

Stand-level biomass estimation for Korean pine plantations based on four additive methods in Heilongjiang province, northeast China

Shidong Xin ¹, Surya Bagus Mahardika ¹, Lichun Jiang ^{*}

¹School of Forestry, Northeast Forestry University, Harbin, China

ECOLOGY

ABSTRACT

Background: Korean pine (*Pinus koraiensis* Siebold & Zucc.) is one of the primary plantation conifer species of economic and ecological importance in northeast China. Forest biomass estimation in the broader landscape has been receiving attention from researchers and forest managers. The development of forest stand biomass models is regarded an effective method to estimate forest biomass at large scales. This study was carried out for developing stand-level biomass models for Korean pine plantations. Four additive methods were compared: Aggregation 1, Aggregation 2, Adjustment, and Disaggregation. All the stand biomass additive modeling systems (i.e., total, root, stem, branch, and leaf) included both stand volume and biomass conversion and expansion factors (BCEFs) as predictors.

Results: The predictive performance of the four additive methods and Constant BCEFs were ranked as follows: Aggregation 1 > Disaggregation > Adjustment > Aggregation 2 > Constant BCEFs. The prediction accuracy of the four additive methods was not consistent across the stand volume intervals.

Conclusion: The model based on the Aggregation 1 method was recommended for predicting stand biomass. However, different additive method should be selected according to the stand volume intervals of the Korean pine plantations.

Keywords: biomass conversion and expansion factors, additive methods, stand biomass

HIGHLIGHTS

Stand biomass models were developed for Korean pine plantations.

Four additive methods were evaluated in this study.

The biomass conversion and expansion factors (BCEFs) showed a significant non-linear relationship with the stand quadratic mean diameter.

The Aggregation 1 method was superior to other methods in estimating stand biomass.

XIN, S.; MAHARDIKA, S. B.; JIANG, L. Stand-level biomass estimation for Korean pine plantations based on four additive methods in Heilongjiang province, northeast China. CERNE, v.28, e-103008, doi: 10.1590/01047760202228013008

 Corresponding author

e-mail: jlcnefu@126.com

Submitted: 03/10/2021

Accepted: 15/02/2022



INTRODUCTION

As a basic unit of forest ecosystems, forest biomass is an indispensable resource in the global carbon cycle and there is correspondingly increasing interest in recent decades in obtaining accurate predictions to quantify carbon stock and determine the availability of forest materials for use as a bioenergy resource (Gómez-García *et al.*, 2015). The practical implications and value of accurate biomass predictions are also directly related to global climate change, while using good management plans based on quality scientific data and methods would be able to help reduce CO₂ emissions and achieve Kyoto Protocol targets (Groen *et al.*, 2006). Recognizing the significance of such scientific advances, researchers have been paying more attention to improving the accuracy of regional-scale estimates of forest biomass (Somogyi *et al.*, 2007; Oliveira and Tomé, 2017; Jagodziński *et al.*, 2018a).

Currently, there are three main approaches of large-scale forest biomass assessment, scaling-up, remote sensing estimation, and direct stand modeling. In general, the tree dendrometric variables are required for tree-level biomass estimation, primarily diameter at breast height (DBH), total tree height (H), crown factors, and dry weight of tree components (Muukkonen, 2007; Zou *et al.*, 2015; Luo *et al.*, 2020). These tree variables, combined with the allometric equation, can develop precision models for estimating tree-level biomass. The stand or local biomass is acquired by then summing the predictions of species-specific individual tree biomass models, however the preliminary preparations are costly and time-consuming. Furthermore, complex error propagation procedures occur in the scaling-up process from tree to stand or local biomass (Castedo-Dorado *et al.*, 2012; Dong *et al.*, 2019). Undoubtedly, remote sensing methods have the unique advantage of providing estimates of forest biomass over larger areas, such as at the national scale (Chi *et al.*, 2015). This technology estimates above-ground biomass (AGB) via total tree height, canopy height, and canopy factors extracted from remote sensing images or LiDAR (Light Detecting and Ranging) waves. Since these variables extracted are influenced by stand density and remote sensing resolution, which affect the precision of machine learning or model prediction, it also needs large amounts of ground sample plots for validation (Huang *et al.*, 2019). In recent years, numerous individual tree biomass models have been established for more than several hundred tree species in different areas worldwide (Zianis and Mencuccini, 2004; Návar, 2009; Zeng *et al.*, 2017), these efforts have laid the foundation for the direct development of stand biomass models.

Forest volume at the regional or national level is a reliable source of information for forest resource assessment and is a basis for biomass and carbon studies (Dixon *et al.*, 1994). Biomass expansion and conversion factors (BCEFs) convert volume to individual tree biomass, and also provide an important tool for converting stand volume to above-ground, below-ground, or total stand biomass (Fang *et al.*, 1998; Jagodziński *et al.*, 2017). A set of available BCEFs default values are provided by IPCC guidelines, which are species-specific averaged values. It is

widely acknowledged that inaccuracies occasionally occur because BCEFs vary depending on forest type and growth conditions, which is even more distinct in early stands. After all, BCEFs change over the stage of development, during the stand development, it is vital to consider applying the constant values (Lehtonen *et al.*, 2004; Jagodziński *et al.*, 2018b). Hence, BCEF models based on stand variables have been established to reduce the uncertainties of applying default BCEF values in forest biomass estimations at large scales (Soares and Tomé, 2012).

Thus far, additive and non-additive are common technical specifications for developing biomass equations. Non-additivity fits the total and each component biomass equations separately, which leads to the possibility that the sum of the component equation predictions not being equal to the total biomass equation predictions (Kozak, 1970). Therefore, to satisfy the statistical efficiency of the biomass equations that the sum of the component equation predictions is equal to the total biomass equation predictions, many researchers have offered various approaches to ensure the additivity of the system of biomass equations (Parresol, 1999; Tang *et al.*, 2000; Affleck and Diéguez-Aranda, 2016; Bronisz and Mehtätalo, 2020; Trautenmüller *et al.*, 2021). As Tang *et al.* (2000; 2008) proposed a proportional model system (referred to as Adjustment) and a disaggregation model system (referred to as Disaggregation). Specifically, Adjustment is a relatively easy method to solve the additivity, where the total is allocated in one step into components (e.g., stem, branch, leaf and root), and the sum of the proportion of each component to the total is equal to 1. In contrast, the Disaggregation fits the total and component equations simultaneously. Parresol (2001) also proposed an aggregation system to achieve additivity (referred to as Aggregation 1), besides, the researchers extend aggregation system that the component equations can be fitted simultaneously after total equations removal (referred to as Aggregation 2) (Affleck and Diéguez-Aranda, 2016; Zhao *et al.*, 2019). However, few comparative assessments have been performed for different additive methods in the literature, especially for predicting biomass in stand level. The nonlinear seemingly unrelated regression (NSUR) and two-stage nonlinear error-in-variable models (TSEM) are the main parameter estimation methods for system of nonlinear simultaneous equations. Due to the NSUR method can be readily implemented in R version 3.5.1 and SAS version 9.3 software (SAS Institute Inc, 2011; R Core Team, 2019). And it has been applied in several studies to guarantee tree biomass and crown additivity (Dong *et al.*, 2015; Fu *et al.*, 2017), therefore, the NSUR method is a relatively popular method for parameter estimation of nonlinear biomass simultaneous equations.

