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# Assessing Tree and Stand Biomass: A Review with Examples and Critical Comparisons

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**ABSTRACT.** There is considerable interest today in estimating the biomass of trees and forests for both practical forestry issues and scientific purposes. New techniques and procedures are brought together along with the more traditional approaches to estimating woody biomass. General model forms and weighted analysis are reviewed, along with statistics for evaluating and comparing biomass models. Additivity and harmonization are addressed, and weight-ratio and density-integral approaches are discussed. Subsampling methods on trees to derive unbiased weight estimates are examined, and ratio and difference sampling estimators are considered in detail. Error components for stand biomass estimates are examined. This paper reviews quantitative principles and gives specific examples for prediction of tree biomass. The examples should prove useful for understanding the principles involved and for instructional purposes. *FOR. SCI.* 45(4): 573–593.

**Additional Key Words:** Model forms, weighting, selection criteria, subsampling, error components.

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**T**HERE IS CONSIDERABLE INTEREST TODAY in estimating the biomass of forests for both practical forestry issues and scientific purposes. Forest biomass is important for commercial uses (e.g., fuelwood and fiber) and for national development planning, as well as for scientific studies of ecosystem productivity, energy and nutrient flows, and for assessing the contribution of changes in forestlands (especially tropical) to the global carbon cycle. Thus, it is not surprising that during the past four decades, research on biomass production by forests has steadily grown in importance (Zeide 1987, Waring and Running 1998). As early as 1950 weight<sup>1</sup> as a measure of wood quantity was used by many of the larger companies in North America and northern Europe (Taras 1967). With the increasing value of wood and

the realization of the shortcomings of traditional volume measurement, that is, the myriad log rules in use, interest in and use of weight for measurement and valuation of trees has rapidly grown (Guttenberg 1973, Husch et al. 1982, Avery and Burkhart 1994). The use of end-product units as a measure of the amount of raw material is rare outside the forest products industry. Raw cotton is not bought and sold in "shirt" or other similar units, nor is crude oil marketed with liters of gasoline as the measurement unit. Of course, a shirt cannot be identified out in a cotton field, but a veneer log or a sawlog can be identified in a forest. Hence volume measurement will continue to be essential. Nonetheless, the current trend is toward decreasing the usage of end-product units as expressions of stem content. The interest in complete tree utilization (roots, stumps, branches, etc.), the use of residues from the manufacture of forest products, fuel quantity in relation to forest fire conditions, and other issues has increased the use and importance of biomass measurement (Husch et al. 1982, Philip 1994).

<sup>1</sup> The term "weight" is commonly used for mass, but strictly speaking this is incorrect. Mass is the measure of the amount of matter present in a body; whereas the weight of a body is the force exerted on its mass by gravity. To know whether mass or force is being measured, the SI uses two units: the kilogram for mass and the newton for force.

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A review of past practices by Cunia (1988) showed that in some instances estimates of biomass content were obtained by ocular means based on intuition and past experience. Later, this was supplemented by (1) measurements performed on subjectively selected samples of trees or plots and (2) results obtained from subjectively designed experiments. Today, forest inventory methods are based on sound statistical designs (de Vries 1986). The bias, if any, is largely reduced, and the error of estimates can be quantified in probabilistic terms. Indeed, research foresters and statisticians have come to recognize the various error components of forest biomass inventory estimates and to develop techniques to account for them. Great progress has been made in the last few decades in the methodology of selection of sample trees and plots and estimation of forest parameters of interest. New and exciting developments in sampling theory, such as importance and randomized branch sampling, have changed the way we view forest inventory (Schreuder et al. 1993). These modern procedures of error components and sampling techniques have provided considerable gains in reliability and efficiency by improving forecasts and corresponding inferences and by reducing the number of samples required and the costs involved.

Remote sensing, geographic information systems, and photogrammetry are powerful interrelated tools for forest resource assessment, as evidenced by the scope of presentations at the First International Conference on Geospatial Information in Agriculture and Forestry (Petoskey 1998). Biomass estimation by using such tools is a fascinating and intricate subject in itself and will not be considered here. Statistical methodologies, such as the expectation-maximization or EM algorithm and its extensions, multiple imputation, and Markov chain Monte Carlo (Rubin 1987, Schafer 1997), are starting to be applied to inventory data as an alternative to growth and yield models for forecasting (Van Deusen 1997). Again, these related methodologies and their use in calculation of biomass constitute a topic needing its own review and development. This article focuses on modeling and sampling procedures, because these have been the main avenues of biometrical research and development on biomass.

The critique starts with general model forms and statistics useful for comparing models. The issue of heteroscedasticity is addressed, and the theory of estimated generalized least squares is presented. I elaborate on the three general procedures to handle the additivity problem and follow with specific illustrative examples. The next three sections deal with bole biomass and the techniques of harmonization, the ratio approach, and density integrals. The next part of the article deals with sampling—ratio-type estimators, randomized branch and importance sampling, and difference sampling. Estimation with a ratio estimator and difference sampling are demonstrated. The article continues with a section on error of inventory estimates and concludes with a look at past and present studies and general thoughts on application and future directions of research.

## 1 Biomass Estimation Techniques

The basic management unit is the forest stand. However, any stand is an aggregation of trees, and the *stand biomass* is defined as the sum of the biomass of the individual trees that comprise the stand. All methods for estimating stand biomass must therefore involve, at least in their developmental stages, a prediction of individual tree biomass and the summation of these quantities to obtain per-hectare stand biomass.

### 1.1 Regression Modeling

The most common procedure for estimating tree biomass is through the use of regression. Trees are chosen through an appropriate selection procedure for destructive sampling, and the weights or mass of the components of each tree are determined and related by regression to one or more dimensions of the standing tree. The tree is normally separated into three aboveground components: (1) bole or main stem, (2) bole bark, and (3) crown (branches and foliage). Occasionally, a fourth component, belowground biomass, which is the stump and major roots within a fixed distance, is considered. See Karizumi (1977), Lossaint and Rapp (1978), Satoo and Sassa (1979), Deans et al. (1996), Kurz et al. (1996), and Reed et al. (1996) for examples on sampling and estimation of belowground biomass. Other tree component schemes are possible and are usually devised based on the milling and pulping technologies of the users for the population of trees of interest. The fresh weight of an individual tree may be determined by weighing all components using field scales or by sampling. For large trees, weighing of the entire tree can be quite time consuming and laborious. Sampling procedures as an alternative to direct weighing of an entire component will be considered later. The process of collecting data and developing biomass relationships falls under the subject of *allometry*, the measure and study of growth or size of a part in relation to an entire organism. West et al. (1997) provide a general theory of allometric scaling laws based on fractal networks of branching tubes, and Broad (1998) gives a theory of multivariate allometry.

#### 1.1.1 General Model Forms

Researchers have used a variety of regression models for estimating total-tree and tree-component biomass. Earlier reviews of biomass studies (e.g., Pardé 1980, Baldwin 1987, Clark 1987, Pelz 1987) indicate that prediction equations generally have been developed utilizing one of the following three forms:

$$\text{Linear (additive error): } Y = \beta_0 + \beta_1 X_1 + \dots + \beta_j X_j + \epsilon \quad (1)$$

$$\text{Nonlinear (additive error): } Y = \beta_0 X_1^{\beta_1} X_2^{\beta_2} \dots X_j^{\beta_j} + \epsilon \quad (2)$$

$$\text{Nonlinear (multiplicative): } Y = \beta_0 X_1^{\beta_1} X_2^{\beta_2} \dots X_j^{\beta_j} \epsilon \quad (3)$$

where  $Y$  = total or component biomass,  $X_j$  = tree dimension variable,  $\beta_j$  = model parameter, and  $\epsilon$  = error term. Some commonly used tree dimension variables are diameter at breast height ( $D$ ),  $D^2$ , total height ( $H$ ),  $D^2H$ , age, and live crown length

(LCL). Diameter at the base of the live crown has been proven to be one of the best predictor variables for crown weight (Clark 1982). On the basis of the pipe model theory (Shinozaki et al. 1964a, 1964b), many researchers have used sapwood area (active conducting tissue) measured at various heights in the stem as a predictor of foliage weight and surface area (e.g., Snell and Brown 1978, Rogers and Hinckley 1979, Kaufmann and Troendle 1981, Waring et al. 1982, Robichaud and Methven 1992). An innovative approach for predicting seedling and sapling biomass has used projected area of the seedling or sapling (as measured by computer-based image analysis) as an explanatory variable. Studies have shown that projected area alone can explain more than 97% of the variation in seedling or sapling mass (Suh and Miles 1988, Norgren et al. 1995). Model (1) produces multiple linear regressions that can be fitted by standard least squares estimation procedures. Model (2) produces nonlinear regression equations that require use of iterative procedures for parameter estimation.

Normally, biomass data exhibit heteroscedasticity; that is, the error variance is not constant over all observations. If Models (1) and (2) are fitted to such data, then weighted analysis, typically involving additional parameters, is necessary to achieve minimum variance parameter estimates (assuming all other regression assumptions are met: e.g., uncorrelated errors). A statistical model consists jointly of a part that specifies the mean  $X'\beta$  and a part describing variation around the mean, and the latter may well need more than one parameter ( $\sigma^2$ ) to be adequate. A weighted analysis procedure, based on modeling the error structure, will be described shortly.

Model (3) nonlinear regression equations are usually transformed into linear (additive error) regression equations by taking the logarithm of both sides of the equation. In this form, the equation parameters can easily be estimated by least squares procedures. Typically, the variance of  $Y$  is not uniform across the domain of one or more of the  $X_j$ 's; however, when transformed to logarithms, Model (3) generally has homoscedastic variance. The logarithmic form is

$$\ln Y = \ln \beta_0 + \beta_1 \ln X_1 + \dots + \beta_j \ln X_j + \ln \epsilon \quad (4a)$$

where  $\ln$  is the natural logarithm. All common goodness-of-fit statistics relate to the transformed equation only and are not directly comparable with the same statistics produced through use of either Models (1) or (2). When the logarithmic transformation is used, it is usually desirable to express estimated values of  $Y$  in arithmetic (i.e., untransformed) units. However, the conversion of the unbiased logarithmic estimates of the mean and variance to arithmetic units is not direct. The antilogarithm of  $\ln Y$  yields the median of the skewed arithmetic distribution rather than the mean. If  $\hat{\mu} = \widehat{\ln Y}$  and  $\hat{\sigma}^2 =$  sample variance of the logarithmic equation, then

$$\begin{aligned} \hat{Y} &\doteq \exp(\hat{\mu} + \sigma^2 / 2) \\ \hat{\sigma}_a^2 &\doteq \exp(2\hat{\sigma}^2 + 2\hat{\mu}) - \exp(\hat{\sigma}^2 + 2\hat{\mu}) \end{aligned} \quad (4b)$$

where  $\hat{Y}$  is the estimated value in arithmetic units and  $\hat{\sigma}_a^2$  is the estimated variance of  $Y$  in arithmetic units (Flewellling

and Pienaar 1981, Yandle and Wiant 1981, Sprugel 1983). There is some evidence that these corrections tend to overestimate the true bias (Madgwick and Satoo 1975, Hepp and Brister 1982). Snowdon (1985), working with *Pinus radiata* D. Don, showed that the square-root transformation was a viable alternative to the logarithmic transformation if curvilinearity between the untransformed predictors and biomass was low. To correct for bias under the square-root transform, add  $\hat{\sigma}$  from the regression to the biomass estimate (Kilikki 1979). A list of commonly used equation forms for biomass estimation can be found in Clutter et al. (1983, p. 8).

