METHOD COMPARISON ON ABOVEGROUND BIOMASS INVESTIGATION IN A *PINUS KESIYA* **VAR.** *LANGBIANENSIS* **NATURAL FOREST BASED ON A CLEAR-CUT PLOT**

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Abstract. To obtain suitable methods for accurately investigating the stand aboveground biomass (AGB) and determining plot size for biomass measurement, the plot-size gradient was set to 100 m², 400 m², 600 m² , 900 m² , and 1500 m² in the 0.3 hm² clear-cut plot of *Pinus kesiya* var. *langbianensis* natural forest of Mojiang county, Pu`er City, Yunnan Province, China. The AGB of each tree in the plot was investigated by a destructive investigation method. The AGB in the different plot sizes was calculated using the biomass model (BM), the biomass-volume regression (BV), the average standard tree of the diameter classes (SDC), the average standard tree of the tree classification (STC), the average standard tree of the stand (STS) and the measurement method (MD). Then, the error differences between these estimation methods were compared with the different plot sizes. The results showed that 1) with the increase in sample size, the mean absolute relative errors (MAREs) of all the methods tended to decrease, and the error values were stable if the plot size was greater than or equal to 400 m^2 . Thus, the plot size for a forest biomass survey should not be less than 400 m². 2) BM, BV, and SDC had a lower mean error (ME) and MARE values. Especially, compared to those of the observed data for the 0.3 hm² sample plots where the MAREs of the BM and BV were less than 15%, and the MARE of SDC was approximately 15% for wood and total AGB, but higher than 20% for the other three components. Therefore, the BM and BV should be used to estimate stand AGB if reliable biomass models or biomass-volume functions are available, the SDC is recommended for measuring AGB without biomass models, and the STS could be used for wood biomass and total AGB.

Keywords: *aboveground biomass, standard tree, biomass model, biomass-volume regression, clear-cut plot, Pinus kesiya var. langbianensis*

Abbreviations: Measurement method (MD); Average standard tree of the stand (STS); Average standard tree of the diameter classes (SDC); Average standard tree of the tree classification (STC); Biomass model (BM); Biomass expansion factors method (BV); Biomass expansion factor (BEF); Diameter at breast height (DBH); Tree height (H); Tree crown width (CW); Tree crown length (CL); Aboveground biomass (AGB)

Introduction

Forest biomass data is an essential source of information for forest carbon sink research and has become the primary data for ecology and forestry research. Therefore, the measurement and estimation of forest biomass remain one of the most c tasks in forestry and ecology research (Lieth and Whittaker, 1975; Feng et al., 1999; Fang et al., 2001, 2002; IPCC, 2006; West, 2009; Zhang, 2018; Townsend et al., 2019; Chen et al., 2022). As the main part of forest biomass, trees account for more than 90% of the total forest biomass (Zhang, 2018; Augusto and Boča, 2022), while aboveground biomass accounts for approximately 60% of the entire tree biomass (Luo et al., 2009, 2015). In particular, aboveground biomass (AGB) is relatively easy to measure and has become the research focus of forest biomass estimation (Meng, 2006; Huang, 2014; Luo et al., 2015; Zhang, 2018).

Forest biomass investigation and estimation mainly include the photosynthesis method, carbon dioxide balance method, remote sensing estimation method, and direct harvesting method (Meng, 2006; West, 2009; Luo et al., 2015; Zhang, 2018). Among them, the direct harvesting method is one of the most effective and feasible methods. It is widely used in forest resource inventories by measuring the biomass of sample trees in sample plots and establishing estimation models suitable for different ranges according to the relationship between biomass and tree measuring factors (Meng, 2006; Zhang, 2018). Among these harvesting methods, the destructive measurement method, biomass model, and biomass estimation parameter method are the three most commonly used methods (Meng, 2006; Somogyi et al., 2007; Zhang, 2018; Dong et al., 2019; He et al., 2021). The biomass model can estimate forest biomass at different scales by establishing models suitable for different ranges (Meng, 2006; Luo et al., 2009, 2015). Biomass estimation parameters, especially the biomass expansion factor (BEF), can determine the conversion from volume to biomass and are widely used in forest biomass estimation at different scales (Fang et al., 2001, 2002; Zhang, 2018; Jagodziński et al., 2018).

Direct measurement or actual field measurement methods can obtain the most accurate data, but the estimation process is often expensive, time-consuming, and laborious and has a destructive influence on the ecosystem (Meng, 2006; Luo et al., 2009, 2015). Moreover, in the process of field investigation, it is challenging to obtain data from clear-cut plots; thus, calculating forest biomass with the survey data per tree and the cutting data from the selected standard trees is a commonly used method (Ma, 2013; Zhou, 2014), and the standard trees used in forestry investigation mainly include those of the total stands, the different diameter classes, and the different tree classifications (Meng, 2006; Zhang, 2018; Chen et al., 2022).

However, due to the time-consuming, high labor needed and lack of measured data on getting stand biomass through sample plot surveys, an estimation method using biomass models based on standard trees is widely used. Generally, the errors between these different estimation methods and different biomass components are rarely described quantitatively, resulting in the estimation accuracy of forest carbon biomass and carbon storage at the regional scale based on stand-level biomass data being unknown (Fang et al., 2002; Fu et al., 2015; Qin et al., 2017; Zhao et al., 2017; Cao, 2017; He et al., 2021; Xu et al., 2021, 2022). For this reason, it is significant to explore the estimation accuracy of the different investigation and estimation methods for other dimensions of forest biomass under different conditions. In particular, in past forestry surveys, basic tree measuring factors such as DBH, tree height, and volume were used mainly, as the direct biomass survey data were not easy to get. The setting of the sample plot size was primarily determined according to the difference in stand volume. Therefore, choosing the appropriate sample plot size for biomass surveys is of great significance regarding the accuracy of survey data.

