Research Article

Biomass Modelling of Androstachys johnsonii Prain: A Comparison of Three Methods to Enforce Additivity

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Three methods of enforcing additivity of tree component biomass estimates into total tree biomass estimates for Androstachys johnsonii Prain were studied and compared, namely, the conventional (CON) method (a method that consists of using the same independent variables for all tree component models, and for total tree model, and the same weights to enforce additivity), seemingly unrelated regression (SUR) with parameter restriction, and nonlinear seemingly unrelated regression (NSUR) with parameter restriction. The CON method was found to be statistically superior to any other method of enforcing additivity, yielding excellent fit statistics and unbiased biomass estimates. The NSUR method ranked second best but was found to be biased. The SUR method was found to be the worst; it exhibited large bias and had a poor fit for the biomass. Therefore, we recommend that only the CON and NSUR methods should be used for further estimates, provided that their limitations are considered, that is, exclusion of contemporaneous correlations for the CON method and consideration of the significant bias of the NSUR method.

1. Introduction

In the early 1960s, Androstachys johnsonii Prain (A. johnsonii) had already been reported to be almost completely restricted to Mozambique [1], presumably due to overexploitation. Five decades later, there is still a lack of studies on this species in any branch of forest science, particularly tree allometry, supporting that this species may indeed be restricted to Mozambique. Moreover, in Mozambique, biomass models have rarely been reported for any tree species, and no such models have been described for A. johnsonii. Isolated studies in Mozambique have focused on Miombo woodlands and some forest plantations and are often part of research theses or forestry projects; therefore, the results are not always made public. Generally, such studies have only considered the aboveground biomass and have not included a breakdown of further tree components.

A. johnsonii woodlands (Mecrusse) are very important. Besides being restricted to Mozambique [1], Mecrusse has important socioeconomic value to local communities, which use stakes of A. johnsonii in the construction of homes, shelters, and furniture and sell them for income generation. At the global scale, Mecrusse is reported to be a tipping point in regional ecological and socioeconomic development [2], hence the importance of modelling and estimating its biomass.

The estimation of aboveground biomass is important to predict the amount of carbon that is sequestered [3–5], to assess nutrient cycling and fluxes and energy wood potentials [4, 6], and to provide estimates for the different tree components [5]. These types of estimates are important for several reasons as follows: (i) stem wood biomass is an important quantity because this component is the only one used in the forest industry, and the carbon therefore remains stored for a long time and is not released into the atmosphere; (ii) in many species, branches and foliage are left in the forest and decompose, releasing CO₂ and nutrients; (iii) in some species, especially broadleaf species, the branches are collected by members of local communities for use as firewood, which will result in release of CO₂;
### Table 1: Summary statistics for the independent and dependent variables.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Minimum</th>
<th>Q0.25</th>
<th>Median</th>
<th>Average</th>
<th>Q0.75</th>
<th>Maximum</th>
<th>SD</th>
<th>CV (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>DBH (cm)</td>
<td>5.00</td>
<td>11.00</td>
<td>17.50</td>
<td>17.59</td>
<td>24.00</td>
<td>32.00</td>
<td>7.51</td>
<td>42.72</td>
</tr>
<tr>
<td>Total tree height, H (m)</td>
<td>5.69</td>
<td>11.21</td>
<td>12.77</td>
<td>12.32</td>
<td>13.90</td>
<td>16.00</td>
<td>2.14</td>
<td>17.35</td>
</tr>
<tr>
<td>Crown height, CH (m)</td>
<td>0.70</td>
<td>3.74</td>
<td>5.16</td>
<td>5.05</td>
<td>6.15</td>
<td>9.92</td>
<td>2.01</td>
<td>39.86</td>
</tr>
<tr>
<td>Live crown length, LCL (m)</td>
<td>1.10</td>
<td>5.50</td>
<td>7.05</td>
<td>7.27</td>
<td>8.90</td>
<td>13.50</td>
<td>2.47</td>
<td>34.05</td>
</tr>
<tr>
<td>Belowground biomass (kg)</td>
<td>2.55</td>
<td>11.66</td>
<td>36.04</td>
<td>47.73</td>
<td>73.49</td>
<td>162.10</td>
<td>41.21</td>
<td>86.33</td>
</tr>
<tr>
<td>Stem wood biomass (kg)</td>
<td>4.95</td>
<td>30.51</td>
<td>103.18</td>
<td>124.07</td>
<td>197.62</td>
<td>357.35</td>
<td>99.50</td>
<td>80.20</td>
</tr>
<tr>
<td>Stem bark biomass (kg)</td>
<td>0.68</td>
<td>3.52</td>
<td>11.17</td>
<td>14.20</td>
<td>22.60</td>
<td>55.80</td>
<td>12.37</td>
<td>87.14</td>
</tr>
<tr>
<td>Crown biomass (kg)</td>
<td>3.04</td>
<td>13.68</td>
<td>37.36</td>
<td>58.39</td>
<td>80.44</td>
<td>216.69</td>
<td>59.08</td>
<td>101.17</td>
</tr>
<tr>
<td>Total tree biomass (kg)</td>
<td>12.48</td>
<td>59.90</td>
<td>204.39</td>
<td>244.39</td>
<td>368.23</td>
<td>752.57</td>
<td>204.33</td>
<td>83.61</td>
</tr>
</tbody>
</table>

Q0.25 = first quartile; Q0.75 = third quartile; SD = standard deviation; CV = coefficient of variation.

(iv) the stump and root system are left in the forest, allowing the stump to either sprout (regrow), continuing the sequestration process, or decompose along with the roots, releasing CO$_2$ and nutrients; and (v) in some tree species, belowground biomass can account for more than one-third of the total biomass [7]. Hence, it is critical to estimate the biomass of all tree components as well as the total tree biomass in order to assess the global carbon balance.

However, the biomass estimates of the considered tree components often do not sum to the estimate of the total tree biomass, and a desired and logical feature of the tree component regression equations is that the predictions of the components sum to the prediction for the total tree. This feature is called additivity. Various authors, such as Goicoa et al. [5], Kozak [8], Cunia [9], Cunia and Briggs [10, 11], Jacobs and Cunia [12], Parresol [4, 13], and Carvalho and Parresol [14], have proposed and/or discussed various methods to ensure the property of additivity.

The objective of this study was to fit independent linear and nonlinear tree component and total tree biomass models and compare three methods of enforcing the property of additivity (the conventional (CON) method, seemingly unrelated regression (SUR) with parameter restriction, and nonlinear seemingly unrelated regression (NSUR) with parameter restriction) for *A. johnsonii* tree species.