Korean pine (*Pinus koraiensis* Siebold & Zucc.) is distributed in northeastern China, Korea, Japan, and Russia. The species is multipurpose and has economic value for timber and edible seeds (Liu *et al.*, 2020). Hence, nut and timber forestry have become two of the main management approaches for Korean pine plantation forest. Furthermore, considering the value of forests in term of ecosystem service provision, Korean pine sequesters comparably

higher amounts of carbon dioxide from the atmosphere, a significant contribution to the mitigation of global warming and its effects.

The objectives of this study were to (1) develop stand biomass prediction tools by BCEF equations and stand volume for Korean pine plantations at stand level, and (2) evaluate the performance of different additive methods (i.e., Aggregation 1, Aggregation 2, Adjustment, and Disaggregation) and Constant BCEFs to estimate the total stand biomass and that of its respective components.

MATERIAL AND METHODS

Study area

A total of 207 Korean pine plots were sampled in four regions in southern Heilongjiang Province (121°11'-135°05' E, 43°26'-53°33' N), namely Dong Jingcheng Forestry Farm (52 plots), Linkou Forestry Farm (45 plots), Mao'er shan Forestry Farm (76 plots) and Meng Jiagang Forestry Farm (34 plots). The climate type of the study area can be classified as cold temperate and temperate continental monsoon. The altitude range of the four study areas is about 170 to 900 m above sea level, the air temperature is between -37°C and +35°C, the average annual precipitation fluctuates from 500 to 700 mm, the parent material is granite bedrock, and the soil is typically dark brown.

Data collection and biomass estimates

The experimental plot areas ranged from 100 to 900 m² and were selected based on different stand densities. The volume of Korean pine within each sample plot was ≥ 65%, the sample plots covered the distribution of the species in the local area, and the initial plantation density of Korean pine was 4400 trees per hectare. All individual trees in the plot were recorded except those with the diameter at breast height (measured at 1.3 m) less than 5cm.

Stand variables were calculated from the sample plot data using the measurement factors of individual trees, where stand quadratic mean diameter was calculated as $\sqrt{\sum DBH_i^2/n}$, where DBH was diameter at breast height, n was the number of trees in the plot, and stand dominant height was the average height of the 100 largest height dominant trees per hectare. Stand volume was calculated as the summation of the volume of the individual trees in each plot with individual-tree volume equations according to the volume table of standing timber in Heilongjiang Province, China (Heilongjiang Forestry Bureau, 1981), which relies on diameter at breast height (DBH). In this study, the sample plots also contain other tree species, so we applied the respective species-specific tree biomass models previously published by forestry researchers (Wang, 2006; Dong et al., 2014, 2015), to obtain the stand total and individual component biomass values in each plot (Table 1).

Biomass conversion and expansion factors (BCEFs) model specification

Stand biomass estimation required BCEFs to be determined, calculated as:

$$BCEF_i = W_i / V \quad (1)$$

Where $BCEF_i$ represents biomass conversion and expansion factors, W_i represents stand biomass of component i , and V is stand volume in m³·ha⁻¹. Component i could be either s , b , l , r or t , which represents stem, branch, leaf, root, and total, respectively.

Although this work has been devoted to the development of BCEFs biomass model, the stand-level total, root, stem, branch, and leaf constant values of BCEFs were calculated as the average value of each plot (Table 2), and the constant value of BCEFs multiplied by the stand volume is also considered the direct method of biomass estimation.

Table 1. Summary statistics of stand variables and stand biomass.

Variables	Minimum	Maximum	Mean	Standard deviations
Dq (cm)	4.62	30.94	15.37	4.61
$H0$ (m)	5.00	20.88	13.73	2.92
A (years)	11.00	47.00	32.90	6.18
N (tree·ha ⁻¹)	300.00	2900.00	1365.36	478.10
V (m ³ ·ha ⁻¹)	4.33	498.69	161.20	91.09
W_t (Mg·ha ⁻¹)	4.05	288.65	98.83	50.92
W_r (Mg·ha ⁻¹)	0.62	54.99	18.35	9.88
W_s (Mg·ha ⁻¹)	2.09	156.70	55.41	27.68
W_b (Mg·ha ⁻¹)	0.83	61.11	19.74	11.03
W_l (Mg·ha ⁻¹)	0.51	15.84	5.33	2.63

Notes: Dq is stand quadratic mean diameter, $H0$ is stand dominant height, A is stand age, N is stand density, V is stand volume, W_t is stand total biomass, W_r is stand root biomass, W_s is stand stem biomass is stand stem biomass, W_b is stand branch biomass, W_l is stand leaf biomass.

Table 2. Summary statistics of stand level BCEFs (Mg·m⁻³).

Components	BCEFs			
	Constant	Minimum	Maximum	Standard Deviation
Total	0.6407	0.2367	0.9362	0.0898
Root	0.1168	0.0426	0.1610	0.0138
Stem	0.3605	0.1402	0.5264	0.0572
Branch	0.1259	0.0398	0.1933	0.0172
Leaf	0.0375	0.0426	0.1171	0.0140

Furthermore, the stand biomass was predicted by constant values, hence it could be compared with the stand biomass predicted from the equations. The following stand biomass estimation model by BCEF equation was defined as:

$$W_i = BCEF_i(X_j)V \tag{2}$$

Where $BCEF_i(X_j)$ is the expression of the functional relationships between biomass conversion and expansion factors and stand variables, and X_j represents stand variables ($j=1, \dots, n$), Symbols used in Equation (2) are the same as in Equation (1).

Stand additive biomass model

Four additive methods were used to construct the stand biomass model: Aggregation 1, Aggregation 2, Adjustment and Disaggregation. Aggregation 1 followed the model structure specified in Parresol (2001), which simultaneously fits a system of correlated linear equations with cross-equation constraints to ensure the additivity of biomass models (referred to as Aggregation 1) by Nonlinear Seemingly Unrelated Regression (NSUR). Then, stand biomass components were constrained to equal the total stand biomass as follows:

$$\begin{cases} W_s = BCEF_s(X_j)V + \varepsilon_s \\ W_b = BCEF_b(X_j)V + \varepsilon_b \\ W_l = BCEF_l(X_j)V + \varepsilon_l \\ W_r = BCEF_r(X_j)V + \varepsilon_r \\ W_t = W_s + W_b + W_l + W_r \end{cases} \tag{3}$$

Where ε_i are inter-correlated error terms. Other symbols used in the equation are the same as in Equations (1-2).

