



Research paper

Evaluation of predictive models for Douglas-fir bark thickness at breast height following 12 biomass harvest treatments

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ABSTRACT

Foresters often require an estimation of bark thickness from a reference height (typically breast height) to accurately estimate the bark or wood volume of a tree. Various models for estimating the bark thickness of interior Douglas-fir (*Pseudotsuga menziesii* var. *glauca*) from measured dbh (diameter at breast height) were evaluated. Sample trees were from northern Rocky Mountain mixed conifer stands that had been subjected to four levels of experimental woody biomass harvesting. Among simple linear, nonlinear, and segmented linear mixed effects models, the segmented linear model performed best. A join point (where the linear equations are linked) for the segmentation was statistically detected at approximately 19.0 cm dbh. The join point seems to indicate the size at which juvenile Douglas-fir trees boost the production of bark tissue, perhaps as those trees express dominance over competing understory vegetation. Woody biomass utilization level had no impact on bark thickness, indicating that the bark:dbh relationship does not depend on biomass utilization intensity. The study results enable accurate bark thickness estimation for interior Douglas-fir in this region, and suggest several silvicultural applications for juvenile Douglas-fir stand management.

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1. Introduction

Estimations of tree bark volume have long been pursued because foresters must know merchantable log volumes, and subtracting bark volume from outside bark volume provides the most convenient calculation method [1]. Numerous mathematical equations accounting for each species' bark thickness have been developed over the past decades (e.g., [2–4]). They generally predict the bark thickness at any given tree height from bark thickness at a certain reference height (typically, diameter at breast height, or dbh; 1.4 m). Accurate prediction of whole tree bark and log volumes are predicated upon the accurate estimate of bark thickness from measured diameter at the reference height, because error in that estimate is expressed and thereby amplified throughout the log.

In an ongoing study of biomass utilization at Montana's Coram Experimental Forest [5,6], we have been quantifying forest vegetation and productivity responses to a variety of biomass harvest treatments. In that work, determining accurate estimates of forest biomass by segregated components is a primary objective, and one

that requires a robust bark predictive model, particularly for Rocky Mountain Douglas-fir (*Pseudotsuga menziesii* (Mirb.) Franco var. *glauca* (Beissn.) Franco). Previous research has produced a variety of models to predict the bark thickness of Douglas-fir using diameter at breast height. For coastal Douglas-fir, Johnson [7] developed a segmented linear equation for the estimation of bark thickness from dbh. Larsen and Hann [8] formulated a nonlinear equation for bark thickness in a similar region. For interior Douglas-fir, Spada [9], Monserud [10], and Dolph [11] each constructed simple linear regression models. Monserud [10] and Dolph [11] found different results among linear models across the regions, implying the necessity of locally-constructed equations for the best predictive performance.

During field surveys at Coram Experimental Forest, we observed an apparent difference in the ratio of bark thickness to tree size between small and large Douglas-fir trees. We theorized that the simple linear approach might be inappropriate, and that segmented linear regression analysis might yield a better predictive model for Douglas-fir in the northern Rocky Mountains. Segmented linear regression has been used to construct stem taper equations (e.g., [2,12,13]). In contrast to more complex models, it provides a simpler method by producing different equations within different

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regions of the explanatory variable space [14]. Two (or more) different linear equations are fitted simultaneously under a constraint: the “join point,” where the linear equations are linked. If it is possible to estimate the join point, then the model can be constructed as multiple linear forms with simplicity and robustness. This study considered segmented, simple linear and nonlinear mixed effects regression to determine the best model for predicting the bark thickness of Douglas-fir from breast-height diameter (dbh) in northern Rocky Mountain forests, and to evaluate whether the relationship of bark thickness to dbh differs significantly among biomass utilization treatments and regeneration harvests.

2. Methods and materials

2.1. Study site

This study was conducted at the site of the interdisciplinary Forest Residues Utilization Research and Development Program at western Montana's Coram Experimental Forest (Flathead National Forest). Established in 1974, a primary purpose of the research program was to evaluate the effects of varying biomass removal levels (and associated post-harvest burning treatments) for each of three common regeneration harvest methods. The present study is one aspect of an ongoing comprehensive analysis of that experiment, focused on the relatively long-term responses of vegetation and site productivity to biomass harvesting in northern Rocky Mountain forests [5].

