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

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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.

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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 CO_2 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 (IPCC, 2006), 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℃ and +35℃, 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 $m^3 \cdot ha^{-1}$. 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:

$$W_i = BCEF_i(x_j)V \quad (2)$$

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, ..., 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:

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

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:

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

$$\widehat{W}_t = \widehat{W}_s + \widehat{W}_b + \widehat{W}_l + \widehat{W}_r \quad (5)$$

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:

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

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

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

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

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

Where $\hat{W}_i$ 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 that was adjusted directly by one step via the following equations:

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

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 ($\hat{e}^2$) of stand biomass models and stand variables were fitted by stepwise regression in the process, equation as:

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

Where $\hat{e}$ are the unweighted residuals for each model, σ^2 is the variance of residuals, φ_{i1}- φ_{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 α = 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 $resid.W_i/\sqrt{X_1^{\varphi_{i1}} \cdots X_p^{\varphi_{ip}}}$ (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.

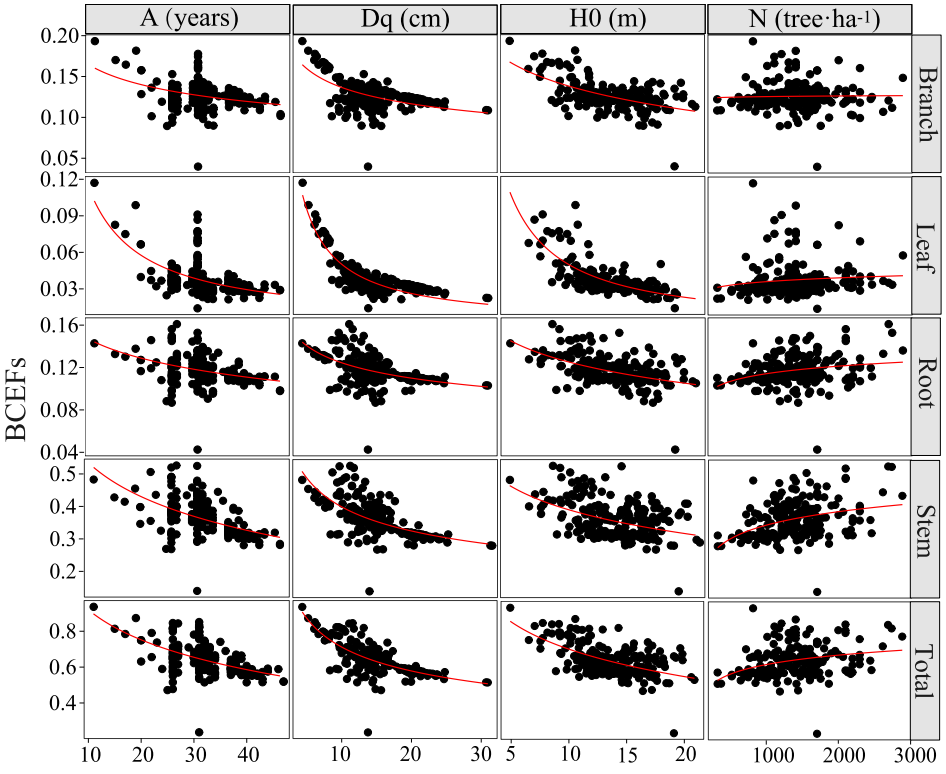

Figure 1. Relationships between BCEFs and stand-level variables: stand age (A), stand quadratic mean diameter (Dq), stand dominant height (H0) and stand density (N). The red line is the fitted curve of BCEFs and stand-level variables.

