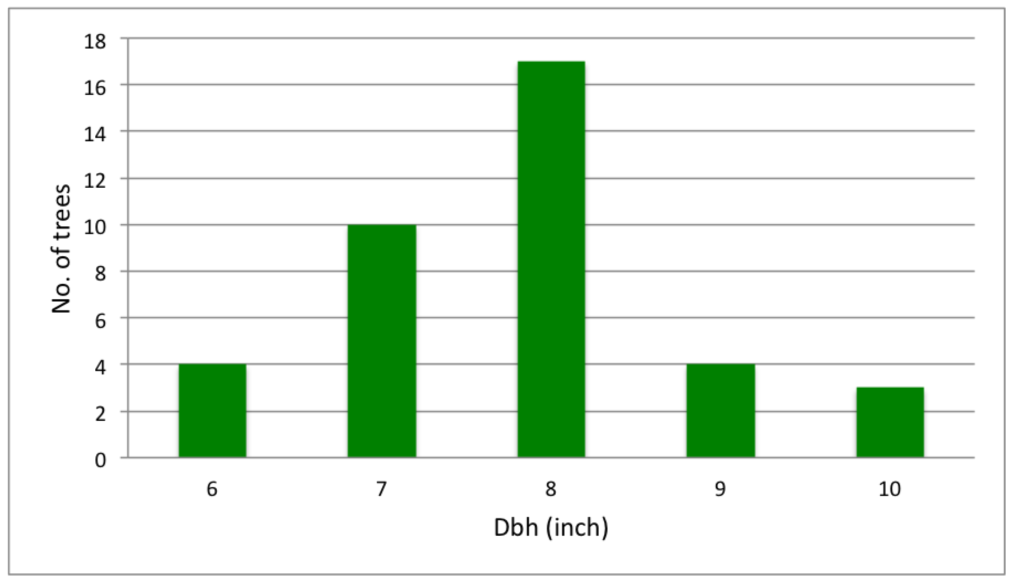


Figure 3.2: Data distribution by 1 inch Dbh class for slash pine - UGA data

The second data set, we call it Legacy data, is comprised of biomass data from various studies in the past. Legacy data are compiled within Forest Inventory and Analysis Program (FIA) biomass project by Phil Radtkey and David Walker of Virginia Tech. Red maple trees used in this study were gathered from studies conducted by Briggs et al. (1989), Clark et al. (1985, 86a, 86b, 86c), and Martin et al. (1998). Out of 136 red maple trees, 16 trees were taken from Briggs et al. (1988), 111 were taken from Clark et al. (1985, 86a, 86b, 86c), and 9 were taken from Martin et al. (1998) studies. These studies covered 15 locations in the north east and southern part of the U.S, ranging from New York to Florida. Whereas, 10 slash pine trees were obtained from a biomass study conducted by Garbett (1977).

For red maple, 136 trees ranging in Dbh from about 5 to 21 inches and ranging in Ht from about 40 to 110 ft and for slash pine 10 trees ranging in Dbh from about 5 to 13 inches and ranging in Ht from about 44 to 72 ft were used for biomass modeling work (Table 3.2).

We excluded observations with Dbh less than and equal to 4.5 inches from the original Legacy data.

Table 3.2: Sample tree characteristics for Legacy data available for biomass modeling

		Dbh (inch)			Tree height (ft)		
Species	No. of trees	min	mean	max	min	mean	max
Red maple	136	4.7	9.2	20.6	40	66.5	110.1
Slash pine	10	4.6	7.9	12.3	44.3	56.4	71.9

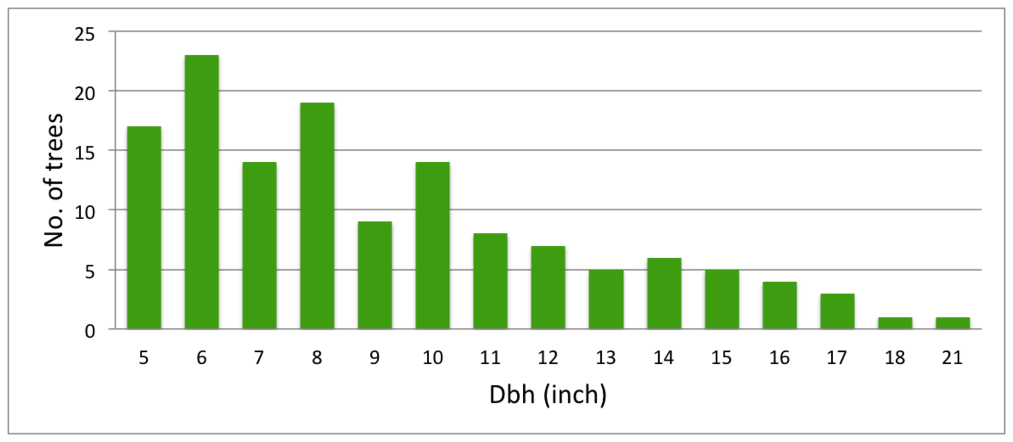


Figure 3.3: Data distribution by 1 inch Dbh class for red maple - Legacy data

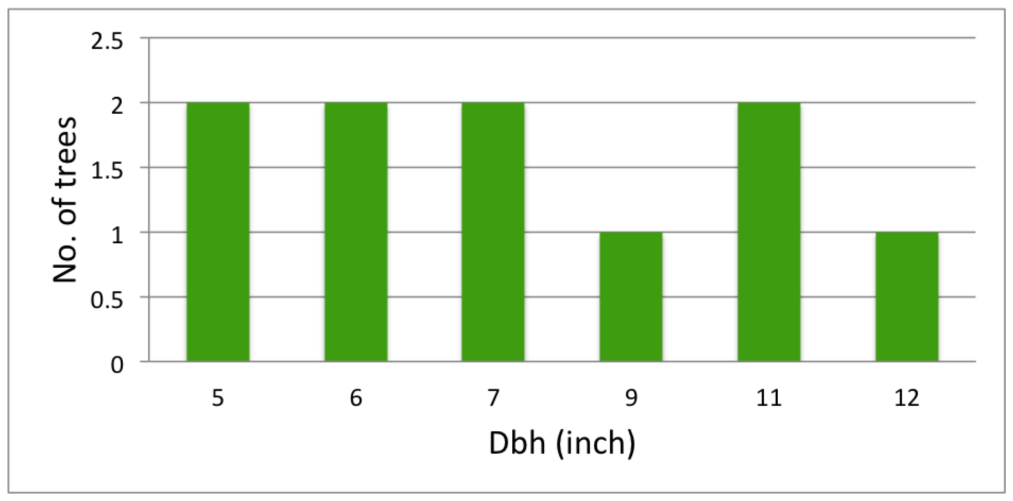


Figure 3.4: Data distribution by 1 inch Dbh class for slash pine - Legacy data

3.2.2 STATISTICAL ANALYSIS

We first, investigated appropriate independent variables for each biomass component using nonlinear regression. The parameters in the component models were estimated using ordinary least squares method (OLS). At this stage, an appropriate weight function if needed was used to stabilize the variance. The final biomass component equations were then fitted simultaneously using nonlinear seemingly unrelated regression (NSUR) with additive error terms in all equations. The underlying biomass equation structure was developed using the form (Parresol 1999)

$$Y = \exp(\beta_0)x_1^{\beta_1}x_2^{\beta_2}\ldots x_n^{\beta_n} + \varepsilon \tag{3.5}$$

The system of equations was fitted following the procedure described by Borders (1989). Borders (1989) suggested following a 3-step fitting procedure to estimate coefficients in system of equations when we have models that are recursive in nature (sequential relationships between some equations) but which also have intercorrelated error components:

1. Coefficients of individual equations are estimated by applying a two-stage instrumental variable technique.
2. Residuals are obtained from step 1 and are used to estimate the cross-equation covariance matrix.
3. Generalized least-squares approach is applied to account for correlated error components.

Borders (1989) further described that the first step is implemented by fitting the equations that do not consist of Right Hand Side (RHS) endogenous variables using OLS. Next, equations with RHS endogenous variables are fitted with OLS and using predicted values of RHS endogenous variables in place of observed values. This procedure is known as an instrumental variable technique. This technique is important as it removes endogeneity from the RHS endogenous variables (Fox 1968). Steps 2 and 3 are implemented using Zellner estimation.

The structural equations that comprise of the system of nonlinear models is specified as

$$\begin{aligned}
y_1 &= f_1(X_1, \beta_1) + \varepsilon_1 \\
y_2 &= f_2(X_2, \beta_2) + \varepsilon_2 \\
&\vdots \\
y_k &= f_k(X_k, \beta_k) + \varepsilon_k \\
y_{total} &= f_{total}(X_1, X_2, \ldots, X_k, \beta_1, \beta_2, \ldots, \beta_k) + \varepsilon_{total} \qquad (3.6)
\end{aligned}$$

where y_1 to y_k are 1 to k biomass components, respectively, and y_{total} is total biomass, X_1 to X_k are predictor variables (tree dimension variables), β_s are regression parameters to be estimated and ε is error term which is identically and independently distributed with $\varepsilon \overset{iid}{\sim} N(0, \sigma^2)$.

Statistical Analysis System (SAS) (SAS 2013) was used to implement fitting procedures. Nonlinear fitting procedure for individual components was carried out with the NLIN procedure and the system of equations fit was implemented using the MODEL procedure. R (R 2013) statistical analysis software was also used for data management and graphical analysis.

We used University of Georgia and Legacy data separately for both species to build models for estimating biomass components. Three types of models which are based on (1) Dbh, (2) Dbh and Ht, and (3) Dbh, Ht and Dcrn were selected and fitted for red maple and slash pine UGA data. These three system of equations were compared using (1) Average residual (AR) (2) Average percent residual (APR) (3) Average absolute residual (AAR) (4) Average absolute percent residual (AAPR) (5) Root mean square error (RMSE) and (6) Percent variance explained (PVE). AR measures average bias in prediction. This indicates the expected error in prediction when several observations are to be combined by averaging. The AAR measures accuracy in model prediction. This signifies the average error from prediction of any one observation (Burk 1986). RMSE, square root of MSE, is the standard deviation of prediction error for unbiased models (Burk 1986). It is a measure of average deviation. PVE measures the goodness of fit of the model. It actually measures how well the fit accounts for the variation in the data. It is a measure similar to fit index or R^2.

$$
\begin{aligned}
\mathrm{AR} &= \frac{\sum_{\mathrm{i}}^{\mathrm{n}}(\mathrm{y_i} - \hat{\mathrm{y}}_\mathrm{i})}{\mathrm{n}} \\
\mathrm{APR} &= \frac{\sum_{\mathrm{i}}^{\mathrm{n}}(\frac{\mathrm{y_i} - \hat{\mathrm{y}}_\mathrm{i}}{\mathrm{y_i}} \times 100)}{\mathrm{n}} \\
\mathrm{AAR} &= \frac{\sum_{\mathrm{i}}^{\mathrm{n}}|(\mathrm{y_i} - \hat{\mathrm{y}}_\mathrm{i})|}{\mathrm{n}} \\
\mathrm{AAPR} &= \frac{\sum_{\mathrm{i}}^{\mathrm{n}}(\frac{|(\mathrm{y_i} - \hat{\mathrm{y}}_\mathrm{i})|}{\mathrm{y_i}} \times 100)}{\mathrm{n}} \\
\mathrm{RMSE} &= \sqrt{\sum_{\mathrm{i}}^{\mathrm{n}} \frac{(\mathrm{y_i} - \hat{\mathrm{y}}_\mathrm{i})^2}{\mathrm{n}}} \\
\mathrm{PVE} &= (1 - \frac{\sum_{\mathrm{i}}^{\mathrm{n}}(\mathrm{y_i} - \hat{\mathrm{y}}_\mathrm{i})^2}{\sum_{\mathrm{i}}^{\mathrm{n}}(\mathrm{y_i} - \bar{\mathrm{y}})^2}) \times 100 \qquad (3.7)
\end{aligned}
$$

where, $\mathrm{y_i}$ refers to the observed i^{th} response value (observed dry weight of components), $\hat{\mathrm{y}}_\mathrm{i}$ is the corresponding predicted response value, and n is the number of observations.

Dbh, and Dbh and Ht based models were used for both species from legacy data. Since Dcrn variable was not available in the Legacy data we could not use it to develop equations that use this information to predict tree biomass. Following are the best selected system of equations based on Dbh, on Dbh and Ht and on Dbh, Ht and Dcrn for red maple and slash pine trees.

3.2.2.1 SYSTEM OF EQUATIONS FOR RED MAPLE - UGA DATA

A Dbh only based equation is the simplest equation form for modeling biomass components. The final system based on Dbh only for red maple from the UGA data is:

$$
\begin{aligned}
\mathrm{Y}_{\mathrm{Stemwood}} &= \mathrm{Dbh}^{\beta_{11}} + \varepsilon_{\mathrm{Stemwood}} \\
\mathrm{Y}_{\mathrm{Stembark}} &= \mathrm{Dbh}^{\beta_{21}} + \varepsilon_{\mathrm{Stembark}} \\
\mathrm{Y}_{\mathrm{Branch}} &= \mathrm{Dbh}^{\beta_{31}} + \varepsilon_{\mathrm{Branch}} \\
\mathrm{Y}_{\mathrm{Foliage}} &= \mathrm{Dbh}^{\beta_{41}} + \varepsilon_{\mathrm{Foliage}} \\
\mathrm{Y}_{\mathrm{Stem}} &= \mathrm{Dbh}^{\beta_{11}} + \mathrm{Dbh}^{\beta_{21}} + \varepsilon_{\mathrm{Stem}} \\
\mathrm{Y}_{\mathrm{Crown}} &= \mathrm{Dbh}^{\beta_{31}} + \mathrm{Dbh}^{\beta_{41}} + \varepsilon_{\mathrm{Crown}} \\
\mathrm{Y}_{\mathrm{Totaltree}} &= \mathrm{Dbh}^{\beta_{11}} + \mathrm{Dbh}^{\beta_{21}} + \mathrm{Dbh}^{\beta_{31}} + \mathrm{Dbh}^{\beta_{41}} + \varepsilon_{\mathrm{Totaltree}} \qquad (3.8)
\end{aligned}
$$

where, left hand side of equations are tree biomass components in pounds (lbs), β_{s} are unknown regression parameters and Dbh is independent variable. This system of equations ensures that the stem biomass is the sum of stem wood and bark biomass. Similarly, crown biomass is the sum of branch and foliage biomass and the total tree biomass is the sum of all components.

In Equation 3.9, we used both Dbh and tree total height (Ht). Everything else is same as defined in Equation 3.8.

$$\begin{aligned}
\mathrm{Y}_{\mathrm{Stemwood}} &= \exp(\beta_{10})\mathrm{Dbh}^{\beta_{11}}\mathrm{Ht}^{\beta_{12}} + \varepsilon_{\mathrm{Stemwood}} \\
\mathrm{Y}_{\mathrm{Stembark}} &= \exp(\beta_{20})\mathrm{Dbh}^{\beta_{21}}\mathrm{Ht}^{\beta_{22}} + \varepsilon_{\mathrm{Stembark}} \\
\mathrm{Y}_{\mathrm{Branch}} &= (\mathrm{Dbh}^2\mathrm{Ht})^{\beta_{32}} + \varepsilon_{\mathrm{Branch}} \\
\mathrm{Y}_{\mathrm{Foliage}} &= (\mathrm{Dbh}^2\mathrm{Ht})^{\beta_{42}} + \varepsilon_{\mathrm{Foliage}} \\
\mathrm{Y}_{\mathrm{Stem}} &= \exp(\beta_{10})\mathrm{Dbh}^{\beta_{11}}\mathrm{Ht}^{\beta_{12}} + \exp(\beta_{20})\mathrm{Dbh}^{\beta_{21}}\mathrm{Ht}^{\beta_{22}} + \varepsilon_{\mathrm{Stem}} \\
\mathrm{Y}_{\mathrm{Crown}} &= (\mathrm{Dbh}^2\mathrm{Ht})^{\beta_{32}} + (\mathrm{Dbh}^2\mathrm{Ht})^{\beta_{42}} + \varepsilon_{\mathrm{Crown}} \\
\mathrm{Y}_{\mathrm{Totaltree}} &= \exp(\beta_{10})\mathrm{Dbh}^{\beta_{11}}\mathrm{Ht}^{\beta_{12}} \\
&\quad +\exp(\beta_{20})\mathrm{Dbh}^{\beta_{21}}\mathrm{Ht}^{\beta_{22}} \\
&\quad +(\mathrm{Dbh}^2\mathrm{Ht})^{\beta_{32}} + (\mathrm{Dbh}^2\mathrm{Ht})^{\beta_{42}} + \varepsilon_{\mathrm{Totaltree}} \qquad (3.9)
\end{aligned}$$

Equation 3.10 is a more complex model than the models above. It consists of Dbh, Ht and Dcrn as independent variables.

$$\begin{aligned}
\mathrm{Y}_{\mathrm{Stemwood}} &= \exp(\beta_{10})(\mathrm{Dbh}^2\mathrm{Ht})^{\beta_{11}} + \varepsilon_{\mathrm{Stemwood}} \\
\mathrm{Y}_{\mathrm{Stembark}} &= \exp(\beta_{20})(\mathrm{Dbh}^2\mathrm{Ht})^{\beta_{21}} + \varepsilon_{\mathrm{Stembark}} \\
\mathrm{Y}_{\mathrm{Branch}} &= \mathrm{Dcrn}^{\beta_{30}}\mathrm{Ht}^{\beta_{31}} + \varepsilon_{\mathrm{Branch}} \\
\mathrm{Y}_{\mathrm{Foliage}} &= (\mathrm{Dbh}^2\mathrm{Ht})^{\beta_{40}} + \varepsilon_{\mathrm{Foliage}} \\
\mathrm{Y}_{\mathrm{Stem}} &= \exp(\beta_{10})(\mathrm{Dbh}^2\mathrm{Ht})^{\beta_{11}} + \exp(\beta_{20})(\mathrm{Dbh}^2\mathrm{Ht})^{\beta_{21}} + \varepsilon_{\mathrm{Stem}} \\
\mathrm{Y}_{\mathrm{Crown}} &= \mathrm{Dcrn}^{\beta_{30}}\mathrm{Ht}^{\beta_{31}} + (\mathrm{Dbh}^2\mathrm{Ht})^{\beta_{40}} + \varepsilon_{\mathrm{Crown}} \\
\mathrm{Y}_{\mathrm{Totaltree}} &= \exp(\beta_{10})(\mathrm{Dbh}^2\mathrm{Ht})^{\beta_{11}} + \exp(\beta_{20})(\mathrm{Dbh}^2\mathrm{Ht})^{\beta_{21}} \\
&\quad +\mathrm{Dcrn}^{\beta_{30}}\mathrm{Ht}^{\beta_{31}} + (\mathrm{Dbh}^2\mathrm{Ht})^{\beta_{40}} + \varepsilon_{\mathrm{Totaltree}} \qquad (3.10)
\end{aligned}$$

3.2.2.2 System of equations for slash pine - UGA data

For slash pine , the following Dbh based system was selected:

$$\begin{aligned}
\mathrm{Y_{Stemwood}} &= \mathrm{Dbh}^{\beta_{11}} + \varepsilon_{\mathrm{Stemwood}} \\
\mathrm{Y_{Stembark}} &= \exp(\beta_{20})\mathrm{Dbh}^{\beta_{21}} + \varepsilon_{\mathrm{Stembark}} \\
\mathrm{Y_{Branch}} &= \exp(\beta_{30})\mathrm{Dbh}^{\beta_{31}} + \varepsilon_{\mathrm{Branch}} \\
\mathrm{Y_{Foliage}} &= \exp(\beta_{40})\mathrm{Dbh}^{\beta_{41}} + \varepsilon_{\mathrm{Foliage}} \\
\mathrm{Y_{Stem}} &= \mathrm{Dbh}^{\beta_{11}} + \exp(\beta_{20})\mathrm{Dbh}^{\beta_{21}} + \varepsilon_{\mathrm{Stem}} \\
\mathrm{Y_{Crown}} &= \exp(\beta_{30})\mathrm{Dbh}^{\beta_{31}} + \exp(\beta_{40})\mathrm{Dbh}^{\beta_{41}} + \varepsilon_{\mathrm{Crown}} \\
\mathrm{Y_{Totaltree}} &= \mathrm{Dbh}^{\beta_{11}} + \exp(\beta_{20})\mathrm{Dbh}^{\beta_{21}} + \exp(\beta_{30})\mathrm{Dbh}^{\beta_{31}} \\
&\quad + \exp(\beta_{40})\mathrm{Dbh}^{\beta_{41}} + \varepsilon_{\mathrm{Totaltree}} \qquad (3.11)
\end{aligned}$$

Equation 3.12 was selected as Dbh and Ht based system of equations.

$$\begin{aligned}
\mathrm{Y_{Stemwood}} &= \exp(\beta_{10})\mathrm{Dbh}^{\beta_{11}}\mathrm{Ht}^{\beta_{12}} + \varepsilon_{\mathrm{Stemwood}} \\
\mathrm{Y_{Stembark}} &= \beta_{20}\mathrm{Dbh}^{\beta_{21}}\mathrm{Ht}^{\beta_{22}} + \varepsilon_{\mathrm{Stembark}} \\
\mathrm{Y_{Branch}} &= \mathrm{DBH}^{\beta_{31}}\mathrm{Ht}^{\beta_{32}} + \varepsilon_{\mathrm{Branch}} \\
\mathrm{Y_{Foliage}} &= \exp(\beta_{40})\mathrm{Dbh}^{\beta_{41}}\mathrm{Ht}^{\beta_{42}} + \varepsilon_{\mathrm{Foliage}} \\
\mathrm{Y_{Stem}} &= \exp(\beta_{10})\mathrm{Dbh}^{\beta_{11}}\mathrm{Ht}^{\beta_{12}} + \beta_{20}\mathrm{Dbh}^{\beta_{21}}\mathrm{Ht}^{\beta_{22}} + \varepsilon_{\mathrm{Stem}} \\
\mathrm{Y_{Crown}} &= \mathrm{DBH}^{\beta_{31}}\mathrm{Ht}^{\beta_{32}} + \exp(\beta_{40})\mathrm{Dbh}^{\beta_{41}}\mathrm{Ht}^{\beta_{42}} + \varepsilon_{\mathrm{Crown}} \\
\mathrm{Y_{Totaltree}} &= \exp(\beta_{10})\mathrm{Dbh}^{\beta_{11}}\mathrm{Ht}^{\beta_{12}} + \beta_{20}\mathrm{Dbh}^{\beta_{21}}\mathrm{Ht}^{\beta_{22}} \\
&\quad + \mathrm{DBH}^{\beta_{31}}\mathrm{Ht}^{\beta_{32}} + \exp(\beta_{40})\mathrm{Dbh}^{\beta_{41}}\mathrm{Ht}^{\beta_{42}} + \varepsilon_{\mathrm{Totaltree}} \qquad (3.12)
\end{aligned}$$

Equation 3.13 is a more complex model than the previous models. It consists of Dcrn as an additional variable in the model.

$$\begin{aligned}
\mathrm{Y}_{\mathrm{Stemwood}} &= \exp(\beta_{10})\mathrm{Dbh}^{\beta_{11}}\mathrm{Ht}^{\beta_{12}} + \varepsilon_{\mathrm{Stemwood}} \\
\mathrm{Y}_{\mathrm{Stembark}} &= \beta_{20}(\mathrm{Dbh}^{2}\mathrm{Ht})^{\beta_{21}} + \varepsilon_{\mathrm{Stembark}} \\
\mathrm{Y}_{\mathrm{Branch}} &= \exp(\beta_{30})\mathrm{Dcrn}^{\beta_{31}} + \varepsilon_{\mathrm{Branch}} \\
\mathrm{Y}_{\mathrm{Foliage}} &= \exp(\beta_{40})\mathrm{Dcrn}^{\beta_{41}} + \varepsilon_{\mathrm{Foliage}} \\
\mathrm{Y}_{\mathrm{Stem}} &= \exp(\beta_{10})\mathrm{Dbh}^{\beta_{11}}\mathrm{Ht}^{\beta_{12}} + \beta_{20}(\mathrm{Dbh}^{2}\mathrm{Ht})^{\beta_{21}} + \varepsilon_{\mathrm{Stem}} \\
\mathrm{Y}_{\mathrm{Crown}} &= \exp(\beta_{30})\mathrm{Dcrn}^{\beta_{31}} + \exp(\beta_{40})\mathrm{Dcrn}^{\beta_{41}} + \varepsilon_{\mathrm{Crown}} \\
\mathrm{Y}_{\mathrm{Totaltree}} &= \exp(\beta_{10})\mathrm{Dbh}^{\beta_{11}}\mathrm{Ht}^{\beta_{12}} + \beta_{20}(\mathrm{Dbh}^{2}\mathrm{Ht})^{\beta_{21}} \\
&\quad +\exp(\beta_{30})\mathrm{Dcrn}^{\beta_{31}} + \exp(\beta_{40})\mathrm{Dcrn}^{\beta_{41}} + \varepsilon_{\mathrm{Totaltree}} \qquad (3.13)
\end{aligned}$$

3.2.2.3 System of equations for Red maple and slash pine - legacy data

For red maple from Legacy data, the following Dbh based system was selected:

$$\begin{aligned}
\mathrm{Y}_{\mathrm{Stemwood}} &= \exp(\beta_{10})\mathrm{Dbh}^{\beta_{11}} + \varepsilon_{\mathrm{Stemwood}} \\
\mathrm{Y}_{\mathrm{Stembark}} &= \exp(\beta_{20})\mathrm{Dbh}^{\beta_{21}} + \varepsilon_{\mathrm{Stembark}} \\
\mathrm{Y}_{\mathrm{Branch}} &= \exp(\beta_{30})\mathrm{Dbh}^{\beta_{31}} + \varepsilon_{\mathrm{Branch}} \\
\mathrm{Y}_{\mathrm{Foliage}} &= \exp(\beta_{40})\mathrm{Dbh}^{\beta_{41}} + \varepsilon_{\mathrm{Foliage}} \\
\mathrm{Y}_{\mathrm{Stem}} &= \exp(\beta_{10})\mathrm{Dbh}^{\beta_{11}} + \exp(\beta_{20})\mathrm{Dbh}^{\beta_{21}} + \varepsilon_{\mathrm{Stem}} \\
\mathrm{Y}_{\mathrm{Crown}} &= \exp(\beta_{30})\mathrm{Dbh}^{\beta_{31}} + \exp(\beta_{40})\mathrm{Dbh}^{\beta_{41}} + \varepsilon_{\mathrm{Crown}} \\
\mathrm{Y}_{\mathrm{Totaltree}} &= \exp(\beta_{10})\mathrm{Dbh}^{\beta_{11}} + \exp(\beta_{20})\mathrm{Dbh}^{\beta_{21}} \\
&\quad +\exp(\beta_{30})\mathrm{Dbh}^{\beta_{31}} + \exp(\beta_{40})\mathrm{Dbh}^{\beta_{41}} + \varepsilon_{\mathrm{Totaltree}} \qquad (3.14)
\end{aligned}$$

The following Dbh and Ht based system was selected

$$\begin{aligned}
Y_{\text{Stemwood}} &= \exp(\beta_{10})\text{Dbh}^{\beta_{11}}\text{Ht}^{\beta_{12}} + \varepsilon_{\text{Stemwood}} \\
Y_{\text{Stembark}} &= \exp(\beta_{20})\text{Dbh}^{\beta_{21}}\text{Ht}^{\beta_{22}} + \varepsilon_{\text{Stembark}} \\
Y_{\text{Branch}} &= \exp(\beta 30)\text{Dbh}^{\beta_{31}} + \varepsilon_{\text{Branch}} \\
Y_{\text{Foliage}} &= \exp(\beta_{40})\text{Dbh}^{\beta_{41}} + \varepsilon_{\text{Foliage}} \\
Y_{\text{Stem}} &= \exp(\beta_{10})\text{Dbh}^{\beta_{11}}\text{Ht}^{\beta_{12}} + \exp(\beta_{20})\text{Dbh}^{\beta_{21}}\text{Ht}^{\beta_{22}} + \varepsilon_{\text{Stem}} \\
Y_{\text{Crown}} &= \exp(\beta 30)\text{Dbh}^{\beta_{31}} + \exp(\beta_{40})\text{Dbh}^{\beta_{41}} + \varepsilon_{\text{Crown}} \\
Y_{\text{Totaltree}} &= \exp(\beta_{10})\text{Dbh}^{\beta_{11}}\text{Ht}^{\beta_{12}} + \exp(\beta_{20})\text{Dbh}^{\beta_{21}}\text{Ht}^{\beta_{22}} \\
&\quad + \exp(\beta 30)\text{Dbh}^{\beta_{31}} + \exp(\beta_{40})\text{Dbh}^{\beta_{41}} + \varepsilon_{\text{Totaltree}} \qquad (3.15)
\end{aligned}$$

For slash pine from Legacy data, the following Dbh based system was selected

$$\begin{aligned}
Y_{\text{Stemwood}} &= \beta_{10}\text{Dbh}^{\beta_{11}} + \varepsilon_{\text{Stemwood}} \\
Y_{\text{Stembark}} &= \beta_{20}\text{Dbh}^{\beta_{21}} + \varepsilon_{\text{Stembark}} \\
Y_{\text{Branch}} &= \text{Dbh}^{\beta_{31}} + \varepsilon_{\text{Branch}} \\
Y_{\text{Foliage}} &= \text{Dbh}^{\beta_{41}} + \varepsilon_{\text{Foliage}} \\
Y_{\text{Stem}} &= \beta_{10}\text{Dbh}^{\beta_{11}} + \beta_{20}\text{Dbh}^{\beta_{21}} + \varepsilon_{\text{Stem}} \\
Y_{\text{Crown}} &= \text{Dbh}^{\beta_{31}} + \text{Dbh}^{\beta_{41}} + \varepsilon_{\text{Crown}} \\
Y_{\text{Totaltree}} &= \beta_{10}\text{Dbh}^{\beta_{11}} + \beta_{20}\text{Dbh}^{\beta_{21}} \\
&\quad + \text{Dbh}^{\beta_{31}} + \text{Dbh}^{\beta_{41}} + \varepsilon_{\text{Totaltree}} \qquad (3.16)
\end{aligned}$$

The following Dbh and Ht based system was selected

$$\begin{aligned}
Y_{\text{Stemwood}} &= \exp(\beta_{10})\text{Dbh}^{\beta_{11}}\text{Ht}^{\beta_{12}} + \varepsilon_{\text{Stemwood}} \\
Y_{\text{Stembark}} &= (\text{Dbh}^{2}\text{Ht})^{\beta_{21}} + \varepsilon_{\text{Stembark}} \\
Y_{\text{Branch}} &= \exp(\beta_{30})\text{Dbh}^{\beta_{31}} + \varepsilon_{\text{Branch}} \\
Y_{\text{Foliage}} &= \text{Dbh}^{\beta_{41}}\text{Ht}^{\beta_{42}} + \varepsilon_{\text{Foliage}} \\
Y_{\text{Stem}} &= \exp(\beta_{10})\text{Dbh}^{\beta_{11}}\text{Ht}^{\beta_{12}} + (\text{Dbh}^{2}\text{Ht})^{\beta_{2}1} + \varepsilon_{\text{Stem}} \\
Y_{\text{Crown}} &= \exp(\beta_{30})\text{Dbh}^{\beta_{31}} + \text{Dbh}^{\beta_{41}}\text{Ht}^{\beta_{42}} + \varepsilon_{\text{Crown}} \\
Y_{\text{Totaltree}} &= \exp(\beta_{10})\text{Dbh}^{\beta_{11}}\text{Ht}^{\beta_{12}} + (\text{Dbh}^{2}\text{Ht})^{\beta_{2}1} \\
&\quad + \exp(\beta_{30})\text{Dbh}^{\beta_{31}} + \text{Dbh}^{\beta_{41}}\text{Ht}^{\beta_{42}} + \varepsilon_{\text{Totaltree}} \qquad (3.17)
\end{aligned}$$

3.2.3 COMPONENT RATION METHOD (CRM)

In addition to system of equations fits, we used the component ratio method (CRM) to estimate total tree and component biomass. Procedures described in Woodall et al. (2010) were used to implement CRM for both red maple and slash pine for UGA and legacy data. CRM is used by the USDA Forest Service Forest Inventory and Analysis Program (FIA) to generate biomass estimates. This method generates biomass estimates by conversion of cubic volume estimates and specific gravity and other information for branches, stems, bark and stumps. CRM consists of a seven major steps (Woodall et al. 2010):

1. measure tree variables in the field

2. compute gross cubic-foot volume (VOLCFGRS) by using those tree measurements and the appropriate volume model

3. compute sound cubic-foot volume (VOLCFSND) of wood in the bole by using VOLCFGRS

4. convert VOLCFSND to mass and estimate bark biomass by utilizing already complied sets of specific gravity (Miles and Smith 2009)
5. estimate tops and limb biomass as a proportion of the bole based on Jenkins et al. (2003)
6. estimate stump volume based on equations from Raile (1982) and convert it to stump biomass
7. estimate total aboveground biomass by summing all aboveground components biomass

Complete procedure of biomass calculation for all sapling, pole and sawtimber by species type, growing condition and region are provided in Woodall et al. (2010).

3.3 Results and Discussion

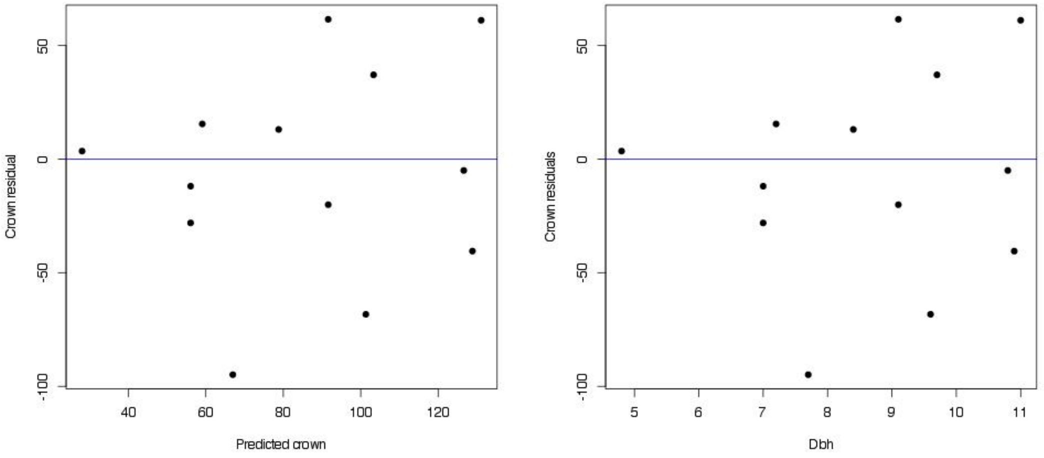
All component models by species, were fitted using nonlinear seemingly unrelated regression. Appropriate weight for each component model was investigated and used if necessary to account for variance heterogeneity in the data. For UGA data, we had very small sample size for both species. We could not find heterogeneity in variance related to tree size such as Dbh , and Ht, hence no weight function was used to stabilize the variance. However, for Legacy data, heterogeneity of variance was apparent and appropriate weight functions were required for most of the components of both species to stabilize the variance.

