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Developing Additive Systems of Biomass Equations for *Robinia pseudoacacia* L. in the Region of Loess Plateau of Western Shanxi Province, China

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Abstract: The accurate estimation of forest biomass is important to evaluate the structure and function of forest ecosystems, estimate carbon sinks in forests, and study matter cycle, energy flow, and the effects of climate change on forest ecosystems. Biomass additivity is a desirable characteristic to predict each component and the total biomass since it ensures consistency between the sum of the predicted values of components such as roots, stems, leaves, pods, and branches and the prediction for the total tree. In this study, 45 *Robinia pseudoacacia* L. trees were harvested to determine each component and the total biomass in the Loess Plateau of western Shanxi Province, China. Three additive systems of biomass equations of *R. pseudoacacia* L., based on the diameter at breast height (D) only and on the combination of D and tree height (H) with D^2H and D^bH^c , were established. To ensure biomass model additivity, the additive system of biomass equations considers the correlation among different components using simultaneous equations and establishes constraints on the parameters of the equation. Seemingly uncorrelated regression (SUR) was used to estimate the parameters of the additive system of biomass equations, and the jackknifing technique was used to verify the accuracy of prediction of the additive system of biomass equations. The results showed that (1) the stem biomass contributed the most to the total biomass, comprising 51.82% of the total biomass, followed by the root biomass (24.63%) and by the pod and leaf biomass, which accounted for the smallest share, comprising 1.82% and 2.22%, respectively; (2) the three additive systems of biomass equations of *R. pseudoacacia* L. fit well with the models and were effective at making predictions, particularly for the root, stem, above-ground, and total biomass ($R^2_{adj} > 0.812$; root mean square error (RMSE) < 0.151). The mean absolute error (MAE) was less than 0.124, and the mean prediction error (MPE) was less than 0.037. (3) When the biomass model added the tree height predictor, the goodness of fit R^2_{adj} increased, RMSE decreased, and the accuracy of prediction was much improved. In particular, the additive system, which was developed based on D^bH^c combination prediction factors, was the most accurate. The additive system of biomass equations established in this study can provide a reliable and accurate estimation of the individual biomass of *R. pseudoacacia* L. in the Loess region of western Shanxi Province, China.

Keywords: *Robinia pseudoacacia* L.; Loess Plateau; additive biomass models; error structure; likelihood analysis; seemingly unrelated regression

1. Introduction

As the most basic quantitative characteristic of a forest ecosystem [1], forest biomass is an integral part of the structure and function of forest ecosystems [2]. Accurate estimation of the above-ground and below-ground biomass is important to evaluate the structure and function of forest ecosystems, estimate carbon sinks in forests, and study matter cycle, energy flow, and the effects of climate change on forest ecosystems [3–7].

There are two main methods for biomass estimation: destructive methods by integral or sampled harvesting and model estimation. The first one is the most accurate method for estimating biomass amounts. Nevertheless, it is time-consuming, expensive to use, and restricts the development in spatial scale [8,9]. In contrast, model estimation has become more popular because of its high accuracy, efficiency, and conciseness [3,4,10]. The most commonly used method for developing biomass models is to link tree biomass or that of tree components, such as stems, branches, leaves, or roots, with one or several easily measurable dendrometric variables, such as the diameter at breast height (D) and tree height (H), using logarithmically transformed data through least squares [4,11,12]. Even though it is necessary to obtain a certain amount of sample tree biomass data destructively during the process of modeling, once the model is developed, the forest inventory data can be used to estimate the biomass of the whole stand in the same type of forest, which guarantees that the results are accurate [3,6,11].

More than 5000 biomass models have been established in China, involving more than 200 species [4]. The models used to estimate tree biomass can be divided in two classes: additive and non-additive [4,13,14]. Some researchers used the power law function as the primary approach to construct biomass models which were not additive and were used to independently estimate the total and component-based biomass of trees [4,15,16]. As a result, the sum of the values estimated by each biomass component model was not equal to the value of total biomass, and the intrinsic correlation and logical consistency between the biomass of each component and the total biomass were ignored [17]. In contrast, the additive approach used to develop biomass equations can ensure that the sum of the predicted values of each component equation is equal to the predicted value of the total biomass equation [8,18,19]. To enable the additivity of biomass models, some parameter estimation methods have been proposed for linear and nonlinear additive biomass models. For the first case, estimation methods include the weighted linear least squares estimator (WLS), a three-stage least squares (3SLS) and seemingly unrelated regression (SUR) [20–22]. In the second case, the estimation methods primarily include nonlinear seemingly unrelated regression (NSUR), maximum likelihood analysis, the error variable model method, and the generalized moment method (GMM) [6,18,23–25]. However, seemingly unrelated regression and nonlinear seemingly unrelated regression are more common and flexible [8,26].

When constructing an additive system of biomass equations based on allometric growth models, it is critical to determine the error structure of model [8,27]. However, this point is often overlooked. Generally speaking, the error structure of the allometric growth model of tree biomass can be divided into additive and multiplicative error. The error structure of the model varies with different tree species and biomass components [14]. The traditional method of analysis of power law data was to obtain a linear relationship by logarithmic transformation on both sides of the equation followed by the use of logarithmic transformation data to be modeled by linear regression [27]. However, some researchers have questioned this method [28–30], believing that the nonlinear regression on original data (NLR) is superior to the linear regression (LR) on logarithmic transformation [31]. In response to these controversies, Xiao [27] used a Monte Carlo simulation to prove that the error distribution determines which method (LR or NLR) performs better and proposed the judgment method of likelihood analysis

to determine the error structure (multiplication or addition) of allometric growth equations. Thus, this should ensure the validity of the biomass model constructed, i.e., the selection of an appropriate model structure to build the biomass model. The likelihood analysis method is considered to conform to the core principles of statistics and is more suitable for determining the model error structure of biomass models [32].