To obtain suitable methods for accurately investigating stand AGB and determining the appropriate size of a sample plot for biomass measurements, we selected the *Pinus kesiya* var. *langbianensis* natural forest in Pu' er city of Yunnan Province, China as the study object, and clear-cut plots with different plot sizes were investigated. Then, the five most common investigation or estimation methods of forest biomass, which include

the measurement method (MD), average standard tree of the stand (STS), average standard tree of the diameter classes (SDC), average standard tree of the tree classification (STC), biomass model (BM), and biomass expansion factors method (BV), were applied to calculate the AGB. Furthermore, the estimation errors of different methods for the forest AGB and the other estimation methods for different sizes were compared and analyzed. The optimal methods or plot sizes for the AGB investigations were explored. Thus, a basis and reference for the investigation and accurate estimation of forest AGB is provided.

Materials and Methods

Pinus kesiya var. langbianensis

Pinus kesiya var. *langbianensis* is an evergreen tree mainly concentrated in parts of Pu`er City, Honghe Prefecture, Xishuangbanna Prefecture, Lincang, and Dehong Prefecture in Yunnan Province of China (Editorial Board of Flora of China, 1978). Because of fast growth, high production rates, and strong ecological adaptability, it has become one of the main species in artificial afforestation in Yunnan Province, especially in southern Yunnan Province (Compilation Committee of Yunnan Forest, 1986; Chen et al., 2002). Thus, it plays an essential role in the forestry industry and ecological conservation in Yunnan Province because of its high environmental, economic, and social values (Wu and Dang, 1992; Wen et al., 2010; Yue and Yang, 2011; Li, 2011).

Sample setting

This study area was conducted in a natural *Pinus kesiya* var. *langbianensis* forest in Yutang township, Mojiang County, Pu 'er City, Yunnan Province. We selected a sample plot with an area of 0.3 hm² (30 m \times 100 m). The coordinates of the southwestern corner of the sample plot were 23°09′58.2″N, 101° 29′14.4″E, and the [altitude](https://fanyi.sogou.com/?fr=common_index_nav_pc&ie=utf8&keyword=&p=40051205#auto/en/javascript:;) was 1530 m. The average age of the selected stand is 35 years, and the total basal area at DBH for all *Pinus kesiya var. langbianensis* is 7.12 m^2 , and the proportion reaches 65.99% of the whole plot. Then, all the trees in the plot were felled to carry out AGB measurements in October and November 2016 (*Figure 1*).

The large sample plot was divided into 30 small sample plots with an area of 10 m \times 10 m each, and 30 plots, 7 plots, 5 plots, 3 plots, and 3 plots with areas of 100 m², 400 m², 600 m², 900 m² and 1500 m², respectively (*Figure* 2) were formed and used to analyze the variation in each component of the stand AGB calculated by the different methods and plot sizes.

In the plots, 512 trees, including 132 *Pinus kesiya* var. *langbianensis* and 380 other tree species were recorded, and for each tree, the species name, diameter at breast height (1.3 m above ground) (DBH), tree height (H), tree crown width (CW), and tree crown length (CL) were recorded and measured. Then, the trees were arranged in corresponding subplots according to their locations (*Table 1*).

Investigation and determination of aboveground biomass

In the clear-cut plot, all standing trees whose DBH is equal and larger than 5 cm in the sample plot were investigated, and the southwestern corner of the sample plot was the origin of the coordinates to record the coordinate position of each tree in the sample

plot (*Figure 3*). Furthermore, according to the biomass measurement method by Zhang (2018), the biomass of wood, bark, branches, and foliage in the plot was measured. The biomass of the stem (including wood and bark) was measured using the weighing or volume density method. The total stems of the trees with DBHs equal to or less than 20 cm were measured by weight, and the fresh weight of the felled trees was measured by segments 2 m in length and sampled from each segment. Then, the biomass values were obtained using the ratios of fresh weight to the corresponding dry matter. However, for the other trees with DBHs greater than 20 cm, the wood and bark biomass values were measured by volume and density (Xu and Zhang, 2002). The corresponding diameters of each 2 m in length section of the felled trees from base to tip were measured, and each sample tree was collected by taking a 3 cm thick disk at a 2 m interval along the tree trunk (Xu and Zhang, 2002). Then, the biomass values of the wood and bark of the sample trees were calculated using the volumes and the corresponding sample density values. Moreover, the branch and foliage biomass were measured by weight, and the samples were taken according to the graded standard branches. Dead branches and fruits were measured by weight and sampled separately. All samples were constantly dried at 105°C to measure the moisture content which was used to calculate the dry weight of the different organs.

Figure 1. The clear-cut plot and biomass measurement in the field. (A) is the stand condition before cutting (By G. L. Ou), (B) is plot setting (By G. L. Ou), (C) is weighting the logs (By G. L. Ou), (D) is stripping the branches (By G. L. Ou), (E) is stripping the tree bark (By J. F. Wang), (F) is weighing the tree crown (By G. L. Ou), (G) is the stand after cutting (By G. L. Ou)

C: 600m²(n=5), C1(A1,A2,A11,A12,A21,A22),C2(A3,A4,A13,A14,A23,A24),C3(A5,A6,A15,A16,A25,A26),

C4(A7, A8, A17, A18, A27, A28), C5(A9, A10, A19, A20, A29, A30)

D: $900m^2(n=3)$, D1(A1~A3,A11~A13,A21~A23),D2(A4~A6,A14~A16,A24~A26),D3(A7~A9,A17~A19,A27~A29) E: 1500m²(n=3),E1(A1~A5,A11~A15,A21~A25),E2(A6~A10,A16~A20,A26~A30),E3(A3~A7,A13~A17,A23~A27)