3.3.1 Red maple - UGA data

All parameters in the Dbh only based system are significantly different from zero at α=0.05 level (Table 3.3). Statistical significance of all parameters indicate that Dbh is important in predicting biomass components. Additionally, the positive coefficient of Dbh for all component equations clearly indicate that the biomass component increases with increase in Dbh. Residual plots (Figures 3.5, and3.6) show that the model fits the data well.

Table 3.3: Parameter estimates, standard errors and test statistics of Dbh based biomass equation fitted in the system of equations (3.8) for red maple - UGA data

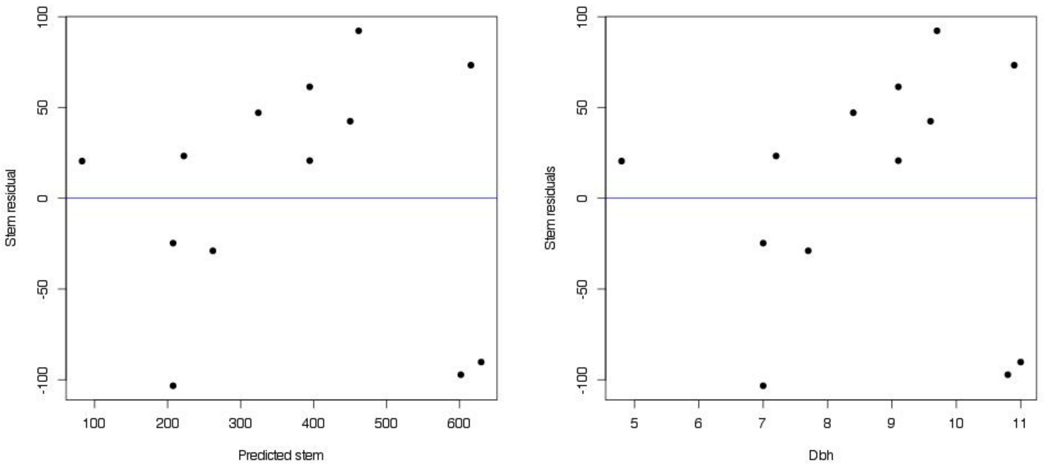
Parameter	Parameter associated with	Estimate	Standard error	t-value	p-value
$\hat{\beta}_{11}$	Dbh	2.58	0.019	37.44	<0.0001
$\hat{\beta}_{21}$	Dbh	2.06	0.037	56.25	<0.0001
$\hat{\beta}_{31}$	Dbh	1.99	0.065	30.43	<0.0001
$\hat{\beta}_{41}$	Dbh	1.07	0.054	19.89	<0.0001



(a) Residual vs predicted crown

(b) Residual vs Dbh

Figure 3.5: Residual plot of crown - Dbh only based system



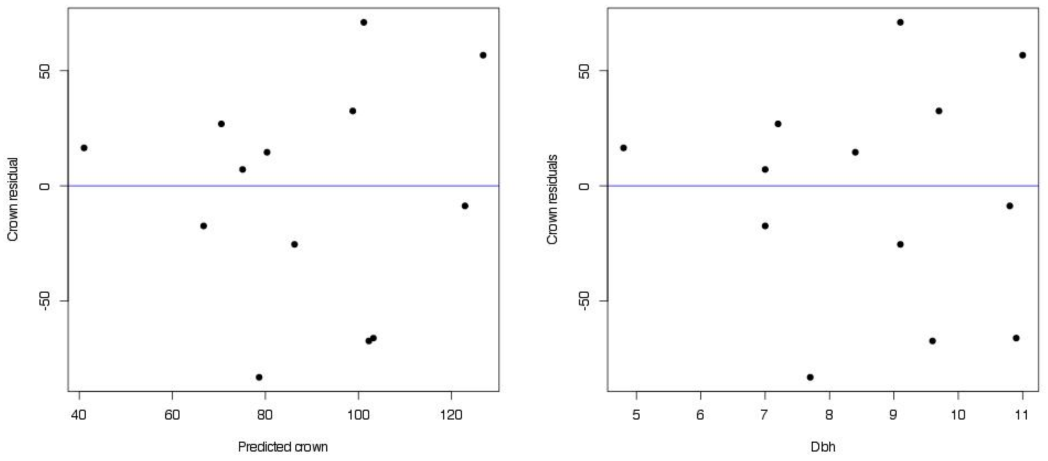
(a) Residual vs predicted stem (b) Residual vs Dbh

Figure 3.6: Residual plot of stem - Dbh only based system

Parameter estimates and their test statistics show that tree height is an important variate for stem equations (Table 3.4). This finding is similar to Lamber et al. (2005) and Bi et al. (2004) where they found tree height was an important variable for stem equations but not for crown equations. Dbh and Ht are positively related with stemwood, bark and total stem biomass (refer Equation 3.9 and Table 3.4) . This implies, for the same Dbh, the total stem biomass increases with increase in tree total height (a logical result). For some components, such as branch and foliage, combination of Dbh and Ht (Dbh^2Ht) is significant. The distribution of residuals show that the model fits the data well (Figures 3.7, and 3.8).

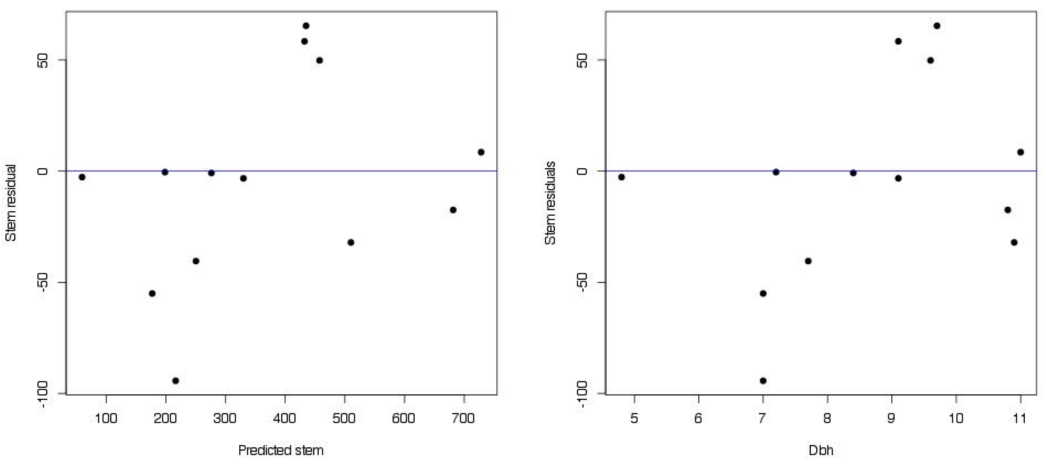
Table 3.4: Parameter estimates, standard errors and test statistics of Dbh and Ht based biomass equation fitted in the system of equations (3.9) for red maple - UGA data

Parameter	Parameter associated with	Estimate	Standard error	t-value	p-value
$\hat{\beta}_{10}$		-2.46	0.868	-2.84	0.0162
$\hat{\beta}_{11}$	Dbh	2.22	0.274	8.10	<0.0001
$\hat{\beta}_{12}$	Ht	0.80	0.229	3.49	0.0050
$\hat{\beta}_{20}$		-6.19	1.668	-3.71	0.0034
$\hat{\beta}_{21}$	Dbh	3.03	0.576	5.26	0.0003
$\hat{\beta}_{22}$	Ht	0.97	0.411	2.35	0.0384
$\hat{\beta}_{32}$	Dbh^2Ht	0.52	0.017	30.26	<0.0001
$\hat{\beta}_{42}$	Dbh^2Ht	0.28	0.016	17.05	<0.0001



(a) Residual vs predicted crown (b) Residual vs Dbh

Figure 3.7: Residual plot of crown - Dbh and Ht based system



(a) Residual vs predicted stem

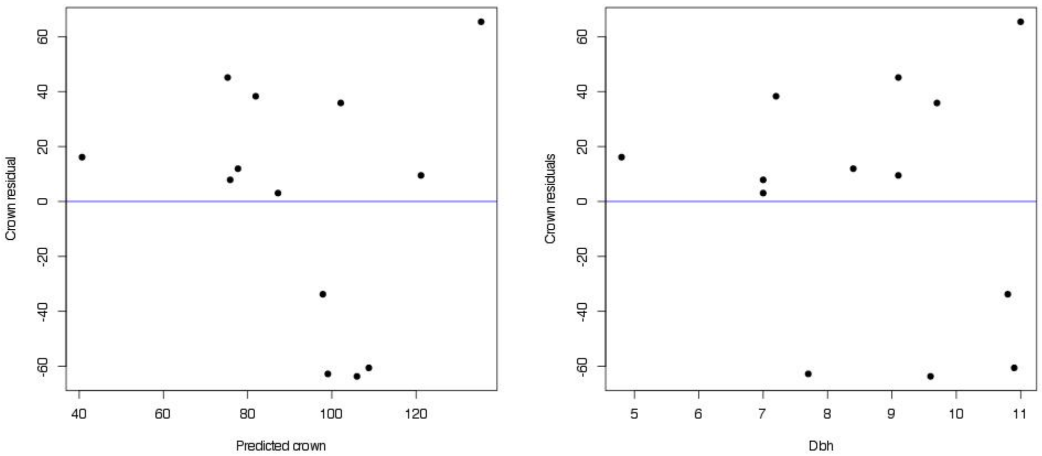
(b) Residual vs Dbh

Figure 3.8: Residual plot of stem - Dbh and Ht based system

The most complex system of equations 3.10 uses Dcrn as an additional variable. Dcrn did not enter all components equations. It was significant in predicting branch and crown biomass but not for predicting stem wood and stem bark biomass. The positive coefficient of Dcrn implies that for the same height, if diameter at the base of crown increases then a tree contains more branch and crown biomass. It is evident from the residual plots that the model satisfies the usual regression assumption of homogeneity of variance (Figures 3.9, and 3.10) and fits the data well.

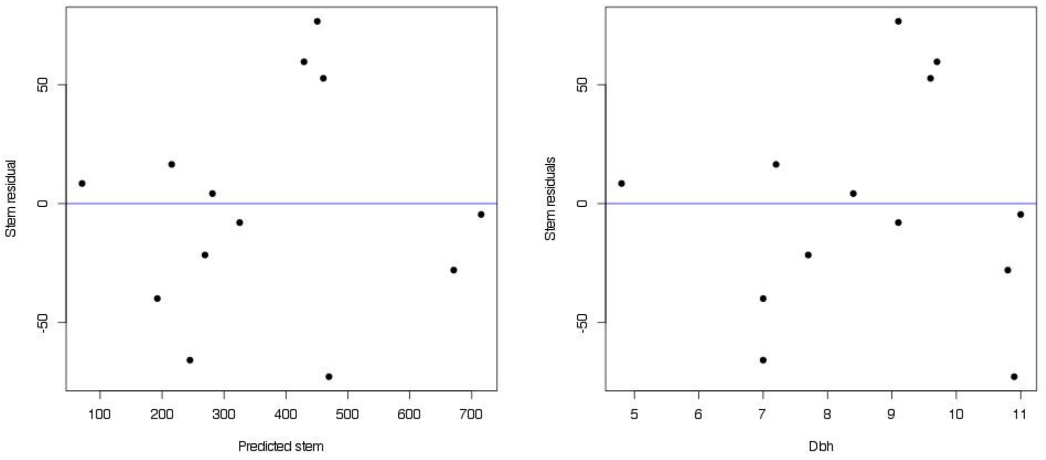
Table 3.5: Parameter estimates, standard errors and test statistics of Dbh, Ht and Dcrn based biomass equation fitted in the system of equations (3.10) for red maple - UGA data

Parameter	Parameter associated with	Estimate	Standard error	t-value	p-value
$\hat{\beta_{10}}$		-2.40	0.718	-3.33	0.0059
$\hat{\beta_{11}}$	Dbh^2Ht	0.95	0.082	11.64	<0.0001
$\hat{\beta_{20}}$		-5.76	1.289	-4.46	0.0008
$\hat{\beta_{21}}$	Dbh^2Ht	1.20	0.147	8.22	<0.0001
$\hat{\beta_{30}}$	Dcrn	1.14	0.453	2.51	0.0272
$\hat{\beta_{31}}$	Ht	0.56	0.224	2.49	0.0286
$\hat{\beta_{40}}$	Dbh^2Ht	-0.51	0.029	-17.59	<0.0001



(a) Residual vs predicted crown (b) Residual vs Dbh

Figure 3.9: Residual plot of crown - Dbh, Ht, and Dcrn based system



(a) Residual vs predicted stem (b) Residual vs Dbh

Figure 3.10: Residual plot of stem - Dbh, Ht, and Dcrn based system

Since Dcrn is not always available in mensurational data, a simple function to predict Dcrn based on Dbh was developed for red maple (Equation 3.18).

$$\hat{\text{Dcrn}} = 2.81 + 0.45\text{Dbh} \tag{3.18}$$

R^2 value for Equation 3.18 was 0.35.

3.3.1.1 MODEL COMPARISON : RED MAPLE (UGA DATA)

For Dbh only system, the average bias in prediction (AR) is not large (Table 3.6). Bark, stem and foliage were over-predicted whereas, branch, crown and total were under-predicted. We find larger percent average bias (APR) for predicting bark (-20.2%), branch (-18.6%) and foliage (-64.97%) components. On average, percent prediction error (AAPR) is higher for branch (50.96%), foliage (82.67%) and crown (47.08%) than other components. For the DBH only system of equations stem wood, bark and total stem biomass are predicted better than crown components. This agrees with Sabatia et al. (2008) findings that PVE values are lower for branch and foliage equations than for bole and total tree biomass.

Table 3.6: Average observed, average predicted component biomass, and fit statistics from Dbh only system (3.8) fitted to UGA red maple data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	285.67	284.43	1.25	- 1.00	38.15	13.66	48.64	86.98
Bark	84.88	88.97	- 4.09	- 20.20	21.62	32.44	28.34	68.50
Stem	370.56	373.40	- 2.84	- 4.18	55.81	16.52	63.72	87.56
Branch	82.37	76.05	6.32	- 18.60	33.18	50.96	42.54	11.95
Foliage	9.68	10.06	- 0.38	- 64.97	3.39	82.67	4.25	42.28
Crown	92.05	86.11	5.94	- 17.01	35.41	47.08	44.69	18.95
Total	462.61	459.51	3.10	- 2.32	65.98	16.93	76.12	86.41

When Ht is added to the models, the error in prediction decreased for stemwood, bark, stem, and total biomass, whereas it has slightly increased for branch, foliage and crown biomass (Table 3.7). In fact, the prediction error has decreased by about 15% for stemwood, 32% for bark, 41% for stem, and 7% for total biomass, whereas, it has increased by about 4% for branch, 15% for foliage and 7% for crown biomass.

RMSE has decreased for stemwood, bark, stem, and total, whereas it has slightly increased for branch, foliage and crown biomass, when Ht is added to the models. The RMSE has decreased by about 19% for stemwood, 32% for bark, 31% for stem and 3% for total biomass, whereas it has increased by about 1% for branch, 13% for foliage, and 3% for crown biomass.

PVE has increased from about 87% to 91% for stemwood, from 69% to 85% for stembark, from 86% to 87% for total biomass when total height is added to the models. For all other components the value of PVE has dropped slightly. Overall, better fit was obtained using height as an additional variable in the model. Similar to Dbh based system of equations, branch, foliage and crown biomass model did not fit the data well as indicated by all fit statistics (Table 3.7).

Table 3.7: Average observed, average predicted component biomass, and fit statistics from Dbh and Ht system (3.9) fitted to UGA red maple data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	285.67	282.25	3.42	1.22	32.37	11.12	39.62	91.36
Bark	84.88	83.37	1.51	4.67	14.64	18.79	19.39	85.25
Stem	370.56	365.62	4.94	2.72	32.97	9.91	43.99	94.07
Branch	82.37	78.74	3.63	-29.05	34.52	57.54	43.04	9.90
Foliage	9.68	10.01	-0.33	-75.82	3.90	96.67	4.79	26.69
Crown	92.05	88.75	3.30	-26.70	37.97	54.43	45.94	14.33
Total	462.61	454.38	8.23	0.46	61.58	14.87	74.05	87.14

When using Dcrn as an additional variable in the models, the average prediction error dropped for most of the components (Table 3.8). For example, comparing with Dbh and Ht based system of equations, the average prediction error has decreased by about 5% for bark and branch, 30% for foliage, 8% for crown, and 5% for total biomass, whereas, it has increased by about 3%, and 7% for stemwood and stem, respectively. Overall, the addition of Dcrn improved the model fit. RMSE from this system of equation is comparable to RMSE from Dbh and Ht based system. Branch and crown biomass models using DCrn fit the data more closely than do the previous models, however prediction of crown components is still rather weak (Table 3.8). Similar results were found in the studies conducted by Sabatia (2007) and Lambert et al. (2005).

Table 3.8: Average observed, average predicted component biomass, and fit statistics from Dbh, Ht and Dcrn system (3.10) fitted to UGA red maple data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	285.67	284.65	1.02	0 1.64	33.38	12.10	40.48	90.98
Bark	84.88	84.19	0.70	- 0.28	13.94	16.79	18.45	86.66
Stem	370.56	368.84	1.72	- 0.52	35.28	10.71	43.94	94.08
Branch	82.37	83.07	- 0.70	- 30.44	32.71	52.59	39.21	25.23
Foliage	9.68	9.94	- 0.26	- 44.58	2.74	60.63	3.59	58.86
Crown	92.05	93.01	- 0.96	- 27.30	34.92	48.49	41.54	29.98
Total	462.61	461.85	0.76	- 3.24	58.48	14.57	70.73	88.27

CRM method applied to UGA red maple data, does not provide adequate fit for bark and branch biomass (Table 3.9). The goodness of fit of stemwood model from CRM is comparable to the Dbh based system.

It should be noted that CRM method includes stump biomass and does not include foliage biomass in total biomass calculation. Whereas, in our data, we do not have stump biomass but we have information on foliage biomass. To make observed values comparable with predicted values from CRM, for the fit statistics below, observed total biomass does not include the foliage component. In fact, the total biomass here is sum of stemwood, bark and branch components. In addition, branch biomass in CRM is defined as branch and tops which is different than our branch biomass data. In CRM tops are defined as the main stem from a minimum top diameter outside bark of four inches to the stem tip. Clearly, our available data do not lend themselves to a clean comparison with CRM, but the fit statistics do indicate that CRM is a poor predictor of components that we do have available.

Table 3.9: Average observed, average predicted component biomass, and fit statistics from component ratio method applied to UGA red maple data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	305.41	275.43	29.98	9.97	40.39	13.71	50.89	82.29
Bark	90.83	29.00	61.83	66.18	61.83	66.18	72.30	- 126.95
Stem	396.25	304.44	91.81	23.07	91.81	23.07	107.15	57.11
Branch	87.41	96.16	- 8.75	- 48.68	42.04	73.56	50.84	- 36.31
Total	483.66	400.60	83.06	16.44	94.67	19.34	112.53	60.54

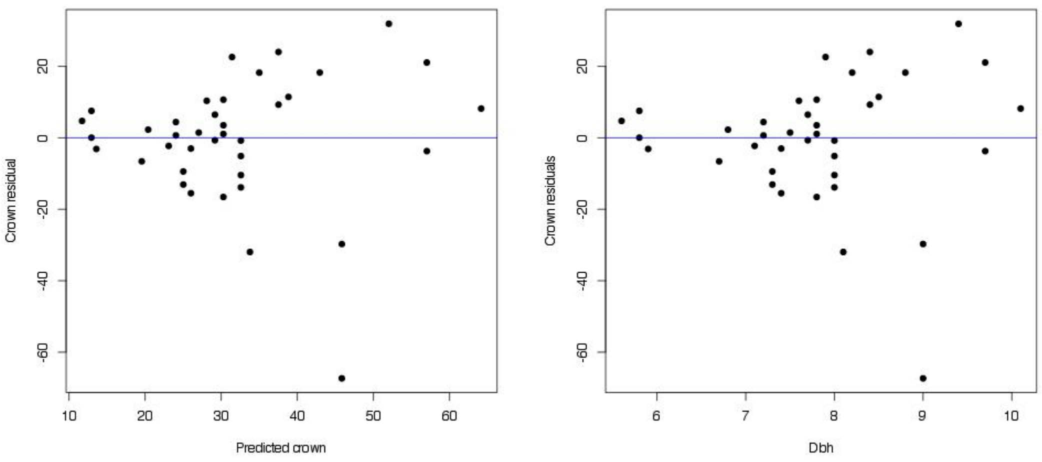
For red maple, the Dbh only system of equations provides the weakest predictions of tree biomass. When we add Ht to the system we improve stem component biomass prediction. When Dcrn is added to the system, improved crown biomass predictions result.

3.3.2 SLASH PINE - UGA DATA

Parameter estimates and fit statistics and residual plots from the final selected Dbh based equation fitted to slash pine is presented in Table 3.10 and Figure 3.11.

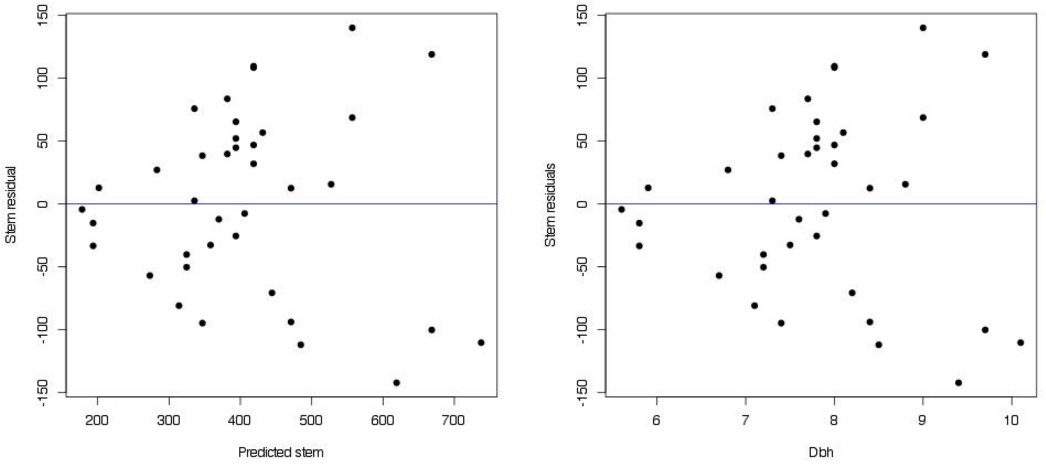
Table 3.10: Parameter estimates, standard errors and test statistics of Dbh based biomass equation fitted in the system of equations (3.11) for slash pine - UGA data

Parameter	Parameter associated with	Estimate	Standard error	t-value	p-value
$\hat{\beta}_{11}$	Dbh	2.68	0.016	169.47	<.0001
$\hat{\beta}_{20}$		0.95	0.396	2.39	0.0222
$\hat{\beta}_{21}$	Dbh	1.97	0.188	10.50	<.0001
$\hat{\beta}_{30}$		-3.50	1.204	-2.91	0.0061
$\hat{\beta}_{31}$	Dbh	3.15	0.560	5.63	<.0001
$\hat{\beta}_{40}$		-2.57	1.379	-1.86	0.0007
$\hat{\beta}_{41}$	Dbh	2.40	0.650	3.69	0.0708



(a) Residual vs predicted crown (b) Residual vs Dbh

Figure 3.11: Residual plot of crown - Dbh only based system



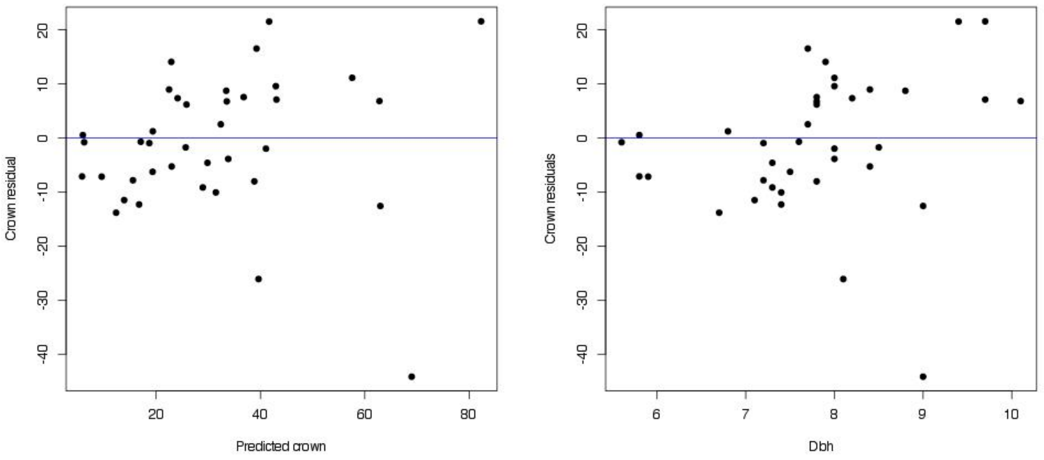
(a) Residual vs predicted stem (b) Residual vs Dbh

Figure 3.12: Residual plot of stem - Dbh only based system

All parameters in the Dbh and Ht based system of equations fitted to slash pine, are significant at α=0.1 (Table 3.11). It is evident from the residual plots that the model satisfies the usual regression assumption of homogeneity of variance (Figures 3.13, and 3.14).

Table 3.11: Parameter estimates, standard errors and test statistics of Dbh and Ht based biomass equation fitted in the system of equations (3.12) for slash pine - UGA data

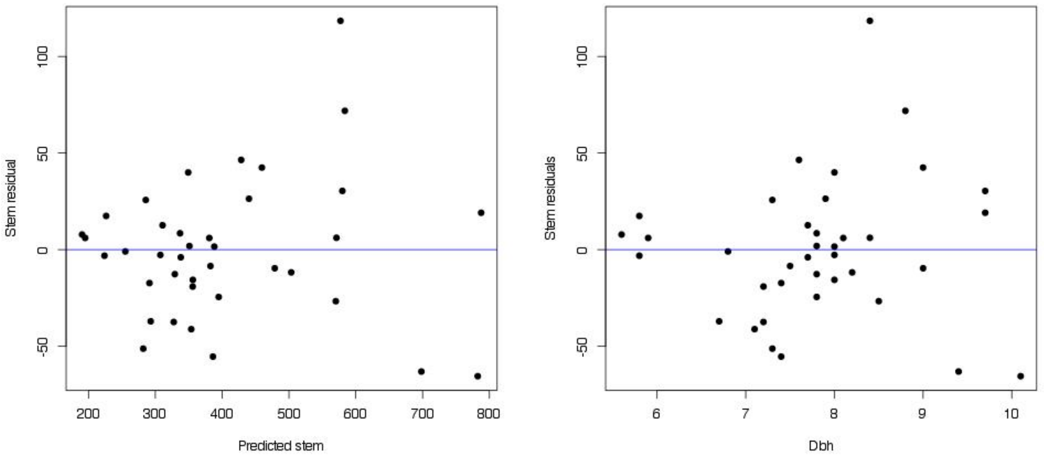
Parameter	Parameter associated with	Estimate	Standard error	t-value	p-value
$\hat{\beta}_{10}$		-3.68	0.361	-10.18	<.0001
$\hat{\beta}_{11}$	Dbh	1.90	0.141	13.49	<.0001
$\hat{\beta}_{12}$	Ht	1.29	0.103	12.45	<.0001
$\hat{\beta}_{20}$		0.76	0.435	1.74	0.0899
$\hat{\beta}_{21}$	Dbh	1.74	0.222	7.84	<.0001
$\hat{\beta}_{22}$	Ht	0.42	0.159	2.61	0.0130
$\hat{\beta}_{31}$	Dbh	5.37	0.619	8.69	<.0001
$\hat{\beta}_{32}$	Ht	-2.00	0.327	-6.11	<.0001
$\hat{\beta}_{40}$		1.99	1.213	1.64	0.1095
$\hat{\beta}_{41}$	Dbh	4.73	0.782	6.05	<.0001
$\hat{\beta}_{42}$	Ht	-2.31	0.465	-4.98	<.0001



(a) Residual vs predicted crown

(b) Residual vs Dbh

Figure 3.13: Residual plot of crown - Dbh and Ht based system



(a) Residual vs predicted stem

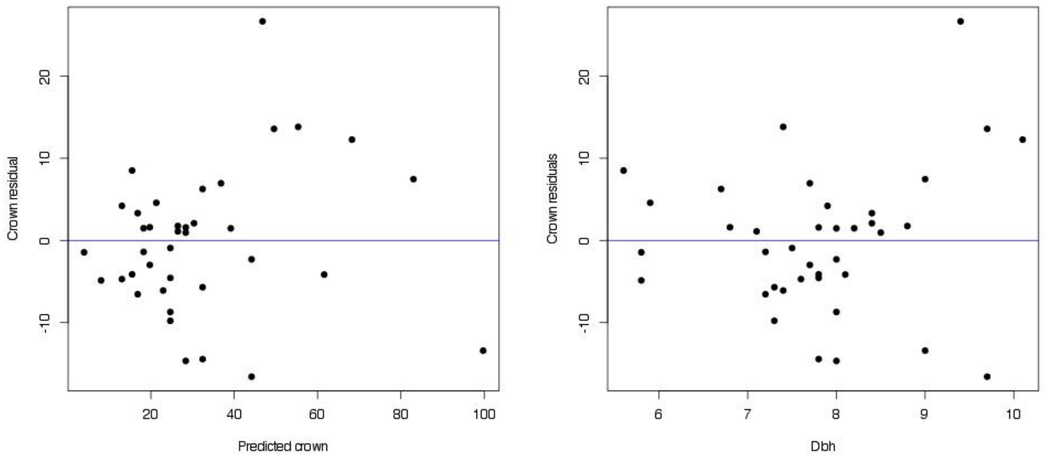
(b) Residual vs Dbh

Figure 3.14: Residual plot of stem - Dbh and Ht based system

Parameter estimates, fit statistics and residual plots for the Dbh, Ht, Dcrn system are presented in Table (3.12) and Figures 3.15 and 3.16. Dcrn is significant in predicting branch and foliage biomass.

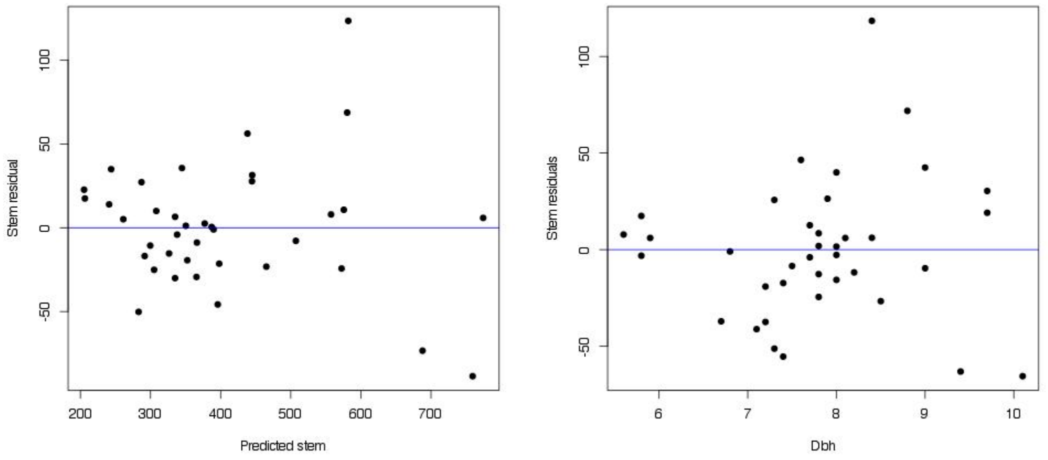
Table 3.12: Parameter estimates, standard errors and test statistics of Dbh, Ht and Dcrn based biomass equation fitted in the system of equations (3.13) for slash pine - UGA data

Parameter	Parameter associated with	Estimate	Standard error	t-value	p-value
$\hat{\beta}_{10}$		-3.46	0.376	-9.21	<.0001
$\hat{\beta}_{11}$	Dbh	1.82	0.144	12.67	<.0001
$\hat{\beta}_{12}$	Ht	1.27	0.106	11.97	<.0001
$\hat{\beta}_{20}$		0.78	0.411	1.91	0.0646
$\hat{\beta}_{21}$	Dbh^2Ht	0.64	0.063	10.21	<.0001
$\hat{\beta}_{30}$		-1.34	0.321	-4.19	0.0002
$\hat{\beta}_{31}$	Dcrn	2.93	0.191	15.31	<.0001
$\hat{\beta}_{40}$		-2.03	0.510	-3.98	0.0003
$\hat{\beta}_{41}$	Dcrn	2.94	0.303	9.72	<.0001



(a) Residual vs predicted crown (b) Residual vs Dbh

Figure 3.15: Residual plot of crown - Dbh, Ht, and Dcrn based system



(a) Residual vs predicted stem (b) Residual vs Dbh

Figure 3.16: Residual plot of stem - Dbh, Ht, and Dcrn based system

As for the red maple, a simple function to predict Dcrn based on Dbh for slash pine (Equation 3.19) was developed.

$$\hat{\text{Dcrn}} = 0.92 + 0.75\text{Dbh} - 0.04\text{Ht} \tag{3.19}$$

R^2 values for Equation 3.19 was 0.61.

3.3.2.1 Model comparison : slash pine (UGA data)

For Dbh only system, higher average percentage bias and error are found for branch, foliage and crown components then for stem components (Table 3.13). The goodness of fit statistics show that more than 70% of variation is explained by the model for stemwood, bark, stem and total biomass and poor fit is clear for branch, foliage and crown components.

Table 3.13: Average observed, average predicted component biomass, and fit statistics from Dbh only system (3.11) fitted to UGA slash pine data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	254.36	255.89	- 1.53	-5.46	49.18	21.10	56.22	73.38
Bark	150.12	150.29	- 0.17	-2.21	20.88	13.95	24.45	71.84
Stem	404.48	406.18	- 1.70	- 2.80	58.77	14.46	70.62	77.84
Branch	21.14	20.86	0.27	-23.70	7.96	46.90	11.21	32.94
Foliage	11.06	10.93	0.13	-36.63	4.37	59.32	6.82	17.43
Crown	32.20	31.79	0.41	-23.82	11.87	46.14	17.39	28.39
Total	436.68	437.97	-1.29	-1.85	51.62	11.70	61.64	84.43

Addition of height in the model significantly increases the model fit (Table 3.14). For example, average prediction bias is close to 0 for all components and the average percent prediction error is smaller for all components compared to Dbh based system. RMSE has significantly decreased for all components. PVE has increased from about 74% to 95%, 72%

to 76%, 78% to 94%, 33% to 65%, 17% to 52%, 28% to 63%, and 84% to 94% for stemwood, bark, stem, branch, foliage, crown and total biomass, respectively. Overall, better fit was obtained using height as an additional variable in the system. Similar to Dbh based system of equations, branch, foliage and crown biomass models predictions are not as good as for stem components.