Research on single-tree additive systems of biomass equations is primarily concentrated in the northeast, north, and south of China. The coniferous species for which models were developed include Korean pine (*Pinus koraiensis* Sieb. et Zucc.), larch (*Larix gmelinii* (Rupr.) Kuzen.), and Mongolian Scotch pine (*Pinus sylvestris* var. *mongolica* Litv.) [8,33,34], and the broad-leaved species include white birch (*Betula platyphylla* Suk.), Mongolian oak (*Quercus mongolica* Fisch. ex Ledeb), *Quercus variabilis* Bl., and Amur linden (*Tilia amurensis* Rupr.) [7,26,33,35,36]. Black locust (*Robinia pseudoacacia* L.) is widely planted as a suitable and primary afforestation tree species owing to its rapid growth, drought tolerance, and nitrogen fixation in the Loess Plateau, China [37–39]. Its planting area in the Loess Plateau comprises 70.37% of the planting area of *R. pseudoacacia* L. in China and comprises 16.85% of the planting area of all the tree species in the Loess Plateau, making it the most widely distributed species of tree in this region [40]. However, there are no reports on the biomass additive modeling of *R. pseudoacacia* L. in this region. To evaluate the structure and functions of the forest ecosystem more effectively and accurately estimate the forest carbon storage, this study (1) analyzed the biomass allocation in each component of *R. pseudoacacia* L.; (2) constructed three additive systems of *R. pseudoacacia* L. biomass using SUR, and (3) tested the accuracy of the additive system of biomass equations using the jackknifing technique.

2. Materials and Methods

2.1. Study Site

The study was performed at the small watershed of Caijiachuan (110°39′45″–110°47′45″ E, 36°14′27″–36°18′23″ N), which is a typical gully area of the Loess Plateau in Ji County, Shanxi Province, China (Figure 1). The area of the watershed is 40.1 km², with an elevation range of 904–1592 m. The climate is a warm, temperate, continental monsoon, with a mean annual temperature of 10 °C and a mean annual rainfall of 579.5 mm. The annual evapotranspiration is approximately 3- to 4-fold the amount of precipitation [41]. According to the soil classification of the Food and Agriculture Organization (FAO) of the United Nations, the soil type in the region is mainly Haplic Luvisols, which are mostly alkaline [42]. This soil type is locally known as cinnamon soil, and it is distributed on loess. The main tree species of artificial forests from the study area are *R. pseudoacacia* L. and Chinese pine (*Pinus tabulaeformis* Carr.), while Manchu rose (*Rosa xanthina* Lindl.), Hawthornleaf raspberry (*Rubus crataegifolius* Bunge), and *Periploca sepium* (*Periploca sepium* Bunge) are the most dominant understory shrub species. The herbaceous cover consists of *Eriophorum vaginatum* (*Carex rigescens*), *Artemisia selengensis* (*Artemisia sacrorum* Ledeb.) and *Radix rubiae* (*Rubia cordifolia* L.), among others.

Figure 1. The location of the study area and sampling sites at the Caijiachuan watershed of the Loess Plateau, China.

2.2. Biomass Sampling

There were 85 sample plots of *R. pseudoacacia* L. established from 2017 to 2019 in the study area, and the size of each plot was 20 m × 20 m. The diameter at breast height (D), which was a $D \geq 5$ cm for all trees, and the height (H) were measured in these sample plots. The range of distribution of the tree height (H) and the diameter at breast height (D) in these plots are all shown in Figure 2A. Forty-five trees were selected as representative for destructive sampling and were used to develop the additive system of biomass models (Figure 2B).

Figure 2. The height and diameter at breast height (D) distribution of all the investigated trees (A) and the destructively sampled trees (B). The vertical bar represents the distribution frequency across 2-cm diameter classes.

The trees selected for sampling were cut at the base using a chain saw, and the branches were removed from the stem and cut into weighable sections. All the pods and leaves were separated from branches and collected into bags to facilitate weighing. The stem of each tree was cut into 2- or 1-m

sections. When H was higher than 10 m, the stem was divided into 2-m sections, and 5-cm thick discs were cut in the middle of each section. In contrast, when H was less than or equal to 10 m, the stem was divided into 1-m sections, and 5-cm thick discs were cut in the middle of each section. A total of 330 discs were collected. Owing to the growth characteristics of the roots of *R. pseudoacacia* L., which were horizontally developed with no obvious taproot, the roots located within a depth of 2 m were excavated manually and weighed [43]. These roots were divided into three classes, which included large roots (diameter ≥ 5 cm), medium roots (diameter 2–5 cm), and small roots (diameter < 2 cm). The fresh weights of branches, pods, leaves, stems, and roots for each tree were determined separately using a 50-kg scale balance. Smaller samples of 300 g were taken for the pods, leaves, and each class of roots; then, they were weighed and used to determine their moisture content. Depending on the size (diameter) of the stem or branch, samples of the branches and stems were cut into 5-cm thick discs to determine the fresh weight using a 2-kg electronic balance with a precision of 0.01 g. All of the samples of pods, leaves, branches, stems, and roots were transported to the laboratory, where they were oven-dried until reaching a constant weight at 85 °C to determine their moisture content. The dry weight of sample was divided by the corresponding fresh weight to obtain the dry/fresh ratio of each component, such as the stems, branches, leaves, pods, and roots. The dry weight (biomass) of each component was obtained by multiplying the dry/fresh ratio by the fresh weight of the corresponding component. For each tree, the sum of branch biomass (W_b), leaf biomass (W_l), and pod biomass (W_p) yielded the crown biomass (W_c). The sum of crown biomass (W_c) and stem biomass (W_s) produced the above-ground biomass (W_a). The sum of each component's biomass produced the total tree biomass (W_t). Table 1 lists the descriptive statistics of each component's biomass (kg), the sub-total biomass (kg), and the total biomass (kg).