The CON method consists of using the same independent variables for all tree component models, and for total tree model, and the same weights to enforce additivity [4]. The SUR and NSUR methods consist in first fitting and selecting the best linear and nonlinear models, respectively, for each tree component. The total tree model is a function of the independent variables used in each component model. Then, all models, including the total, are fitted again simultaneously using joint-generalized least squares under the restriction of the coefficients of regression which ensures the additivity property [4].

### 2. Materials and Methods

#### 2.1. Study Area

*Mecrusse* is a forest type where the main species, many times the only one, in the upper canopy is *A. johnsonii* [15].

In Mozambique, *Mecrusse* woodlands are mainly found in Inhambane and Gaza provinces and in Massangena, Chicualacuala, Mabalone, Chigubo, Guijá, Mabote, Funhalouro, Panda, Mandlakazi, and Chibuto districts. The eastern-most *Mecrusse* patches, covering the last five districts, were defined as the study area. The study area had an extension of 4,502,828 ha [16], of which 226,013 ha (5%) was covered by *Mecrusse* woodlands.

The climate is dry and tropical throughout the study area, except in the west part of the *Panda* district and the southwest part of the *Mandlakazi* district, where the climate is humid and tropical [16–21]. The climate has two seasons: the warm or rainy season from October to March and the cool or dry season from March to September [17–21].

The mean annual temperature is generally greater than 24°C, and the mean annual precipitation varies from 400 to 950 mm [16–21]. According to FAO classification [22], the soils in the study area are mainly Ferralic Arenosols covering more than 70% of the study area [16]. Arenosols, Umbric Fluvisols, and Stagnic soils are also predominant in the northern-most part of the study area [16].

The study area is characterized by a shortage of water resources as well as precipitation; thus, of the five districts that made up the study area, only the districts of Chibuto and Mandlakazi have water resources [16–21], either from precipitation or from lakes and rivers.

#### 2.2. Data Acquisition

A total of 93 trees (2 to 6 per plot) selected across all size classes (Table 1) were destructively sampled within 23 circular plots randomly located in the study area. Diameter at breast height (DBH), total tree height (*H*), crown height (CH), and live crown length (LCL) were measured on the felled trees. Trees were divided into the following tree components: (1) root system, (2) stem wood, (3) stem bark, and (4) crown. Tree components were sampled and the dry weights were estimated as follows.

##### 2.2.1. Root System

The stump height was predefined as being 20 cm for all trees and considered as part of the taproot, as recommended by Parresol [13] and because in larger *A. johnsonii* trees this stump height (20 cm) is affected by

...
the root buttress; therefore, the root collar was also considered part of the taproot. The root system was divided into 3 subcomponents: fine lateral roots, coarse lateral roots, and taproot. Lateral roots with diameters at insertion point on the taproot < 5 cm were considered as fine roots and those with diameters ≥ 5 cm were considered as coarse roots.

First, the root system was partially excavated to the first node, using hoes, shovels, and picks, to expose the primary lateral roots (Figures 1(a)–1(c)). The primary lateral roots were numbered and separated from the taproot with a chainsaw (Figures 1(b) and 1(c)) and removed from the soil, one by one. This procedure was repeated in the subsequent nodes until all primary roots were removed from the taproot and the soil. Finally, the taproot was excavated and removed (Figures 1(d)–1(f)). The complete removal of the root system was relatively easy because 90% of the lateral roots of *A. johnsonii* are located in the first node, which is located close to ground level (Figures 1(a)–1(d)); the lateral roots grow horizontally to the ground level, and do not grow downwards; and because the taproots had, at most, only 4 nodes and at least 1 node (at ground level).

Fresh weight was obtained for the taproot, each coarse lateral root and for all fine lateral roots. A sample was taken from each subcomponent, fresh weighed, marked, packed in a bag, and taken to the laboratory for oven drying. For the taproot, the samples were two discs, one taken immediately below the ground level and another from the middle of the taproot. For the coarse lateral roots, two discs were also taken, one from the insertion point on the taproot and another from the middle of it. For fine roots the sample was 5 to 10% of...
the fresh weight of all fine lateral roots. Oven drying of all samples was done at 105°C to constant weight (i.e., to approximately, 0% moisture content), hereafter, referred to as dry weight.

2.2.2. Stem Wood and Stem Bark. Felled trees were scaled up to a 2.5 cm top diameter. The stem was defined as the length of the trunk from the stump to the height that corresponded to 2.5 cm diameter. The remainder (from the height corresponding to 2.5 cm diameter to the tip of the tree) was considered a fine branch. The stem was divided into sections, the first with 1.1 m length, the second with 1.7 m, and the remaining with 3 m, except the last, whose length depended on the length of the stem. Discs were removed on the bottom and top of the first section and on the top of the remaining sections; that is, discs were removed at heights of 0.2 m (stump height), 1.3 m (breast height), and 3 m, and the successive discs were removed at intervals of 3 m to the top of the stem, and their fresh weights were measured using a digital scale.

Diameters over and under bark were taken from the discs in the North-South direction (previously marked on the standing tree) with the help of a ruler. The volumes over and under the bark of the stem were obtained by summing up the volumes of each section calculated using Smalian's formula [27, 28]. Bark volume was obtained from the difference between volume over bark and volume under bark.

The discs were dipped in drums filled with water for its saturation (3 to 4 months) and subsequent determination of the saturated volume and basic density. The saturated volume of the discs was obtained based on the water displacement method [29] using Archimedes’ principle. This procedure was done twice: before and after debarking; hence, we obtained saturated volume under and over the bark.

Wood discs and respective barks were oven dried at 105°C to constant weight. Basic density was obtained by dividing the oven dry weight of the discs (with and without bark) by the relevant saturated wood volume [27, 30]. Therefore, two distinct basic densities were calculated: (1) basic density of the discs with bark and (2) basic density of the discs without bark.

We estimated the basic density at point of geometric centroid of each section using the regression function of density over height [31]. This density value was taken as representative of each section [31].

2.2.3. Crown. The crown was divided into two subcomponents: branches and foliage. Primary branches, originating from the stem, were classified in two categories: primary branches with diameters at the insertion point on the stem ≥ 2.5 cm were classified as large branches, and those with diameters < 2.5 cm were classified as fine branches.

Large branches were sampled similarly to coarse roots, and fine branches and foliage were sampled similarly to fine roots. All the leaves from each tree were collected and fresh weighed together and a sample was taken for oven drying. The subcomponents branches and foliage were not treated as separated components because in the preliminary analysis the weight of the foliage did not show significant variation with DBH, H, CH, and LCL, exhibiting, therefore, poor fits.

