

Predicting total and component biomass of Chinese fir using a forecast combination method

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Accurate estimates of tree biomass are critical for forest managers to assess carbon stock. Biomass of Chinese fir (*Cunninghamia lanceolata* [Lamb.] Hook.) in southern China was assessed by three alternative methods. In the Separate model approach, total and component tree biomass was directly predicted from a regression equation as a function of tree diameter and height. In the Additive model approach, total biomass was predicted as the sum of predictions from all component biomass equations. The Forecast Combination method involved combining predictions from the total biomass equation with the sum of predictions from component biomass equations. Results indicated that the Separate model method outperformed the Additive model method in predicting total and component biomass. The drawback of the Separate model method is that the total is not equal to the sum of its components. The Forecast Combination method provided the overall best prediction for total and component biomass, and still ensured additivity of component biomass predictions.

Keywords: Additivity, Biomass Predictions, *Cunninghamia lanceolata*, Even-aged Plantations, Tree Allometry

Introduction

Forest biomass comprises the arboreal fraction of all existing plant mass in the forest, including stems, branches, leaves, and roots of forest trees (Sanquetta et al. 2015). Due to its important role as carbon pool in forest ecosystems (Fahey et al. 2010) and the laborious and costly process of measuring trees in the forest, there is a great demand to accurately predict tree biomass. A number of approaches for tree biomass prediction have been put forward. A widely used approach is the direct prediction of biomass using allometric relationships from tree measurements, such as diameter at breast height, total tree height, crown radius, and wood density (Chave et al. 2005, Zhang et al. 2013, Goodman et al. 2014, MacFarlane 2015).

There are two methods for predicting

total tree biomass with allometric equations: tree-level and component-level. The tree-level method involves a regression to predict total tree biomass. In the component-level method, prediction of total tree biomass is the sum of predictions of all tree components (leaves, branches, stem, and roots), obtained from separate regressions. There are strengths and weaknesses for each method. The tree-level biomass model predicts total tree biomass directly, but lacks detailed information on biomass of stems, branches, leaves, and roots. On the other hand, the component-level method provides more detailed information, but total tree biomass obtained by summing component predictions could often suffer from accumulation of errors and subsequently poor accuracy and precision. Moreover, in the component-level method, the

sum of the biomass components can generate inconsistent results, as compared to predictions from the total biomass model (Parresol 1999, Sanquetta et al. 2015). To eliminate this inconsistency, several model estimation methods have been suggested to enforce additivity on a system of biomass equations (Jacobs & Cunia 1980, Reed & Green 1985, Tang et al. 2000, Parresol 2001, Bi et al. 2004).

Forecast combination, introduced by Bates & Granger (1969), is a method to improve forecast accuracy (Newbold et al. 1987). This method combines information generated from different models and distributes errors from these models, thus ensuring consistency of outputs from different models. Zhang et al. (2010) used this method to combine tree-level and stand-level predictions of stand basal area.

The objective of this study was to evaluate current methods of predicting total and component biomass against the forecast combination method.

Materials and methods

Study sites

The plantations studied were at Weimin farm (Shaowu city, Fujian province) and Nianzhu farm (Fenyi city, Jiangxi province) in southern China (Fig. 1). Both sites belong to the subtropical monsoon climate region. In Weimin farm, mean annual precipitation is 1768 mm, mean annual temperature is 17.7 °C, and monthly mean temperature ranges from 6.8 °C in January to 28 °C in July. In Nianzhu farm, mean annual temperature and precipitation are 17.2 °C and