Table 1. Descriptive statistics of the main variables of standard trees ($n = 45$).

Statistics	Tree Age	D	H	W_p	W_b	W_l	W_s	W_r	W_c	W_a	W_t
Minimum	13	6.2	4.7	0.17	2.11	0.23	4.57	3.12	2.74	8.92	12.53
Maximum	37	23.2	14.7	2.53	71.39	6.20	142.28	53.86	79.92	209.52	263.38
Mean	25	12.1	9.6	1.09	14.34	1.41	38.70	16.52	16.84	55.54	62.56
SD	7	4.1	2.5	0.60	15.42	1.08	35.58	13.01	16.86	51.21	56.68

Note: SD, standard deviation; D , diameter at breast height (cm); H , tree height (m); n is the number of all sample trees; W_p is the pod biomass of sample trees (kg); W_b is the branch biomass of sample trees (kg); W_l is the leaf biomass of the sample trees (kg); W_s is the stem biomass of the sample trees (kg); W_r is the root biomass of sample trees (kg); W_c is the crown biomass of sample trees (kg); W_a is the above-ground biomass of sample trees (kg), and W_t is the total biomass of sample trees (kg).

2.3. Error Structure Evaluation of Allometric Biomass Equations

Allometric biomass equations, i.e., $W = a \times D^b$, $W = a \times (D^2H)^b$ and $W = a \times D^b \times H^c$, are usually used to fit models of total and component biomass of individual trees [8,35,42]. Therefore, in this study, $W = a \times D^b$, $W = a \times (D^2H)^b$ and $W = a \times D^b \times H^c$ were used as the basic models to construct additive systems of biomass equations.

Owing to the difference in the error structure in power law and logarithmic transformation models, we used the method of likelihood analysis to determine the appropriate error structures from linear regression (LR) on the log-transformed data and nonlinear regression (NLR) on the original data to select the most suitable model structure to construct the additive systems of biomass equations, as recommended by Xiao and Dong et al. [27,33]. The relative likelihood of those two error structures can be compared with the AICc, a second-order variant of Akaike's information criterion (AIC) that corrects a small sample size [27]. The AICc measures the goodness-of-fit of a statistical model by incorporating the model's likelihood while applying a penalty for extra parameters and correcting for small sample size [27,44]. If $AICc_{\text{norm}} - AICc_{\text{logn}} < -2$, the assumption of normal error is favored over log-normal error. If $AICc_{\text{norm}} - AICc_{\text{logn}} > 2$, it implies the assumption that log-normal error is

avored over normal error. If $|AIC_{C-norm} - AIC_{C-logn}| \leq 2$, this implies that neither model error structure is favored and model averaging may be adopted.

For each component biomass datum of trees, we fitted the allometric equations $W = a \times D^b$, $W = a \times (D^2H)^b$, and $W = a \times D^b \times H^c$ using non-linear regression on the original data (NLR) and linear regression on the log-transformed data (LR) to estimate the model intercept, slope parameters, and σ^2 for each model in this study. The specific steps for constructing the log-likelihood functions for the three models can be found in Xiao et al. [27] and Balantan [32]. In addition, we used the calculated ΔAIC_c value, which is equal to $AIC_{C-NLR} - AIC_{C-LR}$, to select the suitable model error structure.

2.4. Biomass Additivity System Development

For all the components and total biomass equations of trees in this study, the likelihood analysis of the error structures for $W = a \times D^b$, $W = a \times (D^2H)^b$, and $W = a \times D^b \times H^c$ showed that the ΔAIC_c values were much greater than 2 (Table 2), which indicated that linear regression on the log-transformed data (LR) was favored over nonlinear regression on the original data (NLR) to fit the allometric growth equations with $W = a \times D^b$, $W = a \times (D^2H)^b$, and $W = a \times D^b \times H^c$ in this study.

Table 2. Information statistic (ΔAIC_c) of the likelihood analysis for three allometric biomass equations.

Equation Type	Pods	Branch	Leaf	Stem	Crown	Above-Ground	Root	Total
$W = a \times D^b$	30.94	65.04	49.17	48.21	99.75	54.38	45.82	44.01
$W = a \times (D^2H)^b$	31.38	57.91	48.24	48.68	56.03	49.74	46.03	49.06
$W = a \times D^b \times H^c$	31.58	57.65	48.28	89.89	87.44	89.58	94.51	91.39

We based the model structure of the logarithmic function to construct the leaf, pod, branch, stem, root, crown, above-ground, and total biomass model. Moreover, seemingly unrelated regression (SUR) was used to simultaneously fit the total biomass and the biomass of each component to construct the additive systems of biomass equations so that the component model was not independent of the total amount to ensure the additivity of models. Three additive systems of biomass equations with cross-equation constraints on the structural parameters and cross-equation error correlation for biomass components, sub-total biomass (i.e., the above-ground biomass and crown biomass), and total biomass are as follows:

1. Based on the logarithmic function of additive error structure $\lg W_i = \lg a_{ij} + b_{ij} \times \lg D + \varepsilon_i$, we constructed the additive system of *R. pseudoacacia* L. biomass equation, system 1, as follows:

$$\begin{aligned}
 \lg W_p &= \lg a_{11} + b_{12} \times \lg D + \varepsilon_p \\
 \lg W_b &= \lg a_{21} + b_{22} \times \lg D + \varepsilon_b \\
 \lg W_l &= \lg a_{31} + b_{32} \times \lg D + \varepsilon_l \\
 \lg W_s &= \lg a_{41} + b_{42} \times \lg D + \varepsilon_s \\
 \lg W_r &= \lg a_{51} + b_{52} \times \lg D + \varepsilon_r \\
 \lg W_c &= \lg(W_p + W_b + W_l) + \varepsilon_c = \lg(a_{11} \times D^{b_{12}} + a_{21} \times D^{b_{22}} + a_{31} \times D^{b_{32}}) + \varepsilon_c \\
 \lg W_a &= \lg(W_p + W_b + W_l + W_s) + \varepsilon_a \\
 &= \lg(a_{11} \times D^{b_{12}} + a_{21} \times D^{b_{22}} + a_{31} \times D^{b_{32}} + a_{41} \times D^{b_{42}}) + \varepsilon_a \\
 \lg W_t &= \lg(W_p + W_b + W_l + W_s + W_r) + \varepsilon_t \\
 &= \lg(a_{11} \times D^{b_{12}} + a_{21} \times D^{b_{22}} + a_{31} \times D^{b_{32}} + a_{41} \times D^{b_{42}} + a_{51} \times D^{b_{52}}) + \varepsilon_t
 \end{aligned} \tag{1}$$

2. Based on the logarithmic function of additive error structure $\lg W_i = \lg a_{ij} + b_{ij} \times \lg(D^2H) + \varepsilon_i$, we constructed the additive system of *R. pseudoacacia* L. biomass equation, system 2, as follows:

$$\begin{aligned}
 \lg W_p &= \lg a_{11} + b_{12} \times \lg(D^2H) + \varepsilon_p \\
 \lg W_b &= \lg a_{21} + b_{22} \times \lg(D^2H) + \varepsilon_b \\
 \lg W_l &= \lg a_{31} + b_{32} \times \lg(D^2H) + \varepsilon_l \\
 \lg W_s &= \lg a_{41} + b_{42} \times \lg(D^2H) + \varepsilon_s \\
 \lg W_r &= \lg a_{51} + b_{52} \times \lg(D^2H) + \varepsilon_r \\
 \lg W_c &= \lg(W_p + W_b + W_l) + \varepsilon_c = \lg(a_{11} \times (D^2H)^{b_{12}} + a_{21} \times (D^2H)^{b_{22}} + a_{31} \times (D^2H)^{b_{32}}) + \varepsilon_c \\
 \lg W_a &= \lg(W_p + W_b + W_l + W_s) + \varepsilon_a \\
 &= \lg(a_{11} \times (D^2H)^{b_{12}} + a_{21} \times (D^2H)^{b_{22}} + a_{31} \times (D^2H)^{b_{32}} + a_{41} \times (D^2H)^{b_{42}}) + \varepsilon_a \\
 \lg W_t &= \lg(W_p + W_b + W_l + W_s + W_r) + \varepsilon_t \\
 &= \lg(a_{11} \times (D^2H)^{b_{12}} + a_{21} \times (D^2H)^{b_{22}} + a_{31} \times (D^2H)^{b_{32}} + a_{41} \times (D^2H)^{b_{42}} \\
 &\quad + a_{51} \times (D^2H)^{b_{52}}) + \varepsilon_t
 \end{aligned} \tag{2}$$

3. Based on the logarithmic function of additive error structure $\lg W_i = \lg a_{ij} + b_{ij} \times \lg D + c_{ij} \times \lg H + \varepsilon_i$, we constructed the additive system of *R. pseudoacacia* L. biomass equation, system 3, as follows:

$$\begin{aligned}
 \lg W_p &= \lg a_{11} + b_{12} \times \lg D + c_{13} \times \lg H + \varepsilon_p \\
 \lg W_b &= \lg a_{21} + b_{22} \times \lg D + c_{23} \times \lg H + \varepsilon_b \\
 \lg W_l &= \lg a_{31} + b_{32} \times \lg D + c_{33} \times \lg H + \varepsilon_l \\
 \lg W_s &= \lg a_{41} + b_{42} \times \lg D + c_{43} \times \lg H + \varepsilon_s \\
 \lg W_r &= \lg a_{51} + b_{52} \times \lg D + c_{53} \times \lg H + \varepsilon_r \\
 \lg W_c &= \lg(W_p + W_b + W_l) + \varepsilon_c \\
 &= \lg(a_{11} \times D^{b_{12}} \times H^{c_{13}} + a_{21} \times D^{b_{22}} \times H^{c_{23}} + a_{31} \times D^{b_{32}} \times H^{c_{33}}) + \varepsilon_c \\
 \lg W_a &= \lg(W_p + W_b + W_l + W_s) + \varepsilon_t \\
 &= \lg(a_{11} \times D^{b_{12}} \times H^{c_{13}} + a_{21} \times D^{b_{22}} \times H^{c_{23}} + a_{31} \times D^{b_{32}} \times H^{c_{33}} \\
 &\quad + a_{41} \times D^{b_{42}} \times H^{c_{43}}) + \varepsilon_a \\
 \lg W_t &= \lg(W_p + W_b + W_l + W_s + W_r) + \varepsilon_t \\
 &= \lg(a_{11} \times D^{b_{12}} \times H^{c_{13}} + a_{21} \times D^{b_{22}} \times H^{c_{23}} + a_{31} \times D^{b_{32}} \times H^{c_{33}} \\
 &\quad + a_{41} \times D^{b_{42}} \times H^{c_{43}} + a_{51} \times D^{b_{52}} \times H^{c_{53}}) + \varepsilon_t
 \end{aligned} \tag{3}$$

where $\lg$ denotes the natural logarithm with base 10; D is the tree diameter at breast height; H is the tree height; a_{ij} , b_{ij} , and c_{ij} are the regression coefficients, and ε_i represents the model error term.