Table 3.14: Average observed, average predicted component biomass, and fit statistics from Dbh and Ht system (3.12) fitted to UGA slash pine data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	254.36	254.06	0.30	- 0.93	19.36	8.37	24.23	95.05
Bark	150.12	149.94	0.18	- 1.71	18.06	12.40	22.38	76.41
Stem	404.48	404.00	0.48	- 0.29	26.22	6.34	36.01	94.24
Branch	21.14	20.48	0.65	- 5.02	6.32	33.91	8.10	65.01
Foliage	11.06	10.72	0.34	- 13.10	3.38	39.87	5.18	52.44
Crown	32.20	31.21	0.99	- 4.80	9.32	32.71	12.42	63.49
Total	436.68	435.21	1.47	0.13	28.81	6.54	39.14	93.72

Addition of Dcrn improved the model fit for branch, foliage, crown and total biomass components (Table 3.15). In general the addition of Dcrn improved overall model fit as well as individual component predictions (Table 3.15).

Table 3.15: Average observed, average predicted component biomass, and fit statistics from Dbh, Ht, and Dcrn system (3.13) fitted to UGA slash pine data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	254.36	254.58	- 0.22	- 1.57	19.40	8.48	24.22	95.06
Bark	150.12	150.29	- 0.17	- 3.01	17.93	12.82	23.77	73.39
Stem	404.48	404.87	- 0.39	- 1.10	26.44	6.71	37.15	93.87
Branch	21.14	21.09	0.05	- 5.56	3.74	21.64	5.33	84.84
Foliage	11.06	10.91	0.15	- 11.27	3.26	39.06	4.44	65.03
Crown	32.20	32.00	0.20	- 4.44	6.50	24.70	8.59	82.54
Total	436.68	436.87	- 0.19	- 0.92	26.05	6.28	36.25	94.61

CRM predicts the stemwood components for UGA slash pine very well (PVE=93.75) (Table 3.16). It results in very poor fit for bark and branch components.

Table 3.16: Average observed, average predicted component biomass, and fit statistics from component ratio method applied to UGA slash pine data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	254.36	245.64	8.72	2.98	22.51	9.64	27.24	93.75
Bark	150.12	28.66	121.46	81.23	121.46	81.23	126.67	- 655.83
Stem	404.48	274.30	130.19	33.45	130.19	33.45	137.80	15.64
Branch	21.14	45.10	- 23.96	- 188.88	25.03	190.60	30.82	- 406.94
Total	425.62	319.39	106.22	26.32	106.64	26.41	113.83	45.82

Results for UGA slash pine are similar to UGA red maple results. Addition of Ht improves stem component biomass predictions. Addition of DCrn improves crown biomass predictions.

Further, prediction of slash pine component biomass is generally superior to prediction of red maple component biomass. CRM method works well for stemwood biomass component.

3.3.3 Red maple - Legacy data

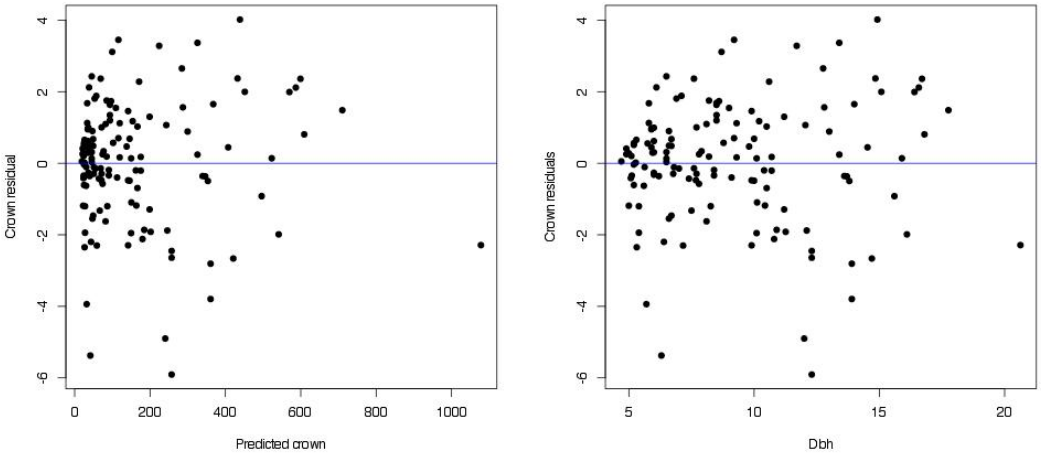
Since Dcrn was not available in the legacy data set, we fitted only Dbh, and Dbh and Ht based system of equations to red maple and slash pine.

Equations for red maple data were weighted as a function of Dbh to account for the heterogeneous variance properties in the data (Parresol 2001). Appropriate weights were determined by refitting the equation with weights in the model. For red maple, for Dbh based system, the weight functions used were DBH^2 for stemwood, bark, foliage, total stem and total biomass, $\sqrt{\mathrm{DBH}^{2.5}}$ for branch biomass, and $\sqrt{\mathrm{DBH}^3}$ for crown biomass equation.

Significant parameters (Table 3.17) and representative residual plots (Figures 3.17 and 3.18) associated with the final Dbh based system of equations fitted to Legacy red maple data show a good fit to the data.

Table 3.17: Parameter estimates, standard errors and test statistics of Dbh based biomass equation fitted in the system of equations (3.14) for red maple - Legacy data

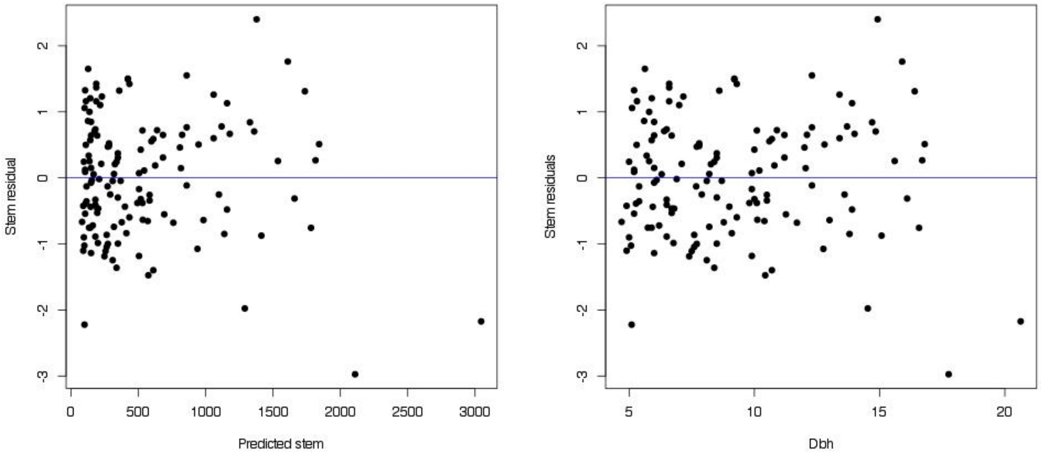
Parameter	Parameter associated with	Estimate	Standard error	t-value	p-value
$\hat{\beta}_{10}$		0.44	0.056	7.84	<.0001
$\hat{\beta}_{11}$	Dbh	2.47	0.024	101.61	<.0001
$\hat{\beta}_{20}$		-1.18	0.126	- 9.33	<.0001
$\hat{\beta}_{21}$	Dbh	2.31	0.056	41.35	<.0001
$\hat{\beta}_{30}$		- 1.67	0.145	- 11.55	<.0001
$\hat{\beta}_{31}$	Dbh	2.84	0.056	50.72	<.0001
$\hat{\beta}_{40}$		- 1.59	0.164	- 9.72	<.0001
$\hat{\beta}_{41}$	Dbh	1.90	0.074	25.62	<.0001



(a) Residual vs predicted crown

(b) Residual vs Dbh

Figure 3.17: Residual plot of crown - Dbh based system



(a) Residual vs predicted stem

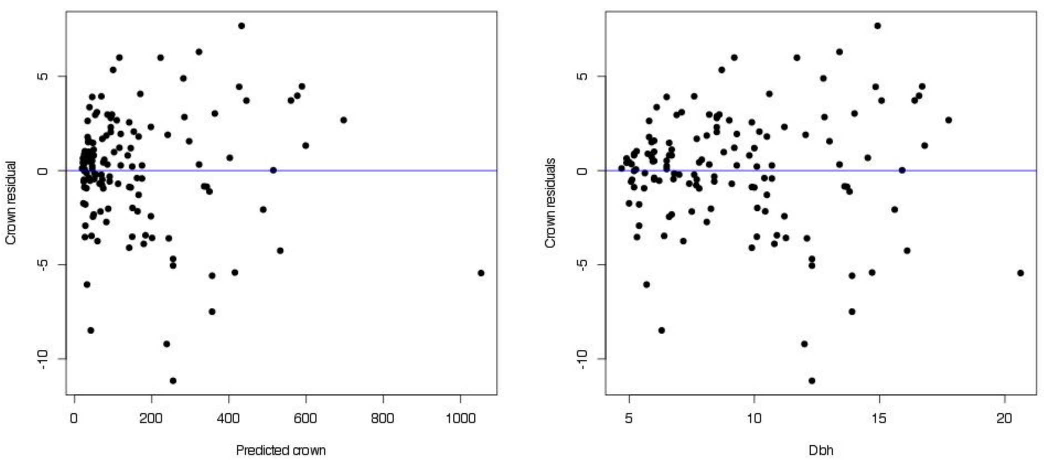
(b) Residual vs Dbh

Figure 3.18: Residual plot of stem - Dbh based system

All parameters in the Dbh and Ht based system of equations are highly significant (Table 3.18). In estimating branch and foliage components, only Dbh is important. We weighted the stemwood, bark and stem, and total biomass equations by using DBH^2, the branch equation by using $\sqrt{\mathrm{DBH}^2}$, the foliage equation by using $\sqrt{\mathrm{DBH}^3}$, and the crown equation by using $\sqrt{\mathrm{DBH}^{2.5}}$. It is evident from the residual plots that the model satisfies the usual regression assumption of homogeneity of variance (Figures 3.19, and 3.20).

Table 3.18: Parameter estimates, standard errors and test statistics of Dbh and Ht based biomass equation fitted in the system of equations (3.15) for red maple - Legacy data

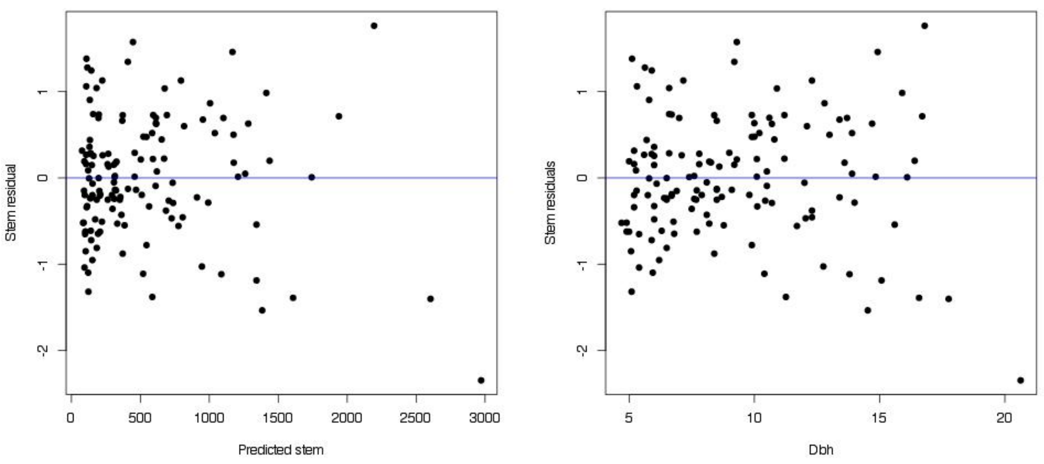
Parameter	Parameter associated with	Estimate	Standard error	t-value	p-value
$\hat{\beta}_{10}$		- 3.03	0.199	- 15.18	<.0001
$\hat{\beta}_{11}$	Dbh	1.99	0.032	62.52	<.0001
$\hat{\beta}_{12}$	Ht	1.07	0.060	17.92	<.0001
$\hat{\beta}_{20}$		- 5.56	0.602	- 9.23	<.0001
$\hat{\beta}_{21}$	Dbh	1.69	0.096	17.50	<.0001
$\hat{\beta}_{22}$	Ht	1.36	0.182	7.52	<.0001
$\hat{\beta}_{30}$		- 1.61	0.148	- 10.82	<.0001
$\hat{\beta}_{31}$	Dbh	2.81	0.058	48.65	<.0001
$\hat{\beta}_{40}$		- 1.62	0.159	- 10.19	<.0001
$\hat{\beta}_{41}$	Dbh	1.90	0.070	27.05	<.0001



(a) Residual vs predicted crown

(b) Residual vs Dbh

Figure 3.19: Residual plot of crown - Dbh and Ht based system



(a) Residual vs predicted stem

(b) Residual vs Dbh

Figure 3.20: Residual plot of stem - Dbh and Ht based system

3.3.3.1 Model comparison : red maple (Legacy data)

For the Dbh only system, higher average percent prediction bias and error are evident for branch, foliage and crown components. The system predicts stem components better than crown components. PVEs for crown components are higher than the Dbh based system fitted to UGA data.

Table 3.19: Average observed, average predicted component biomass, and fit statistics from Dbh only system (3.14) fitted to Legacy red maple data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	466.81	464.90	1.91	- 3.93	69.54	16.47	134.27	92.67
Bark	63.34	62.59	0.74	- 9.21	14.93	25.89	25.54	86.00
Stem	530.14	527.49	2.65	- 3.73	80.65	16.10	155.71	92.34
Branch	140.24	142.21	- 1.96	- 35.00	41.67	55.76	65.62	85.60
Foliage	15.32	15.20	0.13	- 35.01	6.11	57.90	10.14	52.75
Crown	155.57	157.40	- 1.84	- 30.34	43.15	49.83	68.14	86.19
Total	685.71	684.90	0.81	- 3.20	90.73	14.35	177.89	94.12

Overall, better fit was obtained by using height as an additional variable in the system (Table 3.20)

Table 3.20: Average observed, average predicted component biomass, and fit statistics from Dbh and Ht system (3.15) fitted to Legacy red maple data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	466.81	463.59	3.21	- 2.35	55.34	12.15	116.43	94.49
Bark	63.34	62.40	0.93	- 7.36	13.59	23.42	21.42	90.15
Stem	530.14	526.00	4.15	- 2.13	63.88	11.87	132.83	94.43
Branch	140.24	141.01	- 0.76 -	35.43	41.49	56.04	65.75	85.55
Foliage	15.32	15.02	0.30	- 33.19	6.06	56.87	10.14	52.72
Crown	155.57	156.03	- 0.47	- 30.40	42.96	49.92	68.20	86.17
Total	685.71	682.03	3.68	- 2.27	79.96	12.04	160.07	95.24

CRM method performs better when applied to legacy red maple data than UGA red maple data. However, it has lower fit than the systems of equations.

Table 3.21: Average observed, average predicted component biomass, and fit statistics from component ratio method applied to Legacy red maple data

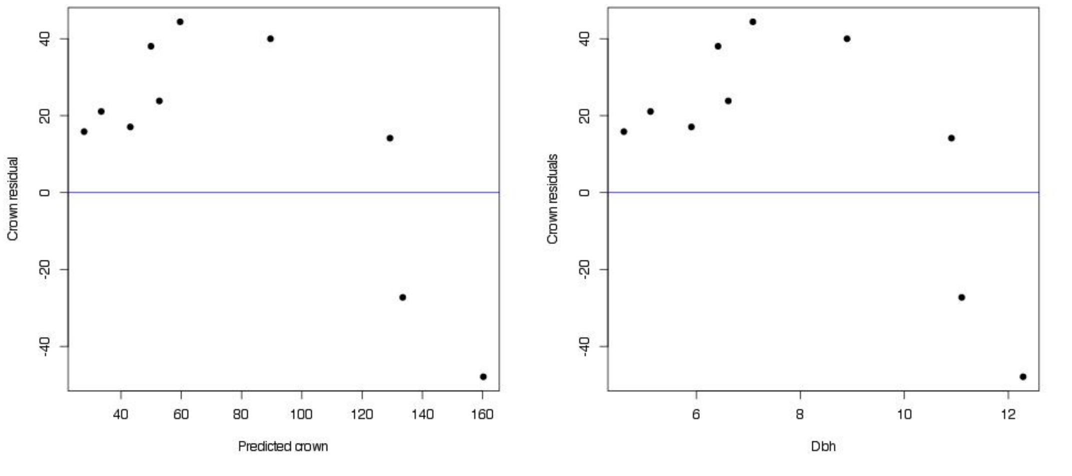
Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	475.24	400.89	74.34	11.82	83.14	16.25	175.07	87.65
Bark	64.51	42.22	22.29	31.08	22.70	32.96	39.65	66.57
Stem	539.74	443.11	96.63	14.83	103.85	17.64	210.56	86.13
Branch	143.10	124.15	18.95	- 77.29	62.48	99.30	109.06	60.63
Total	682.84	567.26	115.58	7.14	132.15	14.66	294.31	83.63

3.3.4 Slash pine - Legacy data

Note that only ten trees were available for slash pine in the legacy database. Consequently we can not draw widely applicable conclusions based on these model fits. However, for sake of completeness we present and discuss results of model fits to this small set of data. All parameters in the Dbh based system of equations fitted to slash pine from Legacy data are significant at α=0.05 (Table 3.22). Weight functions were not required to stabilize the variance. Residual plots from the fitted model are shown in Figures 3.21 and 3.22.

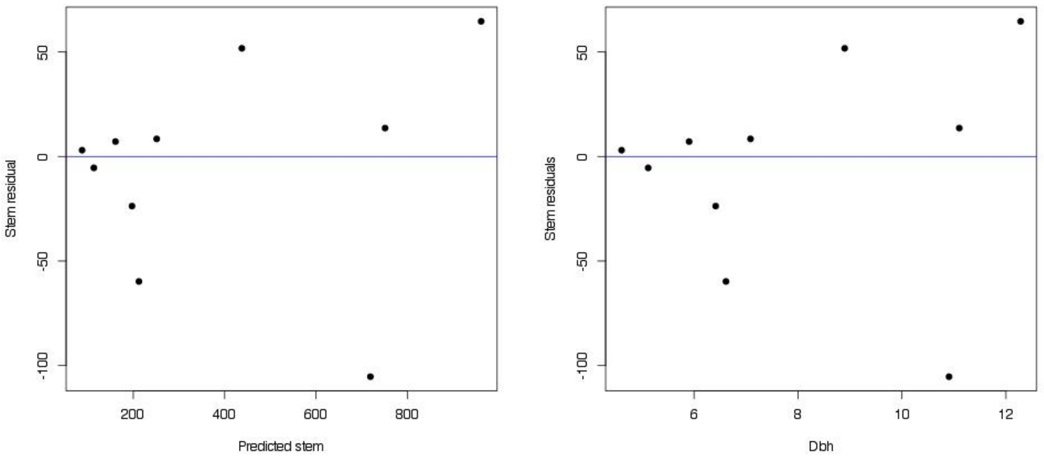
Table 3.22: Parameter estimates, standard errors and test statistics of Dbh based biomass equation fitted in the system of equations (3.16) for slash pine - Legacy data

Parameter	Parameter associated with	Estimate	Standard error	t-value	p-value
$\hat{\beta}_{10}$		1.71	0.698	2.44	0.0371
$\hat{\beta}_{11}$	Dbh	2.47	0.171	14.48	<.0001
$\hat{\beta}_{20}$		0.44	0.035	12.63	<.0001
$\hat{\beta}_{21}$	Dbh	2.26	0.029	77.34	<.0001
$\hat{\beta}_{31}$	Dbh	1.92	0.042	46.16	<.0001
$\hat{\beta}_{41}$	Dbh	1.44	0.071	20.25	<.0001



(a) Residual vs predicted crown (b) Residual vs Dbh

Figure 3.21: Residual plot of crown - Dbh based system



(a) Residual vs predicted stem

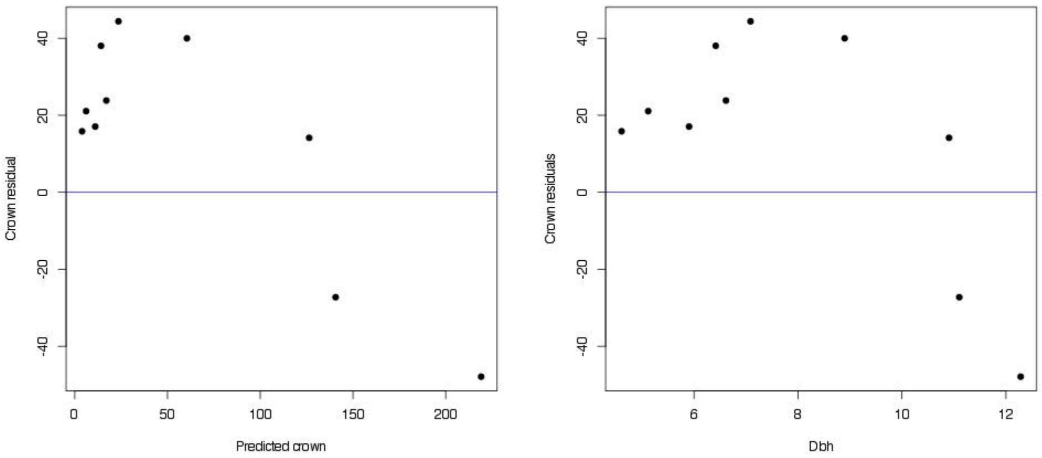
(b) Residual vs Dbh

Figure 3.22: Residual plot of stem - Dbh based system

Significant parameters (Table 3.23) and representative residual plots (Figures 3.23, 3.24) of Dbh and Ht based system fitted to Legacy slash pine data indicate a good fit.

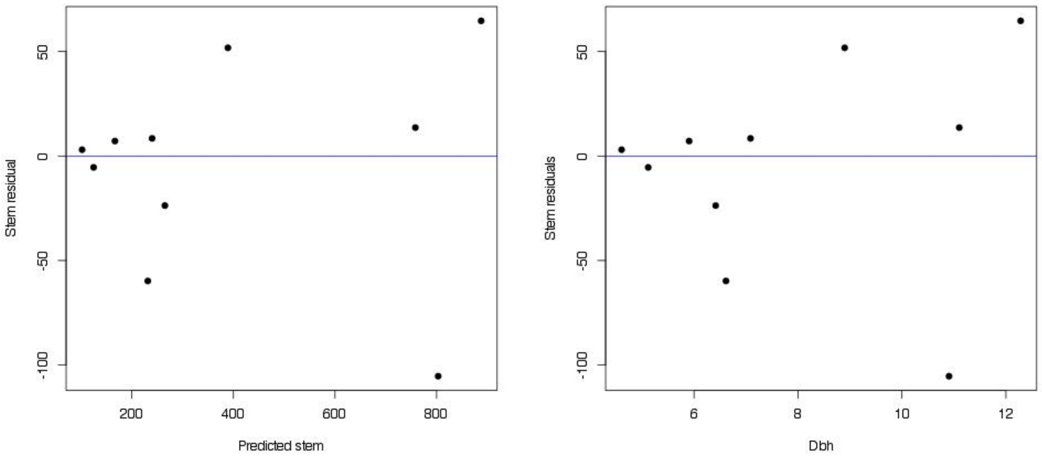
Table 3.23: Parameter estimates, standard errors and test statistics of Dbh and Ht based biomass equation fitted in the system of equations (3.17) for slash pine - Legacy data

Parameter	Parameter associated with	Estimate	Standard error	t-value	p-value
$\hat{\beta}_{10}$		- 4.40	0.576	- 7.63	<.0001
$\hat{\beta}_{11}$	Dbh	1.79	0.108	16.64	<.0001
$\hat{\beta}_{12}$	Ht	1.56	0.172	9.06	<.0001
$\hat{\beta}_{22}$	DBH^2Ht	0.50	0.006	85.02	<.0001
$\hat{\beta}_{30}$		- 4.99	0.697	- 7.15	<.0001
$\hat{\beta}_{31}$	Dbh	4.01	0.284	14.14	<.0001
$\hat{\beta}_{41}$	Dbh	5.29	0.666	7.94	<.0001
$\hat{\beta}_{42}$	Ht	- 2.19	0.391 -	5.61	0.0005



(a) Residual vs predicted crown (b) Residual vs Dbh

Figure 3.23: Residual plot of crown - Dbh and Ht based system



(a) Residual vs predicted stem (b) Residual vs Dbh

Figure 3.24: Residual plot of stem - Dbh based system

3.3.4.1 Model comparison : slash pine (Legacy data)

For Dbh only system when fitted to Legacy slash pine data, models related to stem components explain more than 90% variation in the data. Similar to other systems, average percent error and bias are higher for crown related components.

Table 3.24: Average observed, average predicted component biomass, and fit statistics from Dbh only system (3.16) fitted to Legacy slash pine data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	337.24	335.78	1.46	- 1.01	32.63	10.06	45.06	96.97
Bark	56.53	53.43	3.10	11.87	6.32	14.90	6.60	96.11
Stem	393.77	389.21	4.55	1.59	34.29	8.42	47.37	97.37
Branch	48.41	57.83	- 9.41	- 104.32	18.63	110.94	20.73	83.30
Foliage	15.56	20.08	- 4.52	- 147.01	10.32	158.80	10.98	60.78
Crown	63.98	77.91	- 13.93	- 111.65	28.96	119.64	31.32	78.72
Total	457.75	467.12	- 9.38	- 7.10	37.53	11.73	47.63	98.22

When height is added to the model, average percent bias and error in prediction significantly decreased for most the components (Table 3.25). PVE has increased for all components except for bark for which it has dropped from about 96% to 90%. Overall, better fit was obtained by using height as an additional variable in the system.

Table 3.25: Average observed, average predicted component biomass, and fit statistics from Dbh and Ht system (3.17) fitted to Legacy slash pine data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	337.24	336.00	1.24	0.54	15.06	6.46	21.46	99.31
Bark	56.53	60.76	- 4.23	- 21.96	9.32	26.76	10.41	90.32
Stem	393.77	396.76	- 2.99	- 3.70	17.73	7.65	22.52	99.41
Branch	48.41	47.26	1.15	9.45	6.77	33.37	7.23	97.97
Foliage	15.56	14.98	0.59	14.09	3.89	39.76	4.82	92.44
Crown	63.98	62.24	1.74	11.79	10.49	33.95	11.46	97.15
Total	457.75	459.00	- 1.26	- 1.47	14.32	5.52	23.11	99.58

As for the Legacy red maple data, the CRM method works well for Legacy slash pine data. Except for bark, all other component models provide a good fit to the data. Overall, it does not perform better than the system of equations.

Table 3.26: Average observed, average predicted component biomass, and fit statistics from component ratio method applied to Legacy slash pine data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	367.31	302.45	64.86	21.90	64.86	21.90	74.69	91.47
Bark	60.77	35.29	25.49	49.06	25.49	49.06	26.43	34.37
Stem	428.09	337.74	90.35	26.43	90.35	26.43	99.19	88.14
Branch	52.91	53.75	- 0.84	- 50.41	13.45	59.50	17.42	88.57
Total	481.00	391.49	89.51	22.20	89.51	22.20	102.94	90.72

3.3.5 Model prediction on an independent data set

Model development techniques and evaluation often include various statistics of fit as discussed above. Another performance measure of how well a model represents its real world counterpart is how it performs when used on totally independent data. In this study, we use Dbh and Ht based system of equations developed using UGA data to predict component biomass given the Dbh and Ht from legacy data and vice-versa.

First, we evaluated performance of models fitted to UGA data on the legacy data for both red maple (Table 3.27) and slash pine (Table3.28). We used UGA data for developing the models and legacy data as independent data set to validate the models.

The fit statistics for red maple (Table 3.27) show that the model fits well for the stem biomass but it has a poor fit for crown biomass. Average percent bias and error are smaller for stemwood, stem and total biomass compared to others. For stemwood more than 85% and for stem and total biomass more than 90% of the total variation in the data has been explained by the model. When compared to fit data, the fit statistics from independent data show that the system does not perform as well. However, the poor fit on some components may be due to extrapolation of the data. The range of UGA red maple data used to develop the models consist is from 4.8 to 11 inch for Dbh and is 38.7 to 73.6 ft for Ht whereas these range for Legacy data are 4.7 to 20.6 inch for Dbh and 40 to 110.1 ft.

Table 3.27: Fit statistics from using models fitted to UGA red maple data on the Legacy red maple data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	466.81	438.93	27.88	6.03	60.17	13.95	118.05	94.33
Bark	63.34	169.15	- 105.81 -	109.62	106.90	113.75	203.64	- 789.99
Stem	530.14	608.08	- 77.94 -	6.44	99.31	16.77	192.29	88.32
Branch	140.24	92.55	47.70 -	58.85	76.47	94.92	143.46	31.19
Foliage	15.32	10.72	4.61	- 32.40	7.65	72.18	13.73	13.39
Crown	155.57	10.72	4.61	- 32.40	7.65	72.18	13.73	13.39
Total	685.71	711.34	- 25.63	- 6.89	77.62	13.10	145.66	96.06

The performance of the UGA slash model is better than UGA red maple model. The model fits the data well for all components except for bark (Table 3.28). Fit statistics from this model when evaluated on the independent data is comparable to the fit data (Table 3.14) except for the bark component. The fit statistics show that the model has the worst fit for bark biomass. The plots of observed values with predicted values in Appendix (B) also support that this.

Table 3.28: Fit statistics from using models fitted to UGA slash data on the Legacy slash data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	337.24	278.94	58.30	16.89	58.30	16.89	75.34	91.53
Bark	56.53	161.50	- 104.97	- 183.18	104.97	183.18	124.04	- 1273.40
Stem	393.77	440.43	- 46.67	- 15.49	49.46	16.52	57.60	96.11
Branch	48.41	40.69	7.72	30.64	10.23	39.41	12.87	93.56
Foliage	15.56	17.67	- 2.10	- 18.02	4.75	47.51	5.85	88.86
Crown	63.98	17.67	- 2.10	- 18.02	4.75	47.51	5.85	88.86
Total	457.75	498.79	- 41.05	- 11.14	46.70	13.02	56.27	97.52

The average percent prediction bias and error are higher for branch, foliage and crown models when legacy red maple model was used to predict UGA red maple data. This trend is similar to the fit model (Table 3.20). The goodness of fit statistics (Table 3.29) indicate that the legacy red maple model predicted stemwood, stem and total biomass better than branch components when applied to new data. The plots of observed values with predicted values for various components are presented in Appendix (C).

Table 3.29: Fit statistics from using models fitted to Legacy red maple data on the UGA red maple data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	285.67	295.37	- 9.69	- 3.83	35.64	12.45	45.39	88.66
Bark	84.88	39.84	45.04	49.51	45.04	49.51	56.17	- 23.72
Stem	370.56	335.21	35.35	8.72	46.48	11.93	58.52	89.51
Branch	82.37	94.80	- 12.44	- 42.56	39.67	69.02	52.00	- 31.55
Foliage	9.68	12.41	- 2.72	- 82.40	3.84	89.10	4.62	31.97
Crown	92.05	12.41	- 2.72	- 82.40	3.84	89.10	4.62	31.97
Total	462.61	442.42	20.19	4.40	62.79	14.07	76.95	86.12

Overall, the legacy slash model does not perform well when used for the independent data from UGA study (Table 3.30). Goodness of fit statistics are better for stemwood, stem and total biomass models compared to branch components. Observed versus predicted plots in Appendix (D) also support this.

Table 3.30: Fit statistics from using models fitted to Legacy slash data on the UGA slash data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	254.36	311.88	- 57.52	- 22.54	57.52	22.54	72.82	55.34
Bark	150.12	60.83	89.29	57.74	89.29	57.74	96.52	- 338.80
Stem	404.48	372.71	31.77	8.57	45.07	11.50	52.45	87.78
Branch	21.14	28.90	- 7.76	- 64.09	11.52	74.49	15.56	- 29.15
Foliage	11.06	7.84	3.22	18.14	4.31	43.76	6.26	30.44
Crown	32.20	7.84	3.22	18.14	4.31	43.76	6.26	30.44
Total	436.68	409.44	27.23	7.16	47.55	11.24	56.55	86.90

In general, evaluation of the fitted biomass systems with independent data indicate that stem biomass components are more reliably estimated than are crown components.

3.3.6 MODEL PREDICTION FOR GIVEN DBH, HT AND DCRN

Models 1, 2 and 3 below refer to systems of equations 3.8, 3.9 and 3.10, respectively for red maple. That is, Model 1 is the Dbh only system, Model 2 is the Dbh, total height system, and Model 3 is the Dbh, total height and diameter at base of live crown system. These three system of equations were used to predict biomass components by various Dbh, Dcrn and Ht sizes. Dcrn is not always available in mensurational data hence a regression model based on Dbh was developed to predict Dcrn (Equation 3.18 for red maple and 3.19 for slash).

As expected, the Dbh only model predicts an average of the Dbh and Ht models, where as the Dbh, Ht and Dcrn models simply modify the Dbh, Ht models for crown size. For example, for all height levels, Model 1 predicts 359.60 lbs of total biomass for 8 inch Dbh (Table 3.31). Model 1 over-predicts the total biomass with increase in Dbh. For instance, if we were to predict total biomass using Model 1 for a 50 ft tree, we would be predicting about 24, 110, 242, 426, 668, 974 lbs more total biomass for trees with Dbh 8, 10, 12, 14, 16, and 18 inches, respectively than when using Model 3. This clearly indicates that relative to the Dbh, Ht, Dcrn equation system, the Dbh only equation system has more potential for large prediction errors as tree size increases. Moreover, for a 8 inch Dbh tree with 6.40 inch Dcrn, Model 1 predicts more total biomass relative to the Model 3 for shorter trees and less total biomass for taller trees. But for increase in Dbh, most of the time, we are predicting more total biomass with increase in height.

Model 2 uses more information than Model 1 to predict biomass components. We observed that, for most size combinations considered, Model 2 predicts more total biomass relative to Model 3. This is true for stemwood (Table 3.32), bark (Table 3.33), branch (Table 3.34) and stem (Table 3.36) biomass. For foliage biomass Model 2 predicts less biomass than Model

3 especially for larger Dbh and taller trees. For, for crown component biomass, predictions from Models 2 and 3 are similar. This suggests that both models work equally well when predicting crown component.