Affleck and Diéguez-Aranda (2016) have estimated the parameters through jointly fitting biomass component models with a maximum likelihood (ML) approach, except for total biomass equation, which we define here as Aggregation 2. However, the stand biomass components were fit jointly through NSUR in this study as follows:

$$\begin{cases} W_s = BCEF_s(X_j)V + \varepsilon_s \\ W_b = BCEF_b(X_j)V + \varepsilon_b \\ W_l = BCEF_l(X_j)V + \varepsilon_l \\ W_r = BCEF_r(X_j)V + \varepsilon_r \end{cases} \tag{4}$$

$$\widehat{W}_t = \widehat{W}_s + \widehat{W}_b + \widehat{W}_l + \widehat{W}_r \tag{5}$$

The Adjustment method followed the model structure specified in Tang et al. (2000). Generally speaking, the Adjustment method was the simplest way to realize additivity which needs to jointly fit the total biomass and

the individual biomass separately by Ordinary Least Square (OLS) in the form of the Equations (3). The total stand biomass was then derived according to the proportion of each component. Predicted values of total stand biomass and each respective component were obtained by the following equations:

$$\widehat{W}_s = \frac{BCEF_s(X_j)V}{BCEF_s(X_j)V + BCEF_b(X_j)V + BCEF_l(X_j)V + BCEF_r(X_j)V} \widehat{W}_t \tag{6}$$

$$\widehat{W}_b = \frac{BCEF_b(X_j)V}{BCEF_s(X_j)V + BCEF_b(X_j)V + BCEF_l(X_j)V + BCEF_r(X_j)V} \widehat{W}_t \tag{7}$$

$$\widehat{W}_l = \frac{BCEF_l(X_j)V}{BCEF_s(X_j)V + BCEF_b(X_j)V + BCEF_l(X_j)V + BCEF_r(X_j)V} \widehat{W}_t \tag{8}$$

$$\widehat{W}_r = \frac{BCEF_r(X_j)V}{BCEF_s(X_j)V + BCEF_b(X_j)V + BCEF_l(X_j)V + BCEF_r(X_j)V} \widehat{W}_t \tag{9}$$

$$\widehat{W}_t = BCEF_t(X_j)V \tag{10}$$

Where \widehat{W}_i represents i component biomass estimates, Symbols used in the equation are the same as in Equations (1-2).

The Disaggregation method was proposed by Tang et al. (2008). In this paper, we adopt NSUR to jointly fit simultaneous equations. The characteristic of this method was the total stand biomass was adjusted directly by one step via the following equations:

$$\begin{cases} W_s = \frac{BCEF_s(X_j)V}{BCEF_s(X_j)V + BCEF_b(X_j)V + BCEF_l(X_j)V + BCEF_r(X_j)V} W_t + \varepsilon_s \\ W_b = \frac{BCEF_b(X_j)V}{BCEF_s(X_j)V + BCEF_b(X_j)V + BCEF_l(X_j)V + BCEF_r(X_j)V} W_t + \varepsilon_b \\ W_l = \frac{BCEF_l(X_j)V}{BCEF_s(X_j)V + BCEF_b(X_j)V + BCEF_l(X_j)V + BCEF_r(X_j)V} W_t + \varepsilon_l \\ W_r = \frac{BCEF_r(X_j)V}{BCEF_s(X_j)V + BCEF_b(X_j)V + BCEF_l(X_j)V + BCEF_r(X_j)V} W_t + \varepsilon_r \\ W_t = BCEF_t(X_j)V + \varepsilon_t \end{cases} \tag{11}$$

The symbols used in the equation are the same as in Equations (1-2).

Elimination of heteroscedasticity

The weight function for eliminating heteroskedasticity was strictly selected from stand variables, the squared unweighted residuals ($\hat{\varepsilon}^2$) of stand biomass models and stand variables were fitted by stepwise regression in the process, equation as:

$$\ln(\hat{\epsilon}^2) = \ln(\sigma^2) + \varphi_{i1} \ln(X_1) + \varphi_{i2} \ln(X_2) + \dots + \varphi_{ip} \ln(X_p) \quad (12)$$

Where $\hat{\epsilon}$ are the unweighted residuals for each model, σ^2 is the variance of residuals, $\varphi_{ij} - \varphi_{ip}$ are coefficients of stand variables, and $X_1 - X_p$ are stand variables, i could be either s, b, l, r or t , which represents stem, branch, leaf, root, and total, respectively.

Equation (12) coefficients were retained at the significant level of $\alpha = 0.05$, the weight function may be $1/Dq^{\varphi_{i1}}, 1/V^{\varphi_{i2}}$ or $1/Dq^{\varphi_{i1}}V^{\varphi_{i2}}$. Stand biomass model system was refitted in the SAS/ETS® MODEL, and $resid.W_i/\sqrt{X_1^{\varphi_{i1}} \dots X_p^{\varphi_{ip}}}$ (where $resid.W_i$ is the model residual of W_i) was added in the procedure (SAS Institute Inc, 2011; Harvey, 1976; Zhao *et al.*, 2015).

Model assessment and validation among the four additive methods

The fitting performance of the four additive systems was assessed through the goodness of fit statistic, according to the adjusted coefficient of determination (R^2_{adj}) and root mean square error (RMSE), when the entire data set was involved in the establishment of the model. The leave-one-out cross validation (LOOCV) was used to evaluate model prediction. In this validation process, only one sample is retained from all data sets at a time, and the next one will not be retained. The remaining samples participate in the model fitting (sample size N-1), where N is number of samples. The estimated parameters obtained by model fitting were used to predict the remaining one sample. The process of fitting and testing was repeated N times to complete the

model validation (Kozak and Kozak, 2003). Afterward, mean absolute bias (MAB), mean percentage bias (MPB), and mean relative bias (MRB) were calculated to evaluate the performance of four additive model systems. The above five calculations were made following the equations:

Adjusted coefficient of determination

$$R^2_{adj} = 1 - \frac{\sum_{i=1}^n (y_i - \hat{y}_i)^2}{\sum_{i=1}^n (y_i - \bar{y})^2} \times \left(\frac{n-1}{n-p-1} \right) \quad (13)$$

Root mean square error

$$RMSE = \sqrt{\frac{\sum_{i=1}^n (y_i - \hat{y}_i)^2}{n-1}} \quad (14)$$

Mean absolute bias

$$MAB = \frac{\sum_{i=1}^n |y_i - \hat{y}_i|}{n} \quad (15)$$

Mean percentage bias

$$MPB = 100 \times \frac{\sum_{i=1}^n |y_i - \hat{y}_i|}{\sum_{i=1}^n y_i} \quad (16)$$

Mean relative bias

$$MRB = \frac{100}{n} \sum_{i=1}^n \frac{y_i - \hat{y}_i}{y_i} \quad (17)$$

Where y_i and \hat{y}_i are actual values of biomass, and the predicted values of biomass, respectively, n is the number of samples, \bar{y} is the mean value of the actual value of biomass, and p is the number of model parameters.