The above three additive systems of biomass equations were fitted to the data of total and each component's individual biomass using the method of seemingly unrelated regression (SUR) in R i386 4.0.2 equipped with the package 'systemfit'. This method simultaneously constrains the parameters, considers the structural correlation of errors between the total and component models, and estimates the coefficients of each component biomass model.

2.5. Model Evaluation and Validation

To determine whether the biomass model is reliable and can be used to reasonably and accurately estimate the biomass, we need to assess and evaluate the predictive quality of the different biomass equations. It is well known that the jackknifing technique, also known as the "leave-one-out" method or the Predicted Sum of Squares (PRESS), is a popular verification method [13,36,44]. Thus, in this paper, we used the entire dataset to fit the additive systems of biomass equations and we used the jackknifing technique to evaluate the equations. The model fitting was evaluated by two goodness of fit statistics—the adjusted coefficient of determination (R^2_{Adj}) and root mean square error (RMSE). The statistical indicators of model performance were calculated using the jackknifing technique, including

the mean absolute error (MAE), mean absolute error percentage (MAE%), the mean prediction error (MPE), and the mean prediction error percentage (MPE%) (Equations (4)–(7)).

$$MAE = \frac{\sum_{i=1}^N |W_i - \widehat{W}_{i,-i}|}{N} \quad (4)$$

$$MAE\% = \frac{\sum_{i=1}^N \left(\frac{|W_i - \widehat{W}_{i,-i}|}{W_i} \right)}{N} \times 100 \quad (5)$$

$$MPE = \frac{\sum_{i=1}^N (W_i - \widehat{W}_{i,-i})}{N} \quad (6)$$

$$MPE\% = \frac{\sum_{i=1}^N \left(\frac{W_i - \widehat{W}_{i,-i}}{W} \right)}{N} \times 100 \quad (7)$$

where W_i presents the log-transformed value of the i th observed biomass value; $\widehat{W}_i$ represents the log-transformed of the i th predicted biomass value from the model which was fitted using the entire dataset (sample size N); $\bar{W}_i$ represents the mean value of the log-transformed observed biomass value, and $\widehat{W}_{i,-i}$ represents the predicted value of the i th observed value by the fitted model, which was fitted by $(N-1)$ observations without using the i th observation.

3. Results

3.1. Biomass Allocation

The diameter at breast height (D) varied between 6.2 and 23.2 cm, while the tree height varied between 4.7 and 14.7 cm (Table 1). The partitioning of tree total biomass into five components, namely pods, leaves, stems, branches, and roots, is shown in Figure 3. Among them, the stem biomass had the largest relative contribution to the total biomass, accounting for 51.82% of the dry wood, followed by the root biomass (24.63%); the pod biomass accounted for the smallest proportion (1.82%), followed by the leaf biomass (2.22%); the branch biomass had a share of 19.51% of the total biomass, and the above-ground biomass (i.e., the sum of the stem, branch, leaf, and pod) accounted for 75.37% of the total biomass (Figure 3).

Figure 3. Biomass allocation of *Robinia pseudoacacia* L. IQR represents the interquartile range.

The root to stem ratio is the ratio of root biomass to the above-ground biomass. Among the 45 root biomass samples, the root to stem ratio ranged from 0.18 to 0.50 and was primarily concentrated in the range of 0.2–0.4. The average and standard deviation were 0.33 and 0.07, respectively. When the tree was small, the root biomass accounted for a higher proportion. However, the proportion of root biomass decreased and the proportion of above-ground biomass increased with the increase in D . Thus, the root to stem ratio decreased with the increase in D .

The nonlinear trend of proportion of each component's biomass observations in total biomass as a function of D is presented in Figure 4. The red line represents the fitting relationship between the proportion of biomass of each constituent and D . The red area represents the 95% confidence interval. The results showed that the proportion of stem and above-ground biomass in the total biomass increased with the increase in D and tended to be stable. The proportion of branch biomass gradually increased with the increase in D , demonstrating a positive correlation. In contrast, the proportion of pods, leaf, and root biomass manifested an opposite trend in this study.

Figure 4. Variation in tree component mass fraction according to the diameter at breast height (D).