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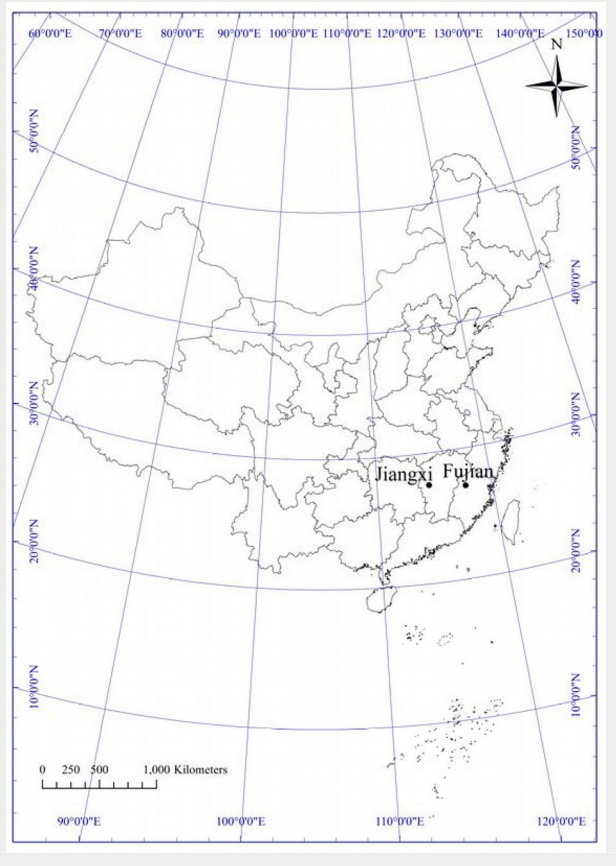
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Fig. 1 - Locations of the Chinese fir study sites in southern China.



1656 mm, respectively.

Weimin farm consisted of stands of 7-, 16- and 28-year-old Chinese firs (*Cunninghamia lanceolata* [Lamb.] Hook.). Nianzhu farm consisted of stands of 28-year-old Chinese firs. One or two trees in each diameter class (2-cm) in each plot (0.06 ha) were randomly destructively sampled, totaling 39 sample trees in Weimin farm and 24 trees in Nianzhu farm (Tab. 1).

Tree diameter at breast height (*D*) and height (*H*) was measured after the tree was felled. The fresh and dry weights of stem, branch, leaf and root were determined separately. From each stem, we sampled a 5-cm thick stem disc cut from the base of each 1-m stem segment, three subsamples of the branches and leaves from the upper, middle, and lower crown (1/3 of crown length, approximately 500

1000 g each), and samples (500-1000 g) from the stump, large structural roots (more than 10 mm), small roots (2-10 mm), and fine roots (less than 2 mm), obtained after excavation of the whole root system to the extent of the crown projection area. All samples were fresh weighted in the field, then transported to the laboratory where they were oven-dried to a constant weight at 105 °C and dry weighted. Dry weight was computed for each tree component by extrapolating the ratio of dry weight to fresh weight from subsamples.

Allometric equations

Standard allometric equations predict tree biomass as a power function of *D* (MacFarlane 2015). Other variables, such as total tree height, have also been proven to be important predictors (Chave et al. 2005,

Molto et al. 2013). The following two widely used equations (Medhurst et al. 1999, Lambert et al. 2005, Zhang et al. 2013, Zhao et al. 2015, Tang et al. 2016) were considered in this study (eqn. 1, eqn. 2):

$$M_i = a_1 D_i^{b_1} + \epsilon_i \tag{1}$$

$$M_i = a_2 (D_i^2 H_i)^{b_2} + \epsilon_i \tag{2}$$

where M_i is the biomass (kg) for the *i*-th tree, *a* and *b* are the regression parameters to be estimated, D_i is the tree diameter (cm), H_i is the total height (m), and ϵ_i is the random error.

The separate model method involves employing separate regression models to predict total tree biomass and its components: branch, leaf, root, and stem. Based on a preliminary analysis, we found that the eqn. 1 performed better than eqn. 2 on modeling branch, leaf and root biomass. However, in terms of the stem and total biomass, the eqn. 2 was better than eqn. 1. Thus, the following equation forms were selected (eqn. 3 to eqn. 7):

$$\text{Branch: } M_{Bi} = a_{3B} D_i^{b_{3B}} + \epsilon_i \tag{3}$$

$$\text{Leaf: } M_{Li} = a_{4L} D_i^{b_{4L}} + \epsilon_i \tag{4}$$

$$\text{Root: } M_{Ri} = a_{5R} D_i^{b_{5R}} + \epsilon_i \tag{5}$$

$$\text{Stem: } M_{Si} = a_{6S} (D_i^2 H_i)^{b_{6S}} + \epsilon_i \tag{6}$$

$$\text{Total: } M_{Ti} = a_{7T} (D_i^2 H_i)^{b_{7T}} + \epsilon_i \tag{7}$$

where all variables are as defined earlier, with added subscripts to denote component types.

