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TITLE:

Development of an Individual-Tree Basal Area Increment Model using a Linear Mixed-Effects Approach

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SUMMARY:

Mixed-effects models are flexible and useful tools for analyzing data with a hierarchical stochastic structure in forestry and could also be used to significantly improve the performance of forest growth models. Here, a protocol is presented that synthesizes information relating to linear mixed-effects models.

ABSTRACT:

Here, we developed an individual-tree model of 5-year basal area increments based on a dataset including 21898 *Picea asperata* trees from 779 sample plots located in Xinjiang Province, northwest China. To prevent high correlations among observations from the same sampling unit, we developed the model using a linear mixed-effects approach with random plot effect to account for stochastic variability. Various tree- and stand-level variables, such as indices for tree size, competition, and site condition, were included as fixed effects to explain the residual variability. In addition, heteroscedasticity and autocorrelation were described by introducing variance functions and autocorrelation structures. The optimal linear mixed-effects model was determined by several fit statistics: Akaike's information criterion, Bayesian information criterion, logarithm likelihood, and a likelihood ratio test. The results indicated that significant variables of individual-tree basal area increment were the inverse transformation of diameter at breast height, the basal area of trees larger than the subject tree, the number of trees per hectare, and elevation. Furthermore, errors in variance structure were most successfully modeled by the exponential function, and the autocorrelation was significantly corrected by first-order autoregressive structure (AR(1)). The performance of the linear mixed-effects model was significantly improved relative to the model using ordinary least squares regression.

INTRODUCTION:

Compared with even-aged monoculture, uneven-aged mixed-species forest management with multiple objectives has received increased attention recently[1-3]. Prediction of different management alternatives is necessary for formulating robust forest management strategies, especially for complex uneven-aged mixed-species forest[4]. Forest growth and yield models have been used extensively to forecast tree or stand development and harvest under various management schemes[5-7]. Forest growth and yield models are classified into individual-tree models, size-class models, and whole-stand growth models[6-8]. Unfortunately, size-class models and whole-stand models are not appropriate for uneven-aged mixed-species forests, which require a more detailed description to support the forest management decision-making process. For this reason, individual-tree growth and yield models have received increased attention throughout the last few decades because of their ability to make predictions for forest stands with a variety of species compositions, structures, and management strategies[9-11].

Ordinary least squares (OLS) regression is the most commonly used method for the development of individual-tree growth models[12-15]. The datasets for individual-tree growth models collected repeatedly over a fixed length of time on the same sampling unit (i.e., sample plot or tree) have a hierarchical stochastic structure, with a lack of independence and high spatial and temporal correlation among observations[10,16]. The hierarchical stochastic structure violates the fundamental assumptions of OLS regression: namely independent residuals and normally distributed data with equal variances. Therefore, the use of OLS regression inevitably produces biased estimates of the standard error of parameter estimates for these data[13,14].

Mixed-effects models provide a powerful tool for analyzing data with complex structures, such as repeated measures data, longitudinal data, and multi-level data. Mixed-effects models consist of both fixed components, common to the complete population, and random components, which is specific to each sampling level. In addition, mixed-effects models take into account heteroscedasticity and autocorrelation in space and time by defining non-diagonal variance-covariance structure matrices[17-19]. For this reason, mixed-effects models have been extensively used in forestry, such as in diameter-height models[20,21], crown models[22,23], self-thinning models[24,25], and growth models[26,27].

Here, the main objective was to develop an individual-tree basal area increment model using a linear mixed-effects approach. We hope that the mixed-effects approach could be broadly applied.

PROTOCOL:

1. Data preparation

1.1. Prepare modeling data, which includes individual-tree information (species and diameter at breast height at 1.3 m) and plot information (slope, aspect, and elevation). In this study, the data were obtained from the 8th (2009) and 9th (2014) Chinese National Forest Inventory in Xinjiang Province, northwest China, which includes 21,898 observations of 779 sample plots. These sample plots are square-shaped with a size of 1 Mu (Chinese unit of area equivalent to 0.067 ha) and are systematically arranged over a grid of 4 km x 8 km.

NOTE: Data for modeling (basal area) increment requires at least one growth period (i.e., two observations).

1.2. Randomly divide the data into two datasets, with 80% of the data from the sample plots used for model fitting (model development dataset), which consists of 17,145 observations from 623 sample plots and 20% for model validation (model validation dataset) which consists of 4,753 observations from 156 sample plots. Descriptive statistics for the key variables used are provided in **Table 1**.

NOTE: This step of the modeling procedure can be omitted, and all data is used for model development.

[Place Table 1 here]

2. Basic model development

2.1. Consult references to identify variables that affect individual-tree basal area increments.

2.2. Select and compute variables based on the data. Generally, the individual-tree basal area increment is affected by three groups of variables: tree size, competition, and site condition[27-30].

2.2.1. Consider tree-size effects such as DBH_1, square of DBH_1 (DBH_1^2), the inverse transformation of DBH_1 ($1/DBH_1$), and the common logarithm of DBH_1 ($\log DBH_1$) or combinations of them.

2.2.2. Consider competitive effects such as both one- and two-sided indices of competition to more comprehensively quantify the level of competition experienced by a tree, as well as its social position within the stand. One-sided competition include BAL and the relative density index ($RD=DBH_1/QMD$); two-sided competition include NT, and BA.

NOTE: The distance dependent competition indices should be considered if data is available.

2.2.3. Consider site effects such as aspect (ASP), slope (SL), and EL. SL and ASP should be included using Stage's transformation[31].

2.3. Select $\log(\mathrm{DBH}_2^2 - \mathrm{DBH}_1^2 + 1)$ (DBH_2^2 denotes square of DBH_2) as the dependent variable.

2.4. Develop the basic model using the stepwise regression method. Ensure that the model is biologically reasonable and exhibits significant differences between independent variables. Utilize the variance inflation factor (VIF) to check for multicollinearity.

2.5. Leave the independent variables with $p < 0.05$ and VIF < 5 in the basic model.

2.6. Output the basic model results and the residual plot. The basic model produced here serves as a foundation for the further development of a mixed-effects model.