3.2. The Biomass Additivity System Construction

The seemingly unrelated regression (SUR) method was used to estimate the parameters of the three additive biomass systems of *R. pseudoacacia* L. The results showed that the p -value of the parameter c , which, in the branch biomass model of system 3, was equal to 0.498, was more than 0.05. Therefore, the independent variable H was not statistically significant; the predictor H should be removed from the branch model, and the parameters of additive biomass system 3 should be estimated again. In addition, the SE, t , and p values estimated from the model parameters showed that the predictors D and H of other models were statistically significant ($\alpha = 0.05$) (Table 3). According to the values of goodness of fit, the three additive systems of biomass equations fit the biomass data well ($R^2_{adj} > 0.812$, and $RMSE < 0.151$) (Table 3). Among them, in system 1, which was developed based on a D single

predictor, with the exception of the pod and leaf biomass models, other components and total biomass models fitted well ($R^2_{adj} > 0.862$ and $RMSE < 0.134$). In system 2, which was developed based on the D^2H combination, with the exception of the branch biomass model, the goodness of fit of the other components and total biomass models fitted better with the introduction of tree height factor ($R^2_{adj} > 0.862$, and $RMSE < 0.131$). Compared with system 1 and system 2, the goodness of fit of system 3, which was developed based on the D^bH^c combination, had the best fitting effect ($R^2_{adj} > 0.864$, and $RMSE < 0.133$).

Table 3. Coefficient estimates and goodness-of-fit statistics for fitting the additive system of the biomass equations using the seemingly unrelated regression (SUR) method ($N = 45$).

System Types	Biomass Components	Parameter	Estimate Values	SE	T-Value	p-Value	R^2_{Adj}	RMSE
System 1	Pod	a	0.013	0.004	3.394	<0.01	0.812	0.136
		b	1.712	0.118	14.531	<0.01		
	Branch	a	0.025	0.006	3.956	<0.01	0.862	0.134
		b	2.43	0.106	22.822	<0.01		
	Leaf	a	0.012	0.004	3.221	<0.01	0.821	0.134
		b	1.83	0.125	14.616	<0.01		
	Stem	a	0.062	0.013	4.775	<0.01	0.899	0.121
		b	2.464	0.088	28.003	<0.01		
	Root	a	0.076	0.013	5.969	<0.01	0.933	0.082
		b	2.087	0.067	30.961	<0.01		
System 2	Canopy	-	-	-	-	-	0.891	0.118
	Above-ground	-	-	-	-	-	0.917	0.110
	Total	-	-	-	-	-	0.927	0.099
	Pod	a	0.007	0.002	3.471	<0.01	0.872	0.108
		b	0.684	0.04	17.104	<0.01		
	Branch	a	0.021	0.006	3.524	<0.01	0.824	0.151
		b	0.859	0.041	21.111	<0.01		
	Leaf	a	0.007	0.002	3.197	<0.01	0.862	0.116
		b	0.718	0.044	16.493	<0.01		
	Stem	a	0.031	0.006	5.269	<0.01	0.938	0.094
		b	0.945	0.027	34.643	<0.01		
System 3	Root	a	0.044	0.007	6.174	<0.01	0.943	0.075
		b	0.793	0.023	35.126	<0.01		
	Canopy	-	-	-	-	-	0.865	0.131
	Above-ground	-	-	-	-	-	0.938	0.096
	Total	-	-	-	-	-	0.946	0.086
	Pod	a	0.005	0.002	3.422	<0.01	0.874	0.107
		b	1.101	0.155	7.124	<0.01		
		c	1.076	0.192	5.61	<0.01		
	Branch	a	0.039	0.009	4.209	<0.01	0.864	0.133
		b	2.288	0.137	16.653	<0.01		
		c	-0.04	0.137	-0.293	0.498		
	Leaf	a	0.006	0.002	3.217	<0.01	0.865	0.115
		b	1.383	0.166	8.35	<0.01		
		c	0.832	0.202	4.118	<0.01		
	Stem	a	0.037	0.004	8.357	<0.01	0.939	0.095
		b	1.847	0.078	23.643	<0.01		
		c	0.941	0.091	10.296	<0.01		
System 3	Root	a	0.046	0.007	6.934	<0.01	0.949	0.072
		b	1.86	0.067	27.558	<0.01		
		c	0.479	0.084	5.722	<0.01		
	Canopy	-	-	-	-	-	0.895	0.122
	Above-ground	-	-	-	-	-	0.943	0.099
	Total	-	-	-	-	-	0.951	0.092

Note: SE represents the standard deviation; R^2_{Adj} represents the adjusted coefficient of determination; RMSE represents root mean square error.

3.3. Biomass Additive System Validation

Model validation statistics (Equations (4)–(7)) were computed for the three additive biomass systems based on the jackknifing technique. The MAE was used to measure the average absolute error between predicted and actual values of the experimental datasets. The MPE was used to measure the average prediction error between predicted and actual values of the experimental datasets. The MAE% represents the percentage of average absolute error, and the MPE% represents the percentage of average prediction error. As shown in Table 4, the average absolute error values of all the equations of the three additive biomass systems of *R. pseudoacacia* L. are less than 0.2, and the average prediction error values are all less than 0.04, which indicates that the additive biomass systems constructed in this study provide an accurate prediction. According to the values of MAE% and MPE% of all the equations in the three additive biomass systems shown in Table 4, it seems that the crown, including the branches, leaves, and pods, has a poor fitting effect, particularly the leaf and pod biomass, when compared with the root, stem, above-ground, and total biomass.

Table 4. Validation of log-transformed biomass equations using the jackknifing technique.

