CONVERTING STEM VOLUME TO BIOMASS WITH ADDITIVITY, BIAS CORRECTION, AND CONFIDENCE BANDS FOR TWO AUSTRALIAN TREE SPECIES

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ABSTRACT

There are increasing requirements for forest management agencies to estimate not only wood volume for timber production, but also biomass accumulation and carbon sequestration rates of their forests for environmental purposes. The common methods of biomass estimation have been to develop allometric equations to predict the biomass of individual trees from diameter or both diameter and height. The biomass equations are usually based on small samples, especially for large trees, due to the time-consuming nature of destructive biomass sampling. Consequently, the predictive performance of biomass equations has been seldom evaluated. Most forest management agencies do, however, have reliable volume estimates that are based on large samples. Converting stem or stand volume estimates, that are already available in forest inventory and growth and yield systems, to biomass seems to be the most convenient and reliable way to estimate forest biomass over a large management area. Adopting this approach, we developed a system of additive equations for converting stem volume into four biomass components (stemwood, bark, branches, foliage) and total above-ground tree biomass using data for two Australian tree species as an example. To correct log transformation bias and at the same time maintain additivity among the component equations, we proposed a regression-based bias correction factor and simultaneously estimated the biomass correction factors for the component equations. The distributional properties of the error in stem volume prediction were incorporated in stochastic simulations of the system of equations to determine the confidence bands of the biomass conversions. Such results would provide a clear indication whether the required precision of biomass prediction is met for a particular objective of investigation and, if not, where improvements can be made.

Keywords: system of additive equations; regression-based bias correction factor; stochastic simulations; biomass distribution.

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INTRODUCTION

Biomass estimation has long been a predominant component of studies on forest productivity and nutrient distribution (e.g., Ovington 1957; Whittaker 1961; Attiwill *et al.* 1978; Feller 1980; Gosz 1980; Turner & Lambert 1983; Adams & Attiwill 1984; Sprugel 1984; Birk & Turner 1992; Wang *et al.* 1995; Santa Regina 2000). Estimating tree and stand biomass for calculating biomass energy, carbon storage, and carbon sequestration rates of forest stands began more recently (Cooper 1983; Grierson *et al.* 1992; Lovenstein & Berliner 1993; Hall 1997; Laiho & Laine 1997; Nelson *et al.* 1999). The common methods of biomass estimation have been to develop allometric equations using log transformed data to predict the biomass of a tree and its components such as stemwood, bark, branches, and foliage either from diameter or from both diameter and height (Ter-Mikaelian & Korzukhin 1997; Parresol 1999). The weaknesses shared by many reported biomass equations are (1) the lack of additivity among the component equations, (2) the existence of an inherent bias due to log transformation, and (3) the lack of confidence bands indicating their predictive performances.

The lack of additivity means inconsistency in logic in the sense that the predicted values from the biomass equations of tree components do not add up to the predicted value from the equation for the total tree biomass (Kozak 1970). To overcome this problem, statistical procedures have been developed for forcing additivity among component equations, both linear (Kozak 1970; Chiyenda & Kozak 1984; Cunia & Briggs 1984, 1985; Parresol 1999) and non-linear (Reed & Green 1985). A critical review of these procedures has been given by Parresol (1999). The existence of an inherent bias in biomass estimation because of the use of logarithmic regression has been well-recognised (Baskerville 1972; Beauchamp & Olson 1973; Wiant & Harner 1979; Flewelling & Pienaar 1981; Sprugel 1983; Snowdon 1991). However, corrections for log transformation bias are not attempted in many reports of biomass equations, even though the bias can be up to 30% or more for certain biomass components (Baskerville 1972; Snowdon 1991). The lack of confidence bands signifies deficiency in statistical estimates of the predictive accuracy of the biomass equations, particularly when applied to data independent of those used for estimating the equations. This deficiency stems largely from a problem of sample sizes. Because of the time-consuming nature of destructive biomass measurements, samples for developing biomass equations are usually small, especially when large trees are involved (Feller 1980; Applegate 1982; Ter-Mikaelian & Korzukhin 1997; Burrows *et al.* 2000). With small sample sizes it is difficult to evaluate the predictive accuracy of biomass equations. Consequently, predictive performance of biomass equations is seldom evaluated and reported (Madgwick 1971; Madgwick & Satoo 1975; Maia Araujo *et al.* 1999), particularly in comparison with the way that many forest growth models are tested (Vanclay & Skovsgaard 1997).

Unlike biomass estimation, forest management agencies generally have more reliable estimates of tree and stand volume in their forest inventory and growth and yield systems. These volume estimates are from stem volume equations constructed from samples that are often many times larger than the sample size for biomass equations. Such samples usually cover a much wider geographical area, and so a greater range of stand conditions, than the biomass samples. In addition, reliable estimates of the predictive accuracy of stem volume equations are available for some species (Bi & Hamilton 1998). Stem volume estimates can be converted to biomass estimates with constant conversion factors (e.g., Whittaker 1961; Adams 1982; Grierson *et al.* 1992) or through regression equations relating biomass to stem

volume (Grundy 1995; Schroeder *et al.* 1997; Usoltsev & Hoffmann 1997). Converting stem or stand volume estimates, that are already available in forest inventory and growth and yield systems, to biomass seems to be the most convenient and reliable way to estimate forest biomass over a large management area (Delcourt *et al.* 1981; Usoltsev & Hoffmann 1997; Schroeder *et al.* 1997). Accurate estimates of stem volume also provide the basis for more accurate estimates of biomass at a local level of management such as compartments. An added advantage of such an approach is that the distributional properties of the error in stem volume prediction estimated from large samples can be used in the evaluation of the accuracy of tree and stand biomass predictions.

The objective of this study was to develop a general method to convert stem volume to biomass that overcomes the weaknesses shared by many allometric biomass equations. Small-sample data for two Australian tree species, *Eucalyptus fastigata* Deane et Maiden and *Acacia dealbata* Link, are used as an example. Firstly, we develop a system of equations to convert stem volume to biomass components with additivity. Then we propose a regression-based estimator for correcting log transformation bias while maintaining additivity. Furthermore, we demonstrate how the predictive performance of such a system of equations that is based on small samples can be more realistically evaluated through stochastic simulations that incorporate the distributional properties of the error in stem volume prediction estimated using large samples.

STUDY AREA

Glenbog State Forest on the south-east tablelands of New South Wales (36°50'S, 149° 50'E), Australia consists of approximately 20 000 ha of wet sclerophyll eucalypt forests at altitudes ranging from 800 to 1200 m. The mean annual rainfall in the area ranges from 700 to 1100 mm. The mean annual temperature is in the range 8.5°–13.5°C, and the mean minimum for the coldest month is –4° to 3°C. The most prevalent tall tree species in the area is *E. fastigata* which can attain heights of more than 40 m on favourable sites. It occurs either in pure stands or in association with other eucalypt species. The most commonly found small tree species is *A. dealbata* which can sometimes reach more than 30 m in height and form pure stands at confined locations (Bi *et al.* 2000).

As part of a growth and yield project in the study area, more than 30 temporary plots were established in the regrowth forests of *E. fastigata* using a stratified random sampling scheme based on forest type (Bi & Jurskis 1996a). Most of these plots were in relatively pure *E. fastigata* stands. Nominal stand age, taken as the time elapsed since the last fire or logging which initiated the regrowth stand, varied mostly between 20 and 72 years among the sample stands (Bi & Jurskis 1996a). The plots were circular and varied in size according to stand density, but had a minimum radius of 15 m and contained at least 50 regrowth trees. Within each plot, diameter at breast height overbark (dbhob) and height of trees with dbhob greater than 10 cm were measured. A nominal age-class was recorded for each tree in one of the following categories: old tree, advance growth, or regrowth. Their morphological characteristics have been detailed by Bi & Jurskis (1996b).

