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Allometric Biomass Models for European Beech and Silver Fir: Testing Approaches to Minimize the Demand for Site-Specific Biomass Observations

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Abstract: In this paper, site-specific allometric biomass models were developed for European beech (*Fagus sylvatica* L.) and silver fir (*Abies alba* Mill.) to estimate the aboveground biomass in Șinca virgin forest, Romania. Several approaches to minimize the demand for site-specific observations in allometric biomass model development were also investigated. Developing site-specific allometric biomass models requires new measurements of biomass for a sample of trees from that specific site. Yet, measuring biomass is laborious, time consuming, and requires extensive logistics, especially for very large trees. The allometric biomass models were developed for a wide range of diameters at breast height, D (6–86 cm for European beech and 6–93 cm for silver fir) using a logarithmic transformation approach. Two alternative approaches were applied, i.e., random intercept model (RIM) and a Bayesian model with strong informative priors, to enhance the information of the site-specific sample (of biomass observations) by supplementing with a generic biomass sample. The appropriateness of each model was evaluated based on the aboveground biomass prediction of a 1 ha sample plot in Șinca forest. The results showed that models based on both D and tree height (H) to predict tree aboveground biomass (AGB) were more accurate predictors of AGB and produced plot-level estimates with better precision, than models based on D only. Furthermore, both RIM and Bayesian approach performed similarly well when a small local sample (of seven smallest trees) was used to calibrate the allometric model. Therefore, the generic biomass observations may effectively be combined with a small local sample (of just a few small trees) to calibrate an allometric model to a certain site and to minimize the demand for site-specific biomass measurements. However, special attention should be given to the H-D ratio, since it can affect the allometry and the performance of the reduced local sample approach.

Keywords: biomass; Romania; site-specific; *Fagus sylvatica*; *Abies alba*; Bayesian model; mixed effect models

1. Introduction

Forests play an important role in mitigating the effects of climate change [1–3], contributing significantly to the uptake of atmospheric carbon dioxide [4]. However, the large uncertainties usually associated with the estimation of forest biomass stock and stock change are an important limitation for the successful implementation of forest-based mitigation programs [2]. As a result, there is an increasing interest from the international scientific community to reduce the uncertainties of forest biomass estimates [5,6].

Forest biomass estimates usually rely on allometric biomass models, which are regression models that predict individual tree aboveground biomass (AGB_i) as a function of easy-to-measure independent variable x_i (e.g., diameter at breast height, D, and/or tree height, H):

$$AGB_i = \beta_0 \cdot x_i^{\beta_1} + \varepsilon_i. \quad (1)$$

Allometric biomass models describe how tree biomass varies with the predictor(s). For trees of similar sizes, the variation in AGB is determined by the genotype, the environmental conditions, and their interaction [7]. For example, the environmental conditions such as temperature and precipitation were shown to affect the allocation of biomass within trees [8], whereas a change in tree biomass allocation due to different levels of tree competition was shown to significantly affect tree biomass allometry [9]. It is well documented that allometric biomass models are species- and site-specific [10–14], and, therefore, specific model parameters should be used for each species and each site. Developing species-specific allometric models, based on sample trees from multiple sites, requires the models to be applied in those same sites. This is required because the mean of site-effects would tend to zero and, therefore, the mean biomass per unit area is unbiased [10]. However, applying a model calibrated for different sites to one single site, could yield biased biomass estimates [13,15]. As a result, calibration of allometric models at the site level becomes compulsory to obtain accurate estimates of biomass at the site level. Moreover, given the small forest property size, especially in the case of private owners [16], estimates of forest biomass over small forest areas are often needed.

Development of unbiased allometric models for new sites requires measuring the biomass of a large enough number of trees from the total tree population [17]. However, measuring the biomass requires extensive logistics and resources, limiting, therefore, the possibility to calibrate the model for each site. The most common fitting method for allometric models is the ordinary least squares regression [18–21]. However, because the residuals of allometric models are heteroscedastic, i.e., the variance increases with a predictor, a weighting approach should be used to account for the heteroscedasticity, which is usually the inverse of the predicted variance for a given value of the predictor. Since the variance is greatest for the largest trees, these trees will bring less effective information into the model (because the weights are calculated as the inverse of variance, large trees are weighted less compared to small trees) [22]. These large trees are also the most difficult to measure (for biomass); therefore, the logistics limitations of measuring biomass make the calibration of these models at site level a very low cost-effective task. Because of that, much interest has been invested in finding ways to make local calibration more affordable. For example, [23] proposed the “small sampling scheme” method, where the smallest two trees were used to detect the most appropriate parameters of the local allometric model from a database of allometric models.

When species-specific biomass observations from other sites are available, the mixed-effects models can be used to enhance the local information (of the site-specific sample). In a similar conceptual approach to [23], just a few local trees can be used to calibrate the intercept of a random intercept model to local conditions, whereas the slopes remain similar for all locations. Therefore, the assumption here is that, at a species level, the allometric scaling is invariant. Although the assumption of invariant allometric scaling has been widely disputed, it was demonstrated that allometric scaling is species-specific [12], but there is no information to support a site-specific allometric scaling. However, it has been shown that the intercept of allometric models vary by site [10]. This approach can be very

convenient since the intercept can be calibrated based on a few small trees, for which the biomass can more easily be measured.

Another approach extensively promoted lately is the Bayesian modelling, since it is considered an effective way to combine prior information with the local observations [24,25]. Compared to random intercept model, the Bayesian approach does not need the observations (biomass data) from other locations; it only needs the parameter values (it could be either theoretical or estimated) which can be integrated with new local information. Therefore, the Bayesian approach can be more versatile, as demonstrated by [26].

The few remnant natural forests, located in remote mountain areas with steep slopes in Eastern and Southern Europe are often dominated by pure and mixed beech and coniferous forests [27–30]. European beech (*Fagus sylvatica* L.) represents one of the widely distributed tree species across Europe [31], in Romania accounting for a third of the Romanian growing stock [32]. Allometric biomass models for European beech have been developed in numerous studies [33–39]. In contrast, fewer studies reported allometric models for silver fir (*Abies alba* Mill.), another species often present in the few remaining mixed virgin forests, sometimes, from the point of view of allometry, being assimilated to Norway spruce [40,41].

