Original Article

Simultaneous Equations to Estimate Aboveground Biomass of *Pinus caribaea var. hondurensis*

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ABSTRACT

This study aimed to develop equations to predict the biomass of trunks, branches, needles and total individual biomass for *Pinus caribaea* var. *hondurensis*. A simultaneous equation system was also adjusted. Twenty (20) trees from the experimental area of the State University of Southwest Bahia (*UESB*), Vitória da Conquista, Bahia, Brazil, were measured and weighed, while 15 traditional models were tested for dry biomass modeling. Of the models tested for total aboveground biomass, trunk biomass and pine needle/leaf biomass, models 9, 9 and 6, respectively obtained the most accurate adjustments. The models with the best performance for branch biomass were model 2 and logistics. The use of the adjustment method for simultaneous equations assured properties of additivity between biomass compartments and total biomass, preventing distortions between the sum of the individual equations for each compartment and the total equation.

Keywords: simultaneous adjustment, aboveground biomass, modeling.

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1. INTRODUCTION

Forests have received increasing attention given their potential to contribute to reducing greenhouse effects due to their capacity to store carbon via natural biomass production (Sanquetta et al., 2011). Thus, forests are important to establish global carbon equilibrium, since different types of forests store different amounts of carbon as a function of their stage of succession, age, management regime and species composition (Watzlawick, 2004).

A tree's biomass can be quantified using two methods: direct and indirect (Rezende, 2000). The direct method involves felling the tree to exactly determine its measurements. However, when a significant number of measurements have been obtained, indirect methods such as regression models can be used, in which mathematical models are developed which allow us to estimate individual biomass and per unit area. Several studies have been carried out using modeling to estimate *Pinus spp.* biomass. For *Pinus caribaea,* the study by Lima et al. (2016) stands out.

In most cases, modeling to estimate tree biomass is performed in order to independently adjust models, meaning that the estimation is performed for each tree compartment (trunk, bark, branches, needles/leaves, miscellaneous). However, the sum of the estimated biomasses according to these equations for each compartment may not produce the same result obtained using an equation for total tree biomass, resulting in inconsistent results. In order to prevent this problem, equations for biomass compartments and for total biomass must be estimated together through simultaneous estimation, considering the principle of additivity (Kozak, 1970).

According to Parresol (1999), the simultaneous estimation technique provides a system of equations with statistically correlated constraints, which in the case of biomass, implies assembling the equations for total estimation and for the compartments with restrictions on the parameters, thereby assuring the additivity (principle). The specific methods to ensure the additivity of regression functions are presented by Cunia (1979) and Jacobs & Cunia (1980). Dong et al. (2014) successfully employed the NSUR process (*Non-linear Seemingly Unrelated Regressions*) to obtain biomass estimates for *Pinus koraiensis* Sieb. et Zucc compartments.

Therefore, the present study aimed to develop allometric equations to estimate the total dry aboveground biomass and the dry biomass of three tree compartments (trunk with bark, needles and branches) for the *Pinus caribaea* species. Moreover, the study also aimed to develop a simultaneous adjustment evaluation for integrated estimates of these biomasses in a compatible manner.

2. MATERIAL AND METHODS

2.1. Characterization of the study area

The data used in this study was obtained from a *Pinus caribaea* var. *hondurensis* stand located in the experimental area of the State University of the Southwest of Bahia (*UESB*), in Vitória da Conquista - BA, Brazil, at the geographic coordinates 14º53 'S and 40º48' W.

The region is characterized by a humid subtropical climate (Cwb) according to the Köppen classification adapted to Brazil (Alvares et al., 2013), with maximum and minimum temperatures of 25.3 °C and 16.1 °C, respectively. Average annual precipitation is 733.9 mm and the altitude is 928 m. The soil of the region is classified as Dystrophic Yellow Latosol (Melo et al., 2013).