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:

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

Where R_i represents the relative rank of model i (i = 1, 2, ..., 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).

$$BCEF_i = a_i Dq^{\beta i} \quad (19)$$

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

After the variables of Equation (19) are determined, then replace $BCEF_i(X_j)$ 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	a_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:

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

Where α_i, β_i, r_1-r_3, and k_1-k_3 are coefficients, $r_1=\alpha_s/\alpha_b$, $r_2=\alpha_l/\alpha_b$, $r_3=\alpha_r/\alpha_b$, $k_1=\beta_s-\beta_b$, $k_2=\beta_l-\beta_b$, $k_3=\beta_r-\beta_b$, ε_i are inter-correlated error terms, and *i* is either *s*, *b*, *l*, *r*, 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_1 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 Mg·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 Mg·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 ~ -0.01), while the stand leaf biomass models were slightly underestimated (0.63 ~ 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	$Dq^{-5.2564}V^{3.2175}$
	Root	0.9747	1.5651	$Dq^{-5.8616}V^{3.0028}$
	Stem	0.9598	5.5262	$V^{0.2599}$
	Branch	0.9762	1.6947	$V^{-0.1426}$
	Leaf	0.9289	0.6988	$V^{-0.4067}$
Aggregation 2	Total	0.9731	8.1938	—
	Root	0.9745	1.5695	$Dq^{-5.2731}V^{3.0382}$
	Stem	0.9597	5.5290	$V^{0.2404}$
	Branch	0.9758	1.7058	$Dq^{-2.9598}V^{1.4731}$
	Leaf	0.9285	0.7008	$Dq^{-2.1290}V^{0.7555}$
Adjustment	Total	0.9730	8.2107	$Dq^{-5.2353}V^{2.8958}$
	Root	0.9747	1.5653	$Dq^{-6.0322}V^{3.7551}$
	Stem	0.9598	5.5262	$V^{0.2633}$
	Branch	0.9761	1.6953	$V^{-0.1484}$
	Leaf	0.9289	0.6986	$V^{-0.4032}$
Disaggregation	Total	0.9739	8.1869	$Dq^{-5.2489}V^{3.1123}$
	Root	0.9738	1.5671	$Dq^{-5.9880}V^{3.6339}$
	Stem	0.9587	5.5127	$V^{0.2638}$
	Branch	0.9755	1.6917	$V^{-0.1432}$
	Leaf	0.9265	0.6996	$V^{-0.4081}$

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 $m^3 \cdot ha^{-1}$, while the prediction ability of Aggregation 2 is better than others when the stand volume is greater than 300 $m^3 \cdot ha^{-1}$.

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 $m^3 \cdot ha^{-1}$ 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 $m^3 \cdot ha^{-1}$ stand volume interval. There is no significant difference between Aggregation 1 and Adjustment. Aggregation 2 performed better when stand volume exceeds 300 $m^3 \cdot ha^{-1}$. 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).