The models were separate in the sense that prediction of total tree biomass from eqn. 7 did not equal the sum of predictions for components from eqn. 3 to 6. In other words, the equations were not constrained to be additive. Parameters of eqn. 3 to 7 were simultaneously obtained by using Seemingly Unrelated Regression (SUR). SAS procedure MODEL (SAS Institute Inc 2009) was used for this purpose.

The Additive model approach was based on the procedure developed by Parresol (2001). The following system of equations was used to predict total tree biomass and its components (eqn. 8 to eqn. 12):

$$\text{Branch: } M_{Bi} = a_{8B} D_i^{b_{8B}} + \epsilon_i \tag{8}$$

$$\text{Leaf: } M_{Li} = a_{9L} D_i^{b_{9L}} + \epsilon_i \tag{9}$$

$$\text{Root: } M_{Ri} = a_{10R} D_i^{b_{10R}} + \epsilon_i \tag{10}$$

$$\text{Stem: } M_{Si} = a_{11S} (D_i^2 H_i)^{b_{11S}} + \epsilon_i \tag{11}$$

$$\text{Total: } M_{TSi} = \hat{M}_{Bi} + \hat{M}_{Li} + \hat{M}_{Ri} + \hat{M}_{Si} + \epsilon_i \tag{12}$$

where the symbol ^ on top of a variable name denotes the predicted value for that variable.

Eqn. 8 to 11 have the same forms as eqn. 3 to 6, respectively. Prediction of total tree

Tab. 1 - Mean and standard deviation (SD) for tree variables and component biomass of Chinese fir by location and age. Values in parentheses are ranges.

Location	Age	n	Stats	D (cm)	H (m)	Stem (kg)	Branch (kg)	Leaf (kg)	Root (kg)
Weimin	7	9	Mean	10.97 (5.7-16.3)	7.28 (4.9-9.3)	14.67	3.60	5.25	6.97
			SD	3.84	1.61	9.08	2.41	4.25	5.56
	16	14	Mean	14.19 (5.6-22.5)	11.48 (5.9-14.8)	34.26	2.63	3.45	11.38
			SD	5.28	2.70	22.57	2.50	3.18	8.90
	28	16	Mean	16.86 (8.7-27.8)	17.07 (10.3-22.7)	71.11	5.72	4.22	18.41
			SD	5.82	3.30	51.04	7.16	3.68	16.03
Nianzhu	28	24	Mean	18.70 (7.5-30.2)	16.89 (10.2-23.2)	86.67	6.82	4.65	21.26
			SD	7.13	3.57	64.90	6.97	4.53	18.18

biomass (eqn. 12) was obtained by summing predictions of component biomass. Again, SUR was used to estimate parameters of this system of equations.

Zhang et al. (2010, 2011a) applied the forecast combination method to combine different types of models for predicting stand basal area and stand survival. A similar approach was applied in this study to predict total tree biomass by combining: (a) direct prediction from the regression model (eqn. 7); and (b) indirect prediction by summing predictions from component models (eqn. 13):

$$\hat{M}_{Fi} = w_1 M_{Ti} + w_2 M_{TSi} \quad (13)$$

where \hat{M}_{Fi} is the prediction of total tree biomass from forecast combination, w_1 and w_2 are weights, with $w_1 + w_2 = 1$, M_{Ti} is the direct prediction of total tree biomass from eqn. 7, and \hat{M}_{TSi} is the indirect prediction of total tree biomass by summing predictions from component biomass equations. Depending on the component biomass equations, two methods of Forecast Combination were considered in this study: (i) FC1 that used the sum of predictions from the Separate model (eqn. 3-6); and (ii) FC2 that used the sum of predictions from the Additive model (eqn. 12). The weight coefficients of the combined tree biomass model could be obtained by the optimal weight method (Zhang et al. 2010 – eqn. 14):

$$W = \frac{E^{-1} R}{R^T E^{-1} R} \quad (14)$$

where (eqn. 15 to eqn. 18):

$$W = (w_1, w_2)^T \quad (15)$$

$$R = (1, 1)^T \quad (16)$$

$$E = \begin{pmatrix} e_1^T e_1 & e_1^T e_2 \\ e_2^T e_1 & e_2^T e_2 \end{pmatrix} \quad (17)$$

$$e_k = (\varepsilon_{k1}, \varepsilon_{k2}, \dots, \varepsilon_{kn}) \quad (18)$$

where ε_{ki} is the prediction error for the tree i using the method k , with $k = 1, 2$, and $i = 1, 2, \dots, m$, being m the total number of trees; T is the transport matrix.