Figure 2. The plot set and their distribution of the different plot sizes in a clear-cut plot with 0.3 hm² . There were only 2 plots for the sample plot of 1500 m 2 for a 0.3 hm² plot, and one plot was added to the crossing area to meet the statistical requirements

Plot area		H_m		$H_t(m)$		D (cm)			N				
(m ²)	n	Max.	Min.	Mean I	Max. I		Min. Mean	Max.		Min. Mean	Max.	Min.	Mean
100	30	21.0	8.0	14.3	25.6	12	21.52	24.3	7.6	16.6	2600	600	1637
400		15.9		13.9	25.6	21.5	23.7	19.0	15.6	17.1	2100	1300	1618
600		17.9	13.9	15.6	25.6	23.5	24.3	18.6	13.9	16.6	1867	1433	1637
900		15.9	13.1	14.3	25.6	23.5	24.5	18.5	15.3	16.4	1900	1489	1674
1500		13.9		13.8	25.6	24.5	25.1	17.5	15.7	16.6	1826	1547	1700

Table 1. The basic characteristics of stand in different sizes

n is the number of Plots, H_m is the average height of the stand (m), H_t is the average dominant height of the stand(m), D is the average diameter at the breast height of the stand(cm), and N is the average tree number per [hectare](https://www.baidu.com/link?url=48DhTEfp90Wdw00fJtPmJyxOzxwfRwxb4CnfibYyymmZ1xS1Zf0M2PmIBijxVBfZPZPtC-Yo1cMS3_kHlPY4t8av-5pQcV4BIU_AxpOpU-G&wd=&eqid=d335938b000482c8000000065e561329)

Figure 3. The distribution of trees and the plots in the clear-cut plot. The circle size is proportional to the tree diameter at breast height (DBH)

Tree aboveground biomass models

Based on the power function model (Meng, 2006; Zhang, 2018), the diameter at breast height (DBH), tree height (H), crown width (CW), crown length (CL), and their combined variables ($DBH²H$ and $CW²CL$) were used as independent variables to fit the better biomass models of aboveground parts (*Table 2*). The determination coefficients (*R 2*) of *Pinus kesiya* var. *langbianensis* and other tree species models were all higher than 0.69. Some models showed that it was higher than 0.90, which can be used to estimate the biomass of aboveground parts of the stand.

Tree species/				Fitting Parameters	Fitting indices				
groups	Components	Models	$\mathfrak a$	h	\mathcal{C}	d	\boldsymbol{e}	\mathbb{R}^2	RMSE
	Wood	$W=a \cdot (DBH^2H)^b$	0.014	1.026					0.940 82.381
	Bark	$W = a \cdot DBH^b$		0.703				0.679	5.025
<i>Pinus kesiya var.</i> langbianensis	$W=a\cdot DBH^b\cdot H^c\cdot CW^d\cdot CL^e$ Branches		0.014	3.211	-1.805 0.559 0.582 0.790				29.048
	needles	$W = a \cdot DBH^b \cdot (CW^2CL)^c$	0.017	0.858	0.442			0.693	3.740
	Aboveground	$W = a \cdot (DBH^2H)^b$	0.017	1.022					0.940 98.780
	Wood	$W = a \cdot (DBH^2H)^b \cdot CL^c$	0.023	1.048	-0.411			0.929	14.615
	Bark	$W=a\cdot DBH^b\cdot H^c\cdot CW^d\cdot CL^e$	0.042	1.421	-0.191 0.475 0.720 0.728				7.389
The other tree species	Branches	$W=a\cdot DBH^b\cdot H^c\cdot CW^d\cdot CL^e$	0.043	1.278	0.965 0.233 -0.305 0.678				7.777
	Foliage	$W = a \cdot (DBH^2H)^b$	0.024	0.617				0.786	2.652
	Aboveground	$W=a\cdot DBH^b\cdot H^c\cdot CW^d\cdot CL^e$	0.093	1.698					0.929 0.157 - 0.277 0.928 21.679

Table 2. The models of individual tree biomass using the trees in the clear-cutting plots

W represents individual biomass of the components (kg), DBH represents Diameter at breast height (cm), H represents Tree height (m), CW represents Tree crown width (m), and CL represents Length of tree crown (m)

Biomass expansion factor models

The methods in Fang et al. (2001, 2002) were used to construct the biomass-volume regression equation for forest biomass with different components of the aboveground part, and the estimation models of forest biomass with different components based on forest volume were constructed through the measured sample plot data (*Table 3*).

Table 3. The estimations of biomass volume regression functions for Pinus kesiya var. langbianensis natural forest

		Fitting indices			
Components	Biomass-volume regression function	\mathbb{R}^2	RMSE		
Wood	$W=6.031+0.443\times V$	0.855	18.422		
Bark	$W=8.016+0.007\times V$	0.652	4.477		
Branches	$W=3.391+0.072\times V$	0.781	7.458		
Foliage	$W=1.345+0.009\times V$	0.674	1.228		
Above-ground	$W=18.484+0.531\times V$	0.822	24.976		

W represents the individual biomass of the components(kg), and V represents the stand volume (m^3)

Plot aboveground biomass calculation

Although many sophisticated methods are used for biomass surveys, the simple models using the standard trees, biomass equations, or biomass expansion factors are the common methods to investigate forest AGB in forestry (Meng, 2006; Zhang, 2018). To estimate the biomass of the aboveground part of the stand, the following methods were used to calculate the AGB for each subplot. The methods included the measured method (MD) (*Eq. 1*), average standard tree of the stand (STS) (*Eq. 2*), average standard tree of the diameter classes (SDC) (*Eq. 3*), average standard tree of the tree classification (STC) (*Eq. 3*), biomass model (BM) (*Eq. 4*), and biomass expansion factor (BV) method (*Eq. 5*).