The site is located in the experimental forest's Upper Abbot Creek basin (48°25'N, 113°59'W), about 20 km east of Columbia Falls, and 9 km south of Glacier National Park. Elevation ranges from 1195 m to 1615 m with 16.7°–38.7° slopes. Mean annual precipitation is 1076 mm (range: 890–1270 mm), occurring primarily in the form of snow [15]. Mean annual temperatures during summer and winter months are about 16 °C, and –7 °C, respectively [16].

The site is characterized by the western larch (*Larix occidentalis* Nutt.) forest cover type (Society of American Foresters Cover Type No. 212; [17]), mixed with Douglas-fir, subalpine fir (*Abies lasiocarpa* (Hook.) Nutt.), and Engelmann spruce (*Picea engelmannii* Parry ex Engelm.). At the lower elevations, broadleaf species such as paper birch (*Betula papyrifera* Marshall), black cottonwood (*Populus balsamifera* L. ssp. *trichocarpa* (Torr. & A. Gray ex Hook.) Brayshaw), and quaking aspen (*P. tremuloides* Michx.) are also present. The subalpine fir – queen's cup (*Clintonia uniflora* (Menzies ex Schult. & Schult. f.) Kunth) (ABLA/CLUN) habitat type is dominant [18,19].

2.2. Experimental design

The experiment was established as a split-plot design with two replicates, three whole-plots, and four sub-plots. The three whole-plots consisted of shelterwood, group selection, and clearcut harvest units. Within each whole-plot harvest unit, four biomass utilization treatment combinations were imposed as sub-plots. Each sub-plot treatment consisted of a combination of biomass

utilization level (high, medium, and low) and post-harvest prescribed burning (burned, unburned) (details in Table 1). Burning was prescribed for reduction of fire hazard; it was performed only at the medium and low utilization levels, because the high utilization level produced woody fuels loads that were insufficient to either warrant or permit burning. The four combinations of biomass utilization levels and post-harvesting treatments (burning treatment) were: 1) High-Unburned, 2) Medium-Unburned, 3) Medium-Burned, and 4) Low-Burned. In each of the clearcut and shelterwood harvest units, the four biomass utilization treatments were oriented longitudinally downslope and adjacent to each other. In the group selection units, eight patches were harvested, and two patches were randomly assigned to each of the four biomass utilization treatments. The experiment was replicated at two elevations (low, high).

Harvesting was conducted via skyline yarder in 1974, and prescribed burning treatment followed in 1975. In the lower shelterwood unit, burning was not achievable (fuel moisture contents exceeded the prescription limits; [21]), resulting in an imbalance in the experimental design and the addition of a Low-Unburned treatment in that unit. The Low-Unburned treatment was excluded for data analyses.

Douglas-fir bare-root seedlings (2-0; two-year-old in the seedbed without transplantation) were planted during 1976–1979. Except for the Medium-Unburned treatment (understory protected treatment), 25 seedlings were planted at 1.8 m spacing on the middle-top area of each sub-plot during each of 4 consecutive years. Within each biomass utilization treatment (sub-plot) of the clearcut and shelterwood units, 10 permanent sampling points were installed (two columns × five rows) spaced at 30.5 m. Five permanent sampling points were located within each cut patch of the group selection harvest units.

2.3. Data collection

From 2012 to 2013, cores were taken with an increment borer from a total 393 trees (Table 2). The sampling procedure was selected according to tree layer and regeneration type. For overwood trees in the shelterwood units, 20 Douglas-fir trees in each biomass utilization treatment were selected, avoiding the edge effect of neighbor sub-plot. Among naturally regenerated trees, 1–2 damage-free crop trees were selected within a 15 m radius of each historical permanent sampling point in all units. Sampling for the planted trees was conducted only in clearcut units. At each tree's breast height (1.37 m), diameter was recorded and two core samples (at right angles) were taken. Bark thickness per core was measured through either a bark gauge inserted at the coring spot, or a digital caliper measurement of the removed core. The average of the two measurements was calculated as the bark thickness per tree.

2.4. Data analysis

Since the data were collected from an experiment with a split-

Table 1
Design of the utilization treatments within harvesting units (from Refs. [19,20]).

Treatment	Cut trees ^a	Max. Size of retained woody materials ^b	Post-harvest treatment
Medium-Unburned	>17.8 cm dbh	7.6 cm × 2.4 m	Understory protected/unburned
High-Unburned	All trees	2.5 cm × 2.4 m	Slashed/unburned
Low-Burned	All trees	14.0 cm × 2.4 m	Slashed/broadcast burned
Medium-Burned	All trees	7.6 cm × 2.4 m	Slashed/broadcast burned

^a Except designated overstory shelterwood trees.