The component predictions were then adjusted to add up to the combined estimator for total tree biomass. This was accomplished by multiplying the component predictions by λ , the adjusting coefficient, which is calculated as (eqn. 19):

$$\lambda = \hat{M}_{Fi} / \hat{M}_{TSi} \quad (19)$$

In this study, the two-fold leave-one-out cross validation scheme was used for model validation. First, the models were fitted using data from the Weimin farm, and then validated using data from the Nianzhu farm. Second, we treated Nianzhu data as the fit data and Weimin data the validation data. Evaluation statistics were computed based on observations pooled from the two validation data sets. The evaluation

Tab. 2 - Parameter estimates and standard errors (SE) of the biomass model using Separate and Additive models in the Weimin and Nianzhu farms.

Parameter	Weimin		Nianzhu	
	Estimates	SE	Estimates	SE
a_{3B}	8.2e-5	6.4e-5	8.84e-4	0.0013
b_{3B}	3.7571	0.2425	2.9377	0.4520
a_{4L}	0.0276	0.0215	0.0009	0.0013
b_{4L}	1.7984	0.2574	2.7953	0.4455
a_{5R}	0.0110	0.0047	0.0200	0.0103
b_{5R}	2.5401	0.1383	2.3165	0.2503
a_{6S}	0.0247	0.0053	0.0397	0.0131
b_{6S}	0.9141	0.0236	0.8647	0.0346
a_{7T}	0.0337	0.0066	0.0435	0.0156
b_{7T}	0.9211	0.0215	0.8897	0.0376
a_{8B}	0.0001	8.6e-5	0.0015	0.0021
b_{8B}	3.7089	0.2966	2.7895	0.4583
a_{9L}	0.0432	0.0396	0.0010	0.0015
b_{9L}	1.6763	0.3055	2.7802	0.4539
a_{10R}	0.0089	0.0041	0.0114	0.0058
b_{10R}	2.6206	0.1480	2.4950	0.2641
a_{11S}	0.0224	0.0049	0.0369	0.0121
b_{11S}	0.9254	0.0239	0.8726	0.0344

statistics of mean difference (MD), mean absolute difference (MAD), and R^2 (Zhang et al. 2010) were used to validate the models. Models with lower MD and MAD values indicate a better fit to the data.

Results and discussion

The stem biomass ranged from 14.67 to 86.67 kg, branches from 2.63 to 6.82 kg, leaves from 3.45 to 5.25 kg, and roots from 6.77 to 21.23 kg (Tab. 1). Stem biomass accounted for more than 50% of the total tree biomass, except the stand of age 7, which could explain the same equation (eqn. 2) of stem and total tree biomass in the preliminary analysis. The parameter estimates and their standard deviation errors were slightly different between the Separate model and Additive models in the Weimin and Nianzhu farms (Tab. 2), being their values more consistent across methods than across farms. For total tree biomass prediction, the MD value obtained using the FC1 method (the Forecast Combination method that used separate models) was 83.46% smaller than that obtained using the additive model and 41.04% smaller than that of the FC2 method (Forecast Combination method that used additive model). Moreover, the FC1 method produced the best R^2 values, while the Sep-

arate model method yielded the lowest MAD value (Tab. 3). Regarding the prediction of component biomass, the FC1 method had the best MAD and R^2 values for all components (except leaf biomass) and the best MD values for two of the four components (Tab. 4).

Fig. 2 displays the predicted vs. observed biomass of total and component biomass. Most of biomass predictions were distributed near the straight line ($y=x$) using any of the four methods used (Fig. 2). It can be noticed that the predictions of leaf biomass showed the lowest accuracy and precision among all the component biomass.

Additive vs. separate model

Parameters of the component regression models in the Additive model approach were subjected to the constraint that the sum of component predictions from the resulting models would be equal to the total biomass (Kozak 1970, Bi et al. 2004, Dong et al. 2014). On the other hand, the Separate model method did not involve any constraints, thus its parameters resulted 19.97% and 6.86% lower for MD, MAD, respectively and 0.47% larger for R^2 than those of the Additive model method used for modeling total tree biomass (Tab. 3). Furthermore, the separate model meth-

Tab. 3 - Evaluation statistics for total tree biomass prediction by method. (§): denotes the best method based on each fitting statistic (MD, MAD, R^2).