It should be noted that the ranges of Dbh, Ht and Dcrn used to develop the models 1, 2 and 3 are 4.8 to 11 inches, 38.7 to 73.6 ft, and 4 to 9.2 inches , respectively. Hence the prediction of biomass components reported in Tables 3.31 through 3.37 beyond the range of these Dbh, Ht and Dcrn variables represent extrapolation.

Table 3.31: Prediction of total biomass from Dbh (Model 1), Dbh and Ht (Model 2) and Dbh, Ht and Dcrn (Model 3) based system of equations for red maple for given Dbh, Dcrn and Ht level

			Ht			
Dbh	Dcrn	Model	50	60	70	80
8	6.40	1	359.60	359.60	359.60	359.60
		2	321.61	369.06	414.87	459.35
		3	335.85	394.04	452.00	509.77
10	7.30	1	607.17	607.17	607.17	607.17
		2	513.24	591.34	666.97	740.57
		3	496.97	585.48	673.93	762.34
12	8.20	1	935.06	935.06	935.06	935.06
		2	763.24	882.02	997.28	1109.65
		3	692.98	818.79	944.81	1071.01
14	9.10	1	1350.40	1350.40	1350.40	1350.40
		2	1077.91	1248.55	1414.41	1576.32
		3	924.45	1094.70	1265.53	1436.86
16	10.00	1	1859.82	1859.82	1859.82	1859.82
		2	1463.38	1698.20	1926.74	2150.10
		3	1191.92	1413.91	1636.96	1860.91
18	10.90	1	2469.56	2469.56	2469.56	2469.56
		2	1925.67	2238.10	2542.52	2840.33
		3	1495.91	1777.09	2059.91	2344.13

Table 3.32: Prediction of stemwood biomass from Dbh (Model 1), Dbh and Ht (Model 2) and Dbh, Ht and Dcrn (Model 3) based system of equations for red maple for given Dbh, Dcrn and Ht level

			Ht			
Dbh	Dcrn	Model	50	60	70	80
		1	215.07	215.07	215.07	215.07
8	6.40	2	196.15	226.98	256.79	285.76
		3	201.47	239.75	277.74	315.48
		1	382.73	382.73	382.73	382.73
10	7.30	2	321.63	372.18	421.06	468.57
		3	308.42	367.03	425.18	482.96
		1	612.92	612.92	612.92	612.92
12	8.20	2	481.77	557.48	630.70	701.86
		3	436.76	519.76	602.11	683.93
		1	912.68	912.68	912.68	912.68
14	9.10	2	677.95	784.49	887.54	987.67
		3	586.14	697.52	808.04	917.84
		1	1288.56	1288.56	1288.56	1288.56
16	10.00	2	911.42	1054.65	1193.17	1327.79
		3	756.26	899.96	1042.56	1184.22
		1	1746.74	1746.74	1746.74	1746.74
18	10.90	2	1183.25	1369.20	1549.05	1723.82
		3	946.86	1126.77	1305.31	1482.68

Table 3.33: Prediction of bark biomass from Dbh (Model 1), Dbh and Ht (Model 2) and Dbh, Ht and Dcrn (Model 3) based system of equations for red maple for given Dbh, Dcrn and Ht level

			Ht			
Dbh	Dcrn	Model	50	60	70	80
		1	72.61	72.61	72.61	72.61
8	6.40	2	49.02	58.47	67.86	77.21
		3	52.54	65.43	78.78	92.52
		1	115.00	115.00	115.00	115.00
10	7.30	2	96.36	114.92	133.39	151.77
		3	89.92	111.99	134.84	158.36
		1	167.44	167.44	167.44	167.44
12	8.20	2	167.37	199.63	231.71	263.63
		3	139.49	173.73	209.17	245.65
		1	230.04	230.04	230.04	230.04
14	9.10	2	266.96	318.41	369.57	420.49
		3	202.19	251.83	303.19	356.08
		1	302.91	302.91	302.91	302.91
16	10.00	2	400.02	477.12	553.78	630.08
		3	278.88	347.35	418.19	491.14
		1	386.12	386.12	386.12	386.12
18	10.90	2	571.49	681.63	791.16	900.16
		3	370.35	461.27	555.35	652.22

Table 3.34: Prediction of branch biomass from Dbh (Model 1), Dbh and Ht (Model 2) and Dbh, Ht and Dcrn (Model 3) based system of equations for red maple for given Dbh, Dcrn and Ht level

			Ht			
Dbh	Dcrn	Model	50	60	70	80
8	6.40	1	62.67	62.67	62.67	62.67
		2	67.15	73.84	80.02	85.79
		3	73.01	80.79	88.02	94.80
10	7.30	1	97.70	97.70	97.70	97.70
		2	84.74	93.18	100.98	108.26
		3	84.82	93.87	102.27	110.15
12	8.20	1	140.43	140.43	140.43	140.43
		2	102.47	112.69	122.12	130.92
		3	96.84	107.17	116.76	125.75
14	9.10	1	190.84	190.84	190.84	190.84
		2	120.34	132.33	143.41	153.74
		3	109.05	120.68	131.48	141.61
16	10.00	1	248.92	248.92	248.92	248.92
		2	138.31	152.10	164.83	176.71
		3	121.43	134.38	146.40	157.68
18	10.90	1	314.67	314.67	314.67	314.67
		2	156.38	171.97	186.36	199.79
		3	133.96	148.25	161.51	173.96

Table 3.35: Prediction of foliage biomass from Dbh (Model 1), Dbh and Ht (Model 2) and Dbh, Ht and Dcrn (Model 3) based system of equations for red maple for given Dbh, Dcrn and Ht level

			Ht			
Dbh	Dcrn	Model	50	60	70	80
		1	9.25	9.25	9.25	9.25
8	6.40	2	9.29	9.77	10.20	10.58
		3	8.84	8.06	7.45	6.97
		1	11.75	11.75	11.75	11.75
10	7.30	2	10.51	11.06	11.54	11.97
		3	13.81	12.59	11.65	10.88
		1	14.28	14.28	14.28	14.28
12	8.20	2	11.63	12.23	12.76	13.24
		3	19.88	18.13	16.77	15.67
		1	16.84	16.84	16.84	16.84
14	9.10	2	12.66	13.32	13.89	14.42
		3	27.06	24.68	22.83	21.33
		1	19.43	19.43	19.43	19.43
16	10.00	2	13.63	14.33	14.96	15.52
		3	35.35	32.23	29.81	27.86
		1	22.04	22.04	22.04	22.04
18	10.90	2	14.55	15.30	15.96	16.56
		3	44.74	40.79	37.73	35.27

Table 3.36: Prediction of stem biomass from Dbh (Model 1), Dbh and Ht (Model 2) and Dbh, Ht and Dcrn (Model 3) based system of equations for red maple for given Dbh, Dcrn and Ht level

			Ht			
Dbh	Dcrn	Model	50	60	70	80
		1	287.68	287.68	287.68	287.68
8	6.40	2	245.17	285.45	324.65	362.97
		3	254.01	305.19	356.52	408.00
		1	497.72	497.72	497.72	497.72
10	7.30	2	417.99	487.10	554.45	620.34
		3	398.34	479.02	560.02	641.31
		1	780.36	780.36	780.36	780.36
12	8.20	2	649.14	757.11	862.41	965.49
		3	576.25	693.49	811.28	929.58
		1	1142.73	1142.73	1142.73	1142.73
14	9.10	2	944.91	1102.90	1257.11	1408.16
		3	788.33	949.35	1111.23	1273.92
		1	1591.47	1591.47	1591.47	1591.47
16	10.00	2	1311.44	1531.77	1746.95	1957.87
		3	1035.14	1247.30	1460.75	1675.36
		1	2132.86	2132.86	2132.86	2132.86
18	10.90	2	1754.75	2050.84	2340.20	2623.97
		3	1317.21	1588.04	1860.66	2134.91

Table 3.37: Prediction of crown biomass from Dbh (Model 1), Dbh and Ht (Model 2) and Dbh, Ht and Dcrn (Model 3) based system of equations for red maple for given Dbh, Dcrn and Ht level

			Ht			
Dbh	Dcrn	Model	50	60	70	80
8	6.40	1	71.92	71.92	71.92	71.92
		2	76.44	83.62	90.22	96.37
		3	81.84	88.85	95.48	101.77
10	7.30	1	109.45	109.45	109.45	109.45
		2	95.25	104.24	112.52	120.23
		3	98.63	106.46	113.91	121.03
12	8.20	1	154.71	154.71	154.71	154.71
		2	114.10	124.92	134.88	144.16
		3	116.73	125.30	133.53	141.43
14	9.10	1	207.68	207.68	207.68	207.68
		2	133.00	145.65	157.30	168.16
		3	136.11	145.36	154.30	162.94
16	10.00	1	268.35	268.35	268.35	268.35
		2	151.94	166.43	179.78	192.23
		3	156.78	166.61	176.21	185.54
18	10.90	1	336.70	336.70	336.70	336.70
		2	170.93	187.27	202.32	216.36
		3	178.70	189.04	199.24	209.22

Tables 3.38 - 3.44 provide prediction of biomass components for slash pine from using three system of equations 3.11, 3.12, 3.13. Models 1, 2 and 3 below refer to system of equations 3.11, 3.12 and 3.13, respectively.

Similar to red maple, the Dbh based equation for slash pine is over-predicts the total biomass with increasing Dbh (Table 3.38). The range of Dbh is 5.6 to 10.1 inches, of Ht is 44.30 to 81.6 ft and of Dcrn is 2.2 to 6.6 inches, that was used to develop models for slash pine. The values of the variables in the table below beyond the respective range represents the extrapolation of the data.

Similar to red maple, Model 2 tends to predict more total and component biomass relative to Model 3. Additionally, differences in stem biomass (stemwood + bark) predictions for Models 2 and 3 (Table 3.43) are smaller than differences in predictions of crown biomass (branch + foliage) (Table 3.44).

Table 3.38: Prediction of total biomass from Dbh (Model 1), Dbh and Ht (Model 2) and Dbh, Ht and Dcrn (Model 3) based system of equations for slash pine for given Dbh, Dcrn and Ht level

			Ht			
Dbh	Dcrn	Model	50	60	70	80
8	6.40	1	451.15	451.15	451.15	451.15
		2	387.69	437.72	495.14	557.12
		3	379.40	439.90	503.32	569.48
10	7.30	1	782.21	782.21	782.21	782.21
		2	656.96	709.70	783.15	868.52
		3	574.54	660.64	751.02	845.42
12	8.20	1	1232.18	1232.18	1232.18	1232.18
		2	1082.18	1104.73	1177.42	1277.95
		3	818.42	933.55	1054.52	1180.97
14	9.10	1	1815.32	1815.32	1815.32	1815.32
		2	1759.75	1688.53	1725.36	1820.98
		3	1116.19	1263.62	1418.65	1580.79
16	10.00	1	2545.32	2545.32	2545.32	2545.32
		2	2829.93	2557.11	2496.53	2550.13
		3	1473.14	1656.02	1848.40	2049.74
18	10.90	1	3435.46	3435.46	3435.46	3435.46
		2	4486.20	3843.20	3587.37	3538.44
		3	1894.62	2115.94	2348.91	2592.80

Table 3.39: Prediction of stemwood biomass from Dbh (Model 1), Dbh and Ht (Model 2) and Dbh, Ht and Dcrn (Model 3) based system of equations for slash pine for given Dbh, Dcrn and Ht level

			Ht			
Dbh	Dcrn	Model	50	60	70	80
8	6.40	1	263.26	263.26	263.26	263.26
		2	200.60	253.65	309.32	367.32
		3	201.87	254.58	309.74	367.09
10	7.30	1	478.76	478.76	478.76	478.76
		2	306.21	387.19	472.16	560.70
		3	303.30	382.49	465.37	551.55
12	8.20	1	780.43	780.43	780.43	780.43
		2	432.61	547.02	667.07	792.16
		3	423.00	533.43	649.02	769.20
14	9.10	1	1179.67	1179.67	1179.67	1179.67
		2	579.41	732.65	893.44	1060.97
		3	560.37	706.67	859.79	1019.01
16	10.00	1	1687.27	1687.27	1687.27	1687.27
		2	746.28	943.66	1150.75	1366.54
		3	714.95	901.61	1096.97	1300.10
18	10.90	1	2313.55	2313.55	2313.55	2313.55
		2	932.95	1179.70	1438.59	1708.35
		3	886.34	1117.74	1359.93	1611.76

Table 3.40: Prediction of bark biomass from Dbh (Model 1), Dbh and Ht (Model 2) and Dbh, Ht and Dcrn (Model 3) based system of equations for slash pine for given Dbh, Dcrn and Ht level

			Ht			
Dbh	Dcrn	Model	50	60	70	80
8	6.40	1	155.31	155.31	155.31	155.31
		2	142.50	153.71	163.87	173.22
		3	136.77	153.68	169.61	184.73
10	7.30	1	241.14	241.14	241.14	241.14
		2	209.98	226.50	241.48	255.25
		3	181.95	204.45	225.63	245.75
12	8.20	1	345.43	345.43	345.43	345.43
		2	288.23	310.91	331.47	350.38
		3	229.74	258.15	284.90	310.30
14	9.10	1	468.10	468.10	468.10	468.10
		2	376.75	406.40	433.27	457.98
		3	279.81	314.42	347.00	377.94
16	10.00	1	609.07	609.07	609.07	609.07
		2	475.13	512.51	546.40	577.57
		3	331.93	372.98	411.63	448.33
18	10.90	1	768.26	768.26	768.26	768.26
		2	583.02	628.89	670.48	708.72
		3	385.90	433.63	478.56	521.23

Table 3.41: Prediction of branch biomass from Dbh (Model 1), Dbh and Ht (Model 2) and Dbh, Ht and Dcrn (MOdel 3) based system of equations for slash pine for given Dbh, Dcrn and Ht level

			Ht			
Dbh	Dcrn	Model	50	60	70	80
		1	21.30	21.30	21.30	21.30
8	6.40	2	28.60	19.87	14.60	11.18
		3	26.86	20.86	15.82	11.65
		1	43.05	43.05	43.05	43.05
10	7.30	2	94.86	65.89	48.42	37.08
		3	58.76	48.51	39.52	31.70
		1	76.51	76.51	76.51	76.51
12	8.20	2	252.62	175.48	128.95	98.75
		3	108.91	93.34	79.32	66.76
		1	124.40	124.40	124.40	124.40
14	9.10	2	578.28	401.69	295.19	226.05
		3	181.26	159.31	139.19	120.82
		1	189.53	189.53	189.53	189.53
16	10.00	2	1184.94	823.10	604.86	463.19
		3	279.71	250.34	223.07	197.84
		1	274.78	274.78	274.78	274.78
18	10.90	2	2231.06	1549.77	1138.87	872.12
		3	408.13	370.28	334.83	301.69

Table 3.42: Prediction of foliage biomass from Dbh (Model 1), Dbh and Ht (Model 2) and Dbh, Ht and Dcrn (MOdel 3) based system of equations for slash pine for given Dbh, Dcrn and Ht level

			Ht			
Dbh	Dcrn	Model	50	60	70	80
8	6.40	1	11.27	11.27	11.27	11.27
		2	15.99	10.49	7.34	5.39
		3	13.90	10.78	8.16	6.00
10	7.30	1	19.25	19.25	19.25	19.25
		2	45.92	30.12	21.09	15.49
		3	30.53	25.19	20.50	16.42
12	8.20	1	29.82	29.82	29.82	29.82
		2	108.72	71.32	49.93	36.66
		3	56.78	48.62	41.28	34.72
14	9.10	1	43.16	43.16	43.16	43.16
		2	225.32	147.79	103.47	75.98
		3	94.75	83.22	72.66	63.02
16	10.00	1	59.46	59.46	59.46	59.46
		2	423.58	277.84	194.52	142.83
		3	146.55	131.08	116.73	103.46
18	10.90	1	78.87	78.87	78.87	78.87
		2	739.17	484.85	339.44	249.25
		3	214.25	194.28	175.59	158.12

Table 3.43: Prediction of stem biomass from Dbh (MOdel 1), Dbh and Ht (Model 2) and Dbh, Ht and Dcrn (Model 3) based system of equations for slash pine for given Dbh, Dcrn and Ht level

			Ht			
Dbh	Dcrn	Model	50	60	70	80
8	6.40	1	418.58	418.58	418.58	418.58
		2	343.10	407.36	473.19	540.54
		3	338.64	408.26	479.34	551.82
10	7.30	1	719.90	719.90	719.90	719.90
		2	516.18	613.69	713.64	815.95
		3	485.25	586.94	691.00	797.30
12	8.20	1	1125.86	1125.86	1125.86	1125.86
		2	720.84	857.94	998.54	1142.54
		3	652.73	791.58	933.92	1079.50
14	9.10	1	1647.77	1647.77	1647.77	1647.77
		2	956.16	1139.05	1326.71	1518.96
		3	840.18	1021.09	1206.79	1396.94
16	10.00	1	2296.34	2296.34	2296.34	2296.34
		2	1221.41	1456.17	1697.16	1944.11
		3	1046.88	1274.59	1508.60	1748.44
18	10.90	1	3081.81	3081.81	3081.81	3081.81
		2	1515.97	1808.59	2109.07	2417.07
		3	1272.24	1551.38	1838.50	2132.99

Table 3.44: Prediction of crown biomass from Dbh (Model 1), Dbh and Ht (Model 2) and Dbh, Ht and Dcrn (Model 3) based system of equations for slash pine for given Dbh, Dcrn and Ht level

			Ht			
Dbh	Dcrn	Model	50	60	70	80
		1	32.58	32.58	32.58	32.58
8	6.40	2	44.60	30.36	21.94	16.57
		3	40.76	31.64	23.98	17.65
		1	62.31	62.31	62.31	62.31
10	7.30	2	140.78	96.01	69.51	52.56
		3	89.29	73.70	60.01	48.12
		1	106.33	106.33	106.33	106.33
12	8.20	2	361.34	246.79	178.88	135.41
		3	165.69	141.96	120.60	101.47
		1	167.56	167.56	167.56	167.56
14	9.10	2	803.59	549.48	398.66	302.02
		3	276.01	242.53	211.85	183.84
		1	248.99	248.99	248.99	248.99
16	10.00	2	1608.52	1100.94	799.38	606.02
		3	426.26	381.42	339.80	301.30
		1	353.65	353.65	353.65	353.65
18	10.90	2	2970.23	2034.61	1478.30	1121.36
		3	622.38	564.57	510.41	459.81

3.4 Conclusion

In this study, we used two independent individual tree biomass data sets (UGA data and legacy data), to fit systems of biomass prediction equations for red maple and slash pine. Nonlinear regression with parameter estimated using ordinary least square method was used to investigate important variables for individual biomass components. For UGA data, independent variables Dbh, Ht, and Dcrn were tested for each component equation. Dcrn variable was not available in legacy data, therefore only Dbh and Dbh and Ht based biomass prediction equations were developed. For each data set and species, final biomass component equations were fitted simultaneously following the procedure described by Borders (1989). Borders' (1989) method is an instrumental technique known as nonlinear seemingly unrelated regression (NSUR). NSUR accounts fro cross equation correlation among equations within a system and allows for cross equation parameter constraints as well. Using this method it was possible to ensure that individual biomass component equation estimates were constrained to sum to total tree biomass.

Detailed analysis of fit statistics evaluated with both fit data and independent data indicate that more tree size information (e.g. Dbh, Ht, Dcrn) leads to better predictions of component biomass than does less tree size information (Dbh only or Dbh and Ht). Further, it is evident that stem biomass components are more reliably predicted than crown biomass components for all models considered.

Our work suggests that individual tree biomass prediction equations that rely on Dbh only are not useful for predicting total tree or tree component biomass. Further, it is clear that improved crown biomass prediction equations will require more detailed crown size measurements from the field. These measures include crown length, crown width, number of branches, and possibly others. Further work needs to be carried out to identify the most beneficial tree and crown measurements that will improve component biomass prediction models.

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3.6 APPENDIX A: CORRELATION OF RESIDUALS

Table 3.45: Correlations of residuals - Dbh based system of equations for red maple (UGA data)

	stemwood	Bark	Branch	Foliage	Stem	Crown	Total
Stemwood	1.00	0.32	0.23	-0.27	0.91	0.19	0.87
Bark	0.32	1.00	-0.45	-0.04	0.69	-0.43	0.33
Branch	0.23	-0.45	1.00	0.47	-0.03	1.00	0.56
Foliage	-0.27	-0.04	0.47	1.00	-0.22	0.54	0.13
Stem	0.91	0.69	-0.03	-0.22	1.00	-0.05	0.81
Crown	0.19	-0.43	1.00	0.54	-0.05	1.00	0.55
Total	0.87	0.33	0.56	0.13	0.81	0.55	1.00

Table 3.46: Correlations of residuals - Dbh and Ht based system of equations for red maple (UGA data)

	Stemwood	Bark	Branch	Foliage	Stem	Crown	Total
Stemwood	1.00	-0.01	0.56	-0.05	0.90	0.52	0.85
Bark	-0.01	1.00	-0.23	-0.28	0.43	-0.25	0.10
Branch	0.56	-0.23	1.00	0.57	0.40	1.00	0.85
Foliage	-0.05	-0.28	0.57	1.00	-0.17	0.64	0.30
Stem	0.90	0.43	0.40	-0.17	1.00	0.36	0.81
Crown	0.52	-0.25	1.00	0.64	0.36	1.00	0.83
Total	0.85	0.10	0.85	0.30	0.81	0.83	1.00

Table 3.47: Correlations of residuals - Dbh, Ht and Dcrn based system of equations for red maple (UGA data)

	Stemwood	Bark	Branch	Foliage	Stem	Crown	Total
Stemwood	1.00	-0.03	0.58	0.09	0.91	0.56	0.89
Bark	-0.03	1.00	-0.36	-0.03	0.39	-0.35	0.04
Branch	0.58	-0.36	1.00	0.62	0.38	1.00	0.82
Foliage	0.09	-0.03	0.62	1.00	0.07	0.67	0.44
Stem	0.91	0.39	0.38	0.07	1.00	0.37	0.84
Crown	0.56	-0.35	1.00	0.67	0.37	1.00	0.82
Total	0.89	0.04	0.82	0.44	0.84	0.82	1.00

Table 3.48: Correlations of residuals - Dbh based system of equations for slash pine (UGA data)

	Stemwood	Bark	Branch	Foliage	Stem	Crown	Total
Stemwood	1.00	0.45	- 0.58	-0.58	0.95	-0.60	0.92
Bark	0.45	1.00	-0.32	-0.39	0.70	-0.36	0.70
Branch	-0.58	-0.32	1.00	0.85	-0.58	0.98	-0.38
Foliage	-0.58	-0.39	0.85	1.00	-0.60	0.94	-0.42
Stem	0.95	0.70	-0.58	-0.60	1.00	-0.61	0.97
Crown	-0.60	-0.36	0.98	0.94	-0.61	1.00	-0.41
Total	0.92	0.70	-0.38	-0.42	0.97	-0.41	1.00

Table 3.49: Correlations of residuals - Dbh and Ht based system of equations for slash pine (UGA data)

	Stemwood	Bark	Branch	Foliage	Stem	Crown	Total
Stemwood	1.00	0.19	0.22	0.07	0.79	0.17	0.78
Bark	0.19	1.00	0.01	-0.12	0.75	-0.04	0.68
Branch	0.22	0.01	1.00	0.74	0.16	0.96	0.45
Foliage	0.07	-0.12	0.74	1.00	-0.03	0.90	0.26
Stem	0.79	0.75	0.16	-0.03	1.00	0.09	0.95
Crown	0.17	-0.04	0.96	0.90	0.09	1.00	0.40
Total	0.78	0.68	0.45	0.26	0.95	0.40	1.00

Table 3.50: Correlations of residuals - Dbh, Ht and Dcrn based system of equations for slash pine (UGA data)

	Stemwood	Bark	Branch	Foliage	Stem	Crown	Total
Stemwood	1.00	0.20	0.10	-0.10	0.78	0.01	0.80
Bark	0.20	1.00	-0.27	-0.36	0.77	-0.35	0.70
Branch	0.10	-0.27	1.00	0.54	-0.11	0.90	0.10
Foliage	-0.10	-0.36	0.54	1.00	-0.29	0.85	-0.10
Stem	0.78	0.77	-0.11	-0.29	1.00	-0.22	0.97
Crown	0.01	-0.35	0.90	0.85	-0.22	1.00	0.01
Total	0.80	0.70	0.10	-0.10	0.97	0.01	1.00

Table 3.51: Correlations of residuals - Dbh based system of equations for red maple (Legacy data)

	Stemwood	Bark	Branch	Foliage	Stem	Crown	Total
Stemwood	1.00	0.41	0.06	- 0.05	0.98	0.05	0.76
Stembark	0.41	1.00	0.15	- 0.27	0.60	0.10	0.54
Branch	0.06	0.15	1.00	0.19	0.09	0.99	0.65
Foliage	- 0.05	- 0.27	0.19	1.00	- 0.11	0.33	0.11
Stem	0.98	0.60	0.09	- 0.11	1.00	0.07	0.80
Crown	0.05	0.10	0.99	0.33	0.07	1.00	0.63
Total	0.76	0.54	0.65	0.11	0.80	0.63	1.00

Table 3.52: Correlations of residuals - Dbh and Ht based system of equations for red maple (Legacy data)

	Stemwood	Bark	Branch	Foliage	Stem	Crown	Total
Stemwood	1.00	0.41	0.06	- 0.05	0.98	0.05	0.76
Stembark	0.41	1.00	0.15	- 0.27	0.60	0.10	0.54
Branch	0.06	0.15	1.00	0.19	0.09	0.99	0.65
Foliage	- 0.05	- 0.27	0.19	1.00	- 0.11	0.33	0.11
Stem	0.98	0.60	0.09	- 0.11	1.00	0.07	0.80
Crown	0.05	0.10	0.99	0.33	0.07	1.00	0.63
Total	0.76	0.54	0.65	0.11	0.80	0.63	1.00

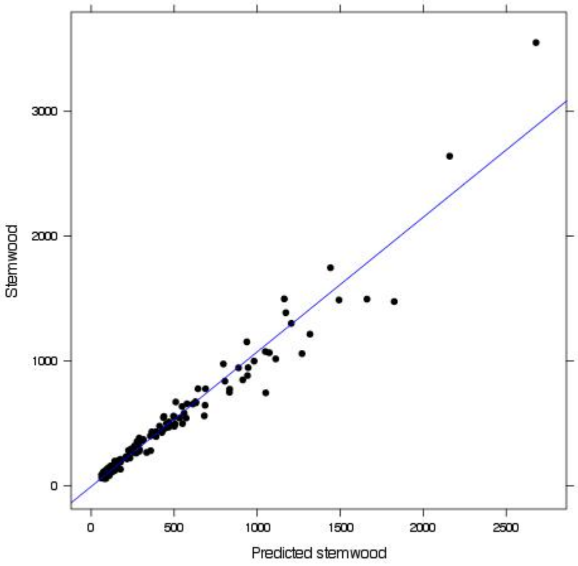
Table 3.53: Correlations of residuals - Dbh based system of equations for slash pine (Legacy data)

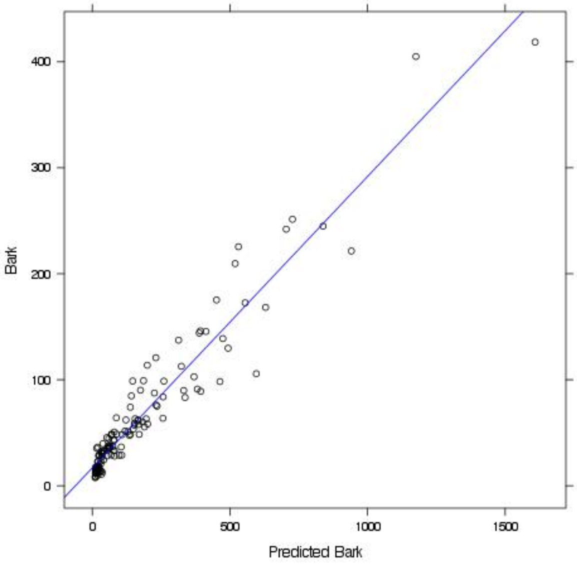
	Stemwood	Bark	Branch	Foliage	Stem	Crown	Total
Stemwood	1.00	0.29	- 0.10	- 0.36	0.99	- 0.19	0.86
Stembark	0.29	1.00	- 0.97	- 0.98	0.41	- 0.98	- 0.24
Branch	- 0.10	- 0.97	1.00	0.95	- 0.23	0.99	0.42
Foliage	- 0.36	- 0.98	0.95	1.00	- 0.48	0.98	0.16
Stem	0.99	0.41	- 0.23	- 0.48	1.00	- 0.32	0.78
Crown	- 0.19	- 0.98	0.99	0.98	- 0.32	1.00	0.34
Total	0.86	- 0.24	0.42	0.16	0.78	0.34	1.00

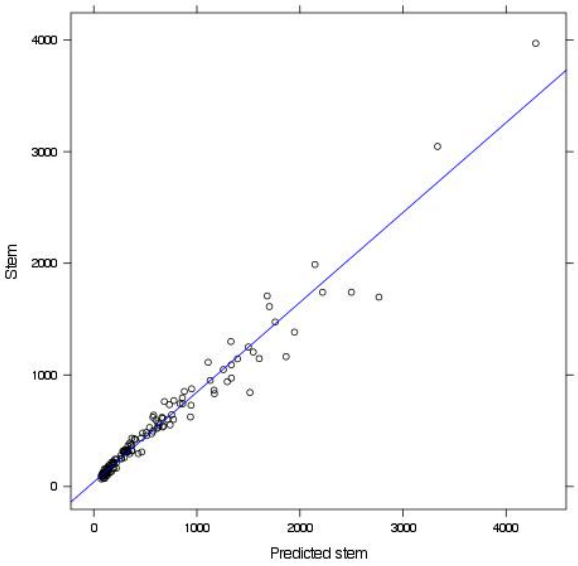
Table 3.54: Correlations of residuals - Dbh and Ht based system of equations for slash pine (Legacy data)

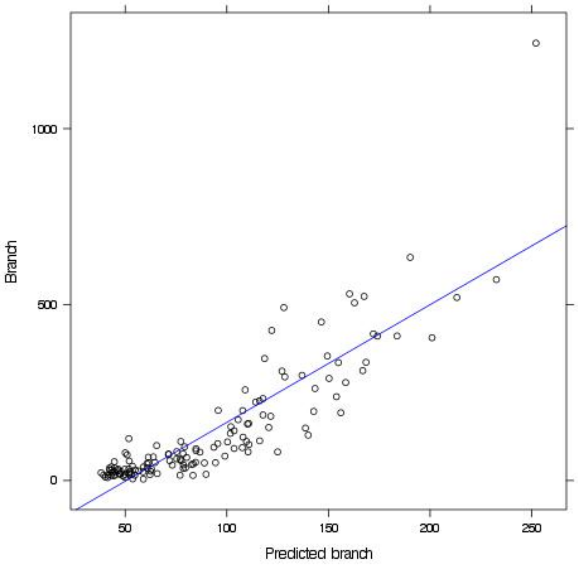
	Stemwood	Bark	Branch	Foliage	Stem	Crown	Total
Stemwood	1.00	- 0.14	0.26	- 0.27	0.05	0.89	0.89
Stembark	- 0.14	1.00	- 0.56	- 0.45	- 0.54	0.33	0.05
Branch	0.26	- 0.56	1.00	0.80	0.97	- 0.01	0.47
Foliage	- 0.27	- 0.45	0.80	1.00	0.93	- 0.46	0.01
Stem	0.05	- 0.54	0.97	0.93	1.00	- 0.20	0.30
Crown	0.89	0.33	- 0.01	- 0.46	- 0.20	1.00	0.87
Total	0.89	0.05	0.47	0.01	0.30	0.87	1.00