^b Live and dead down logs (small-end diameter × length); for dead down logs, they were removed if sound enough to yard.

Table 2
Description of samples.

Regeneration cutting (whole-plot)	Min. DBH (cm)	Mean DBH (SD) (cm)	Max. DBH (cm)	Sample size
Shelterwood	7.0	44.1 (15.9)	78.5	167
Group selection	9.1	16.7 (5.9)	35.9	56
Clearcut	5.6	15.3 (4.9)	34.1	170

plot design, mixed effects models were used for all model forms considered. For example, in the linear mixed effects model, dbh was treated as a covariate, regeneration harvests and biomass utilization treatment were considered fixed effects, and block (i.e., low and high elevation) was treated as a random effect. Therefore, the model was constructed as:

$$y_{ijkl} = \beta_0 + \beta_1 x_{ijkl} + \alpha_i + B_k + \varepsilon_{(1)ik} + \gamma_j + \varepsilon_{(2)ijk} + \varepsilon_{ijkl} \quad (1)$$

where y_{ijkl} , x_{ijkl} are the bark thickness and dbh respectively of the l th tree in regeneration harvest type i with biomass utilization treatment j in elevation block k , α_i = effect of regeneration harvest type i (whole-plot effect), B_k = k th elevation effect (random effect), γ_j = j th biomass utilization treatment effect (sub-plot effect), $\varepsilon_{(1)ik}$, $\varepsilon_{(2)ijk}$, and ε_{ijkl} are the whole-plot, sub-plot error, and the variation among trees in a subplot. The β_0 and β_1 are model parameters.

Second, a segmented linear regression model [14] was constructed for the relationship between bark thickness and dbh. Since the join point of the two different regression lines is not known, the model has a nonlinear form. For convenience of description, letting β_0 = summation of the intercept and all fixed effects and ε_i = summation of all error terms, then Eq. (1) can be simplified as:

$$y_i = \beta_0 + \beta_1 x_i + \varepsilon_i \quad (2)$$

where y_i and x_i are bark thickness and dbh of the i th tree, respectively.

If we assume the slope of this relationship between bark thickness and dbh changes for dbh values exceeding the value θ , Eq. (2) can be segmented at θ via:

$$y_i = \begin{cases} \beta_0 + \beta_1 x_i + \varepsilon_i & \text{if } x_i \leq \theta \\ \gamma_0 + \gamma_1 x_i + \varepsilon_i & \text{if } x_i > \theta \end{cases} \quad (3)$$

where θ = the join point where the two segmented linear lines meet. Since the lines should meet where $x = \theta$, we can impose a constraint of $\beta_0 + \beta_1 \theta = \gamma_0 + \gamma_1 \theta$. Therefore, Eq. (3) can be rewritten as:

$$y_i = \begin{cases} \beta_0 + \beta_1 x_i + \varepsilon_i & \text{if } x_i \leq \theta \\ (\beta_0 + \beta_1 \theta - \gamma_1 \theta) + \gamma_1 x_i + \varepsilon_i & \text{if } x_i > \theta \end{cases} \quad (4)$$

Letting $I_{\theta} = 1$ if $X_i > \theta$, and $I_{\theta} = 0$ if $X_i \leq \theta$, the model can be simplified to one equation:

$$y_i = (1 - I_{\theta})(\beta_0 + \beta_1 x_i) + I_{\theta}[(\beta_0 + \beta_1 \theta - \gamma_1 \theta) + \gamma_1 x_i] + \varepsilon_i \quad (5)$$

The above model is nonlinear, since products of two parameters exist (e.g., $\beta_1 \theta$) and since θ appears in the support of the indicator function I_{θ} .