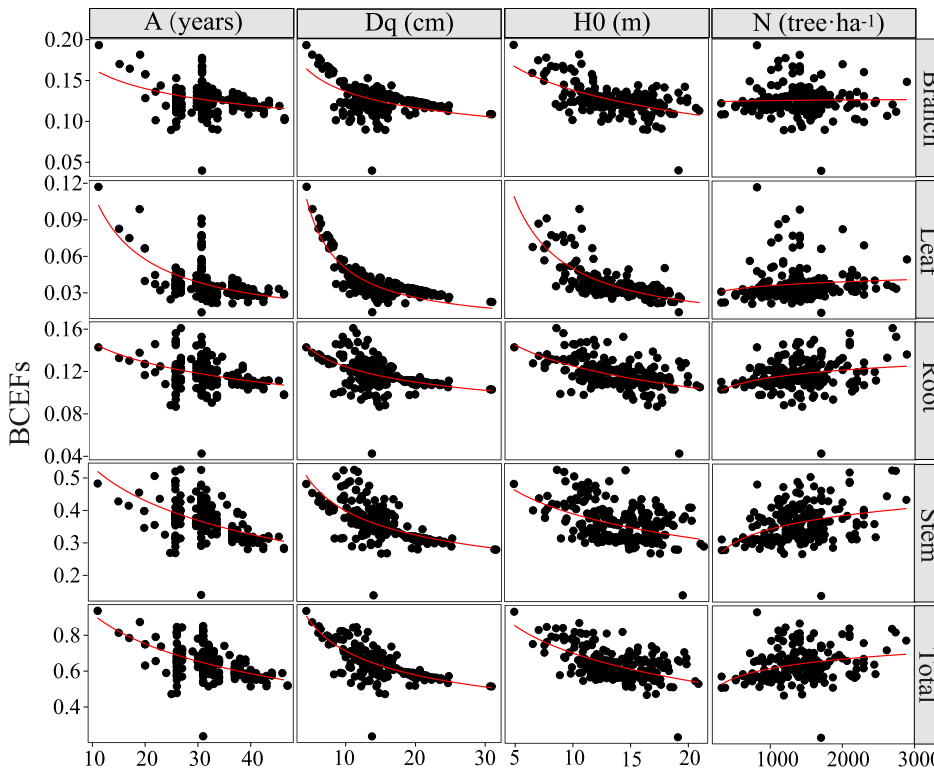


Figure 1. Relationships between BCEFs and stand-level variables: stand age (A), stand quadratic mean diameter (Dq), stand dominant height (H0) and stand density (N). The red line is the fitted curve of BCEFs and stand-level variables.

Table 3. The parameter estimates and standard errors (SEs) of stand biomass models (Aggregation 1, 2, and Adjustment).

Additive method	Component	α_i		β_i	
		Estimate	SE	Estimate	SE
Aggregation 1	Total	—	—	—	—
	Root	0.1794**	0.0044	-0.1614**	0.0080
	Stem	1.0908**	0.0374	-0.4090**	0.0117
	Branch	0.1466**	0.0073	-0.0631*	0.0170
	Leaf	0.0937**	0.0094	-0.3733**	0.0346
Aggregation 2	Total	—	—	—	—
	Root	0.1732**	0.0058	-0.1510**	0.0109
	Stem	0.9969**	0.0570	-0.3807**	0.0198
	Branch	0.1625**	0.0087	-0.1009**	0.0180
	Leaf	0.1129**	0.0113	-0.4395**	0.0342
Adjustment	Total	1.3840**	0.0314	-0.2880**	0.0074
	Root	0.1792**	0.0045	-0.1610**	0.0083
	Stem	1.0658**	0.0453	-0.4010**	0.0147
	Branch	0.1474**	0.0077	-0.0648*	0.0178
	Leaf	0.0954**	0.0096	-0.3797**	0.0346

Notes: ** represents the coefficient estimates at the significance $p < 0.0001$, *represents the coefficient estimates at the significance $p < 0.005$.

Ranking of modeling systems

The relative rank method proposed by Poudel and Cao (2013) was used in this study. This method can comprehensively evaluate the performance of each model system and reflect the ranking situation. It can also describe the exact position of each model relative to others. In this ranking system, the best and worst models have relative ranks of 1 and m , respectively. The calculation is defined as:

$$R_i = 1 + \frac{(m - 1)(S_i - S_{min})}{S_{max} - S_{min}} \tag{18}$$

Where R_i represents the relative rank of model i ($i = 1, 2, \dots, m$), S_i represents the statistical indicators produced by model i , S_{min} and S_{max} are the minimum and maximum values of S_i respectively.

RESULTS

Determination of model system variables

A correlation analysis was implemented to study the values of BCEFs plotted against the stand-level variables (A, Dq, H0 and N) (Figure 1). The results of establishing BCEF equations with these variables indicated that Dq was the best stand-level variable, and so we determined that the form of the basic stand biomass model was equation (19).

$$BCEF_i = \alpha_i Dq^{\beta_i} \tag{19}$$

Where Dq represents quadratic mean diameter, α_i and β_i are coefficients, and others variables are as previously defined.

After the variables of Equation (19) are determined, then replace $BCEF_i(X)$ in Equations (2-4 and 6-11)

Table 4. The stand biomass model's parameter estimates and standard error (SE) (Disaggregation).

Additive method	Parameters	Estimate	SE
Disaggregation	α_t	1.3837**	0.0679
	β_t	-0.2897**	0.0171
	r_1	7.4267**	0.8125
	k_1	-0.3464**	0.0380
	r_2	0.6370**	0.0823
	k_2	-0.3082**	0.0444
	r_3	1.2218**	0.1024
	k_3	-0.0971*	0.0285

Notes: ** represents the coefficient estimates at the significance $p < 0.0001$, *represents the coefficient estimates at the significance $p < 0.005$.

with $\alpha_i Dq^{\beta_i}$ to determine the total stand biomass and component model form. Equation (11) can be simplified to the following form:

$$\begin{cases} W_s = \frac{r_1 Dq^{k_1}}{r_1 Dq^{k_1} + 1 + r_2 Dq^{k_2} + r_3 Dq^{k_3}} \alpha_t Dq^{\beta_t V} + \varepsilon_s \\ W_b = \frac{1}{r_1 Dq^{k_1} + 1 + r_2 Dq^{k_2} + r_3 Dq^{k_3}} \alpha_t Dq^{\beta_t V} + \varepsilon_b \\ W_l = \frac{r_2 Dq^{k_2}}{r_1 Dq^{k_1} + 1 + r_2 Dq^{k_2} + r_3 Dq^{k_3}} \alpha_t Dq^{\beta_t V} + \varepsilon_l \\ W_r = \frac{r_3 Dq^{k_3}}{r_1 Dq^{k_1} + 1 + r_2 Dq^{k_2} + r_3 Dq^{k_3}} \alpha_t Dq^{\beta_t V} + \varepsilon_r \\ W_t = \alpha_t Dq^{\beta_t V} + \varepsilon_t \end{cases} \quad (20)$$

Where $\alpha_r, \beta_r, r_1-r_3$ and k_1-k_3 are coefficients, $r_j = \alpha_s / \alpha_b$, $r_2 = \alpha_l / \alpha_b$, $r_3 = \alpha_r / \alpha_b$, $k_1 = \beta_s - \beta_b$, $k_2 = \beta_l - \beta_b$, $k_3 = \beta_r - \beta_b$, ε_i are inter-correlated error terms, and i is either $s, b, l, r, \text{ or } t$, which represents stem, branch, leaf, root and total, respectively.