$$
B_i = \sum W_i \tag{Eq.1}
$$

$$
B_i = N \cdot W'_i \tag{Eq.2}
$$

$$
B_i = \sum_{j=0}^{m} (N_j \cdot W_{ij})
$$
 (Eq.3)

$$
B_i = \sum \hat{W}_i \tag{Eq.4}
$$

$$
B_i = a_i + b_i \cdot V \tag{Eq.5}
$$

where B_i is the biomass value of the aboveground part of component *i* in the sample plot, *N* is the number of trees in the sample plot, N_i is the number of trees in grade *j* tree classification in the sample plot for the SDC method or the number of trees in grade *j* diameter in the sample plot for STC; W_i is the biomass of component *i* of the tree in the sample plot, W_i ['] is the biomass of the average standard wood in the sample plot for component *i* using the STS method, *Wij* is the biomass of grade *j* standard wood in the sample plot for component *i* using the SDC or STC method, \hat{W}_i is the biomass estimation value of aboveground part *i* calculated by the biomass models for the trees in the sample plot, and *V* is the stand volume.

Finally, the biomass of each component (kg) was converted into the biomass per unit area (t/hm^2) according to the sample area.

Comparison of estimation precision

The mean error (ME) and the mean absolute relative error (MARE) were selected to compare the estimation accuracy. On the one hand, the measured biomass values of different components with different sample plot sizes were taken as true values, and the estimation accuracy of the five methods varied with the sample plot size. On the other hand, the measured value of the biomass for each dimension in the large clear-cut plot (0.3 hm^2) was taken as the true value, and the estimation accuracy of the five methods varied with the sample plot size. The least significant difference test (LSD) method in SPSS software was used to analyze the significance of the different estimation methods and different sample plot sizes of the aboveground biomass estimations.

Results

Estimation values of aboveground biomass

According to the aboveground biomass measured in the 0.3 hm^2 clear-cut plot, the biomass of the wood, bark, branches, foliage, and other aboveground parts were 128.81 t/hm², 10.03 t/hm², 22.98 t/hm², 3.72 t/hm², and 165.54 t/hm², respectively. The biomass of the different components obtained by the BM and MD was closer to that in the 0.3 hm^2 plot, and the value of the BM was slightly higher than that of the MD. Thus, the changing trend of the two methods was consistent with the sample plot area size, and the change was stable. The values from the BV changed minimally from the sample plot size, and its values were also closer to those of MD. The biomass values calculated by the other three estimation methods differed substantially from the measured values under the corresponding sample plot sizes and the measured values obtained from the 0.3 hm² plot. The change amplitudes of the values were greater with the sample size than with the other factors, especially for the estimation values of STS and SDC. In addition, the branches, wood, and aboveground biomass values showed a similar variation trend with sample plot size (*Figure 4 and Table 4*).

Plot Area		Methods $(t/hm2)$								
(m ²)	Components	MD	STS	SDC	STC	BM	BV			
	Aboveground	165.54	159.73	163.32	159.42	168.28	166.65			
100	Bark	10.03	8.17	9.69	9.21	10.64	9.97			
	Branches	22.98	22.12	22.82	22.34	23.45	23.48			
	Foliage	3.72	3.57	3.75	3.38	3.86	3.86			
	Wood	128.81	125.87	127.06	124.49	129.45	129.65			
	Aboveground	172.41	161.94	176.26	177.07	175.70	166.27			
	Bark	10.05	7.84	10.86	7.99	10.72	9.96			
400	Branches	23.82	21.97	24.33	28.21	24.31	23.43			
	Foliage	3.81	4.06	3.92	4.58	3.95	3.85			
	Wood	134.73	128.06	137.14	136.29	135.81	129.32			
	Aboveground	165.54	155.85	164.19	168.22	168.28	166.65			
	Bark	10.03	8.41	10.28	9.91	10.64	9.97			
600	Branches	22.98	19.59	22.03	20.10	23.45	23.48			
	Foliage	3.72	4.00	3.59	3.85	3.86	3.86			
	Wood	128.81	123.85	128.29	134.36	129.45	129.65			
	Aboveground	164.18	147.51	181.24	149.70	168.19	165.73			
	Bark	10.43	11.07	12.78	10.85	10.97	9.96			
900	Branches	22.31	18.21	26.18	20.10	22.88	23.36			
	Foliage	3.77	3.32	5.31	3.53	3.89	3.84			
	Wood	127.67	114.92	136.97	115.21	128.95	128.88			
	Aboveground	165.54	152.16	159.64	132.36	168.28	166.65			
	Bark	10.03	7.89	9.53	7.74	10.64	9.97			
1500	Branches	22.98	18.51	19.33	15.68	23.45	23.48			
	Foliage	3.72	4.35	3.33	3.06	3.86	3.86			
	Wood	128.81	121.41	127.45	105.88	129.45	129.65			

Table 4. The mean of the biomass values using the six methods

MD represents a measured method, STS represents the average standard tree of stand method, SDC represents the average standard tree of the diameter classes method, STC represents the average standard tree of the tree classification method, BM represents the biomass model method, and BV represents the biomass-volume regression method

Figure 4. The aboveground biomass of Pinus kesiya var. langbianensis stands with different plot sizes using six methods

Difference analysis of aboveground biomass estimations

Differences between the values from six estimation methods with the measured data of the 0.3 hm² plot

For the average error index, the ME of MD was close to zero compared with the true value of the data obtained from the 0.3 hm^2 plot, and the ME changed little with the plot size. The changing trend of ME for BM and BV with sample plot size was consistent with that of MD. Compared with MD, the absolute values of ME for the other five estimation methods were often higher. Moreover, the ME of BV varied little with the sample size, and the SDC also had better estimation performance, especially when the sample size was 600 m^2 or less. The SDC often had a smaller absolute value of ME, even though its absolute value was smaller than that of BM. The STC and STS had higher absolute values of ME. In addition, from the variation trend of the different components with sample plot size, both wood and aboveground biomass showed similar variation (*Table 5*).