Method	MD	MAD	R^2
Separate model	0.5761	8.0296 ^(§)	0.9772
Additive model	-0.7199	8.6210	0.9726
Combined using Separate model	0.1191 ^(§)	8.0469	0.9780 ^(§)
Combined using Additive model	0.2020	8.0802	0.9776

Tab. 4 - Evaluation statistics for component biomass prediction by method. (§): denotes the best method based on each fitting statistic (MD, MAD, R²).

Component	Method	MD	MAD	R ²
Branch	Separate model	-0.1511	1.9476	0.6601
	Additive model	-0.487	2.0743	0.6371
	Combined using Separate model	-0.0853 ^(§)	1.9307 ^(§)	0.6786 ^(§)
	Combined using Additive model	-0.3997	2.0213	0.6755
Leaf	Separate model	0.7034 ^(§)	2.0181 ^(§)	0.4952 ^(§)
	Additive model	0.4883	2.0838	0.4424
	Combined using Separate model	0.7343	2.0768	0.4332
	Combined using Additive model	0.5259	2.1002	0.4311
Root	Separate model	-0.2353	3.2619	0.8807
	Additive model	-0.2625	3.3982	0.8686
	Combined using Separate model	-0.0046 ^(§)	3.2564 ^(§)	0.8905 ^(§)
	Combined using Additive model	-0.0466	3.2853	0.8872
Stem	Separate model	-0.298	4.7543	0.9832
	Additive model	-0.4586	4.9985	0.9831
	Combined using Separate model	0.1986	4.2931 ^(§)	0.9865 ^(§)
	Combined using Additive model	0.1224 ^(§)	4.5509	0.9851

od produced the best MD, MAD and R² values for all components. The sole exception using the latter method was leaf biomass, which showed a lower MD value (Tab. 4). However, due to lack of additivity con-

straint, the sum of predictions from different biomass components was not equal to the prediction of total tree biomass in the Separate model approach (Sanquetta et al. 2015). Therefore, the advantage of a com-

patible, additive system for total and component biomass in the Additive model method was also accompanied by a decrease in the accuracy and precision of predictions.