Three different mixed effects models were constructed: (1) linear mixed effects model (without segmentation; Eqs. (1) and (2)) nonlinear model (basic model form: $y_i = \beta_0 X_i^{\beta_1} + \beta_2 + \varepsilon_i$; modified from Refs. [8] and [22]) with mixed effects (i.e., $\alpha_i + B_k + \varepsilon_{(1)ik} + \gamma_j + \varepsilon_{(2)ijk}$ from Eqs. 1, and (3) segmented linear model (Eq. (5)) with mixed effects ($\alpha_i + B_k + \varepsilon_{(1)ik} + \gamma_j + \varepsilon_{(2)ijk}$ from Eq. (1)). The variance of the residuals for all three models showed quadratic increases with dbh, so a weighted least squares approach was

introduced to deal with the nonconstant error variance; specifically, the variance of the error term was weighted proportionally by the inverse of the squared dbh. Non-significant treatment effects were eliminated from the models. The final models were compared to each other via the Akaike Information Criterion (AIC; [23]) and the Predicted Residual Sum of Squares (PRESS) statistic [24]. All statistical analyses were conducted using the *nlme* package [25] in R [26].

3. Results

The residual plots indicated that the weighted least squares approach effectively accounted for the variance heteroscedasticity problems for all models. Whereas dbh was a highly significant variable across all tested models (Table 3), the biomass utilization treatment variables did not explain the Douglas-fir bark thickness for any of the mixed effects models ($p = 0.93, 0.21$, and 0.25 for the simple linear, nonlinear, and segmented linear mixed effects model, respectively). On the other hand, the regeneration harvests significantly affected bark thickness for both the nonlinear and segmented linear mixed effects models. The final nonlinear mixed effects model was constructed as:

$$\hat{y} = 0.0793 \cdot x^{1.4521} + 4.6797 - 3.1178 \cdot I_1 - 2.7990 \cdot I_2 \quad (6)$$

where x = dbh, $I_1 = \begin{cases} 1 & \text{if group selection} \\ 0 & \text{otherwise} \end{cases}$, $I_2 = \begin{cases} 1 & \text{if clearcut} \\ 0 & \text{otherwise} \end{cases}$, respectively.

The result indicated that the clearcut and group selection units showed a lower mean bark thickness (by approximately 2.8 and 3.1 mm) than the shelterwood unit ($p < 0.0001$ and $p = 0.0513$, respectively) (Fig. 1a).

The join point was estimated at 19.0 cm dbh (p -value < 0.0001). Therefore, the final segmented linear mixed effects model was constructed as:

$$\hat{y} = \begin{cases} 4.1212 + 0.2484 \cdot x - 2.4466 \cdot I_1 - 2.1419 \cdot I_2 & \text{if } X \leq 19.0 \\ -3.2868 + 0.6379 \cdot x - 2.4466 \cdot I_1 - 2.1419 \cdot I_2 & \text{if } X > 19.0 \end{cases} \quad (7)$$

where x = dbh, $I_1 = \begin{cases} 1 & \text{if group selection} \\ 0 & \text{otherwise} \end{cases}$, $I_2 = \begin{cases} 1 & \text{if clearcut} \\ 0 & \text{otherwise} \end{cases}$.

The segmented linear model indicates that the mean bark thickness of Douglas-fir increases by about 0.25 mm for each 1-cm increment in dbh, up to 19.0 cm. Beyond that point, the mean bark thickness increases by about 0.64 mm for each 1-cm increment of dbh (illustrated by Fig. 1b). Similar to the nonlinear model, bark thickness tends to be lower in the group selection and clearcut units than the shelterwood unit ($p = 0.0267$ and $p = 0.0274$, respectively).

Among the three models, the segmented linear mixed effects model exhibited the overall lowest AIC value (2056.681) (Table 3). On the other hand, the simple linear mixed effects model yielded the lowest PRESS statistic (6646.245), indicating the best agreement between actual and predicted bark thicknesses.

Table 3

Model parameters, their standard errors (SE), and corresponding p-values of each model. Model evaluation statistics (AIC and PRESS) for each model were represented. Symbols for each parameter are described in the text.

Model Parameter	Estimate	SE	p-value	AIC	PRESS
Simple linear mixed effects model				2113.395	6646.245
β_0 (intercept)	-0.4752	0.9118	0.6025		
β_1 (dbh)	0.5128	0.0163	<0.0001		
Nonlinear mixed effects model				2073.932	6870.609
β_0 (coefficient of dbh)	0.0793	0.0298	0.0080		
β_1 (power of dbh)	1.4521	0.0910	<0.0001		
β_2 (intercept)	4.6797	0.7313	<0.0001		
β_3 (effect of group selection)	-3.1178	0.7126	0.0513		
β_4 (effect of clearcut)	-2.7990	0.6597	0.0485		
Segmented linear mixed effects model				2056.681	6831.373
β_0 (intercept when $x \leq \theta$)	4.1211	0.7169	<0.0001		
β_1 (slope when $x \leq \theta$)	0.2483	0.0496	<0.0001		
θ (join point)	19.0212	1.4466	<0.0001		
γ_1 (slope when $x > \theta$)	0.6379	0.0245	<0.0001		
β_2 (effect of group selection)	-2.4466	0.5898	0.0267		
β_3 (effect of clearcut)	-2.1419	0.5232	0.0274		