The following aims were set for this study: (i) developing allometric biomass models for European beech and silver fir to be used to estimate biomass of a European beech-silver fir virgin forest located in Southern Carpathians; (ii) investigating whether the local calibration of allometric models can be done appropriately based on a reduced sample of site-specific observations using a random intercept model or a Bayesian model; and (iii) assessing how these models and approaches perform in predicting AGB in a 1-ha sample plot of this virgin forest.

2. Materials and Methods

2.1. Materials

2.1.1. Study Site

The study was conducted in Făgăraș Mountains ($45^{\circ}40'0.420''$ N and $25^{\circ}10'14.359''$ E, Southern Carpathians, Romania). Having the aim to develop allometric models to estimate the biomass in the UNESCO Șinca virgin forest (351.8 ha), the study site is located in the immediate neighborhood of the virgin forest. The study site has similar composition and structure to the virgin forest and, before 2009, when the first silvicultural interventions were applied, was itself regarded as a virgin forest. The species composition is dominated by European beech (*Fagus sylvatica* L.) and silver fir (*Abies alba* Mill.). The climate is temperate continental with a mean annual temperature of 6.1°C and average annual rainfall of 1100 mm. The bedrock consists of crystalline schists, and the soils are predominantly cambisols [42].

2.1.2. Biomass Datasets

Dataset #1

Dataset #1 consists of site-specific biomass observations from the study site. A destructive sampling method took place in July and August 2018 for European beech trees and in 2019, for silver fir trees. To avoid the effects of thinning on tree allometry, the sample trees were selected from stand patches that presented no stumps from silvicultural interventions. Since the trees within the virgin forests have a large range of diameters and reach greater dimensions than those in managed forests [27], the trees felled for the biomass determination were selected to cover a large range of diameters at breast height (D-range) as wide as possible, with at least one tree in each 10 cm D-class. The information from a 1-ha sample plot (presented in the next section) was used to determine the D-range. A total of 29 trees were destructively sampled, 15 European beech and 14 silver fir trees (Table 1).

Table 1. The characteristics of site-specific sample trees (full sample). Note: D is the diameter at breast height; H is the tree height; AGB is the aboveground biomass.

Characteristic	European Beech	Silver Fir
Sample size	15	14
D range (cm)	5.7–86.3	6.3–92.6
D mean (standard deviation) (cm)	32.8 (26.1)	35.8 (27.0)
H range (m)	6.2–40.3	3.5–43.5
H mean (standard deviation) (cm)	22.8 (12.5)	21.2 (13.8)
AGB range (kg)	6.0–8447.1	4.2–4042.9
AGB mean (standard deviation) (kg)	1561.4 (2382.7)	1034.6 (1316.9)

For each sample tree, D (in cm, with a precision of 0.1 cm) and the total height (H, in m, with a precision of 0.01 m) were recorded. The selected trees were cut down and fresh biomass was measured. The trees were first separated into stem and branches (with the leaves/needles attached) and then each fraction was weighed. For large stem sections and big branches, we used a crane with ± 0.001 Mg precision and 3 Mg capacity [43], whereas for smaller branches, we used an electronic scale with a precision of ± 0.1 kg. For each stem, at least 5 sample discs were taken from different tree heights, to determine moisture content. The wood discs were weighed fresh, and then transported to the laboratory and dried in the oven at 70 °C for at least 5 days, until the constant weight was achieved and weighed again. The mean value of dry-to-fresh weight ratio of sampled wood discs for each tree was used to convert the fresh stem mass into dry stem mass. Tree crown was divided into three sections (i.e., lower, middle, and upper) and 3–4 branches per section were randomly selected to determine the branch-to-foliage ratio. Each sampled branch was weighed in the field with a ± 0.1 kg precision. For European beech, the leaves were detached from the branches in the field, and each fraction was weighed. For silver fir, the sample branches were taken into the laboratory and dried in the oven for 1–2 days (at 70 °C) to ease separation of needles from branches. After separation, the two fractions were dried until constant weight. Each fraction was weighed again, and the ratio of foliage/branches weight was determined. To determine the moisture content of branches and foliage, fresh samples for each fraction were randomly selected within each crown layer and weighed with a precision of ± 0.01 g. The samples were dried in the oven at 70 °C until the constant mass was reached. The dry biomass of each component was determined, and then the dry AGB was calculated for each individual tree.

Dataset #2

Dataset #2 (the reduced site-specific sample) was derived from Dataset #1 (Table 1) and consisted of the smallest 7 trees for each of the two species (European beech and silver fir); the sample size was set to 7, because it was considered to be the minimum sample size that could be used in this context. The range of the sample trees attributes is presented in Table 2.

Table 2. The characteristics of reduced site-specific sample (Dataset #2).

Characteristic	European Beech	Silver Fir
Sample size	7	7
D range (cm)	5.7–20.0	6.3–27.9
D mean (standard deviation) (cm)	11.1 (5.8)	14.2 (7.9)
H range (m)	6.2–19.8	3.5–19.8
H mean (standard deviation) (m)	11.4 (5.2)	9.3 (5.8)
AGB range (kg)	6.0–182.2	4.2–358.9
AGB mean (standard deviation) (kg)	65.1 (73.9)	84.2 (128.8)

Dataset #3

Dataset #3 consists of Dataset #1, plus a generic dataset (Table 3), that was not specific to our site. The generic observations were extracted, for each of the two species, from two international databases of tree biomass observations [35,44].

Table 3. The characteristics of the generic biomass sample and Dataset #3.

Characteristic	Generic Dataset		Dataset #3	
	European Beech	Silver Fir	European Beech	Silver Fir
Sample size	144	102	159	116
D range (cm)	5.2–62.1	5.1–64.0	5.2–86.3	5.1–92.6
H range (m)	9.2–33.0	4.1–28.9	6.2–40.3	3.5–43.5
AGB range (kg)	6.6–3116.2	7.0–1652.3	6.0–8447.1	4.2–4042.9
Number of sites	10	10	11	11
References	[35,44]		[35,44] and this study	

Dataset #4

Dataset #4 consists of the generic dataset presented in Table 3, plus the reduced site-specific sample, presented in Table 2.