2.2. Data collection

Twenty (20) trees of the *Pinus caribaea* var. *hondurensis* species from a 10-year-old plantation with spacing of 3 m x 3 m were selected and felled. The selection was made within the diametric range of 8.2 to 23.7 cm, distributed into five DBH classes (diameter at breast height) with an amplitude of four centimeters in each class. Therefore, two trees per DBH class were felled. Class amplitude was based on the standard deviation mean of DBH with bark for the population. The number of sample trees used was defined based on studies from the related literature, which adopted a sample number between 10 and 40 trees (Soares et al., 2010; Azevedo et al., 2011; Pelissari et al., 2011). The selected trees were submitted to DBH measurement, and total tree height (TH) was measured after felling. Green biomass quantification was performed by the direct method, with each tree separated into 3 compartments

for weighing: trunk with bark, needles and branches (dry and green branches).

Next, sample portions representative of the needle/leaf and branch biomasses were selected to quantify dry biomass, using about 300 grams per compartment. For the trunk, 3 discs per tree were extracted for dry biomass determination (from the base, middle and upper portions of the tree). For these determinations, the samples were dried in a drying oven with air circulation at a temperature of 65 °C until reaching constant weight. The dried sample portions were weighed in an electronic 1 g precision scale and the dry biomass percentages of each compartment were calculated based on the ratio (Equation 1):

$$DM(\%) = \frac{(DW)}{(GW)} * 100 \qquad (1)$$

DM= dry matter (%);

DW= total dry weight of the compartment (g);

GW= total green weight of the compartment (g).

After determining the moisture content of the samples, it was possible to relate this to the green biomass in the field, thus obtaining the estimated dry biomass for the compartments of each tree.

2.3. Statistical analysis and adjustment of mathematical models

A simple linear correlation matrix was designed with the DBH, TH and wood density (ρ) information obtained for the 20 tree samples for subsequent construction of models to estimate total dry biomass and dry biomass for each tree compartment (trunk, needles/leaves and branches).

Fifteen (15) allometric models were tested, of which 9 were linear and 6 were non-linear (biological growth models), totaling 60 adjusted models (total dry biomass, trunk with bark, needles/leaves and branches) (Table 1). The selected non-linear models only considered one independent variable and were used to estimate biomass as a function of the most easily obtained variable (DBH); these methods included: Weibull (1951), Logistic (Nelder, 1961), Gompertz (Laird, 1965), Schumacher (1939), Silva-Bailey (Silva, 1986) and Richards (1959).

To correct the logarithmic discrepancy of the linearized models, the adjustment statistics were recalculated by applying the Meyer Correction Factor (Equation 2).

Table 1. Tested models for estimating total dry biomass and the compartments of *Pinus caribae*a var. *hondurensis* in Vitoria da Conquista, Bahia, Brazil.

Model Number		Model
Linear models	[1]	$Y = \beta_0 + \beta_1.DBH + \varepsilon$
	[2]	$Y = \beta_0 + \beta_1.DBH + \beta_2.DBH^2 + \varepsilon$
	[3]	$Y = \beta_0 + \beta_1.DBH + \beta_2.DBH^2.TH + \varepsilon$
	[4]	$Y = \beta_0 + \beta_1.DBH + \beta_2.DBH^2 + \beta_3.DBH^2.TH + \varepsilon$
	[5]	$Y = \beta_0 + \beta_1.DBH^2 + \beta_2.DBH^2.TH + \varepsilon$
	[6]	$Y = \beta_0 + \beta_1.DBH + \beta_2.TH + \varepsilon$
	[7]	$log\ Y = \beta_0 + \beta_1.log(DBH) + \varepsilon$
	[8]	$log\ Y = \beta_0 + \beta_1.log(DBH) + \beta_2.log(TH) + \varepsilon$
	[9]	$log\ Y = \beta_0 + \beta_1.log(DBH) + \beta_2.log(TH) + \beta3.log(\rho) + \varepsilon$
Non-linear models	[10] Weibull	$f(x) = \beta_0.(1 - e^{-\beta_1.x^{\beta_2}}) + \varepsilon$
	[11] Logistic	$f(x) = \beta_0 / (1 + \beta_2.e^{-\beta_2.x}) + \varepsilon$
	[12] Gompertz	$f(x) = \beta_0.e^{-\beta_1.e^{-\beta_2.x}} + \varepsilon$
	[13] Schumacher	$f(x) = \beta_0.e^{-\beta_1.\left(\left(\frac{1}{x}\right)\right)} + \varepsilon$
	[14] Silva-Bailey	$f(x) = \beta_0.e^{(\beta_1.(\beta_2^x))} + \varepsilon$
	[15] Richards	$f(x) = \beta_0.(1 - e^{\beta_1 * x})^{\beta_2} + \varepsilon$