2.2.4. Tree Component Dry Weights. Dry weights of coarse and fine roots, large and fine branches, and foliage were obtained from the "fresh weight/oven dry weight" ratio of the respective samples by multiplying it by the relevant subcomponent total fresh weight. Dry weights of the root system and crown were obtained by summing up the relevant subcomponents’ dry weights.

Dry weights of each stem section (with and without bark) were obtained by multiplying respective densities by relevant stem section volumes. Stem (wood + bark) and stem wood dry weights were obtained by summing up each section’s dry weight with and without bark, respectively. The dry weight of the stem bark was obtained from the difference between the dry weights of stem and stem wood. Finally, the total tree biomass was obtained by adding the component dry weights.

2.3. Data Analysis. Several linear and nonlinear regression model forms were tested for each tree component and for the total tree using weighted least squares (WLS). The weight functions were obtained by iteratively finding the optimal weight that homogenises the residuals and improves other fit statistics. Independent tree component models were fitted with the statistical software package R [32] and the functions lm and nls for linear models and nonlinear models (the latter of which using the Gauss-Newton algorithm). The best linear and nonlinear biomass equations selected are given in (1) and (2), respectively. Among the tested weight functions \(1/D, 1/D^2, 1/DH, 1/DLCL, 1/D^2H, 1/D^2LCL\), the best weight function was found to be \(1/D^2H\), for all tree component equations (linear or nonlinear). Although, the selected weight function might not be the best one among all possible weights, it is the best approximation found. Consider

\[
\begin{align*}
\hat{Y}_{\text{Roots}} &= b_0 + b_1 D^2 H, \\
\hat{Y}_{\text{Stem-wood}} &= b_0 + b_1 D^2 H, \\
\hat{Y}_{\text{Stem-bark}} &= b_0 + b_1 D^2 H, \\
\hat{Y}_{\text{Crown}} &= b_0 + b_1 D^2 LCL^{0.25}, \\
\hat{Y}_{\text{Total-tree}} &= b_0 + b_1 D^2 H, \\
\end{align*}
\]

\[\text{(1)}\]

\[
\begin{align*}
\hat{Y}_{\text{Roots}} &= b_0 (D^2 H)^{b_1}, \\
\hat{Y}_{\text{Stem-wood}} &= b_0 D^{b_1} H^{b_2}, \\
\hat{Y}_{\text{Stem-bark}} &= b_0 D^{b_1} H^{b_2}, \\
\hat{Y}_{\text{Crown}} &= b_0 D^{b_1} LCL^{b_3}, \\
\hat{Y}_{\text{Total-tree}} &= b_0 (D^2 H)^{b_4}. \\
\end{align*}
\]

\[\text{(2)}\]

The CON method used the same independent variables for all tree component models and the total tree model and used the same weight functions [4], achieving additivity automatically [5]. For this method, the most frequent best linear model form in (1) among tree components was used for all other components and for total tree biomass. The most frequent
model form in (1) is \( \hat{Y} = b_0 + b_1 D^2 H \); therefore, the structural system of equations for the CON method is given in:

\[
\hat{Y}_{\text{Roots}} = b_{00} + b_{11} D^2 H, \\
\hat{Y}_{\text{Stem-wood}} = b_{20} + b_{21} D^2 H, \\
\hat{Y}_{\text{Stem-bark}} = b_{30} + b_{31} D^2 H, \\
\hat{Y}_{\text{Crown}} = b_{40} + b_{41} D^2 H, \\
\hat{Y}_{\text{Total-tree}} = \hat{Y}_{\text{Roots}} + \hat{Y}_{\text{Stem-wood}} + \hat{Y}_{\text{Stem-bark}} + \hat{Y}_{\text{Crown}} = (b_{10} + b_{30} + b_{50}) + (b_{11} + b_{31} + b_{51}) D^2 H = b_{50} + b_{51} D^2 H.
\]

The SUR method consisted of first fitting and selecting the best linear models for each tree component. The total tree model was a function (sum) of the independent variables used in each tree component model. Then, all models, including the total, were fitted again simultaneously using joint-generalized least squares (also known as SUR) under the restriction of the coefficients of regression, which ensured additivity.

The best linear model forms were found to be \( \hat{Y} = b_0 + b_1 D^2 H \) for belowground, stem wood, and stem bark biomasses and \( \hat{Y} = b_0 + b_1 D^2 \text{LCL}^{0.25} \) for the crown biomass. Summing up the best model forms from each tree component, the model form obtained for the total tree biomass was \( \hat{Y} = b_0 + b_1 D^2 H + b_2 D^2 \text{LCL}^{0.25} \).

However, the system of equations obtained by combining the best linear model forms per component under parameter restriction will not yield effective and precise estimates because, according to SAS Institute Inc. [33], for SUR to be effective, the models must use different regressors.

This requirement is not verified, as three of the four components have identical regressors. Indeed, according to Srivastava and Giles [34], applying SUR to system of the best equations given above is of no benefit when the component equations have identical explanatory variables. Moreover, as stated by Greene [35] and Bhattacharya [36], a system of linear SUR equations with identical regressors yields ineffective estimates of coefficient vectors when compared to equation-by-equation ordinary least squares (OLS).

To eliminate the ineffectiveness caused by identical regressors, SUR was applied using second best regression equations for belowground and stem wood biomasses such that the different tree component equations could have different regressors. The resulting system of equations of biomass additivity is given in (4). However, the results of SUR using the best independent model forms are given in Tables 2 and 3, for demonstration proposes of the ineffectiveness caused by identical regressors. Consider

\[
\hat{Y}_{\text{Roots}} = b_{10} + b_{11} D^2 + b_{12} H, \\
\hat{Y}_{\text{Stem-wood}} = b_{20} + b_{21} D^2, \\
\hat{Y}_{\text{Stem-bark}} = b_{30} + b_{31} D^2 H, \\
\hat{Y}_{\text{Crown}} = b_{40} + b_{41} D^2 \text{LCL}^{0.25}, \\
\hat{Y}_{\text{Total}} = (b_{10} + b_{20} + b_{30} + b_{40}) + (b_{11} + b_{21}) D^2 + b_{33} D^2 H + b_{41} D^2 \text{LCL}^{0.25} + b_{52} H = b_{50} + b_{51} D^2 + b_{52} D^2 H + b_{53} D^2 \text{LCL}^{0.25} + b_{54} H.
\]

Note from the equations in (4) that the intercepts of all tree component biomass models are forced (constrained, restricted) to sum to the intercept of the total tree biomass model, the coefficients of regression for the regressor \( D^2 \) in the root system and stem wood biomass models are
constrained to sum to the coefficient of regression for $D^2$ in the total tree biomass model, and the coefficients for the regressors $H$, $D^2H$, and $D^2LCL$ in the root system, stem bark, and crown biomass models, respectively, are constrained to be equal to the coefficients of the same regressors in the total tree biomass model, thereby achieving additivity.