Coefficient estimates for stand biomass model systems

The coefficient estimates and standard errors (SEs) of the four additive methods are shown in Table 3 and Table 4. It can be seen that the parameter estimates of stand components of Aggregation 1, Aggregation 2, and Adjustment are relatively close. Nevertheless, the standard errors of Aggregation 2 are slightly higher, and all coefficient estimates have minor standard errors except r_l in Table 4.

Comparison of four additive modeling approaches

The R^2_{adj} , RMSE and weight functions for stand biomass equations were shown in Table 5. The results indicated that the total and component biomass models

based on Aggregation 1, Aggregation 2, Adjustment and Disaggregation fitted the data well, with $R^2_{adj} > 0.92$ and $RMSE < 8.22 \text{ Mg}\cdot\text{ha}^{-1}$. The stand leaf biomass models had lower R^2_{adj} and the stand total and stem biomass models had larger RMSE in all model systems. Only the RMSE of the total stand biomass model with Adjustment and Disaggregation had a difference of about $0.02 \text{ Mg}\cdot\text{ha}^{-1}$. Table 5 also listed the weight functions of the total and components biomass models.

Validation of stand biomass models

In this study, we used the leave-one-out cross-validation method to evaluate the prediction precision of stand biomass systems among four additive modeling approaches. The advantage of this method was that each model could be tested without losing samples. The validation statistics of the stand additive biomass model were shown in Table 6. The most stand total and component biomass models were slightly overestimated ($-3.19 \sim -0.01$), while the stand leaf biomass models were slightly underestimated ($0.63 \sim 1.49$). The total and root models based on Aggregation 1 are slightly better than the other three additive methods. The stem model based on Aggregation 2 performs best. Adjustment is slightly better for branch and leaf model than for the other three additive methods. Overall, we rank the prediction precision of the additive systems as follows: Aggregation 1 > Disaggregation > Adjustment > Aggregation 2, and their sum ranks were 11.9913, 12.4599, 12.7691, and 13.9094, respectively (Table 6).

Table 5. Goodness-of-fit statistics and weight functions for four additive stand biomass modeling methods.

Additive method	Component	R^2_{adj}	RMSE	Weight functions
Aggregation 1	Total	0.9730	8.1990	$Dq^{-5.2564} \sqrt{3.2175}$
	Root	0.9747	1.5651	$Dq^{-5.8616} \sqrt{3.0028}$
	Stem	0.9598	5.5262	$\sqrt{0.2599}$
	Branch	0.9762	1.6947	$\sqrt{-0.1426}$
	Leaf	0.9289	0.6988	$\sqrt{-0.4067}$
Aggregation 2	Total	0.9731	8.1938	—
	Root	0.9745	1.5695	$Dq^{-5.2731} \sqrt{3.0382}$
	Stem	0.9597	5.5290	$\sqrt{0.2404}$
	Branch	0.9758	1.7058	$Dq^{-2.9598} \sqrt{1.4731}$
	Leaf	0.9285	0.7008	$Dq^{-2.1290} \sqrt{0.7555}$
Adjustment	Total	0.9730	8.2107	$Dq^{-5.2353} \sqrt{2.8958}$
	Root	0.9747	1.5653	$Dq^{-6.0322} \sqrt{3.7551}$
	Stem	0.9598	5.5262	$\sqrt{0.2633}$
	Branch	0.9761	1.6953	$\sqrt{-0.1484}$
	Leaf	0.9289	0.6986	$\sqrt{-0.4032}$
Disaggregation	Total	0.9739	8.1869	$Dq^{-5.2489} \sqrt{3.1123}$
	Root	0.9738	1.5671	$Dq^{-5.9880} \sqrt{3.6339}$
	Stem	0.9587	5.5127	$\sqrt{0.2638}$
	Branch	0.9755	1.6917	$\sqrt{-0.1432}$
	Leaf	0.9265	0.6996	$\sqrt{-0.4081}$

Table 6. Leave-one-out cross-validation statistics for four additive methods.

Additive method	Component	MAB	MPB	MRB	Rank
Aggregation 1	Total	4.9072	4.9654	-1.4970	2.0000
	Root	0.9024	4.9165	-1.1518	1.9333
	Stem	3.7343	6.7394	-3.1812	3.7820
	Branch	1.1392	5.7719	-0.3887	2.0695
	Leaf	0.5501	10.3250	1.4096	2.2065
Aggregation 2	Total	4.9468	5.0054	-0.6169	3.0000
	Root	0.9172	4.9974	-0.4505	3.0000
	Stem	3.6312	6.5533	-1.7273	1.0000
	Branch	1.1695	5.9256	-0.4658	3.9094
	Leaf	0.5559	10.4345	0.6395	3.0000
Adjustment	Total	4.9266	4.9850	-1.4449	2.9207
	Root	0.9046	4.9286	-1.2019	2.2982
	Stem	3.7469	6.7622	-3.0061	3.8796
	Branch	1.1335	5.7430	-0.5104	2.0000
	Leaf	0.5491	10.3066	1.2035	1.6706
Disaggregation	Total	4.9373	4.9958	-0.9841	2.9373
	Root	0.9076	4.9449	-0.9461	2.3620
	Stem	3.7150	6.7024	-2.8976	3.2430
	Branch	1.1459	5.8059	-0.0179	1.6889
	Leaf	0.5499	10.3208	1.4806	2.2287

The graphical comparisons between actual stand biomass and predicted values were showed in Figure 2. It indicated that four additive methods showed similar performance. However, Constant BCEFs would lead to overestimation of stand biomass.

Furthermore, four additive methods were also compared by different stand volume (Figure 3). Aggregation 1 and Adjustment are slightly better than Disaggregation and Aggregation 2 in the stand volume interval of 0–300 m³·ha⁻¹, while the prediction ability of Aggregation 2 is better than others when the stand volume is greater than 300 m³·ha⁻¹.

DISCUSSION

As expected, the constant BCEF values and stand volumes did not provide accurate predictions of stand biomass (Soares and Tomé, 2004), in contrast, our results indicated that the BCEF equations were more suitable for total stand biomass and component biomass estimation (Figure 2). Regarding BCEF equations, including observed stand variables, stand quadratic mean diameter was selected as a predictor for BCEFs of total and component biomass estimation of Korean pine plantations (Figure 1). These findings are similar to previous findings that stand quadratic mean diameter has a good correlation with BCEF values (Castedo-Dorado et al., 2012; Dong et al., 2019). However, Lehtonen et al. (2004) found that stand age and BCEFs were strongly correlated for Scots pine, Norway spruce, and

birch using Finnish National Forest Inventory (NFI) data. The inconsistency in stand variables may be due to the slower growth of Korean pine, and the fact that plantation forests are subject to anthropogenic management (intermediate cuttings, etc.). Thus, the correlation between BCEFs and stand quadratic mean diameter are more evident.