Where: Y = Dry biomass of each compartment (kg); DBH = diameter at breast height (cm); TH = total height (m); ρ = density of wood (g.cm^{-3}); log = logarithm in base 10; β_0, β_1, β_2 and β_3 = regression coefficients; f(x) = total dry biomass or dry biomass of the compartments (kg); e = exponential; x = DBH (cm); ε = random error.

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$$FCM=10^{0,5*(S_{yx}^2)} \qquad (2)$$

Where:

S_{yx} = Standard error of estimate.

Four different performance evaluation criteria were used to evaluate the models: Schlaegel determination coefficient ($R^2_{adj.}$), standard error of the percentage estimate (Syx%), Akaike Information Criterion (AIC) and graphical residual analysis. The graphical residual analysis was applied to visualize the deviations between the real and estimated values, and to identify any tendencies in the residual distribution of the equation. Homogeneity of variance, and normality and independence of residues were determined through the Breush-Pagan, Shapiro-Wilk and Durbin-Watson tests, respectively, all at 5% probability.

Moreover, the simultaneous estimation was developed by a system of equations, which made it possible to reconcile the estimates, meaning that the sum result of the equations from each compartment is similar to that of the equation for total individual dry biomass, ensuring the biomass additivity of tree components (Parresol, 1999).

Performance of the simultaneous adjustment followed the procedures described by Sanquetta et al. (2015) for biomass estimation. Therefore, the best performance model for each biomass compartment was selected, selecting models of the same nature (in the case of this study, only linear models). Next, the selected models were adjusted at the same time, establishing restrictions for the parameters in order to ensure that the equation for total biomass corresponded to the sum of the equations for each component i. The calculation was performed using iterative convergence to minimize the sum of squares of the residues using the Gauss-Newton method (Parresol, 2001). Each regression was adjusted using the biomass determined in the independent adjustment (Formulas 3, 4, 5 and 6). Thus, the procedure was applied using the PROC MODEL option of SAS, according to the following specifications:

$$Y_{trunk}=f_1(X_{1j},\beta_{1j})+e_1 \qquad (3)$$

$$Y_{needles}=f_2(X_{2j},\beta_{2j})+e_2 \qquad (4)$$

$$Y_{branches}=f_3(X_{3j},\beta_{3j})+e_3 \qquad (5)$$

$$Y_{total}=f_{total}(X_{1j},X_{2j},X_{3j},\beta_1,\beta_2,\beta_3)+e_{total} \qquad (6)$$

In which:

Y = Biomass of each tree compartment (kg);

f = as a function of

See;

X = variables;

β_n= parameters.

Analysis of the performance of simultaneous adjustments was realized using the same statistical criteria employed to evaluate the independent models.

3. RESULTS AND DISCUSSION

Evaluating the descriptive statistics of the dependent and independent variables, an average diameter of 16.48 cm was observed for *Pinus caribaea* individuals, with a minimum value of 8.20 cm and a maximum of 23.70 cm; average total height of 11.06 m, ranging from 6.40 m to 14.20 m; and mean density of 0.44 g.cm^{-3} with a standard deviation of 0.15 g cm^{-3} (Table 2).