The NSUR method had the same characteristics and was performed using the same procedures as the SUR method except that the system of equations was composed of nonlinear models. For reference, please see Brandeis et al. [3], Parresol [13], Carvalho and Parresol [14], and Carvalho [37]. The system of equations (including the total tree biomass) obtained by combining the best nonlinear model forms per component under parameter restriction is given by

$$
\begin{align*}
\bar{Y}_{\text{Roots}} &= b_{10} (D^2 H)_1 b_{11}, \\
\bar{Y}_{\text{Stem-wood}} &= b_{20} D^{b_{21}} H^{b_{22}}, \\
\bar{Y}_{\text{Stem-bark}} &= b_{30} D^{b_{31}} H^{b_{32}}, \\
\bar{Y}_{\text{Crown}} &= b_{40} D^{b_{41}} LCL^{b_{42}}, \\
\bar{Y}_{\text{Total}} &= b_{10} (D^2 H)_1 b_{11} + b_{20} D^{b_{21}} H^{b_{22}} + b_{30} D^{b_{31}} H^{b_{32}} + b_{40} D^{b_{41}} LCL^{b_{42}}.
\end{align*}
$$

Note that the coefficients of regression of each regressor in each tree component model are forced (constrained, restricted) to be equal to coefficients of the equivalent regressor in total tree model, allowing additivity.

The systems of equations in (4) and (5) were fitted using PROC SYSLIN and PROC MODEL in SAS software [33], respectively, using the ITSUR option. Restrictions (constraints) were imposed on the regression coefficients by using SRESTRICT and RESTRICT statements in PROC SYSLIN and PROC MODEL procedures, respectively. The start values of the parameters in PROC MODEL were obtained by fitting the logarithmized models of each component in Microsoft Excel.

### 2.4. Model Evaluations and Comparison

The best tree component and total tree biomass equation were selected by running various possible regressions on combinations of the independent variables (DBH, H, and LCL) and evaluating them using the following goodness of fit statistics: adjusted coefficient of determination (Adj.$R^2$), standard deviation of the residuals (S$_{\text{est}}$) and CV of the residuals, mean relative standard error (MRSE), mean residual (MR), and graphical analysis of the residuals. The computation and interpretation of these fit statistics were previously described by Goicoa et al. [5], Gadow and Hui [38], Meyer [39], Magalhães [40], and Ruiz-Peñado et al. [41]. The best models are those with highest Adj.$R^2$, smallest S$_{\text{est}}$, and CV of the residuals, MRSE, and MR and with the residual plots showing no heteroscedasticity, no dependencies or systematic discrepancies.

In addition to the goodness of fit statistics described above, the methods of enforcing additivity were compared using percent standard error of the expected value and percent standard error of the predicted value, as computed in Table 4. The smaller the percent standard error of the expected and percent standard error of the predicted values is, the better the model is in predicting the biomass.

SUR and NSUR methods were used instead of, for example, simply summing the best component biomass models (i.e., Harmonization procedure [42]), because in the latter case the total biomass is not modelled and therefore its fit

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**Table 4: Standard error of the expected and predicted values for different methods.**

<table>
<thead>
<tr>
<th>Statistic</th>
<th>Absolute form</th>
<th>Relative form</th>
</tr>
</thead>
<tbody>
<tr>
<td>Standard error of the expected value for CON</td>
<td>$S(E(y_0)) = S_{x} x \left(1 + \frac{(x_0 - \bar{x})^2}{SS_{x}}\right)$</td>
<td>$S(E(y_0)) % = \frac{S(E(y_0))}{\bar{y}_i} \times 100$</td>
</tr>
<tr>
<td>Standard error of the predicted value for CON</td>
<td>$S(y_0 - \bar{y}) = S_{x} x \left(1 + \frac{(x_0 - \bar{x})^2}{SS_{x}}\right)$</td>
<td>$S(y_0 - \bar{y}) % = \frac{S(y_0 - \bar{y})}{\bar{y}_i} \times 100$</td>
</tr>
<tr>
<td>Standard error of the expected value for SUR</td>
<td>$S(E(y_0)) = \sqrt{S_{y}^2 + f_i(b)^T \Sigma_i f_i(b)}$</td>
<td>$S(E(y_0)) % = \frac{S(E(y_0))}{\bar{y}_i} \times 100$</td>
</tr>
<tr>
<td>Standard error of the predicted value for SUR</td>
<td>$S(y_0 - \bar{y}) = \sqrt{S_{y}^2 + f_i(b)^T \Sigma_i f_i(b)}$</td>
<td>$S(y_0 - \bar{y}) % = \frac{S(y_0 - \bar{y})}{\bar{y}_i} \times 100$</td>
</tr>
<tr>
<td>Standard error of the expected value for NSUR</td>
<td>$S(E(y_0)) = \sqrt{S_{y}^2 + \Sigma_{NSUR} \psi_i(\theta_i)}$</td>
<td>$S(E(y_0)) % = \frac{S(E(y_0))}{\bar{y}_i} \times 100$</td>
</tr>
<tr>
<td>Standard error of the predicted value for NSUR</td>
<td>$S(y_0 - \bar{y}) = \sqrt{S_{y}^2 + \Sigma_{NSUR} \psi_i(\theta_i)}$</td>
<td>$S(y_0 - \bar{y}) % = \frac{S(y_0 - \bar{y})}{\bar{y}_i} \times 100$</td>
</tr>
</tbody>
</table>

Sources: Parresol [13], Lambert et al. [23], Parresol and Thomas [24], Snedecor and Cochran [25], and Yanai et al. [26].
Table 5: Regression coefficients and goodness of fit statistics for the best linear and nonlinear models in (3) and (4), respectively.