### 1.1.2 Comparing Alternative Models

Schlaegel (1982) recommends the reporting of a series of statistics for evaluating goodness-of-fit and for use in comparing alternative biomass models. The first, an  $R^2$  statistic, is called the fit index ( $FI$ ). Kvålseth (1985) examined eight alternative  $R^2$  statistics;  $FI$  corresponds to his  $R_1^2$ , which is the one he recommended. Model predictions, if not already in original units, are transformed back to the original units, correcting for any bias if needed. The total sum of squares ( $TSS$ ) and the residual sum of squares ( $RSS$ ) are calculated as

$$TSS = \sum_{i=1}^n (Y_i - \bar{Y})^2, \quad RSS = \sum_{i=1}^n (Y_i - \hat{Y}_i)^2$$

where  $\bar{Y}$  = arithmetic mean of  $Y$  (total or component biomass) and  $n$  = number of sample observations. The fit index is

$$FI = 1 - (RSS / TSS) \quad (5)$$

The second statistic is the standard error of estimate in actual units ( $S_e$ ). It is calculated as

$$S_e = \sqrt{RSS / (n - p)} \quad (6)$$

where  $p$  = number of model parameters. The third statistic, useful for making quick comparisons between models, is the coefficient of variation ( $CV$ ) expressed as a percent:

$$CV = (S_e / \bar{Y}) \times 100 \quad (7)$$

The fourth statistic that Schlaegel recommends is one proposed by Furnival (1961) based on normal likelihood functions. The general formula for Furnival's index ( $I$ ) is

$$I = [f'(Y)]^{-1} \times RMSE \quad (8)$$

where  $f'(Y)$  is the derivative of the dependent variable with respect to biomass, the brackets signify the geometric mean, and  $RMSE$  is the root mean square error of the fitted equation. The index reduces to the usual estimate of the standard error about the curve when the dependent variable is biomass. When the dependent variable is some function of biomass, the index may be regarded as an average standard error transformed to units of biomass. The way Furnival derived the index puts it in inverse order as compared to likelihood, that is, a large value indicates a poor fit and vice-versa. The fifth statistic, suggested by Meyer (1938) and recommended by Schlaegel, is the percent standard error [ $S(\%)$ ]. Knowledge can be obtained about the model by calculating the  $i$ th residual's size relative to  $\hat{Y}_i$ , all values being

in actual biomass units. For each residual, the percent standard error is  $S(\%)_i = \left[ |Y_i - \hat{Y}_i| / \hat{Y}_i \right] \times 100$ . This statistic indicates the size of error as a percent of the mean of the distribution of  $Y_i$ . The expected value of  $S(\%)_i = 0$  because the expected value of  $Y_i - \hat{Y}_i = 0$ . Thus, if all  $S(\%)_i$ 's are nearly 0, the equation is very precise. Naturally, the  $S(\%)_i$ 's usually fluctuate widely. For reporting purposes, I recommend taking all residuals into account to form a composite statistic, the mean percent standard error ( $\bar{S}(\%)$ ) of predictions, defined as

$$\bar{S}(\%) = \frac{100}{n} \sum_{i=1}^n |Y_i - \hat{Y}_i| / \hat{Y}_i \quad (9)$$

The sixth statistic is the percent error ( $P_e$ ). It is a precision index using the percent standard error and the chi-square test. Let  $P_e$  represent the relative difference in percent of the estimate of tree or component weight to its true value. This statistic computes the value of  $P_e$  that would be necessary to assure a nonsignificant  $\chi^2$  test. The percent error is defined as

$$P_e = \left[ \frac{(196)^2}{\chi^2_{(n-p)}} \sum_{i=1}^n \left( \frac{\hat{Y}_i}{Y_i} - 1 \right)^2 \right]^{1/2} \quad (10)$$

where the  $\alpha = 0.05$  value for  $\chi^2$  with  $\nu$  degrees of freedom is approximated by

$$\chi^2_{(\nu)} = 0.853 + \nu + 1.645(2\nu - 1)^{1/2}$$

For derivation of this statistic see Schlaegel (1982). Finally, Schlaegel advocates reporting the necessary information for the construction of prediction confidence intervals. This usually involves reporting the model mean square error ( $MSE$ ) and the sums of squares and cross products matrix, i.e.,  $(X'X)^{-1}$  or more generally the  $Cov(\hat{\beta})$ .

To summarize, statistics useful for model evaluation and comparison are: (1) fit index ( $FI$ ), (2) standard error of estimate in biomass units ( $S_e$ ), (3) coefficient of variation based on  $S_e$  ( $CV$ ), (4) Furnival's index ( $I$ ), (5) mean percent standard error ( $\bar{S}(\%)$ ), (6) percent error ( $P_e$ ) of the residuals, and (7) information needed for building prediction confidence intervals. Another useful model selection procedure—prevalent in the statistics literature—is the Akaike Information Criterion ( $AIC$ ). For a description and discussion of the  $AIC$ , see Judge et al. (1988, p. 848).

A number of researchers have published accounts of comparisons of alternative biomass regression models. Crow (1971) used  $FI$  as a means with which to compare models. Although the transformed allometric equation [Model (4)] proved superior, Model (1) was found to be almost as reliable when there was a relatively small range in tree sizes. Schreuder and Swank (1971, 1976) used  $FI$  and  $I$  to compare a weighted linear model with six other models based on the family of power transformations defined by Box and Cox (1964). They found that the  $FI$  criterion could give misleading results, but that Furnival's index was a useful tool in comparison of models for estimating biomass. Crow and Laidly (1980) also used the likelihood approach to show that weighted linear

[weighted Model (1)] and weighted nonlinear [weighted Model (2)] equations were acceptable alternatives to the transformed allometric model. Jacobs and Monteith (1981) obtained similar results. The maximum likelihood approach, or Furnival's index, reflects not only the magnitude of residuals but also possible departures from assumptions of normality and homogeneity of variance. These findings lead to two conclusions: (1) Furnival's index can generally be recommended as one of the most useful statistics for evaluating and comparing biomass models, and (2) weighted regressions are important and often necessary for developing biomass models of high precision.

### 1.1.3 Weighting Biomass Models

Forest modelers are typically faced with multiplicative heteroscedasticity in their data (Parresol 1993). It is often the case that the error variance (or disturbance) is functionally related to predictor variables in regression. Harvey (1976) and Judge et al. (1988) have shown that if the error variance is a function of a small number of unknown parameters, and if these parameters can be consistently estimated, then estimated generalized least squares (EGLS) estimation will provide asymptotically efficient estimates of the model parameters.

In the general linear statistical model  $y = X\beta + \epsilon$ ,  $X$  is a  $(T \times K)$  observable nonstochastic matrix,  $\beta$  is a  $(K \times 1)$  vector of parameters to be estimated,  $y$  is a  $(T \times 1)$  observable random vector, and the error vector,  $\epsilon$ , is a  $(T \times 1)$  unobservable random vector with properties  $E[\epsilon] = 0$  and  $E[\epsilon\epsilon'] = \Phi = \sigma^2\Psi$ , where  $\Psi$  is a  $(T \times T)$  diagonal matrix. Heteroscedasticity exists when the diagonal elements of  $\Psi$  are not all identical. In the general heteroscedastic specification  $\Phi = \text{diag}(\sigma_1^2, \sigma_2^2, \dots, \sigma_T^2)$ . If we assume that each  $\sigma_t^2$  is an exponential function of  $P$  explanatory variables then

$$E[\epsilon_t^2] = \sigma_t^2 = \exp[z_t'\alpha] \quad t = 1, 2, \dots, T \quad (11)$$

where  $z_t' = (z_{t1}z_{t2}\dots z_{tP})$  is a  $(1 \times P)$  vector containing the  $t$ th observation on  $P$  nonstochastic explanatory variables and  $\alpha = (\alpha_1\alpha_2\dots\alpha_P)'$  is a  $(P \times 1)$  vector of unknown coefficients. The first element in  $z_t$  is taken as unity ( $z_{t1} \equiv 1$ ), and the other  $z$ 's could be identical to, or functions of, the  $x$ 's. The normal convention is to parameterize the scale factor  $\sigma^2$  as  $\exp(\alpha_1)$ , or  $\alpha_1 = \ln \sigma^2$ . This means the expression in (11) can be written as

$$\sigma_t^2 = \sigma^2 \exp[z_t^*\alpha^*] \quad (12)$$

where  $z_t^* = (z_{t2}\dots z_{tP})$  and  $\alpha^* = (\alpha_2\dots\alpha_P)'$ . The covariance matrix can now be written as

$$\sigma^2\Psi = \sigma^2 \begin{bmatrix} \exp(z_1^*\alpha^*) & & & \\ & \exp(z_2^*\alpha^*) & & \\ & & \ddots & \\ & & & \exp(z_T^*\alpha^*) \end{bmatrix} \quad (13)$$

In order to estimate  $\alpha$  we first take logarithms of Equation (11) to obtain

$$\ln \sigma_i^2 = z_i' \alpha \quad (14)$$

Since the  $\sigma_i^2$  are not known, we use instead the squares of the ordinary least squares (OLS) residuals.<sup>2</sup> These residuals (denoted  $e_i$ ) are likely to reflect the size of  $\sigma_i^2$ , that is, large when  $\sigma_i^2$  is large and small when  $\sigma_i^2$  is small. Adding  $\ln e_i^2$  to both sides of Equation (14) yields

$$\ln e_i^2 + \ln \sigma_i^2 = z_i' \alpha + \ln e_i^2$$

or

$$\ln e_i^2 = z_i' \alpha + v_i \quad (15)$$

where  $v_i = \ln e_i^2 - \ln \sigma_i^2 = \ln(e_i^2 / \sigma_i^2)$ . In matrix notation, Model (15) can be written as  $q = Z\alpha + v$  where the vector  $q = (\ln e_1^2 \ln e_2^2 \dots \ln e_T^2)'$ . One way to estimate  $\alpha$  is to apply OLS to Model (15) which yields  $\hat{\alpha} = (Z'Z)^{-1}Z'q$ . Harvey (1976) showed that if the  $e_i$ 's are normally distributed then the intercept  $\alpha_1$  will not be consistently estimated, but the remaining elements in  $\hat{\alpha}$  will be consistent or unbiased.

Substituting  $\hat{\alpha}^*$  for  $\alpha^*$  in expression (13), we obtain the estimated covariance matrix  $\hat{\Phi} = \hat{\sigma}^2 \hat{\Psi}$ . The EGLS estimator is formed as

$$\hat{\beta} = (X' \hat{\Phi}^{-1} X)^{-1} X' \hat{\Phi}^{-1} y = (X' \hat{\Psi}^{-1} X)^{-1} X' \hat{\Psi}^{-1} y \quad (16)$$

Fortunately,  $\hat{\beta}$  only depends on the consistently estimated elements of  $\hat{\alpha}$ , since  $\hat{\alpha}_1$  can be factored out as a proportionality constant. The covariance matrix of  $\hat{\beta}$  is

$$\hat{\sigma}^2 (X' \hat{\Psi}^{-1} X)^{-1} \quad (17)$$

where  $\hat{\sigma}^2 = (y - X\hat{\beta})' \hat{\Psi}^{-1} (y - X\hat{\beta}) / T - K$

The usual hypothesis tests and interval estimates are based on this matrix. For prediction intervals on some future value  $y_0$  the sampling error is estimated by

$$\hat{\sigma}^2 (\hat{\psi}_0 + x_0' X' \hat{\Psi}^{-1} X)^{-1} x_0 \quad (18)$$

where  $\hat{\psi}_0$  is the scalar  $\exp(z_0' \hat{\alpha}^*)$

To test the hypothesis of homoscedastic errors versus heteroscedastic errors you simply test  $H_0: \alpha^* = 0$  against  $H_1: \alpha^* \neq 0$ . Let  $R$  be the matrix  $(Z'Z)^{-1}$  with its first row and first column removed. If the  $e_i$ 's are normally distributed then  $\hat{\alpha}^* \sim N[\alpha^*, 4.9348R]$  (Harvey 1976) and the following statistic (Judge et al. 1988, p. 370), based on the distribution of quadratic forms in normal variables, tests the above null hypothesis:

$$\frac{\hat{\alpha}^{*'} R^{-1} \hat{\alpha}^*}{4.9348} \sim \chi_{(P-1)}^2 \quad (19)$$

<sup>2</sup> Some statisticians, such as Carroll and Rupert (1988, p. 79-82), suggest that better performance can be obtained using absolute residuals over squared residuals.

Note that the numerator is the regression (or explained) sum of squares obtained when estimating  $\alpha$  and that this test is asymptotically equivalent to the  $F$  test for testing that all coefficients, except the intercept, are 0.

Gregoire and Dyer (1989) and Williams and Gregoire (1993) advocate the use of maximum likelihood (ML) with a specified error structure for fitting weighted regressions. Carroll and Ruppert (1988) discuss the increased efficiency of maximum likelihood (under normality) over generalized least squares, with increases of about 8% being common. The ML procedure requires solving for both first and second partial derivatives and results in a simultaneous system of nonlinear equations. In contrast, the EGLS estimator is simple and direct, requires no special software to implement, and is almost as efficient as ML. If iterated, the EGLS procedure converges to the ML estimates under normality.