The development of additivity models is an important approach for stand biomass estimation. However, some works of literature which did not consider additivity and predicted total and components separately have also been reported (Cunliffe et al., 2020; Kenzo et al., 2020). In this study, four additive methods were used to establish the stand biomass model to provide technical support for broader landscape Korean pine biomass assessment. Although the differences in the prediction accuracy of different additivity methods are small (Table 6), the predicted values of stand biomass from applying different additivity methods may show significant differences when estimating the stand biomass in large-scale forests.

Among the four additivity methods, the advantage of Aggregation 1, Aggregation 2, and Disaggregation lies in the simultaneous fitting and joint solution of the total and component biomass equations. The NSUR can consider inherent correlation among stand components and a total of the same plot; it obtains more effective statistics than Adjustment (OLS) (Parresol, 1999, 2001; Bi et al., 2004; Nord-Larsen et al., 2017). Besides, compared with Adjustment, the other three additive methods had a smaller number of parameters (Table 3, 4). However, the

advantage of Adjustment is that its parameter estimation process is relatively simple and easy to converge than other additive methods. Disaggregation requires the formula simplification during the development of the stand biomass model to reduce the number of parameters, which has the disadvantage of making model construction relatively complex. Furthermore, this study does not consider the logarithmic transformation because the anti-log transformation process may lead to a systematic deviation (Baskerville, 1972). The predicted value of BCEFs needs to multiply the correction factors, making the predicted values of stand biomass challenging to ensure the additive.

Since the estimation of total stand biomass is a greater concern in forest biomass monitoring, this study compared the prediction accuracy of the four additive-based total stand biomass models in different stand

volume intervals. The results showed that the selection of the appropriate additive method is crucial to the prediction of total stand biomass in different stand volume intervals (at 100 m³·ha⁻¹ intervals) (Figure 3). The MAB and MPB of the Aggregation 1 and Adjustment methods were slightly better than the other two additive methods in the 0-300 m³·ha⁻¹ stand volume interval. There is no significant difference between Aggregation 1 and Adjustment. Aggregation 2 performed better when stand volume exceeds 300 m³·ha⁻¹. If the forest stand volume is concentrated in specific interval, different additive method should be selected for prediction according to the actual situation. In addition, stand volume in this study was an estimated variable, so propagation errors predicted by individual tree volume models were expected (McRoberts and Westfall, 2016).

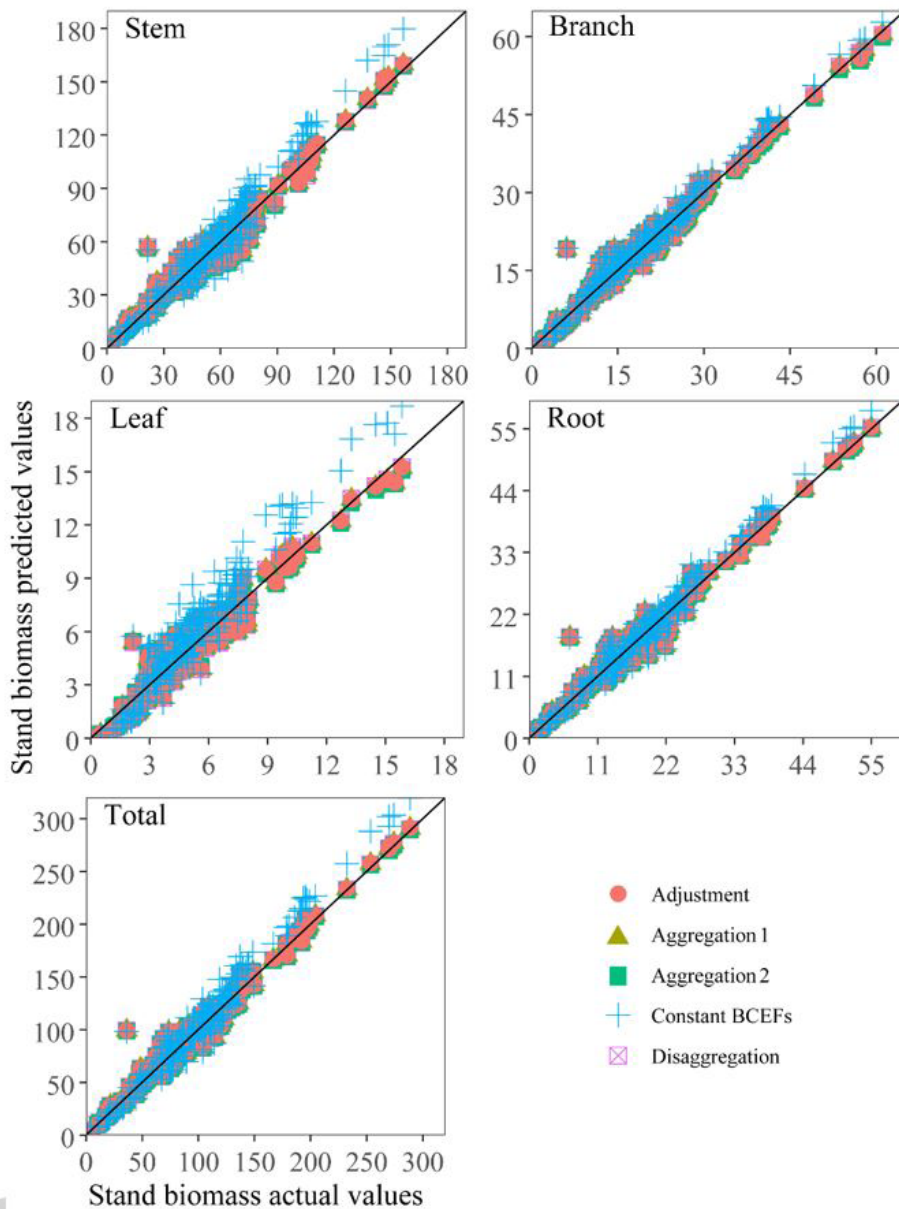


Figure 2. Comparisons of stand biomass (stem, branch, leaf, root, and total) predictions with Adjustment, Aggregation 1, Aggregation 2, Disaggregation and Constant BCEFs.

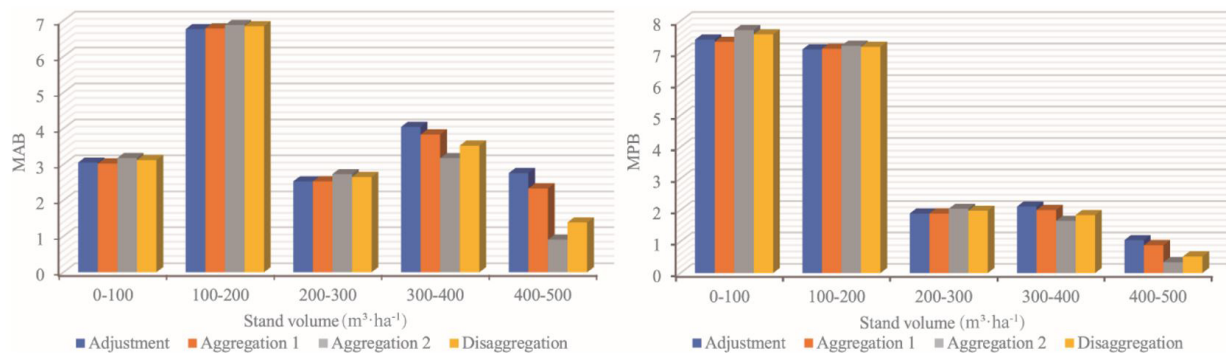


Figure 3. The predictive ability of the total biomass model of Korean pine plantations based on four additivity methods (Adjustment, Aggregation 1, Aggregation 2, Disaggregation) in different stand volume intervals.