| Tree component | Weight function | $b_0$ (±SE) | $b_1$ (±SE) | $b_2$ (±SE) | Adj. $R^2$ (%) | $S_{y|x}$ (kg) | CV (%) | MRSE (kg) | MR (kg) |
|----------------|----------------|-------------|-------------|-------------|----------------|----------------|--------|-----------|--------|
| **Linear models** | | | | | | | | | |
| Roots          | $1/D^2H$        | 0.0252 (±0.0334) | 0.0097 (±0.00002) | 0.0194 (±0.0001) | 94.94 | 9.59 | 20.10 | 0.1520 | $-2.05E-14$ |
| Stem wood      | $1/D^2H$        | 0.6616 (±0.1145) | 0.0251 (±0.0004) | 0.0409 (±0.0014) | 97.49 | 16.66 | 15.84 | 0.0255 | $-7.96E-16$ |
| Stem bark      | $1/D^2H$        | 0.1895 (±0.3503) | 0.0028 (±0.0001) | 0.0353 (±0.0001) | 84.24 | 4.97 | 34.97 | 0.3397 | $-1.96E-16$ |
| Crown          | $1/D^2H$        | $-1.9106$ (±0.1521) | 0.0984 (±0.0044) | 0.1190 (±0.005)  | 84.24 | 27.06 | 46.34 | 1.0292 | $-2.43E-01$ |
| Total tree     | $1/D^2H$        | 1.4066 (±0.2198)  | 0.0494 (±0.0008) | 0.1732 (±0.0017) | 97.61 | 34.92 | 14.29 | 0.0247 | $-1.24E-15$ |
| **Nonlinear models** | | | | | | | | | |
| Roots          | $1/D^2H$        | 0.0091 (±0.0024) | 1.0074 (±0.0841) | 1.1002 (±0.0857) | 94.94 | 10.40 | 21.79 | 0.1480 | $1.90E-05$ |
| Stem wood      | $1/D^2H$        | 0.0197 (±0.0063) | 1.8210 (±0.0567) | 1.3081 (±0.1559) | 97.71 | 18.83 | 15.18 | 0.0272 | $-3.40E-04$ |
| Stem bark      | $1/D^2H$        | 0.0022 (±0.0019) | 1.7451 (±0.1564) | 1.4084 (±0.4355) | 84.84 | 5.70 | 40.11 | 0.3770 | $-2.04E-03$ |
| Crown          | $1/D^2H$        | 0.0350 (±0.0137) | 2.1318 (±0.1385) | 0.5290 (±0.1482) | 84.42 | 26.89 | 46.05 | 0.5396 | $-2.59E-01$ |
| Total tree     | $1/D^2H$        | 0.0533 (±0.0093) | 0.9920 (±0.0196) | 0.9710 (±0.0204) | 97.60 | 38.68 | 15.83 | 0.1192 | $1.10E-05$ |

$SE = $ standard error; ** = significant at α ≥ 5%; * * = not significant at any probability level.

statistics are unknown and because the sum of tree component models with the best fits does not guarantee good fit in the total model and might produce biased estimates for whole tree biomass [6] and, further, because SUR and NSUR, unlike the CON method, take into account the contemporaneous correlation among residuals of the component equations [4, 13, 14, 24]. Nevertheless, the standard deviation and CV of the residuals for the harmonization approach (HAR) were compared with those obtained for SUR and NSUR approaches. Since, in HAR procedure, the total tree biomass is obtained simply by summing the best component models, the standard deviation of the residuals can be computed using the variance of a sum (6) [4, 13]. Consider

$$ S_{y|x}(\text{Total}) = \sqrt{\sum_{i=1}^{n} S_{y-x(i)}^2 + 2 \sum S_{i,j}} $$

(6)

where $S_{y-x}(\text{Total})$ and $S_{y-x(i)}$ are the standard deviation of the residuals of the total tree biomass model and of the $i$th tree component biomass model and $S_{i,j}$ is the covariance of $i$th and $j$th tree component biomass models.

The CV of the residuals is, therefore, computed as

$$ CV(\text{Total}) = \frac{S_{y-x}(\text{Total})}{\bar{Y}_{\text{total}}} \times 100, $$

(7)

where $\bar{Y}_{\text{total}}$ is the average total tree biomass (per tree).

3. Results

3.1. Independent Tree Component and Total Tree Models. The fit statistics and the coefficient of regression for the best tree component and total tree models are given in Table 5 for linear and nonlinear models.

All linear and nonlinear regression equations yielded satisfactory fit statistics. The linear models presented an adjusted $R^2$ varying from 84.24% for stem bark and crown biomass regressions to 97.61% for total tree biomass regression; the precision, as measured by the coefficient of variation (CV) of the residuals, varied from 14.29% for total tree biomass regression to 46.34% for crown biomass regression. On the other hand, the adjusted $R^2$ for nonlinear models varied from 84.42% for crown biomass regression to 97.60% for total tree biomass regression, and the CV of the residuals varied from 15.18% to 46.05%. For either linear or nonlinear models, the biases, as measured by the mean residual (MR), were found to be statistically not significant using Student’s $t$-test, and relatively poor fit statistics were found for stem bark and crown biomass regressions.

3.2. Forcing Additivity. In the models in (1), the most frequent best linear model form is $\tilde{Y} = b_0 + b_1 D^2H$, which was found to be the best for the root system, stem wood, stem bark, and total tree biomasses. This model form was also ranked as the second model form for crown biomass. Therefore, to enforce additivity using the CON approach, this model form was generalized for all tree components and for total tree biomasses. This model form was also ranked as the second model form for crown biomass. Therefore, to enforce additivity using the CON approach, this model form was generalized for all tree components and of the residual biomasses, as can be seen from (3). Tables 6 and 7 illustrate the regression coefficients and the goodness of fit statistics, respectively, for the CON method presented in (3), the SUR method in (4), and the NSUR method in (5).

3.2.1. The CON Method. The results of the CON method were the same as for equation-by-equation WLS in Table 5, except that the model for crown biomass was replaced in order to have the same regressors as the remaining tree components. Better performances were found for total tree, belowground, and stem wood biomass regressions.

The graphs of the residuals against predicted values for the CON method are presented in Figure 2 and did not show any particular trend or heteroscedasticity. The cluster of points was contained in a horizontal band, showing no particular trend, with the residuals almost evenly distributed under and over the axis of abscissa, meaning that there were not obvious model defects.
Table 6: Coefficients of regression for CON, SUR, and NSUR methods.