System Types	Biomass Models	MAE	MAE%	MPE	MPE%
System 1	$\lg W_p = -1.886 + 1.712 \times \lg D$	0.110	32.603	0.018	−40.887
	$\lg W_b = -1.602 + 2.43 \times \lg D$	0.103	12.428	0.020	1.891
	$\lg W_l = -1.921 + 1.83 \times \lg D$	0.106	6.779	0.016	30.548
	$\lg W_s = -1.208 + 2.464 \times \lg D$	0.075	5.900	0.028	1.805
	$\lg W_r = -1.119 + 2.087 \times \lg D$	0.064	6.223	0.016	1.457
	$\lg W_c = \lg(W_p + W_b + W_l)$	0.086	8.755	0.023	2.122
	$\lg W_a = \lg(W_p + W_b + W_l + W_s)$	0.069	4.587	0.029	1.794
	$\lg W_t = \lg(W_p + W_b + W_l + W_s + W_r)$	0.066	3.949	0.027	1.588
System 2	$\lg W_p = -2.155 + 0.684 \times \lg(D^2H)$	0.075	−7.685	0.016	−36.259
	$\lg W_b = -1.678 + 0.859 \times \lg(D^2H)$	0.124	13.819	0.036	3.640
	$\lg W_l = -2.155 + 0.718 \times \lg(D^2H)$	0.090	9.327	0.014	30.352
	$\lg W_s = -1.509 + 0.945 \times \lg(D^2H)$	0.060	4.504	0.021	1.432
	$\lg W_r = -1.357 + 0.793 \times \lg(D^2H)$	0.055	5.391	0.018	1.649
	$\lg W_c = \lg(W_p + W_b + W_l)$	0.101	9.889	0.037	3.374
	$\lg W_a = \lg(W_p + W_b + W_l + W_s)$	0.064	4.221	0.029	1.803
	$\lg W_t = \lg(W_p + W_b + W_l + W_s + W_r)$	0.058	3.515	0.027	1.589
System 3	$\lg W_p = -2.301 + 1.101 \times \lg D + 1.076 \times \lg H$	0.079	0.737	0.005	−12.431
	$\lg W_b = -1.409 + 2.288 \times \lg D$	0.105	10.346	0.013	1.287
	$\lg W_l = -2.222 + 1.383 \times \lg D + 0.832 \times \lg H$	0.091	7.942	0.007	14.290
	$\lg W_s = -1.432 + 1.847 \times \lg D + 0.941 \times \lg H$	0.062	4.630	0.013	0.934
	$\lg W_r = -1.337 + 1.86 \times \lg D + 0.479 \times \lg H$	0.051	5.114	0.013	1.203
	$\lg W_c = \lg(W_p + W_b + W_l)$	0.086	8.638	0.017	1.584
	$\lg W_a = \lg(W_p + W_b + W_l + W_s)$	0.058	3.767	0.017	1.060
	$\lg W_t = \lg(W_p + W_b + W_l + W_s + W_r)$	0.052	3.135	0.018	1.072

Note: MAE represents the mean absolute error; MAE% represents mean absolute error percentage; MPE represents the mean prediction error; MPE% represents the mean prediction error percentage.

By comparing the model validation statistics of the three biomass additive systems (Table 4), it seems that system 3 is the best. According to the residual diagram of system 3, the residuals of each component have an irregular distribution, while the main distribution range was between −0.5 and 0.5. The residuals plot does not show any heteroscedastic behavior for any of the models in system 3 (Figure 5). From an analysis of variance of the predicted and observed values of each component and total biomass in system 3, it seems that there were no significant differences for pod ($t = -0.004$, $p = 0.996$), branch ($t = -0.008$, $p = 0.994$), leaf ($t = -0.003$, $p = 0.998$), stem ($t = -0.009$, $p = 0.993$), root ($t = 0.013$, $p = 0.990$), crown ($t = -0.100$, $p = 0.992$), above-ground ($t = -0.008$, $p = 0.993$) and total

biomass ($t = 0.001$, $p = 1.000$). Besides, the trend in the observed and estimated values of the pods, stems, roots, above-ground, and total biomass showed a relatively good coincidence with the linear equation ($y = x$) (Figure 6).

Figure 5. Residuals chart of the best model, system 3, with the predicted value of logarithmic transformation as abscissa.

Figure 6. Scatter plot of the predicted and actual biomass values of each component with the best model, system 3. The solid red line refers to the fitting line between the measured values and predicted values. The dark red area is a 95% confidence interval, and the light red area is a 95% prediction interval. The dashed line in black color indicates the 1:1 equivalence.

4. Discussion

4.1. Biomass Allocation

The diameter at breast height (D) is a representative index of biomass allocation; moreover, trees with different sizes of diameter at breast height (D) have different biomass allocation strategies [15,45]. The proportion of pod, leaf, and root biomass decreased with the increase in D , while the proportion of biomass in branches, in stems, and above ground increased (Figure 4). The contribution of the stems to the total biomass was the largest, followed by the roots, pods, and leaves, which had the smallest contribution. These results are consistent with most of the previous research results [15,33,46]. Nevertheless, the research results of Dimobe and Nogueira Junior et al. [19,47] have shown that the biomass allocated to branches is larger than that of stems, which may be owing to the younger age of trees (11–12 years). The results by Dong et al. [33] showed that the contribution of stem and branch biomass of *B. platyphylla* increased with the increase in D , which was consistent with the results of this study. In contrast, the percentage of leaf biomass of *B. platyphylla* increased with the increase in D , which may be related to the shape and size of the leaves. As such, owing to different tree species and forest ages, the proportion of biomass in each component is different, and these differences also reflect the morphological and ecological traits of different tree species [22]. In addition, our results show that the above-ground biomass accounts for approximately 75% of the total biomass, and the below-ground biomass accounts for the rest, which is approximately 25%. The root to stem ratio is primarily concentrated in the range of 0.2–0.4, with an average value of 0.33, which is consistent with the results of other studies [33,42].