BIOMASS SAMPLING

For biomass sampling, four plots were selected across the range of site productivity using the site productivity index derived by Bi & Jurskis (1996a) for these stands. A total of 15

regrowth and advance growth *E. fastigata* were destructively sampled across the diameter range of trees in the four plots. Diameter at breast height (ob) of the sample trees ranged from 10.3 to 80.8 cm and height ranged from 9 to 45 m (Fig. 1). After felling, sectional measurements of overbark stem diameter and bark thickness were taken along the stem at 1.5-m intervals for calculating overbark and underbark sectional volumes as described by Bi & Hamilton (1998). In addition, discs approximately 5 cm thick were cut at 1.3 m and at two to four relatively evenly spaced points along the stem, depending on tree size. The height above ground was recorded for all points where discs were taken. The discs were then taken back to the laboratory for determining the basic densities of sapwood, heartwood, and stem bark.
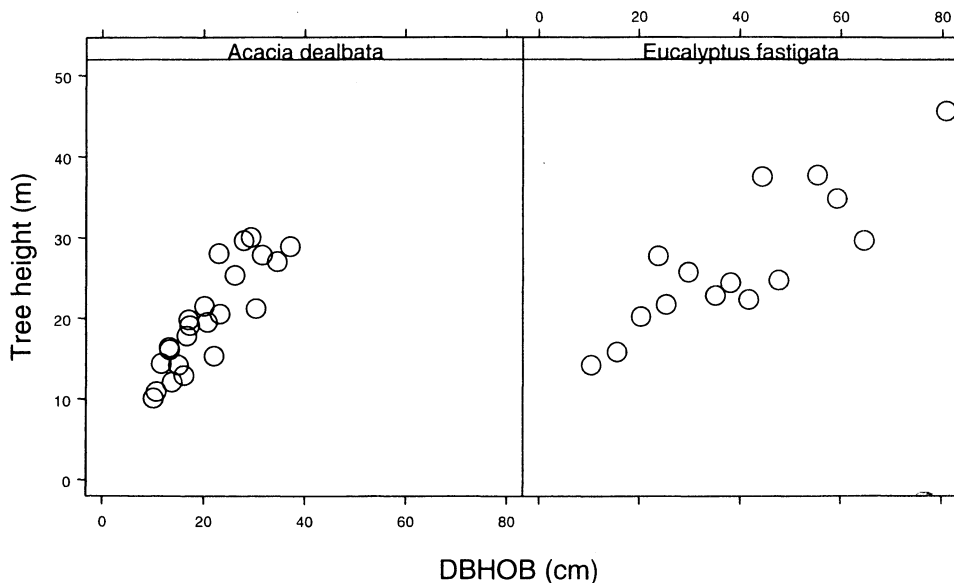

FIG. 1–Height and diameter at breast height overbark (dbhob) of the sample trees.

Diameter of all branches, either live or dead, was measured at about 5 cm from the forking point on the stem, and their height above ground level was recorded. Branches exceeding 18 cm in diameter on large trees were treated as separate leaders. The diameter and the height of the forking point of each leader were recorded. Branch measurements were made on the leaders in the same way as on the main stem. After branch measurements had been made, the crown was divided into upper and lower crown using the height measurements of live branches. From each crown stratum, a random sample of between one and six live branches was taken, depending on the crown size. The foliage and twigs (<1 cm in diameter) were separated manually from each sample branch. Fresh weights of foliage, twigs, and branch wood were obtained using a field balance. A subsample of about 0.5 kg of leaves was taken from each sampled branch. Subsamples of twigs and branches were taken initially from each branch, but there was little variation in moisture content among the branches of a tree and so, to expedite the sampling process, a subsample of twigs weighing about 0.5–0.7 kg and a subsample of branch wood with bark weighing about 2–3 kg were taken from each tree. All dead branch samples were cut off the stem and weighed in the field, together with the broken

pieces collected from the floor. Depending on the number of dead branches present, a subsample of branchwood weighing about 1–3 kg was taken. For *A. dealbata*, 24 trees were sampled across its diameter range in the four plots. Diameters at breast height (ob) of the sample trees ranged from 10 to 37 cm and height ranged from 10 to 31 m (Fig. 1). Field measurements were taken in the same way as for *E. fastigata*, but without partitioning the crown. All dead branches were collected and weighed, and a subsample of dead branches weighing about 1–2 kg was taken to the laboratory.

All subsamples weighed in the field were oven dried in the laboratory at 70°C until a constant weight was reached, to determine the dry weight to fresh weight ratio. The total dry weight of foliage of each sample branch was obtained by multiplying the fresh weight of foliage by the dry:fresh weight ratio for foliage. The total dry weight of twigs and branch wood of the sample branches was calculated in the same way, and the sum of the two components was taken as the total branch biomass. To determine the total dry weight of foliage and of branches for a tree, three regression equations were developed relating the biomass of foliage, live branches, and dead branches to branch diameter on log scales by pooling subsamples from all trees. Then for all non-sample branches, the biomass of foliage and branch wood was calculated from branch diameter using the regression equations. Log-transformation bias was corrected using a regression-based bias correction factor (to be described in detail later in this paper). The total foliage biomass of a tree was calculated as the sum of foliage dry weight of all live branches of the tree. The total branch biomass of a tree was calculated by summing the dry weight of all live and dead branches of the tree. The basic density of sapwood and heartwood, and the bark density of disc samples were determined (in grams per cubic centimetre) by cutting small cube samples from each disc and using water immersion techniques similar to that described by Feller (1980) and Bradstock (1981). This was done several days or more after the disc samples were taken in the field because the foliage and branch samples were dried and weighed first in the laboratory. As a reviewer correctly pointed out, because the shrinkage during this period was not taken into account, application of the basic density to green stem volume may over-estimate stem biomass. Overbark and underbark sectional volumes were calculated for both species as described by Bi & Hamilton (1998). In addition, sapwood and heartwood volumes in each stem section were also calculated. The heartwood and sapwood biomass of each stem section was first calculated by multiplying the heartwood and sapwood volumes of the section with the corresponding basic densities. The total biomass of stemwood of each stem section was then calculated as the sum of the heartwood and sapwood biomass of that section. The biomass of stem bark was calculated in the same way. Since *E. fastigata* is a rough bark species, overbark measurement with a tape will measure the "apparent" volume rather than true volume, and application of bark density measured using water immersion techniques to "apparent" bark volume may over-estimate bark biomass. Total stemwood and bark biomass for the whole tree was calculated as the sum of sectional stemwood and bark biomass from ground to tip.

Model Specification, Estimation, and Diagnostics

A system of five equations with multiplicative error terms, cross-equation constraints on the structural parameters, and cross-equation correlation are specified to convert stem volume to four tree biomass components and total tree biomass with additivity:

$$Y_1 = e^{\beta_1} V^{\beta_2} e^{\varepsilon_1}$$
$$Y_2 = e^{\beta_3} V^{\beta_4} e^{\varepsilon_2}$$
$$Y_3 = e^{\beta_5} V^{\beta_6} e^{\varepsilon_3}$$
$$Y_4 = e^{\beta_7} V^{\beta_8} e^{\varepsilon_4}$$
$$Y_5 = (e^{\beta_1} V^{\beta_2} + e^{\beta_3} V^{\beta_4} + e^{\beta_5} V^{\beta_6} + e^{\beta_7} V^{\beta_8}) e^{\varepsilon_5} \tag{1}$$

where Y_1 to Y_5 represent stemwood, stem bark, branch, leaf, and total tree biomass respectively (in kilograms), V is underbark stem volume (in cubic metres), $\beta_1, \beta_2,...,\beta_8$ are coefficients. The error terms can be expressed in matrix algebra notation as follows:

$$\boldsymbol{\varepsilon} = [\varepsilon_1, \varepsilon_2, \varepsilon_3, \varepsilon_4, \varepsilon_5]' \tag{2}$$