The average total individual dry biomass was 50.31 kg. The trunk presented the largest participation in the individual compartment total biomass (39.18 kg), representing on average 77.88% of the total aboveground biomass, followed by branch biomass (7.70 kg) with 15.3% and needle biomass (3.43 kg) with 6.82%. Similar relative values of aboveground biomass were found by Giongo et al. (2011) for 23-year-old *Pinus elliottii* plantations, located in the municipality of Rio Branco do Sul (PR, Brazil), in which the proportion of trunk biomass represented 81% of total biomass. In analyzing carbon stock in *Pinus spp* plantations in the State of Paraná, Balbinot et al. (2007) also found

Table 2. Descriptive statistics of dependent and independent variables used when adjusting models for biomass estimation.

Variable	Mean	Standard Deviation	N
DBH (cm)	16.48	3.64	20
TH (m)	11.06	1.90	20
ρ (g.cm^{-3})	0.44	0.15	20
Trunk Biomass (kg)	39.18	20.96	20
Needle/Leaf Biomass (kg)	3.43	2.01	20
Branch Biomass (kg)	7.70	4.28	20
Total Biomass (kg)	50.31	26.42	20

that the trunk compartment represented the highest percentage of biomass, with an upward trend as the tree grew.

3.1. Correlation analysis between the variables involved

Using simple linear correlation analysis it was possible to observe that the total aboveground biomass and the trunk, needle and branch compartment biomasses were more strongly correlated with DBH than with total height (TH) (Table 3). The high correlation observed between TH and DBH variables (Table 4) indicates similarity in these variables for explaining biomass variation. When analyzing *Pinus taeda* and *Pinus elliottii*, Schikowski et al. (2013) also found high correlation values between DBH and total height (r = 0.97). On the other hand, density had a low correlation with the total and component biomasses when compared to other independent variables such as DBH and total height.

Table 3. Correlations between the biometric variables used in the settings.

	DBH (cm)	TH (m)	ρ (g.cm^{-3})	Needle Biomass (kg)	Branch Biomass (kg)	Trunk Biomass (kg)	Total Biomass (kg)
DBH (cm)	1						
TH (m)	0.813	1					
ρ (g.cm^{-3})	0.173	0.018	1				
Needle Biomass (kg)	0.734	0.712	0.355	1			
Branch Biomass (kg)	0.797	0.618	0.573	0.726	1		
Trunk Biomass (kg)	0.877	0.723	0.500	0.851	0.849	1	
Total Biomass (kg)	0.881	0.728	0.516	0.868	0.891	0.995	1

Table 4. Adjusted models for biomass in different *Pinus caribaea* compartments.