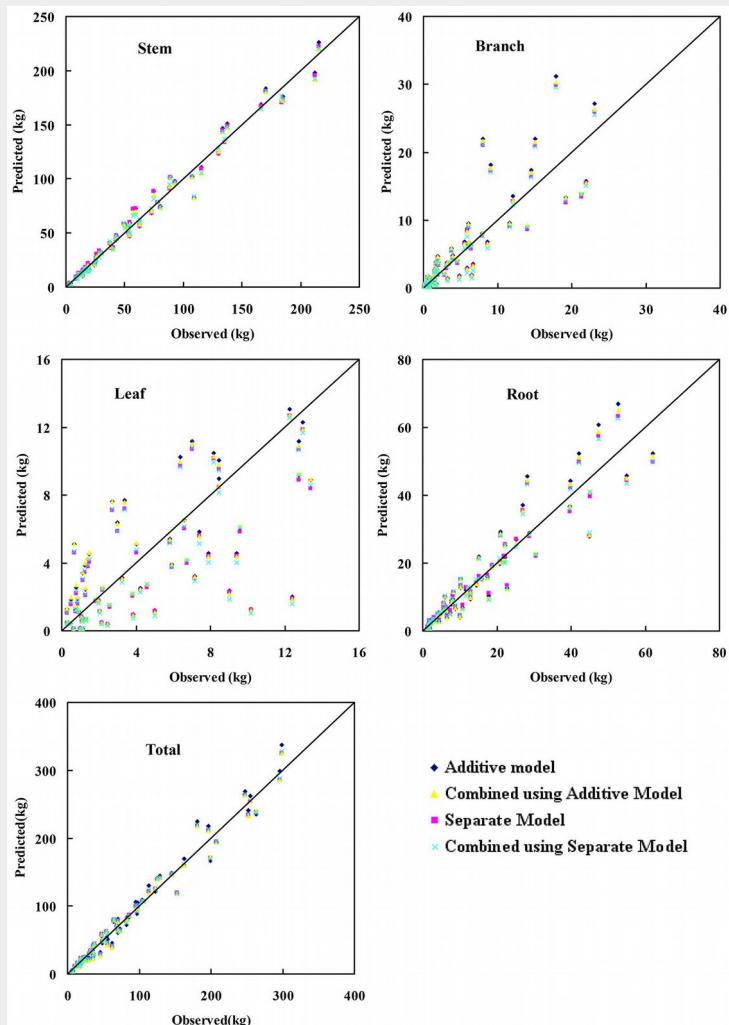
Forecast combination

This approach involves a combined estimator, which is the weighted average of the predictions from the total biomass equation and the sum of predictions of component biomass from either (a) the separate model, or (b) the additive model. Yue et al. (2008) used the variance-covariance method to calculate weight coefficients for the combined model. Zhang et al. (2011b) reported that the optimal weight method (*i.e.*, the ordinary least squares estimate of the weights) performed better than the variance-covariance method. Here, the optimal weight method was used to calculate weight coefficients of combined model of tree biomass. Compared to the method using the additive model (FC₂), the Forecast Combination method that used the separate model (FC₁) gave better values of MD, MAD, and R² for total and component biomass prediction (Tab. 3, Tab. 4). The only exceptions were MD values for leaf and stem biomass. The sum of component predictions from the Separate model was not subject to any constraint, and therefore could be different from the prediction from the total biomass equation. The combined predictions of FC₁ method benefit from non-constraint of the Separate model, thus increasing the accuracy and precision as compared to the FC₂ estimation.

Forecast combination vs. additive model

Tree biomass additivity has long been recognized as a desirable property of biomass estimation. Several studies have successfully solved the logical inconsistency between the components and total tree predictions (Reed & Green 1985) by developing a system of additive biomass equations estimated by the SUR method, thus providing a statistically correlated system of equations with restrictions (Parresol 2001, Bi et al. 2010). In this study, a forecast combination with adjusted coefficient (a consistent value) was applied, ensuring the additivity of the component biomass. It is worth noting that the adjusted coefficient may vary across the biomass components, because the ratio between each component depends on site quality, stand density, age or tree size.

The FC₁ method outperformed the Additive model method in predicting the total tree biomass, based on all three evaluation statistics. The FC₁ method also produced better values of MD, MAD, and R² for predicting branch, root, and stem biomass. For leaf biomass, the FC₁ method resulted in better MAD, but worse MD and R² values, as compared to the Additive model method (Tab. 3, Tab. 4).

Fig. 2 - Observed vs. predicted total and component biomass by each method.

Forecast combination vs. separate model

In the Separate model method, the prediction of total tree biomass for each tree is directly derived from the total biomass regression equation. The FC1 method combined the information from this prediction and the sum of predictions from regression equations for each component biomass. The result is an improvement of two (MD and R^2) out of three fitting statistics for total tree biomass predictions obtained using the FC1 method, as compared with the Separate model method (Tab. 3). Indeed, the MD value derived from FC1 method was 79.33% smaller than that obtained using the Separate model method, while the R^2 value from FC1 method was slightly larger than that of the Separate model method.

For the component biomass, predictions from the Separate model method were unadjusted predictions from the regression models. These predictions were then adjusted such that the resulting sum matched the combined estimator for total biomass in the FC1 method.

Based on all three evaluation statistics, the FC1 method showed better performances in predicting branch, root, and stem biomass as compared to the Separate model, whereas the latter method yielded more accurate predictions of leaf biomass. The opposite trend observed in leaf biomass predictions might be due to low R^2 values of separate leaf biomass model (Tab. 4). In the forecast combination method, the implicit assumption was that the relationship between observed and predicted values from different models was stable. If this relationship remains relatively unchanged from the sample data to the population, then the combined value should provide better predictions than those by any model alone (Zhang et al. 2011b). However, in this study the relationship in leaf biomass was not stable, as inferred from R^2 values ranging from 0.43 to 0.49 (Tab. 4).

Conclusions

The Forecast Combination method takes advantages of information from tree-level and component-level models, by providing an estimator that combines predictions from these models. To ensure additivity, component predictions from the Separate model were adjusted to match the combined estimator for total tree biomass. This approach was superior to the Additive model method in predicting total tree biomass and all of its components, except for leaf biomass.

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