The properties of $\boldsymbol{\varepsilon}$ are

$$E(\boldsymbol{\varepsilon}) = 0 \tag{3}$$

and

$$Cov(\boldsymbol{\varepsilon}) = E(\boldsymbol{\varepsilon\varepsilon}') = \begin{bmatrix} \sigma_{11} & \sigma_{12} & \sigma_{13} & \sigma_{14} & \sigma_{15} \\ \sigma_{21} & \sigma_{22} & \sigma_{23} & \sigma_{24} & \sigma_{25} \\ \sigma_{31} & \sigma_{32} & \sigma_{33} & \sigma_{34} & \sigma_{35} \\ \sigma_{41} & \sigma_{42} & \sigma_{43} & \sigma_{44} & \sigma_{45} \\ \sigma_{51} & \sigma_{52} & \sigma_{53} & \sigma_{54} & \sigma_{55} \end{bmatrix} \otimes I_T = \Sigma \otimes I_T \tag{4}$$

where $E(\boldsymbol{\varepsilon})$ and $Cov(\boldsymbol{\varepsilon})$ denote the expectation and covariance of ε, σ_{ii} represents the variance of $\boldsymbol{\varepsilon}_i$, (i=1, ...,5), σ_{ij} represents the covariance between the error term of the ith and the jth equation, (j=1,...,5), $\otimes$ denotes the Kronecker product, T denotes the number of observations, and I_T is an identity matrix of order T. The random errors follow a multivariate normal (MVN) distribution, i.e., $\boldsymbol{\varepsilon} \sim N(0,\Sigma)$. Taking logarithmic transformation on both sides of Equation (1), the system of equations becomes

$$y_1 = \beta_1 + \beta_2 \ln V + \varepsilon_1$$
$$y_2 = \beta_3 + \beta_4 \ln V + \varepsilon_2$$
$$y_3 = \beta_5 + \beta_6 \ln V + \varepsilon_3$$
$$y_4 = \beta_7 + \beta_8 \ln V + \varepsilon_4$$
$$y_5 = \ln(e^{\beta_1} V^{\beta_2} + e^{\beta_3} V^{\beta_4} + e^{\beta_5} V^{\beta_6} + e^{\beta_7} V^{\beta_8}) + \varepsilon_5 \tag{5}$$

where ln denotes natural logarithm and $y_i = \ln Y_i$. This system of five nonlinear equations can be written in a more compact form as:

$$y_1 = f_1(V, \boldsymbol{\beta}) + \varepsilon_1$$
$$y_2 = f_2(V, \boldsymbol{\beta}) + \varepsilon_2$$
$$y_3 = f_3(V, \boldsymbol{\beta}) + \varepsilon_3$$
$$y_4 = f_4(V, \boldsymbol{\beta}) + \varepsilon_4$$
$$y_5 = f_5(V, \boldsymbol{\beta}) + \varepsilon_5 \tag{6}$$

where $\boldsymbol{\beta} = [\beta_1, \beta_2,...,\beta_8]$. The same coefficient vector appears in all equations so that the coefficients can be shared by two equations as imposed by the cross-equation restrictions on the structural parameters for ensuring additivity.

Clearly, this system of equations falls into the framework of seemingly unrelated regressions (SUR) of Zellner (1962). Although Zellner's SUR estimator was first derived for a system of linear equations, it can be extended to a system of nonlinear equations such as the system specified above (Gallant 1975; Srivastava & Giles 1987; Judge *et al.* 1988). When the random errors follow a multivariate normal distribution, a system of nonlinear equations can also be estimated by maximum likelihood estimation. The maximum likelihood estimators for the coefficients and the cross-equation covariance matrix, Σ, have been given

in detail by Judge *et al.* (1988) for such systems of nonlinear equations. The maximum likelihood estimator of the coefficients in our model (6) is

$$
\arg \min_{\beta} |S| = \arg \min_{\beta} \left\| \begin{bmatrix} \varepsilon'_1\varepsilon_1 & \varepsilon'_1\varepsilon_2 & \varepsilon'_1\varepsilon_3 & \varepsilon'_1\varepsilon_4 & \varepsilon'_1\varepsilon_5 \\ \varepsilon'_2\varepsilon_1 & \varepsilon'_2\varepsilon_2 & \varepsilon'_2\varepsilon_3 & \varepsilon'_2\varepsilon_4 & \varepsilon'_2\varepsilon_5 \\ \varepsilon'_3\varepsilon_1 & \varepsilon'_3\varepsilon_2 & \varepsilon'_3\varepsilon_3 & \varepsilon'_3\varepsilon_4 & \varepsilon'_3\varepsilon_5 \\ \varepsilon'_4\varepsilon_1 & \varepsilon'_4\varepsilon_2 & \varepsilon'_4\varepsilon_3 & \varepsilon'_4\varepsilon_4 & \varepsilon'_4\varepsilon_5 \\ \varepsilon'_5\varepsilon_1 & \varepsilon'_5\varepsilon_2 & \varepsilon'_5\varepsilon_3 & \varepsilon'_5\varepsilon_4 & \varepsilon'_5\varepsilon_5 \end{bmatrix} \right\| \tag{7}
$$

where $\varepsilon'_i\varepsilon_j = [y_i - f_i(V,\beta)]'[y_j - f_j(V,\beta)]$. The maximum likelihood estimator for Σ is S/T, where S is defined in Equation (7). Since the loss of degree of freedom is not taken into account, the estimator tends to under-estimate the true value of Σ. The estimation of the structural parameters is consistent and asymptotically efficient.

The system of Equation (5) was fitted to the data for each species through the PROC MODEL procedure of SAS (SAS Institute Inc. 1988). Parameter estimates were obtained using both SUR and the maximum likelihood method. The two methods produced very similar parameter estimates. The approximate standard errors for the parameters from the maximum likelihood method were slightly larger. To be conservative and for the sake of parsimony, only the maximum likelihood estimates were reported (Table 1). The differences in branch and foliage exponents between the species largely reflected their differences in tree form. For each component equation, a generalised value of R^2 was calculated to indicate the goodness of fit:

$$
R^2 = 1 - \frac{\sum_{i=1}^{T}(y_i - \hat{y}_i)^2}{\sum_{i=1}^{T}(y_i - \bar{y})^2} \tag{8}
$$

where y_i and $\hat{y}_i$ are the observed and predicted values of log transformed biomass, and $\bar{y}$ is the mean observed value of log transformed biomass (Table 1). The asymptotic estimates of across equation error covariance matrix in Equation (4) are

TABLE 1–Parameter estimates and their asymptotic standard errors for the two species. Two values of R^2 are shown for each component equation: one in logarithmic space calculated according to Equation (8) and the other (in brackets) in arithmetic space calculated after taking back transformation from logarithm.

Biomass component	Parameters	E. fastigata			A. dealbata		
		Asymptotic estimate	Asymptotic standard error	R^2	Asymptotic estimate	Asymptotic standard error	R^2
Stemwood	β_1	6.5342	0.0142	0.997	6.4241	0.0170	0.999
	β_2	1.0370	0.0195	(0.989)	1.0091	0.0082	(1.000)
Stem bark	β_3	5.1351	0.0418	0.984	4.6649	0.0659	0.951
	β_4	0.9303	0.0379	(0.975)	0.8213	0.0627	(0.878)
Branch	β_5	4.6038	0.0815	0.935	4.6511	0.0860	0.818
	β_6	1.3072	0.0625	(0.404)	0.6456	0.0423	(0.793)
Foliage	β_7	2.6209	0.0893	0.925	1.9507	0.2063	0.623
	β_8	0.9379	0.0705	(0.727)	0.4672	0.0874	(0.667)
Total biomass				0.994			0.992
				(0.954)			(0.994)

$$\hat{\Sigma} = \begin{bmatrix} 0.0067 & 0.0094 & 0.0123 & 0.0031 & 0.0100 \\ 0.0094 & 0.0309 & 0.0109 & -0.0072 & 0.0172 \\ 0.0123 & 0.0109 & 0.2193 & 0.1479 & 0.0428 \\ 0.0031 & -0.0072 & 0.1479 & 0.1310 & 0.0200 \\ 0.0100 & 0.0172 & 0.0428 & 0.0200 & 0.0190 \end{bmatrix} \qquad (9)$$

for *E. fastigata* and

$$\hat{\Sigma} = \begin{bmatrix} 0.0007 & 0.0001 & -0.0012 & 0.0007 & 0.0005 \\ 0.0001 & 0.0409 & 0.0086 & -0.0110 & 0.0087 \\ -0.0123 & 0.0086 & 0.1549 & 0.1020 & 0.0341 \\ 0.0007 & -0.0110 & 0.1020 & 0.2156 & 0.0234 \\ 0.0005 & 0.0087 & 0.0341 & 0.0234 & 0.0099 \end{bmatrix} \qquad (10)$$

for *A. dealbata*. The diagonal elements of the asymptotic covariance matrices in Equations (9) and (10) showed that the asymptotic error variance of branch and foliage components was much greater than that of the stemwood and total biomass for both species. Consequently, the data points of stemwood and total biomass scattered more closely along the fitted lines than that of the branch and foliage biomass (Fig. 2).