Compart-ment	Models	β_0	β_1	β_2	β_3	$R^2_{adjusted}$	S_{yx}	$S_{yx}\%$	AIC
	1	-1.590150	0.196665			0.52	0.67	40.51	-14.22
	2	-1.948940	0.244898	-0.001535		0.50	0.69	41.65	-12.26
	3	-0.913616	0.123530	0.000160		0.50	0.68	41.29	-12.61
	4	-2.764560	0.411565	-0.014287	0.000511	0.50	0.68	41.28	-11.83
	5	0.143643	0.002459	0.000244		0.48	0.69	42.10	-11.82
	6	**-2.275050**	**0.124748**	**0.169092**		**0.54**	**0.66**	**39.92**	**-2.95**
	7	-3.610890	3.075550			0.34	0.78	47.57	-7.79
Needles	8	-4.346510	1.553010	2.478750		0.21	0.86	52.10	-3.30
	9	-4.144330	1.153360	2.895130	0.402694	0.33	0.79	47.91	-5.87
	Weibull	14.249000	0.008268	0.981603		0.33	0.79	47.94	-6.63
	Logistc	3.001940	229.280000	0.342447		0.51	0.68	41.15	-12.74
	Gompertz	3.557660	14.485300	0.179183		0.50	0.68	41.31	-12.58
	Schumacher	12.790900	33.839500			0.52	0.67	40.46	-14.27
	Silva-Bailey	0.000471	6.685170	1.011990		0.42	0.74	44.78	-9.35
	Richards	1230.970000	0.002059	0.041189		0.35	0.78	47.15	-7.3
	1	-3.889810	0.470515			0.62	1.32	34.24	13.07
	2	**-8.138820**	**1.041710**	**-0.018173**		**0.62**	**1.32**	**34.12**	**13.00**
	3	-6.100170	0.709462	-0.000522		0.62	1.32	34.31	14.00
	4	-7.830960	0.978800	-0.013359	-0.000193	0.60	1.36	35.12	15.73
Branches	5	-0.914562	0.026467	-0.000828		0.57	1.41	36.55	16.53
	6	-3.478740	0.513679	-0.101489		0.60	1.36	35.10	14.92
	7	-4.087750	3.770120			< 0.1	2.24	57.93	34.10
	8	-4.070990	3.804810	-0.056476		< 0.1	2.31	59.69	36.16
	9	-3.664760	3.001840	0.780123	0.809088	0.49	1.53	39.64	20.57

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Table 4. Continued...

Compart-ment	Models	β_0	β_1	β_2	β_3	$R^2_{adjusted}$	S_{yx}	$S_{yx}\%$	AIC
Branches	Weibull	24.540500	0.013693	0.921127		0.37	1.70	43.90	23.87
	Logistc	**5.606350**	**9764.160000**	**0.630520**		**0.67**	**1.24**	**32.06**	**11.29**
	Gompertz	6.081330	111.365000	0.347799		0.66	1.25	32.38	11.69
	Schumacher	27.271000	32.069500			0.62	1.33	34.32	13.16
	Silva-Bailey	0.015851	4.175830	1.016570		0.45	1.59	41.17	21.30
	Richards	289.876000	0.006522	0.130443		0.42	1.63	42.15	22.24
Trunk	1	-23.174300	2.627070			0.76	5.38	21.00	69.20
	2	-22.386500	2.521170	0.003369		0.74	5.54	27.53	71.20
	3	-21.124700	2.405510	0.000484		0.74	5.53	27.50	71.15
	4	-24.042300	2.859530	-0.022520	0.001038	0.73	5.69	28.31	73.10
	5	-3.836320	0.093832	-0.000818		0.72	5.72	28.45	72.51
	6	-24.130300	2.526690	0.236025		0.74	5.53	27.50	71.15
	7	-2.479460	3.058660			0.60	6.86	34.12	78.92
	8	-2.455810	3.107610	-0.079690		0.58	7.07	35.15	89.96
	9	**-2.097130**	**2.398640**	**0.658970**	**0.714370**	**0.91**	**3.27**	**16.24**	**50.88**
	Weibull	44.320700	0.000059	3.291160		0.75	5.40	26.88	70.24
	Logistc	37.743500	503.069000	0.384253		0.77	5.25	26.11	69.08
	Gompertz	44.278100	22.501300	0.203564		0.76	5.30	26.37	69.48
	Schumacher	200.267000	38.189200			0.76	5.33	26.51	68.83
	Silva-Bailey	0.003229	7.312350	1.010560		0.61	6.78	33.72	79.31
	Richards	1114.300000	0.007622	0.152434		0.50	7.69	38.23	84.33
Total	1	-28.654200	3.294250			0.77	6.57	25.66	77.22
	2	-32.474000	3.807750	-0.016337		0.75	6.76	26.38	79.18
	3	-28.138400	3.238490	0.000122		0.75	6.76	26.40	79.22
	4	-34.637600	4.249870	-0.050165	0.001356	0.74	6.95	27.12	81.07
	5	-4.607220	0.122758	-0.001402		0.73	7.09	27.69	81.12
	6	-29.884100	3.165110	0.303637		0.94	6.76	26.37	81.12
	7	-2.449460	3.120210			0.56	9.04	35.29	89.96
	8	-2.453570	3.111700	0.013862		0.53	9.31	36.35	92.00
	9	**-2.093310**	**2.399600**	**0.755784**	**0.717524**	**0.91**	**4.17**	**16.29**	**60.67**
	Weibull	52.996800	0.000056	3.341420		0.77	6.59	25.72	78.17
	Logistc	45.936500	576.539000	0.400757		0.78	6.39	24.92	76.91
	Gompertz	52.869900	25.695400	0.217948		0.78	6.44	25.15	77.27
	Schumacher	237.114000	36.883600			0.77	6.55	25.55	77.05
	Silva-Bailey	0.007198	7.831580	1.002840		0.17	12.41	48.44	103.49
	Richards	1319.590000	0.007903	0.158058		0.52	9.45	36.89	92.6