4.2. Construction of Biomass Additivity System

Biomass additivity is an ideal characteristic to predict component biomass and total forest biomass. It eliminates the inconsistency between the sum of the prediction value of each component and the whole tree [18,48]. In addition to the logical consistency, considering the intrinsic correlation between biomass components, the additive biomass system is more efficient compared with cases in which the biomass equation is estimated separately [19,23]. It is critical to determine the error structure of the model to construct an additive biomass system based on an allometric growth equation [8,26]. Most of the biomass models of *R. pseudoacacia* L. in the Loess Plateau were fitted by the least square method. However, during the process of model construction, the error structure of the model was not considered, and the additive relationship between the components and the total biomass was ignored [49–51]. Therefore, the likelihood analysis method was used to analyze the error structure, and the logarithmic transformation model structure was selected to construct the additive biomass system of *R. pseudoacacia* L. by the method of seemingly unrelated regression (SUR) in this study.

Logarithmic transformation has been widely used by scientists as a mathematical operation method since the emergence of electronic calculators [52]. In addition, it has also been widely used in the study of allometric growth, since it is convenient in the conversion between logarithmic and arithmetic data. For example, in the past, the least square method was used to fit logarithmically transformed data, and then, the linear equation was inversely transformed to obtain the power function of the original scale. However, many researchers believe that the traditional method of fitting allometric growth equations is defective. In contrast, nonlinear regression should be used to fit the original data [28–30,53]. Whether or not to use logarithmic transformation in the analysis of power law data has aroused a critical discussion, and different views have been expressed [28,29,31,54,55]. Among them, Gingerich [56] and Kerkhoff and Enquist [55] believed that a fundamental difference between linear regression (LR) of log-transformed data and nonlinear regression (NLR) of untransformed data lies in the assumption of model error structure (multiplication error or additive error) [24,25,27]. Therefore, to select the appropriate model structure (LR or NLR), it is necessary and crucial to determine the error structure (multiplication or addition) in the construction of the biomass model. Xiao et

al. [27] proposed the likelihood analysis method to determine the error structure of allometric growth equations, and this method was effectively verified by Ballantyne et al. [32].

Because a logarithm-transformed biomass equation predicts the logarithm value of biomass, it is necessary to carry out anti-log transformation to obtain the predicted biomass on the original scale. It is well known that this process of anti-log transformation often underestimates the predicted biomass. Therefore, Baskerville et al. [57] proposed a correction factor (CF), $CF = \exp(RSE^2/2)$, which is usually used to correct the systematic deviation introduced by anti-log transformation. However, Madgwick and Satoo [58] found that if the correction factor was applied, the biomass would be overestimated by the inverse transformation, and it was suggested that the correction factor could be ignored if the deviation of the inverse transformation was relatively small compared with the overall error of biomass estimation. In this study, the correction factor values of all the biomass equations were less than 1.01. Therefore, the error of model estimation in the process of anti-log transformation is small and can be ignored in practical use. In addition, if the conversion coefficient is used, the additivity of biomass models among the components will be destroyed. Therefore, in this study, it was unnecessary to use the correction factor for the *R. pseudoacacia* L. biomass models against the anti-log transformation. This result is also consistent with those of previous studies [7,59].

4.3. Verification and Application of Biomass Additivity System

In this study, three additive systems of *Robinia pseudoacacia* L. biomass were constructed based on *D*, tree height, and their combination. The inclusion of tree height as an additional predictor improved the goodness of fit and the accuracy of prediction of the biomass model. Among the used metrics, R^2_{adj} increased and RMSE decreased. However, compared with the stem, root, above-ground, and total biomass models, the fitting performance of the canopy biomass models, including the pods, branches, and leaves, was relatively low, particularly the biomass models of leaves and pods, an effect that was also commonly observed in other studies [19,25,33,35]. These may be because the development of branches and leaves is more susceptible to internal factors, such as the stand density and competition from neighboring trees, and external factors, such as the soil, climate change, seasonal change, and site conditions, of stand growth [19]. According to the biomass allocation analysis, the biomass of leaves and pods accounted for 2.22% and 1.82% of the total biomass, respectively—therefore, for a relatively small proportion. To improve the fitting performance of the crown biomass model, some studies have added crown height, crown width, and crown length as additional predictors into the allometric growth equation or biomass additive system, which significantly improved the fitting and performance [33,60]. In future research, crown height, crown width, and crown length could be added into the additive system of biomass equations to improve the accuracy of the crown biomass model.

The relationship between biomass amount and easily measured variables varied with the DBH, stand age, stand type, and growth conditions. In this study, three biomass additive systems were constructed for the Loess region of western Shanxi Province. The tree diameters ranged from 6.5 to 23.2 cm, and the tree heights ranged from 4.7 to 14.7 m. Each system included five components, two subtotals, and the total biomass of *R. pseudoacacia* L. Therefore, the biomass equations established in this study are more suitable for estimation in the Loess region of western Shanxi Province.

5. Conclusions

In this study, three additive biomass systems of equations were developed to estimate the amount of biomass in *Robinia pseudoacacia* L. forests located in the Loess Plateau of western Shanxi Province. The results showed that most of the biomass equations of the three additive systems fitted well with the biomass data, particularly for the root, stem, above-ground, and total biomass models. The overall ranking of models based on the fitting performance and validation statistics was in the following order: system 3 > system 2 > system 1. In general, the three additive biomass systems can provide a reliable and accurate estimation of the individual plant biomass of *R. pseudoacacia* L. trees in the Loess Plateau of western Shanxi Province, China. However, the developed additive systems of biomass equations

should be used with caution to predict tree biomass beyond the data and regional boundaries of this study.

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