#### 1.1.4 Biomass Additivity

A desirable feature of tree component regression equations is that the predictions for the components sum to the prediction for the total tree. Kozak (1970), Chiyenda and Kozak (1984), and Cunia and Briggs (1984, 1985a) have discussed the problem of forcing additivity on a set of tree biomass functions. The means to forcing additivity can be grouped into three different procedures depending on how the individual components are aggregated.

In procedure 1, the total biomass sample regression function is defined as the sum of the individually calculated best regression functions of the biomass of its  $k$  components:

$$\begin{aligned} \hat{y}_1 &= f_1(x_1') \\ \hat{y}_2 &= f_2(x_2') \\ &\vdots \\ \hat{y}_k &= f_k(x_k') \\ \hat{y}_{\text{total}} &= \hat{y}_1 + \hat{y}_2 + \dots + \hat{y}_k \end{aligned} \quad (20)$$

Reliability (i.e., confidence intervals) of the total biomass prediction can be determined from variance properties of linear combinations:

$$\text{Var}(\hat{y}_{\text{total}}) = \sum_{i=1}^k \text{Var}(\hat{y}_i) + 2 \sum_{i < j} \text{Cov}(\hat{y}_i, \hat{y}_j) \quad (21)$$

where

$$\begin{aligned} \text{Cov}(\hat{y}_i, \hat{y}_j) &= \rho_{y_i y_j} \sqrt{\text{Var}(\hat{y}_i) \text{Var}(\hat{y}_j)} \\ \rho_{y_i y_j} &= \text{correlation between } Y_i \text{ and } Y_j \end{aligned}$$

In procedure 2, the additivity of the components is ensured by using the same independent variables (and the same weight function) in the (weighted) least squares linear regressions of the biomass of each component and that of the total. Under this method, one can compute the regression coefficients of the total equation simply by summing the regression coefficients of the (assumed independent) component equations (the  $b_i$  vectors), that is,

$$\begin{aligned} \hat{y}_1 &= \mathbf{x}'\mathbf{b}_1 \\ \hat{y}_2 &= \mathbf{x}'\mathbf{b}_2 \\ &\vdots \\ \hat{y}_k &= \mathbf{x}'\mathbf{b}_k \\ \hat{y}_{\text{total}} &= \mathbf{x}'[\mathbf{b}_1 + \mathbf{b}_2 + \dots + \mathbf{b}_k] \end{aligned} \quad (22)$$

This result holds only under the restrictive assumption that the  $k$  components  $y_i$  ( $i = 1, \dots, k$ ) are independent, which implies that the  $\epsilon_i$  ( $i = 1, \dots, k$ ) are uncorrelated. Regression statistics and reliability of estimates can be computed for the total equation (see Chiyenda and Kozak 1984). Under independence, the variance of  $\hat{y}_{\text{total}}$  is simply the sum of the variances of the  $\hat{y}_i$ 's, the covariance terms drop out of Equation (21), thus

$$\text{Var}(\hat{y}_{\text{total}}) = \sum_{i=1}^k \text{Var}(\hat{y}_i)$$

Procedure 2 allows no flexibility for using different component equation forms. Chiyenda and Kozak (1984), however, generalized procedure 2 using restricted least squares to allow for different equation forms.

Procedure 3 is the most general and flexible method and the most difficult to employ. Statistical dependencies among sample data are accounted for using generalized least squares regression with dummy variables techniques to calculate a set of regression functions such that: (1) each component regression contains its own independent variables, and the total-tree regression is a function of all independent variables used; (2) each regression can use its own weight function; and (3) the additivity is ensured by setting constraints (i.e., linear restrictions) on the regression coefficients. The Cunia and Briggs (1984, 1985a) procedure 3 is the same as using joint-generalized least squares, also called "seemingly unrelated regressions" (SUR), for a set of contemporaneously correlated linear statistical models with cross-equation constraints. The structural equations for the system of models of biomass additivity can be specified as

$$\begin{aligned} y_1 &= f_1(X_1) + \epsilon_1 \\ y_2 &= f_2(X_2) + \epsilon_2 \\ &\vdots \\ y_k &= f_k(X_k) + \epsilon_k \\ y_{\text{total}} &= f_{\text{total}}(X_1, X_2, \dots, X_k) + \epsilon_{\text{total}} \end{aligned} \quad (23)$$

and redundant columns in  $f_{\text{total}}$  are eliminated. When the stochastic properties of the error vectors are specified, along with the linear restrictions, the structural equations become a statistical model for efficient parameter estimates and reliable prediction intervals. The procedure 3, or SUR, method is preferable to procedures 1 and 2 for several reasons. Procedure 2 requires the assumption of independence among components on the same tree, which is unrealistic. Another consideration against procedure 2 is that loading the same predictor variables in all equations

permits the very real possibility of multicollinearity. This can cause unstable parameter estimates and inflated standard errors. In fact, applying joint-generalized least squares to the set of equations in (22) is of no benefit because the covariances between the equations get concentrated out when each equation has identical explanatory variables (Srivastava and Giles 1987). Thus, it is as if the equations are independent, and the same results are obtained as when applying least squares to each equation separately. If disturbances or errors in the different equations are correlated (contemporaneous correlation), then procedure 1 [formulation in (20)] is inferior to procedure 3 [formulation in (23)] because SUR takes into account the contemporaneous correlations and results in lower variance. With the ready availability of econometric software, such as SAS/ETS® (SAS Institute Inc., SAS Campus Drive, Cary, NC 27513), complicated statistical procedures like SUR can easily be implemented. A comprehensive reference on SUR is Srivastava and Giles (1987).

### 1.1.5 Example

At this juncture, an example is in order to demonstrate equation selection, weighted analysis, equation additivity, and goodness-of-fit statistics. Consider the sample of 39 willow oak (*Quercus phellos* L.) trees in Table 1. Trees for destructive sampling were selected from 10 natural bottomland hardwood stands in Mississippi. Trees were felled, separated into components of bolewood, bole bark, and crown, and weighed in the field. The 39 trees given in Table 1 are a subset of a larger dataset from a biomass study by Schlaegel (1981), used here for illustrative purposes. Scatterplots of the data, a stepwise regression procedure, and residual analyses were used to select the following individually "best" biomass component equations:

$$\begin{aligned} \hat{Y}_{\text{wood}} &= b_0 + b_1 D^2 H \\ \hat{Y}_{\text{bark}} &= b_0 + b_1 D^2 \\ \hat{Y}_{\text{crown}} &= b_0 + b_1 \frac{D^2 H \times LCL}{1000} + b_2 H \end{aligned} \quad (24)$$

For total tree biomass, the best individual equation was

$$\hat{Y}_{\text{total}} = b_0 + b_1 D^2 H \quad (25)$$

Scatterplots of the residuals over  $D^2 H$  for  $Y_{\text{wood}}$  and  $Y_{\text{total}}$  (Figure 1A) and over  $D^2$  for  $Y_{\text{bark}}$  revealed similar fan patterns of increasing error variance. This type of heteroscedasticity is common and is usually modeled as a power function, that is,  $\sigma_i^2 = \sigma^2 X_i^k$ , where  $X$  is  $D^2 H$  or  $D^2$ . Hence, the following variance function was fitted to the OLS residuals from the bolewood, bole bark, and total biomass regressions:

$$e^2 = \exp[a_1 + a_2 \ln X]$$

or

$$\ln e^2 = a_1 + a_2 \ln X \quad (26)$$

**Table 1. Green weight data for willow oak trees from the state of Mississippi, USA.**

Tree	Dbh (cm)	Height (m)	LCL	Age (yr)	Green weight			
					Wood	Bark	Crown	Tree
1	73.2	29.0	16.2	93	4,463.4	572.9	186.4	5,222.7
2	30.5	18.3	10.4	40	550.7	83.9	44.9	679.5
3	48.3	22.9	11.9	69	1,689.2	225.0	93.4	2,007.6
4	69.6	27.4	18.3	74	3,441.5	435.5	178.3	4,055.3
5	28.7	19.8	11.6	38	482.2	75.3	45.4	602.9
6	53.1	32.0	14.9	78	2,281.6	307.5	57.2	2,646.3
7	45.7	32.0	17.7	79	1,771.3	230.4	24.9	2,026.6
8	46.5	30.5	17.4	83	1,611.6	228.2	17.2	1,857.0
9	33.8	25.9	10.1	68	861.8	122.5	20.0	1,004.3
10	55.4	30.5	13.1	70	2,952.9	367.4	65.3	3,385.6
11	30.5	24.4	9.1	75	679.9	125.2	17.7	822.8
12	70.1	30.5	13.4	81	3,867.8	546.1	79.4	4,493.3
13	41.9	24.4	12.2	79	1,289.1	185.5	36.7	1,511.3
14	42.9	25.9	13.7	76	1,495.5	201.4	71.7	1,768.6
15	66.3	35.1	17.7	81	4,091.0	413.2	99.3	4,603.5
16	40.6	25.9	11.6	64	1,264.2	175.5	12.7	1,452.4
17	28.7	21.3	9.8	75	485.8	67.6	19.1	572.5
18	80.5	32.0	17.4	93	5,782.0	657.7	186.9	6,626.6
19	66.5	33.8	16.8	106	4,085.1	524.4	112.0	4,721.5
20	61.2	29.0	17.1	71	2,621.4	225.4	82.6	2,929.4
21	21.8	25.9	11.3	35	292.6	51.7	5.0	349.3
22	29.0	24.4	8.8	35	616.4	94.3	21.8	732.5
23	49.8	27.4	16.2	35	1,757.2	220.0	63.5	2,040.7
24	34.3	27.4	10.4	37	902.2	144.7	21.8	1,068.7
25	43.2	27.4	15.5	41	1,251.5	212.3	20.9	1,484.7
26	25.1	24.4	8.8	38	437.7	63.5	6.4	507.6
27	29.7	25.9	13.7	40	704.4	89.4	10.0	803.8
28	34.8	25.9	13.1	40	906.7	117.5	23.1	1,047.3
29	38.6	27.4	13.4	41	1,309.5	148.8	26.8	1,485.1
30	49.8	22.9	14.3	40	1,497.3	160.1	49.0	1,706.4
31	36.1	25.9	16.5	34	794.3	116.6	20.9	931.8
32	37.1	21.3	11.0	67	846.9	120.7	26.8	994.4
33	33.0	21.3	9.8	67	635.5	89.8	27.7	753.0
34	57.7	25.9	18.6	84	2,545.1	371.0	70.3	2,986.4
35	53.8	25.9	12.2	87	2,275.7	359.3	32.7	2,667.7
36	57.9	27.4	10.1	89	2,822.3	379.2	61.2	3,262.7
37	75.4	27.4	13.7	91	3,782.1	579.2	61.7	4,423.0
38	57.2	25.9	12.2	86	2,055.7	362.0	45.4	2,463.1
39	69.1	27.4	14.6	87	3,618.4	498.1	87.1	4,203.6

Note: DBH is diameter breast height and LCL is live crown length.

For the crown model, variance was assumed proportional to a power of  $D^2H \times (LCL/1000)$  based on a fan pattern of increasing variance. With increasing tree height, however, variance appeared to expand then decrease (Figure 1B), suggesting a negative quadratic trend or  $\sigma_i^2 = \sigma^2 \exp[-kH_i^2]$ . Combining these two heteroscedastic trends into one multiplicative error model results in

$$\ln e^2 = a_1 + a_2 \ln \frac{D^2H \times LCL}{1000} - a_3H^2 \quad (27)$$

Table 2 gives the coefficients, weight functions, and heteroscedasticity tests [Equation (19)] from the EGLS fit of the three willow oak component biomass functions and the total tree function. As readily seen in Table 2, all the heteroscedasticity tests are significant, indicating the need for modeling the error structure. The statistics [Equations (5)–(10)] recommended by Schlaegel (1982) are shown in Table 3 for each of the four equations.<sup>3</sup> The mean percent

standard error is around 8% to 11% for the wood, bark, and total tree regressions but over 32% for the crown regression; and the fit index is lowest for the crown regression, which also has the highest coefficient of variation and percent error. All in all this shows (not surprisingly!) that crown biomass has greater variability than wood, bark, or total biomass.