A high association was observed between the growth variables (height and diameter) and the biomass amounts (total and compartments). Silveira (2009) also observed that DBH and height are strongly correlated with biomass, and reported that using the diameter variable in its pure or combined form is essential for models that seek to estimate biomass or carbon. When estimating biomass and carbon in native Atlantic Forest species using different models, Lacerda et al. (2009) concluded that the models that use the independent DBH variable in its pure form present a better fit.

The high correlation of biomass with DBH is important since the latter variable (DBH) is an easily measured characteristic, making it possible to estimate the dependent variables quickly and efficiently.

3.2. Adjusting traditional allometric models

The results of traditional adjustments using linear and non-linear models are presented in Table 4. It should be pointed out that the models for estimating total biomass and trunk biomass as a function of the DBH,

height and density variables provide more precise adjustments. The coefficient of determination adjusted for total biomass models ranged from 0.17 to 0.94, while the standard error of the estimate varied between 16.29% and 48.44%, which shows great variation for these statistics.

The model with the best performance for estimating total individual biomass was model 9, which had the best adjustment indicators ($R^2_{adj} = 0.91$; $S_{yx} = 16.29\%$; AIC = 60.67) and balanced graphical residual distribution (Figure 1). Model 6 also had high adjusted coefficient of determination, despite presenting a higher standard error of estimation and AIC value, in addition to a less uniform graphical residual distribution when compared to model 9. For the estimation of the trunk biomass, the model with the best fit was also model 9, with better results for the statistical indicators ($R^2_{adj} = 0.91$; $S_{yx} = 16.24\%$; AIC = 50.88) and a more balanced residual distribution (Figure 1).

Equations for the biomass estimation of needles/leaves and branches presented less satisfactory performance when compared to total biomass and trunk equations. Similar to the present study, Behling et al. (2012) found lower adjustments of the equations for biomass estimates of canopy compartments in relation to those used for biomass estimates of the trunk and total biomass in a settlement of *Acacia mearnsii* at seven-years of age.

For the branch compartment, the best fit was obtained for the logistic model ($R^2_{adj} = 0.67$; $S_{yx} = 32.06\%$; AIC=11.29). The linear model with the best fit was model 2 ($R^2_{adj} = 0.62$; $S_{yx} = 34.12$; AIC = 13.00). Models 1 and 3 presented precision statistics similar to those for model 2, however the latter presented better results and better graphical residual distribution (Figure 1).