3. Linear mixed-effects model development with the package "nlme" in R software

3.1. Read the model development dataset and load the Package "nlme".

```
>model.development.dataset=read.csv("E:/DATA/JoVE/modelingdata.csv",
  header=TRUE)
>library(nlme)
```

3.2. Select sample plots as random effects to develop the mixed-effects model.

3.3. Fit all possible combinations of random effects with the maximum likelihood (ML) method and output the results.

```
>Model<-lme(Y~1/DBH1+BAL+NT+EL,data=model.development.dataset,
  method="ML", random =~1|PLOT)
>summary(Model)
```

3.3.1. Set random =~1 is the intercept to random parameters. Change the random statements until all combinations are fitted. For example, to set 1/DBH_1 and BAL as random parameters, the code is as follows: random =~1/DBH_1+BAL-1. In addition, in the process of fitting, the codes may report errors due to the nonconvergence of the fitted model.

3.4. Select the best model by Akaike's information criterion (AIC), the Bayesian information criterion (BIC), the logarithm likelihood (Loglik), and likelihood ratio test (LRT).

```
>anova(Model.1, Model.6)
>anova(Model.6, Model.23)
>anova(Model.23, Model.30)
```

3.5. Determine the structure of R_i. Address the heteroscedasticity and autocorrelation of R_i[32]. The R_i is written as follows:

$$R_i=\sigma^2 G_i^{0.5}\Gamma_i G_i^{0.5} \tag{1}$$

where σ^2 is an unknown scaling factor that is equal to the model residual variance, G_i is a diagonal matrix describing heteroscedasticity, and Γ_i is a matrix describing autocorrelation.

3.5.1. Observe whether the residuals have heteroscedasticity from the residual plot. If there is heteroscedasticity (the residuals have a clear pattern or trend), introduce three frequently used variance functions—the constant plus power function, the power function, and the exponential function—to model the errors variance structure.

```
>Model.30.1<-lme(Y~1/DBH1+BAL+NT+EL,data=model.development.dataset,
  method="ML",random=~1/DBH1+BAL+NT|PLOT,weights=varConstPower(form=~
  fitted(.)))
>summary(Model.30.1)
>Model.30.2<-lme(Y~1/DBH1+BAL+NT+EL,data=model.development.dataset,
  method="ML",random=~1/DBH1+BAL+NT|PLOT,weights=varPower(form=~
  fitted(.)))
>summary(Model.30.2)
>Model.30.3<-lme(Y~1/DBH1+BAL+NT+EL,data=model.development.dataset,
  method="ML",random=~1/DBH1+BAL+NT|PLOT,weights=varExp(form=~ fitted(.)))
>summary(Model.30.3)
```

3.5.2. Determine the best variance function for the model according to the AIC, BIC, Loglik, and LRT.

```
>anova(Model.30, Model.30.1)
>anova(Model.30, Model.30.2)
>anova(Model.30, Model.30.3)
```

3.5.3. Introduce three commonly used autocorrelation structures—the compound symmetry structure (CS), first-order autoregressive structure [AR(1)], and a combination of first-order autoregressive and moving average structures [ARMA(1,1)]—to account for autocorrelation.

```
>Model.30.3.1<-lme(Y~1/DBH1+BAL+NT+EL,data=model.development.dataset,
  method="ML",random=~1/DBH1+BAL+NT|PLOT,weights=varExp(form=~fitted(.)),
  corr= corCompSymm())
>summary(Model.30.3.1)
>Model.30.3.2<-lme(Y~1/DBH1+BAL+NT+EL,data=model.development.dataset,
  method="ML", random=~1/DBH1+BAL+NT|PLOT,weights=varExp(form=~ fitted(.)),
  corr=corAR1())
>summary(Model.30.3.2)
>Model.30.3.3<-lme(Y~1/DBH1+BAL+NT+EL,data=model.development.dataset,
  method="ML",random=~1/DBH1+BAL+NT|PLOT,weights=varExp(form=~ fitted(.)),
  corr=corARMA(q=1,p=1))
>summary(Model.30.3.3)
```

3.5.4. Determine the best autocorrelation structure according to the AIC, BIC, Loglik, and LRT.

```
>anova(Model.30.3, Model.30.3.2)
```

NOTE: The G_i and Γ_i cannot be defined if there is no heteroscedasticity and autocorrelation.

3.6. Output the final results of the mixed-effects model using the restricted maximum likelihood (REML) method.

```
>Mixed.model<-lme(Y~1/DBH1+BAL+NT+EL,data=model.development.dataset,
  method="REML",random=~1/DBH1+BAL+NT|PLOT,weights=varExp(form=~
  fitted(.)), corr=corAR1())
>summary(Mixed.model)
```

4. Bias correction

4.1. Transform the predicted values of basal area increment using the final model on a logarithmic scale to the original scale. However, such a linear back transformation of predicted value from a log-transformed model produces an associated log-transformation bias. To deal with the log-bias, a correction factor was derived and integrated into the prediction equation, which estimates actual predicted basal area increment for a given tree [Equation (2)]:

$$\widehat{BAI}' = \exp(\widehat{BAI} + (\sigma_{plot}^2 + \sigma^2) / 2 - 1) \qquad (2)$$

where $\widehat{BAI}$ is predicted logarithmic value of basal area increment from the model, while $\widehat{BAI}'$ is the predicted back transformed value of basal area increment for 5 years after correcting for log-transformation bias. σ^2_{plot} is variance from random effects at plot and σ^2 is residual variance.

4.2. Convert basal area increment ($\widehat{BAI}'$) to the diameter increment.

5. Model prediction and evaluation

5.1. Prepare the model validation dataset produced in section 1.2 for prediction.

5.2. Use the linear mixed-effects model to predict individual-tree basal area increment. The random components were calculated using the following best linear unbiased predictor:

$$\hat{b}_i \approx \widehat{D}\hat{Z}_i^T(\hat{Z}_i\widehat{D}\hat{Z}_i^T + \hat{R}_i)^{-1}\hat{e}_i \tag{3}$$

where $\hat{b}_i$ is a vector for the random components; $\widehat{D}$ is the variance-covariance matrix for between-plots variability; $\hat{Z}_i$ is the design matrix for the random components acting at the complementary observations; $\hat{e}_i$ is the residual vector whose components are given by the difference between the basal area increments and the predicted increments using the fixed-effects model.

5.3. Evaluate and compare the predictive ability of the basic model and the linear mixed-effects model using the following three statistical indicators[23,33].

$$R^2=1-\frac{\sum_{i=1}^{n}(obj_i-est_i)^2}{\sum_{i=1}^{n}(obj_i-\overline{obj}_i)^2} \tag{4}$$

$$\text{Bias}=\frac{\sum_{i=1}^{n}|(obj_i-est_i)|}{N} \tag{5}$$

$$\text{RMSE}=\sqrt{\frac{\sum_{i=1}^{n}(obj_i-est_i)^2}{N-1}} \tag{6}$$

where obj_i is the basal area increments, est_i is the predicted basal area increments, $\overline{obj}_i$ is the mean of observations, and N is the number of observations.