In terms of the MARE, the values of SDC, BM, BV, and STC showed a gradually decreasing trend with plot size increasing, and the values were stable at approximately 10% after the sample plot area reached 400 m² . Compared to the other models, the BM had lower MARE values when the sample areas were 100 m^2 and 400 m^2 , but the SDC had lower MARE values when the sample area was larger than 400 m^2 (except the MD). The BV had the lowest MARE values, especially for bark biomass. The MARE of STC and STS varied greatly with plot size, and most tree parts had higher MARE values, especially the MARE values of bark, branch, and foliage, which were more than 20%. However, the STS had a similar absolute value of average error as the BM and SDC

when the sample area was 400 m^2 or more because the significance tests were insignificant. In addition, except for the STC for both wood and aboveground biomass, the MARE values of the other four estimation methods gradually decreased with increasing sample plot size. However, for the other three components, the MARE values of BM, SDC, and MD show a decreasing trend with increasing plot size, but the changing trend of the other two methods was not apparent; in addition, the error values were larger (*Table 6*).

Components	Plot area	Estimation methods (t/hm^2)							
	(m ²)	MD	STS	SDC	STC	BM	BV		
	100	$-0.002bB$	2.604aA	$-0.076bB$	$-4.316cAB$	0.642bB	1.114bA		
Wood	400	5.922aA	$-0.746bA$	7.227aA	7.479aA	7.000aA	0.726bA		
	600	$-0.002bB$	$-4.964cAB$	$-0.422bB$	5.552aA	0.642bB	1.114bA		
	900	$-1.144aB$	$-13.891bB$	$-5.849abC$	$-13.171bB$	0.136aB	0.192aB		
	1500	$-0.002aB$	$-7.398bB$	$-0.862aB$	$-22.933cB$	0.642aB	1.114aA		
	100	$-0.001aA$	$-1.658aA$	$-0.313aA$	$-0.817aA$	0.612aA	$-0.061aA$		
	400	0.016aA	$-2.193bA$	0.288aA	$-2.037bAB$	0.690aA	$-0.066aA$		
Bark	600	$-0.001aA$	$-1.623aA$	0.308aA	$-0.117aA$	0.612aA	$-0.061aA$		
	900	0.402aA	1.035aA	$-0.268aA$	0.841aA	0.935aA	$-0.073aA$		
	1500	$-0.001aA$	$-2.145bA$	$-0.401aA$	$-2.287bB$	0.612aA	$-0.061aA$		
	100	0.005aB	$-0.141aA$	0.049aA	$-0.637aAB$	0.472aA	0.502aA		
	400	0.836 _b A	$-1.005bA$	1.266bA	5.230aA	1.330bA	0.449 _{bA}		
Branches	600	0.005aB	$-3.387bB$	$-0.937aAB$	$-2.878bAB$	0.472aA	0.502aA		
	900	$-0.667aB$	$-4.774bB$	$-2.265abB$	$-2.859abAB$	$-0.101aA$	0.377aA		
	1500	0.005aB	$-4.473abB$	$-3.436abB$	$-7.301bB$	0.472aA	0.502aA		
	100	0.001aA	$-0.012aA$	0.070aA	$-0.344aA$	0.138aA	0.136aA		
	400	0.093aA	0.343aA	0.200aA	0.856aA	0.227aA	0.130aA		
Foliage	600	0.001aA	0.283aA	$-0.120aA$	0.127aA	0.138aA	0.136aA		
	900	0.053aA	$-0.401aA$	$-0.071aA$	$-0.182aA$	0.165aA	0.121aA		
	1500	0.001aA	0.633aA	$-0.324aA$	$-0.656aA$	0.138aA	0.136aA		
	100	0.003bB	0.793bA	$-0.270bB$	$-6.114cB$	2.742aB	0.835bA		
	400	6.867aA	$-3.601bAB$	8.982aA	11.528aA	10.159aA	0.511bA		
Above-ground	600	0.003bB	$-9.692cAB$	$-1.171bB$	2.684aAB	2.742aB	0.835bA		
	900	$-1.355aB$	$-18.031cB$	$-8.453bB$	$-15.372cB$	2.646aB	0.067aB		
	1500	0.003aB	$-13.384bB$	$-5.023bBC$	$-33.177cC$	2.742aB	0.835aA		

Table 5. The difference test on the mean error of aboveground biomass of Pinus kesiya var. langbianensis stands between the predicted values of the estimation methods and measured data of the clear-cutting plots

MD represents a measured method, STS represents the average standard tree of stand method, SDC represents the average standard tree of the diameter classes method, STC represents the average standard tree of the tree classification method, BM represents the biomass model method, and BV represents the biomass-volume regression method. *Capital letters indicate the significant test between different areas under the same estimation method for each component, while lower letters indicate the significant test between different estimation methods under the same sampling size for each component