Further graphical examinations of the estimated systems of equations in relation to the data for both species suggested that specification of Model (5) was appropriate and there were no marked departures from homogeneous error variance for all biomass components for both species. Since the random errors were assumed to follow a multivariate normal distribution (MVN), i.e., $\varepsilon \sim N(0,\Sigma)$ and the estimated Σ was to be used in stochastic simulations later in the paper, tests for multivariate normality were carried out to detect significant departures from the MVN assumption. The tests were also to ascertain whether the estimated Σ provides an adequate summary of the interrelations among the error terms, a main objective of any tests for MVN as stated by Cox & Small (1978). Over 50 tests for assessing multivariate normality have been proposed (Looney 1995). However, there is no uniformly most-powerful test for assessing multivariate normality when the alternative distribution is unknown (Ozturk & Romeu 1992; Looney 1995). The multivariate skewness and kurtosis tests proposed by Mardia (1980) remain among the most powerful, general, and easy to implement (Ozturk & Romeu 1992). Mardia's tests of the residuals of the system of equations showed no significant departures from MVN at a significance level of $\alpha=0.05$ for both species.

Bias Correction for a System of Additive Biomass Equations

As given by Flewelling & Pienaar (1981), the correction for log transformation bias for a single equation may be written as:

$$\hat{Y}_c = \theta\hat{Y} = \theta \exp(\hat{y}) \qquad (11)$$

where $\hat{Y}_c$ is the estimated value of biomass after bias correction, $\hat{Y} = \exp(\hat{y})$, and $\hat{y}$ is the estimated value of log transformed biomass, exp represents the exponential function, and θ is the correction factor. Several estimators of θ have been proposed (Finney 1941; Bradu & Mundlad 1970; Baskerville 1972; Teekens & Koerts 1972; Evans & Shaban 1976). They are generally based upon the sample variance (s^2) of the log transformed biomass, y, as reviewed by Flewelling & Pienaar (1981). The accuracy of these estimators would naturally depend upon how well the population variance is estimated, and thus is also dependent on the sample size. However, in small samples typical of those used in biomass studies, the variance will
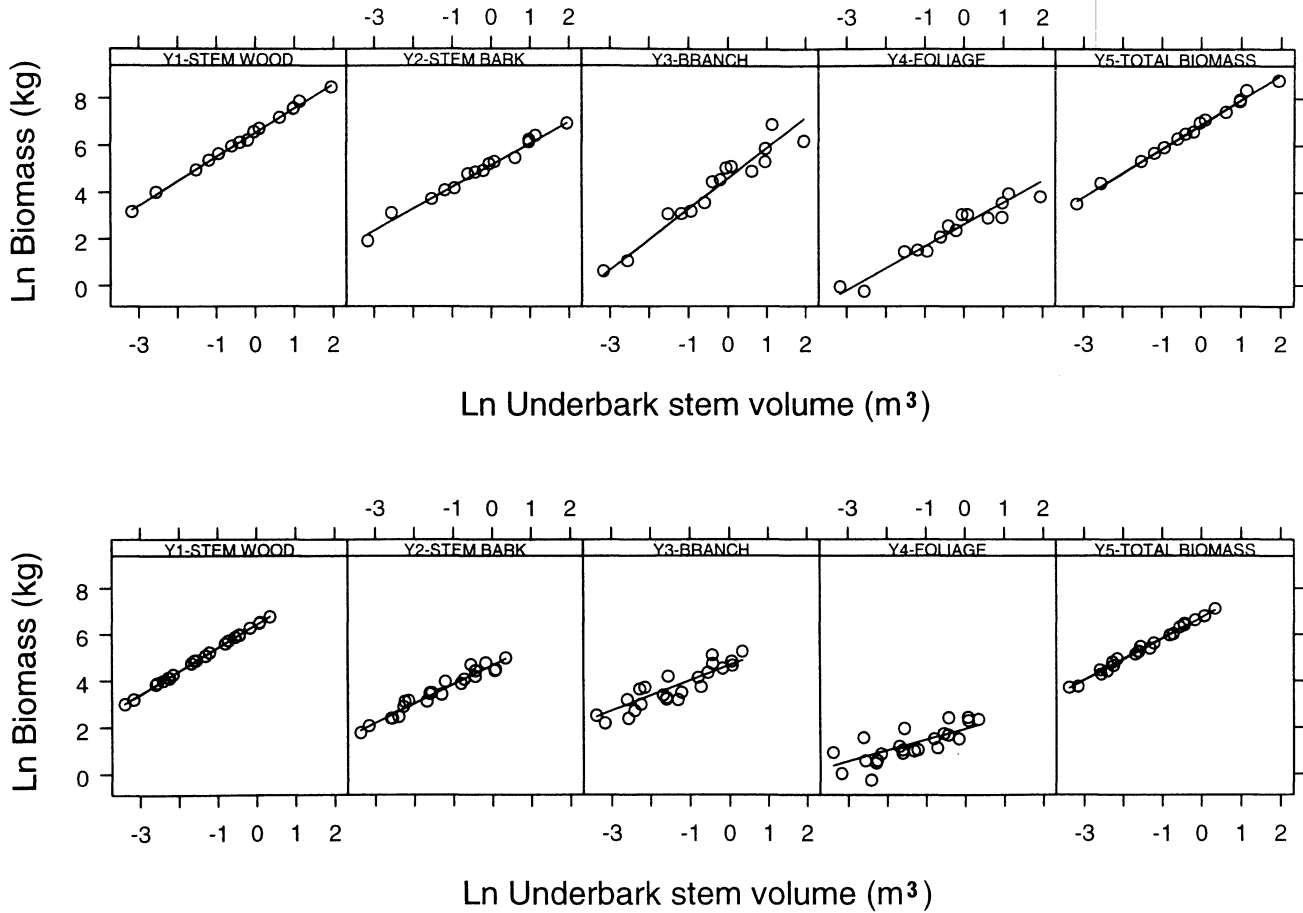
be poorly estimated (Snowdon 1991) and, therefore, bias corrections by these estimators may still be less than adequate for the objective of bias correction in a practical situation. As an alternative to these estimators of θ, Snowdon (1991) proposed a simple and more reliable

FIG. 2–Observed values of biomass components plotted against stem volume on log scales for *E. fastigata* (top) and *A. dealbata* (bottom) together with fitted lines.

estimator which is the ratio of the arithmetic sample mean and the mean of the back-transformed predicted values of log biomass. Since it is based on the mean, the ratio estimator is sensitive to extreme values (Snowdon 1991). This sensitivity represents a shortcoming, particularly for small samples containing few large trees such as those in this study. Furthermore, these existing correction factors were proposed for a single equation. Additivity among the component equations will not be maintained after bias correction when these bias correction factors are applied separately to each component equation of a system of additive equations as shown below:

$$\hat{Y}_{1c} = \theta_1 \hat{Y}_1$$
$$\hat{Y}_{2c} = \theta_2 \hat{Y}_2$$
$$\hat{Y}_{3c} = \theta_3 \hat{Y}_3$$
$$\hat{Y}_{4c} = \theta_4 \hat{Y}_4$$
$$\hat{Y}_{5c} = \theta_5 \hat{Y}_5 \tag{12}$$

where $\hat{Y}_{ic}$ (i=1,...,5) is the estimated value of biomass after bias correction for the biomass component corresponding to $\hat{Y}_i$, $\hat{Y}_i = \exp(\hat{y}_i)$, and $\hat{y}_i$ is the estimated value of log transformed biomass as in Equations (5) and (6).