Model 6 had the best fit ($R^2_{adj} = 0.54$; $S_{yx} = 39.92\%$; AIC = -2.95) in terms of the estimation of needle/leaf biomass, with a better graphical residual distribution (Figure 1). In all cases, the variance between the errors was constant for different observations, diagnosing data homoscedasticity, and the residual distribution was independent; meaning that the residues are not correlated in series, guaranteeing accuracy of the estimates. On the other hand, the results for the normality test showed that the residues presented normal distribution only for total aboveground biomass and for the branch and needle compartment biomasses, with the trunk biomass

presenting non-normal distribution. Normality of the residues is essential so that the results of adjusting the linear regression model are reliable; therefore, the use of the model to predict the trunk biomass should be applied with caution. All tested models had a significant F value indicating a relationship between the variables. In a study with models similar to those used in the present study, Schikowski et al. (2013), when analyzing the biomass of *Pinus spp*. also found good results in the adjustments for total and trunk biomass, with high R^2_{adj} values and low S_{yx} values.

Incompatibility between total biomass and tree compartment estimates was observed when the equations were estimated independently. In other words, there was an inconsistency in the overall estimation of tree biomass, since the sum of the estimated values for biomass by compartment was not equal to the result of the equation for total tree biomass, indicating a need to apply simultaneous adjustments to ensure additivity of the estimates.

The result for simultaneous adjustment is shown in Table 5. We can see that the SUR method does not aim to improve performance of the equations, but rather to reconcile the biomass estimates by compartment and for total biomass. We also found that the residual distribution showed the same tendency when the two estimation methods were compared. Simultaneous adjustment maintained the homogeneity of variance of the data and also ensured independence of the residues. Furthermore, according to Behling et al. (2012), simultaneous adjustment has an advantage in the estimation process since it does not present distortions between the sum of the biomass obtained from the equations of each compartment and the total equation, as is the case in the independent adjustment.

When studying *Pinus pinaster* stands in central Portugal, Viana et al. (2013) found good-quality simultaneous predictive adjustment statistics for total aboveground biomass. Correia et al. (2008) found that standard errors generally decreased with simultaneous adjustment, leading to greater quality of the final models when estimating the total biomass and aboveground compartments of *Pinus pinea* located in southern Portugal. Simultaneous equations for biomass prediction were also developed for the *Quercus suber* and *Quercus ilex* species (Paulo & Tomé, 2006).
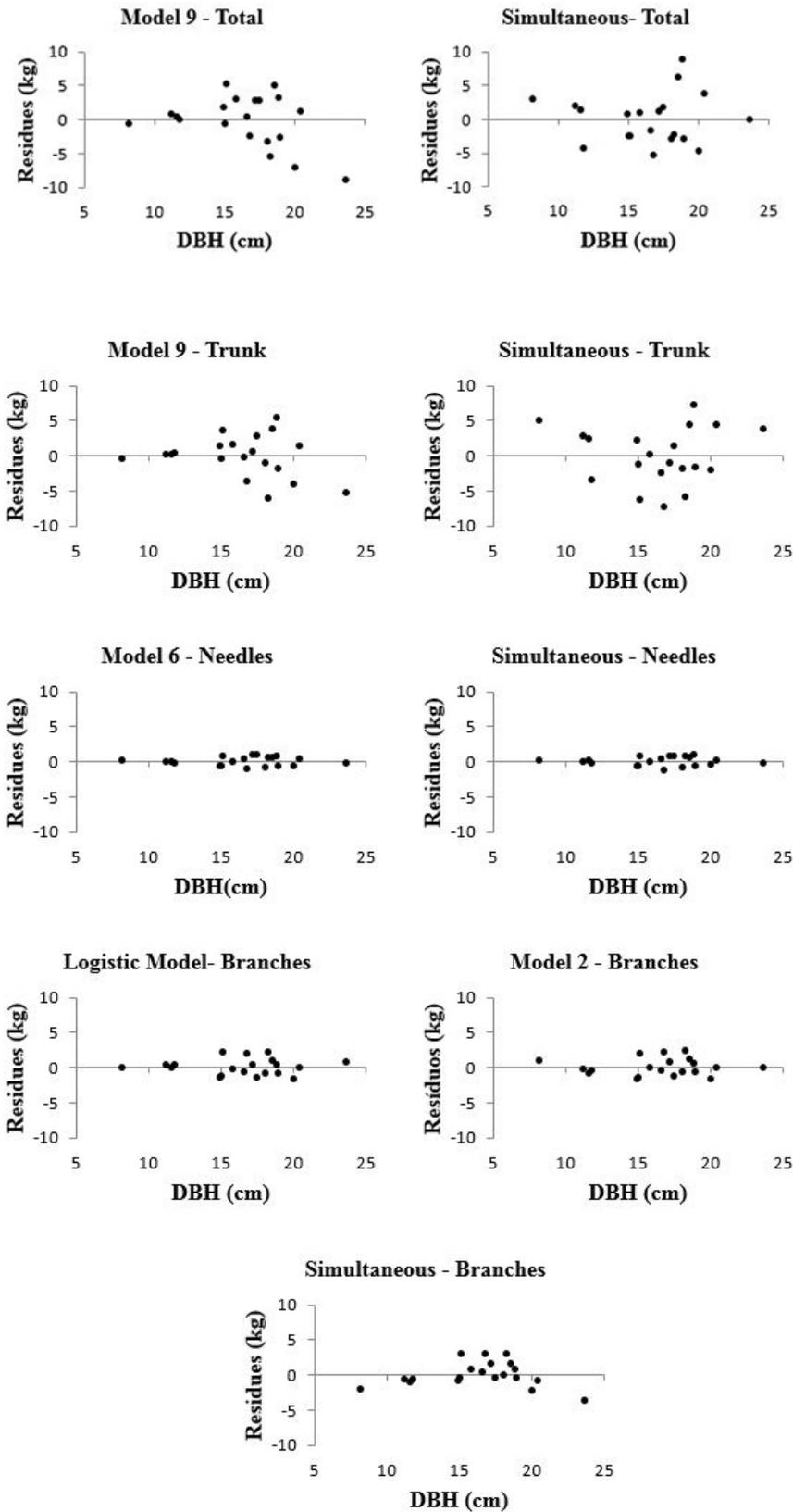
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Figure 1. Absolute residual distribution resulting from the model adjustments for compartments.