REPRESENTATIVE RESULTS:

The basic basal area increment model for *P. asperata* was expressed as Equation (7). The parameter estimates, their corresponding standard errors, and the lack-of-fit statistics are shown in **Table 2**. The residual plot is shown in **Figure 1**. Pronounced heteroscedasticity of the residuals was observed.

$$\log(\text{DBH}_2^2 - \text{DBH}_1^2 + 1) = \beta_1 + \beta_2 1/\text{DBH}_1 + \beta_3\text{BAL} + \beta_4\text{NT} + \beta_5\text{EL} + e_i \tag{7}$$

[Place Table 2 here]

[Place Figure 1 here]

There were 31 possible combinations of random-effects parameters for Equation (7). After fitting, 30 combinations reached convergence (**Table 3**). Among these 30 combinations, Model 30 of Equation (8) was selected since it yielded the lowest AIC (9083), the lowest BIC (9207), the largest LogLik (-4525), and the LRT was significantly different when compared with the other models.

$$\log(\mathrm{DBH}_2^2 - \mathrm{DBH}_1^2 + 1) = (\beta_1 + b_1) + (\beta_2 + b_2)1/\mathrm{DBH}_1 + (\beta_3 + b_3)\mathrm{BAL} + (\beta_4 + b_4)\mathrm{NT} + \beta_5\mathrm{EL} + e_i \quad (8)$$

where β_1–β_5 are the fixed effects parameters and b_1–b_4 are the random-effects parameters.

[Place Table 3 here]

The linear mixed-effects models with variance functions and correlation structures are shown in **Table 4**. According to the AIC, BIC, Loglik, and LRT, the exponential function and AR(1) were selected as the best variance function and autocorrelation structure, respectively.

[Place Table 4 here]

The final linear mixed-effects individual-tree basal area increment model was proposed using the REML method [Equation (9)]. The estimated fixed parameters, their corresponding standard errors, and the lack-of-fit statistics are shown in **Table 5**. The residual plot of the final model is shown in **Figure 2**. A significant improvement was observed in the residuals.

$$\log(\mathrm{DBH}_2^2 - \mathrm{DBH}_1^2 + 1) = (2.8086 + b_1) + (-6.24021 + b_2)1/\mathrm{DBH}_1 + (-0.1324 + b_3)\mathrm{BAL} + (-0.0001 + b_4)\mathrm{NT} - 0.0003\mathrm{EL} + e_i \quad (9)$$

where

$$b_i = \begin{bmatrix} b_1 \\ b_2 \\ b_3 \\ b_4 \end{bmatrix} \sim \mathrm{N}\left\{\begin{bmatrix} 0 \\ 0 \\ 0 \\ 0 \end{bmatrix}, \psi_i = \begin{pmatrix} 0.1302 & -0.2088 & -0.0271 & -1.59\mathrm{E}-05 \\ -0.2088 & 6.1589 & -0.0552 & -2.28\mathrm{E}-04 \\ -0.0271 & -0.0552 & 0.0143 & 1.19\mathrm{E}-05 \\ -1.59\mathrm{E}-05 & -2.28\mathrm{E}-04 & 1.19\mathrm{E}-05 & 1.73\mathrm{E}-08 \end{pmatrix}\right\}$$

$$e_i \sim \mathrm{N}(0, R_i = 0.0886 G_i^{0.5} \Gamma_i G_i^{0.5})$$

$$G_i = \exp(-0.0104 y_i);\ \Gamma_i = \mathrm{AR}(1),\ \rho = 0.04245$$

[Place Table 5 here]

[Place Figure 2 here]

Table 6 listed the three prediction statistics of Equation (7) and Equation (9). Compared with the basic model, the performance of the linear mixed-effects model was significantly improved.

[Place Table 6 here]

FIGURE AND TABLE LEGENDS:

Figure 1. Residual plot derived from Equation (7). The residuals have a clear trend, i.e., pronounced heteroscedasticity of the residuals was observed.

Figure 2. Residual plot derived from Equation (9). Compared with Figure 1, a significant improvement was observed in the residuals.

Table 1. Summary statistics for fitting and validation data. DBH_1: initial diameter at breast height at 1.3 m (DBH), DBH_2: DBH measured after 5 years of growth, QMD: quadratic mean diameter, ID: diameter increment for 5 years ($DBH_2 – DBH_1$), BAL: the basal area of trees larger than the subject tree (the subject tree: the tree which was calculated the competition indices), NT: the number of trees per hectare, BA: basal area per hectare, EL: elevation, S.D.: standard deviation.

Table 2. Basic model results. The estimated parameters, their corresponding standard errors, and the lack-of-fit statistics derived from Equation (7). VIF: variance inflation factor, AIC: Akaike's information criterion, BIC: Bayesian information criterion, and Loglik: logarithm likelihood.

Table 3. Evaluation indices of each linear mixed-effects model. ▲: random-effects parameter was selected for fitting; LRT: likelihood ratio test.

Table 4. Comparisons of the linear mixed-effects individual-tree basal area increment models performance with different variance functions and different correlation structures. CS: compound symmetry structure, AR(1): a first-order autoregressive structure, ARMA(1,1): a combination of first-order autoregressive and moving average structures; [a] Likelihood ratio was calculated for Model 30; [b] Likelihood ratio was calculated for Model 30.3.

Table 5. Mixed-effects model results. The estimated fixed parameters, their corresponding standard errors, and the lack-of-fit statistics derived from Equation (9).

Table 6. Evaluation indices of the basic model and the linear mixed-effects model. A significant improvement was observed from the three prediction statistics.

DISCUSSION:

A crucial issue for the development of mixed-effects models is to determine which parameters can be treated as random effects and which should be considered fixed effects[34,35]. Two methods have been proposed. The most common approach is to treat all parameters as random effects and then have the best model selected by AIC, BIC, Loglik, and LRT. This was the method employed by our study[35]. An alternative is to fit basal area increment models for every sample plot with OLS regression. Parameters that have high variability and less overlap in confidence intervals across the sample plots among these models can be regarded as random ones[17].