CONCLUSION

We developed four systems of additive stand-level biomass models for Korean pine plantations across the species' main distribution areas in Heilongjiang Province, Northeast China. The BCEFs correlate best with the quadratic mean diameter (D_q). There was no single additive method to predict stand biomass that was best for all stand total and component biomass regarding the stand biomass predictions. Overall, the four additive method systems followed the order of Aggregation 1 > Disaggregation > Adjustment > Aggregation 2 > Constant BCEFs according to the relative rank.

Consequently, The Aggregation1 was recommended for the prediction of stand biomass in Korean pine plantations when the stand volume has a wider interval. However, when predicting the total stand biomass, the parameter estimates of the Aggregation 1 was recommended for Korean pine plantation with stand volume in the range of 0-300 m³·ha⁻¹, while Aggregation 2 was recommended for stand volumes greater than 300 m³·ha⁻¹. None of the additivity methods outperformed the other additive methods for both stand total and component predictions. If a study is more concerned with the prediction of biomass of a component, the appropriate additive method should be selected according to the prediction accuracy. This study also provides an alternative solution to estimate biomass at the stand level when tree level data are not available.

ACKNOWLEDGMENTS

This research was Supported by the Fundamental Research Funds for the Central Universities (2572022AW11) and Heilongjiang Province Applied Technology Research and Development Plan Project of China (GA19C006). We also want to extend our sincere thanks to Nathan J. Roberts (Northeast Forestry University) for the final revised English manuscript.

AUTHORSHIP CONTRIBUTION

Project Idea: SX, LJ
 Funding: SX, LJ
 Database: SX, LJ
 Processing: SX, LJ
 Analysis: SX, LJ, SBM
 Writing: SX
 Review: LJ, SBM

REFERENCES

- AFFLECK, D. L.; DIÉGUEZ-ARANDA, U. Additive nonlinear biomass equations: a likelihood-based approach. *Forest Science*, v. 62, n. 2, p. 129–140, 2016.
- BASKERVILLE, G. L. Use of logarithmic regression in the estimation of plant biomass. *Canadian Journal of Forest Research*, v. 2, n. 1, p. 49–53, 1972.
- BI, H.; TURNER, J.; LAMBERT, M. J. Additive biomass equations for native eucalypt forest trees of temperate Australia. *Trees*, v. 18, n. 4, p. 467–479, 2004.
- BRONISZ, K.; MEHTÁTALO, L. Seemingly unrelated mixed-effects biomass models for young silver birch stands on post-agricultural lands. *Forests*, v. 11, n. 4, p. 381, 2020.
- CASTEDO-DORADO, F.; GÓMEZ-GARCÍA, E.; DIÉGUEZ-ARANDA, U.; BARRIO-ANTA, M.; CRECENTE-CAMPO, F. Aboveground stand-level biomass estimation: a comparison of two methods for major forest species in northwest Spain. *Annals of Forest Science*, v. 69, n. 6, p. 735–746, 2012.
- CHI, H.; SUN, G.; HUANG, J.; GUO, Z.; NI, W.; FU, A. National forest aboveground biomass mapping from ICESat/GLAS data and MODIS imagery in China. *Remote Sensing*, v. 7, n. 5, p. 5534–5564, 2015.
- CUNLIFFE, A. M.; MCINTIRE, C. D.; BOSCHETTI, F.; SAUER, K. J.; LITVAK, M.; ANDERSON, K.; BRAZIER, R. E. Allometric relationships for predicting aboveground biomass and sapwood area of one-seed Juniper (*Juniperus monosperma*) trees. *Frontiers in Plant Science*, v. 11, p. 94, 2020.
- DIXON, R. K.; SOLOMON, A. M.; BROWN, S.; HOUGHTON, R. A.; TREXIER, M. C.; WISNIEWSKI, J. Carbon pools and flux of global forest ecosystems. *Science*, v. 263, n. 5144, p. 185–190, 1994.
- DONG, L.; ZHANG, L.; LI, F. A compatible system of biomass equations for three conifer species in Northeast, China. *Forest Ecology and Management*, v. 329, p. 306–317, 2014.
- DONG, L.; ZHANG, L.; LI, F. Developing additive systems of biomass equations for nine hardwood species in Northeast China. *Trees*, v. 29, n. 4, p. 1149–1163, 2015.
- DONG, L.; ZHANG, L.; LI, F. Evaluation of stand biomass estimation methods for major forest types in the eastern Da Xing'an Mountains, Northeast China. *Forests*, v. 10, n. 9, p. 715, 2019.
- FANG, J.; WANG, G. G.; LIU, G.; XU, S. Forest biomass of China: an estimate based on the biomass–volume relationship. *Ecological Applications*, v. 8, n. 4, p. 1084–1091, 1998.