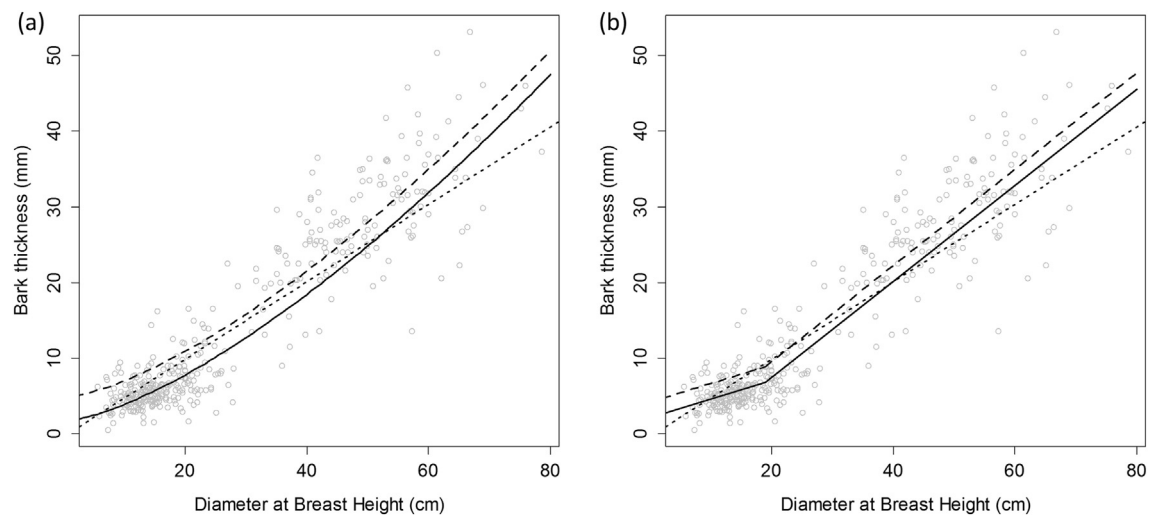


Fig. 1. Bark thickness at breast height predictions of Douglas-fir from (a) nonlinear mixed effected model and (b) segmented linear mixed effects model. Solid and dashed line represent the each model's prediction for clearcut unit and shelterwood unit, respectively. Dotted line represents the prediction through the simple linear mixed model. The prediction line for group selection was omitted since the line was undistinguishable from the line for clearcut.

4. Discussion

Tree bark figures prominently among wood industry residues, as it can comprise 10–20% of total log volumes [27]. Emerging biofuel-based energy production technologies may utilize bark as a feedstock and thereby increase its demand; others that rely on clean wood fiber will likely exact low bark tolerances in their forest biomass feedstock supplies, and require segregating bark volumes from wood volumes. In both cases, it will become increasingly important to make accurate predictions of bark volumes from tree and log measurements.

In this study, biomass utilization level was consistently a non-significant factor, indicating that the relationship between bark and dbh does not depend on that aspect of treatment history. Many sample trees regenerated after the conclusion of the treatments, and any effects on the bark:dbh relationship should have had a full opportunity for expression. Although we detected a regeneration harvest effect in the nonlinear and segmented models, this outcome was likely attributed to the fact that the larger tree samples were mainly collected from just the shelterwood units. In other words, it seems that the significance of regeneration harvest

originated not from true treatment effect but from this imbalance in sampling. We assume that any effect of treatment history upon wood and bark formation would likely manifest indirectly via its effect on site productivity; thus, the fact that no real treatment history effect was observed here indicates that either (1) the harvest and utilization treatments had no effect on site productivity, or (2) the bark:dbh relationship is one that is driven by tree level dynamics that are unaffected by site productivity.