To account for heteroscedasticity and autocorrelation, three variance functions and three autocorrelation structures were introduced. Consistent with the results of Calama and Montero[17] and Uzoh and Oliver[27], the exponential function and AR(1) were determined to be the optimal variance function and autocorrelation structure, respectively.

There are two most commonly used methods in statistical software programs to estimate mixed-effects models: ML and REML[17]. ML is more flexible because models that differ in either their fixed effects or their random effects can be directly compared. However, the estimator for the variance obtained by ML is biased because ML does not account for the fact that the intercept and slope are estimated as well (as opposed to being known for certain). REML can provide superior ML estimates. Therefore, when the model comparisons were completed, the REML method was used for final model fitting[17,18,36].

In this study, we found that the individual-tree basal area increment model for *P. asperata* using a linear mixed-effects approach represented a significant improvement over the basic model using OLS regression. Mixed-effects models provide an efficient tool for modeling data with hierarchical stochastic structure, making it widely applicable in fields such as agriculture, biology, economics, manufacturing, and geophysics.

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DISCLOSURES:

The authors have nothing to disclose.

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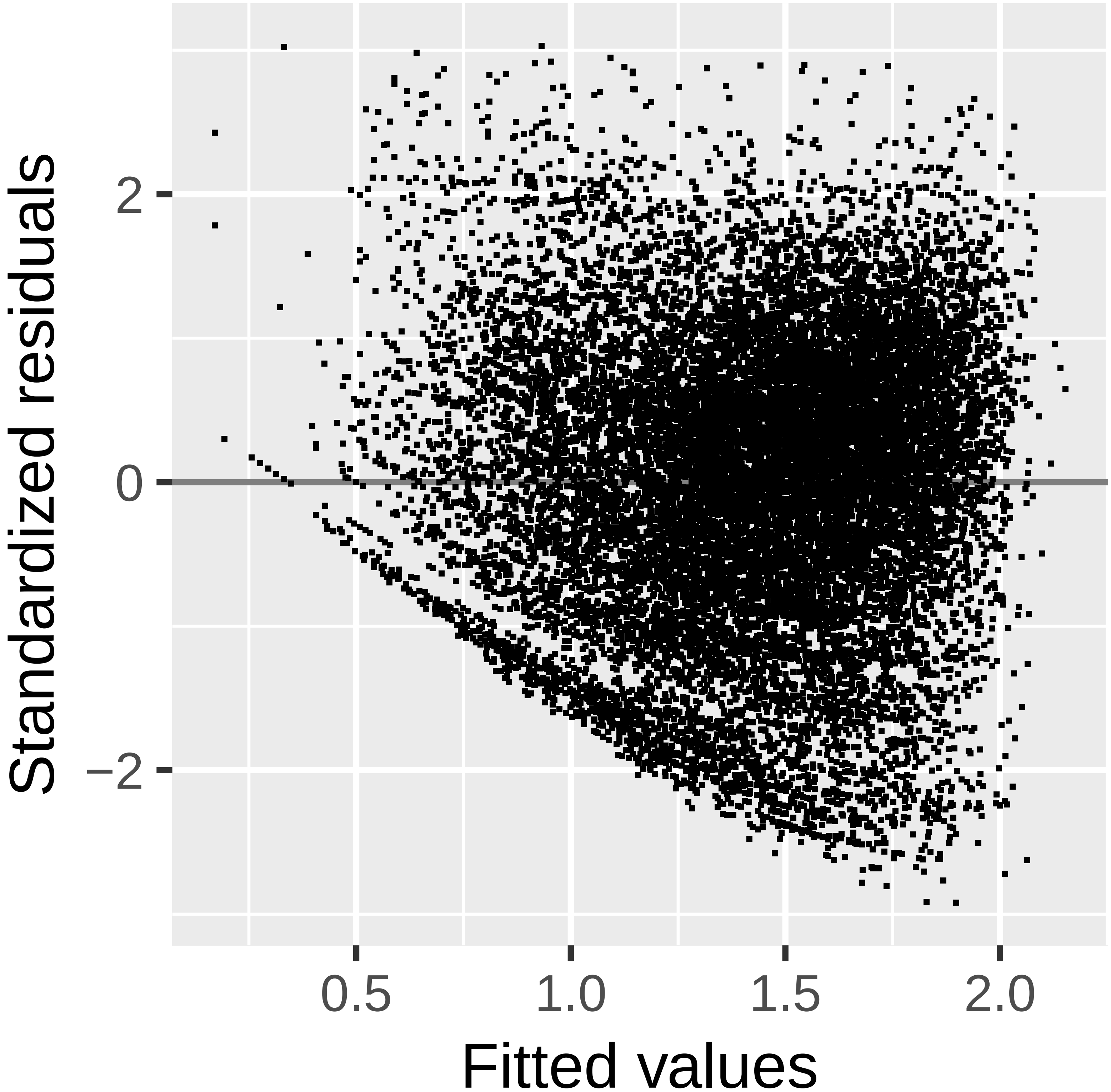
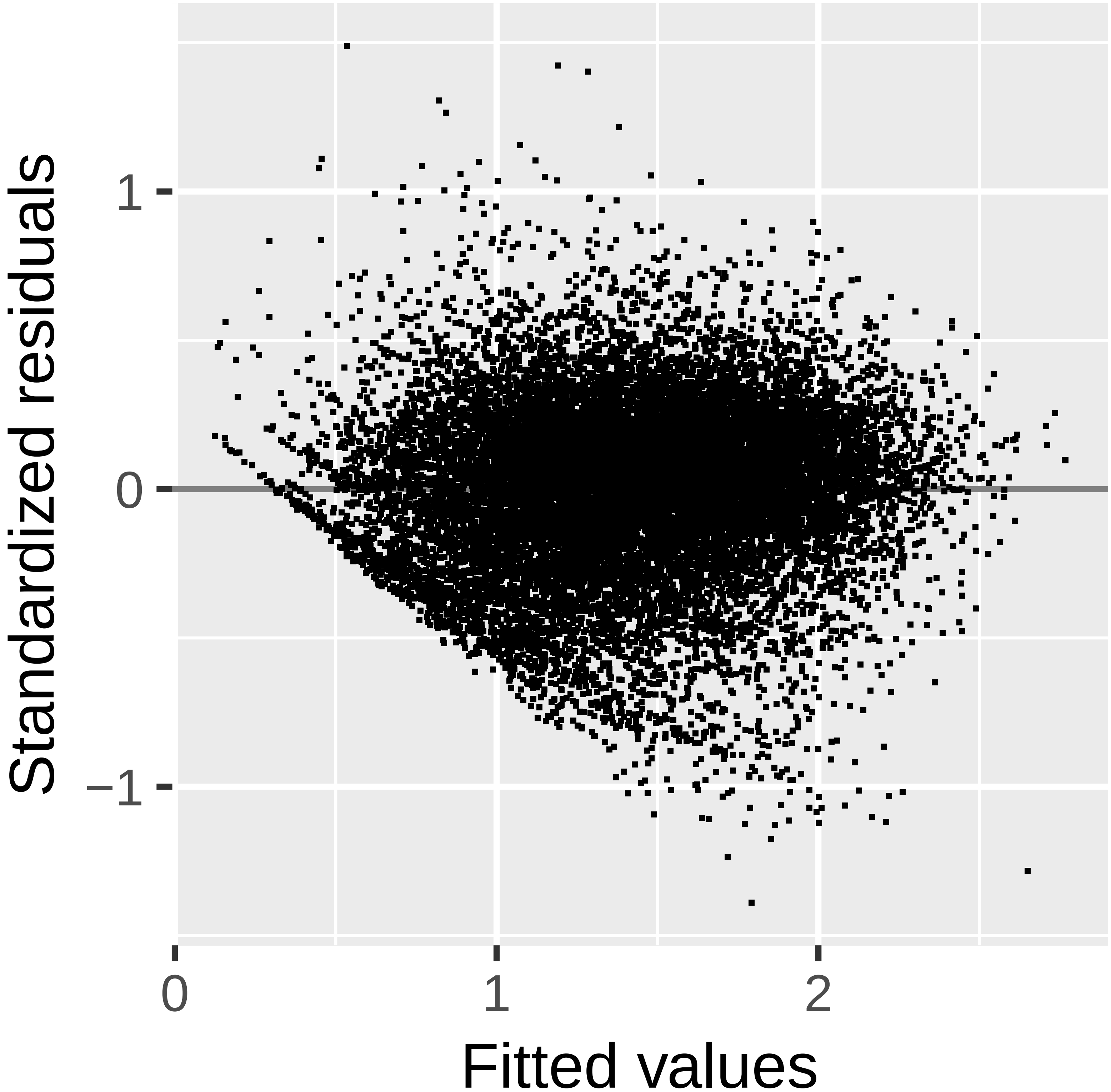
36 Pinheiro, J. C., Bates, D. M. Mixed-effects models in S and S-Plus. *Publications of the American Statistical Association.* **96** (455), 1135-1136 (2000).