3.7 Appendix B: Actual vs predicted plots by components from predicting Legacy red maple data using UGA model









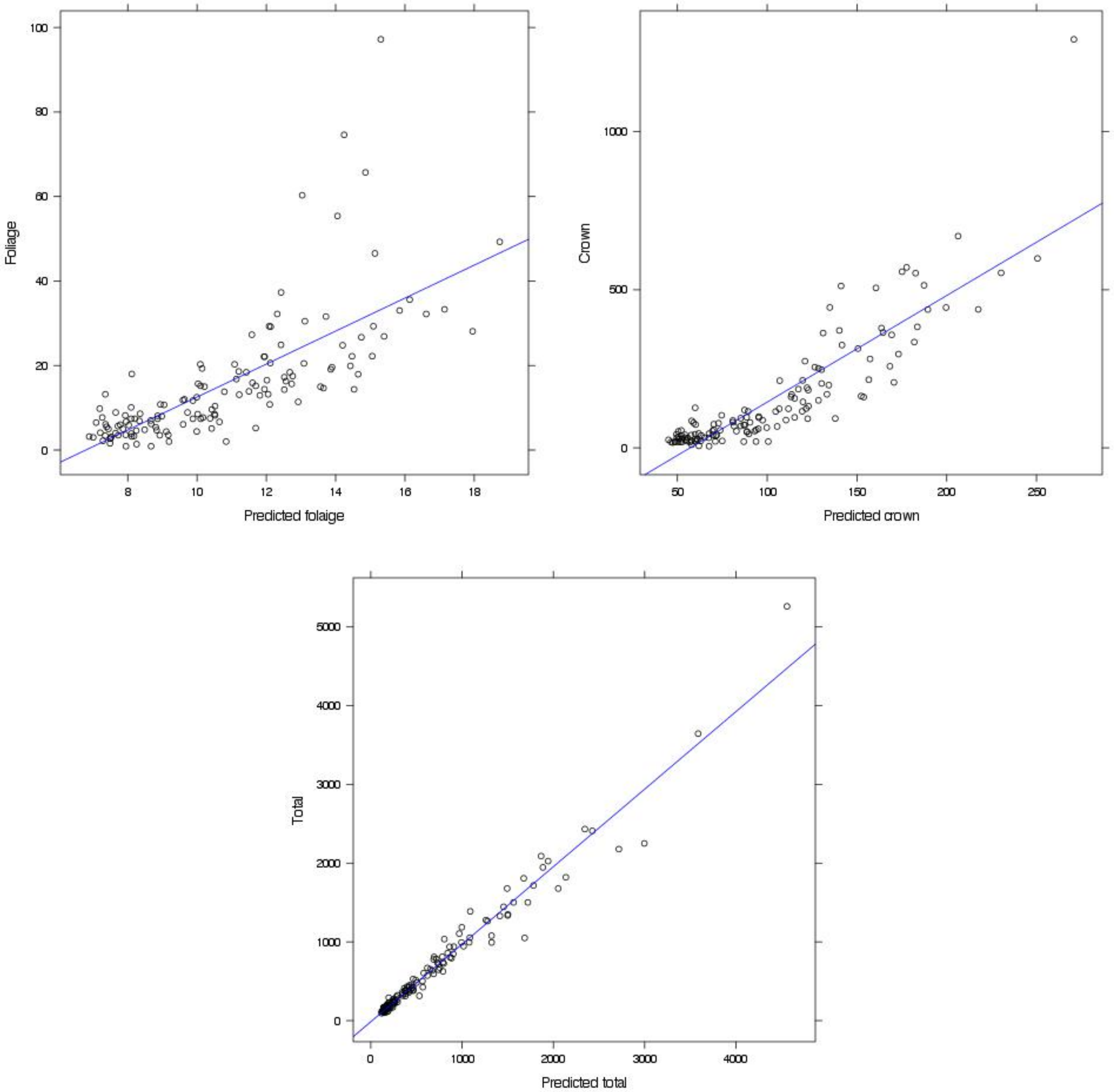
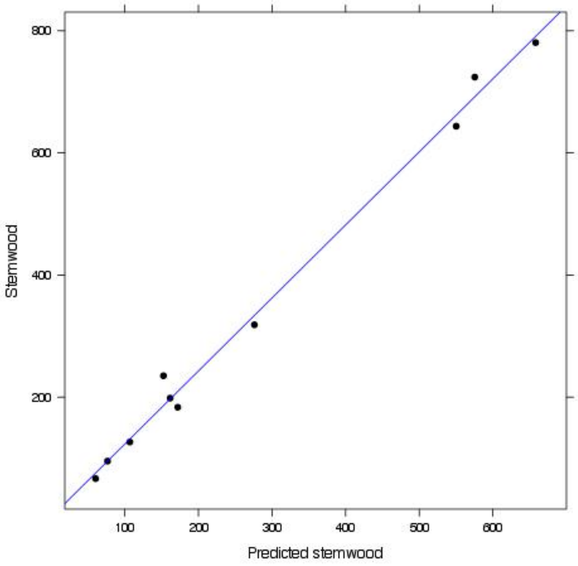
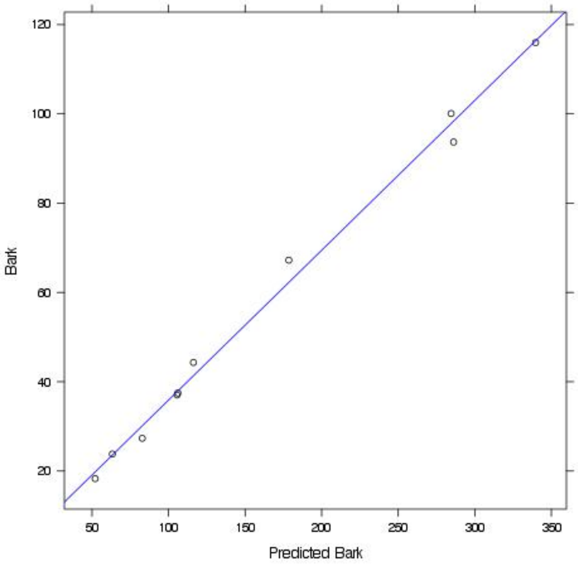
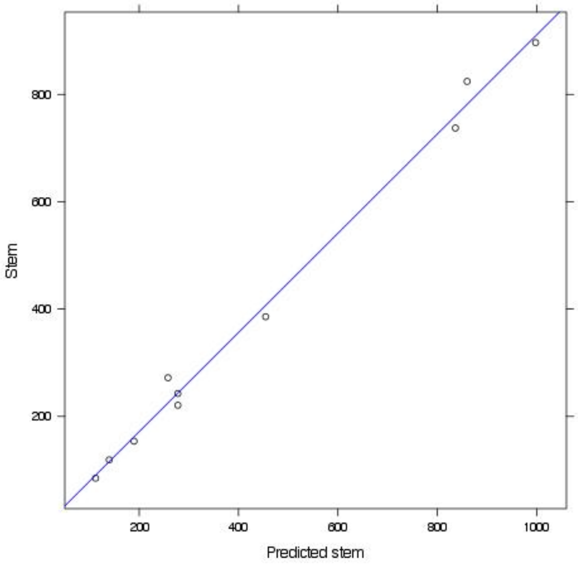


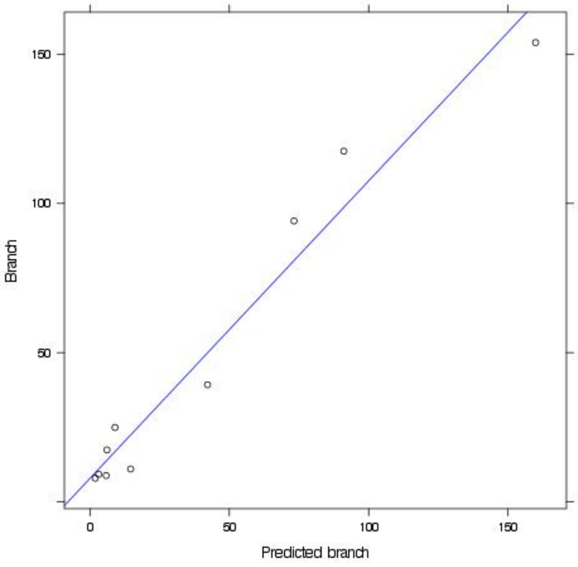
Figure 3.25: Actual vs predicted plots of various components from predicting Legacy red maple using UGA red maple model

3.8 Appendix C: Actual vs predicted plots by components from predicting Legacy slash pine data using UGA model









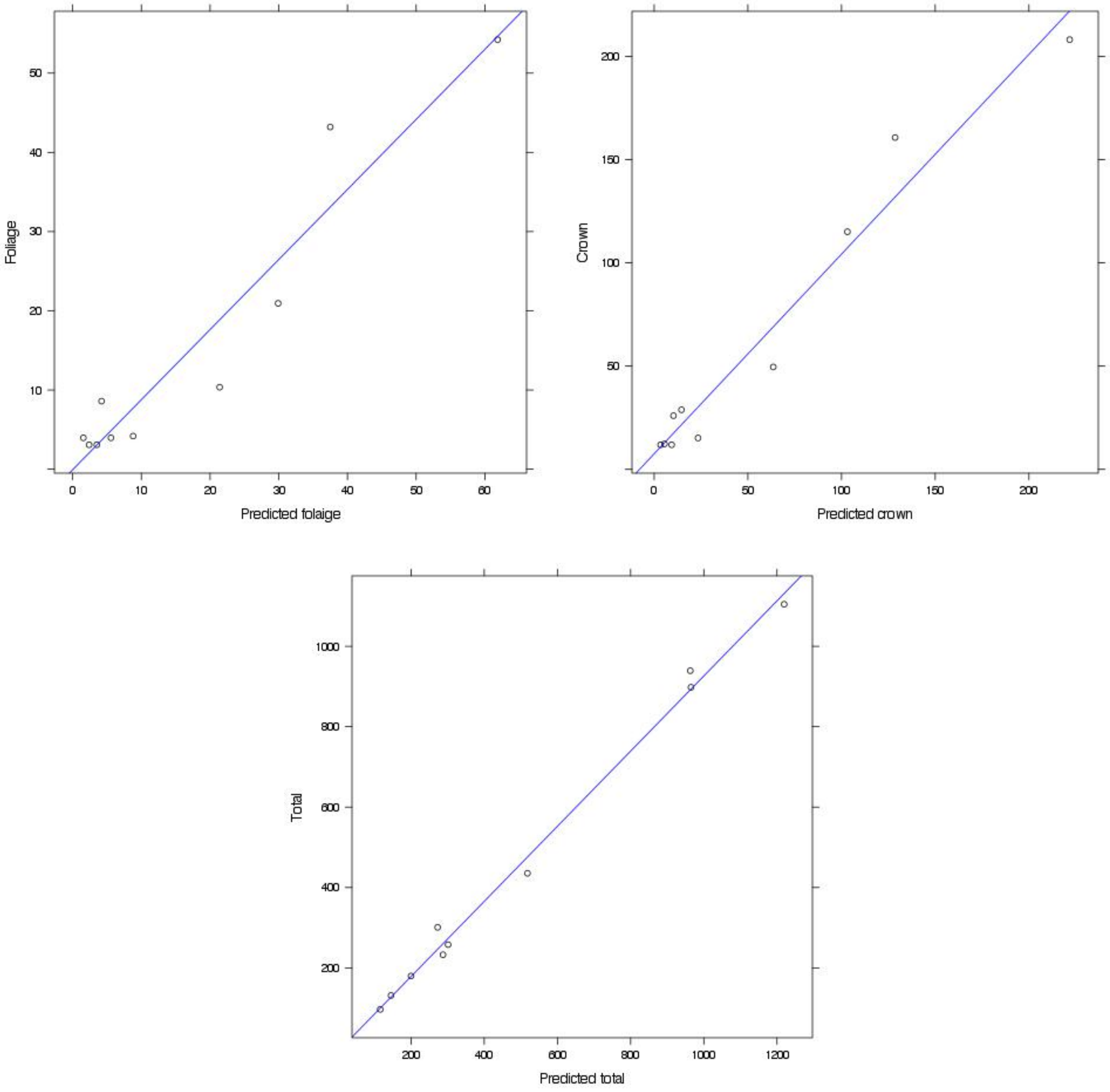
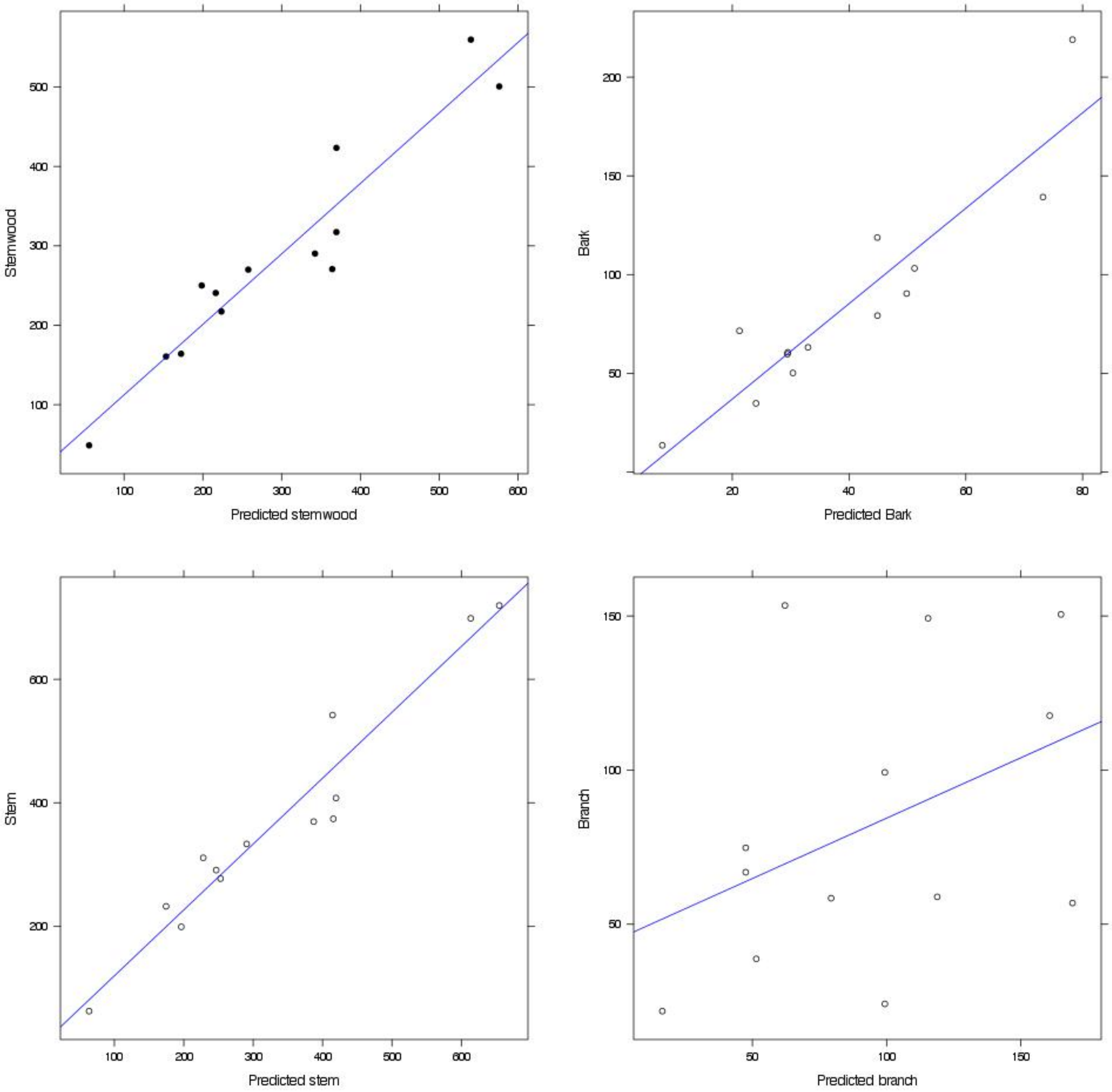


Figure 3.26: Actual vs predicted plots of various components from predicting Legacy slash pine using UGA slash model

3.9 Appendix D: Actual vs predicted plots by components from predicting UGA red maple data using Legacy model



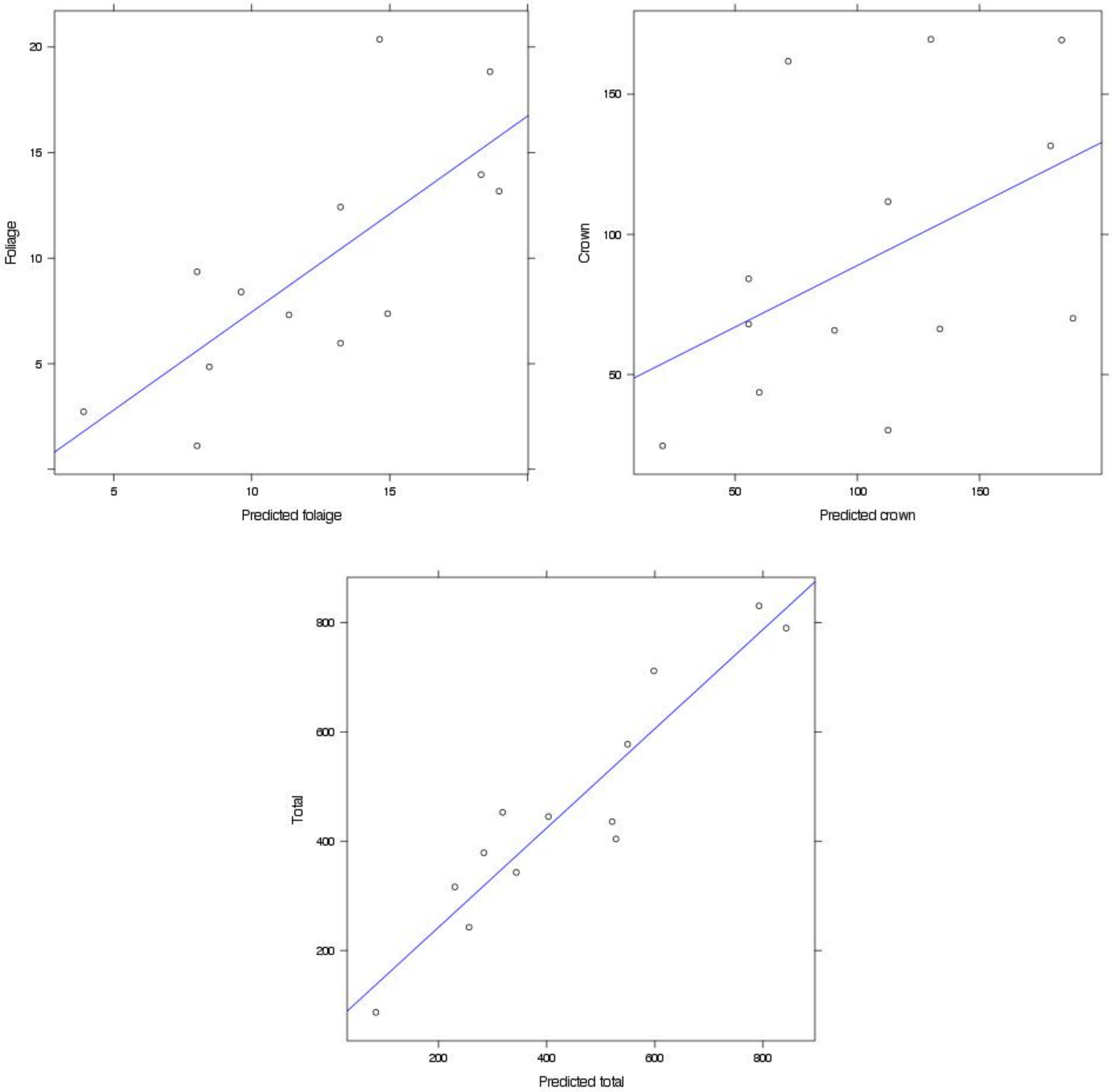
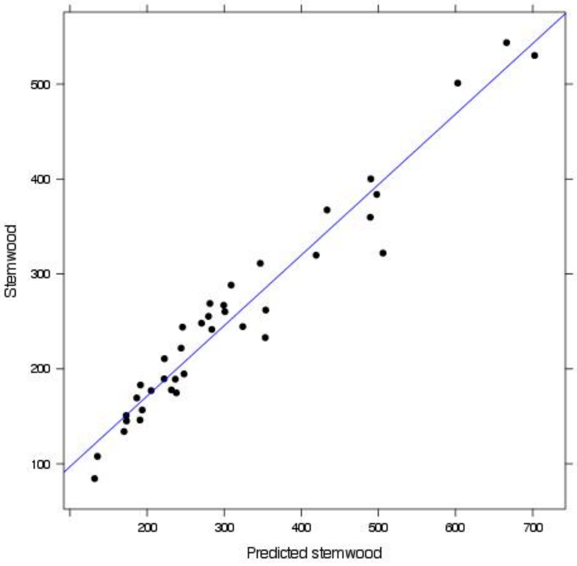
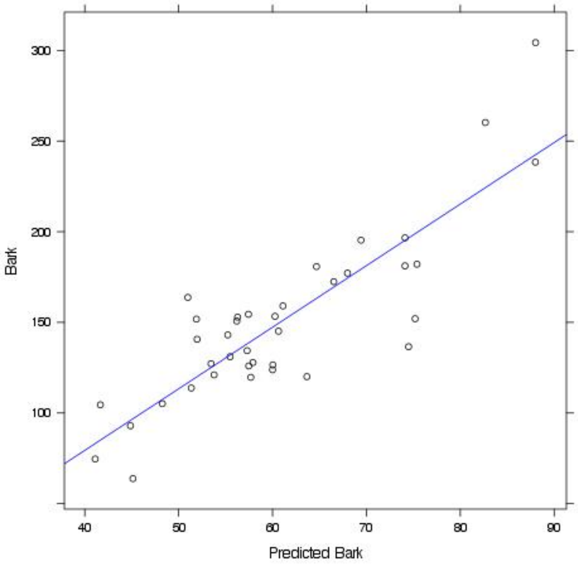
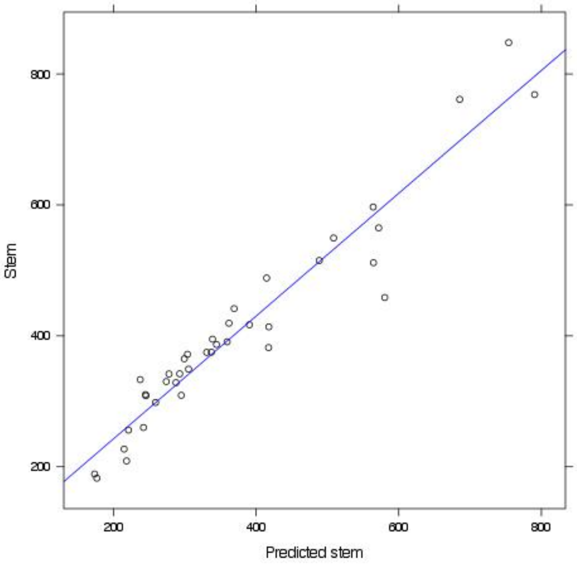


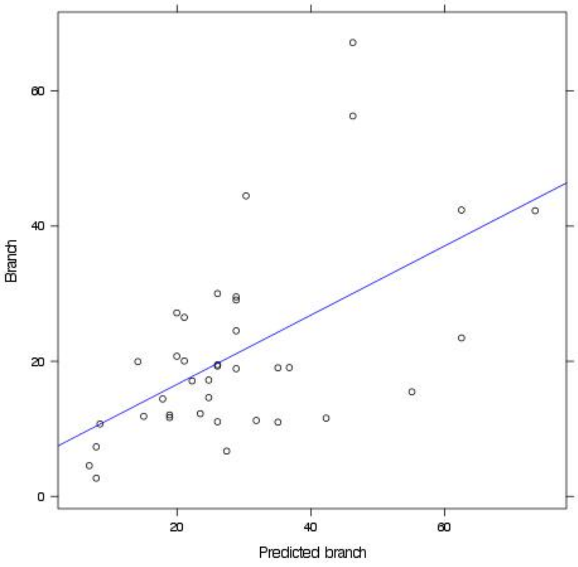
Figure 3.27: Actual vs predicted plots of various components from predicting UGA red maple using Legacy red maple model

3.10 Appendix E: Actual vs predicted plots by components from predicting UGA slash data using Legacy model









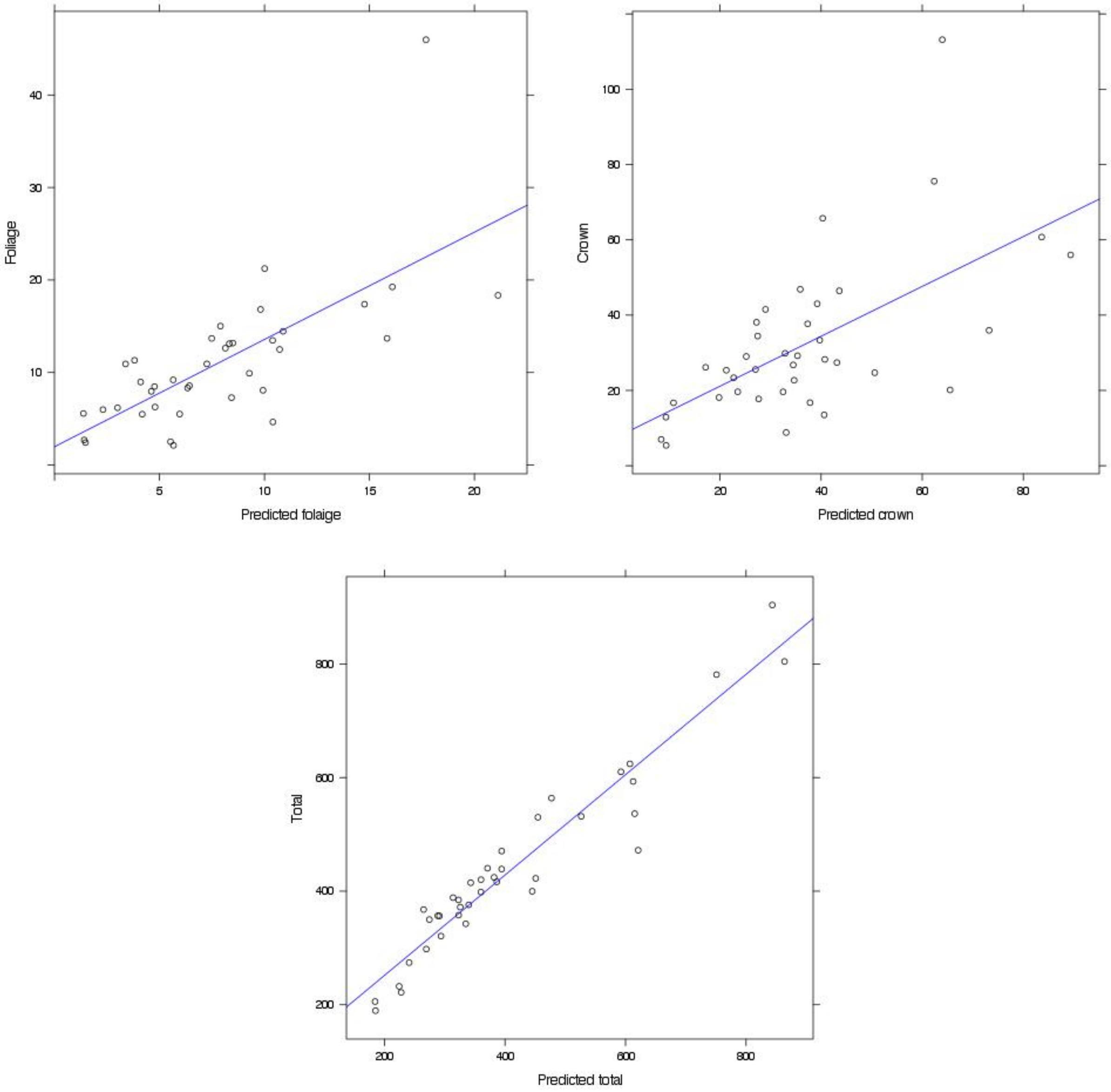


Figure 3.28: Actual vs predicted plots of various components from predicting UGA slash pine using Legacy slash pine model

Chapter 4

Use of compatible taper, volume equations to estimate individual tree total and component biomass

4.1 Introduction

Various studies on individual tree taper, volume, and weight equations have been conducted in recent decades. The term “taper” is used to express the decrease in stem diameter with increase in stem height. Tree total height (Ht), diameter at breast height (Dbh), and height at a specific point above ground level are independent variables used in establishing taper equations (Clutter et al. 1983). Using taper equations, stem inside-bark or outside-bark diameter can be predicted at any given tree height, or conversely tree height can be predicted at any given diameter (Li et al. 2012). These equations are also used as a basis for deriving volume equations, merchantable volume equations, and weight equations. Individual tree volume and weight equations are important for obtaining estimates of standing tree volume and biomass. Volume equations derived by integration of taper equations are useful in estimating total, as well as merchantable, stem volume. Theoretically correct taper/volume functions fitted to appropriate data are often preferred over existing volume tables/equations for prediction of individual tree volume as they provide accurate estimates of diameter outside-bark (dob) or diameter inside-bark (dib) at any specified height (Li and Weiskittel 2010). It is important to note that, stem taper is an important factor that determines quality of timber as it has direct impact on efficiency of timber processing, hence the market value of timber (Knauft 2004).

Taper equations differ by species as tree form varies by species. Also, a single equation may not be sufficient to cover all stand conditions in which a single species may be grown (Clutter et al. 1983) and no single taper model is applicable for all purposes (McClure and Czaplewski 1986). Furthermore, Newnham (1998) explained that no single theory or model form is available that can be applied to various stem forms of all species. Hence, researchers have developed different forms of taper equations that are used for various purposes.

Depending upon the form, the taper equation can be used to estimate upper-stem diameters and volume of the stem between stump and the top of the tree. They can also be used in estimating volume of a section of a log or main stem. Many studies have focused on developing relationships between taper functions, volume equations, and weight equations (Behre 1923, Demaerschalk 1972, Bailey 1994, Zhang et al. 2002). Volume equations can be developed by integrating taper functions when the equation is rotated around the longitudinal direction of a tree (Bruce et al. 1968). In this way, the volume and taper equations are compatible, meaning the estimated volume using the volume function is the same as the volume obtained by integrating the taper equation along the bole. Kozak (2004) points out that taper functions are useful in estimating:

- outside or inside-bark diameter at any given point of the stem
- tree height at a given diameter
- total outside or inside-bark volume of a tree
- outside or inside merchantable volume to any merchantable height or minimum upper-stem diameter from any stump height
- volumes of any length log

Fonweban et al. (2011) stated that taper equations can be categorized based on the variety of functional form of models as: simple (e.g Kozak et al. 1969), polynomial (e.g. Bruce et al.

1968), segmented polynomial (e.g. Max and Burkhart 1976), geometric-orientated (e.g. Parresol and Thomas 1996), and variable-exponent taper functions (e.g. Kozak 1988). Although many equations have been used to model taper in the forestry literature, a very common approach is to divide a tree into different segments and apply a mathematical function on each segment where the regression function represents the change in stem diameter with increase in tree height (Li and Weiskittel 2010). Max and Burkhart (1976) used this approach by splining polynomials used in different sections of tree stems. They divided a tree into three sections using two join points in which the lower section represents a neiloid shape and the upper and middle sections represent conic and parabolic shape, respectively. Another commonly used approach in taper modeling is the use of a variable-exponent function (e.g. Kozak 1988; 2004). The variable-exponent model uses different exponents to represent different stem shapes moving from ground to top of tree. (Li and Weiskittel 2010).

These variations in model forms are due to variation in stem form, which is influenced by factors such as genetics, climate, site quality, species types, and stand characteristics (Muhairwe et al. 1994). Heger (1965) stated that if two trees with comparable Ht and Dbh are considered, trees with less taper can have up to 20% more volume than trees with more taper.

In this study, our main goal is to make use of the taper function along with a small sample of data where we have information on wood density and specific gravity, to estimate component biomass. That is we make use of a compatible taper-volume set of equations, but we are not carrying out a study of tree taper in and of itself. For this purpose we used a revised version of the Fang et al. (2000) compatible taper-volume models to fit the data for red maple (*Acer rubrun*) and slash pine (*Pinus elliottii*). Outside-bark and inside-bark taper-volume models were developed for both species using two sets of data, one from a relatively small set of trees recently obtained in a whole tree biomass study carried out at the University of Georgia (UGA) and the other from a large regionwide taper database consisting of individual tree taper data from across the southern U.S. which was obtained over the past 30 years (Legacy data). A compatible function for total volume is derived by direct integration of the taper model. We fitted the taper model and estimated the parameters using nonlinear ordinary least square (NOLS) method. The estimated parameters from the taper model were then used to predict total volume of a tree. This predicted volume was used to obtain individual tree and component dry biomass. This is an indirect method of predicting tree biomass. Since it is expensive and time consuming to obtain weight information from the field, an indirect method such as this can make use of available taper-volume functions and newly acquired wood density, specific gravity and crown component biomass information to estimate total and component tree biomass. Finally, we compared the prediction of individual tree and component biomass from additive biomass system of equations, developed for red maple and slash pine in Chapter 3, and from the indirect taper-volume approach put forth in this chapter.

4.2 Materials and methods

4.2.1 Data

Taper measurement data from the UGA study and Legacy data were used separately, to model taper-volume functions for this study. Two species, red maple and slash pine, were selected for modeling from each set of data. The architecture of these two species is quite different. Slash pine, a softwood tree species, has more regular tree structure than red maple, a hardwood tree species. Of course, the two species not only differ in stem taper characteristics, but their crown structures are quite different. Slash pine being an excurrent crown form and red maple a deliquesent crown form.

Trees from the UGA data were destructively sampled and intensively measured. Pertinent measurements for biomass calculation and modeling include-diameter at breast height (Dbh) (0.1 inch), total tree height (0.1 foot), height to live crown (0.1 foot), diameter outside-bark at ground line, stump height, 2.75 feet, 4.5 feet, 8 feet and then every 4 feet up the stem (0.1 inch). All stems were then sectioned at 4.5 feet, 8 feet and every 8 feet up the bole to a minimum dob of 4 inches. Each section was weighed. A disk was removed from the base of each bolt. All disks were weighed green with and without bark, had diameter measured with and without bark and then debarked disks were soaked until saturation. Saturated disk volume was determined using water displacement and then disks were dried at 105° C until weight change stopped. Additionally, a sample of bark from each disk was selected, weighed green, saturated and had its volume determined using water displacement and finally dried to constant weight at 105° C.

Total tree volume was calculated using a combination of neiloid, paraboloid and cone shapes. Measured diameters at the lower and upper end of each bolt (main stem section) were used to calculate each bolt volume. Newton's formula was used to calculate the volume of a stem from base to 4.5 feet using three diameter measurements and assuming the stem shape is represented by a neiloid frustrum. The tip of the tree stem from the minimum four inch dob top was assumed to be represented by a cone. Smalian's formula was used to calculate volume of four foot stem sections between 4.5 feet and the four inch dob top diameter. Total tree volume was then obtained by summing the volumes of the component bolts.

Thirty eight slash pine trees ranging in Dbh from about 6 to 10 inches and ranging in Ht from about 44 to 82 ft (Table 4.1), and 14 red maple trees ranging in Dbh from about 5 to 15 inches and ranging in Ht from about 39 to 74 ft were available for taper-volume modeling work from the UGA data.

Table 4.1: Sample tree characteristics for UGA data available for taper-volume model by species

		Dbh (inch)			Tree height (ft)		
Species	No. of trees	min	mean	max	min	mean	max
Slash pine	38	5.60	7.80	10.10	44.30	60.16	81.60
Red maple	14	4.80	9.07	14.70	38.70	57.61	73.60

The second data set, Legacy data, consisted of taper measurement data from previous taper/volume studies (Clark et al. 1991). For slash pine, 868 trees ranging in Dbh from about 5 to 21 inches and ranging in Ht from about 21 to 103 ft and for red maple 905 trees ranging in Dbh from about 5 to 32 inches and ranging in Ht from about 29 to 114 ft were used for taper-volume modeling work (Table 4.2). Diameters were measured to the nearest 0.1 inch. Several other measurements, such as dob (0.1 inch) and dib (0.1 inch) at various heights from the ground (taper measurement), total tree height (ft), total tree outside and inside-bark volume, and cumulative outside and inside-bark volume, were available in this data set.

Table 4.2: Sample tree characteristics for legacy data* available for the taper-volume model by species

		Dbh (inch)			Tree height (ft)		
Species	No. of trees	min	mean	max	min	mean	max
Slash pine	868	4.6	9.12	20.8	21	61.36	103
Red maple	905	4.6	11.63	32	29	61.14	114

**Legacy data are compiled within Forest Inventory and Analysis (FIA) biomass project by Phil Radtkey and David Walker of Virginia Tech.*

Number of trees by one inch Dbh class for each species by data type are given in Tables 4.3, 4.4, 4.5, and 4.6 and corresponding distributions are shown in Figures 4.1, 4.2, 4.3, and 4.4.