- FU, L.; SHARMA, R. P.; WANG, G.; TANG, S. Modelling a system of nonlinear additive crown width models applying seemingly unrelated regression for Prince Rupprecht larch in northern China. *Forest Ecology and Management*, v. 386, p. 71–80, 2017.
- GÓMEZ-GARCÍA, E.; BIGING, G.; GARCÍA-VILLABRILLE, J. D.; CRECENTE-CAMPO, F.; CASTEDO-DORADO, F.; ROJO-ALBORECA, A. Cumulative continuous predictions for bole and aboveground woody biomass in *Eucalyptus globulus* plantations in northwestern Spain. *Biomass and Bioenergy*, v. 77, p. 155–164, 2015.
- GROEN, T.; NABUURS, G. J.; SCHELHAAS, M. J. Carbon accounting and cost estimation in forestry projects using CO₂ Fix V. 3. *Climatic Change*, v. 74, n. 1, p. 269–288, 2006.
- HARVEY, A. C., 1976. Estimating regression models with multiplicative heteroscedasticity. *Econometrica: Journal of the Econometric Society*, v. 44, p. 461–465.
- HEILONGJIANG FORERSTRY BUREAU. Stump volume table of Heilongjiang Province, 1981.
- HUANG, H.; LIU, C.; WANG, X.; ZHOU, X.; GONG, P. Integration of multi-resource remotely sensed data and allometric models for forest aboveground biomass estimation in China. *Remote Sensing of Environment*, v. 221, p. 225–234, 2019.
- JAGODZIŃSKI, A. M.; DYDESKI, M. K.; GĘSIKIEWICZ, K.; HORODECKI, P. Tree and stand-level biomass estimation in a *Larix decidua* Mill. Chronosequence. *Forests*, v. 9, n. 10, p. 587, 2018a.
- JAGODZIŃSKI, A. M.; DYDESKI, M. K.; GĘSIKIEWICZ, K.; HORODECKI, P.; CYSEWSKA, A.; WIERCZYŃSKA, S.; MACIEJCZYK, K. How do tree stand parameters affect young Scots pine biomass?—Allometric equations and biomass conversion and expansion factors. *Forest Ecology and Management*, v. 409, p. 74–83, 2018b.
- JAGODZIŃSKI, A. M.; ZASADA, M.; BRONISZ, K.; BRONISZ, A.; BIJAK, S. Biomass conversion and expansion factors for a chronosequence of young naturally regenerated silver birch (*Betula pendula* Roth) stands growing on post-agricultural sites. *Forest Ecology and Management*, v. 384, p. 208–220, 2017.
- KENZO, T.; HIMMAPAN, W.; YONEDA, R.; TEDSORN, N.; VACHARANGKURA, T.; HITSUMA, G.; NODA, I. General estimation models for above- and below-ground biomass of teak (*Tectona grandis*) plantations in Thailand. *Forest Ecology and Management*, v. 457, p. 117701, 2020.
- KOZAK, A. Methods for ensuring additivity of biomass components by regression analysis. *The Forestry Chronicle*, v. 46, n. 5, p. 402–405, 1970.
- KOZAK, A.; KOZAK, R. Does cross validation provide additional information in the evaluation of regression models? *Annals of Forest Science*, v. 33, n. 6, p. 976–987, 2003.
- LEHTONEN, A.; MÄKIPÄÄ, R.; HEIKKINEN, J.; SIEVÄNEN, R.; LISKI, J. Biomass expansion factors (BEFs) for Scots pine, Norway spruce and birch according to stand age for boreal forests. *Forest Ecology and Management*, v. 188, n. 1–3, p. 211–224, 2004.
- LIU, K.; HE, H.; XU, W.; DU, H.; ZONG, S.; HUANG, C.; WU, M.; TAN, X.; CONG, Y. Responses of Korean pine to proactive managements under climate change. *Forests*, v. 11, n. 3, p. 263, 2020.
- LUO, Y.; WANG, X.; OUYANG, Z.; LU, F.; FENG, L.; TAO, J. A review of biomass equations for China's tree species. *Earth System Science Data*, v. 12, n. 1, p. 21–40, 2020.
- MCCROBERTS, R. E.; WESTFALL, J. A. Propagating uncertainty through individual tree volume model predictions to large-area volume estimates. *Annals of Forest Science*, v. 73, n. 3, p. 625–633, 2016.
- MUUKKONEN, P. Generalized allometric volume and biomass equations for some tree species in Europe. *European Journal of Forest Research*, v. 126, n. 2, p. 157–166, 2007.
- NÁVAR, J. Allometric equations for tree species and carbon stocks for forests of northwestern Mexico. *Forest Ecology and Management*, v. 257, n. 2, p. 427–434, 2009.
- NORD-LARSEN, T.; MEILBY, H.; SKOVSGAARD, J. P. Simultaneous estimation of biomass models for 13 tree species: effects of compatible additivity requirements. *Canadian Journal of Forest Research*, v. 47, n. 6, p. 765–776, 2017.
- OLIVEIRA, T. S.; TOMÉ, M. Improving biomass estimation for *Eucalyptus globulus* Labill at stand level in Portugal. *Biomass and Bioenergy*, v. 96, p. 103–111, 2017.
- PARRESOL, B. R. Assessing tree and stand biomass: a review with examples and critical comparisons. *Forest Science*, v. 45, n. 4, p. 573–593, 1999.
- PARRESOL, B. R. Additivity of nonlinear biomass equations. *Canadian Journal of Forest Research*, v. 31, n. 5, p. 865–878, 2001.
- POUDEL, K. P.; CAO, Q. V. Evaluation of methods to predict Weibull parameters for characterizing diameter distributions. *Forest Science*, v. 59, n. 2, p. 243–252, 2013.
- R Core Team, R Foundation for Statistical Computing: Vienna, Austria. R: A Language and Environment for Statistical Computing, 2019.
- SAS Institute Inc, SAS Institute Inc.: Cary, NC, USA. SAS/ETS® 9.3. User's Guide, p. 3302. 2011
- SOARES, P.; TOMÉ, M. Analysis of the effectiveness of biomass expansion factors to estimate stand biomass. *Modeling Forest Production*, p. 368–374, 2004.
- SOARES, P.; TOMÉ, M. Biomass expansion factors for *Eucalyptus globulus* stands in Portugal. *Forest Systems*, v. 21, n. 1, p. 141–152, 2012.
- SOMOGYI, Z.; CIENCIALA, E.; MÄKIPÄÄ, R.; MUUKKONEN, P.; LEHTONEN, A.; WEISS, P. Indirect methods of large-scale forest biomass estimation. *European Journal of Forest Research*, v. 126, n. 2, p. 197–207, 2007.
- TANG, S.; ZHANG, H.; XU, H. Study on establish and estimate method of compatible biomass model. *Scientia Silvae Sinicae*, v. 36, p. 19–27, 2000.
- TANG, S.; LANG, K.; LI, H. Statistics and computation of biomathematical models. Science Press: Beijing, China, 2008.
- TRAUTENMÜLLER, J. W.; NETTO, S. P.; BALBINOT, R.; WATZLAWICK, L. F.; DALLA CORTE, A. P.; SANQUETTA, C. R.; BEHLING, A. Regression estimators for aboveground biomass and its constituent parts of trees in native southern Brazilian forests. *Ecological Indicators*, v. 130, p. 108025, 2021.
- WANG, C. Biomass allometric equations for 10 co-occurring tree species in Chinese temperate forests. *Forest Ecology and Management*, v. 222, n. 1–3, p. 9–16, 2006.
- ZENG, W.; DUO, H.; LEI, X.; CHEN, X.; WANG, X.; PU, Y.; ZOU, W. Individual tree biomass equations and growth models sensitive to climate variables for *Larix* spp. in China. *European Journal of Forest Research*, v. 136, n. 2, p. 233–249, 2017.
- ZHAO, D.; KANE, M.; MARKEWITZ, D.; TESKEY, R.; CLUTTER, M. Additive tree biomass equations for midrotation loblolly pine plantations. *Forest Science*, v. 61, n. 4, p. 613–623, 2015.
- ZHAO, D.; WESTFALL, J.; COULSTON, J. W.; LYNCH, T. B.; BULLOCK, B. P.; MONTES, C. R. Additive biomass equations for slash pine trees: comparing three modeling approaches. *Canadian Journal of Forest Research*, v. 49, n. 1, p. 27–40, 2019.
- ZIANIS, D.; MENCUCINI, M. On simplifying allometric analyses of forest biomass. *Forest Ecology and Management*, v. 187, n. 2–3, p. 311–332, 2004.
- ZOU, W.; ZENG, W.; ZHANG, L.; ZENG, M. Modeling crown biomass for four pine species in China. *Forests*, v. 6, n. 2, p. 433–449, 2015.