Standardized residuals
2
0
−2
0.5
1.0
1.5
2.0
Fitted values


Standardized residuals
1
0
−1
0
1
2
Fitted values

Variables	Fitting data				Validation data			
	Min	Max	Mean	S.D.	Min	Max	Mean	S.D.
DBH_1 (cm)	5	124.8	19.9	13.2	5	101.5	19.5	13.4
QMD (cm)	6.7	82.3	22.5	8.5	9.2	73.3	21.8	9.2
ID (cm)	0.1	14.4	1.1	1	0.1	16.9	1	1.1
BAL (m^3)	0	5.2	1.7	0.9	0	5.4	1.7	1
NT (trees/ha)	14.9	3642	1072	673.7	14.9	3418	1205	829.3
BA (m^2/ha)	0.1	77.5	34.2	13.9	0.1	80.6	34.5	15.3
EL (m)	2	3302	2189	340.3	1441	3380	2256	308.3

	Estimate	Standard error	t-test	P-value	VIF
int	2.41	2.26E-02	106.78	<2e-16	-
$1/DBH_1$	-5.84	7.57E-02	-77.19	<2e-16	1.12
BAL	-9.54E-02	3.34E-03	-28.54	<2e-16	1.08
NT	-1.58E-04	4.74E-06	-33.31	<2e-16	1.12
EL	-1.10E-04	9.07E-06	-12.13	<2e-16	1.05
		AIC = 16789			
		BIC = 16836			
		Loglik = -8389			

Model	Random parameters					AIC	BIC	LogLik	LRT	P-value
	int	$1/DBH_1$	BAL	NT	EL					
1	▲					10175	10230	-5081		
2		▲				11630	11684	-5808		
3			▲			11772	11826	-5879		
4				▲		10556	10611	-5271		
5					▲	10259	10313	-5123		
6	▲	▲				9268	9338	-4625	911.1 (1 vs 6)	<.0001
7	▲		▲			9411	9481	-4697		
8	▲			▲		10179	10249	-5081		
9	▲				▲	10179	10249	-5080		
10		▲	▲			10829	10899	-5406		
11		▲		▲		9532	9601	-4757		
12		▲			▲	9335	9405	-4659		
13			▲	▲		9803	9873	-4892		
14			▲		▲	9465	9535	-4723		
15				▲	▲	10200	10270	-5091		
16	▲	▲	▲			Nonconvergence				
17	▲	▲		▲		9271	9364	-4624		
18	▲	▲			▲	9274	9367	-4625		
19	▲		▲	▲		9417	9510	-4696		
20	▲		▲		▲	9417	9510	-4697		
21	▲			▲	▲	10184	10277	-5080		
22		▲	▲	▲		9332	9425	-4654		
23		▲	▲		▲	9132	9225	-4554	142.7 (23 vs 6)	<.0001
24		▲		▲	▲	9293	9386	-4634		
25			▲	▲	▲	9443	9536	-4709		
26	▲	▲	▲	▲		9083	9207	-4525		
27	▲	▲	▲		▲	9086	9210	-4527		
28	▲	▲		▲	▲	9280	9404	-4624		
29	▲		▲	▲	▲	9425	9549	-4696		
30		▲	▲	▲	▲	9083	9207	-4525	56.8 (30 vs 23)	<.0001
31	▲	▲	▲	▲	▲	9091	9254	-4525		

Model	Variance function	Correlation structure	AIC	BIC	LogLik	LRT	P-value
30	No	Independent	9083	9207	-4525		
30.1	ConstPower	Independent	9075	9215	-4520	11.8[a]	0.0028
30.2	Power	Independent	9073	9205	-4520	11.7[a]	6.00E-04
30.3	Exponent	Independent	9073	9204	-4519	12.3[a]	5.00E-04
30.3.1	Exponent	CS	Nonconvergence				
30.3.2	Exponent	AR(1)	9050	9189	-4507	24.9[b]	<.0001
30.3.3	Exponent	ARMA(1,1)	Nonconvergence				