Table 4.3: Number of trees by 1 inch Dbh class with average Dbh and Ht for slash pine - UGA data

Dbh class	Number of trees	Average Dbh	Average Ht
6	4	5.78	55.63
7	10	7.19	57.24
8	17	7.98	59.66
9	4	9.05	64.98
10	3	9.83	72.27

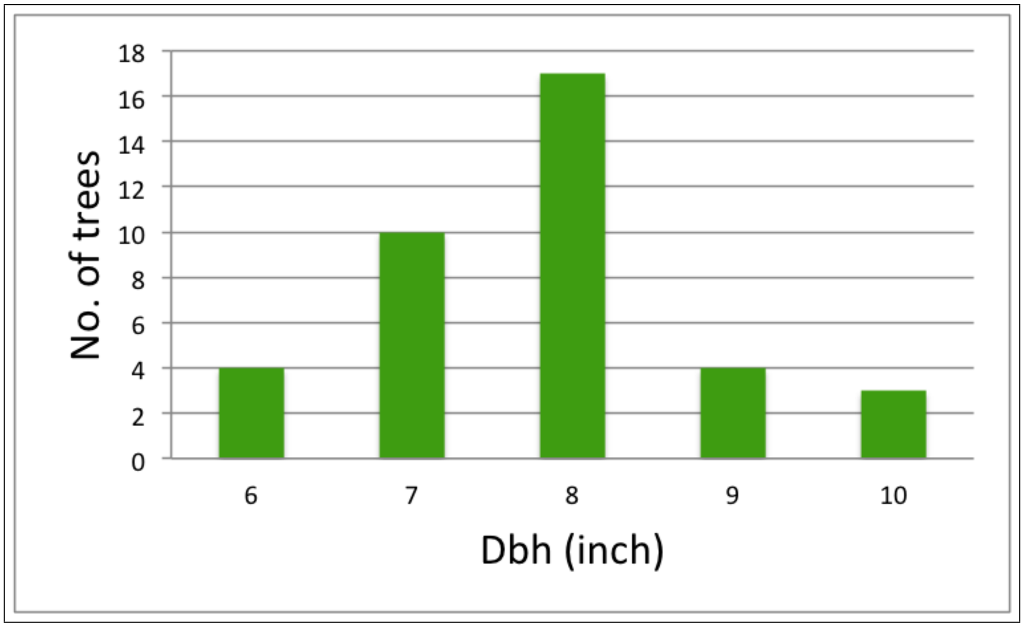


Figure 4.1: Data distribution by 1 inch Dbh class for slash pine - UGA data

Table 4.4: Number of trees by 1 inch Dbh class with average Dbh and Ht for red maple - UGA data

Dbh class	Number of trees	Average Dbh	Average Ht
5	1	4.80	38.70
7	3	7.07	54.97
8	2	8.05	53.70
9	2	9.10	58.80
10	2	9.65	59.90
11	3	10.90	64.93
15	1	14.70	63.40

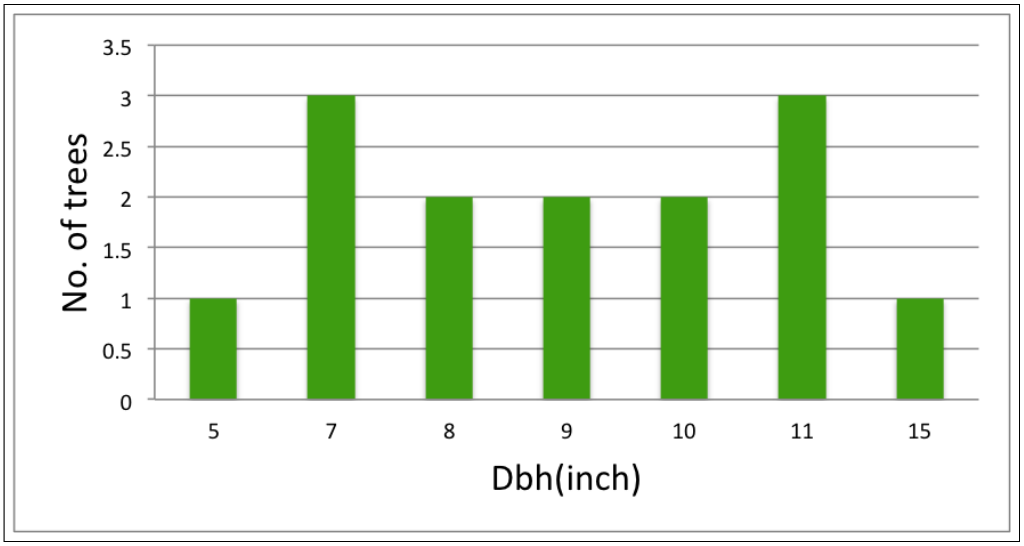


Figure 4.2: Data distribution by 1 inch Dbh class for red maple - UGA data

Table 4.5: Number of trees by 1 inch Dbh class with average Dbh and Ht for slash pine - Legacy data

Dbh class	Number of trees	Average Dbh	Average Ht
5	102	5.16	43.33
6	151	6.04	47.36
7	155	7.08	53.92
8	95	8.11	58.74
9	96	9.03	62.84
10	80	10.01	65.63
11	58	11.03	68.64
12	59	12.01	71.39
13	22	13.03	76.18
14	27	14.07	77.63
15	8	15.01	75.50
16	5	15.86	78.60
17	4	17.20	80.00
18	4	18.05	79.75
20	1	19.70	93.00
21	1	20.80	86.00

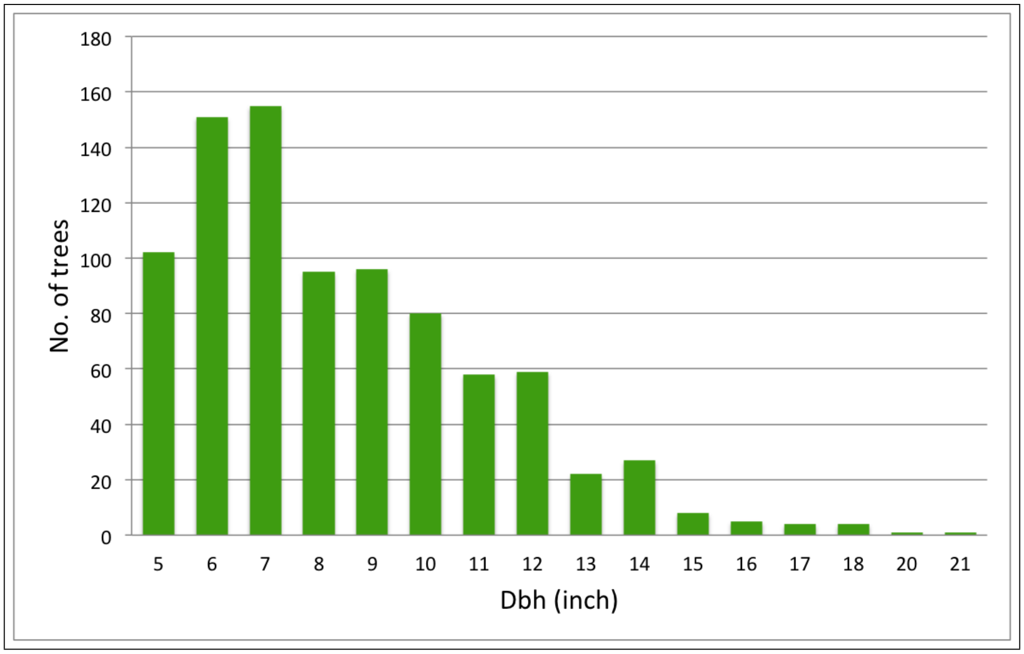


Figure 4.3: Data distribution by 1 inch Dbh class for slash pine - Legacy data

Table 4.6: Number of trees by 1 inch Dbh class with average Dbh and Ht for red maple - Legacy data

Dbh class	Number of trees	Average Dbh	Average Ht
5	83	5.18	44.13
6	99	6.06	46.66
7	88	7.07	49.53
8	86	8.05	52.74
9	72	9.02	55.82
10	80	10.08	56.69
11	70	11.02	63.07
12	52	12.07	63.21
13	48	13.05	66.25
14	47	14.05	67.00
15	42	15.04	67.43
16	36	16.13	71.11
17	23	17.04	72.52
18	18	18.09	72.78
19	14	18.98	71.43
20	14	19.96	77.00
21	6	20.90	72.17
22	7	22.10	82.14
23	4	22.98	80.25
24	3	24.17	78.33
25	2	24.90	79.00
26	3	26.17	82.67
27	2	27.20	85.00

Table 4.6 – continued from previous page

Dbh class	Number of trees	Average Dbh	Average Ht
28	3	28.37	78.33
29	2	28.80	91.00
32	1	32.00	85.00

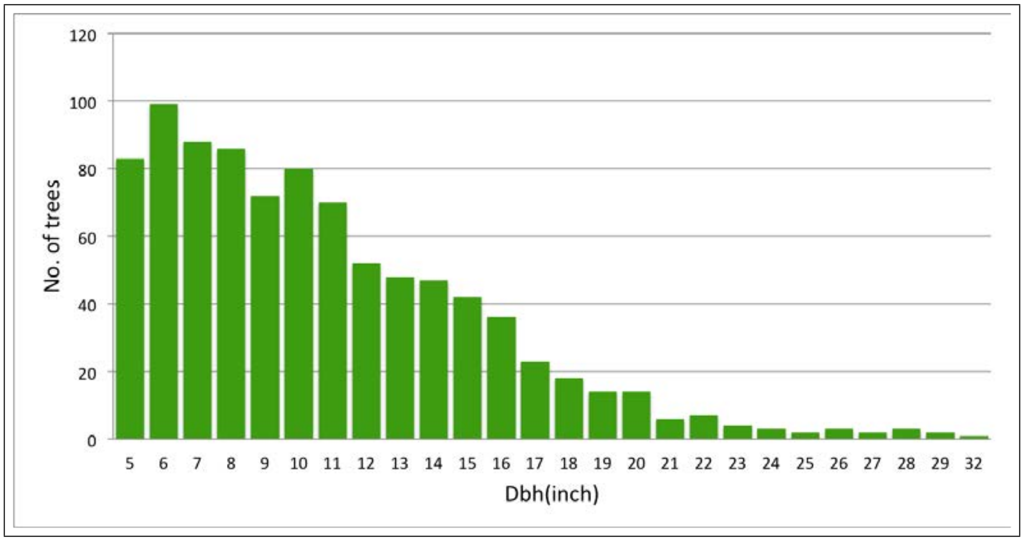


Figure 4.4: Data distribution by 1 inch Dbh class for red maple - Legacy data

4.2.2 Statistical analysis

A revised version of Fang et al. (2000) segmented taper-volume function was selected as a base model, which has the form

$$
\begin{aligned}
d &= c_1[Ht^{\frac{k-\beta_1}{\beta_1}}(1-p)^{\frac{k-\beta}{\beta}}\alpha_1^{I_1+I_2}\alpha_2^{I_2}]^{1/2} \\
\beta &= \beta_1^{1-(I_1+I_2)}\beta_2^{I_1}\beta_3^{I_2}, \quad \alpha_1 = (1-p_1)^{\frac{(\beta_2-\beta_1)k}{\beta_1\beta_2}}, \quad \alpha_2 = (1-p_2)^{\frac{(\beta_3-\beta_2)k}{\beta_2\beta_3}} \\
c_1 &= \frac{D}{(Ht-4.5)^{\frac{k-\beta_1}{2\beta 1}}}, \quad k = \frac{\pi}{576}, \quad p = \frac{h}{Ht}, \quad p_1 = \frac{4.5}{Ht} \\
I_1 &= \begin{cases} 1, & p_1 \le p \le p_2 \\ 0, & \text{otherwise} \end{cases} \\
I_2 &= \begin{cases} 1, & p_2 \le p \le 1 \\ 0, & \text{otherwise} \end{cases} \\
V &= c_1^2 Ht^{\frac{k}{\beta_1}}[\beta_1 t_0 + (I_1+I_2)(\beta_2-\beta_1)t_1 + I_2(\beta_3-\beta_2)\alpha_1 t_2 - \beta(1-p)^{\frac{k}{\beta}}\alpha_1^{I_1+I_2}\alpha^{I_2}] \\
t_0 &= (1-p_0)^{\frac{k}{\beta_1}}, \quad t_1 = (1-p_1)^{\frac{k}{\beta_1}}, \quad t_2 = (1-p_2)^{\frac{k}{\beta_2}} \\
p_0 &= \frac{stumpht}{Ht}
\end{aligned}
\tag{4.1}
$$

where

d = diameter outside-bark (inch) at some specified height Ht

h = height (ft) from base of the tree to upper-stem diameter d

Ht = total tree height (ft)

D = diameter at breast height (inch)

k = constant (for English units - Dbh in inch and Ht in ft) to convert Dbh into basal area

p = proportion of height h to total height (h/Ht)

p_1 = first join point (inflection point) (relative height of Dbh measurement)

p_2 = second join point

β_1, β_2 and β_3 = stem form factors for three corresponding stem-segments, 1, 2 and 3, respectively.

In general, form factor represents the ratio of the volume of a tree to the volume of a specified geometric solid with similar length and basal diameter. Commonly, the form factor is based on a cylinder with the same length and diameter as the tree. All other variables, such as β, α_1, α_2, c_1, t_0, and t_1, are functions of these variables and parameters.

The taper function presented above is a generalized form of three separate taper functions representing three separate stem segments in a tree. These three separate functions along with their range in a stem section can be presented as:

$$\begin{aligned} d &= c_1[Ht(1-p)]^{\frac{k-\beta_1}{2\beta_1}} \quad \text{for} \quad 0 \leq p \leq p_1 \\ d &= c_2[Ht(1-p)]^{\frac{k-\beta_2}{2\beta_2}} \quad \text{for} \quad p_1 \leq p \leq p_2 \\ d &= c_3[Ht(1-p)]^{\frac{k-\beta_3}{2\beta_3}} \quad \text{for} \quad p_2 \leq p \leq 1 \end{aligned} \tag{4.2}$$

where, c_1, c_2, and c_3 are constants associated with each segment. The functions for the first and the second segment are continuous at the first join point, p_1, and the functions for second and the third stem segments are continuous at the second join point, p_2.

V in Equation 4.1 is a cubic volume equation which is obtained by integrating the taper function. Cubic foot volume of a desired section above ground level can be estimated using the volume equation. Fang et al. (2000) used three segments each with its own form factor to model the stem profile. In their work, the join points of the stem segments were set to be unknown; hence, were estimated as parameters and the model insured that total stem volume was obtained by integrating the taper function. Furthermore, the volume implied by integration of the taper function was consistent with a total stem volume prediction equation that was fitted simultaneously. In this study, the Fang et al. (2000) model was formulated as a three segment model with the first join point at p_1 (4.5/H), and the taper function was constrained to pass through Dbh at 4.5 feet above ground level. The second join point is at

p_2, which is generalized as a function of Dbh and/or total height. This formulation of the Fang et al. (2000) taper-volume function 4.1 is very flexible as it allows the upper join point, p_2, and form factors β_1, β_2 and β_3 to vary with tree Dbh and Ht

$$\begin{aligned} p_2 &= 1/(1+\exp(-(\text{pp1}+\text{pp2}\ \log(\text{Ht})+\text{pp3*Dbh}))) \\ \beta_1 &= \text{bb1}+\text{bb2*Dbh}+\text{bb3*Ht} \\ \beta_2 &= \text{mm1}+\text{mm2*Ht}+\text{mm3*Dbh} \end{aligned} \tag{4.3}$$

where, pp1, pp2, pp3, bb1, bb2, mm1, mm2, mm3 are parameters and estimated from the data. Of course for any given species/set of data, p_2, β_1 and β_2 may be functions of Ht only or Dbh only or both.

It is interesting to investigate the properties of the three form factors, β_1, β_2 and β_3, associated with, lower, middle and upper section of stem, respectively. When these form factor parameters are normalized by dividing by a constant "k", where "k" is 0.005454154 (conversion factor to ft^2 from inch^2), the form factors are smallest at the bottom, largest in the middle, and moderate at the top. These normalized form factors are, in fact, comparable to the form factors for a neiloid (0.250), parabolid (0.500) and cone (0.333), respectively.

This taper function has some nice properties: it is a continuous function at join points, d is predicted to be 0 when h=H and d is predicted to be Dbh at 4.5 feet above ground level. The two join points occur at some upper stem height h and at 4.5 ft from the ground.

The number of inflection points required to model stem taper varies by species, site conditions, and other tree growth factors (Fang et al. 2000). For most of the species, it is sufficient to include two inflection points to represent tree taper, one near Dbh of a tree and the other at an upper point on the bole. However, in our UGA data, we found that when modeling inside bark taper and volume for both species that one inflection point (two segment model) was sufficient. The two segment model is, in fact, a reduced form of the Equation 4.1 and is presented as

$$
\begin{aligned}
d &= c_1[Ht^{\frac{k-\beta_1}{\beta_1}}(1-p)^{\frac{k-\beta}{\beta}}\alpha_1^{I_1}]^{1/2} \\
\beta &= \beta_1^{1-I_1}\beta_2^{I_1}, \quad \alpha_1 = (1-p_1)^{\frac{(\beta_2-\beta_1)k}{\beta_1\beta_2}}, \\
c_1 &= \frac{Dbhib}{(Ht-4.5)^{\frac{k-\beta_1}{2\beta 1}}}, \quad k = \frac{\pi}{576}, \quad p = \frac{h}{Ht}, \quad p_1 = \frac{4.5}{Ht} \\
I_1 &= \begin{cases} 1, & p_1 \le p \le 1 \\ 0, & \text{otherwise} \end{cases} \\
V &= c_1^2 Ht^{\frac{k}{\beta_1}}[\beta_1 t_0 + I_1(\beta_2-\beta_1)t_1 - \beta(1-p)^{\frac{k}{\beta}}\alpha_1^{I_1}] \\
t_0 &= (1-p_0)^{\frac{k}{\beta_1}}, \quad t_1 = (1-p_1)^{\frac{k}{\beta_1}} \\
p_0 &= \frac{stumpht}{Ht}
\end{aligned}
\tag{4.4}
$$

The two-segment model consists of two form factor parameters; β_1 and β_2, as described above. The inside-bark model is different than outside bark model in that it requires volume inside bark (vib), diameter inside bark (dib), and Dbh inside bark (Dbhib) variables to fit the model. Dbhib is not typically available from tree measurement data, hence we developed an appropriate Dbh based function to predict Dbhib for both species for both data sets. Parameters for this Dbhib equations were estimated using ordinary least squares (OLS) and the model fitting was implemented in SAS using REG procedure.

Our study involves development of compatible taper and volume models where parameters were estimated for the taper function, which was then integrated to estimate stem volume. We fitted the taper equation using nonlinear ordinary least square (NOLS) approach. The function was fitted to both red maple and slash pine, separately. Therefore, there are two taper models (outside and inside-bark) for red maple and two for slash pine for each of our data sets.. All model fitting was implemented in Statistical Analysis System (SAS) (SAS 2013). The simple linear fitting procedure was implemented in SAS using REG procedure and nonlinear fitting procedure was done using the MODEL procedure. R (R 2013) statistical analysis software was also used for data management and graphical analysis. We also tried to fit taper-volume equation in a system using nonlinear seemingly unrelated regression (NSUR) but in some cases we could not get convergence for NSUR.

4.2.2.1 BIOMASS CALCULATION

Using diameter outside-bark and diameter inside-bark taper equations, tree volume outside-bark and volume inside-bark, respectively, were estimated. The estimated volume was used to compute dry biomass. Hence, the procedure to calculate dry biomass begins with volume prediction from compatible taper-volume functions. In the process of biomass calculation we require green density and specific gravity information, which were calculated as

A) *GD (Green weight wood density)*

$$\begin{aligned} \mathrm{GD_i} &= \frac{\mathrm{GWIB_i}}{\mathrm{TVIB_i}} \\ \overline{\mathrm{GD}} &= \sum_{\mathrm{i}}^{\mathrm{n}} \frac{\mathrm{GD_i}}{\mathrm{n}} \end{aligned} \tag{4.5}$$

B) *SG (Wood specific gravity green volume dry weight)*

Disk data were used to calculate specific gravity for each tree.

$$\begin{aligned} \mathrm{SG_j} &= \frac{\mathrm{DwtDsk_j}}{\mathrm{GvolDsk_j}} \\ \mathrm{SG_i} &= \frac{\sum_{\mathrm{j=1}}^{\mathrm{k}} (\mathrm{SG_j})(\mathrm{A_j})}{\sum_{\mathrm{j=1}}^{\mathrm{k}} \mathrm{A_j}} \\ \mathrm{A} &= 0.005454154^{*}\mathrm{Dib}^2 \\ \overline{\mathrm{SG}} &= \sum_{\mathrm{i=1}}^{\mathrm{n}} \frac{\mathrm{SG_i}}{\mathrm{n}} \end{aligned} \tag{4.6}$$

where,

$\mathrm{GD_i}$ = green weight wood density for tree i (lbs/ft^3), where i from 1 to n trees

GWIB_i = green weight of stem inside bark for tree i (lbs)

TVIB_i = total volume of stem inside bark for tree i (ft^3)

$\overline{\text{GD}}$ = average green weight wood density by species (lbs/ft^3)

SG_j = specific gravity (gm/cc) of disk j, where j from 1 to k (number of disks)

SG_i = specific gravity (gm/cc) of for tree i

$\overline{\text{SG}}$ = average specific gravity by species (gm/cc)

DwtDsk_j = dry weight of disk j (gm)

GvolDsk_j = green volume of disk j (cc)

Dib = disk diameter inside bark (inch)

A = area of disk (ft^2)

n = number of trees

Table 4.7 reports calculated variables, required for biomass calculation, for both red maple and slash pine. When we predict dry biomass of new trees, we consider these variables as already given.

Table 4.7: Variables required to calculate dry biomass

Species	$\overline{\text{GD}}$(lbs \ ft^3)	$\overline{\text{SG}}$ (gm \ cc)
Red maple	53.49	0.48
Slash pine	63.99	0.56

To calculate stem wood, stem bark, and crown component biomass from green volume estimates above, we make use of the information and relationships shown in Equations 4.7

through 4.14 below. Calculation in the following a 8-step process can easily be carried out by using hand held calculator or in other software such as in SAS using data step procedure. Variables $\overline{\mathrm{GD}}$ and $\overline{\mathrm{SG}}$ are considered as given variables while calculating dry biomass. $\hat{\mathrm{Vol}}_{\mathrm{ob}}$ and $\hat{\mathrm{Vol}}_{\mathrm{ib}}$ are predicted volumes for given Dbh and Ht of a tree using the taper-volume model.

1) $\mathrm{GW}_{\mathrm{W_i}}$ *(Green weight of wood biomass for tree i)*

$$\mathrm{G\hat{W}}_{\mathrm{W_i}} = \hat{\mathrm{Vol}}_{\mathrm{ib}} \times \overline{\mathrm{GD}} \tag{4.7}$$

2) $\mathrm{DW}_{\mathrm{W_i}}$ *(Dry weight of wood biomass for tree i)*

$$\mathrm{D\hat{W}}_{\mathrm{W_i}} = \mathrm{G\hat{W}}_{\mathrm{W_i}} \times \overline{\mathrm{SG}} \tag{4.8}$$

3) $\mathrm{DW}_{\mathrm{B_i}}$ *(Dry weight of bark biomass for tree i)*

$$\begin{aligned} \mathrm{D\hat{W}}_{\mathrm{B_i}} &= \mathrm{D\hat{W}}_{\mathrm{W_i}} \times \hat{\mathrm{R}}_{\mathrm{BS_i}} \\ \text{where,} \quad \hat{\mathrm{R}}_{\mathrm{BS_i}} &= \frac{\hat{\mathrm{Y}}_{\mathrm{Stembark_i}}}{\hat{\mathrm{Y}}_{\mathrm{Stemwood_i}}} \end{aligned} \tag{4.9}$$

4) $\mathrm{DW}_{\mathrm{WB_i}}$ *(Dry weight of stem (wood and bark) biomass for tree i)*

$$\mathrm{D\hat{W}}_{\mathrm{WB_i}} = \mathrm{D\hat{W}}_{\mathrm{W_i}} + \mathrm{D\hat{W}}_{\mathrm{B_i}} \tag{4.10}$$

5) $\mathrm{DW}_{\mathrm{Br_i}}$ *(Dry weight of branch biomass for tree i)*

$$\begin{aligned} \mathrm{D\hat{W}}_{\mathrm{Br_i}} &= \mathrm{D\hat{W}}_{\mathrm{W_i}} \times \hat{\mathrm{R}}_{\mathrm{BrS_i}} \\ \text{where,} \quad \hat{\mathrm{R}}_{\mathrm{BrS_i}} &= \frac{\hat{\mathrm{Y}}_{\mathrm{Branch_i}}}{\hat{\mathrm{Y}}_{\mathrm{Stemwood_i}}} \end{aligned} \tag{4.11}$$

6) $\mathrm{DW}_{\mathrm{F_i}}$ *(Dry weight of foliage biomass for tree i)*

$$\begin{aligned} \mathrm{D\hat{W}}_{\mathrm{F_i}} &= \mathrm{D\hat{W}}_{\mathrm{W_i}} \times \hat{\mathrm{R}}_{\mathrm{FS_i}} \\ \text{where,} \quad \hat{\mathrm{R}}_{\mathrm{FS_i}} &= \frac{\hat{\mathrm{Y}}_{\mathrm{Foliage_i}}}{\hat{\mathrm{Y}}_{\mathrm{Stemwood_i}}} \end{aligned} \tag{4.12}$$

7) $\mathrm{DW}_{\mathrm{Crn_i}}$ *(Dry weight of crown biomass for tree i)*

$$\hat{\mathrm{DW}}_{\mathrm{Crn_i}} = \hat{\mathrm{DW}}_{\mathrm{Br_i}} + \hat{\mathrm{DW}}_{\mathrm{F_i}} \tag{4.13}$$

8) $\mathrm{DW}_{\mathrm{T_i}}$ *(Dry weight of total biomass for tree i)*

$$\hat{\mathrm{DW}}_{\mathrm{T_i}} = \hat{\mathrm{DW}}_{\mathrm{WB_i}} + \hat{\mathrm{DW}}_{\mathrm{Crn_i}} \tag{4.14}$$

where,

$\hat{\mathrm{R}}_{\mathrm{BS_i}}$ = estimated bark to stem wood (without bark) ratio

$\hat{\mathrm{R}}_{\mathrm{B_rS_i}}$ = estimated branch to stem wood ratio

$\hat{\mathrm{R}}_{\mathrm{FS_i}}$ = estimated foliage to stem wood ratio

$\hat{\mathrm{Y}}_{\mathrm{Stembark_i}}$ = estimated bark weight for tree i, from using Dbh and Ht based system of equations fitted to UGA data (Equation in chapter3)

$\hat{\mathrm{Y}}_{\mathrm{Stemwood_i}}$ = estimated stem inside bark weight for tree i, from using Dbh and Ht based system of equations fitted to UGA data (Equation in chapter3)

$\hat{\mathrm{Y}}_{\mathrm{Branch_i}}$ = estimated branch weight for tree i, from using Dbh and Ht based system of equations fitted to UGA data (Equation in chapter3)

$\hat{\mathrm{Y}}_{\mathrm{Foliage_i}}$ = estimated foliage weight for tree i, from using Dbh and Ht based system of equations fitted to UGA data (Equation in chapter3)

Legacy and UGA taper-volume models were used to predict UGA data that were used to fit the explicit biomass prediction system of equations from chapter 3. Prediction of dry biomass using the taper-volume function was compared against prediction of dry biomass from using Dbh and Ht based system of equations in chapter 3 for both species. The accuracy and precision of diameter prediction as well as volume prediction of each model were compared using both graphical techniques and numeric analysis of residuals. The statistics obtained from residuals used to compare the precision and accuracy include (1) Average residual (AR) (2) Average percent residual (APR) (3) Average absolute residual (AAR) (4) Average absolute percent residual (AAPR) (5) Root mean square error (RMSE) and (6) Percent variance explained (PVE). AR measures average bias in prediction. This indicates the expected error in prediction when several observations are to be combined by averaging. The AAR measures accuracy in model prediction. This signifies the average error from prediction of any one observation (Burk 1986). RMSE, square root of MSE, is the standard deviation of prediction error for unbiased models (Burk 1986). It is a measure of average deviation. PVE measures the goodness of fit of the model. It actually measures how well the fit accounts for the variation in the data. It is a measure similar to fit index or R^2.

$$\begin{aligned}
\mathrm{AR} &= \frac{\sum_{\mathrm{i}}^{\mathrm{n}}(\mathrm{y_i}-\hat{\mathrm{y}}_{\mathrm{i}})}{\mathrm{n}} \\
\mathrm{APR} &= \frac{\sum_{\mathrm{i}}^{\mathrm{n}}(\frac{\mathrm{y_i}-\hat{\mathrm{y}}_{\mathrm{i}}}{\mathrm{y_i}}\times 100)}{\mathrm{n}} \\
\mathrm{AAR} &= \frac{\sum_{\mathrm{i}}^{\mathrm{n}}|(\mathrm{y_i}-\hat{\mathrm{y}}_{\mathrm{i}})|}{\mathrm{n}} \\
\mathrm{AAPR} &= \frac{\sum_{\mathrm{i}}^{\mathrm{n}}(\frac{|(\mathrm{y_i}-\hat{\mathrm{y}}_{\mathrm{i}})|}{\mathrm{y_i}}\times 100)}{\mathrm{n}} \\
\mathrm{RMSE} &= \sqrt{\sum_{\mathrm{i}}^{\mathrm{n}}\frac{(\mathrm{y_i}-\hat{\mathrm{y}}_{\mathrm{i}})^2}{\mathrm{n}}} \\
\mathrm{PVE} &= (1-\frac{\sum_{\mathrm{i}}^{\mathrm{n}}(\mathrm{y_i}-\hat{\mathrm{y}}_{\mathrm{i}})^2}{\sum_{\mathrm{i}}^{\mathrm{n}}(\mathrm{y_i}-\bar{\mathrm{y}})^2})\times 100 \qquad (4.15)
\end{aligned}$$

where, y_i refers to the observed i^{th} response value (observed dry weight of components), $\hat{y}_i$ is the corresponding predicted response value, and n is the number of observations.

4.3 Results and discussion

4.3.1 Taper-volume outside and inside-bark model for slash pine using legacy data

Three segment taper function was fitted to the Legacy data outside bark. For the outside-bark taper-volume model for slash pine, all parameters are significant at α =0.05 except pp1, which is marginally significant at $\alpha = 0.15$ (Table 4.8). Statistical significance of pp1, pp2 and pp3 indicate that the second join point (p_2) in the taper model varies by tree size (Dbh and Ht). Similarly, bb1 and bb2 are significant in the model, indicating the form factor associated with the first segment of stem, β_1, varies by Dbh. Similarly, the significant parameters mm1, mm2 and mm3 indicate the form factor associated with second stem-segment, β_2, varies by tree Ht and Dbh. The form factor associated with the last stem-segment, β_3, is also highly significant, which was estimated using the data.

The parameters such as p_2, bet1, and bet2 can be calculated using Equation 4.3. For example, for an average size slash tree with 8 inch Dbh and 60 ft tall

p_2 = 1/1(+exp(-(pp1+pp2*ln(Ht)+pp3*Dbh)))
= 1/1(+exp(-(-2.94806+1.738988*ln(60)-0.22149*8))) = 0.917.

bet1 = bb1 + bb2*Dbh =0.000863 - 0.00003 *8 = 0.000623.

bet2 = mm1+mm2*Ht + mm3*Dbh=0.002273 + 0.000007785 -0.00003*Dbh =0.0025001.

The value of p_2 shows that the second join point occurs near the total tree height. Specifically, the second outside-bark join point for this average size slash tree is around 92% of the total height that is around 55 ft from the ground level.

For this average size slash β_1 is 0..000623, β_2 is 0.0025001, and β_3 is 0.001978. The resulting normalized form factors are 0.114, 0.458 and 0.363, respectively for β_1, β_2, and β_3. These outside-bark form factors are smallest at the bottom, largest in the middle, and moderate at the top. These form factors are comparable to the form factors for a neiloid (0.250), paraboloid (0.500) and cone (0.333), respectively.

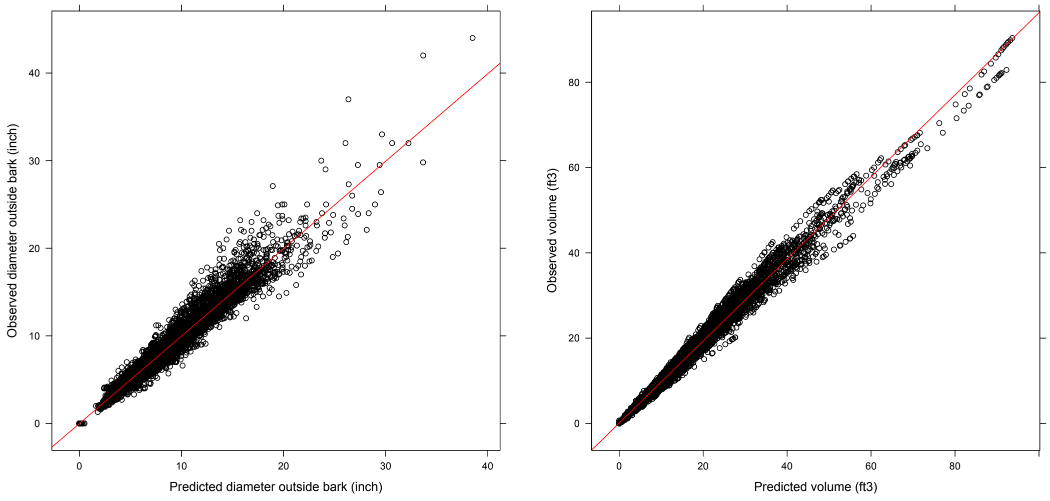
Table 4.8: Parameter estimates, approximate standard errors (Approx. SE) and test statistics for outside-bark taper-volume function for slash pine - Legacy data

Parameter	Estimate	Approx. SE	t-value	p-value
pp1	- 2.948060000	2.054900000	- 1.43	0.1500
pp2	1.738988000	0.524800000	3.31	0.0000
pp3	- 0.221490000	0.026000000	- 8.52	<.0001
bb1	0.000863000	0.000004884	176.62	<.0001
bb2	- 0.000030000	0.000000376	- 81.07	<.0001
mm1	0.002273000	0.000023000	98.80	<.0001
mm2	0.000007785	0.000000493	15.78	<.0001
mm3	- 0.000030000	0.000002002	- 14.94	<.0001
bet3	0.001978000	0.000051000	38.94	<.0001

The fit statistics show that the taper model fits the data very well (Table 4.9). The prediction (APRED) of dob and vob are very close to the actual values (AOBS). The model explains more than 98% of variation about the mean values of d and V. Also, plots of observed versus predicted dob and vob also indicate very good fit for the slash pine taper function (Figure 4.5). The residual plots show reasonable residual patterns (see Appendix A).