Under procedure 1 for additivity, total tree biomass is simply the sum of the components. For example, using the coefficients in Table 2 and the set of equations in (24), a tree with  $D = 30$  cm,  $H = 18$  m, and  $LCL = 10$  m, gives:  $\hat{Y}_{wood} = 468.2$  kg,  $\hat{Y}_{bark} = 91.8$  kg, and  $\hat{Y}_{crown} = 43.4$  kg; therefore,

$$\hat{Y}_{total} = 468.2 + 91.8 + 43.4 = 603.4 \text{ kg}$$

The sampling error for each component prediction is computed using Equation (18), giving:  $\text{Var}(\hat{Y}_{wood}) = 2028.89$ ,  $\text{Var}(\hat{Y}_{bark}) = 221.19$ , and  $\text{Var}(\hat{Y}_{crown}) = 139.45$ . The correlations between the (weighted) biomass components are:

$$\hat{\rho}_{y_{wood}y_{bark}} = 0.26, \hat{\rho}_{y_{wood}y_{crown}} = 0.31, \text{ and } \hat{\rho}_{y_{bark}y_{crown}} = 0.14;$$

therefore, using Equation (21) we obtain

<sup>3</sup> A SAS program is available from the author for computing these statistics.

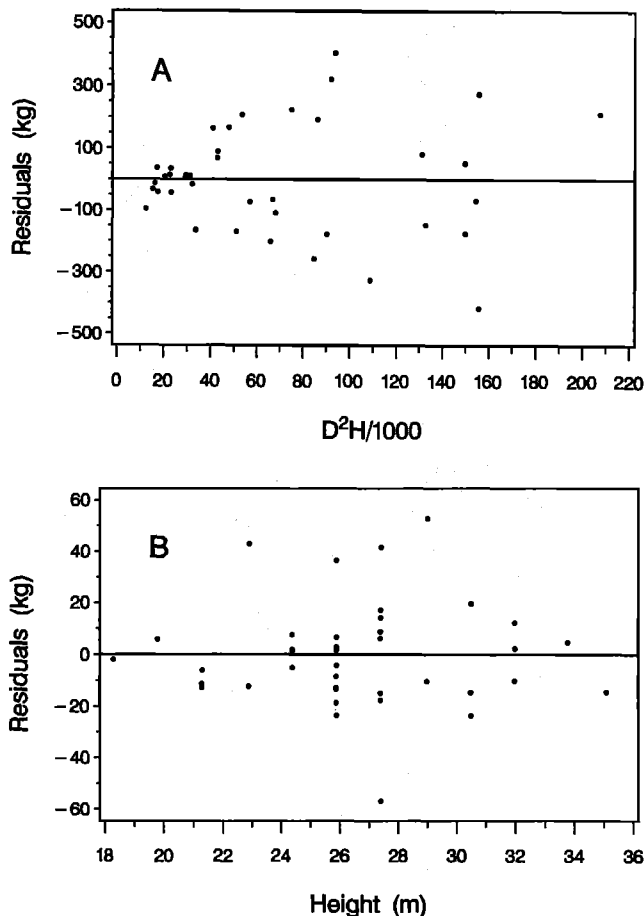


Figure 1. Scatterplots of ordinary least squares residuals from (A) total tree willow oak biomass regression showing fan pattern of increasing variance, and (B) willow oak crown biomass regression showing negative quadratic trend in variance.

$$\begin{aligned} \hat{\text{Var}}(\hat{Y}_{\text{total}}) &= 2028.89 + 221.19 + 139.45 \\ &\quad + 2 \cdot 0.26 \cdot \sqrt{2028.89 \cdot 221.19} \\ &\quad + 2 \cdot 0.31 \cdot \sqrt{2028.89 \cdot 139.45} \\ &\quad + 2 \cdot 0.14 \cdot \sqrt{221.19 \cdot 139.45} \\ &= 3116.84 \end{aligned}$$

Prediction confidence intervals are constructed as

$$\hat{Y} \pm t_{(\alpha/2)} \sqrt{\hat{\text{Var}}(\hat{Y})}$$

For an approximate 95% prediction limit, we will use  $\pm 2\sqrt{3116.84}$  giving

$$603.4 \text{ kg} \pm 111.7 \text{ kg} \quad (28)$$

From Equation (25), the best individual equation for tree biomass, we obtain an alternate value of

$$\hat{Y}_{\text{total}} = 557.6 \text{ kg with } \hat{\text{Var}}(\hat{Y}_{\text{total}}) = 2644.31;$$

hence an approximate 95% prediction interval is

$$557.6 \text{ kg} \pm 102.8 \text{ kg} \quad (29)$$

In considering the prediction intervals in (28) and (29), one can see that the price for additivity using procedure 1 is an expanded interval ( $\pm 111.7$  vs.  $\pm 102.8$ ), indicating a loss of efficiency.

Suppose we wish to consider a set of linear models whereby we allow statistical dependence among components and the total tree biomass. A set or system of linear models whose parameters are estimated by SUR with linear restrictions should result in efficient estimates and additive predictions. Reasonable equations and variance functions for the willow oak sample data are:

$$\begin{aligned} \hat{Y}_{\text{wood}} &= b_{10} + b_{11}D^2H; \\ \hat{\sigma}^2 &= (D^2H)^{1.95} \end{aligned}$$

$$\begin{aligned} \hat{Y}_{\text{bark}} &= b_{20} + b_{21}D^2H; \\ \hat{\sigma}^2 &= (D^2H)^{1.745} \end{aligned}$$

$$\begin{aligned} \hat{Y}_{\text{crown}} &= b_{30} + b_{31} \frac{D^2H \times LCL}{1000} + b_{32}H; \\ \hat{\sigma}^2 &= \left[ \frac{D^2H \times LCL}{1000} \right]^{1.646} \times \exp[-0.00406H^2] \end{aligned} \quad (30)$$

$$\begin{aligned} \hat{Y}_{\text{total}} &= b_{40} + b_{41}D^2H + b_{42} \frac{D^2H \times LCL}{1000} + b_{43}H; \\ \hat{\sigma}^2 &= (D^2H)^{1.844} \end{aligned}$$

Table 2. Coefficients, weight functions, and heteroscedasticity tests from best individual component and total tree regressions for willow oak biomass sample data ( $n = 39$ ).

Model*	$b_0$	$b_1$	$b_2$	Weight function	$\chi^2$	P
Wood	25.749477	0.027310		$(D^2H)^{1.950}$	18.1	<0.0001
Bark	-0.515317	0.102529		$(D^2)^{1.864}$	12.7	0.0004
Crown	117.195175	0.057502	-4.616870	$(D^2H \times LCL/1000)^{1.646} \times \exp[-0.00406H^2]$	9.4	0.0091
Total	46.380555	0.031558		$(D^2H)^{2.084}$	20.7	<0.0001

\* Model forms:

$$Y_{\text{wood}} = \beta_0 + \beta_1 D^2H + \epsilon, Y_{\text{bark}} = \beta_0 + \beta_1 D^2 + \epsilon,$$

$$Y_{\text{crown}} = \beta_0 + \beta_1 D^2H \times LCL/1000 + \beta_2 H + \epsilon,$$

$$Y_{\text{total}} = \beta_0 + \beta_1 D^2H + \epsilon,$$

where  $D$  is diameter breast height,  $H$  is tree height, and  $LCL$  is live crown length.



**Table 3. Goodness-of-fit statistics for the individually best willow oak component and total tree biomass equations.**

Model	FI	S <sub>e</sub>	CV	I	S̄ (%)	P <sub>e</sub>
Wood	0.98	182.32	9.50	134.83	7.47	15.76
Bark	0.94	41.01	16.08	30.48	11.00	31.19
Crown	0.81	21.15	38.67	15.33	32.15	80.32
Total	0.98	217.37	9.76	279.40	7.80	16.34

Note: FI is fit index, S<sub>e</sub> is standard error of estimate in actual biomass units, CV is coefficient of variation expressed from actual biomass units, I is Furnival's Index, S̄ (%) is mean percent standard error of predictions, and P<sub>e</sub> is percent error. See text for definitions.

where  $b_{40} = b_{10} + b_{20} + b_{30}$ ,  $b_{41} = b_{11} + b_{21}$ ,  $b_{42} = b_{31}$ , and  $b_{43} = b_{32}$ . For system parsimony, I altered the  $Y_{bark}$  equation from that used in (24). Note that a separate variance function is specified for each equation in the set. The coefficients for the variance functions were determined by regressing on the OLS residuals [Model (15)] from the four equations. A brief explanation of fitting these equations by SUR follows.

The system of four equations in (30) can be written in the usual matrix algebra notation as

$$\begin{aligned} y_1 &= X_1 \beta_1 + \epsilon_1 \\ y_2 &= X_2 \beta_2 + \epsilon_2 \\ y_3 &= X_3 \beta_3 + \epsilon_3 \\ y_4 &= X_4 \beta_4 + \epsilon_4 \end{aligned}$$

Combining all equations into one big model yields

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \\ y_4 \end{bmatrix} = \begin{bmatrix} X_1 & 0 & 0 & 0 \\ 0 & X_2 & 0 & 0 \\ 0 & 0 & X_3 & 0 \\ 0 & 0 & 0 & X_4 \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \\ \beta_3 \\ \beta_4 \end{bmatrix} + \begin{bmatrix} \epsilon_1 \\ \epsilon_2 \\ \epsilon_3 \\ \epsilon_4 \end{bmatrix} \quad (31)$$

(4T×1)                      (4T×11)                      (11×1)                      (4T×1)

or alternatively

$$y = f(\beta) = X\beta + \epsilon$$

where  $T$  is number of observations (39 for this data). The matrix of weights can be written as

$$\Psi = \begin{bmatrix} \Psi_1 & 0 & 0 & 0 \\ 0 & \Psi_2 & 0 & 0 \\ 0 & 0 & \Psi_3 & 0 \\ 0 & 0 & 0 & \Psi_4 \end{bmatrix} \quad (4T \times 4T)$$

where  $\Psi_i$  is defined as in Equation (13), and let  $\Delta = \sqrt{\Psi^{-1}}$ . The implicit assumptions for Model (31) are:  $E[\epsilon_i] = 0$  and  $E[\Delta_i \epsilon_i \Delta_j' \epsilon_j] = \sigma_{ij} I$ ;  $i, j = 1, 2, 3, 4$ , and  $I$  is a  $T$  dimensional identity matrix.

The variances and covariances of Model (31) are unknown and must be estimated. To estimate the  $\sigma_{ij}$ , we first estimate each equation by EGLS [Equation (16)] and obtain the residuals  $e_i = y_i - X_i b_i$ . Consistent estimates of the variances and covariances are then given by

$$\hat{\sigma}_{ij} = \frac{1}{(T - K_i)^{1/2} (T - K_j)^{1/2}} e_i' \hat{\Delta}_i' \hat{\Delta}_j e_j \quad (32)$$

where the degrees-of-freedom corrections  $K_i$  and  $K_j$  are the number of coefficients per equation. If we define  $\hat{\Sigma}$  as the matrix containing the estimates  $\hat{\sigma}_{ij}$  from (32), then the unrestricted SUR estimator for  $\beta$  can be written as

$$\hat{\beta} = [X' \hat{\Delta}' (\hat{\Sigma}^{-1} \otimes I) \hat{\Delta} X]^{-1} X' \hat{\Delta}' (\hat{\Sigma}^{-1} \otimes I) \hat{\Delta} y \quad (33)$$

where  $\otimes$  denotes the Kronecker or direct product. The restricted SUR estimator is obtained by minimizing  $(\hat{\Delta} y - \hat{\Delta} X \beta)' (\hat{\Sigma}^{-1} \otimes I) (\hat{\Delta} y - \hat{\Delta} X \beta)$  subject to the linear restrictions  $R\beta = r$ . It is given by

$$\hat{\beta}^* = \hat{\beta} + \hat{C}R'(R\hat{C}R')^{-1}(r - R\hat{\beta}) \quad (34)$$

where

$$\hat{C} = [X' \hat{\Delta}' (\hat{\Sigma}^{-1} \otimes I) \hat{\Delta} X]^{-1}$$

and  $\hat{\beta}$  is from (33). The linear restrictions  $b_{40} = b_{10} + b_{20} + b_{30}$ ,  $b_{41} = b_{11} + b_{21}$ ,  $b_{42} = b_{31}$ , and  $b_{43} = b_{32}$ , can be written alternatively as  $b_{10} + b_{20} + b_{30} - b_{40} = 0$ ,  $b_{11} + b_{21} - b_{41} = 0$ ,  $b_{31} - b_{42} = 0$ , and  $b_{32} - b_{43} = 0$ . Writing these restrictions in the format  $R\beta = r$  yields

$$\begin{bmatrix} 1 & 0 & 1 & 0 & 1 & 0 & 0 & -1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & -1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & -1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 1 & 0 & 0 & 0 & -1 \end{bmatrix} \begin{bmatrix} \beta_{10} \\ \beta_{11} \\ \beta_{20} \\ \beta_{21} \\ \beta_{30} \\ \beta_{31} \\ \beta_{32} \\ \beta_{40} \\ \beta_{41} \\ \beta_{42} \\ \beta_{43} \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}$$