2.1.3. Inventory Plot

A one-hectare permanent inventory plot (100 m × 100 m) was established in Šinca virgin forest in 2003 and reinventoried in 2013. Each living tree with a D greater than 5 cm was recorded by species and measured for D using a caliper and for H using a Vertex IV hypsometer (Haglöf, Sweden). In total, 259 silver fir and 153 European beech trees were recorded. The range of D was between 5 and 99.2 cm for silver fir and between 5 and 97.5 cm for European beech.

We applied all allometric models developed in this study to estimate the total plot AGB in order to investigate how the models behaved. Since the true AGB at plot level is unknown, our analysis was not meant to show which model gives the most accurate AGB estimate at plot level, but to highlight any relative differences between AGB estimates, as resulted from different allometric models.

2.2. Development of Allometric Biomass Models

2.2.1. Linear Regression Model on Log-Transformed Data (LM)

To fit the allometric biomass models, two approaches are common: (i) fitting nonlinear models directly in the original scale, accounting, however, for the commonly heterogeneous variance of residuals and (ii) log-transforming all variables and fitting a linear model on log–log transformed data. However, using log–log transformation implies a bias during back transformation, since the normal distribution of residuals in logarithmic scale becomes lognormal after back transformation, and because the mean of the lognormal distribution is usually larger than 1.0 (i.e., the 1.0 value represents the back transformed mean of residuals in log-scale, $\exp(0) = 1$). In this study, we adopted the logarithmic transformation approach, because the generally small sample size available would not be sufficient for developing specific functions to account for heteroscedasticity, necessary with the first approach. A second reason is that the transformation did account well for the heteroscedasticity of residuals.

Within this approach, the models rely exclusively on local data (on Dataset #1). The linear allometric models on log–log transformed data have the following forms:

$$\ln(AGB)_i = \beta_{01} + \beta_{11} \ln(D)_i + \varepsilon_1 \quad (2)$$

$$\ln(AGB)_i = \beta_{02} + \beta_{12} \ln(D)_i + \beta_{22} \ln(H)_i + \varepsilon_2 \quad (3)$$

After back transformation, Equations (2) and (3) become:

$$A\hat{G}B_i = \exp(\hat{\beta}_{01}) \cdot D_i^{\hat{\beta}_{11}} \cdot \exp\left(\frac{\hat{\sigma}_1^2}{2}\right) \cdot \exp(\varepsilon_1) \quad (4)$$

$$A\hat{G}B_i = \exp(\hat{\beta}_{02}) \cdot D_i^{\hat{\beta}_{12}} \cdot H_i^{\hat{\beta}_{22}} \cdot \exp\left(\frac{\hat{\sigma}_2^2}{2}\right) \cdot \exp(\varepsilon_2), \quad (5)$$

where $\exp\left(\frac{\hat{\sigma}_1^2}{2}\right)$ and $\exp\left(\frac{\hat{\sigma}_2^2}{2}\right)$ are the correction factors and CF [45,46], based on residual variances $\hat{\sigma}_1^2$ and $\hat{\sigma}_2^2$ resulted from Equations (2) and (3), respectively. For Equations (2) and (3), we checked all regression assumptions and presented the results only if the assumptions were violated.

2.2.2. Random Intercept Models (RIM)

The model forms presented in Equations (2) and (3) were used to develop mixed-effects models with random intercept effect (the random effect was represented by the site), whereas the coefficients of the variables were entered in the models as fixed-effects. Four models were fitted for each tree species: (i) Equation (2) based on Dataset #3, (ii) Equation (3) based on Dataset #3, (iii) Equation (2) based on Dataset #4, and (iv) Equation (3) based on Dataset #4. For each of these models, the slope was similar for all sites, whereas the intercept varied by site. The total number of sites was 11, for each model and each dataset, see Tables 3 and 4. The parameter estimates corresponding to the study site (Sinca forest) were retained for further analysis and used to derive biomass predictions for European beech and silver fir trees.

Table 4. The characteristics of Dataset #4.

Characteristic	European Beech	Silver Fir
Sample size	151 (i.e., 144 + 7)	109 (i.e., 102 + 7)
D range (cm)	5.2–62.1	5.1–64.0
H range (m)	6.2–33.0	3.5–28.9
AGB range (kg)	6.0–3116.2	4.2–358.9
Number of sites	11	11

2.2.3. Bayesian Models

The structure of the fitted Bayesian models is similar to Equations (2) and (3). The Bayesian model requires prior information for model parameters and residuals. The prior information was derived from the generic dataset (Table 3) for each of the two species. We fitted random intercept and slope models (with the site grouping factor as random effect) to the generic dataset in order to obtain the parameter estimates and their standard errors, that were further used to construct the priors. The priors were defined in JAGS (Just Another Gibbs Sampling) as probability density functions (“dnorm” function in R [47]), characterized by parameter estimates and the precision term that was calculated as the inverse of parameter variance. For example, the intercept of model based on D only for European beech was -1.94 , and its standard error was 0.171 . The precision term was calculated as the inverse of squared 0.171 , which was 34 .

As for the RIM, we developed four types of Bayesian models for each of the two species: (i) Equation (2) based on Dataset #1, (ii) Equation (3) based on Dataset #1, (iii) Equation (2) based on Dataset #2, and (iv) Equation (3) based on Dataset #2.

2.3. Evaluation of Calibration Approaches

To evaluate the fitting approaches, we compared the predicted tree AGB with the observed tree AGB in logarithmic scale and further calculated the root mean squared deviation (RMSD):

$$RMSD = \sqrt{\frac{\sum_{i=1}^n [\ln(\hat{AGB})_i - \ln(AGB)_i]^2}{n}}, \quad (6)$$

where $\ln(\hat{AGB})_i$ is the predicted $\ln(AGB)$ for i^{th} tree, $\ln(AGB)_i$ is the observed $\ln(AGB)$ of i^{th} tree, and n is the sample size.