<table>
<thead>
<tr>
<th>Tree component</th>
<th>Weight function</th>
<th>(b_0) (±SE)</th>
<th>(b_1) (±SE)</th>
<th>(b_2) (±SE)</th>
<th>(b_3) (±SE)</th>
<th>(b_4) (±SE)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>CON method</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Roots</td>
<td>(1/D^2H)</td>
<td>0.2522 (±0.6334)</td>
<td>0.0097 (±0.0002)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Stem wood</td>
<td>(1/D^2H)</td>
<td>0.6616 (±1.1451)</td>
<td>0.0251 (±0.0004)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Stem bark</td>
<td>(1/D^2H)</td>
<td>0.1895 (±0.3504)</td>
<td>0.0028 (±0.0001)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Crown</td>
<td>(1/D^2H)</td>
<td>0.3033 (±1.5640)</td>
<td>0.0118 (±0.0006)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total tree</td>
<td>(1/D^2H)</td>
<td>1.4066 (±2.1984)</td>
<td>0.0494 (±0.0008)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>SUR method</strong></td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Roots</td>
<td>(1/D^2H)</td>
<td>1.6513 (±2.3498)</td>
<td>0.0216 (±0.0407)</td>
<td>−0.4056 (±0.2584)</td>
<td></td>
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</tr>
<tr>
<td>Stem wood</td>
<td>(1/D^2H)</td>
<td>−3.8911 (±0.9553)</td>
<td>0.2106 (±0.0473)</td>
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<tr>
<td>Stem bark</td>
<td>(1/D^2H)</td>
<td>0.1285 (±0.3260)</td>
<td>0.0014 (±0.0001)</td>
<td></td>
<td></td>
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<tr>
<td>Crown</td>
<td>(1/D^2H)</td>
<td>−1.9730 (±1.5045)</td>
<td>0.1114 (±0.0044)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total tree</td>
<td>(1/D^2H)</td>
<td>−4.0843 (±3.1723)</td>
<td>0.3122 (±0.0668)</td>
<td>0.0014 (±0.0001)</td>
<td>0.1114 (±0.0044)</td>
<td>−0.4056 (±0.2584)</td>
</tr>
<tr>
<td><strong>NSUR method</strong></td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Roots</td>
<td>(1/D^2H)</td>
<td>0.0075 (±0.0022)</td>
<td>1.0137 (±0.0326)</td>
<td></td>
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<tr>
<td>Stem wood</td>
<td>(1/D^2H)</td>
<td>0.0131 (±0.0040)</td>
<td>1.7962 (±0.0549)</td>
<td>1.4113 (±0.1470)</td>
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<tr>
<td>Stem bark</td>
<td>(1/D^2H)</td>
<td>0.0001 (±0.0001)</td>
<td>1.6545 (±0.1942)</td>
<td>1.7332 (±0.5460)</td>
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<tr>
<td>Crown</td>
<td>(1/D^2H)</td>
<td>0.0407 (±0.0159)</td>
<td>2.2302 (±0.1343)</td>
<td>0.3146 (±0.1214)</td>
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<td></td>
</tr>
<tr>
<td>Total tree</td>
<td>(1/D^2H)</td>
<td></td>
<td></td>
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</tr>
</tbody>
</table>

SE = standard error; "*" = significant at \(\alpha \geq 5\); "*" = not significant at any probability level.

Table 7: Fit statistics for CON, SUR, and NSUR methods.

<table>
<thead>
<tr>
<th>Tree component</th>
<th>Weight function</th>
<th>Adj.(R^2) (%)</th>
<th>(S_{yx}) (kg)</th>
<th>CV (%)</th>
<th>MRSE (kg)</th>
<th>MR (kg)</th>
<th>(\bar{\sigma}_i)</th>
<th>(\sigma^2_{\text{SUR}})</th>
<th>(\sigma^2_{\text{NSUR}})</th>
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<tbody>
<tr>
<td><strong>CON method</strong></td>
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<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Roots</td>
<td>(1/D^2H)</td>
<td>94.94</td>
<td>9.59</td>
<td>20.10</td>
<td>0.1520</td>
<td>−2.05E−14</td>
<td>—</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Stem wood</td>
<td>(1/D^2H)</td>
<td>97.49</td>
<td>19.66</td>
<td>15.84</td>
<td>0.0255</td>
<td>−7.96E−16</td>
<td>—</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Stem bark</td>
<td>(1/D^2H)</td>
<td>84.24</td>
<td>4.97</td>
<td>34.97</td>
<td>0.3397</td>
<td>−1.96E−16</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>Crown</td>
<td>(1/D^2H)</td>
<td>82.16</td>
<td>25.11</td>
<td>43.01</td>
<td>1.5596</td>
<td>1.71E−15</td>
<td>—</td>
<td>—</td>
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</tr>
<tr>
<td>Total tree</td>
<td>(1/D^2H)</td>
<td>97.61</td>
<td>34.92</td>
<td>14.29</td>
<td>0.0247</td>
<td>−1.24E−15</td>
<td>—</td>
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<td>—</td>
</tr>
<tr>
<td><strong>SUR method</strong></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Roots</td>
<td>(1/D^2H)</td>
<td>82.44</td>
<td>22.06</td>
<td>46.24</td>
<td>0.1378</td>
<td>0.1769*</td>
<td>0.0581</td>
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<tr>
<td>Stem wood</td>
<td>(1/D^2H)</td>
<td>72.47</td>
<td>60.59</td>
<td>48.83</td>
<td>0.1732</td>
<td>0.6599*</td>
<td>0.5943</td>
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</tr>
<tr>
<td>Stem bark</td>
<td>(1/D^2H)</td>
<td>52.84</td>
<td>10.56</td>
<td>74.38</td>
<td>0.2403</td>
<td>0.0930*</td>
<td>0.0157</td>
<td>0.9906</td>
<td>—</td>
</tr>
<tr>
<td>Crown</td>
<td>(1/D^2H)</td>
<td>81.96</td>
<td>27.22</td>
<td>46.62</td>
<td>1.4330</td>
<td>−0.1188*</td>
<td>0.1053</td>
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<tr>
<td>Total tree</td>
<td>(1/D^2H)</td>
<td>86.88</td>
<td>96.67</td>
<td>39.56</td>
<td>0.0791</td>
<td>0.8109*</td>
<td>9.1562</td>
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<tr>
<td><strong>NSUR method</strong></td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Roots</td>
<td>(1/D^2H)</td>
<td>92.76</td>
<td>12.84</td>
<td>26.92</td>
<td>0.1168</td>
<td>0.0805*</td>
<td>0.0244</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Stem wood</td>
<td>(1/D^2H)</td>
<td>92.27</td>
<td>35.66</td>
<td>28.74</td>
<td>0.0440</td>
<td>0.316*</td>
<td>0.1718</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Stem bark</td>
<td>(1/D^2H)</td>
<td>78.12</td>
<td>6.85</td>
<td>48.25</td>
<td>0.2084</td>
<td>0.0423*</td>
<td>0.0072</td>
<td>4.7801</td>
<td>—</td>
</tr>
<tr>
<td>Crown</td>
<td>(1/D^2H)</td>
<td>85.27</td>
<td>26.41</td>
<td>45.23</td>
<td>0.8348</td>
<td>−0.0049</td>
<td>0.0859</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total tree</td>
<td>(1/D^2H)</td>
<td>67.76</td>
<td>53.32</td>
<td>21.82</td>
<td>0.0321</td>
<td>0.4296*</td>
<td>6.7590</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

"*" = significant at \(\alpha \geq 5\); "*" = not significant at any probability level.