The covariance matrix of the restricted parameter estimates is calculated as follows

$$\hat{\Sigma}_{\hat{\beta}^*} = \hat{C} - \hat{C}R'(R\hat{C}R')^{-1}R\hat{C} \quad (35)$$

One can construct the biomass tables and the associated  $(1 - \alpha)$  confidence intervals for the predicted mean value and for a predicted value of an individual (new) outcome by the formulas:

$$\hat{y} = \mathbf{x}_i \hat{\beta}^* \quad (36a)$$

= biomass estimate from *i*th system equation

$$\hat{y} \pm t_{(\alpha/2)} \sqrt{S_y^2} = \text{mean value confidence limits} \quad (36b)$$

$$\hat{y} \pm t_{(\alpha/2)} \sqrt{S_y^2 + \hat{\sigma}_{ii}^2 \hat{\psi}} = \text{confidence limits} \quad (36c)$$

for an individual prediction

where  $\mathbf{x}_i$  is the vector for the *i*th system equation,  $S_y^2 = \mathbf{x}_i' \hat{\Sigma}_{\beta} \mathbf{x}_i$  = variance of  $\hat{y}$ ,  $\hat{\sigma}^2$  is the estimated variance of Model (31) (i.e.,  $\mathbf{e}' \hat{\Delta}' (\hat{\Sigma}^{-1} \otimes I) \hat{\Delta} \mathbf{e} / df_{\text{error}}$ ), and  $\hat{\sigma}_{ii}^2 \hat{\psi}$  is the estimate of the conditional variance of the *i*th system equation [ $\hat{\sigma}_{ii}^2$  is the *i*, *i*th element of  $\hat{\Sigma}$  re Equation (32) and  $\hat{\psi}$  is the estimated weight]. Table 4 gives coefficients and their standard errors from the unweighted (each  $\psi \equiv 1$ ) restricted SUR fit (RSUR) and the weighted restricted SUR fit (WRSUR).<sup>4</sup> Note how weighting reduces the majority of standard errors, dramatically for some (three of the coefficients had standard errors reduced in excess of 50%), and hence achieves more efficient parameter estimates.

Using the coefficients in Table 4, if  $D = 30$  cm,  $H = 18$  m,  $LCL = 10$  m, and  $i = 4$  (total biomass), we have from (36a):

$$\mathbf{x}'_4 = [0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 1 \ 16200 \ 162 \ 18]$$

and

$$\hat{y} = \hat{\beta}_{40}^* + 16200 \hat{\beta}_{41}^* + 162 \hat{\beta}_{42}^* + 18 \hat{\beta}_{43}^* = 583.8 \text{ kg}$$

The prediction limits for this point estimate can be calculated from (36c). For this example we have

$$S_y^2 = 279.895, \hat{\sigma}^2 = 0.832,$$

$$\hat{\sigma}_{44} = 3.99 \times 10^{-5}, \text{ and}$$

$$\psi = 57855638,$$

for an approximate 95% prediction interval ( $t = 2$ ) of

$$583.8 \text{ kg} \pm 93.8 \text{ kg} \quad (37)$$

The SUR prediction interval on  $\hat{Y}_{\text{total}}$  in (37) is narrower than the least squares prediction interval on  $\hat{Y}_{\text{total}}$  in (29). One might expect the individually best regression on  $\hat{Y}_{\text{total}}$  to have the smallest variance, because it is the best estimator that is a linear unbiased function of  $\mathbf{y}_{\text{total}}$ . However, because of the existence of contemporaneous correlations, it is possible to obtain a better linear unbiased estimator that is a function of  $\mathbf{y}_{\text{wood}}$ ,  $\mathbf{y}_{\text{bark}}$ ,  $\mathbf{y}_{\text{crown}}$ , and  $\mathbf{y}_{\text{total}}$ . Thus, even under the constraint of additivity, the SUR estimator can achieve lower variance and be a more efficient estimator. Clearly, procedure 3, the SUR estimator, is the method of choice for additivity.

### 1.1.6 Bole Biomass and Harmonization

Often the biomass of chief interest is just the tree bole, particularly for dry weight yield. What is frequently needed is a means to predict bole biomass for different merchantability limits. For example, bole biomass components can be defined in the following nested fashion. The first component, the entire bole, contains in its entirety the second component, the bole to a 10 cm top diameter, which in turn contains the entire third component, the tree bole up to a 15 cm top, and so on. When calculating a separate regression function for each component, the problem that usually arises is that the regression lines may cross each other; consequently, the estimate of the biomass of a nested component may exceed that of the next larger component. The process of forcing several simultaneous regressions to behave logically with respect to each other is known as *harmonization*. Jacobs and Cunia (1980) and Cunia and Briggs (1985b) solved the intersection problem by (1) using the same model form for all components and (2) making all regressions parallel by restricting the slopes to be identical. Further, they controlled the spacing between consecutive regressions to follow a reasonable pattern. They reasoned that the difference between the inter-

<sup>4</sup> A SAS/IML and a GAUSS matrix language program are available from the author for fitting Model (31).

**Table 4. Results from fitting the willow oak data with seemingly unrelated regressions.**

	RSUR		WRSUR		Reduction in SE <sup>a</sup> (%)
	Estimate	SE	Estimate	SE	
$\beta_{10}$	59.186526	48.243531	29.634908	19.354063	60
$\beta_{11}$	0.026598	0.000558	0.027190	0.000587	-5
$\beta_{20}$	29.651015	10.383880	17.612412	4.406701	58
$\beta_{21}$	0.003225	0.000120	0.003435	0.000124	-3
$\beta_{30}$	133.106587	26.624556	106.065804	17.471978	34
$\beta_{31}$	0.061543	0.005081	0.056544	0.004325	15
$\beta_{32}$	-5.336039	1.114125	-4.153695	0.730026	34
$\beta_{40}$	221.944128	62.183373	153.313124	28.802732	54
$\beta_{41}$	0.029824	0.000623	0.030624	0.000643	-3
$\beta_{42}$	0.061543	0.005081	0.056544	0.004325	15
$\beta_{43}$	-5.336039	1.114125	-4.153695	0.730026	34

NOTE: RSUR is restricted seemingly unrelated regressions, and WRSUR is weighted restricted seemingly unrelated regressions.

<sup>a</sup> Computed as  $[\text{std err}(\text{RSUR}) - \text{std err}(\text{WRSUR})] / \text{std err}(\text{RSUR}) \times 100$ .

cepts is a function of both squared log (that is, top diameters and the length of the log, which is a function of top diameter. Hence, the intercepts of the various regressions should be related as

$$\beta_{i0} = \alpha_0 + \alpha_1 z_i + \alpha_2 z_i^2 \quad (38)$$

where  $z_i$  is the top diameter of the  $i$ th component. Cunia and Briggs (1985b) recognized that the harmonized regression functions were serially correlated because the various components were not independent, being measured on the same trees. As with the additivity problem, Cunia and Briggs put forth a procedure that allowed the estimation of the covariance matrix of the sample biomass values and circumvented the problem of storing and inverting large covariance matrices. They constructed a giant size regression with dummy variables that contained all of the individual component regressions, and they estimated the parameters with generalized least squares. Again, as with the additivity problem, their procedure is equivalent to using joint-generalized least squares with cross-equation constraints. With the proper software, such as the GAUSS™ matrix language (Aptech Systems, Inc., 23804 S.E. Kent-Kangley Road, Maple Valley, WA 98038), SUR is easy to implement.

Though the harmonization technique solves the intersection problem of nested component bole regressions and logically spaces the intercepts, it is based on assumptions of parallelism and precise spacing between consecutive regressions, assumptions which may or may not be true for any particular tree population. Another drawback is that each standard of utilization requires another equation to be added to the set of regressions. Two techniques that do not require these assumptions and minimize the number of equations are (1) the weight-ratio approach and (2) the density-integral approach. Both approaches provide a system to calculate total bole biomass and merchantable bole biomass to any standard of utilization expressed as a function of stump height, and of top diameter or section height.

#### 1.1.7 Weight-Ratio Approach

To circumvent the equation cross-over problem, Honer (1964) devised a two-step method to calculate merchantable volume to any utilization specification. First, he developed an equation to predict total tree volume. Second, he developed an equation to predict the proportion or ratio of merchantable volume to total volume given the merchantability limits. When attention shifted to estimating tree biomass, it was natural to apply the ratio approach thus avoiding similar problems encountered in tree volume estimation (Williams 1982).

The weight-ratio approach uses the following relationship:

$$\hat{w} = \hat{R}\hat{W} \quad (39)$$

where  $w$  is merchantable weight,  $W$  is total weight, and  $R$  is  $w/W$ . Interested persons may refer to Honer (1964), Burkhart (1977), and Van Deusen et al. (1981) for the early developmental work on the ratio approach. Parresol et al. (1987)

reviewed a number of ratio models from the forestry literature. Parresol and Thomas (1989) compared the density-integral approach against the weight-ratio approach and concluded that the density-integral approach gave more precise estimates of sectional and total bole weight.

#### 1.1.8 Density-Integral Approach

Parresol and Thomas (1989) introduced the density-integral methodology. The generalized density-integral model for stem biomass is

$$w = H \int_{x_l}^{x_u} \rho(x) f(x) dx + \epsilon \quad (40)$$

where  $H$  is total tree height,  $x$  is relative height,  $\rho(x)$  is a function giving density or stem specific gravity at  $x$ ,  $f(x)$  is an equation expressing stem profile in cross-sectional area as a function of  $x$ ,  $w$  is bole dry mass of wood between limits  $x_l$  and  $x_u$ , and  $\epsilon$  is stochastic error. For a specific biomass model, one needs to define  $\rho$  and  $f$ . See Tasissa and Burkhart (1998) for recent work on modeling specific gravity and Maguire and Batista (1996) for a review of taper models. For the derivation of the generalized density-integral model and examples of its use see the articles by Parresol and Thomas (1989, 1996), and Thomas et al. (1995).

One could fit stem profile [ $f(x)$ ] and density [ $\rho(x)$ ] independently and place them into Model (40) for prediction of biomass. However, as with the additivity problem and the harmonization problem, it is important to recognize that the data for stem profile (i.e., volume), density, and mass are not independent, coming from the same trees. One would expect mass, density, and volume to be correlated at the same measurement bolt on the tree. This contemporaneous correlation, if not accounted for, leads to inefficient estimates of the parameters. In addition, observed stem mass should be incorporated into the fitting process. Joint-generalized least squares or SUR, as previously outlined, takes into account contemporaneous correlations and leads to efficient estimates. Parresol and Thomas (1996) showed that parameter estimates ( $\hat{\beta}_i$ 's) from SUR estimation of the simultaneous equations from the density integral had smaller standard errors than from OLS estimation of  $f(x)$  and  $\rho(x)$ .

#### 1.2 Sampling on the Tree

The process of physically collecting biomass data can be very labor intensive. In short rotation woody biomass programs, trees usually do not attain large sizes, and field weighing of the entire tree to measure fresh weight is not overly difficult. The various tree components, as determined by the scheme used, can be measured directly as soon as they are separated from the tree. The only possible error may be due to faulty measurement instruments or methods. However, if biomass expressed as dry weight is required, direct measurement may be too expensive and time consuming for the larger components such as the bole. The only practical alternative is subsampling. Small samples are selected from the tree component by some usually random procedure. Green and oven-dry weights of these samples are determined in the laboratory and the results are used to estimate the entire tree component. Note that the "measurement" of biomass is

defined as the process of direct determination of the biomass of the entire tree component of interest, whereas the "estimation" of biomass is defined as the process of determination of the biomass by subsampling.