		Estimation methods								
Components	Plot area	(%)								
	(m ²)	MD	STS	SDC	STC	BM	BV			
	100	34.796bA	41.330aA	34.772bA	31.056bA	32.171bA	30.634bA			
Wood	400	17.801bB	16.666bB	18.890bB	31.877aA	14.766bB	20.701bB			
	600	19.174bAB	17.561bB	17.600bB	32.226aA	16.535bB	15.281bB			
	900	15.849bB	18.248bB	11.255bB	31.789aA	14.932bB	12.367bB			
	1500	10.930bB	7.350bB	7.533bB	17.803aB	9.733bB	8.779bB			
	100	40.728aA	40.964aA	40.677aA	38.199aB	32.359aA	6.715bA			
	400	11.725bB	22.822aB	18.129aB	20.816aC	12.360bB	4.397bA			
Bark	600	5.373bB	32.756aAB	12.983bB	31.639aBC	10.395bB	3.174bAB			
	900	7.763cB	34.856bAB	12.749cB	62.916aA	9.324cB	2.941bAB			
	1500	6.213bB	21.384aB	14.411abB	22.799aC	6.106bB	1.910bB			
	100	41.787aA	48.542aA	41.496aB	40.357aB	34.770abA	29.973bA			
	400	20.884bB	22.775bB	19.284bB	61.092aA	18.345bB	20.438bAB			
Branches	600	17.472bB	26.614aB	20.952abB	20.820abC	16.738bB	15.280bB			
	900	12.001bB	25.398aB	11.941bB	27.268aC	15.475bB	12.142bB			
	1500	15.270bB	20.266abB	14.951bB	31.771aBC	14.488bB	8.575bC			
	100	37.183abA	42.693aA	39.469aA	31.460bB	27.036bA	23.369bA			
	400	17.924cB	27.459bA	18.836cB	58.320aA	12.866cB	16.065cAB			
Foliage	600	16.574bB	38.002aA	9.364cB	35.974aB	12.002bcB	12.986bcB			
	900	14.958cB	34.213bA	24.551bcAB	45.049aB	10.023cB	10.036cB			
	1500	0.976dC	17.006bB	11.519cB	27.885aB	5.015cB	6.621cB			
	100	34.257aA	38.614aA	33.636aA	29.769aA	31.180aA	32.847aA			
	400	16.536bB	14.387bB	17.137bB	30.070aA	14.062bB	22.185bB			
Above-ground	600	16.628bB	16.398bB	15.253bB	24.512aA	16.479bB	16.370bB			
	900	13.935bB	14.304bB	10.496bB	32.052aA	14.923bB	13.284bB			
	1500	10.270bB	8.085bB	6.665bB	20.041aB	9.497bB	9.412bB			

Table 6. The difference test on the mean absolute relative error of aboveground biomass of Pinus kesiya var. langbianensis stands between the predicted values of the estimation methods and measured data of the clear-cutting plots

MD represents a measured method, STS represents the average standard tree of stand method, SDC represents the average standard tree of the diameter classes method, STC represents the average standard tree of the tree classification method, BM represents the biomass model method, BV represents the biomass-volume regression method. *Capital letters indicate the significant test between different areas under the same estimation method for each component, while lower letters indicate the significant test between different estimation methods under the same sampling size for each component

Differences between the five estimation methods and the measured data (MD)

The ME values of the BM and BV varied little with the size of the sample plot and were superior to those of the other three methods. In particular, both approaches had minimally different results if the sample plot area was more than 400 m^2 , except for the results for wood and aboveground biomass. Compared to the other methods, the STC and STS had higher absolute values of ME. While the SDC usually had a smaller absolute ME when the sample plot size was 600 m^2 or less, especially when it was

100 m² and 400 m², the stand bark biomass had the smallest absolute ME when the plot size was 600 m^2 . Moreover, wood and aboveground often had higher ME values, while the biomass of bark and foliage had lower ME values (the absolute value of ME mainly was less than 1 t/hm²) (*Table 7*).

Table 7. The difference test on the mean error of aboveground biomass of Pinus kesiya var. langbianensis stands between the predicted values of the estimation methods and measured data of the different plot areas

	Plot area	Estimation methods							
Components	(m ²)			(t/hm ²)					
		STS	SDC	STC	BM	BV			
Wood	100	2.61aA	$-0.07bA$	$-4.31cA$	0.64 _b A	0.84 _b A			
	400	$-6.67bB$	1.31aA	1.56aA	1.08aA	$-5.41bB$			
	600	$-4.96cAB$	$-0.42bA$	5.55aA	0.64 _b A	0.84 _b A			
	900	$-12.75bB$	$-4.71aB$	$-12.03bB$	1.28aA	1.21aA			
	1500	$-7.40abB$	$-0.86aA$	$-22.93bB$	0.64aA	0.84aA			
	100	$-1.66bAB$	$-0.31aA$	$-0.82aA$	0.61aA	$-0.06aA$			
	400	$-2.21bB$	0.27aA	$-2.05bB$	0.67aA	$-0.08aA$			
Bark	600	$-1.62bA$	0.31aA	$-0.12aA$	0.61aA	$-0.06aA$			
	900	0.63aA	$-0.67aA$	0.44aA	0.53aA	$-0.48aA$			
	1500	$-2.14bB$	$-0.40aA$	$-2.29bB$	0.61aA	$-0.06aA$			
	100	$-0.15aA$	0.04aA	$-0.64aB$	0.47aA	0.50aA			
	400	$-1.84bA$	0.43 _b A	4.39aA	0.49 _b A	$-0.39bA$			
Branches	600	$-3.39bAB$	$-0.94aA$	$-2.88abB$	0.47aA	0.50aA			
	900	$-4.11bB$	$-1.60aA$	$-2.19abB$	0.57aA	1.04aA			
	1500	$-4.48bB$	$-3.44bB$	$-7.31bC$	0.47aA	0.50aA			
	100	$-0.01aA$	0.07aA	$-0.35aA$	0.14aA	0.14aA			
	400	0.25aA	0.11aA	0.76aA	0.13aA	0.04aA			
Foliage	600	0.28aA	$-0.12aA$	0.13aA	0.14aA	0.14aA			
	900	$-0.45aA$	$-0.12aA$	$-0.24aA$	0.11aA	0.07aA			
	1500	0.63aA	$-0.33aA$	$-0.66aA$	0.14aA	0.14aA			
	100	0.79aA	$-0.27aA$	$-6.12bA$	2.74aA	1.11aA			
	400	$-10.47bB$	2.11aA	4.66aA	3.29aA	$-6.14bB$			
Above-ground	600	$-9.69bB$	$-1.17abA$	2.68aA	2.74aA	1.11aA			
	900	$-16.68cB$	$-7.10bB$	$-14.02cAB$	4.00aA	1.55aA			
	1500	-13.39 bcB	$-5.03abB$	$-33.18cB$	2.74aA	1.11aA			