Table 5. Results of simultaneous equation adjustments for predicting biomass of *Pinus caribaea* compartments.

Compartment	Simultaneous model	β_0	β_1	β_2	β_3	R^2_{adj}	$S_{yx}\%$
Needles	bsneedles = $\beta_0+\beta_1$DBH+β_2TH	-1.943	0.160	0.087		0.53	40.34
Branches	bsbranches = $\beta_0+\beta_1$DBH+β_2DBH^2	8.631	-1.213	0.054		0.23	48.66
Trunk	bstrunk = $\beta_0+\beta_1$DBH+$\beta_2$ht+$\beta_3\rho$	-41.5	1.760	1.374	39.377	0.84	21.80
Total	bstotal = bsneedles+bsbranches+bstrunk					0.86	19.93

Where: bstrunk = dry biomass of the trunk with bark; bsbranches = dry biomass of the branches; bsneedles = dry biomass of the needles; bstotal = total dry biomass.

4. CONCLUSION

The trunk was the compartment with the highest contribution to total individual biomass, representing on average 77.88% of total individual tree biomass.

Total individual biomass and trunk, branch and needle compartment biomass values were more strongly correlated with DBH. A strong relationship between total aboveground biomass and the trunk and branch compartment biomass was observed, which is due to their cumulative character.

Models 9 and 6 showed the best performance for predicting total dry biomass, and for trunk and needle biomasses, respectively. The best results for predicting branch biomass were obtained with linear model 2 and the logistic model.

Applying the SUR method guarantees the additivity properties between biomass compartments and total biomass, avoiding distortions between the sum of the individual equations for each compartment and the total equation, which occurs when independent equations are used. Therefore, the simultaneous biomass adjustment allows for obtaining compatible estimates, providing better references for the integrated management of these variables.

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