### 1.2.1 Ratio-Type Estimators

Briggs et al. (1987) described a procedure they used to measure the green weight and to estimate, by subsampling, the dry weight of the aboveground components of randomly selected sugar maple (*Acer saccharum* Marsh.) trees. Foliage and branch dry weights were determined by direct measurement. Bole wood and bole bark dry weight were estimated by stratified subsampling and subsequent application of ratio-type estimators. A brief description of their procedure follows. After measurement of diameter and total height, each tree was felled, and ten plastic sheets were placed on the ground surrounding the tree. Beginning at the base of the crown and working towards the top, the tree branches with their leaves attached were removed and separated into ten piles such that each pile had a similar distribution of branches and foliage with respect to weight and point of origin from the crown. For each of the ten piles, all of the foliage was picked from the branches and placed in paper bags. Foliage and branches were weighed for green weight and then sent to a laboratory for oven drying and direct measurement of dry weight. The bole of each sample tree was divided into three sections of equal length. For each section, three integers were randomly selected from 1 to 100. Each of these numbers was multiplied (as a decimal number) by the section length to obtain the location of a sample disk for the determination of the

fresh and dry weight. For example, if the random number was 24 and the section length was 5.0 m, then a disk would be located at  $0.24 \times 5.0 = 1.2$  m from the base of that section. Each of the three bole sections was cut into logs of various lengths and weighed on a 90 kg capacity field scale. Disks approximately 5 cm in width were removed from the bole at the randomly selected locations, weighed, and transported to the laboratory. Foliage, branches, and disks were placed in forced air kilns at 65°C until constant weights were obtained. The oven-dry weight was determined individually for each pile of branches and foliage, as well as for each disk of each individual sample tree. The bark was removed from each disk, dried at 65°C, and its weight was recorded.

The three bole sections can be considered as strata, and three disks are selected at random from each section, hence the method of disk selection is stratified random sampling. Because the green weight of the entire bole, individual sections, and disks are known, and the oven-dry weights of the sample disks are measured, one can estimate oven-dry weight of the bole by a stratified ratio estimator. Notation and definitions for the ratio estimator are shown in Exhibit A.

Because the  $D_h$ 's are independent random variables, the oven-dry weight of the bole and its error can be estimated by

$$\begin{aligned}
 D &= \Sigma D_h = \text{stratified ratio estimator of the dry weight of} \\
 &\quad \text{wood and bark of the bole} \\
 B &= \Sigma B_h = \text{estimator of the bias of } D \\
 S_D^2 &= \Sigma S_{D_h}^2 = \text{estimator of the variance of } D
 \end{aligned}
 \tag{42}$$

#### Exhibit A

$$\begin{aligned}
 G_h &= \text{green weight of section } h \\
 g_{hk} &= \text{green weight of wood and bark of disk } k \text{ in stratum } h \\
 d_{hk} &= \text{oven-dry weight of wood and bark of disk } k \text{ in stratum } h \\
 m_h &= 3 = \text{number of sample disks per strata} \\
 \bar{g}_h &= \Sigma g_{hk} / m_h \\
 \bar{d}_h &= \Sigma d_{hk} / m_h \\
 M_h &= G_h / \bar{g}_h = \text{conceptual number of disks of weight } \bar{g}_h \text{ in section } h \\
 \frac{M_h - m_h}{M_h} &= \text{finite population correction factor of section } h \\
 S_{d_h}^2 &= \Sigma (d_{hk} - \bar{d}_h)^2 / (m_h - 1) = \text{sample variance of the } m_h \text{ dry disk values within section } h \\
 S_{g_h}^2 &= \Sigma (g_{hk} - \bar{g}_h)^2 / (m_h - 1) = \text{sample variance of the } m_h \text{ green disk values within section } h \\
 S_{d_h g_h} &= \Sigma (d_{hk} - \bar{d}_h)(g_{hk} - \bar{g}_h) / (m_h - 1) = \text{sample covariance} \\
 r_h &= \bar{d}_h / \bar{g}_h = \text{ratio estimator of oven-dry weight to green weight of section } h \\
 D_h &= G_h r_h = M_h \bar{d}_h = \text{ratio estimator of oven-dry weight of section } h \\
 B_h &= (M_h - m_h)(r_h S_{g_h}^2 - S_{d_h g_h}) / (m_h \bar{g}_h) = \text{estimator of the bias of } D_h \\
 S_{D_h}^2 &= M_h (M_h - m_h) (S_{d_h}^2 - 2r_h S_{d_h g_h} + r_h^2 S_{g_h}^2) / m_h = \text{estimator of the variance of } D_h
 \end{aligned}
 \tag{41}$$

**Table 5. Morphological data for the four example sweetgum trees.**

Tree	Dbh (cm)	Total height (m)	Bole length (m)	Green weight of bole (wood + bark) (kg)			
				Bottom	Middle	Top	Total
1	15.5	14.6	13.5	57.5	25.2	7.6	90.3
2	33.0	24.7	24.0	435.1	162.8	24.0	621.9
3	48.8	29.9	28.4	1,447.1	805.5	92.5	2,345.1
4	67.8	34.4	29.8	2,785.0	1,707.8	403.3	4,896.1

Note: The strata (bottom, middle, top) are of equal length, being 1/3 x bole length.

If we define  $d_{hk,w}$  = oven-dry weight of wood of disk  $k$  in stratum  $h$ , and  $d_{hk,b}$  = oven-dry weight of bark of disk  $k$  in stratum  $h$ , and if these values are substituted for  $d_{hk}$  in (41), then one can define the estimators  $D_w$  and  $D_b$ , the stratified ratio estimators of the oven-dry weight of wood and bark, respectively, of the tree bole, as well as the corresponding estimators of their errors. Briggs et al. (1987) give examples of calculations for three sugar maple trees. Tables 5 and 6 present morphological data and disk weights from four sweetgum (*Liquidambar styraciflua* L.) trees from a stand in west-central Mississippi. Tables 7 and 8 show the calculations for the stratified ratio estimator. These trees are part of a larger dataset that was used to develop weight tables for sweetgum (Schlaegel 1984).

Kleinn and Pelz (1987) in Germany estimated both green and dry weight of the bole including bark by simple ratio estimates of volume/green weight and green weight/dry weight on the basis of five disks that were selected with a probability proportional to estimated volume. That is, random numbers between 0 and 1 were drawn, and proportional cumulative volumes up the stem were estimated and disks removed from the tree at these points. For example, say 0.333 is randomly drawn, then a disk is removed at the point on the stem where it is estimated one-third cumulative volume occurs. For crown green and dry weight, a few branches were selected and weighed and a regression of the form

$$\hat{W} = b_0 + b_1 D^2 L \quad (43)$$

was fitted, where  $W$  is branch weight,  $D$  is branch base diameter, and  $L$  is branch length. All branches on the tree were subsequently measured for  $D$  and  $L$ , then weights were estimated and summed for total crown weight. Branches were chosen for weighing as follows. Within the crown of the tree, five locations along the main stem were determined randomly with a probability proportional to stem diameter. For each location the nearest (unselected) node of branches was selected, and from this node a branch was randomly chosen for measurement. Error of estimates can be determined based on formulas given earlier for ratio estimators and regression variance.

Valentine et al. (1984), as well as Cunia (1979), point out the well-known fact that ratio estimators are biased. Indeed, Briggs et al. (1987) acknowledge this but argue that in their procedure, bole biomass is based on nine disks, so bias is expected to be negligible. Ratio-type estimators have the advantage of being simple to understand and apply. However, efficient, unbiased techniques are available which typically involve only two to four sample disks. These will be discussed next.

### 1.2.2 Randomized Branch and Importance Sampling

Valentine et al. (1984) and Gregoire et al. (1995b) describe two procedures, randomized branch sampling (RBS) and importance sampling, for selecting sample paths to obtain unbiased estimates of the biomass content of the tree. A sample path—from which bole disks, crown branches, and foliage are selected—extends from the butt to a terminal bud and has selection probabilities associated with it. The path is

**Table 6. Green and dry weights of the three randomly selected disks per stratum for the four example sweetgum trees.**

Tree	Stratum	Disk 1 location <sup>a</sup> (m)	Disk 1		Disk 2 location (m)	Disk 2		Disk 3 location (m)	Disk 3	
			$g_{h1}$	$d_{h1}$		$g_{h2}$	$d_{h2}$		$g_{h3}$	$d_{h3}$
			(kg)		(kg)		(kg)		(kg)	
1	Bottom	2.0	0.586	0.269	2.6	0.540	0.258	3.6	0.461	0.238
1	Middle	2.2	0.280	0.133	2.4	0.271	0.129	2.9	0.246	0.119
1	Top	0.0	0.176	0.095	2.4	0.081	0.028	4.3	0.012	0.009
2	Bottom	3.1	2.408	1.083	3.5	2.286	1.008	6.4	1.832	0.810
2	Middle	4.5	1.018	0.470	4.9	0.888	0.431	5.7	0.720	0.341
2	Top	1.0	0.325	0.139	6.2	0.036	0.016	7.0	0.020	0.015
3	Bottom	3.0	8.157	3.444	3.2	8.092	3.426	9.2	6.000	2.670
3	Middle	2.7	5.744	2.754	4.4	5.287	2.395	5.6	4.160	1.938
3	Top	1.5	0.998	0.499	2.2	0.815	0.410	3.5	0.545	0.259
4	Bottom	4.7	13.254	6.162	7.5	12.554	6.003	8.0	12.251	5.828
4	Middle	2.0	9.995	4.693	6.0	8.192	3.902	7.4	7.149	3.544
4	Top	1.2	4.399	2.355	2.6	3.045	1.639	9.8	0.601	0.299

Note:  $g_{hk}$  is the green weight of disk  $k$  in stratum  $h$  and  $d_{hk}$  is the dry weight of disk  $k$  in stratum  $h$ . Each disk is approximately 5 cm thick.

<sup>a</sup> Within a stratum, the base of a disk was randomly located by generating a uniform random (0,1) number and multiplying it by the stratum length.

**Table 7. Statistics associated with the estimation of the bole oven-dry weight for the three sections of the four example sweetgum trees.**

Stratum	$\bar{d}_h$	$\bar{g}_h$	$S_{d_h}^2$	$S_{d_h g_h}$	$S_{g_h}^2$	$r_h$	$D_h$	$B_h$	$S_{D_h}^2$
	(kg)		(kg <sup>2</sup> )				(kg)		(kg <sup>2</sup> )
Tree 1									
Bottom	0.255	0.529	0.00025	0.00099	0.00400	0.482	27.72	0.062	0.8346
Middle	0.127	0.266	0.00005	0.00013	0.00031	0.478	12.05	0.002	0.0043
Top	0.044	0.090	0.00204	0.00363	0.00678	0.491	3.73	-0.092	0.2567
Tree 2									
Bottom	0.967	2.175	0.01989	0.04271	0.09213	0.445	193.41	-0.053	1.6051
Middle	0.414	0.875	0.00438	0.00977	0.02232	0.473	77.00	0.055	1.4357
Top	0.057	0.127	0.00508	0.01223	0.02947	0.446	10.71	0.448	0.4281
Tree 3									
Bottom	3.180	7.416	0.19516	0.54204	1.50556	0.429	620.49	0.894	89.0315
Middle	2.362	5.064	0.16726	0.32861	0.66467	0.467	375.79	-0.190	44.0265
Top	0.389	0.786	0.01472	0.02763	0.05193	0.495	45.82	-0.093	0.4082
Tree 4									
Bottom	5.998	12.686	0.02791	0.08322	0.26464	0.473	1,316.65	0.238	132.6241
Middle	4.046	8.445	0.34567	0.84494	2.07306	0.479	818.24	1.166	159.8811
Top	1.431	2.682	1.08923	2.00885	3.70521	0.534	215.21	-0.580	2.6900

NOTE:  $\bar{d}_h$  is mean dry disk weight of stratum  $h$ ,  $\bar{g}_h$  is mean wet disk weight of stratum  $h$ ,  $S_{d_h}^2$  is the variance of  $d_h$ ,  $S_{d_h g_h}$  is the covariance,  $S_{g_h}^2$  is the variance of  $g_h$ ,  $r_h$  is the ratio estimator of dry to green weight of stratum  $h$ ,  $D_h$  is ratio estimator of dry weight of stratum  $h$ ,  $B_h$  is the bias of  $D_h$ , and  $S_{D_h}^2$  is the variance of  $D_h$ . See text for details.