The simple linear model showed the best prediction accuracy based on the PRESS cross-validation process (Table 3). However, the join point and statistical significance of the nonlinear model indicate that the ratio (slope) of bark thickness to dbh is not constant across the whole range of tree diameters (Fig. 2), indicating that the simple linear model might be too simplistic to explain bark thickness. The model selection criterion (AIC) suggested the best model among the three was the segmented mixed effects model. In addition, the segmented model yielded a better PRESS statistic than the nonlinear model. Furthermore, if it is possible to find the physiological evidence for the join point from external subsequent studies, then a considerable amount of uncertainty can be decreased and the model fit improves, since the model takes a

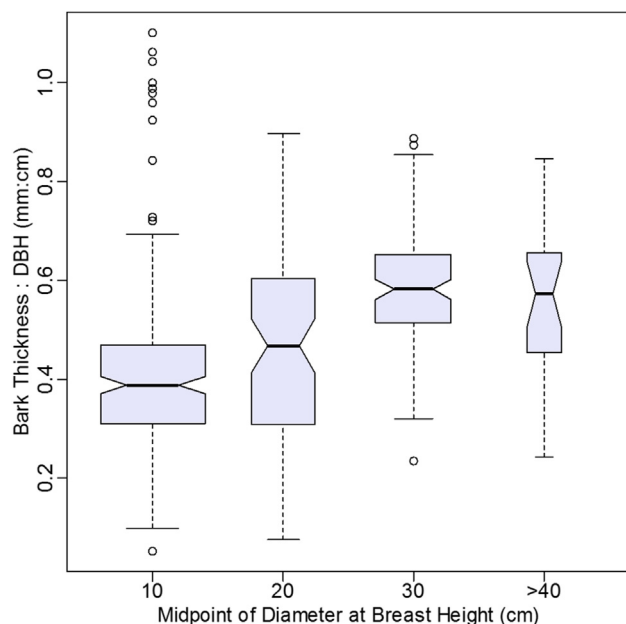


Fig. 2. The ratio of bark thickness of Douglas-fir to dbh according to size class. The x-axis represents the midpoint of each dbh class.

simple linear form. Therefore, we conclude that the simpler (albeit segmented) linear regression model provided the best result for modeling bark thickness.

Similar conclusions have been reached by other studies. Brickell [3] investigated 10 species (including Douglas-fir) in western Montana, and recommended the simpler form for bark thickness prediction. The simple linear regression model's performance has been found superior to more complex models for radiata pine (*Pinus radiata* D. Don) in Australia [28], white spruce (*Picea glauca* (Moench) Voss) in Alaska [29], and lodgepole pine (*Pinus contorta* Douglas ex Loudon var. *latifolia* Engelm. ex S. Watson) in central Oregon [22].

In their study, Garber and Maguire [22] attributed the superior performance of the simple model to a narrow range of size classes and geographic distribution comprising their samples, and theorized that a more complex model form could be required to explain variances as the sample range increases. Yet, the question of how the bark:dbh relationship changes across geographic space remains unclear. Monserud [10] and Dolph [11] each found that model parameters were slightly different among regions with the same model form, implying that model application indeed has geographical limitations. Yet, other researchers (e.g., [28,29]) maintained that their models were quite tolerant of geographic location. The narrow geographic range from which our samples were drawn prevents our addressing this issue.

Compared with other models, segmentation yielded the model (linear) with best performance for our dataset. Johnson [7] similarly observed a diameter join point in a Douglas-fir dataset from western Oregon and Washington (25.4 cm, versus this study's 19.0 cm), but did not describe the rationale used to determine that point. In both cases, however, the possible existence of a join point indicates that the allometric ratio between dbh and bark may not be constant. Nonconstant allometric ratios are uncommon, but have been observed for other tree components. For example, the foliage-sapwood area relationship has been shown to change by competition level in lodgepole pine [30], and by site quality in young Douglas-fir [31]. Reports have also shown that the biomass allocation pattern differs according to the degree of competition for

several species, such as loblolly pine (*Pinus taeda* L.) [32] and Scots pine (*Pinus sylvestris* L.) [33].

Predicted bark volumes computed from the segmented regression model were significantly different from the volumes predicted by the nonlinear model (paired t-test; $P < 0.0001$). The magnitude of difference in predicted bark volume between our segmented model and a conventional nonlinear model [2] is illustrated in Fig. 3 for a range of Douglas-fir tree sizes. The differences may appear modest, but they amplify to levels that are beyond trivial once adjusted up to stand scales.