3.2.2. SUR Method. As can be verified from Table 7, the adjusted \(R^2\) varied from 52.84% for stem bark to 86.88% for total tree biomass regression, and the CVs of the residuals varied from 39.56% for total tree biomass regression to 74.38% for stem bark. All tree components and total tree models were found to be biased, and all of these models underestimated the biomass, except for the crown biomass, which was overestimated, as was observed from the mean
residual (MR). Using Student’s *t*-test, these biases (MRs) were found to be statistically significant (statistically different from zero).

The biases, model defects (under and/or overestimation, heteroscedasticity), and patterns that indicated systematic discrepancies are illustrated by the graph of the residuals in Figure 3. Analyses of the residuals for SUR did not reveal heteroscedasticity but showed that the residuals were mostly agglomerated over the axis of abscissas, meaning that the designed models predicted biomass values smaller than the observed ones, underestimating the biomass (producing positive residuals). This happened to all tree components, except for the crown biomass.

3.2.3. NSUR Method. Component models (Tables 6 and 7) showed an adjusted $R^2$ varying from 78.12% for stem bark to 92.76% for roots. The lowest adjusted $R^2$ was found for the total tree model (67.76%). The CVs of the residuals varied from 21.82% for total tree to 48.25% for the stem bark model. All tree components (except the crown) and the total tree models were biased, underestimating the biomass significantly, as shown by the observation that the MRs were significantly different from zero.

Overall, the distribution of the residuals (Figure 4) was satisfactory. Minor defects were found for crown and total tree models.
Comparing the different methods based on the relative standard errors of the expected and predicted values for total tree biomass, computed from 11 randomly selected trees from different diameter classes (Table 8), we found that the conventional method had the smallest average standard errors of the expected and predicted total tree biomass values (2.02% and 2.20%, resp.), followed by the NSUR method (3.52% and 3.68%, resp.), and lastly the SUR method (7.72% and 7.75%, resp.). These data indicated that the CON method yielded narrower confidence and prediction intervals than the NSUR and SUR methods.

4. Discussion

4.1. Independent Tree Component and Total Tree Models. Linear and nonlinear models were fitted for tree component and total tree biomass estimation. The difference between the performance of the selected linear and nonlinear tree component models is negligible. However, Salis et al. [43], Ter-Mikaelian and Korzukhin [44], and Schroeder et al. [45] found nonlinear models to perform better than the linear ones.

The crown models for both linear and nonlinear models were found to be less accurate and precise than the other tree components.
component models, as evaluated by its adjusted $R^2$ and CVs of the residuals, suggesting more variability. According to Pardé [46], as cited by Carvalho and Parresol [14], this is because of the variability of the internal crown structure, number of branches, and variation in wood density along the branches.

4.2. Additivity. Based on all of the results and analyses, the CON method was significantly superior to the SUR and NSUR methods and showed the best fit statistics for every tree component and total tree biomass models, including the largest adjusted $R^2$, smallest CV of the residuals, and no significant model bias or defects. However, although the CON method was found to be statistically superior, it should be noted that it holds only under the assumption of independence among components [4], implying that the residuals are interrelated, therefore not taking into account contemporaneous correlations.

Among the methods that consider contemporaneous correlations (i.e., SUR and NSUR), NSUR appeared superior to SUR. For all tree components, NSUR was superior to SUR, with the higher adjusted $R^2$, smaller CV of the residuals, and less bias. However, the total tree model of the SUR method presented a higher adjusted $R^2$ when compared to the total tree model of the NSUR method. Figure 5 shows that the SUR method described the data quite poorly, whereas the CON and NSUR methods described the data satisfactorily, even for the total tree model, for which the SUR method had the higher adjusted $R^2$ value than the NSUR method.
Table 8: Relative standard errors (%) of the expected and predicted total tree biomass values for 11 randomly selected trees.

<table>
<thead>
<tr>
<th>D</th>
<th>H</th>
<th>CH</th>
<th>LCL</th>
<th>CON S(𝐸(𝑦_0))%</th>
<th>S(𝑦_0 − ̂𝑦)%</th>
<th>SUR S(𝐸(𝑦_0))%</th>
<th>S(𝑦_0 − ̂𝑦)%</th>
<th>NSUR S(𝐸(𝑦_0))%</th>
<th>S(𝑦_0 − ̂𝑦)%</th>
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<td>5.00</td>
<td>7.60</td>
<td>6.50</td>
<td>1.10</td>
<td>9.8935</td>
<td>10.7478</td>
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<td>57.3862</td>
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<td>8.00</td>
<td>9.16</td>
<td>2.12</td>
<td>7.04</td>
<td>2.4664</td>
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<td>1.3087</td>
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<td>13.46</td>
<td>2.89</td>
<td>10.57</td>
<td>1.3843</td>
<td>1.3873</td>
<td>1.9000</td>
<td>1.9000</td>
<td>2.2690</td>
<td>2.2690</td>
</tr>
<tr>
<td>30.50</td>
<td>15.05</td>
<td>2.16</td>
<td>12.89</td>
<td>1.4515</td>
<td>1.4529</td>
<td>1.9571</td>
<td>1.9571</td>
<td>2.6660</td>
<td>2.6660</td>
</tr>
</tbody>
</table>

Average 2.0167 2.1930 7.7198 7.7489 3.5182 3.6801

S(𝐸(𝑦_0))% = relative standard error of the expected value; S(𝑦_0 − ̂𝑦)% = relative standard error of the predicted value.

Table 9: t-test for the restriction imposed for weighted SUR.