Evaluation of model calibration is often performed at goodness of fit level only. However, [22] showed that the coefficient of variation was not a good indicator of predictive performance of allometric models. As a result, we propagated the model parameters through a Monte Carlo error propagation procedure to calculate the mean predicted biomass at plot level and its standard error.

The Monte Carlo propagation procedure was defined as:

- (1) For the k^{th} replication ($K = 5000$, K is the total number of replications), a set of allometric model parameters and residuals were sampled from a multivariate normal distribution and a univariate normal distribution, respectively.
 - (a) Sampling a residual value from a normal distribution with the mean zero and standard deviation equal to residual standard error of the allometric model;
 - (b) Sampling a set of model parameter values from a bivariate normal distribution (for models using only D as predictor of AGB) or a trivariate normal distribution (for models based on both D and H to predict AGB);
 - (c) Calculate the predicted $\ln(AGB)$ for each tree within the 1 ha inventory plot (Section 2.1.3), based on the model parameters sampled at step 1.b and the residual sampled at step 1.a;
 - (d) Back transform the predicted $\ln(AGB)$, using a correction factor (CF) calculated as in Section 2.2.1;
 - (e) Calculate the total plot AGB by addition of individual tree predictions;
- (2) Steps (1.a) to (1.e) were repeated for a number of $K = 5000$ times to calculate:
 - (a) Mean predicted plot biomass, as the mean of values obtained at step 1.e;
 - (b) Standard error of the mean (values at step 1.e), which, because of using a single plot, equals the standard deviation of the sample mean.

Step 2 was repeated $n_{\text{rep}} = 5000$, to stabilize the mean and the standard error. The values further reported are (i) the mean of mean values at step 2.a and (ii) the mean of the standard error values at step 2.b.

To highlight the role of variance–covariance matrix in the plot-level biomass estimation, we calculated the plot biomass also based on model parameter point estimates.

2.4. Data Processing

The analysis was performed in R [48] and Jags (Bayesian models) [49] using the packages “nlme” [50] and “R2jags” [47].

3. Results

3.1. Allometric Biomass Models

The parameter estimates of the different allometric biomass models are presented in Table 5. Both the models based on a single predictor (D only) and on two predictors (D and H) were fitted.

The simple regression models (i.e., LM; Table 5) fitted well to the data, and, despite of relatively limited sample size, the coefficients of determination (R^2) for models based on single predictor were 0.9972 for European beech and 0.9862 for silver fir, whereas for models based on D and H, the R^2 increased to 0.9986 for European beech and to 0.9921 for silver fir. The reason for these large coefficients of determination is related to the wide D range of the sample trees (Table 1).

Table 5. The parameters of allometric biomass models predicting tree aboveground biomass (AGB), by fitting approach and predictor combination. Standard errors of model parameters are presented in parenthesis. RSE is the residual standard error; CF is the correction factor and was calculated as in Equations (4) or (5); LM is the linear regression model on log-transformed data (Section 2.2.1); RIM is the random intercept model (Section 2.2.2); ln(D) is the logarithm of diameter at breast height; ln(H) is the logarithm of tree height.

Fitting Approach	Dataset	Predictors	Model Form	β_0 (SE)	β_1 (SE)	β_2 (SE)	RSE	CF
European Beech								
LM	#1	ln(D)	Equation (2)	-2.6634 (0.1254)	2.6368 (0.0384)	N.A.	0.1337	1.0089
		ln(D), ln(H)	Equation (3)	-3.1632 (0.1761)	2.1468 (0.1489)	0.6909 (0.2060)	0.1000	1.0050
RIM	#3	ln(D)	Equation (2)	-2.1312 (0.0901)	2.4714 (0.0253)	N.A.	0.1712	1.0148
		ln(D), ln(H)	Equation (3)	-3.0039 (0.1389)	2.1151 (0.0495)	0.6733 (0.0845)	0.1450	1.0106
Bayesian model	#4	ln(D)	Equation (2)	-2.1625 (0.0997)	2.4368 (0.0284)	N.A.	0.1683	1.0143
		ln(D), ln(H)	Equation (3)	-2.9793 (0.1593)	2.1191 (0.0511)	0.6512 (0.0916)	0.1474	1.0109
#1	Bayesian model	ln(D)	Equation (2)	-2.1768 (0.1148)	2.4884 (0.0345)	N.A.	0.2042	1.0211
		ln(D), ln(H)	Equation (3)	-3.0637 (0.1076)	2.1497 (0.0445)	0.6553 (0.0605)	0.1091	1.0060
#2	Bayesian model	ln(D)	Equation (2)	-2.1456 (0.1115)	2.4349 (0.0398)	N.A.	0.2363	1.0283
		ln(D), ln(H)	Equation (3)	-2.9856 (0.1508)	2.1347 (0.0525)	0.6324 (0.0680)	0.1475	1.0109
Silver Fir								
LM	#1	ln(D)	Equation (2)	-3.4141 (0.3106)	2.6997 (0.0922)	N.A.	0.2965	1.0449
		ln(D), ln(H)	Equation (3)	-2.9687 (0.2907)	1.3301 (0.4839)	1.4460 (0.5051)	0.2344	1.0278
RIM	#3	ln(D)	Equation (2)	-2.4756 (0.1106)	2.4219 (0.0346)	N.A.	0.2033	1.0209
		ln(D), ln(H)	Equation (3)	-2.8079 (0.0984)	1.7737 (0.0708)	0.8745 (0.0920)	0.1624	1.0133
Bayesian model	#4	ln(D)	Equation (2)	-2.5086 (0.1205)	2.3561 (0.0375)	N.A.	0.1824	1.0168
		ln(D), ln(H)	Equation (3)	-2.7987 (0.1126)	1.8076 (0.0751)	0.8040 (0.0992)	0.1548	1.0121
#1	Bayesian model	ln(D)	Equation (2)	-2.3284 (0.1598)	2.3859 (0.0471)	N.A.	0.3965	1.0818
		ln(D), ln(H)	Equation (3)	-2.7679 (0.1609)	1.9264 (0.0771)	0.6847 (0.0897)	0.2788	1.0396
#2	Bayesian model	ln(D)	Equation (2)	-2.3553 (0.1591)	2.3316 (0.0552)	N.A.	0.4064	1.0861
		ln(D), ln(H)	Equation (3)	-2.6917 (0.1707)	1.9063 (0.0810)	0.6305 (0.0969)	0.3192	1.0523