Table 4.9: Average observed, average predicted dob and vob, and fit statistics from Legacy slash taper - volume outside-bark model

Variables	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
dob	7.43	7.46	-0.0229	-0.67	0.259	3.505	0.405	98.90
vob	8.75	9.01	-0.263	-3.41	0.553	6.560	1.235	98.93



(a) dob

(b) vob

Figure 4.5: Actual vs predicted dob and vob for slash pine - Legacy model

Similar to the outside-bark taper-volume model, parameters (Table 4.10), fit statistics (Table 4.11) and residual plots (see Appendix A) for inside-bark model indicate good fits to the data. The taper-volume inside-bark model requires diameter at breast height inside-bark (Dbhib) to predict dib and vib of a stem. We developed the simple Dbh based Equation 4.16 to predict Dbhib for slash pine.

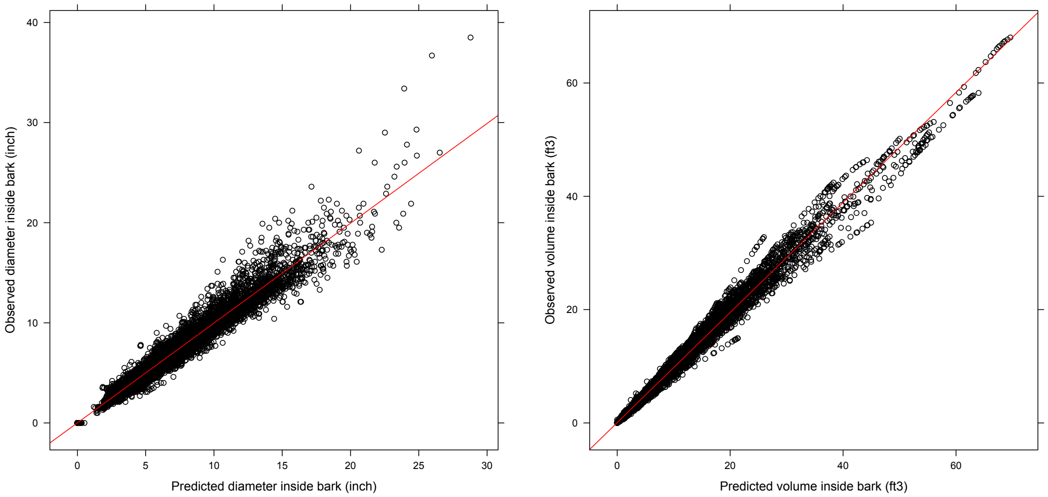
$$\text{Db}\hat{\text{h}}\text{ib} = -0.62 + 0.91 \times \text{Dbh} \tag{4.16}$$

Table 4.10: Parameter estimates, approximate standard errors (Approx. SE) and test statistics for inside-bark taper- volume function for slash pine - Legacy data

Parameter	Estimate	Approx. SE	t-value	p-value
pp1	- 2.5680300000	1.2438000000 -	2.06	0.0400
pp2	1.2552110000	0.3252000000	3.86	0.0000
pp3	- 0.1681900000	0.0194000000 -	8.66	<.0001
bb1	0.0009410000	0.0000078030	120.65	<.0001
bb2	- 0.0000089900	0.0000007189 -	12.50	<.0001
bb3	- 0.0000053800	0.0000001829 -	29.40	<.0001
mm1	0.0023220000	0.0000300000	76.75	<.0001
mm2	- 0.0000300000	0.0000029680 -	9.46	<.0001
mm3	0.0000078350	0.0000006807	11.51	<.0001
bet3	0.0021610000	0.0000200000	107.31	<.0001

Table 4.11: Average observed, average predicted dib and vib, and fit statistics from Legacy slash taper - volume inside-bark model

Variables	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
dib	6.35	6.36	-0.015	-0.64	0.242	3.922	0.372	98.81
vib	6.55	6.68	-0.137	-3.06	0.422	7.000	0.925	98.94



(a) dib

(b) vib

Figure 4.6: Actual vs predicted dib and vib for slash pine - Legacy model

The fitted curve in Appendix A for both outside and inside-bark models show good agreement between model predictions and observed data trend.

4.3.2 TAPER-VOLUME OUTSIDE AND INSIDE-BARK MODEL FOR RED MAPLE USING LEGACY DATA

Similar to slash pine, the 3-segment model was fitted to Legacy red maple data. For both outside and inside-bark model, p_2 was found to not vary with Dbh and Ht. The parameter estimates and fit statistics for outside (Tables 4.12, 4.13) and inside-bark (Tables 4.14, 4.15) model indicate good fits to the data.

Table 4.12: Parameter estimates, approximate standard errors (Approx. SE) and test statistics for outside-bark taper-volume function for red maple - Legacy data

Parameter	Estimate	Approx. SE	t-value	p-value
p2	0.59152500	0.01360000	43.41	<.0001
bb1	0.00074300	0.00000837	88.82	<.0001
bb2	- 0.00001000	0.00000056	- 17.93	<.0001
mm1	0.00194800	0.00002400	80.01	<.0001
mm2	- 0.00003000	0.00000109	- 31.70	<.0001
mm3	0.00000717	0.00000046	15.75	<.0001
bet3	0.00220000	0.00003200	68.14	<.0001

Table 4.13: Average observed, average predicted dob and vob, and fit statistics from Legacy red maple taper - volume outside-bark model

Variables	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
dob	8.86	8.82	0.004	-0.628	0.437	5.29	0.695	98.35
vob	13.67	17.68	-0.001	-2.521	1.200	7.913	3.553	97.18

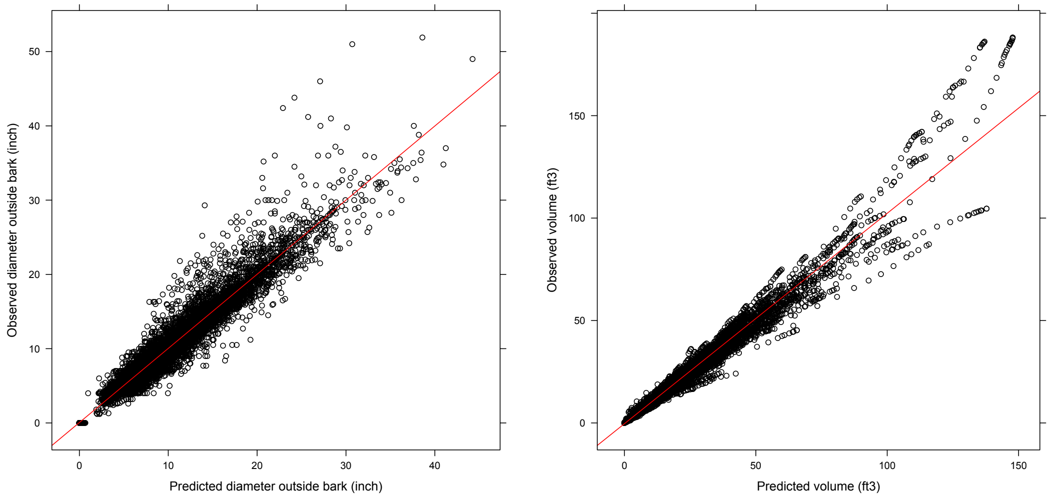
Table 4.14: Parameter estimates, approximate standard errors (Approx. SE) and test statistics for inside-bark taper-volume function for red maple - Legacy data

Parameter	Estimate	Approx. SE	t-value	p-value
p2	0.58606700	0.01390000	42.05	<.0001
bb1	0.00072900	0.00000826	88.21	<.0001
bb2	- 0.00000952	0.00000056	- 17.15	<.0001
mm1	0.00186100	0.00002400	76.98	<.0001
mm2	- 0.00003000	0.00000109	- 30.16	<.0001
mm3	0.00000749	0.00000045	16.49	<.0001
bet3	0.00215300	0.00003100	68.60	<.0001

Table 4.15: Average observed, average predicted dob and vob, and fit statistics from Legacy red maple taper - volume inside-bark model

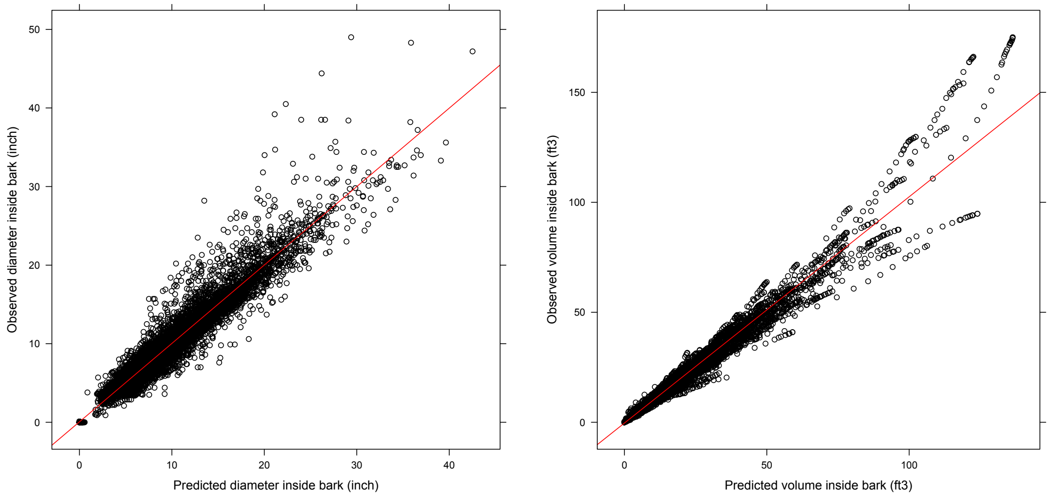
Variables	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
dib	8.26	8.22	0.004	-0.633	0.424	5.67	0.672	98.30
vib	12.03	12.03	-0.003	-2.63	1.08	8.09	3.224	97.11

The average versus observed plots for both outside (Figure 4.7) and inside-bark (Figure 4.8) show a slight deviation in predicted values from the actual values specially in larger volume. The residual plots in Appendix (B) show that the both outside and inside-bark model fits the data well. In addition, fit plots shown in Appendix (B) show that the predicted value follow the observed data trend well.



(a) dob (b) vob

Figure 4.7: Actual vs predicted dob and vob for red maple - Legacy model



(a) dib (b) vib

Figure 4.8: Actual vs predicted dib and vib for red maple - Legacy model

As for slash pine, we developed a Dbh based Equation 4.17 to predict Dbhib for red maple.

$$\hat{\text{Dbhib}} = -0.14 + 0.95 \times \text{Dbh} \tag{4.17}$$

4.3.3 TAPER-VOLUME OUTSIDE AND INSIDE-BARK MODEL FOR SLASH PINE AND RED MAPLE FROM UGA DATA

A 3-segment taper-volume model was fitted to outside bark and a 2-segment model was fitted to inside bark data for both species from our UGA study. Parameter estimates and various fit statistics for outside-bark (Tables 4.16, 4.17) and inside-bark (Tables 4.18, 4.19) models show that these models for slash pine reasonably work well.

Table 4.16: Parameter estimates, approximate standard errors (Approx. SE) and test statistics for outside-bark taper - volume equation for slash pine - UGA data

Parameter	Estimate	Approx. SE	t-value	p-value
pp1	8.290034	2.108400	3.93	<.0001
pp2	-2.302510	0.483500	-4.76	<.0001
pp3	-0.099270	0.054300	-1.83	0.0682
bb1	0.001007	0.000130	7.76	<.0001
bb2	-0.000040	0.000016	-2.36	0.0188
mm1	0.005900	0.000746	7.91	<.0001
mm2	-0.000040	0.000011	-3.90	0.0001
mm3	-0.000220	0.000094	-2.40	0.0167
bet3	0.002450	0.000013	186.24	<.0001

Table 4.17: Average observed, average predicted dob and vob, and fit statistics from UGA slash outside-bark taper - volume model

Variables	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
dob	5.26	5.25	0.0052	-0.264	0.150	3.645	0.300	99.32
vob	6.81	6.87	-0.0522	-1.71	0.279	4.322	0.395	99.17

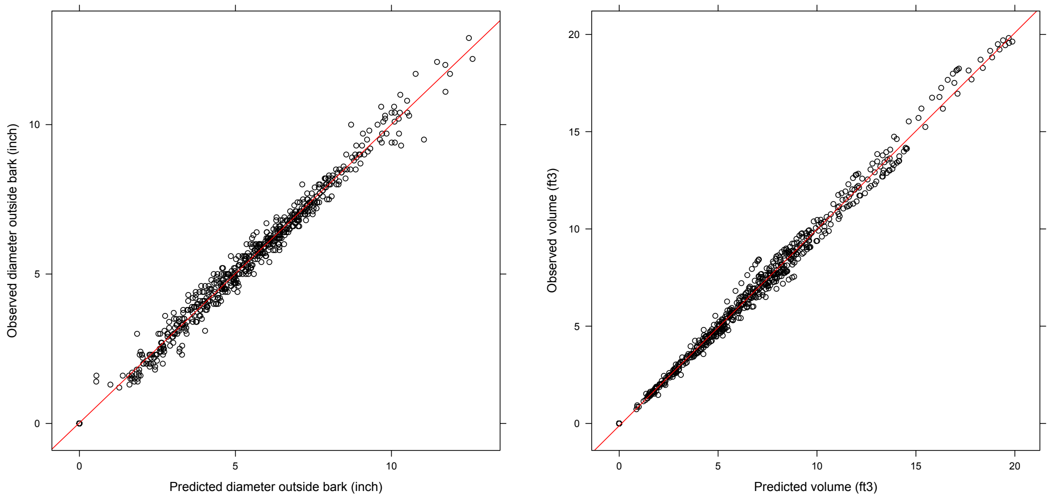
Table 4.18: Parameter estimates, approximate standard errors (Approx. SE) and test statistics for inside-bark taper - volume equation for slash pine - UGA data

Parameter	Estimate	Approx. SE	t-value	p-value
bet1	0.0007	0.000017	41.77	<.0001
bet2	0.0025	0.000009312	269.32	<0.0001

Table 4.19: Average observed, average predicted dib and vib, and fit statistics from UGA slash inside-bark taper - volume model

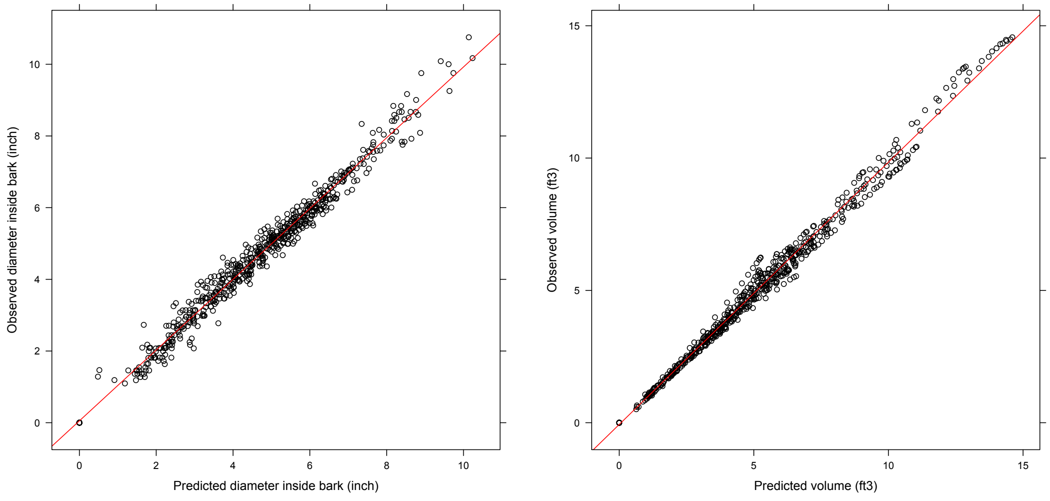
Variables	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
dib	4.53	4.54	-0.0054	-0.36	0.142	3.88	0.197	99.11
vib	4.95	5.06	-0.1122	-2.92	0.235	4.92	0.324	98.97

Plots of observed versus predicted dob and vob (Figure 4.9), dib and vib (Figure 4.10), various residual and fitted plots (see Appendix C) indicate very good fit for the slash pine taper function.



(a) dob (b) vob

Figure 4.9: Actual vs predicted diameter and vob for slash pine- UGA model



(a) dib (b) vib

Figure 4.10: Actual vs predicted diameter and volume inside-bark for slash pine- UGA model

As for the other inside bark taper-volume models we developed an equation to predict dbhib from dbh (Equation 4.18) for UGA slash data.

$$\hat{\text{Dbhib}} = 0.02 + 0.84 \times \text{Dbh} \tag{4.18}$$

Similar to slash pine, UGA red maple data were fitted with 3-segment outside and 2-segment inside bark taper-volume models. As for slash pine the model for red maple shows a good fit to the data. Parameter estimates, fit statistics for outside (Tables 4.20, 4.21) and inside bark (Tables 4.22, 4.23) model below also indicate that these models fit the UGA red maple data very well.

Table 4.20: Parameter estimates, approximate standard errors (Approx. SE) and test statistics for outside-bark taper - volume equation for red maple - UGA data

Parameter	Estimate	Approx. SE	t-value	p-value
pp1	33.011010	8.278700	3.99	<.0001
pp2	- 6.758210	1.810200	-3.73	0.0000
pp3	-0.430640	0.061600	-6.99	<.0001
bb1	0.000883	0.000141	6.27	<.0001
bb2	0.000050	0.000015	3.31	0.0000
bb3	-0.000010	0.000003	-4.31	<.0001
mm1	0.002459	0.000153	16.07	<.0001
mm3	-0.000050	0.000017	-3.21	0.0000
bet3	0.003130	0.000068	46.07	<.0001

Table 4.21: Average observed, average predicted dob and vob, and fit statistics from UGA red maple outside-bark taper - volume model

Variables	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
dob	6.53	6.53	-0.0033	-0.454	0.202	3.531	0.306	99.22
vob	9.23	9.56	-0.3233	-4.136	0.448	5.474	0.602	99.44

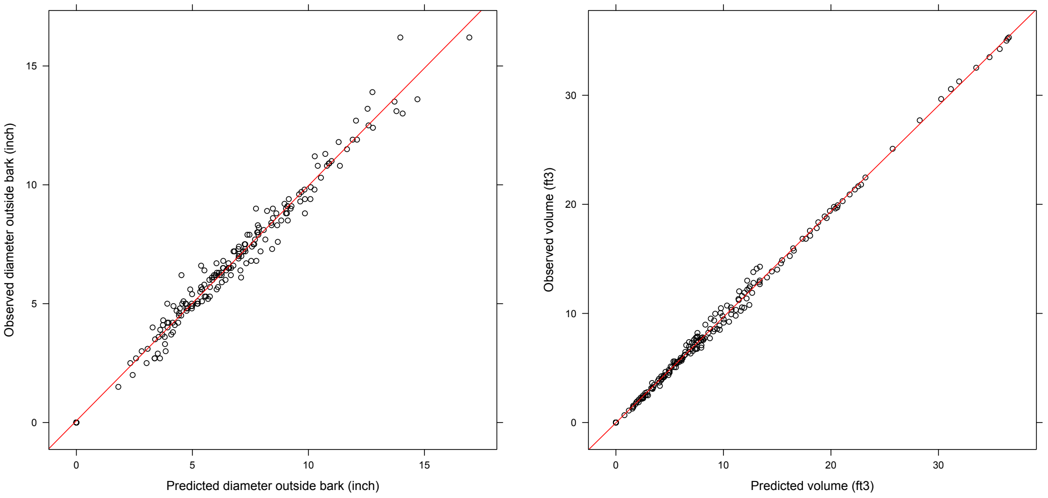
Table 4.22: Parameter estimates, approximate standard errors (Approx. SE) and test statistics for inside-bark taper - volume equation for red maple - UGA data

Parameter	Estimate	Approx. SE	t-value	p-value
bet1	0.0006	0.00004	14.90	<.0001
bet2	0.0022	0.000035	63.64	<0.0001

Table 4.23: Average observed, average predicted dob and vob, and fit statistics from UGA red maple inside bark taper - volume model

Variables	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
dib	6.15	6.24	-0.0659	-2.3403	0.3554	7.2	0.523	97.22
vib	8.29	8.65	-0.3604	-6.806	0.8172	8.477	1.321	96.56

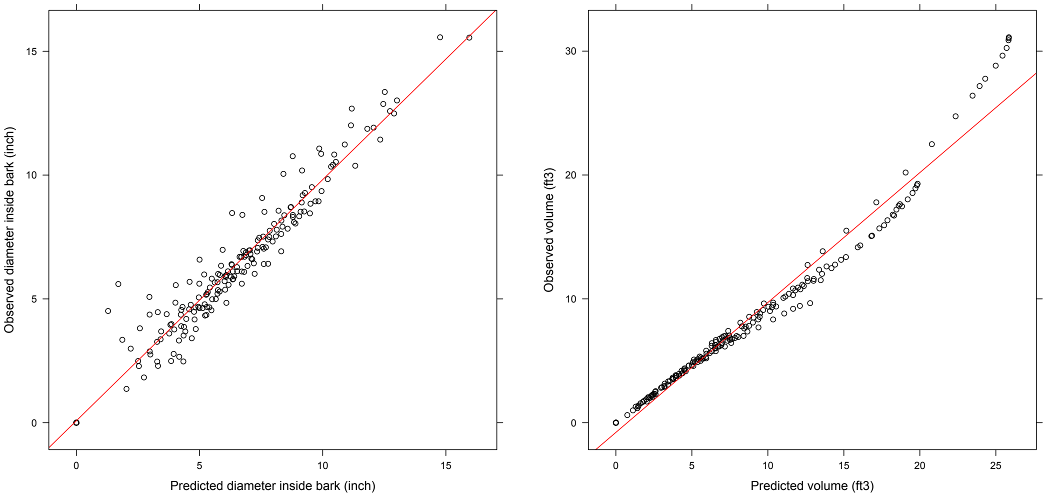
The various observed and predicted plots for outside (Figure 4.11) , inside bark (Figure 4.12), residual plots and fitted plot (see Appendix D) show that both outside and inside bark models are appropriate.



(a) dob

(b) vob

Figure 4.11: Actual vs predicted dob and vob for red maple- UGA model



(a) dib

(b) vib

Figure 4.12: Actual vs predicted dib and vib for red maple- UGA model

As discussed above, it was necessary to fit a function to predict dbhib from dbh for use in the inside bark taper-volume functions for UGA red maple data. The function (Equation 4.19) fits the data very well.

$$\hat{\text{Dbhib}} = 0.63 + 0.88 \times \text{Dbh} \tag{4.19}$$

4.4 Biomass prediction comparison

Using the taper-volume equations and the other required variables from UGA destructive sampling data, we estimated total as well as component biomass for both red maple and slash pine. The biomass prediction from this method was compared with the prediction from system of equations that was developed in Chapter 3. Specifically, we used Legacy and UGA slash and red maple taper-volume functions to predict total and component biomass for each species. The prediction from this method was compared with prediction from the system of equations. The criteria used to compare prediction include AR, APR, AAR, AAPR, RMSE and PVE.

4.4.1 Prediction comparison for slash pine

On average, all biomass components are slightly under-predicted when using the explicit system of equations (Table 4.24). The larger percentage bias and larger percentage error in prediction are for foliage, branch and crown components. The stemwood, stem and total biomass models show better fit than other components as indicated by higher PVE.

Table 4.24: Average observed, average predicted biomass and fit statistics from fitting system of equations based on Dbh and Ht for UGA slash data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	254.36	254.06	0.30	- 0.93	19.36	8.37	24.23	95.05
Bark	150.12	149.94	0.18	- 1.71	18.06	12.40	22.38	76.41
Stem	404.48	404.00	0.48	- 0.29	26.22	6.34	36.01	94.24
Branch	21.14	20.48	0.65	- 5.02	6.32	33.91	8.10	65.01
Foliage	11.06	10.72	0.34	- 13.10	3.38	39.87	5.18	52.44
Crown	32.20	31.21	0.99	- 4.80	9.32	32.71	12.42	63.49
Total	436.68	435.21	1.47	0.13	28.81	6.54	39.14	93.72

The UGA slash pine taper-volume biomass estimation approach predicted observed biomass components similarly to the explicit system of biomass equations. As for the system of equations, the largest percentage bias and percentage error in prediction are for branch, foliage, and crown component models (Table 4.25). Stemwood, stem and total stem biomass predictions are closer to observed values than are crown component predictions.

Table 4.25: Average observed, average predicted biomass and fit statistics for UGA slash taper-volume model when used to predict UGA slash data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	254.36	264.20	- 9.84	- 6.98	25.00	11.69	30.57	92.13
Bark	150.12	157.46	- 7.33	- 7.52	21.29	14.89	25.50	69.36
Stem	404.48	421.65	- 17.17	- 6.17	39.94	10.39	47.66	89.91
Branch	21.14	21.84	- 0.70	- 10.62	6.21	34.78	7.91	66.65
Foliage	11.06	11.49	- 0.42	- 18.80	3.53	41.68	5.11	53.65
Crown	32.20	33.32	- 1.13	- 10.41	9.19	33.33	12.14	65.10
Total	436.68	454.98	- 18.30	- 5.70	41.83	10.07	50.34	89.62

All the components are over-predicted when using Legacy taper-volume model to predict UGA slash data (Table 4.26). Similar to the other two methods, higher prediction bias and prediction error are evident for branch, foliage and crown predictions.

Table 4.26: Average observed, average predicted biomass and fit statistics for legacy slash taper-volume model when used to predict UGA slash data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	254.36	270.54	- 16.18	- 7.91	24.77	11.23	31.24	91.78
Bark	150.12	160.37	- 10.25	- 8.64	21.26	15.09	25.74	68.80
Stem	404.48	430.91	- 26.43	- 7.19	38.06	9.90	48.34	89.62
Branch	21.14	22.27	- 1.13	- 12.37	6.49	36.21	8.33	62.96
Foliage	11.06	11.67	- 0.61	- 20.89	3.65	43.42	5.27	50.77
Crown	32.20	33.94	- 1.74	- 12.17	9.65	34.97	12.76	61.47
Total	436.68	464.86	- 28.18	- 6.75	40.36	9.65	52.97	88.50

Below, we compare the fit statistics for major component (stemwood, crown and total) biomass using the explicit biomass system of equations, the UGA taper-volume model indirect approach (UGA taper-volume) and the Legacy taper-volume indirect model (Legacy taper-volume). Average percent prediction biases for the UGA taper-volume model and legacy taper-volume model are close to each other but higher than the explicit system of equations (Table 4.27). Prediction error is smallest for the explicit system of equations and largest for Legacy taper-volume model for all three components. The average percent prediction errors for both UGA taper-volume and Legacy taper-volume models are similar. For stem and total biomass models, RMSE from the System of equations is smaller than the other two estimation approaches. Whereas, crown biomass RMSE is very close from all three approaches. The goodness of fit statistics show very good fit, specifically for stem and total biomass models. It is usually higher for system of equations followed by UGA taper-volume model.

In general, as expected, the system of equations, a direct approach of estimating biomass, outperforms the other two approaches. However, based on the fit statistics, UGA taper-volume equation is comparable to the system of equations which indicates that the taper-volume equation approach of predicting component biomass is reliable.

Table 4.27: Comparing fit statistics from system of equation, UGA taper model and Legacy taper model prediction for UGA slash pine data

Components	Method	APR	AAPR	RMSE	PVE
Stem	System of equations	- 0.29	6.34	36.01	94.24
	UGA taper-volume	- 6.17	10.39	47.66	89.91
	Legacy taper-volume	- 7.19	9.90	48.34	89.62
Crown	System of equations	- 4.80	32.71	12.42	63.49
	UGA taper-volume	- 10.41	33.33	12.14	65.10
	Legacy taper-volume	- 12.17	34.97	12.76	61.47
Total	System of equations	0.13	6.54	39.14	93.72
	UGA taper-volume	- 5.70	10.07	50.34	89.62
	Legacy taper-volume	- 6.75	9.65	52.97	88.50

4.4.2 Prediction comparison for red maple

When using the red maple explicit system of equations, we find slight under-prediction of biomass for all components except for foliage (Table 4.28). Similar to slash pine, the average percent bias and percent error in prediction are higher for branch, foliage and crown components than for stem components. Goodness of fit statistics show that stemwood, stembark, stem and total components models, each explain more than 85% of variation in the data. However, very poor fit is found for branch, foliage and crown components.

Table 4.28: Average observed, average predicted biomass and fit statistics from fitting system of equations based on Dbh and Ht for UGA red maple data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	285.67	282.25	3.42	1.22	32.37	11.12	39.62	91.36
Bark	84.88	83.37	1.51	4.67	14.64	18.79	19.39	85.25
Stem	370.56	365.62	4.94	2.72	32.97	9.91	43.99	94.07
Branch	82.37	78.74	3.63	- 29.05	34.52	57.54	43.04	9.90
Foliage	9.68	10.01	- 0.33	- 75.82	3.90	96.67	4.79	26.69
Crown	92.05	88.75	3.30	- 26.70	37.97	54.43	45.94	14.33
Total	462.61	454.38	8.23	0.46	61.58	14.87	74.05	87.14

From using UGA red maple taper - volume model to predict UGA red maple data, we obtain higher average percentage bias and error in prediction on the same components (branch, foliage and crown) as above (Table 4.29). Branch, foliage and crown biomass models have poor (low PVE) fit relative to other components.

Table 4.29: Average observed, average predicted biomass and fit statistics for UGA red maple taper - volume model when used to predict UGA red maple data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	285.67	275.82	9.85	0.98	31.50	11.59	41.22	90.65
Bark	84.88	80.97	3.91	5.25	13.74	16.91	19.29	85.41
Stem	370.56	356.79	13.76	2.66	38.09	10.80	45.52	93.65
Branch	82.37	77.83	4.54	- 29.57	35.22	59.01	42.97	10.18
Foliage	9.68	9.96	- 0.28	- 80.81	4.19	103.73	5.08	17.72
Crown	92.05	87.79	4.26	- 27.53	38.97	56.41	46.14	13.58
Total	462.61	444.58	18.03	0.10	63.33	16.22	74.89	86.85

When the Legacy red maple taper - volume model is used, we have the highest percent bias and error in foliage prediction compared to other components (Table 4.30). The percent prediction error is higher for branch foliage and crown components. Goodness of fit statistics show that the all component predictions, except branch, foliage and crown models, fit the data well.

Table 4.30: Average observed, average predicted biomass and fit statistics for legacy red maple taper - volume model when used to predict UGA red maple data

Components	AOBS	APRED	AR	APR	AAR	AAPR	RMSE	PVE
Stemwood	285.67	247.17	38.51	12.01	43.49	14.51	56.98	82.13
Bark	84.88	72.71	12.17	15.70	14.94	18.32	22.06	80.92
Stem	370.56	319.88	50.68	13.49	53.30	14.19	67.82	85.90
Branch	82.37	69.49	12.87	- 15.67	35.89	53.17	45.22	0.54
Foliage	9.68	8.88	0.81	- 61.33	4.12	91.51	5.20	13.78
Crown	92.05	78.37	13.68	- 13.73	38.89	49.68	48.67	3.85
Total	462.61	398.25	64.36	11.22	81.76	17.44	100.08	76.51

We compared the fit statistics for major component (stemwood, crown and total) biomass predictions resulting from using the three methods for red maple. On average, for stem and total biomass, larger percent bias and percent error in prediction are obtained from using Legacy taper-volume model than the other two methods (Table 4.31). However, for crown biomass, these statistics are lower for the Legacy model. The RMSE values from system of equations are close to RMSE from using UGA taper-volume equation and these RMSE values are smaller than RMSE from Legacy taper-volume model. In fact, comparing with the system of equations, RMSE has increased by only about 3% for stem, less than 0.5% for crown and about 1% for total biomass model, when the UGA taper-volume model is used. Further, compared with the system of equations, the RMSE value has increased by about 54% for stem, 6% for crown and 35% for total biomass model, when Legacy taper-volume model is used. There is a large increase in RMSE for these components when Legacy taper-volume is used. Goodness of fit statistics show that system of equations and UGA taper-volume model predict the stem and total biomass reasonably well.

Overall, based on the fit statistics, when we do not have direct measurements on biomass, we can use UGA red maple taper-volume equation to predict individual tree and components biomass. This indirect approach shows less agreement between predictions and observed biomass components than the explicit system of biomass equations.

Table 4.31: Comparing fit statistics from system of equation, UGA taper model and Legacy taper model prediction for UGA red maple data

Components	Method	APR	AAPR	RMSE	PVE
Stem	System of equations	2.72	9.91	43.99	94.07
	UGA taper	2.66	10.80	45.52	93.65
	Legacy taper	13.49	14.19	67.82	85.90
Crown	System of equations	- 26.70	54.43	45.94	14.33
	UGA taper	- 27.53	56.41	46.14	13.58
	Legacy taper	- 13.73	49.68	48.67	3.85
Total	System of equations	0.46	14.87	74.05	87.14
	UGA taper	0.10	16.22	74.89	86.85
	Legacy taper	11.22	17.44	100.08	76.51

4.5 Conclusion

Although simple taper functions represent the general taper of trees, they do not reflect the entire stem profile well; hence, they produce bias especially near the butt and the top section of tree stems (Jiang 2004). More flexible, segmented taper functions represent the stem profile with different sub-functions for various parts of the stem, therefore reducing prediction error. In this study, we used a revised version of Fang et al. (2000) compatible taper-volume function, which is a complex and very flexible system that provides very accurate estimates of upper stem diameter and stem volume. We used three segments or two segments functions depending upon the data type and significance of the parameters.

Major characteristics of our function are: (1) the segmented taper-volume function is continuous at join (inflection) points, (2) the function is constrained to go through Dbh (3) the first join point is at 4.5/Ht and the second join point, is allowed to vary with Dbh and Ht, and is estimated from the data, (4) each segment has its own form factor parameter, (5) first and second form factor parameters are allowed to vary with Dbh and/or Ht whereas the third is estimated directly from the data, (6) when relative height (h) = total height (Ht) , the diameter at the top of the tree (d) is 0, (7) volume is 0 at the stump height (i.e. when $h = h_0$, V_m=0), (8) the segmented taper-volume functions are compatible, that is when integrated taper function results in volume function, (9) parameters in the function have a biological basis and hence are informative, (10) cubic foot volume of any stem section can be predicted using the function and, (11) the segmented taper-volume function represents the stem profile very well.

We fitted segmented taper-volume function for outside and and inside-bark diameter for slash pine and red maple. Two sets of data, one from UGA study and the other from legacy data were separately used to build models. We found the taper functions provide a good fit on diameter and volume prediction. When using inside-bark taper-volume function, diameter inside-bark (Dbhib) is required. Therefore, we developed a species specific function that predicts Dbhib based on Dbh for both data sets.