STS represents the average standard tree of the stand method, SDC represents the average standard tree of the diameter classes method, STC represents the average standard tree of the tree classification method, BM represents the biomass model method, and BV represents the biomass-volume regression method. *Capital letters indicate the significant test between different areas under the same estimation method for each component, while lower letters indicate the significant test between different estimation methods under the same sampling size for each component

Compared with STS and STC, the MARE values of SDC, BM, and BV were smaller, and the values of wood and aboveground biomass were mainly less than 10%, even though the variation within the sample plot size was slight. The MARE values of the BM and BV were consistent with the changing trend in sample plot size and showed a gradually decreasing trend as the sample plot size increased; then, these models tended to have lower MARE values when the sample plot size was larger than 400 m^2 . The MARE value of the SDC was opposite to the changing trend of the sample plot size, and the SDC had a lower MARE value when the sample plot area was 100 m^2 and 400 m^2 . The STC and STS had the highest MARE values, especially for bark and foliage biomass, and the values were more than 20%, even though the change rule was not evident in the plot size. In addition, the MARE values of the different estimation methods varied a little with the plot size for wood and aboveground biomass. In contrast, the estimation error for bark and foliage biomass changed significantly with the sample plot size (*Table 8*).

	Plot area	Estimation methods								
Components	(m ²)			(%)						
		STS	SDC	STC	BM	BV				
	100	13.32aA	2.65 _b A	14.74aA	10.72aA	15.77aA				
Wood	400	16.97aA	3.56bA	15.26aA	5.50bB	8.79abB				
	600	12.49aA	5.72bA	16.11aA	4.57bB	4.53bC				
	900	16.98aA	5.60 _b A	16.92aA	2.83 _b BC	3.51 _b C				
	1500	17.87aA	3.36bA	18.72aA	1.27bC	1.61 _b C				
	100	26.49bA	5.00cA	20.76 _b B	28.80bA	55.35aA				
	400	21.81aA	9.33bA	22.16aB	13.31abAB	13.71abB				
Bark	600	36.27aA	8.90bA	37.11aB	9.93 _b B	7.23 _b B				
	900	33.32bA	8.24cA	60.53aA	12.88cAB	7.28cB				
	1500	20.38aA	8.48bA	21.57aB	8.69bB	8.12bB				
	100	21.70aA	3.93 _b B	28.08aA	26.01aA	29.86aA				
	400	16.51abA	8.33bAB	37.89aA	12.48abB	24.43aA				
Branches	600	21.33aA	11.99bA	22.70aAB	7.61bB	13.52abAB				
	900	19.41aA	6.93 _b B	17.50aB	7.57 _b B	4.92 _b B				
	1500	20.73bcA	15.12bcA	31.91aA	2.20cC	7.19bB				
	100	28.03aA	9.48bA	31.19aB	30.78aA	33.28aA				
	400	18.95bB	9.27cA	57.63aA	14.11bcB	20.56bB				
Foliage	600	30.07aA	9.68cA	20.36bB	13.63bcB	15.45bcB				
	900	21.64abAB	10.03bA	30.19aB	14.99bB	15.73bB				
	1500	16.89bB	12.41bA	27.07aB	4.00cC	5.61cC				
	100	13.74aA	2.56cA	15.55aA	9.62 _b A	15.03aA				
	400	15.65aA	3.27bA	18.41aA	6.15 _b A	10.01abA				
Above-ground	600	10.14aA	5.03bA	12.09aB	3.51bAB	2.79 _b B				
	900	13.75aA	5.15bA	19.19aA	2.55bB	2.40 _b B				
	1500	11.59bA	3.33cA	20.90aA	1.75cB	1.58cB				

Table 8. The difference test on the mean absolute relative error of aboveground biomass of Pinus kesiya var. langbianensis stands between the predicted values of the estimation methods and measured data of the different plot areas

STS represents the average standard tree of the stand method, SDC represents the average standard tree of the diameter classes method, STC represents the average standard tree of the tree classification method, BM represents the biomass model method, and BV represents the biomass-volume regression method. *Capital letters indicate the significant test between different areas under the same estimation method for each component, while lower letters indicate the significant test between different estimation methods under the same sampling size for each component

Discussion

Plot size selection for biomass investigation

The plot size was crucial in ensuring the accuracy of forest plot investigations (Zhang, 2018). In this study, there was no significant difference in the average error indexes of the different components for the biomass estimation values between plot sizes and methods. This result was related to the fact that small sample plots of various sizes were part of the 0.3 hm^2 sample plot, so the estimated average value was mainly close to the measured value of the large sample plot. In addition, the three standard tree methods (SDC, STS, and STC) tended to have higher accuracy due to the higher sampling survey proportion when the sample plot area and the number of trees in the sample plot were small. In addition, these methods had smaller error values if the plot size was smaller than the measured values. These results showed that selecting a smaller sampling area was feasible to ensure a certain number of sample plots when the forest distribution was relatively homogeneous. In contrast, when the heterogeneity of forest distribution was high, the small sample size did not accurately reflect the basic characteristics of the stand.

When the measured biomass data of the 0.3 hm^2 sample plot were the true values, the average absolute relative error showed a gradual decrease with the increase in the sample plot size and a gradual and stable change trend after 400 hm^2 . Moreover, the MD, BM, BV, and SDC methods showed an average absolute relative error for the 400 m^2 and above sampling areas, and this error was significantly higher than that in the 100 m^2 plot; however, there was no significant difference between the 400 m^2 plots and other larger sampling sizes. The average absolute relative error values of the biomass of all the components mainly ranged between 10 and 20% when the sample plot area was 400 m^2 , so it was recommended that the sample plot size for forest biomass investigations should not be less than 400 m^2 . If the estimation accuracy were further improved, the plot size would need to be increased to 1500 m^2 . In addition, the average absolute relative error was less than 10% when the total biomass of wood and aboveground parts was investigated by the MD, BV, and SDC methods in plot size greater than 400 m^2 . However, the estimation errors for the branches, foliage, and bark were rarely less than 10% due to their more significant variation.