	Estimate	Standard error	t-Test	P-value
int	2.8086	7.99E-02	35.14	<0.01
$1/DBH_1$	-6.2402	1.56E-01	-40.01	<0.01
BAL	-0.1324	8.07E-03	-16.41	<0.01
NT	-0.0001	2.26E-05	-4.921	<0.01
EL	-0.0003	3.32E-05	-7.86	<0.01
		AIC = 9105		
		BIC = 9244		
		Loglik = -4535		

Model	Bias	RMSE	R^2
Basic model	0.297	0.377	0.479
Mixed-effects model	0.221	0.286	0.699

Name of Material/Equipment	Company	Catalog Number	Comments/Description
Computer	acer		
Microsoft Office 2013			
R x64 3.5.1			

Dear Editor and Reviewers:

Thank you for your comments concerning our manuscript entitled "Individual-tree basal area increment model for *Picea asperata* using a linear mixed-effects approach" (ID: JoVE60827R2). Those comments are all valuable and very helpful for revising and improving our paper, as well as the important guiding significance to our researches. We have studied comments carefully and have made correction which we hope meet with approval. Revised portion are marked in red in the paper.

Thank you so much!

Jinghui Meng

Editorial comments:

Changes to be made by the Author(s):

1. Please take this opportunity to thoroughly proofread the manuscript to ensure that there are no spelling or grammar issues. The JoVE editor will not copy-edit your manuscript and any errors in the submitted revision may be present in the published version.

Responds: We have thoroughly proofread the manuscript to ensure that there are no spelling or grammar issues.

2. Please upload each Figure individually to your Editorial Manager account. Please combine all panels of one figure into a single image file.

Responds: We have uploaded each Figure individually to my Editorial Manager account.

3. Please submit each figure as a vector image file to ensure high resolution throughout production: (.psd, ai, .eps, .svg).

Responds: We have submitted each figure as a vector image file (.eps) to ensure high resolution throughout production.

4. Please revise the table of the essential supplies, reagents, and equipment. The table should include the name, company, and catalog number of all relevant materials in separate columns in an xls/xlsx file. Please sort the Materials Table alphabetically by the name of the material.

Responds: We have revised the table of the essential supplies, reagents, and equipment.

5. Please remove the embedded figure(s) from the manuscript. All figures should be uploaded separately to your Editorial Manager account. Each figure must be accompanied by a title and a description after the Representative Results of the manuscript text.

Responds: We have removed the embedded figure(s) from the manuscript.

6. Please remove the embedded Table from the manuscript. All tables should be uploaded separately to your Editorial Manager account in the form of an .xls or .xlsx file. Each table must be accompanied by a title and a description after the Representative Results of the manuscript text.

Responds: We have removed the embedded Table from the manuscript.

7. Please ensure that all text in the protocol section is written in the imperative tense as if telling someone how to do the technique (e.g., “Do this,” “Ensure that,” etc.). The actions should be described in the imperative tense in complete sentences wherever possible. Avoid usage of phrases such as “could be,” “should be,” and “would be” throughout the Protocol. Any text that cannot be written in the imperative tense may be added as a “Note.” However, notes should be concise and used sparingly. Please include all safety procedures and use of hoods, etc.

8. The Protocol should contain only action items that direct the reader to do something. Please move the discussion about the protocol to the Discussion.

9. Please add more details to your protocol steps. Please ensure you answer the “how” question, i.e., how is the step performed? Alternatively, add references to published material specifying how to perform the protocol action.

Responds: We have made some changes following your suggestions.

10. Please provide all user input commands so that the protocol fits our publication standard.

Responds: We have provided all user input commands.

Reviewers' comments:

Reviewer #1:

The authors do a nice work on showing the readers how to develop the mixed effects model of tree growth. What the modelers should account for when they get the data sets. It is helpful for modelers when they model forest growth. Also the authors showed the codes and explained each code in line. The manuscript is easily read and well organized. I recommend accept the manuscript.

Responds: Thank you!

Some minor comments:

L154: What is the X1.DBH1?

Responds: It should be $1/DBH_1$, we have corrected the error in the manuscript.

L222: What the former method the authors used is "ML", but here used "REML"

Responds: ML is more flexible because models that differ in either their fixed effects or their random effects can be directly compared. We therefore chose "ML" as the former method. However, the estimator for the variance obtained by ML is biased because ML does not account for the fact that the intercept and slope are estimated as well (as opposed to being known for certain). REML can provide superior ML estimates. Therefore, when the model comparisons were completed, the REML method was used for final model fitting. In the Discussion section, we have discussed this question.

Reviewer #2:

General comments

Using an exemplary dataset this paper presents instructions on how to conduct mixed effects modeling to develop a linear mixed model predicting tree basal are increment. Clarification is needed for some of the modeling steps, i.e. provision of more details as well as additional coding. See details below.

Moreover, I suggest to

1) switch to a nonlinear approach, i.e. y=exp(b0+b1*DBH+b2*ln(DBH)+b3*….), because i) the response variable does not have to be transformed, ii) predictions not re-transformed, and iii) it allows for more flexibility, i.e. a plausible, sigmoidal curve of the predicted response variable.

Responds: We totally agreed with your suggestion. In many ways, nonlinear models are superior to linear models. However, we chose the linear model because of the following considerations: i) the nonlinear models use iterative optimization procedures to compute the parameter estimates, which require providing starting values for the unknown parameters. It might be difficult to determine the proper starting values in certain conditions. ii) when considering too many random parameters in the mixed-effects model, the linear models can more easily converge and are much simpler to handle than the nonlinear models. iii) generally, the linear models were more extensively used than the nonlinear models to produce individual tree growth model. Therefore, the linear mixed-effects model is used to predict the individual trees basal area increment.

2) Also, modeling/predicting DBH increment appears to result in more accurate findings compared to BA increment (see e.g. Weiskittel et al. 2011).

Responds: When developing the basic model, we evaluated the frequently used dependent variables, namely the diameter increment ($DBH_2 - DBH_1$), squared diameter increment (DBH_2^2- DBH_1^2), squared diameter increment plus a constant value of one (DBH_2^2- DBH_1^2 + 1), and the common logarithmic transformation of each using absolute bias (Bias), root mean square error (RMSE), and the coefficient of determination (R^2). Additionally, residual plots were also produced to inspect the homogeneity of the variance and normality of the residuals. After comparing and testing these dependent variables, log(DBH_2^2- DBH_1^2 + 1) was selected as the dependent variable for our basal area increment model since it performed best in terms of the normality and homogeneity of the residuals, and lack-of-fit statistics. Similar results were also reported by many research (Calama and Montero, 2005; Adame et al., 2008 and Lhotka and Loewenstein, 2011).