To reduce bias and also maintain additivity, we propose to use a regression-based estimator of the bias correction factor, θ, for a single equation at first, and then to simultaneously estimate the bias correction factors for the components. For a single equation such as the component equation for total tree biomass, the multiplicative error term can be expanded into additive terms as follows:

$$Y_5 = \hat{Y}_5 e^{\varepsilon^*_5} = \hat{Y}_5 [E(e^{\varepsilon^*_5}) + e^{\varepsilon^*_5} - E(e^{\varepsilon^*_5})] \tag{13}$$

Let $\theta_5 = E(e^{\varepsilon^*_5})$ and $\xi_5 = \hat{Y}_5(e^{\varepsilon^*_5} - \theta_5)$, we have

$$Y_5 = \theta_5 \hat{Y}_5 + \xi_5 \tag{14}$$

where $\hat{Y}_5 = \exp(\hat{y}_5)$ is the predicted value of Y_5, treated here as a fixed regressor known without error, $e^{\varepsilon^*_5}$ is the associated multiplicative error term, ξ_5 is the new additive error term with $E(\xi_5) = 0$ and $Var(\xi_5) = \hat{Y}_5^2 Var(e^{\varepsilon^*_5})$. It is obvious that the weighted least squares estimator of θ_5 is

$$E\left[\frac{Y_5}{\hat{Y}_5}\right] \text{ or } \frac{1}{n}\sum \frac{Y_5}{\hat{Y}_5} \text{ in the sample case, where n is the number of sample trees.}$$

This weighted least squares estimator is equivalent to dividing both sides of Equation (13) with $\hat{Y}_5$. The weighted error term, $(e^{\varepsilon^*_5} - \theta_5)$, now has a zero mean and a variance equal to $Var(e^{\varepsilon^*_5})$. The distribution of the weighted error term has the same shape as that of the lognormal variate $e^{\varepsilon^*_5}$, but obviously its location has shifted to the left by θ_5. In this case, the least squares estimator of θ_5 is still unbiased, although statistical inferences based on the assumption of normal distribution are no longer valid (Wackerly *et al.* 1996).

In order to maintain additivity after bias correction, one may well suggest that the bias correction factors for the biomass components in Equation (12) be estimated through the following system of equations, using the seemingly unrelated regression estimator:

$$Y_1 = \theta_1 \hat{Y}_1 + \xi_1$$
$$Y_2 = \theta_2 \hat{Y}_2 + \xi_2$$

$$Y_3 = \theta_3 \hat{Y}_3 + \xi_3$$
$$Y_4 = \theta_4 \hat{Y}_4 + \xi_4$$
$$Y_5 = \theta_1 \hat{Y}_1 + \theta_2 \hat{Y}_2 + \theta_3 \hat{Y}_3 + \theta_4 \hat{Y}_4 + \xi_5 \tag{15}$$

Although this system of equations has cross-equation error correlations, they cannot be estimated through seemingly unrelated regression equations in the same manner as Model (5). In this system of equations, the component equation for total tree biomass is a linear combination of all other component equations. The variance and covariance matrix needs to be a positive definite matrix to preclude the possibility of any linear dependencies among the error terms in the system of equations (Srivastava & Giles 1987).

To overcome this problem, the bias correction factor for total tree biomass, θ_5, in Equation (12), was estimated in a single equation at first to obtain the estimated value of total tree biomass with bias correction, $\hat{Y}_{5c}$. Then $\hat{Y}_{5c}$ was used as a cross-equation constraint to obtain the final estimates of bias correction factors for other biomass components as follows:

$$Y_1 = \theta_1 \hat{Y}_1 + \xi_1$$
$$Y_2 = \theta_2 \hat{Y}_2 + \xi_2$$
$$Y_3 = \theta_3 \hat{Y}_3 + \xi_3$$
$$Y_4 = \theta_4 \hat{Y}_4 + \xi_4$$
$$\hat{Y}_{5c} = \theta_1 \hat{Y}_1 + \theta_2 \hat{Y}_2 + \theta_3 \hat{Y}_3 + \theta_4 \hat{Y}_4 + \xi_5 \tag{16}$$

The system of Equations (16) was fitted to the data for each species through the PROC MODEL procedure of SAS (SAS Institute Inc. 1988) to obtain parameter estimates using the nonlinear weighted least squares method and $\hat{Y}_i^{-1}$ (i = 1 – 5) as weights as described above.

The estimated bias correction factors for the component equations are

$$\hat{Y}_{1c} = 1.028 \hat{Y}_1$$
$$\hat{Y}_{2c} = 1.058 \hat{Y}_2$$
$$\hat{Y}_{3c} = 1.076 \hat{Y}_3$$
$$\hat{Y}_{4c} = 1.106 \hat{Y}_4$$
$$\hat{Y}_{5c} = 1.028 \hat{Y}_1 + 1.058 \hat{Y}_2 + 1.076 \hat{Y}_3 + 1.106 \hat{Y}_4 \tag{17}$$

for *E. fastigata* and

$$\hat{Y}_{1c} = 1.006 \hat{Y}_1$$
$$\hat{Y}_{2c} = 1.031 \hat{Y}_2$$
$$\hat{Y}_{3c} = 1.000 \hat{Y}_3$$
$$\hat{Y}_{4c} = 1.080 \hat{Y}_4$$
$$\hat{Y}_{5c} = 1.006 \hat{Y}_1 + 1.031 \hat{Y}_2 + 1.000 \hat{Y}_3 + 1.080 \hat{Y}_4 \tag{18}$$

for *A. dealbata* (Fig. 3). The estimated bias correction factor for $\hat{Y}_3$, the branch component of *A. dealbata*, was initially 0.986, slightly less than 1, and so constraint was arbitrarily imposed so that all estimated factors were greater or equal to one.

Stochastic Simulations

Since the equations for converting stem volume to biomass are based on small samples, it is difficult to obtain any reliable statistics on their prediction accuracy in the way shown by Bi & Hamilton (1998), Bi (1999), and Bi (2000) for volume and taper functions using large
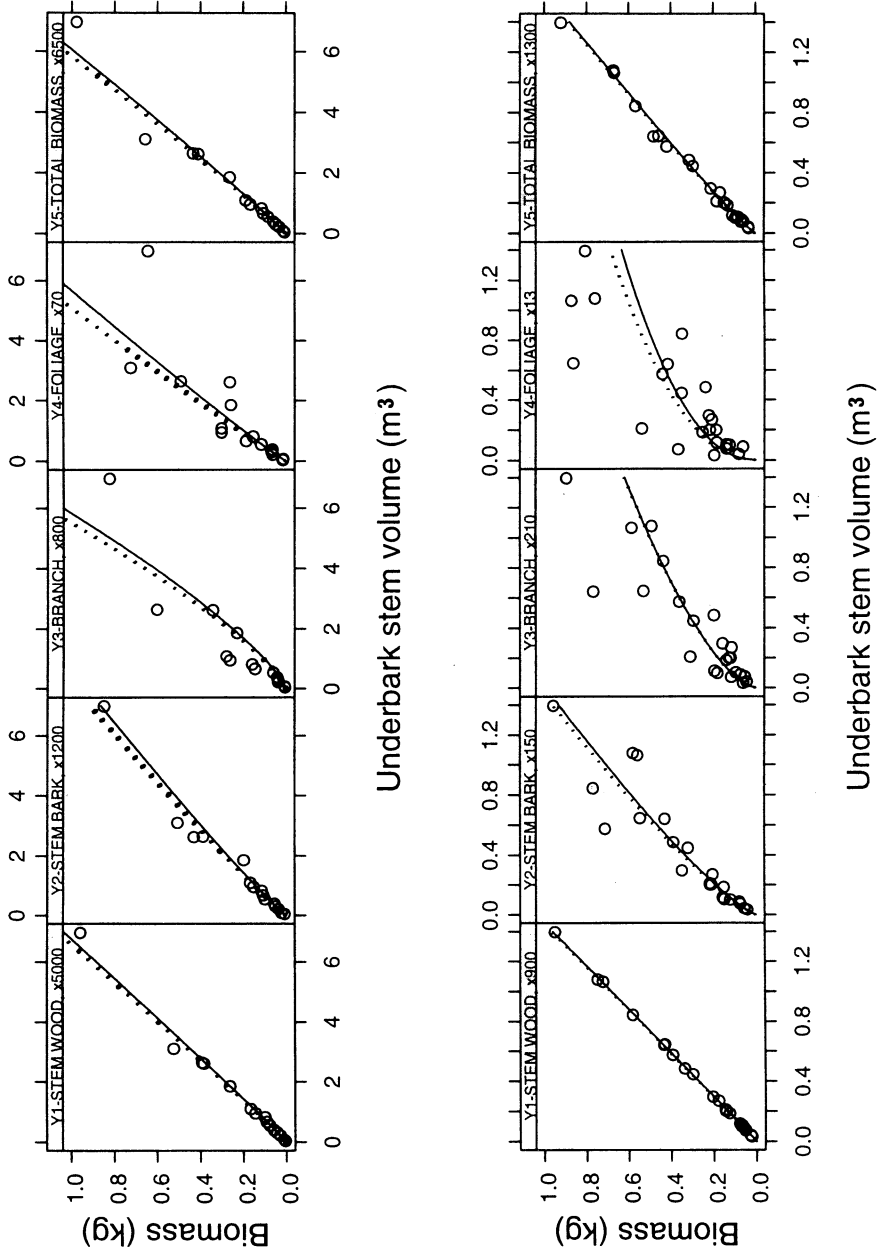
FIG. 3.–Observed values of biomass components plotted against stem volume for *E. fastigata* (top) and *A. dealbata* (bottom) together with the fitted lines after back-transformation from logarithm. Dotted lines show predicted values after bias correction. To obtain absolute values for the y-axis, multiply the relative scales by the number after the code of biomass component in the strip.