Moreover, the plot size gradient from 100 m² to 1500 m² was set in a 0.3 hm² plot, and the sampling positions were overlapping. The overlapping data are regarded as the constraints because of the strong autocorrelation pattern induced by the overlapping scheme (Sharon, 2011; Jackson and Mosleh, 2012; Mayabadi and Saadatfar, 2022), then would lead to a bias estimation (Mayabadi and Saadatfar, 2022). But the overlapping sampling was applied in determining the minimum sampling areas in the forestry and vegetation surveys (Ulrich and Buszko, 2007; Yang et al., 2010; Yuan et al., 2019). In addition, due to the difficulty of biomass and the high cost of entirely clear-cutting plots, completely independent plots had not been applied in this study.

Biomass estimation precision results from estimation methods

The selection of biomass investigation methods was the key to obtaining accurate biomass data (Zhang, 2018). Among the six methods used to investigate or estimate the aboveground biomass of the forest stand in this study, both BM and the BV methods could be used as the preferred methods for forest biomass investigation in the future because they often had lower estimation errors for the different plot sizes. In this study,

the biomass model of a single tree was based on 512 trees in the sample plot. The biomass-volume regression equation at the stand level was also obtained based on the measured data of the sample plot; thus, the models had higher applicability. Therefore, it was essential to determine the biomass models or biomass-volume regression equations suitable for local stands. Due to the uncertainty in estimating forest stand and even regional forest biomass with the biomass model method (Fu et al., 2015; Qin et al., 2017), it has been of great significance to construct a universal and species-appropriate biomass model that ensured a sure prediction accuracy (Luo et al., 2009). A large number of biomass models have been built to date (Ter-Mikaelian and Korzukhin, 1997; Chojnacky, 2002; Jenkins et al., 2004; Zianis et al., 2005; Huang, 2014; Luo et al., 2015), and technical regulations for modeling methods of standing tree biomass (LY/T 2258-2014) and technical rules for the sample collection of standing tree biomass modeling (LY/T 2259-2014) have been established in China as forestry standards of biomass models and biomass tables for *Spruce, Larch, Pinus yunnanensis, Pinus massoniana, Cryptomeria fortunei,* oak and other tree species; however, these models, regulations, and standards need to be further supplemented and improved. Moreover, due to the uncertainty differences in biomass models under different site conditions, the models should be revised or verified in time (Zhao et al., 2017).

Moreover, the SDC method is a better option if the biomass model is not available and the sample plot cannot be measured because this method had a minor average error absolute value, especially when the sample plot size was 600 m^2 or less, which was even smaller than that of the BM method. In addition, the BV method also had a minor average error absolute value. Fang et al. (2001, 2002) constructed the biomass-volume regression equations for the main tree species or tree species groups in China by using the national forest resources continuous inventory data and determined the nationalscale forest biomass estimation based on the continuously changing biomass expansion factor. However, the sample numbers used in these equations were not uniform, and the equations may not be applicable in a specific region. Therefore, constructing the biomass-volume regression equations of the main tree species and tree species groups in the different areas is of great significance for forest biomass estimation at different scales.

Variations in the different components

Considering the variation in different components, branches, foliage, and bark often had significant uncertainties, and their estimation errors were often larger (Tahvanainen and Forss, 2008; Subedi and Sharma, 2012; Goodman et al., 2014); thus, their biomass determinations required a more extensive sampling area. Therefore, the SDC and BM methods were adopted rather than the STS and STC methods. However, for the STS method, the average relative absolute errors of the wood biomass and the total aboveground biomass were often less than 20%; for example, when the sample plot size was 400 m^2 , the average relative absolute error of the wood biomass was 16.97%, while that of the total aboveground biomass was 15.65%. Thus, it is possible to use the STS method for a certain investigation. The STS method could also provide a specific theoretical basis for estimating the forest aboveground biomass using the average standard tree data from forest management inventory data (FMI) in the subcompartments.

Conclusions

In this study, the aboveground biomass and estimation errors for *Pinus kesiya* var. *langbianensis* natural forest were estimated by comparing and analyzing six methods, including BM, BV, SDC, STC, STS, and MD. The results showed that the average relative absolute error of the various methods tended to decrease with increasing sample plot size, especially when compared with the measured true value data of the 0.3 hm^2 sample plot. When the sample plot size was greater than or equal to 400 m^2 , the estimation error was significantly lower than the 100 m^2 plot. Still, the error differences between 400 $m²$ and the other larger sample plot sizes were not significant. Therefore, the sample plot size for a biomass investigation of various components of aboveground parts of a stand should not be smaller than 400 m². Moreover, the BM, BV, and SDC methods mostly had lower average absolute error values and average relative absolute error values. Therefore, if reliable biomass models or biomass-volume regression equations are available, the BM and BV methods are the better selections for forest aboveground biomass investigation; otherwise, the SDC method would be better. The STS method could be used when the survey object is forest wood or/and aboveground biomass. In addition, the results would be applied to natural forests with a simple stand structure or artificial forests. Still, the biomass estimation method and the size determination of sample plots for the natural forests with more complex stand structures need further research. Furthermore, the canopy width and length factors were used in the biomass equation for single trees in this study to obtain a higher accuracy model. Introducing canopy factors in the estimation model also helps get more accurate biomass survey data in future sample plot surveys for remote sensing biomass estimation.

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