3) The title should emphasize that this is a method paper. The name of the species thus should be omitted.

Responds: We have omitted the name of the species and changed the title.

4) And details on the dataset provided appear in the abstract and text only. There should be a paragraph that describes and summarizes the provided dataset.

Responds: We have added the information that describes and summarizes the provided dataset in the manuscript (L103-107, L113-116 and Table 1).

5) In addition, I think a brief description on how to derive the OLS (basic) model should be presented too. The authors should cite Zuur et al. 2009. Mixed effects models and extensions in ecology with R. Springer Science & Business Media.

Responds: In Protocol section (2. Basic model development), we have provided the steps for the OLS (basic) model development. However, because of the limit on the amount of content, we were unable to present more detailed information.

A revised manuscript that addresses the outlined shortcomings and deficiencies might be suitable for publication in JoVE.

Specific comments

59-60 maybe recently but not in general

Responds: We have changed the description (L59-60).

68-71 throughout the last few decades but not overall

Responds: We have changed the description (L69-72).

104 Data for modeling (BA) increment…

Responds: We have made some changes following your suggestion (L109).

106- This step of the modeling procedure should be optional (or omitted) in my opinion. There is disagreement whether reducing the number of observations for model development in order to create an independent dataset for validation purposes is really beneficial. See Kozak & Kozak CJFR 33(6): 976-987.

Responds: We have made some changes following your suggestion (L118-119).

115- tree vigor is missing, i.e. crown ratio, height diameter ratio

Responds: We totally agreed with your comments, unfortunately our national forest inventory (NFI) data, which was used to develop the model in this study, did not contain crown and tree height information.

119- or combinations of them

Responds: We have added the information following your suggestion (L133-134).

123- It is beneficial and advisable to mention that competition can be separated into and quantified as one- and two-sided (among others) and that a metric of either group should be part of the model (Weiskittel et al. 2011). Crown competition factor and crown competition factor in larger trees can also be listed.

Responds: We have considered one-sided (BAL, RD) and two-sided (NT, BA) competition when developing the basic model following your suggestion, and BAL and NT were included in the model to represent the comprehensive effects of aboveground and belowground competition. Unfortunately, crown competition factor and crown competition factor in larger trees can not be listed since our data did not contain crown information (L136-139).

133 Provide R function and code for the calculation of VIFs.

Responds: the R function and code for the calculation of VIFs as follows. However, because of the limit on the amount of content, the code was not provided in the manuscript.

```
>library(car)
>vif(Basic.model)
```

157-158 What do the authors mean by 'Replace this part until all combinations are fitted.'? Please clarify.

Responds: We have made some changes in the manuscript (L174-176).

173 Provide details and code on 'Test for heteroscedasticity in the residual plot.'

Responds: We have made some changes about "heteroscedasticity" (L193-194).

178- Provide details and code on how to address heteroscedasticity in specific explanatory variables, e.g. varExp(form=~DBH)

Responds: We have provided details and code in the manuscript (L198-207).

219- It is unclear how this works: how does the function know where autocorrelation needs to be addressed? The authors may want to mention that autocorrelation can also be addressed in the random effects, e.g. plots nested within years: …|year/plot

Responds: Yes, we want to mention that autocorrelation can also be addressed in the random effects, e.g. plots nested within years: …|year/plot. Because the modeling data in this study was obtained from repeated measurements, the autocorrelation should be addressed. Introducing random effects could correct autocorrelation. In addition, we further introduced three correlation structures to refine our model. Finally, based on the lack-of-fit statistics, AR(1) were determined as the optimum option for correcting the autocorrelation.

241 Please provide reference for calculation of R squared.

Responds: We have provided reference for calculation of R squared (L276).

255 Information on how to specify the random effects structure during model development is missing and needs to be provided.

Responds: We have made some changes in the manuscript (L176-178).

274-275 Absolute values of the residuals decreased but the overall pattern (normality!?) did not. Please clarify.

Responds: We have changed the description in the manuscript (L310-311).

Reviewer #3:

Manuscript Summary:

The manuscript is presented well with good protocol and steps for the development of effective model for the individual tree basal area. The manuscript once published would add value to the field of forest growth models.

Major Concern:

1. The manuscript as per the title should clearly reflect the final model developed and its applicability, which is currently missing in the manuscript. If the manuscript is only about comparing methodology/protocol to be used then the title of the manuscript needs to be changed.

Responds: We have changed the title into " Development of an individual-tree basal area increment model using a linear mixed-effects approach".

2. The biological processed that effect tree growth are non-linear. Most growth models in the past have used multiple linear regression (after transforming the dependent variable) but later studies have shown that transforming back the dependent variable results in potential bias. Therefore, various methods such as non-linear regression, generalized linear regression (glm) were used which doesn't require transformation of the dependent variable. In the current manuscript, it seems log transformation is applied to the dependent variable (DBH), which might have introduced biases while transforming. Such biases and how it was corrected needs to be clearly indicated.

Responds: In this study, we used log-transform the dependent variable to account for heterogeneity. Thank you for your reminding of the log-bias, we dealt with the log-bias in the revision (4. Bias correction：L247-260).

3. Similarly, several methods exist to correct the non-linear function of tree growth. Please clearly explain why mixed effects model is better and whether the authors considered other methods such as glm and spline function and if these were compared as well.

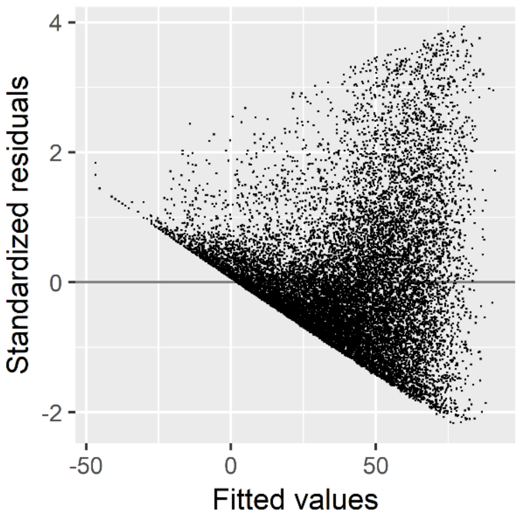
Responds: In this study, we focused on the development of a linear mixed-effect model for basal area increment, so we did not consider and compare other methods.