The alternative calibration approaches (i.e., RIM and Bayesian) produced parameter estimates that were more or less comparable to those obtained with the regression approach, depending on the species and on whether using the full site-specific sample of trees (i.e., Dataset #3 for RIM and Dataset #1 for Bayesian model) or the reduced one (i.e., Dataset #4 for RIM and dataset #2 for Bayesian). Compared to the Bayesian approach, the RIMs produced more similar parameter estimates to the log-linear regression (Table 5). However, since the parameters of these models are inversely correlated,

it is expected that large slope estimates are paired to small intercept values and vice-versa. The models based on reduced sample size (i.e., RIM based on Dataset #4 and Bayesian model based on Dataset #2) produced parameter estimates that were very similar to those resulted from the full sample (Table 5).

Notable differences in parameter estimates were observed for silver fir, especially when the two predictors (D and H) were used together. The parameter of D, which usually is close to 2.0 (in models where D and H are used together to predict AGB), was in this case 1.3301 and the parameter of H, which normally is less than 1.0, was 1.4460. This means that for trees of similar H, an increase in D by 1% produced an increase in AGB of 1.33%; likewise, for trees of similar D, a 1% increase in H yielded 1.446% increase in AGB. The parameters of the alternative fitting approaches were slightly different, the parameter of D being closer to 2.0 (i.e., 1.77–1.92; Table 5), whereas the parameter of H was lower than 1.0 (i.e., 0.63–0.87; Table 5).

The residual standard errors (RSE), which in the case of log-transformed allometric models, shows a form of the coefficient of variation of predicted biomass [22,51] and, in turn, indicates the intrinsic variability of AGB for any given tree size (i.e., D or D and H), were generally smaller for European beech than for silver fir (Table 5). This implies that the correction factors of the back transformation were also smaller.

We plotted the predicted AGB against the observed AGB (for Dataset #1, see Figure 1) to highlight any anomalies in models fitting the data. Figure 1 shows that predicted AGB followed better the observed AGB for European beech compared to silver fir. Addition of H as a predictor of AGB resulted in improvements of AGB prediction accuracy for both species. The accuracy levels are reflected by the RMSD values presented in Figure 1, which, alternatively, can be visually assessed by looking at how closely the observations are to the diagonal (i.e., 1:1) line.

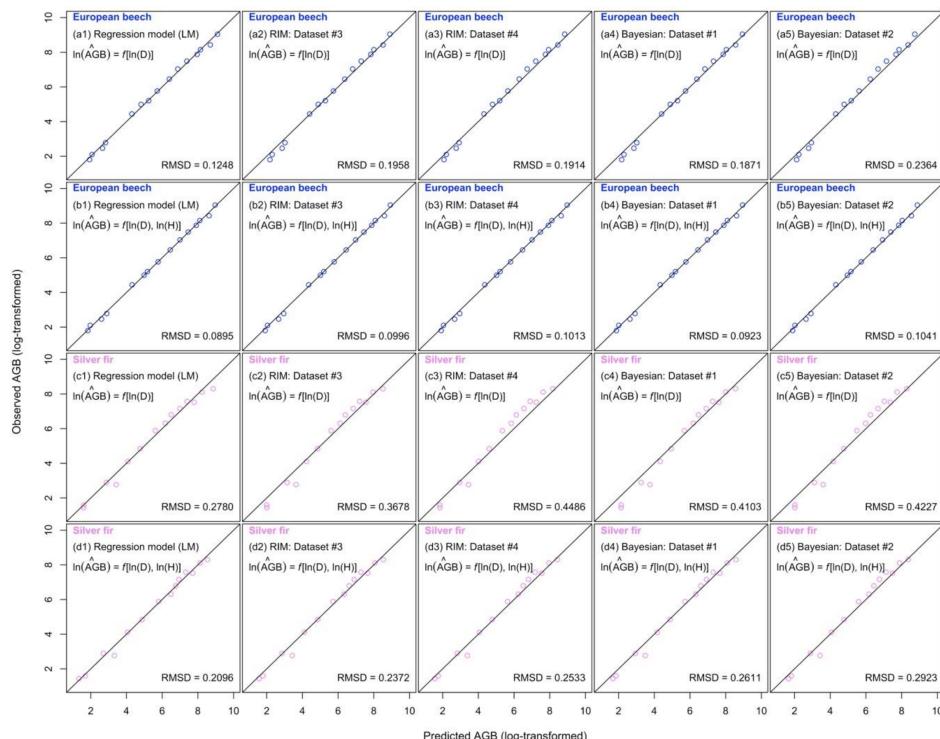


Figure 1. The observed $\ln(\text{AGB})$ against the predicted $\ln(\text{AGB})$. Note: AGB is the aboveground biomass; the values are presented in log-scale for two species, two predictor combination, and five fitting approaches. The data used for validation is from Dataset #1. LM is the linear regression model on log-transformed data (Section 2.2.1); RIM is the random intercept model (Section 2.2.2); $\ln(D)$ is the logarithm of diameter at breast height; $\ln(H)$ is the logarithm of tree height; $\ln(\text{AGB})$ is the logarithm of aboveground biomass; RMSD is the root mean squared deviation (Section 2.3).

As expected, the models based on reduced sample (i.e., RIM based on Dataset #4 and Bayesian model based on Dataset #2) showed a slight reduction in prediction accuracy compared to models based on full local sample (i.e., RIM based on Dataset #3 and Bayesian model based on Dataset #1) and to the regression model (LM). The increase in RMSD was larger for silver fir than for European beech and, as expected, was larger for models based on D only compared to models based on D and H. Therefore, the reduced sample gives better results when used with models based on D and H (as predictors of AGB).

For European beech, the Bayesian approach showed similar accuracy to RIM (RMSD was 0.0923 vs. 0.0996 for full sample and 0.1041 vs. 0.1013 for reduced sample). For silver fir, however, RIM performed better, producing smaller RMSD values (Figure 1).