a series of connected branch segments or internodes, where a branch is defined as the entire stem system that develops from a single bud. A segment is a part of a branch between two consecutive nodes. The butt, by definition, is the first node and has selection probability  $q_1 = 1$ . The second node occurs at the point of live tree limbs. To continue the path, a selection probability is assigned to each branch emanating from the second node, and one is chosen at random. Valentine et al. suggest assigning a selection probability as the product of the squared diameter and length for a branch, divided by the sum of these products for all branches at the node. The second segment of the path has selection probability  $q_2$ . The path continues to the next node, where a branch is selected by RBS with probability  $q_3$  and so on until a terminal shoot is reached with probability  $q_n$ . The  $q_i$ 's are conditional probabilities. The unconditional probability of selection for the  $k$ th segment in the path is

$$Q_k = \prod_{r=1}^k q_r \quad (44)$$

All material that is not part of the path can be discarded. This is a big advantage of RBS; as a result, researchers can significantly reduce project time and labor costs. Aboveground

**Table 8. Summary statistics for the four example sweetgum trees.**

Tree	$D$	Bias	$S_D^2$	95% Confidence limits	
				Lower	Upper
	(kg)		(kg <sup>2</sup> )	(kg)	(kg)
1	43.49	-0.027	1.0957	41.40	45.58
2	281.12	0.449	3.4689	277.40	284.84
3	1,042.10	0.611	133.4661	1,018.99	1,065.21
4	2,350.11	0.824	295.1952	2,315.75	2,384.47

NOTE:  $D$  is the stratified ratio estimate of the bole dry weight (wood + bark) and  $S_D^2$  is the estimate of the variance of  $D$  used for constructing confidence intervals.

biomass can be estimated from a single path, but two or more paths are needed to compute a standard error of the estimate. Estimation of the green weight of the tree involves the weights of each of the  $n$  segments of the path. Denote the weight of the  $k$ th segment as  $b_k$ , then an unbiased estimate of tree weight is

$$\hat{b} = \sum_{k=1}^n \frac{b_k}{Q_k} \quad (45)$$

where  $Q_k$  is defined in Equation (44). For an unbiased estimate of green foliage weight,  $\hat{f}$ , substitute  $f_k$  for  $b_k$  in Equation (45), where  $f_k$  is the weight of the foliage attached to the  $k$ th segment.

Valentine et al. (1984) developed a procedure based on importance sampling (a technique of Monte Carlo integration) for selecting disks that produces unbiased estimates of dry weight. To begin, each segment in the selected path is enlarged by the inflation factor  $1/Q_k$ , so the enlarged stem represents the entire tree. Visualize the inflated path as being composed of thin disks of constant thickness and known volume. One of these disks is selected at random with probability proportional to its volume. If the dry weight of that inflated disk is measured and divided by its selection probability, the result is an unbiased estimate of the dry weight of the tree.

In practice, Valentine et al. (1984) used a continuous (segmented linear) interpolation function to predict the cross-sectional area (volume per unit length) of all points along the path. They measured diameter at numerous points along the path for this purpose. Denote the diameter of the stem at a distance  $L_s$  from the butt as  $D(L_s)$ , and define a quantity proportional to the inflated cross-sectional area as

$$A(L_s) = D(L_s)^2 / Q_k \quad (46)$$

Now the interpolation function,  $S(L)$ , is fitted to the values  $A(L_s)$  and integrated over the length,  $\lambda$ , of the path to approxi-

mate the inflated woody volume of the path, that is,

$$V(\lambda) = \int_0^\lambda S(L)dL \quad (47)$$

A point,  $\theta$ , for cutting a disk is randomly selected with probability proportional to  $S(L)$ . The point is chosen which satisfies  $V(\theta) = uV(\lambda)$ , where  $u$  is a random number from a uniform (0,1) distribution. Next, determine the dry weight per unit thickness (Valentine et al. used 10-cm-thick disks) of the disk cut at  $L = \theta$  as  $B(\theta)$ . The inflated weight per unit thickness of the disk is

$$B^*(\theta) = B(\theta) / Q_k \quad (48)$$

where  $k$  is the index of the path segment in which  $\theta$  occurs. Finally, the unbiased estimate of the true woody dry weight of the tree is computed as

$$\hat{w} = B^*(\theta)V(\lambda) / S(\theta) \quad (49)$$

If multiple paths are selected on the tree from RBS, obtain a disk from each path and use Equation (49) to compute an estimate from each disk, then average the estimates to produce one combined estimate. For further details and examples on RBS and importance sampling, see the papers by Valentine and Hilton (1977), Valentine et al. (1984), Gregoire et al. (1986), de Gier (1989), and Gregoire et al. (1995b).

### 1.2.3 Bole Mass by Difference Sampling

This section describes an innovative technique for obtaining an unbiased estimate of tree bole biomass. Gregoire et al. (1986) showed how to unbiasedly estimate bole volume by importance sampling. Van Deusen and Baldwin (1993) used importance sampling in conjunction with the density-integral concept of Parresol and Thomas (1989) to obtain an unbiased estimate of tree bole dry mass. The procedure requires obtaining increment cores at breast height and another randomly selected height. The specific gravity of the cores and their associated cross-sectional areas are then used to unbiasedly estimate bole mass.

In the density-integral model the bole woody mass to some height  $h$  is

$$w(h) = \int_0^h \rho(x)a(x) dx \quad (50)$$

where  $a(x)$  is the cross-sectional area at height  $x$ . If  $dx$  represents disk thickness, then  $a(x) dx$  is volume, and volume times density yields mass. Thus  $\rho(x)$  is the ratio of mass to volume. Taking the derivative with respect to  $h$  and rearranging gives

$$\rho(h) = w'(h) / a(h) \quad (51)$$

A reasonable function for  $\rho(h)$  depends on the properties of  $w(h)$  and the volume function,  $v(h)$ , which is the integral of  $a(h)$ . Both functions increase monotonically up the stem starting from 0 at the base and going to total woody mass  $W$ , and total volume  $V$ , at total height  $H$ . For volume to height  $h$ , Van Deusen and Baldwin (1993) used

$$v(h) = V - V \left( \frac{H-h}{H-k} \right)^\alpha \quad (52)$$

where  $k$  is stump height. Differentiating Equation (52) gives

$$a(h) = \alpha V (H-h)^{\alpha-1} (H-k)^{-\alpha} \quad (53)$$

Using the same functional form for mass gives

$$\hat{w}'(h) = \beta W (H-h)^{\beta-1} (H-k)^{-\beta} \quad (54)$$

Dividing Equation (54) by Equation (53), as indicated in Equation (51), and simplifying results in

$$\hat{\rho}(h) = \frac{W\beta}{V\alpha} (H-h)^{\beta-\alpha} (H-k)^{\alpha-\beta} \quad (55)$$

It should be pointed out that any function that gives volume to some height  $h$ , as does Equation (52), can be used for approximating  $\rho(h)$ .

Importance sampling is used for estimating the value of any definite integral. Since Equation (50) (the density-integral model) describes bole woody mass as a definite integral, a sampling scheme that utilizes the above equations can be developed. Van Deusen and Baldwin (1993) devised a scheme to estimate the difference between the model and actual bole biomass. This approach, called "difference sampling," combines importance sampling and control variate methods. The desired difference can be written as

$$w(h) - \hat{w}(h) = \int_0^h \frac{w'(x) - \hat{w}'(x)}{f(x)} f(x) dx \quad (56)$$

where  $f(x)$  is a probability density function (PDF). Equation (56) conveys that we can draw a height,  $X_i$ , from the PDF,  $f(x)$ , and measure  $w'(X_i)$  to contrast with the model-based estimate  $\hat{w}'(X_i)$  for an unbiased estimate of the difference,  $w(h) - \hat{w}(h)$ . Hence, a procedure based on difference sampling for obtaining unbiased estimates of bole mass would use

$$W_D(h) = \hat{w}(h) + \frac{1}{n} \sum_{i=1}^n \frac{w'(X_i) - \hat{w}'(X_i)}{f(X_i)} \quad (57)$$

A PDF should be chosen that will lead to most of the measurements being low on the stem, where much of the wood mass occurs and where measurement cost is low. Define  $r = (h-x)/h$ , the relative distance from the upper height limit of interest on the bole. Note that total height  $H$  is just a special case. A simple cumulative density function (CDF) for  $r$  is

$$F(r) = r^\gamma, \quad 0 \leq r \leq 1 \quad (58)$$

Using the inverse transform method, a random height in terms of  $x$  is drawn as

$$X_i = h(1 - u_i^{1/\gamma}) \quad (59)$$

where  $u_i$  is a uniform random variate,  $u_i \sim U(0,1)$ . Differentiating (58) gives the PDF in terms of  $x$  as

$$f(x) = \gamma r^{\gamma-1} = \gamma \left( \frac{h-x}{h} \right)^{\gamma-1} \quad (60)$$

Substituting (60) into Equation (57) yields the suggested difference sampling formula

$$W_D(h) = \hat{w}(h) + \frac{h^{\gamma-1}}{\gamma n} \sum_{i=1}^n \frac{w'(X_i) - \hat{w}'(X_i)}{(h - X_i)^{\gamma-1}} \quad (61)$$

To implement the procedure defined by (61), first recall that Equation (54) provides a model for  $\hat{w}'(h)$ , and Equation (52) gives a model for  $\hat{w}(h)$  after changing the  $v$ 's to  $w$ 's. Second, generate a uniform random variate,  $u_i$ , and substitute this into Equation (59) to generate a measurement height,  $X_i$ . Third, measure the cross-sectional area,  $a(X_i)$ , on the tree and take a core to obtain  $\rho(X_i)$  since  $w'(X_i) = \rho(X_i)a(X_i)$ . The  $\gamma$ -parameter in Equation (59) influences the probability of where  $X_i$  occurs on the bole. Based on simulations, Van Deusen and Baldwin (1993) showed that a value of  $\gamma = 3$  kept measurement heights low (nearly 90% of the time less than half tree height, and 60% of the time less than one-quarter tree height) while minimizing poor predictions on individual trees.

The only remaining element needed is an estimate of total woody mass  $W$  for use in Equations (52) and (54). Note that one can easily obtain  $w'(1.3)$  by taking a core at breast height to determine density and then by multiplying this density by the measured basal area  $a(1.3)$ . The following equation is derived from Equation (54) by letting  $h = 1.3$  m and rearranging terms:

$$\hat{W} = w'(1.3)(H - 1.3)^{1-\beta} \frac{(H - k)^\beta}{\beta} \quad (62)$$

If this estimate of  $W$  is used, then  $\hat{w}'(h)$  is constrained to predict the measured value at 1.3 m regardless of  $\beta$ .

Difference sampling can be used to provide an unbiased estimate of the biomass of a stand of trees. The procedure can be applied to each tree on a sample plot to give an unbiased estimate of the plot mass. These plot-mass estimates can then be used in the usual way to produce sample estimates of stand biomass. To illustrate the above procedure, consider again the 39 willow oak trees in Table 2. Let us estimate the total bole woody mass, excluding bark, of each tree (above stump), hence  $h = H$ . One random height only will be drawn ( $n = 1$ ), and we will set  $\gamma = 3$ ,  $\beta = 3$ , and  $k = 0.5$  in the formulas. In the willow oak dataset, a measure of specific gravity occurs every 1.5 m along the stem, so the random height will be adjusted to the nearest height where cross-sectional area and specific gravity measurements were recorded. Also,  $w'(1.5)$  will be used instead of  $w'(1.3)$  to determine  $\hat{W}$  of Equation (62). Results are given in Table 9. The total woody mass for the 39 trees is 40,987 kg, whereas the difference sampling estimate is 39,099 kg, a difference of only 4.6%. In this example, only one random height per tree was drawn, but in practice usually two to four random heights may be drawn and measurements taken at those points along the bole. This, of course, should improve the accuracy and precision of  $W_D(h)$ .

## 2 The Error of Forest Biomass Inventory Estimates

Historically, attempts have been made to estimate forest biomass using "mean tree" techniques. For example, the weight of the tree of average girth would be determined and multiplied by the number of trees (Attiwill and Ovington 1968). This generally proved unsatisfactory and today large-scale inventories based on sound statistical designs are in place in many parts of the world. Most sampling designs of forest inventory consist of two principal phases. In the first phase, a relatively large sample of trees is selected, and the trees are measured for diameter, height, and possibly other characteristics. The sample trees are usually in clusters defined in terms of sample plots of fixed area or horizontal (Bitterlich) sample points. These trees are not measured for biomass. In the second phase, a relatively small sample of trees is selected, and the trees are measured for biomass and the same characteristics as the first phase trees. The second phase trees are used to estimate a relationship between tree characteristics (diameter, height, age, etc.) and biomass, usually, though not always, expressed as a regression function. This relationship is then applied to the trees of the first phase sample to calculate forest inventory estimates of average biomass per unit area. When previously constructed biomass regressions are available, the second phase sample is no longer necessary. However, a critical assumption is being made that the tree population for which the regression function was calculated and the tree populations currently being inventoried are very similar. Some recent studies dealing with forest biomass estimates from inventory data include Brown et al. (1989) and Brown and Lugo (1992) in the neotropics, Brown et al. (1991) in South and Southeast Asia, and Monserud et al. (1996) in Russia. Two excellent references on forest inventory methodology are de Vries (1986) and Schreuder et al. (1993).