samples. For a tree with a given diameter and tree height, the predicted stem volume will have to be used as the independent variable in Equation (5) to predict biomass, unless the *true* stem volume calculated from taper measurements is available. Thus, in practice the error in stem volume prediction will be an additional component of the error in biomass estimation, as shown below:

$$Y_1 = e^{\beta_1} (\hat{V} + \varepsilon_v)^{\beta_2} e^{\varepsilon_1}$$
$$Y_2 = e^{\beta_3} (\hat{V} + \varepsilon_v)^{\beta_4} e^{\varepsilon_2}$$
$$Y_3 = e^{\beta_5} (\hat{V} + \varepsilon_v)^{\beta_6} e^{\varepsilon_3}$$
$$Y_4 = e^{\beta_7} (\hat{V} + \varepsilon_v)^{\beta_8} e^{\varepsilon_4}$$
$$Y_5 = (e^{\beta_1} (\hat{V} + \varepsilon_v)^{\beta_2} + e^{\beta_3} (\hat{V} + \varepsilon_v)^{\beta_4} + e^{\beta_5} (\hat{V} + \varepsilon_v)^{\beta_6} + e^{\beta_7} (\hat{V} + \varepsilon_v)^{\beta_8}) e^{\varepsilon_5} \qquad (19)$$

where $\hat{V}$ is predicted total stem volume from a volume equation and ε_v represents the error in stem volume prediction. Since volume equations are often developed using large samples, reliable estimates of the distributional properties of ε_v are available in some cases (Bi & Hamilton 1998). The errors in biomass prediction can be more realistically evaluated by taking into account both ε_v and ε in Equation (19) through stochastic simulation.

The volume equation for $E.$ fastigata developed by Bi & Hamilton (1998) using taper data from 949 sample trees is as follows:

$$V = \hat{V} + \varepsilon_v = 0.2195 D^2 H + \varepsilon_v \qquad\qquad R^2 = 0.989 \qquad (20)$$

where D is diameter overbark at breast height (in metres), H is total tree height (in metres), and R^2 is as defined in Equation (8). The selection of equation form, the determination of the weight function, and model diagnostics have been given in detail by Bi & Hamilton (1998). The weight function was $(D^2 H)^{-0.90}$; the weighted error term followed a normal distribution with zero mean and a standard deviation of 0.0224 as given by the root mean squared error of the weighted least squares regression. From these results, one can easily show the distribution of the error term ε_v in Equation (20) in terms of $\hat{V}$: $\varepsilon_v \sim N(0, \sigma^2(\hat{V}))$, where $\sigma^2(\hat{V}) = [0.0224(\hat{V}/0.2195)^{0.90}]^2$. Through the same procedures, a volume equation for $A.$ dealbata was developed using the best available taper data from a small number of 24 sample trees

$$V = \hat{V} + \varepsilon_v = 0.3458 D^2 H + \varepsilon_v \qquad\qquad R^2 = 0.984 \qquad (21)$$

where $\varepsilon_v \sim N(0, \sigma^2(\hat{V}))$ and $\sigma^2(\hat{V}) = [0.04357(\hat{V}/0.3458)^{1.45}]^2$.

To obtain the confidence limits for the error in biomass prediction for the two species, stochastic simulations of the two error components ε_v and ε in Equation (19) were carried out over a range of $\hat{V}$. For $E.$ fastigata, 400 values of $\hat{V}$ ranging from 0.025 to 10 m^3 with an even increment of 0.025 were used in the simulation; for $A.$ dealbata, 150 values of $\hat{V}$ ranging from 0.01 to 1.5 m^3 with an even increment of 0.01 were used. For each value of $\hat{V}$, 1000 random samples were generated for ε_v from the univariate normal distribution $N(0, \sigma^2(\hat{V}))$. In addition, 1000 sets of 5 random variates were generated for ε from the multivariate normal distribution $N(0, \hat{\Sigma})$ through the Cholesky decomposition of the estimated variance and covariance matrix, $\hat{\Sigma}$, given in Equations (9) and (10) for the two species. The algorithm for statistical computing was given in detail by Tong (1990). For each value of $\hat{V}$, the mean, the 2.5[th], and the 97.5[th] percentiles of the 1000 estimates of each of the five biomass components were taken as the predicted value of the stochastic simulations and the 0.95 confidence limits of prediction error at that point. The confidence limits for all points over the range of $\hat{V}$ collectively formed confidence bands for the estimated biomass components. To evaluate the relative width of the confidence bands, the difference between each of the confidence limits and the mean was divided by the mean to obtain percentage confidence bands. In addition, the stochastic simulations were repeated without incorporating ε_v, i.e., letting $\varepsilon_v = 0$, to see the magnitude of change in the width of the confidence bands if stem volume is measured instead of predicted.

As well as the confidence bands for the error of biomass prediction, biomass distribution in terms of the percentage of total above-ground biomass allocated to each biomass component and the 95% confidence limits were also obtained from the simulations. The mean percentage of total biomass allocated to each of the four components and the associated 95% confidence interval were also calculated and plotted against stem volume. The component equation for stemwood biomass, $Y_1 = e^{\beta_1}V^{\beta_2}e^{\varepsilon_1}$, was divided by V on both sides such that $Y_1/V = e^{\beta_1}V^{\beta_2-1}e^{\varepsilon_1}$, where Y_1/V is obviously the basic density of the stemwood for the whole stem, not individual stem sections. Since $\beta_2 - 1$ is greater than zero for both species, this relationship showed how the basic density of stemwood increases with tree size. The mean basic density of stemwood and its 95% confidence interval were calculated and plotted against stem volume.

The estimation of stemwood biomass is most precise among the four biomass components for both species, as shown by the relatively narrower 95% confidence bands (Fig. 4 and 5). The branch and foliage components are the least precisely estimated as shown by the much wider confidence bands. The width of the confidence bands largely reflects the values of the diagonal elements of the variance and covariance matrices for the two species in Equations (9) and (10). As expected, the confidence bands are not symmetrical due to the log normal distribution of the multiplicative error terms in Equation (19). The differences in the shape of the confidence bands between the two species are quite noticeable, particularly for the stemwood component and total tree biomass (Fig. 5). The relative confidence bands are generally wider for *A. dealbata* than for *E. fastigata*, apart from the branch component. For *A. dealbata*, the confidence bands for stemwood biomass and total biomass became much narrower when $\varepsilon_v = 0$. In comparison, the width of the confidence bands for the same biomass components for *E. fastigata* was also reduced when $\varepsilon_v = 0$, but to a much lesser extent. In addition to these differences, the shape of the confidence bands differed between the two species (Fig. 5).

Biomass distribution varied with tree size and also between species (Fig. 6). The mean proportion of stemwood increased with tree size from more than 50% to 77% for *A. dealbata*, whilst that of *E. fastigata* decreased slightly with tree size from 71% to 67%. The mean proportion of bark decreased with tree size for both species, from about 17% to less than 12% for *A. dealbata* and from about 24% to 13% for *E. fastigata*. The mean proportion of branch biomass decreased with tree size from about 30% to 11% for *A. dealbata*, whilst that of *E. fastigata* increased with tree size from 5% to 20%. The mean proportion of foliage decreased with tree size for both species, from about 4% to less than 1% for *A. dealbata* and from about 2% to 1% for *E. fastigata*. The confidence bands of the percentage biomass were relatively wide for the branch and foliage components. The mean basic density of stemwood increased with tree size for both species. However, the 95% confidence interval was much narrower for *A. dealbata* (Fig. 7).