3.2. Comparison of Biomass Estimates on 1 ha Sample Plot

Applying the allometric models, to estimate the biomass at plot level, provides a way to examine the performance of the models. Since the true biomass at plot level is not known, we just compared the model estimates against each other.

The individual tree predictions (from 1 ha sample plot) that are based on parameter estimates (Table 3) are shown in Figure 2. The AGB tree predictions resulted from RIM or Bayesian approaches were compared to the regression approach predictions (i.e., LM vs. RIM and LM vs. Bayesian). The results confirm the above observation that models based on D and H give more reliable (or consistent) predictions of AGB (Figure 2, b vs. a).

The models based on full sample (i.e., models based on Dataset #1 and Dataset #3) produced more consistent estimates when compared to those based on the reduced sample. However, the differences were not substantially large. For example, the RIM approach based on Dataset #3 produced tree AGB predictions that were on average +0.1% and −0.4% different (for European beech and silver fir, respectively) to LM (Figure 2b1). However, the RIM based on Dataset #4 (reduced sample) were on average −2.8% and −6.7% (for European beech and silver fir, respectively) different to LM (Figure 2b2). The full sample (Dataset #1) Bayesian-based estimates differed by −0.1% and +2.9% (for European beech and silver fir, respectively) to LM; for the Bayesian-based reduced sample, the differences were −3.9% and −6.0% (for European beech and silver fir, respectively). The relative differences in tree AGB predictions between LM and the alternative fitting approaches (Figure 2) were larger for small trees, especially for silver fir. This result may have been the consequence of the anomalous parameter estimates for silver fir, when D and H were used as predictors of AGB.

Mean biomass per hectare varied between 370,296 kg ha^{−1} for RIM using the reduced sample (Dataset #4) and based on single predictor and 542,758 kg ha^{−1} for simple regression model based on D only (Table 6). Therefore, the plot AGB estimates varied more when a single predictor of AGB was used. On the other hand, the models based on both D and H produced more stable AGB estimates at plot level (i.e., differences between estimates resulted from different fitting approaches were smaller). In addition, the standard errors of mean AGB were smaller when both D and H were used as predictors. Overall, the Bayesian models resulted in larger standard errors compared to both RIM and LM.

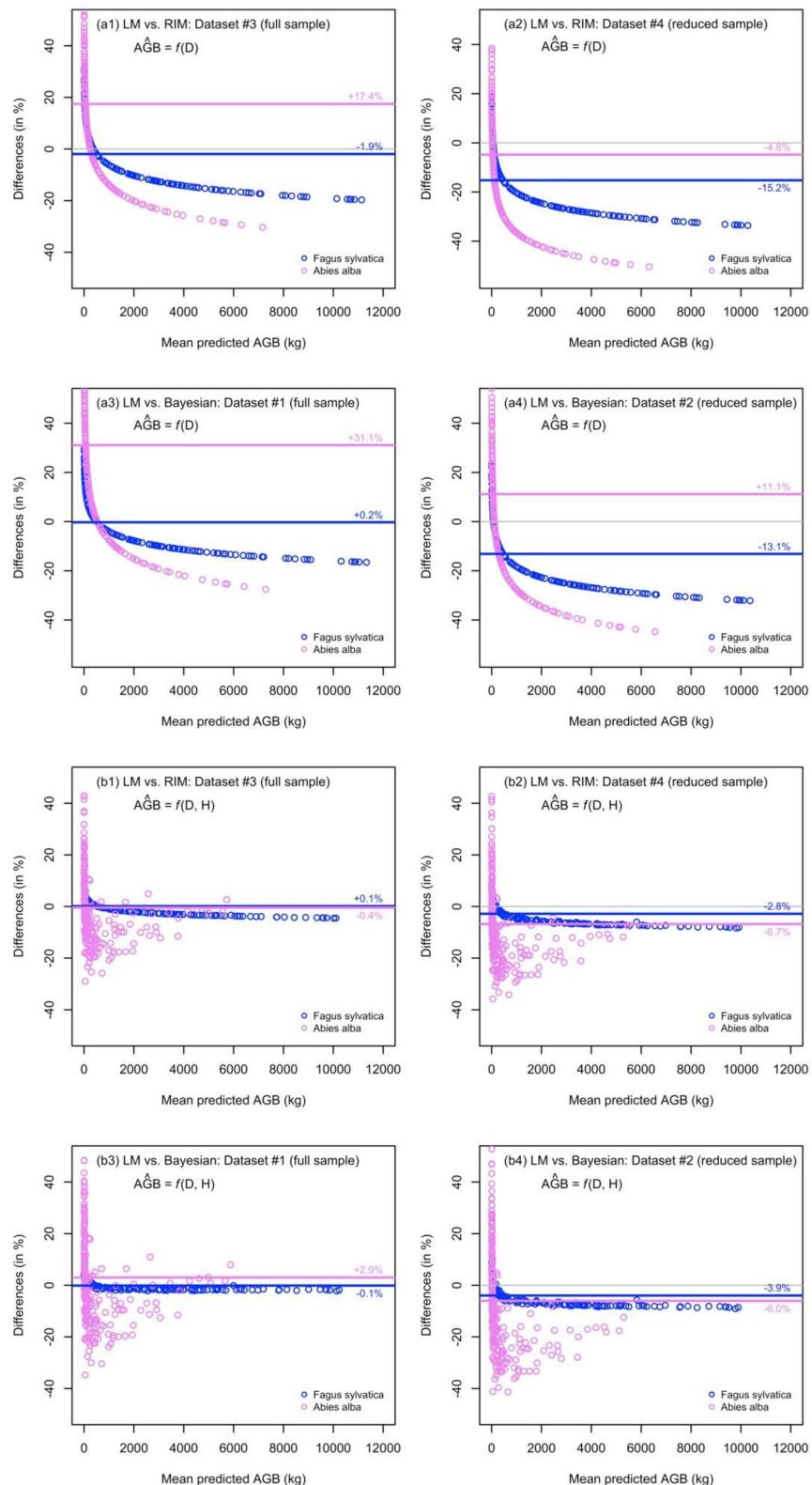


Figure 2. The Bland-Altman plots comparing individual tree AGB predictions. Note: the mean differences are calculated as the mean of relative individual differences (not differences between sum of individual AGB estimates).