The error of the forest inventory estimates has two main components. First is the component due to the random selection of the sample units of the first phase. Successive applications of the same selection procedure to the same forest area result in different sets of sample trees and, thus, different sets of estimates. The size of this component is greatly affected by (1) the sampling design of the first phase, (2) the sample size, (3) the type of estimator used (for given sample data and required parameter to estimate, there are generally several estimators, each having its own precision), and (4) the inherent variation between the sample units. The second component is associated with the sample of the second phase, that is, with the error of the biomass regression. The size of this component is affected by (1) the sampling design used to select these trees, (2) the sample size, (3) the estimation procedure, and (4) the inherent variation of the tree biomass values about the regression function. These two components constitute what is known as the *sampling error*.

An approach proposed by Cunia (1965, 1987a) can be used to combine the error from the first phase sample plots with the error from the second phase sample trees. This approach requires that the estimators be of the form



**Table 9. Comparison of actual bole wood dry mass with difference sampling estimate for willow oak trees from the state of Mississippi, USA.**

Tree	<i>H</i> (m)	True mass (kg)	$\rho(1.5)$ (kg/m <sup>3</sup> )	$a(1.5)$ (m <sup>2</sup> )	$\hat{W}$ (kg)	<i>X</i> (m)	$\rho(X)$ (kg/m <sup>3</sup> )	$a(X)$ (m <sup>2</sup> )	$w'(X)$	$\hat{w}'(X)$	$W_D(H)$
1	29.0	2,493.4	584	0.361	2,152.5	18.0	603	0.092	55.69	33.75	2,203.3
2	18.3	309.4	596	0.061	243.4	3.0	599	0.052	30.96	30.31	243.7
3	22.9	941.7	613	0.173	869.7	3.0	601	0.143	85.95	91.93	867.0
4	27.4	1,772.7	536	0.364	1,886.8	3.0	530	0.273	144.55	173.13	1,874.8
5	19.8	277.1	608	0.053	229.4	9.0	613	0.028	17.01	11.16	235.9
6	32.0	1,301.4	585	0.177	1,160.9	6.0	605	0.125	75.56	75.33	1,161.1
7	32.0	1,000.6	554	0.161	996.1	4.5	565	0.114	64.42	72.31	992.6
8	30.5	885.4	544	0.146	852.5	19.5	567	0.037	21.25	11.46	877.6
9	25.9	464.9	573	0.073	383.6	6.0	590	0.056	32.96	27.81	386.5
10	30.5	1,558.1	564	0.234	1,413.7	10.5	582	0.143	83.23	62.83	1,429.5
11	24.4	376.5	574	0.064	316.6	12.0	575	0.031	17.73	10.70	325.7
12	30.5	2,117.9	580	0.372	2,309.8	4.5	575	0.230	132.19	173.49	2,290.8
13	24.4	721.7	580	0.112	566.2	1.5	580	0.112	65.25	65.25	566.2
14	25.9	802.9	551	0.133	672.3	9.0	557	0.091	50.68	35.15	684.4
15	35.1	2,290.2	593	0.327	2,370.9	1.5	593	0.327	193.86	193.86	2,370.9
16	25.9	662.7	588	0.123	665.3	4.5	582	0.095	55.35	55.77	665.0
17	21.3	272.2	578	0.058	256.6	6.0	607	0.037	22.75	20.02	258.3
18	32.0	3,029.1	582	0.471	3,072.5	1.5	582	0.471	274.33	274.33	3,072.5
19	33.8	2,147.3	568	0.268	1,796.3	1.5	568	0.268	152.25	152.25	1,796.3
20	29.0	1,438.8	560	0.261	1,491.9	15.0	603	0.071	42.54	37.90	1,498.6
21	25.9	171.0	600	0.032	178.5	3.0	600	0.026	15.33	17.14	177.8
22	24.4	365.6	617	0.061	328.3	9.0	647	0.031	19.95	17.11	330.6
23	27.4	1,009.7	607	0.189	1,108.2	7.5	692	0.112	77.85	67.63	1,114.6
24	27.4	523.5	603	0.087	507.2	16.5	630	0.031	19.42	9.29	528.5
25	27.4	667.2	564	0.131	716.5	9.0	591	0.064	37.57	37.39	716.6
26	24.4	240.4	589	0.042	214.5	6.0	596	0.030	17.91	15.96	215.6
27	25.9	394.2	606	0.062	347.1	13.5	640	0.024	15.44	9.77	355.4
28	25.9	510.8	580	0.090	477.0	0.5	590	0.152	89.48	56.34	488.5
29	27.4	732.1	591	0.104	592.3	4.5	602	0.080	48.43	47.87	592.6
30	22.9	836.9	606	0.177	878.4	4.5	612	0.130	79.39	79.38	878.4
31	25.9	440.0	584	0.084	451.8	3.0	584	0.067	39.14	43.38	450.0
32	21.3	468.6	526	0.094	377.2	1.5	526	0.094	49.30	49.30	377.2
33	21.3	356.5	580	0.074	329.2	3.0	588	0.060	35.40	36.76	328.6
34	25.9	1,385.7	561	0.270	1,391.7	4.5	560	0.236	132.39	116.68	1,399.4
35	25.9	1,240.6	587	0.205	1,102.5	1.5	587	0.205	120.17	120.17	1,102.5
36	27.4	1,530.4	567	0.245	1,345.0	4.5	562	0.193	108.28	108.71	1,344.8
37	27.4	2,056.6	560	0.359	1,942.0	12.0	543	0.191	103.55	70.98	1,976.4
38	25.9	1,208.4	464	0.243	1,034.6	12.0	576	0.131	75.65	36.59	1,079.8
39	27.4	1,984.5	567	0.329	1,807.0	9.0	585	0.241	140.87	94.29	1,841.4
SUM		40,986.8									39,099.3

Note:  $\rho(1.5)$  is ratio of mass to volume at height 1.5 m (i.e., specific gravity measured at height 1.5 m  $\times$  1000),  $a(1.5)$  is bole cross-sectional area at 1.5 m,  $W$  is estimate of bole dry mass via Equation (62),  $X$  is a random height generated from Equation (59),  $w'(X)$  is  $\rho(X)a(X)$ ,  $\hat{w}'(X)$  is a model-based estimate of  $w'(X)$  via Equation (54), and  $W_D(H)$  is the difference sampling estimate of bole biomass via Equation (61).

$$\hat{w} = b_1z_1 + b_2z_2 + \dots + b_mz_m = \mathbf{b}'\mathbf{z} \quad (63)$$

where  $\mathbf{b}$  is the coefficient vector from the biomass regression function and  $\mathbf{z}$  is a vector of statistics calculated from the data of the sample points or plots. It is assumed that (1) the regression of tree biomass on  $X$  is of the linear form  $y = X\beta + \epsilon$ , (2) the vector  $\mathbf{z}$  is defined so that  $\hat{w}$  is an unbiased estimate of the parameter of interest  $\mu$ , that is,

$$\mu = \beta'\mu_z = E[\mathbf{b}']E[\mathbf{z}]$$

and (3) the vectors  $\mathbf{b}$  and  $\mathbf{z}$  are statistically independent. The variance of  $w$  is calculated as

$$S_{ww} = \mathbf{b}'S_{zz}\mathbf{b} + z'S_{bb}z \quad (64)$$

where  $S_{zz}$  and  $S_{bb}$  are the covariance matrices of  $\mathbf{z}$  and  $\mathbf{b}$ . The first term of  $S_{ww}$  is the variance component associated with the error of the sample plots, and the second term is the variance component associated with the biomass regression. The definition of  $\mathbf{z}$  depends on (1) the sampling design by which the plots or points are chosen, (2) the specific parameter  $\mu$  one wishes to estimate, and (3) the variables  $\mathbf{x}'$  used in the biomass regression function.

Cunia (1987a,b,c,d,e,f), in a series of papers, described in detail the steps of the above approach for combining the first and second phase error components when the parameter  $\mu$  of interest is the average biomass per hectare and the sampling designs were: (1) simple random sampling, (2) stratified sampling, (3) two-stage sampling, (4) double sampling, (5) Continuous Forest Inventory (CFI) without Sampling with Partial Replacement

(SPR), and (6) CFI with SPR. Details and examples on all these designs are provided in Cunia's papers.

### 3 Discussion

In earlier drafts of this article, I was chided by reviewers for using the terms *weight* and *mass* interchangeably. Weight and mass, though related, are not the same (see footnote 1). I have made an effort throughout this retrospection to refer to either weight or mass as appropriate, and to use the term *weight* with those techniques, such as the ratio-type estimators of 1.2.1, that deal with weight estimation, and to use the term *mass* with those techniques, such as the density-integral model of 1.1.8, that truly deal with estimation of mass. This is as it should be, and researchers in the future should properly distinguish the two.

Research on estimating biomass components of trees and forests has a long tradition. Information on many species for different sites and stand structures is available. Of historical interest are the volumes put out by the IUFRO working group that was initiated by Harold Young: Forest biomass studies 1971, IUFRO biomass studies 1973, and Oslo biomass studies 1976. These volumes were published by the University of Maine at Orono. Two important books on biomass are Satoo (1982), dealing primarily with Japanese efforts to systematize forest biomass data and estimation, and Madgwick (1994), a comprehensive work dealing with the single species *Pinus radiata* D. Don. A short list of current articles dealing with biomass estimation is: Korsmo (1995) on seven hardwood species in Norway; Usol' Tev and Vanclay (1995) on Scots pine (*Pinus sylvestris* L.) in Kazakhstan; Wang et al. (1995) on aspen (*Populus tremuloides* Michx.) in British Columbia; Tahvanainen (1996) on seven *Salix* clones in Finland; Bartelink (1997) on beech (*Fagus sylvatica* L.) in the Netherlands; and in the People's Republic of China, Li et al. (1996) on Japanese red pine (*Pinus densiflora* Sieb. and Zucc.), and Zhou et al. (1997) on *Manglietia hainanensis* Dandy.

There are many ways to determine tree biomass. Ratio-type estimators, difference sampling estimators, and others are appropriate if one only needs estimates of the total woody biomass of the tree (or bole). If, however, one wants to develop weight-ratio or density-integral type models, a more intensive sampling scheme on the bole (such as systematic sampling) would be more appropriate. Under short-rotation woody biomass programs, trees typically do not attain a large size, so development of weight-ratio or density-integral models is probably not labor efficient or cost effective. Older plantations and trees that attain a large size might yield a mix of products in the bole such as pulpwood, fuelwood, and small dimensional lumber. For these plantations and trees, development of prediction systems for merchandizing tree boles would be advantageous, and intensive sampling schemes to develop such prediction systems would be cost effective in the long run.

Modeling tree biomass has been a wide-ranging effort in forestry. It is important to be cognizant of the error structure

to achieve efficient estimates and to construct valid standard errors and confidence regions. New research is showing that spatial and temporal correlation is common in all types of forestry data, and modeling these correlations in tree and plot data can provide considerable gains in efficiency and estimation (Gregoire et al. 1995a, Goelz and Burk 1996, Gregoire and Schabenberger 1996). Future efforts in modeling tree and stand biomass and updating inventory estimates should take into account these correlations. Further, normally distributed errors are almost always assumed and rarely verified. Williams and Schreuder (1996) have looked at the normality assumption with volume models and offer alternative error distributions that could well be applied to biomass models.

As alluded to in the introduction, remote sensing will play an ever increasing role in stand biomass estimation and forest productivity in general (de Gier and Sakouhi 1995, Gholz et al. 1997), with much research being needed in this area. Large-scale forest inventories, such as those conducted by state and federal agencies, are looking to methodologies such as imputation for updating current biomass. Tree and stand biomass modeling and sampling may well be supplanted by remote sensing and multivariate statistical analysis or, preferably, linked with them in the future.

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