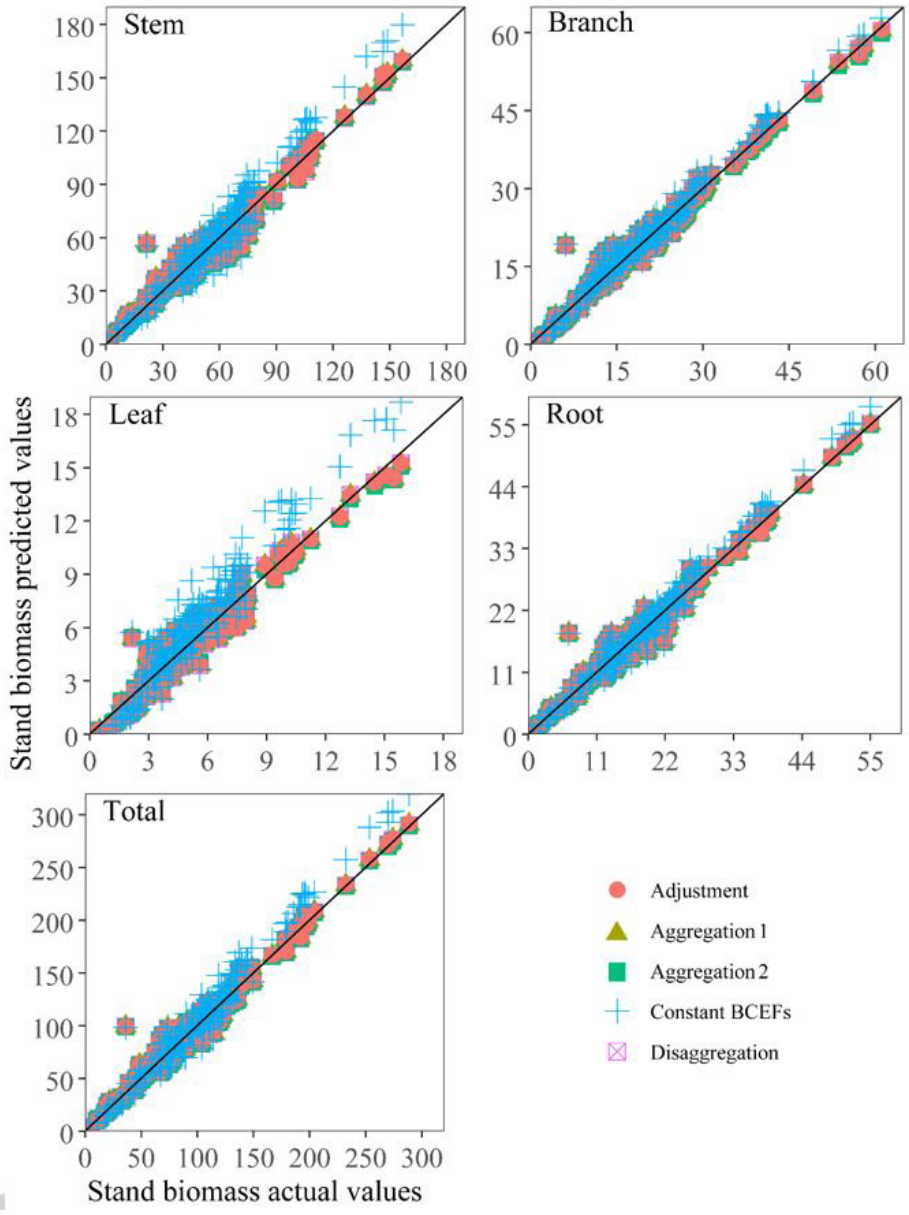

Figure 2. Comparisons of stand biomass (stem, branch, leaf, root, and total) predictions with Adjustment, Aggregation 1, Aggregation 2, Disaggregation and Constant BCEFs.

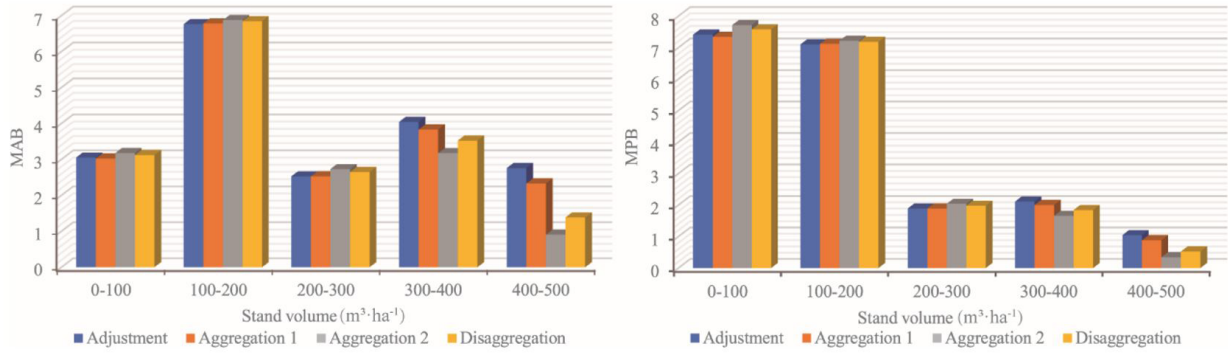

Figure 3. The predictive ability of the total biomass model of Korean pine plantations based on four additivity methods (Adjustment, Aggregation 1, Aggregation 2, Disaggregation) in different stand volume intervals.

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 (Dq). 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 $m^3 \cdot ha^{-1}$, while Aggregation 2 was recommended for stand volumes greater than 300 $m^3 \cdot ha^{-1}$. 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.

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AUTHORSHIP CONTRIBUTION

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