We have shown that the taper-volume indirect method (using the UGA data) of component biomass estimation predicts similarly to the explicit individual tree biomass system of equations. Hence, we can say that it is reasonable to use compatible taper/volume systems that are known to represent tree volume for a given species in a given region in this indirect approach to biomass estimation. However, to use this method we do in fact need to have some ratios available for things such as bark/wood biomass, foliage/wood biomass, branch/wood biomass. Typically, these ratios are difficult and expensive to develop and only a small number of trees are usually sampled to develop them (e.g. our UGA data). However, taper/volume data is much cheaper to obtain and much larger data sets are available for taper/volume modeling. In this study, we have shown that a reasonable process to use to estimate tree biomass components and ultimately stand, forest, regional and ultimately national scale estimates of tree biomass can indeed be performed using the taper-volume indirect method along with ratios developed from smaller regional biomass studies.

4.6 REFERENCES

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4.7 APPENDIX A: RESIDUAL DIAGNOSIS OF FITTED TAPER MODEL - LEGACY MODEL

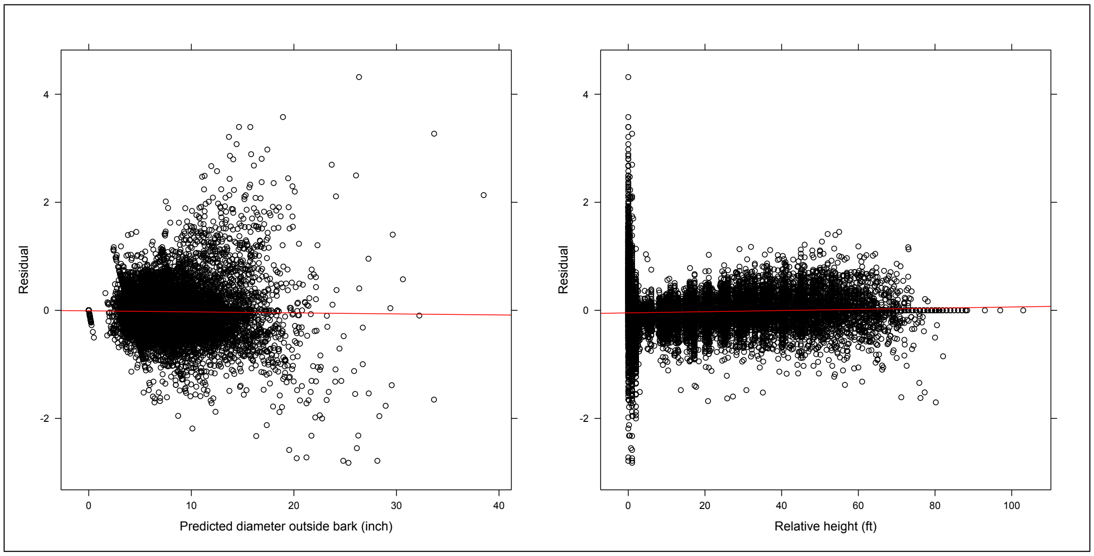

Figure 4.13: Residual plots of fitted taper model of dob for slash pine- Legacy model

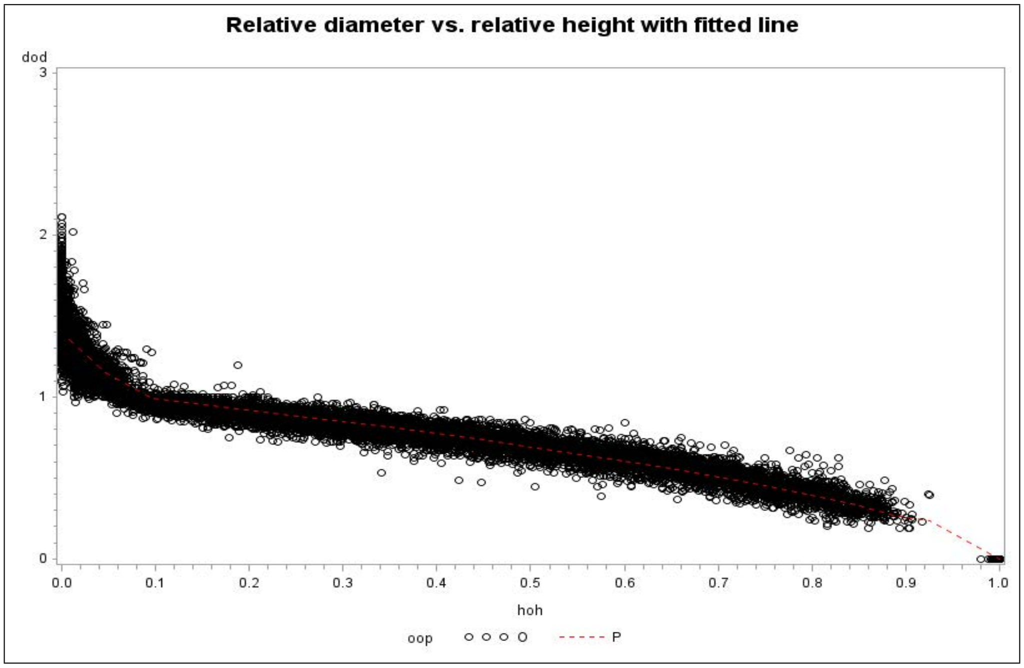

Figure 4.14: Plot of relative height with relative dob with fitted line for slash pine - Legacy model

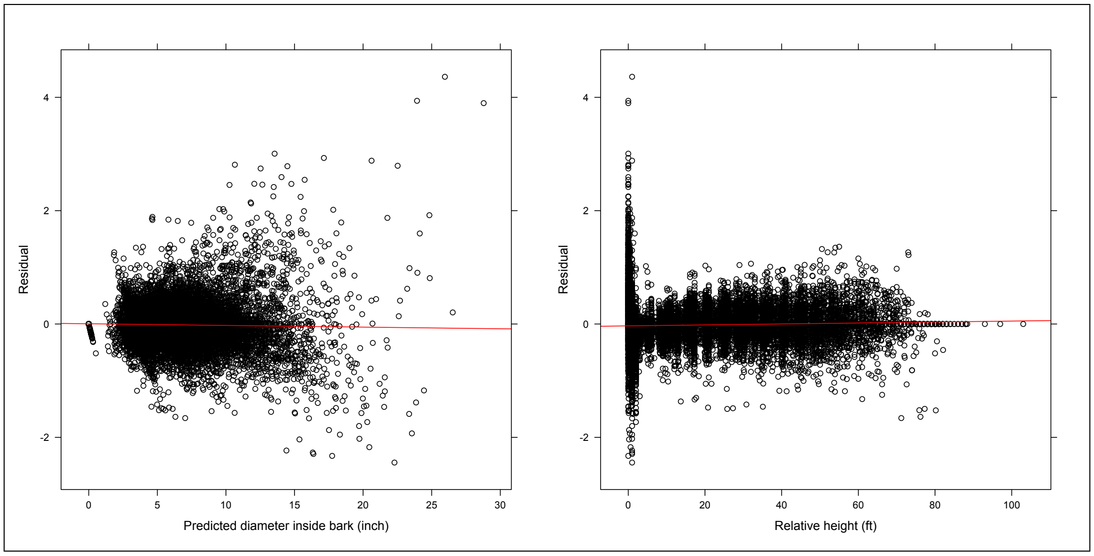

Figure 4.15: Residual plots of fitted taper model of dib for slash pine - Legacy model

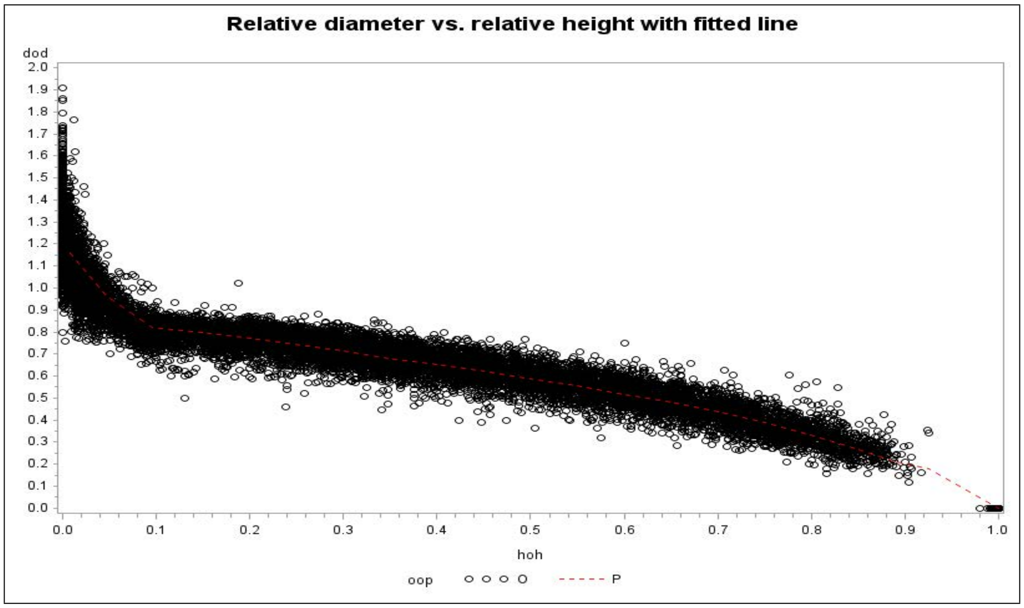

Figure 4.16: Plot of relative height with relative dib with fitted line for slash pine

4.8 Appendix B: Residual diagnosis of fitted taper model of diameter outside and inside-bark for red maple - Legacy model

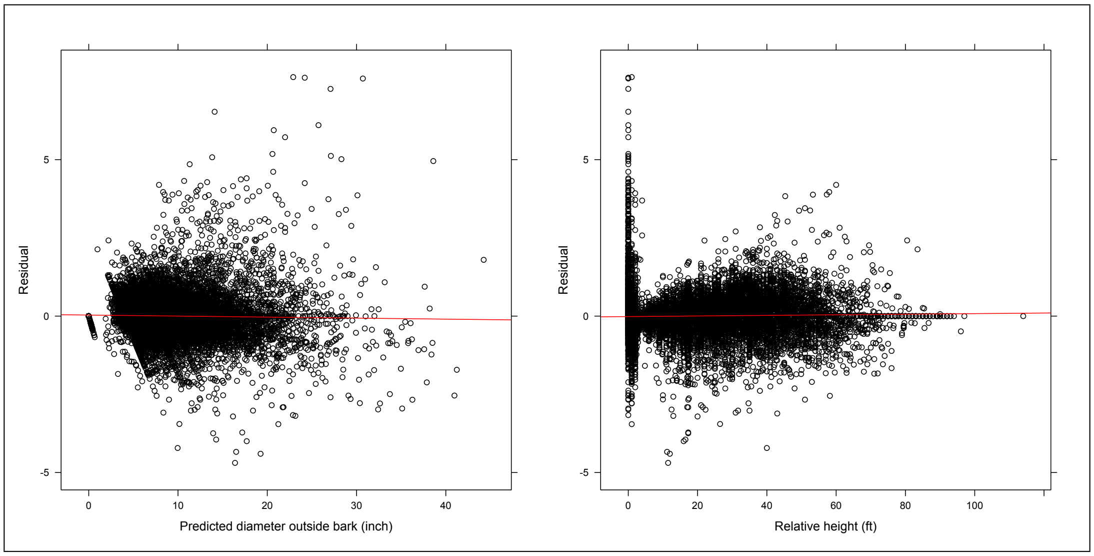

Figure 4.17: Residual plots of fitted taper model of dob for red maple- Legacy model

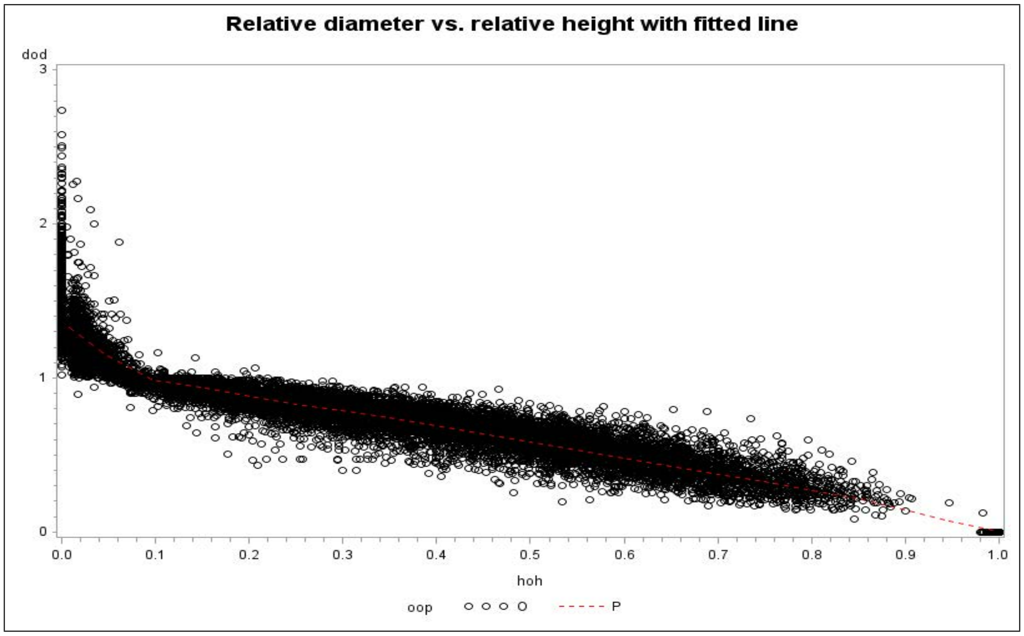

Figure 4.18: Plot of relative height with relative dob with fitted line for red maple

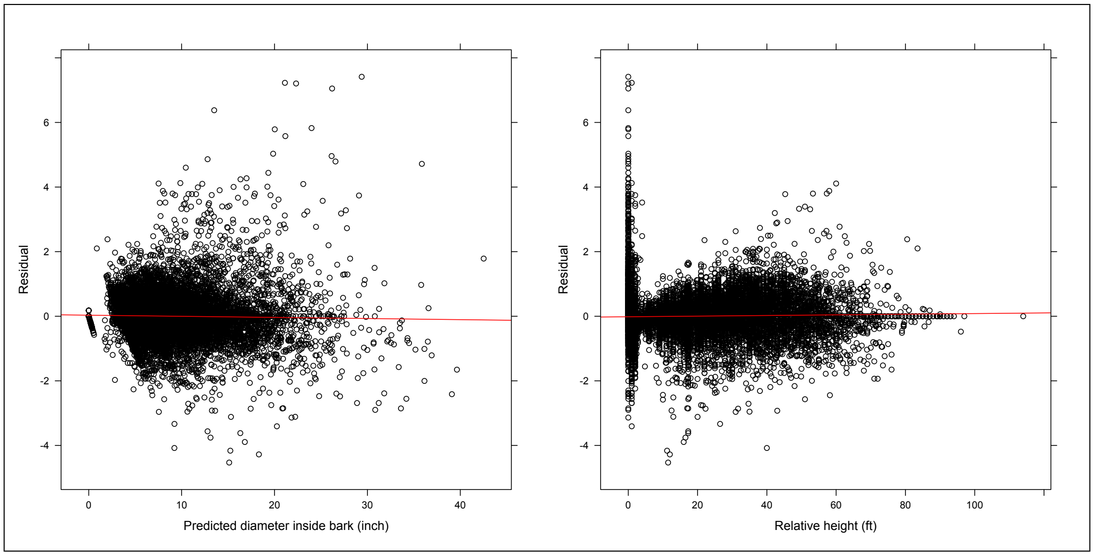

Figure 4.19: Residual plots of fitted taper model of dib for red maple- Legacy model

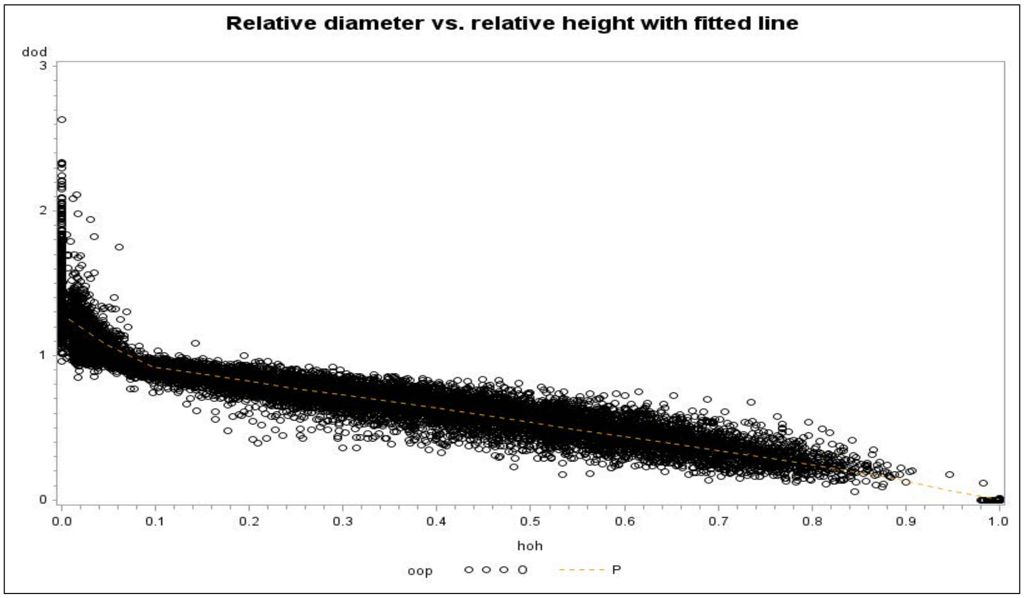

Figure 4.20: Plot of relative height with relative dib with fitted line for red maple

4.9 Appendix C: Residual diagnosis of fitted taper model of diameter outside and inside-bark for slash pine - UGA model

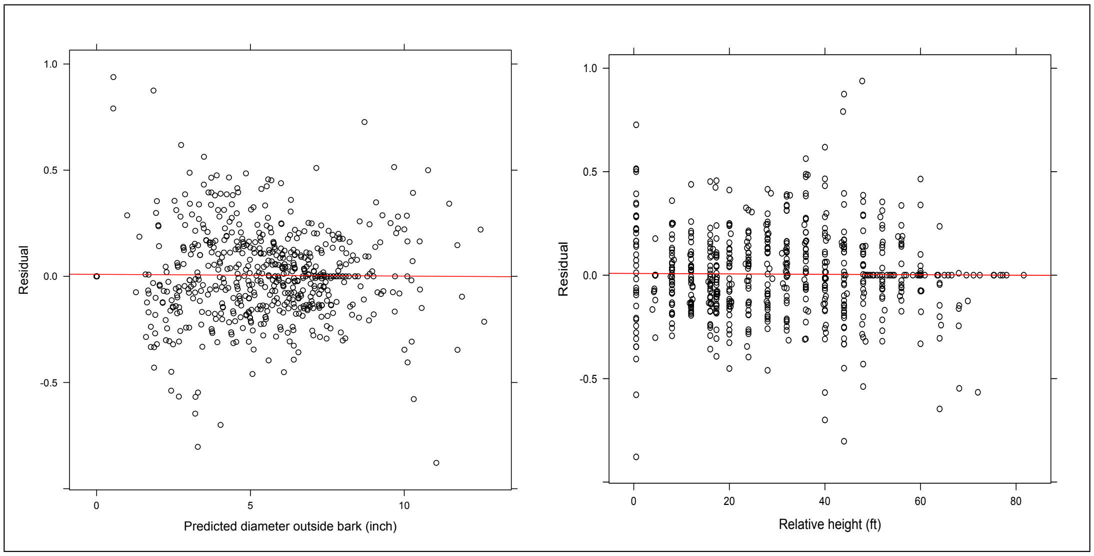

Figure 4.21: Residual plots of fitted taper model of dob for slash pine- UGA model

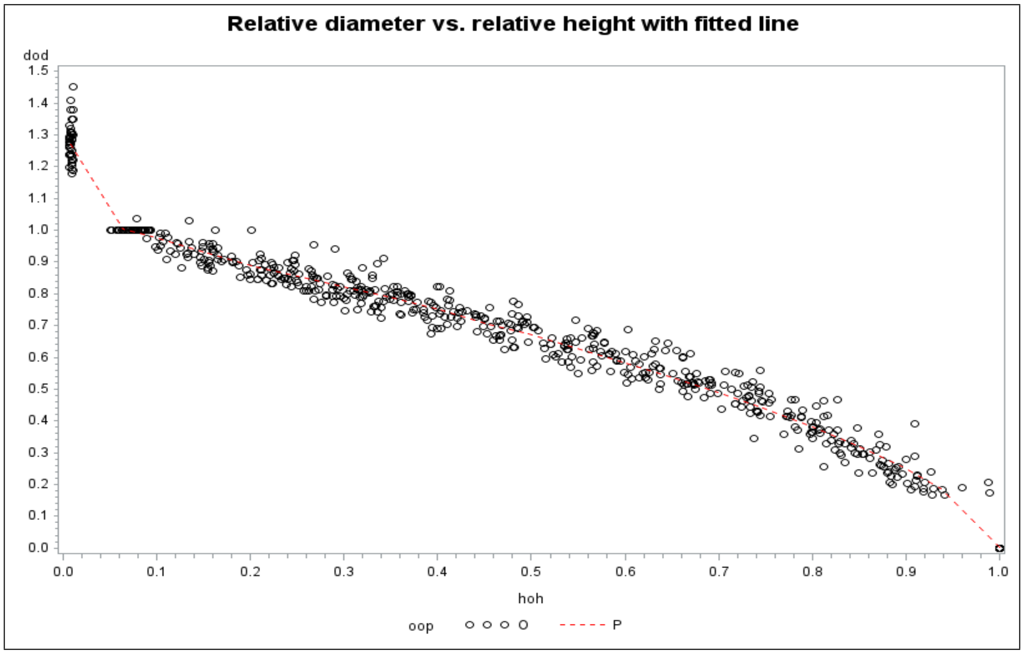

Figure 4.22: Plot of relative height with relative dob with fitted line for slash pine

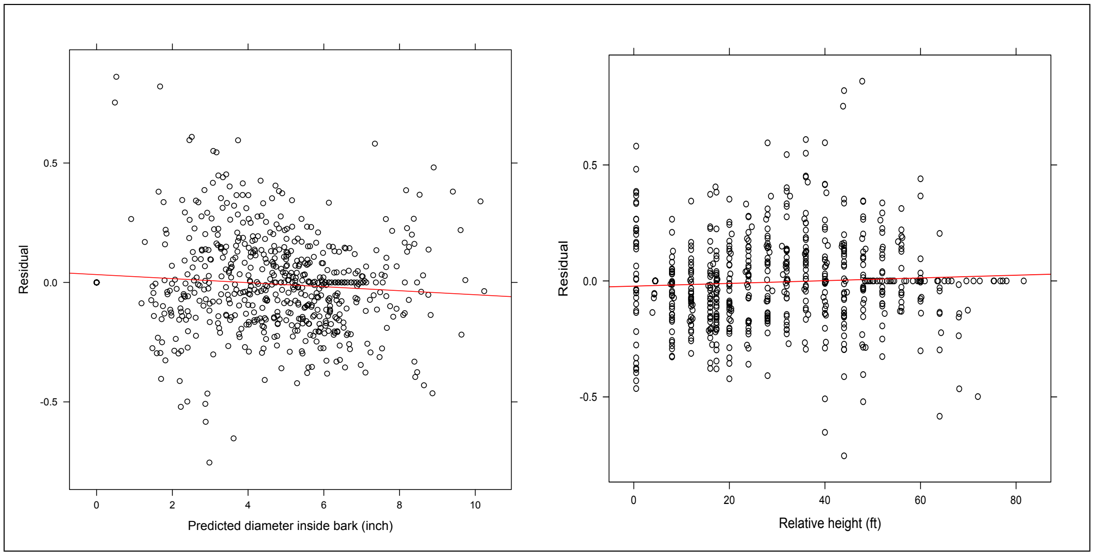

Figure 4.23: Residual plots of fitted taper model of dib for slash pine- UGA model

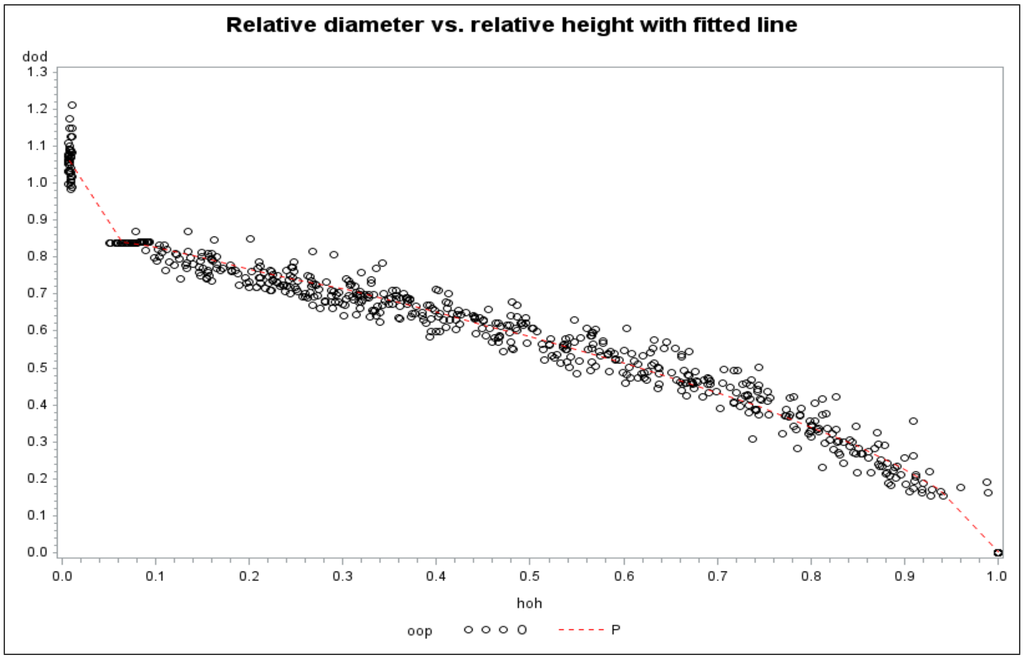

Figure 4.24: Plot of relative height with relative dib with fitted line for slash pine

4.10 APPENDIX D: RESIDUAL DIAGNOSIS OF FITTED TAPER MODEL OF DIAMETER OUTSIDE AND INSIDE-BARK FOR RED MAPLE - UGA MODEL

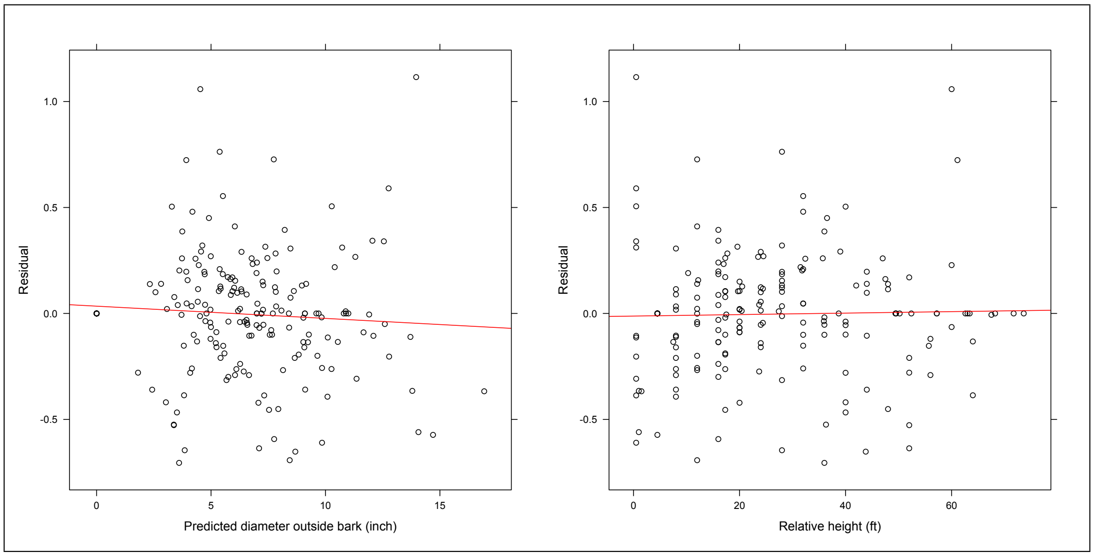

Figure 4.25: Residual plots of fitted taper model of dob for red maple- UGA model

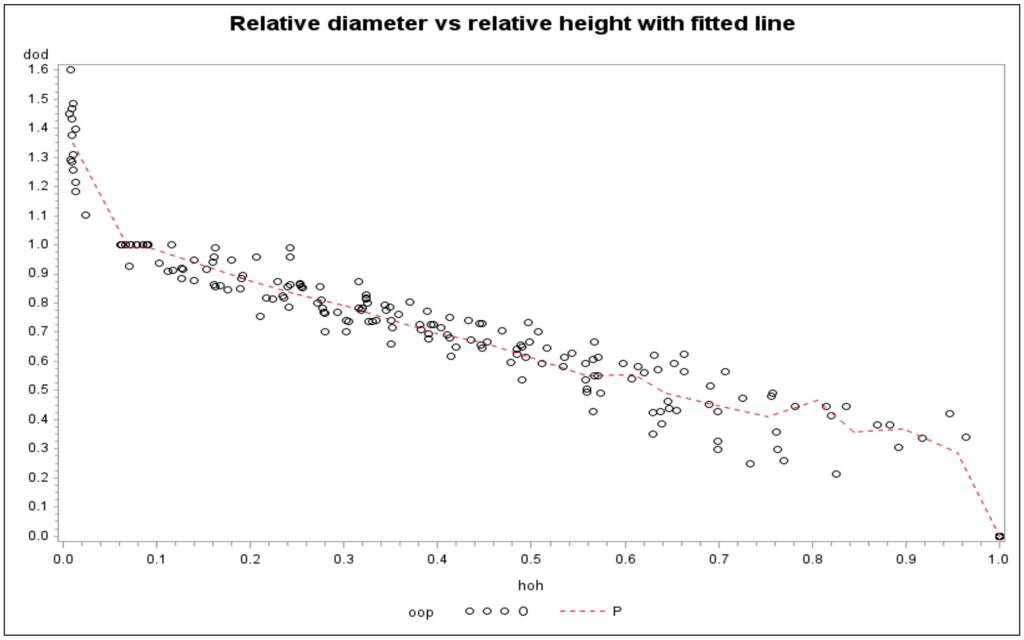

Figure 4.26: Plot of relative height with relative dob with fitted line for red maple

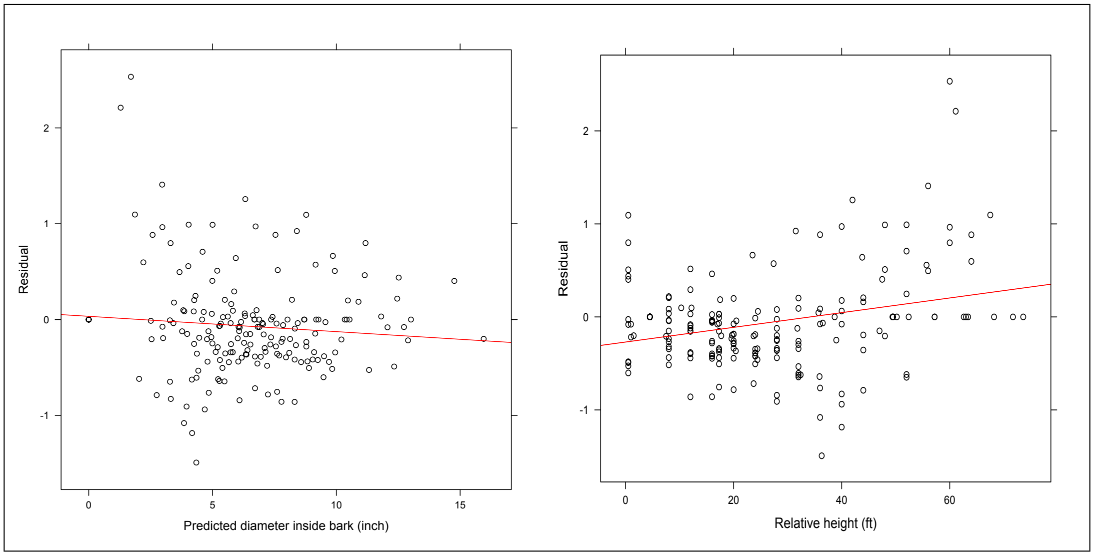

Figure 4.27: Residual plots of fitted taper model of dib for red maple- UGA model

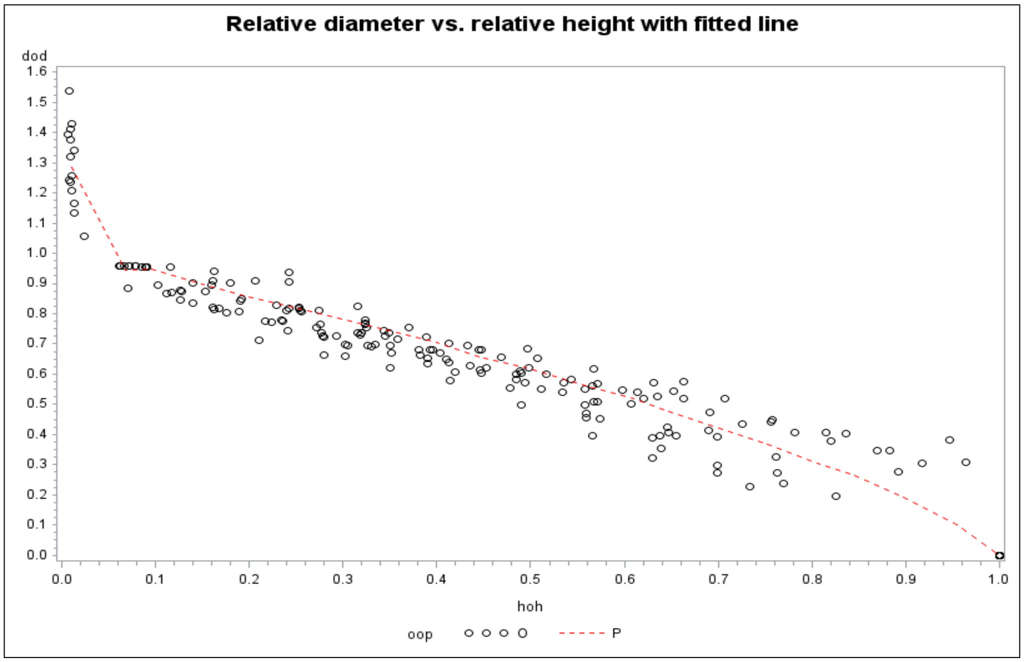

Figure 4.28: Plot of relative height with relative dib with fitted line for red maple