<table>
<thead>
<tr>
<th>Restriction</th>
<th>DF</th>
<th>Parameter estimate</th>
<th>Standard error</th>
<th>t value</th>
<th>Pr &gt;</th>
<th>t</th>
</tr>
</thead>
<tbody>
<tr>
<td>b_{50} = b_{20} + b_{30} + b_{40}</td>
<td>−1</td>
<td>0.6255</td>
<td>0.1204</td>
<td>5.2</td>
<td>&lt;0.0001</td>
<td></td>
</tr>
<tr>
<td>b_{51} = b_{11} + b_{41}</td>
<td>−1</td>
<td>2230.6100</td>
<td>355.3158</td>
<td>6.27</td>
<td>&lt;0.0001</td>
<td></td>
</tr>
<tr>
<td>b_{52} = b_{31}</td>
<td>−1</td>
<td>390.4832</td>
<td>43.5058</td>
<td>8.98</td>
<td>&lt;0.0001</td>
<td></td>
</tr>
<tr>
<td>b_{53} = b_{41}</td>
<td>−1</td>
<td>2270.8888</td>
<td>24.8653</td>
<td>9.13</td>
<td>&lt;0.0001</td>
<td></td>
</tr>
<tr>
<td>b_{54} = b_{32}</td>
<td>−1</td>
<td>4.7892</td>
<td>1.4875</td>
<td>3.22</td>
<td>0.0010</td>
<td></td>
</tr>
</tbody>
</table>

Note: the restrictions are as stated in (4).
Figure 5: Observed biomass versus DBH values and regression lines obtained from the different methods of achieving additivity for (a) belowground, (b) stem wood, (c) stem bark, (d) crown, and (e) total tree biomass.
Table 10: t-test for the restriction imposed for weighted NSUR.

| Restriction Parameter estimate | Standard error | t value | Pr > |t| |
|-------------------------------|----------------|---------|------|---|
| Res1                          | −3162.70        | 356.20  | −8.88| <0.0001 |
| Res2                          | −210.46         | 23.76   | −8.86| <0.0001 |
| Res3                          | −4392.79        | 489.80  | −8.97| <0.0001 |
| Res4                          | −178.30         | 19.99   | −8.92| <0.0001 |
| Res5                          | −150.95         | 16.78   | −9.00| <0.0001 |
| Res6                          | −6811.46        | 732.60  | −9.30| <0.0001 |
| Res7                          | −20.27          | 2.19    | −9.25| <0.0001 |
| Res8                          | −17.20          | 1.85    | −9.31| <0.0001 |
| Res9                          | −877.64         | 94.86   | −9.25| <0.0001 |
| Res10                         | −111.99         | 12.20   | −9.18| <0.0001 |
| Res11                         | −84.74          | 8.80    | −9.63| <0.0001 |

Note: res1 to res11 are the restrictions imposed to each of the 11 regression coefficients in the total tree model, as stated in (5).

SUR when compared to the case where the models are fitted independently.

Due to the large bias found using the SUR method, this method cannot be used for biomass estimation of any tree component. However, because the bias is far smaller than that of the SUR method, the NSUR method can be used for biomass estimation as long as the bias is considered. Moreover, while the NSUR method is not superior to the CON method in terms of bias, it does have the advantage of considering contemporaneous correlation, which the CON method does not.

The CV of the residuals for total tree biomass model obtained using the HAR procedure for the linear and nonlinear models was 72.4 and 69%, respectively; 83 and 216% larger than the CV for total tree model obtained using the SUR and NSUR procedures, respectively. This shows that, in this case, the model for total biomass obtained using SUR or NSUR procedure provides more precise results than what would be obtained by summing up the individual component models to the total (HAR procedure).

4.3. Extrapolation. The models fitted in this research (separately or simultaneously) are based on a dataset of 93 trees with diameters varying from 5 to 32 cm. A. johnsonii trees can reach diameters at breast height (DBHs) larger than 35 cm. In a forest inventory of A. johnsonii tree with a minimum DBH of 10 cm, Magalhães and Soto [48] (unpublished data) found only 13 trees per ha with DBHs larger than or equal to 30 cm, corresponding to only 5% of trees per ha. In this study, using 23 plots randomly distributed in the study area and a minimum DBH of 5 cm, we found only 19 trees per ha with diameters larger than or equal to 32.5 cm, corresponding to 1.54% of the total number of trees per ha. This implied that no serious bias would be added when extrapolating the models (independent tree component or NSUR models) outside the diameter range used to fit the models since very few trees were found outside the diameter range.

4.4. Effect of the Measurement Procedures on the Estimates. In this study, wood density was obtained by dividing oven dry weight (at 105 °C) of the discs (with and without bark) by the relevant saturated wood volume [27, 30] (air not included). It is noteworthy to mention that different definitions of the weight and volume of the discs would potentially influence the estimates of density and therefore biomass. For example, Husch et al. [28] define density as the ratio of oven dry weight and green volume (air included). Compared to the definition adopted by us, such a definition would potentially lead to large values of wood density and consequently wood biomass, as saturated volume is the maximum volume [49] and is expected to be larger than green volume.

Moura et al. [49] found no significant differences between those densities, as according to these authors, the densities must be quite the same because volume is not expected to vary above the fibre saturation point (FSP). FSP of a wood is here defined as the maximum possible amount of water that the composite polymers of the cell wall can hold at a particular temperature and pressure [50], excluding, therefore, free and adsorbed water. Differences in wood density and biomass estimates could also be found if the discs were dried to different moisture content (e.g., 12%) or if a different drying temperature was used (e.g., 65 °C).

Stem was defined as the length from the top of the stump to the height corresponding to 2.5 cm diameter. Differences among stem definitions (e.g., different stump height or different minimum top diameter, stump considered as part of the stem) would affect the biomass estimates, especially stem and root biomasses. Different estimates of root biomass could also be found if the root system was partially removed, as performed by many authors (e.g., [41, 51–54]), if the depths of excavation were predefined [41, 51, 55], if fine roots were excluded [56, 57], and if root sampling procedures were applied, for example, where only a number of roots from each root system are fully excavated, and then the information from the excavated roots is used to estimate biomass for the roots not excavated [58–60].

5. Conclusions

This study showed that CON method was found to be unbiased and to fit the tree component and total tree biomass well; however, the CON method had the disadvantage of not
considering contemporaneous correlations. Among methods that consider contemporaneous correlations, NSUR was far superior to SUR and fit the biomass reasonably well; however, both methods were significantly biased. The CON method can be used safely as long as its limitation is considered. The NSUR method can also be used as long as the bias is accepted and taken into account. Moreover, we recommend that the SUR method should not be used due to its bias and poor description of biomass data. Since the data sets used to build the models (both independent and simultaneous) represented many variations (all diameters, soils, and climatic ranges), the selected models can be used for extrapolation.

Appendix

See Figure 1 and Tables 2 and 3.

The Table 3 shows the results of SUR using the system of the best linear model forms. However, as 3 of the 5 equations in the system use the same independent variables, the SUR is not effective: it has lower adjusted $R^2$, sometimes negative, larger CV of the residuals, larger system variance ($\hat{\sigma}^2_{SUR}$) and larger component covariance errors ($\hat{\sigma}_{ij}$) when compared to the results in Tables 6 and 7. The most jeopardized equations are those sharing the same independent variables.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

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