DISCUSSION

There are several hundred native tree species in Australia (Boland *et al.* 1992), but allometric biomass equations are available for only a small number of species. Most of these equations are based on small samples that are confined to particular study sites within certain geographical areas. Consequently, the predictions from these biomass equations when applied to trees over a large geographical area may not have the required level of accuracy.
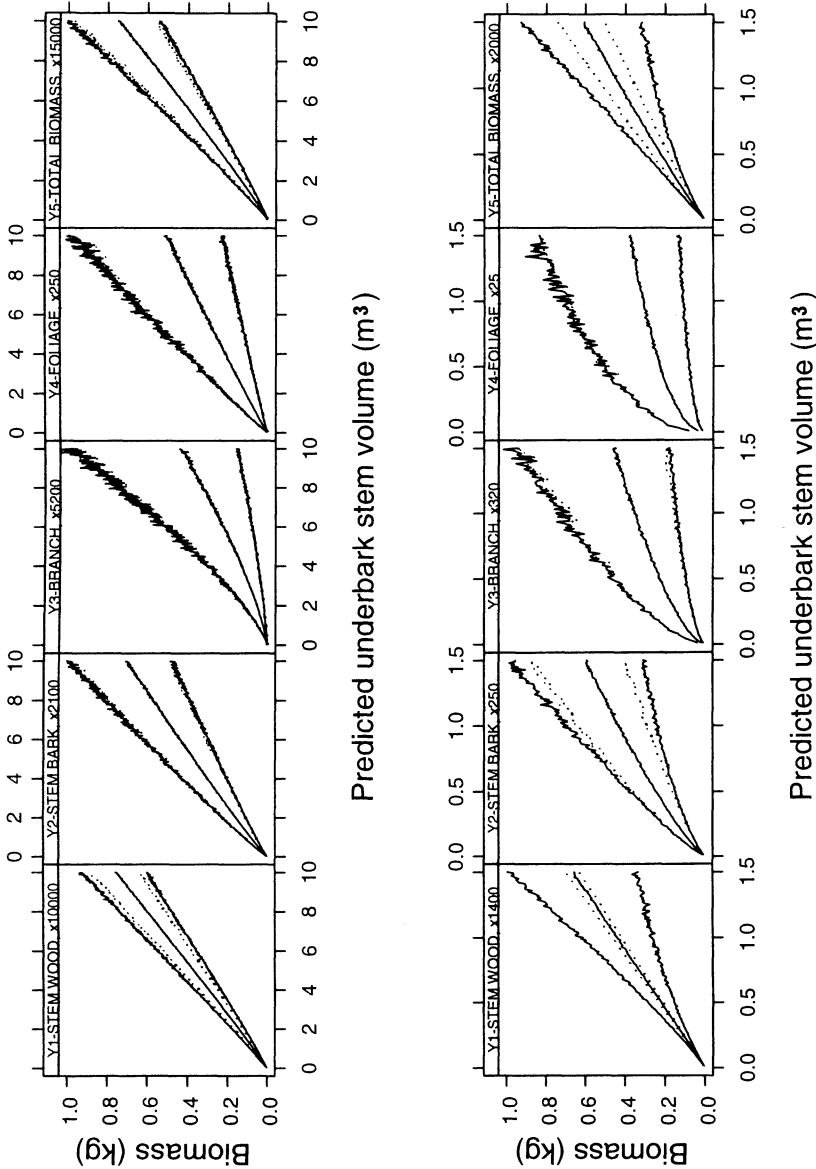
FIG. 4—The mean and 95% confidence bands of the stochastic predictions for all biomass components of *E. fastigata* (top) and *A. dealbata* (bottom). To obtain absolute values for the y-axis, multiply the relative scales by the number after the code of biomass component in the strip. The dotted lines show confidence bands when letting $\varepsilon_i = 0$ in the stochastic simulations (*see* text).

In comparison, stem volume equations are usually constructed using samples that are often many times larger than the sample size for biomass. Converting stem volume estimates, that are already available in forest inventory and growth and yield systems, to biomass estimates should provide more reliable estimates of biomass at a more local management level such as site class, compartments, or stands as demonstrated by Schroeder *et al.* (1997) and Usoltsev & Hoffmann (1977). Rather than using a constant conversion factor (e.g., Whittaker 1961; Adams 1982; Grierson *et al.* 1992), the conversions from stem volume to biomass can be achieved through a system of additive equations, as shown in this paper.
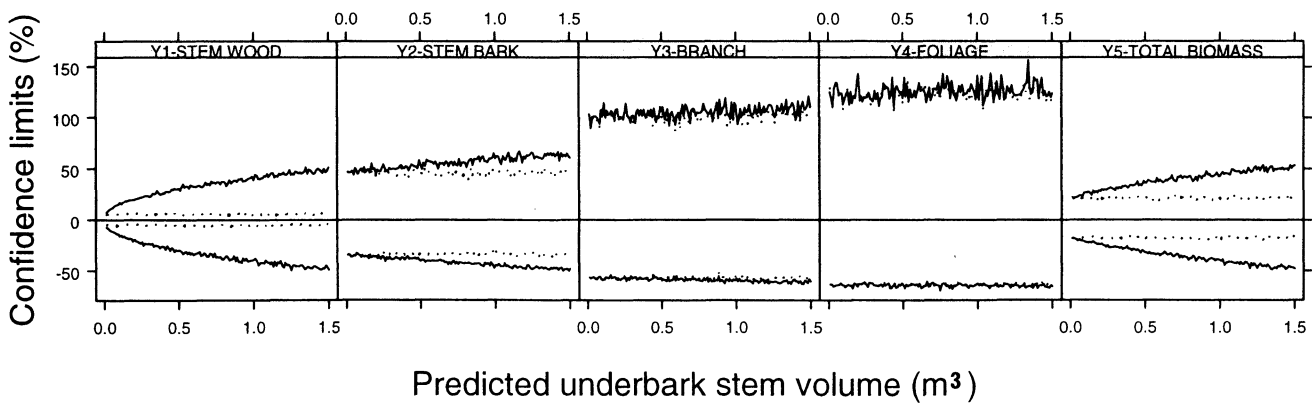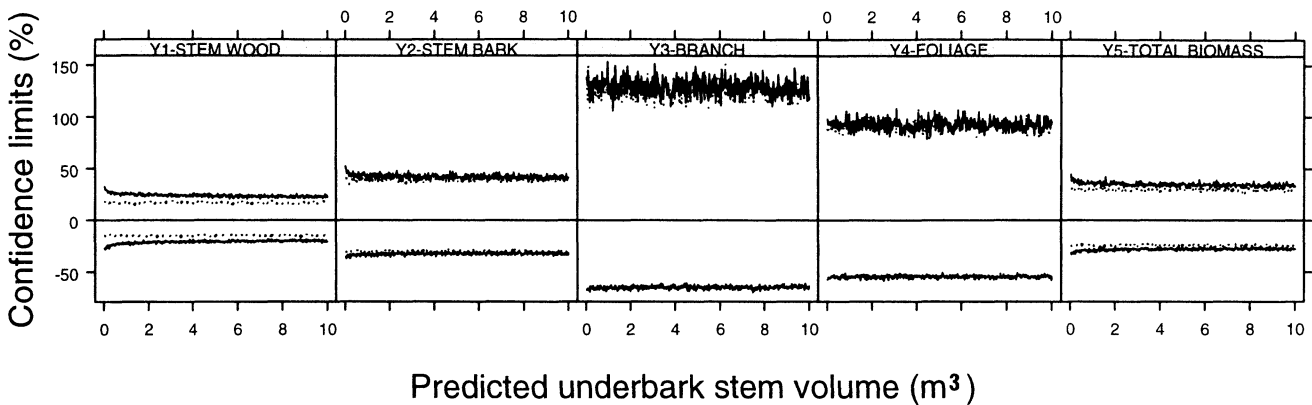
FIG. 5–Percentage confidence bands of the stochastic predictions for all biomass components of *E. fastigata* (top) and *A. dealbata* (bottom). The dotted lines show confidence bands when letting $\varepsilon_v = 0$ in the stochastic simulations (*see* text).