Table 6. Mean biomass per hectare and its standard error by model type and predictor combinations, presented for both species and for each individual species.

Fitting Approach	Biomass Dataset	Model Type	Both Species		European Beech		Silver Fir	
			Mean (kg/ha)	SE (kg/ha)	Mean (kg/ha)	SE (kg/ha)	Mean (kg/ha)	SE (kg/ha)
LM	#1	Equation (2)	542,758	71,118	410,860	57,906	131,881	41,260
		Equation (3)	505,277	49,181	378,396	39,159	126,881	29,754
RIM	#3	Equation (2)	455,408	68,745	350,901	64,759	104,514	23,054
		Equation (3)	484,465	59,552	368,402	56,126	115,934	19,398
	#4	Equation (2)	370,296	55,126	293,328	52,952	76,972	15,297
		Equation (3)	459,387	57,947	354,853	55,409	104,537	16,992
Bayesian	#1	Equation (2)	487,053	100,743	364,564	77,672	122,523	64,197
		Equation (3)	497,354	76,448	376,447	68,229	120,921	34,488
	#2	Equation (2)	438,556	175,137	318,630	129,117	119,831	118,287
		Equation (3)	460,279	76,274	352,865	61,428	107,410	45,214

The reduced sample approach resulted in similar AGB estimates at plot level. The RIM (based on Dataset #4) predicted $459,387 \text{ kg ha}^{-1}$, whereas the Bayesian model (based on Dataset #2) predicted $460,279 \text{ kg ha}^{-1}$. However, both values are smaller compared to AGB estimate resulted from LM, by approximately 9% (Table 6). At the species level, the differences were larger for silver fir (approximately 15%–17%) than for European beech (approximately 6%).

The alternative fitting approaches based on full sample (i.e., Dataset #1 with Bayesian model and Dataset #3 with RIM) predicted plot AGB values that were closer to LM estimate (i.e., $505,277 \text{ kg ha}^{-1}$). Nevertheless, at the species level, the situation was similar: the differences to LM estimate were larger for silver fir (approximately 4%–8%) than for European beech (approximately 0.5%–2%).

4. Discussion

In this paper, we developed site-specific allometric biomass models for European beech and silver fir to be used in Șinca virgin forest, Romania. The parameters of the site-specific allometric models, developed within this study, that use D to predict AGB (Equation (2)) differ slightly from those reported, for the same species, at European level [35,38,52]. For example, for European beech, the slope (also called the scaling exponent) of the generic allometric model based on D was 2.36 [38] and 2.45 [52], whereas for our site-specific model was 2.64. The intercepts (of the models in log-scale), however, were bigger for the generic model (i.e., -1.66 and -2.07 , respectively) and smaller for our site-specific sample (i.e., -2.66). For silver fir, the differences were as large as for European beech. The scaling exponent of the generic model was 2.45 and for the site-specific model was 2.70, whereas the intercepts were -2.39 and -3.41 , respectively. For both species in this study, we reported slope values that were close to the theoretical scaling exponent value of 2.67 predicted by the “General model for the origin of allometric scaling laws” [53]. For our study, the slope estimates indicate that an increase in D by 1.0% causes an increase in AGB, of 2.64% and 2.70%, for European beech and silver fir, respectively; a lower increase is documented at European level (2.36% for European beech and 2.45% for silver fir). These larger parameters for our site indicate that trees of similar D exhibit greater AGB in Șinca compared to European averages, which may have been caused by a larger H for any given D or by a larger crown for any given D and H in the virgin forest, with respect to the averages in European forests. However, more similar parameters to our models were reported for European beech in the Netherlands, where the reported slope was 2.60 and the intercept was -2.53 [34].

When both D and H were used as predictors of AGB the effect of D on AGB was conditional on a constant H. Therefore, the parameter of D shows the increase in AGB produced by 1% increase in D while H was constant. For European beech, the scaling exponents were in line with those published in the literature; the scaling exponent of D was 2.15, which was similar to that reported by [33] and very close to the value of 2.20 reported by [36]. The scaling exponent of H (that shows the proportional increase in AGB caused by 1% increase in H, under constant D) was somehow different; a value of 0.69 was derived in this study, whereas [36] reported a value of 0.56 and [33] reported a value of 1.14.

Therefore, compared to our sample of European beech trees from Šinca forest, the trees sampled from Czech Republic seems to have a greater effect of H on AGB. The increase in H by 1%, for trees of similar D, produced more AGB in Czech Republic than in our site.

For models based on D and H, the scaling exponent of D was approximately 2.0, whereas the scaling exponent of H was smaller than 1.0 for most species [35]. Consequently, it has also been shown that the ratio between the parameter estimate of D and parameter estimate of H (i.e., the Q-ratio) is frequently larger than 2.0, usually between 3 and 4 [54]. In the case of silver fir, the parameters showed quite a different pattern compared to European beech and other species. The scaling exponent of D (i.e., 1.33), surprisingly, was smaller than the scaling exponent of H (i.e., 1.45), showing a Q-ratio of 0.92 [54]. That means, in the case of silver fir, a 1% increase in D (while H constant) produced a 1.33% increase in AGB, whereas a 1% increase in H (under constant D) produced a 1.45% increase in AGB. Although allometric biomass models for silver fir are rare, a similar anomaly was reported in a recent paper [40]. Specifically, the parameter of D was 1.06 and the parameter of H was 1.40, which may support the hypothesis that these parameters may be influenced by an atypical biomass allocation pattern at the species level (for silver fir). Other authors, e.g., [41], have also reported allometric biomass models for silver fir. However, the different model formulation does not allow us to compare the parameter estimates. Silver fir foliage tolerance under a shaded environment may be the starting point to speculate on the reported divergence. For small trees, the ratio between H and D should be higher compared to large trees, since the small trees often grow in a stronger competition. However, it is illustrated in Figure 3a that the smallest silver fir trees have a H-D ratio that is comparable to that of largest trees and is much smaller compared to that of European beech trees (despite its similar shade tolerance behavior). This result could be a consequence of ungulate browsing, which for the studied area was reported to be more frequent on silver fir than on European beech [27]. As a result, in the case of small trees, for similar D, the silver fir trees are much shorter compared to European beech (Figure 3b). Therefore, the increase in H seems to be much more accelerated for silver fir trees compared to European beech, up to about $D \approx 35$ cm, when the silver fir trees reach a maximum H-D ratio of about 0.8 (Figure 3a). For large trees, the H-D ratios become comparable for the two species. The accelerated increase in H during early development stages resulted in a larger effect of H on AGB. Therefore, we argue that in the case of silver fir, the different pattern in H-D ratio is the reason for the anomalous parameter estimates.