To illustrate, consider a fully-stocked, even-aged, uniform stand of Douglas-fir with a quadratic mean diameter of 25.4 cm. Following the rationale of Cochran et al. [34], a stand density index (SDI; [35]) of 939 can be assumed for the fully-stocked stand [36]. Using equations by Maguire and Hann [10], the difference in the predicted bark volume estimate between the segmented linear model and the simple linear model is 5 dm³ per 25.4-cm dbh tree (Fig. 4, in the case of clearcut unit). At the stand level, this difference translates to 5.29 m³ ha⁻¹. Assuming a bark specific gravity of 480 kg m⁻³ [37], that difference results in a bark weight disparity of 2500 kg per hectare. Moreover, the discrepancy in bark volume links directly to error in bolewood volume prediction, since bark thickness is used as a determinant of numerous log volume prediction equations (e.g., [2,4,38]).

5. Conclusion

For prediction of Rocky Mountain Douglas-fir bark thickness, dbh proved a significant variable; harvesting treatment was also significant, but we attribute this result to a weakness in the sampling design rather than actual treatment effect. Since biomass utilization level was a non-significant factor, we conclude that treatment history fails to materially affect the relative formation of wood and bark, and that the bark:dbh relationship remains constant, irrespective of treatment history. Among fitted models, a segmented linear regression model performed best, with greater prediction accuracy than a simple nonlinear model and applicability for various management objectives. The existence of a join point may be a manifestation of tree growth and vegetation dynamics, but remains a subject for further investigation. Quantitatively identifying the segmented linear model's join point is

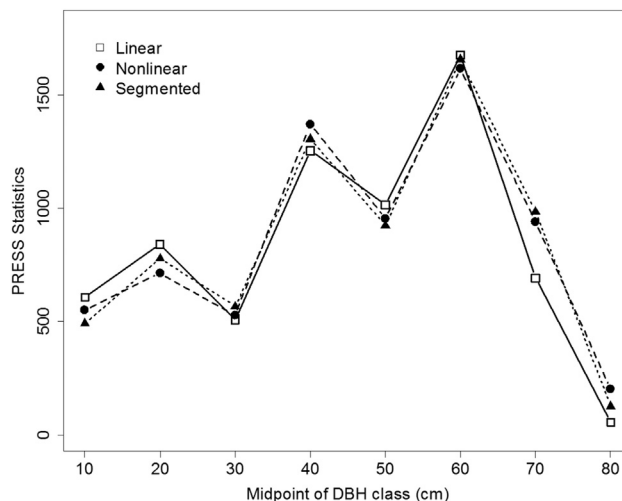


Fig. 3. Comparison of model performances according to Douglas-fir dbh size classes. Solid, dashed, and dotted lines represent the simple linear, nonlinear, and segmented linear regression model, respectively.

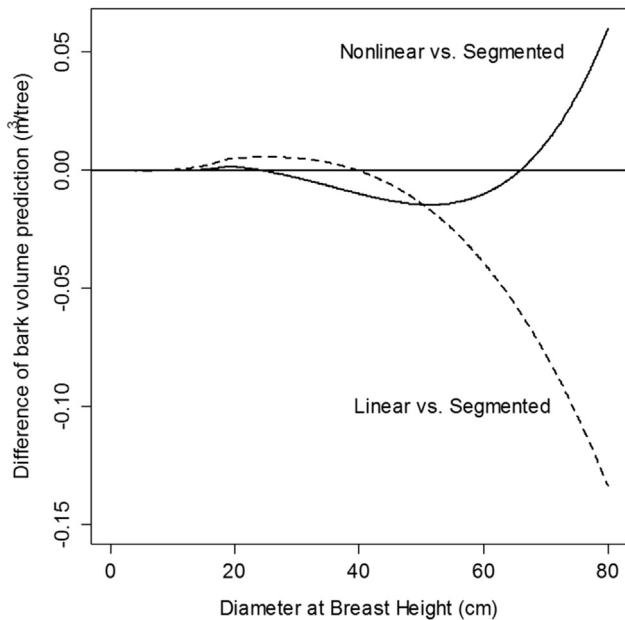


Fig. 4. The prediction differences of Douglas-fir bark thickness (dbh as a predictor) by this study's segmented linear regression model versus the nonlinear model (solid line) and the simple linear regression model (dashed line).

computationally challenging but involves a relatively straightforward model reparameterization and nonlinear fitting algorithm. Such a technique may be used to improve the bark:dbh models for other species and locations.

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