4. The manuscript fails to describe why and how the competition indices of basal area of trees than the subject tree (BAL), number of trees per hectare (NT) and relative density index were chosen for the development of model. These competition indices are classified as the distance independent competition indices and are more suitable for even-aged forests. The manuscript conveys that model is developed for un-even aged mixed forests and in such cases, distance dependent competition indices would be more appropriate. Please clearly indicate the reasons for using the distance independent indices.

Responds: We totally agree with you that distance dependent competition indices would be more appropriate for un-even aged mixed forests. Unfortunately, the main reason for ignoring distance dependent competition indices was related to limitations from the dataset in the study, since there is no coordinate information. For better generality or applicability of the model, we selected the distance-independent competition indices.

5. All growth models face the problem of heteroscedasticity. The problem increases as the DBH or height increases, which means the prediction variabilities increases as the tree size increases resulting in to a funnel shaped residual plots. This is usually corrected through linear transformation of the dependent variable or through other models such as spline function. In this manuscript, the log transformation and lme is used. The residual plots (figure 1 and figure 2) seems to be generated straight from the model where log transformation of the dependent variables still exists. The actual residual plots after back transforming the dependent variable have to be generated (which is predicted DBH - Observed DBH without log function) and then plot against DBH (at least). These residual plots will show whether there is any heteroscedasticity in the model.

Responds: We have generated the actual residual plots following your suggestions as follows. Pronounced heteroscedasticity of the residuals was observed. However, in order to compare the improvement of the mixed-effects model, we retained the contents of the manuscript (Figure 1 and Figure 2).



6. The manuscript suggests individual basal area model, while the manuscript uses DBH as the dependent variable. Please specify why DBH is better than Basal area.

Responds: In this study, we used basal area increment, i.e., log(DBH_2^2 - DBH_1^2 +1) (DBH_2^2 denotes square of DBH_2) as the dependent variable. When developing the basic model, we evaluated the frequently used dependent variables, namely the diameter increment (DBH_2 – DBH_1), squared diameter increment (DBH_2^2 - DBH_1^2), squared diameter increment plus a constant value of one (DBH_2^2 - DBH_1^2 + 1), and the common logarithmic transformation of each using absolute bias (Bias), root mean square error (RMSE), and the coefficient of determination (R^2). Additionally, residual plots were also produced to inspect the homogeneity of the variance and normality of the residuals. After comparing and testing these dependent variables, log(DBH_2^2 - DBH_1^2 + 1) was selected as the dependent variable for our basal area increment model since it performed best in terms of the normality and homogeneity of the residuals, and lack-of-fit statistics.

Minor Concern:

1. It would have been better if data and site description are provided, which is currently

lacking.

Responds: We have added the information that describes and summarizes the provided dataset in the manuscript (L103-107, L113-116 and Table 1).

2. Please re-look at the title of the manuscript

Responds: We have changed the title of the manuscript.

3. In all the equations, please clearly indicate what each parameter means? Like what is DBH (with superscript 2 and subscript 2) means?

Responds: We have indicated the means of each parameter in all the equations.

4. In all table, please clearly indicate actual p values

Responds: In all table, we have made some changes.

Reviewer #4:

Manuscript Summary:

Dear Editorial Board and authors of the manuscript. Thanks to giving a chance to make a review of the manuscript "Development of an individual-tree basal area increment model using a linear mixed effect model". The text is readable for me. However, I have some comments and I would ask authors to consider them. Description of the process in model development is clear for me and it is always hard to describe it in understandable and complex way. However, this modelling "piece of cake" that authors are dealing with is valuable for other researchers. After considering my comments and from other reviewers I would agree with publishing.

Major Concerns:

The research topic is actual, but I miss one important chapter there - evaluation of sufficient amount of data. It should be included in discussion as a paragraph or (better) to add it into the process of described work flow.

Responds: We have added the information that describes and summarizes the provided dataset in the manuscript (L103-107, L113-116 and Table 1).

Minor Concerns:

At the end of abstract, there should be a "…first-order autoregressive structure (AR(1))", because others (AIC, BIC…) are here in abstract explained or are in key words (OLS).

Responds: We have added the information following your suggestion.

I would prefer to add some diagram of work flow, because in present form, the reader might be lost in process.

Responds: In the revised version, we have changed the modeling steps to make it easier for readers to understand, unfortunately due to the limitation of the manuscript instructions, we did not provide some diagram of work flow.

L132 QMD (not explained = quadratic mean diameter)

Responds: We have added the explanation.

L138 "Forest structural diversity effects include…"

Equation 4 - I found formula for Simpson´s diversity index in other literature, but in form how it is here in manuscript, should not it be 1/ instead of 1- ?

Equations 3 and 4 - S and n should be explained better to understand differences. In present form, it is not sufficiently clear.

Responds: In the latest version of the manuscript, we have deleted the information about "Forest structural diversity effects".

L154 5-year growth appeared suddenly here and reader might be confused (I would add this information to NOTE in point 1.1).

Responds: We have made some changes following your suggestion.

L155 DDS is square diameter increment. I would use abbreviation SDI (as square diameter increment), since basal area increment also contain I as INCREMENT.

Responds: We have removed this abbreviation.

L224 "ower" to "power", right?

Responds: We have corrected this error.

Table 4 - why there is number LogLik with 3 decimal places for model 1?

Responds: We have corrected this error.

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CERTIFICATE OF LANGUAGE EDITING

The English writing of the following manuscript was carefully edited by a native English speaker.

Manuscript Information

ID	LE202004070048
Editing date	2020-04-09
Title	Individual-tree basal area increment model for Picea asperata using a linear mixed-effects approach
Corresponding author	Jinghui Meng
Language writing before editing	☐ Very poor ☐ Poor ☐ Fair ■ Good ☐ Very good ☐ Excellent
Recommendation after language editing	☐ Submitting to target journal directly ■ Submitting to target journal after minor revision ☐ Re-editing required after major revision ☐ Not suitable for publication
Overview comments	Thank you for using editorbar. I found this manuscript to be very well written. I have edited to improve the word choice, flow, and the naturalness of the phrasing. I have also ensured that there were no grammatical errors and have enhanced sentence structure. I included several comments to note where improvements could be made. Please read my comments to ensure that I have not altered your intended meaning. Best of luck on the manuscript. Sincerely, Chris A.

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