Biomass additivity is a desirable characteristic of a system of equations for predicting tree component as well as total tree biomass since it eliminates the inconsistency between the sum of predicted values for the tree components and the prediction for the total tree. Different model specifications and estimation methods have been suggested for forcing additivity on
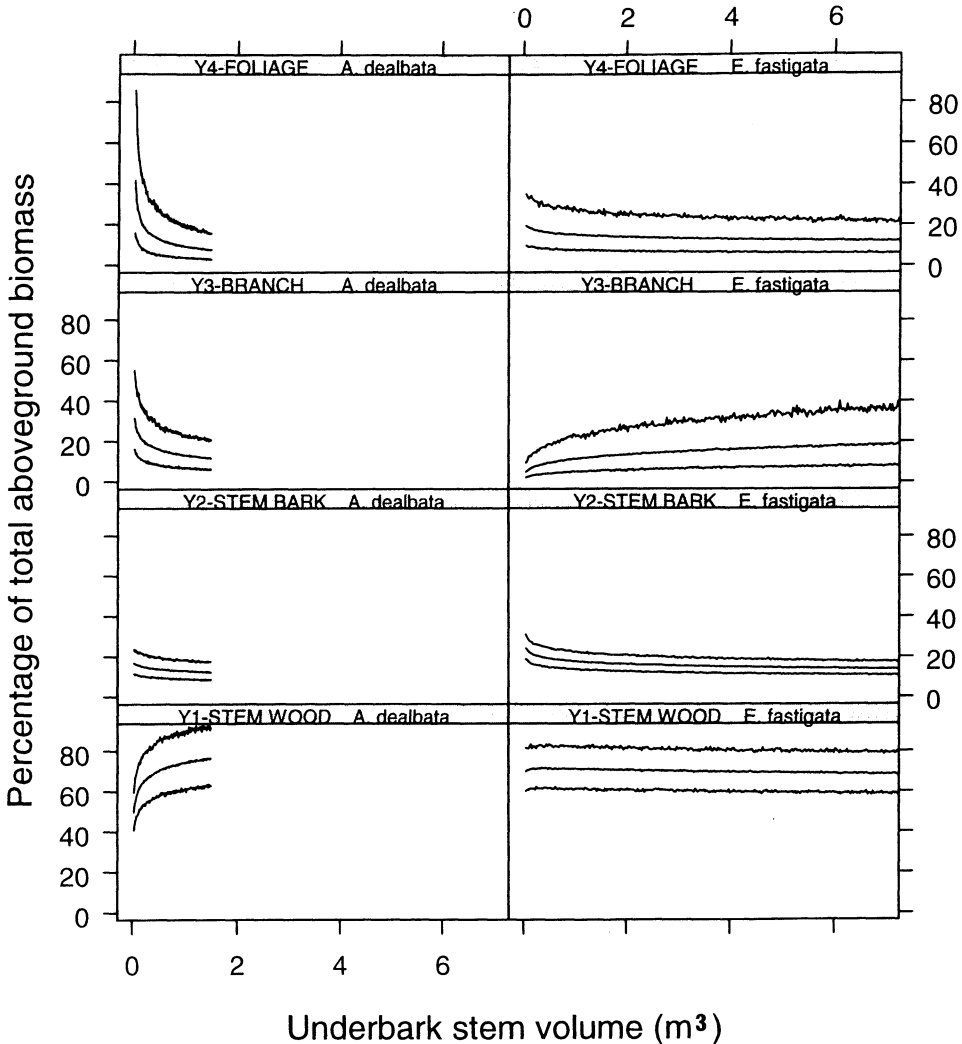
FIG. 6–The mean and 95% confidence bands of biomass distribution for the two species
     obtained from the stochastic predictions.

a set of biomass equations (Kozak 1970; Chiyenda & Kozak 1984; Cunia & Briggs 1984,
1985; Reed & Green 1985). The deterministic part of the model specification as in Equation
(1) of this paper is similar to that reported by Reed & Green (1985) for demonstrating the use
of a loss function in the estimation of the system of equations for predicting biomass from
diameter with additivity. But the specification of the error terms is quite different. Multiplicative
error terms are specified in this paper, while additive error terms were used by Reed & Green
(1985). Further, the specification of the error structure in this paper explicitly incorporates
the cross-equation error correlation, the correlation that naturally exists among biomass
components of the same tree. Taking this correlation into account would result in more
efficient estimation of the system of equations than non-linear OLS, and the gain in
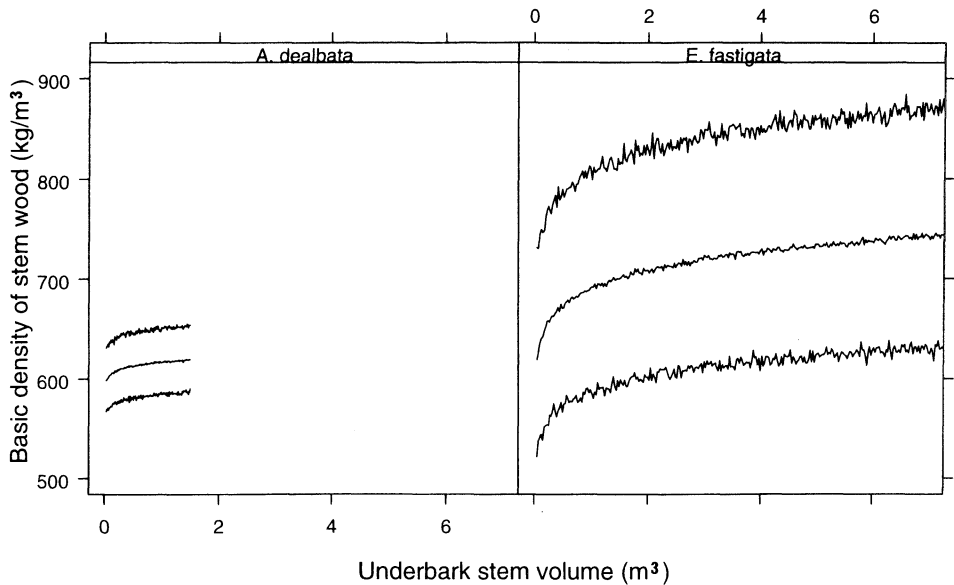
FIG. 7–The mean and 95% confidence bands of the basic density of stemwood for the two species obtained from the stochastic predictions.

efficiency can be expected to increase with sample size according to statistical theory (Zellner 1962; Srivastava & Giles 1987; Judge *et al.* 1988). In a recent review of tree and stand biomass assessments, Parresol (1999) showed an example of a system of linear equations, whose parameters were estimated by SUR with linear restrictions, that resulted in more efficient parameter estimation and additive predictions of biomass. Even under the constraint of additivity, the SUR estimator still achieved lower variance and was a more efficient estimator than other methods (Parresol 1999). This example clearly demonstrated that the SUR estimator is the method of choice for efficient parameter estimates and additive predictions of biomass.

As with single biomass equations, log transformation bias also exists in a system of additive equations as specified in this paper. Although several estimators of the bias correction factor θ in Equation (11) have been proposed for a single equation (Finney 1941; Bradu & Mundlak 1970; Baskerville 1972; Teekens & Koerts 1972; Evans & Shaban 1976; Snowdon 1991), none will maintain additivity among the component equations when applied individually to each component equation in a system of additive biomass equations. The regression-based bias correction factor and the procedures for its estimation proposed in this paper represent the first attempt to correct log transformation bias and maintain additivity for a system of biomass equations. Like those estimators for a single equation, the performance of the regression-based bias correction factor is also data-dependent. Detailed statistical properties of the regression-based bias correction factor and the estimation procedure for a system of additive equations need to be examined in relation to sample size, sampling methods, and other characteristics of the sample data in future research.

Apart from efficient estimates and additive predictions of biomass, using a system of additive equations has an added advantage in that the estimated cross-equation error

covariance matrix can be used to evaluate more realistically the precision of biomass prediction through stochastic simulations. The results provide a clear indication as to whether the required precision of biomass prediction is met for a particular objective of investigation and, if not, where improvements can be made. For example, the confidence bands for stemwood and total biomass were much narrower for *A. dealbata* when stem volume V was known (Fig. 4 and 5). This reduction in the width of the confidence bands indicated that there is much to be gained in the precision of biomass prediction by increasing the precision of stem volume estimates using a larger sample size for volume equations. So far, little such statistical information on precision has accompanied published biomass predictions.

ACKNOWLEDGMENTS

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