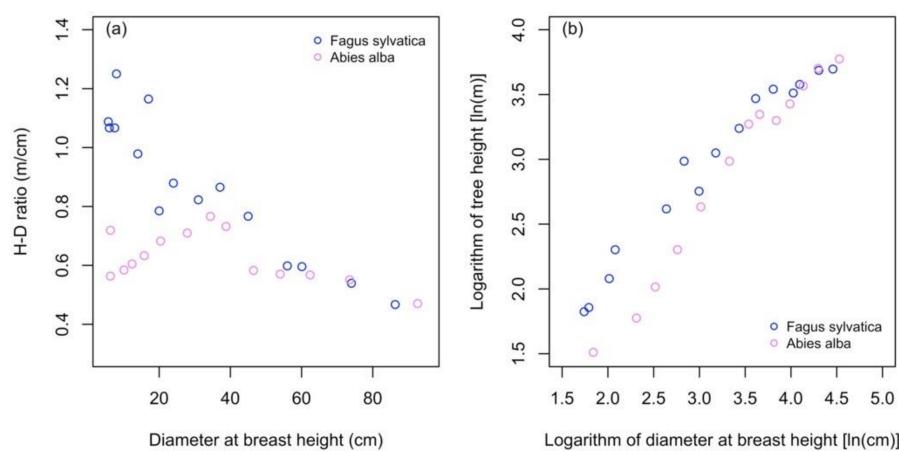


Figure 3. The H-D ratio by D (H is the tree height; D is the diameter at breast height) (a) and the relationship between H and D in log-scale (b), for European beech and silver fir (site-specific biomass datasets). Note: the plotted trees are from Dataset #1.

The obtained results indicate that a RIM or a Bayesian model can be successfully used to combine measurements available from other locations with a site-specific reduced sample of small trees, in order to calibrate the allometric model at site level. These approaches would minimize the effort for biomass

measurements, however, with a trade-off in prediction accuracy. The presented analysis takes a further step from some previous ideas in which a small sample of small trees is used to calibrate an allometric model for the entire covariate range in order to accurately predict the biomass [23].

Although both the Bayesian approach and the RIM can combine the information from other locations with the site-specific observations, there is a crucial difference between these two approaches. To apply RIM the user needs access to the raw observations from other locations, however, the Bayesian approach uses only the model outputs resulted from these observations (i.e., no raw data is required). Therefore, if availability of raw observations data is limited, then Bayesian approach should be preferred. Since Bayesian model does not use the raw data from other locations, the model is fitted based on reduced sample only. Therefore, in the presented analysis, the Bayesian model was based on 7 observations only, whereas the corresponding RIM was based on 151 trees for European beech and 101 trees for silver fir, respectively (Dataset #4; Table 4). Since Bayesian model was fitted on a smaller number of observations, it was also more difficult to accurately estimate the variance-covariance matrix, which is needed to propagate the errors from model parameters and residuals to plot level biomass prediction.

The main assumption of RIM is that the slopes of all sites are similar and only the intercepts differ between sites. Using just a few small trees to calibrate the model for the entire D range implies that the slope parameters are informed primarily by the observations from other locations, whereas the site-specific sample will inform mainly the intercept. In other words, the reduced sample of small trees is used mainly to calibrate the intercept, whereas the slope parameters are derived from the species-specific dataset (generic dataset).

A reduced sample of small trees can successfully be used to calibrate an allometric model locally, however, special attention should be given to:

- (a) The H-D ratio, which should be checked in advance. As we observed in our analysis with silver fir trees, the H-D ratio can affect the parameter estimates, which affect further the performance of small trees sample approach. Therefore, the user should check whether the H-D ratio decreases relatively linearly with the increase in tree size.
- (b) Either a random intercept model or a Bayesian model can be used with the reduced sample approach. Preference to one of the methods can be decided based on the raw data availability. Nevertheless, access to raw observations should not be an issue given the increasing trend in publication of biomass datasets, e.g., [44,55–58].
- (c) The generic biomass sample should contain as many species-specific observations as possible, including very large trees (D-range should match that of the local population for which the models are developed).
- (d) The reduced sample of small trees should contain a large enough number of trees to calibrate mainly the intercept; at least 6–7 trees should be used (the greater the number, the better the result). It is recommended that trees with $D < 5$ cm should not be used with the reduced sample approach, since the allometry of very small trees can be affected by the competition with herbaceous plants.
- (e) Using the reduced sample approach should always be performed using no less than D and H as predictors; other additional predictors can be used, because using both variables, the biomass estimates were more precise.

5. Conclusions

We developed site-specific allometric biomass models for European beech and silver fir, to be used to estimate aboveground biomass in Șinca virgin forest in Romania. Two approaches (i.e., random intercept model and Bayesian model) that use a reduced sample of small trees to calibrate the model locally were further tested. We conclude that (i) the reduced sample approach performed well, producing accurate AGB estimates; for European beech, the approach worked better than for silver fir, and we argued that this may be due to the H-D ratio anomaly that we found for silver fir; (ii) at

plot level, both the Bayesian and RIM performed equally well, although the Bayesian models resulted in larger standard errors of mean AGB per hectare, therefore, lower precision; and (iii) the models based on both D and H performed better (produced more accurate and precise AGB estimates) than those based on D only; therefore, we recommend to use both variables with the reduced sample approach.

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