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**Comparison of taper functions applied to eucalypts of varying genetics in Brazil:
Application and evaluation of the penalized mixed spline approach**

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Abstract

Taper functions have been widely used with an existing array of model forms and methods. However, comparisons of contrasting statistical methods have been more limited. This study aimed to assess contrasting statistical approaches for achieving accurate stem taper and individual tree volume predictions, with focus on the novel penalized mixed spline (PMS) approach. The approaches were tested using four different eucalyptus genetic families planted in Brazil. For comparison, the predictions of diameter outside bark (dob) and volume using a 5th degree polynomial, the polynomial of integer and fractional powers, a segmented taper function, a variable exponent taper function, and a semi-parametric PMS were conducted. Comparisons using the generalized functions of every stem taper function with genetic family as an extra random component were also conducted. Data-splitting was used to test the accuracy of each taper function. PMS and the generalized PMS were the most accurate for both dob and volume, while the generalized PMS approach displayed more stable volume predictions along the stem. The other approaches were more variable across the tree size classes examined. Overall, the study highlights the applicability of the PMS methodology for predicting tree taper and volume that warrants future assessment and application.

Keywords: parametric regression, semi-parametric regression, eucalyptus, stem form, volume

1. Introduction

A combination of high quality data from forest inventory and precise techniques to evaluate the data is essential to provide the information needed for decision making at both the stand and forest levels. This key information is often derived from the use of a stem taper function. This function enables the description of the shape of the tree bole, which makes possible the merchandizing of multiple products from a specific forest (Gomat et al. 2011).

In the past, European researchers used different geometric solids of revolution for stem profile studies (Ferreira 1999). However, one problem regarding the use of a fixed solid of revolution is that a tree displays different shapes along its stem. In 1903, Höjer developed the first taper function, which was applied to *Picea abies* (L.) Karst. (Löetsch et al. 1973). Although the first taper function was developed in 1903, only in the 1970s did the interest for the development of more powerful approaches dramatically increase (Gomat et al. 2011). Over time, a variety of taper approaches have been used such as polynomials (Goulding and Murray 1976), variable exponent form (Demaerschalk 1972; Ormerod 1973; Kozak et al. 1988; Kozak 2004), and segmented polynomial (Max and Burkhart 1976; Parresol et al. 1987). Despite their wide use and varying model forms, comparisons of taper equation performance in predicting both stem form and volume for a given species is less common (Li and Weiskittel 2010).

The best approach for modeling stem taper has varied among regions and species. For example, Assis et al. (2001) studying taper functions applied to eucalyptus in Brazil suggested the desirable capability of polynomials, where the authors discussed the efficiency of the polynomial of integer and fractional powers to describe the shape of the tree bole for older stands and/or larger trees. Figueiredo-Filho et al. (1996) studying *Pinus taeda* in southern Brazil also highlighted the consistent performance of the 5th degree polynomial. Among 32 fitted taper

functions, Rojo et al. (2005) described the superior behavior of the variable exponent form of Kozak (2004) to predict the stem taper of *Pinus pinaster* Ait. in Galicia. They emphasized the function's high flexibility and strong predictive capabilities. Developing a compatible stem volume and taper equation system for three species in Turkey, Brooks et al. (2008) pointed out the performance consistency and the satisfactory estimates provided by the segmented polynomial taper function of Max and Burkhart (1976). For three conifer species in eastern North America, Li and Weiskittel (2010) showed that the best taper equation varied depending on species, available data, and whether accuracy for stem form and volume was desired, but indicated that the Kozak (2004) model generally performed well.

Assis et al. (2001) pointed out the difficulty when using a single taper approach to describe different species and a wide range of tree size classes. Bi (2000) associated this problem with the number of parameters of low biological interpretation in most taper equations. Therefore, the most accurate taper function may be specific to the species, tree size class, and region, which highlights the need for the development of a generalized and flexible approach. This is particularly the case for eucalyptus plantations in Brazil, which have short rotations and a dramatic change in the tree size from one year to another (Scolforo et al. 2016). Thus, a lack of flexibility could easily result in highly biased estimates. In addition, the lack of studies assessing the flexibility and stability of different taper functions across tree size classes is a major shortcoming for plantations in this country.

Generally, traditional parametric approaches are used to fit stem taper equations. Semi-parametric and nonparametric methods have also been used. This has included smoothing splines (Lappi 2006), B-splines (Kublin et al. 2013), neural networks (Özçelik et al. 2010), and generalized additive models (Robinson et al. 2011). Similar to the comparison of stem taper

model forms, the assessment of the performance of parametric and nonparametric methods have been less common. For example, Robinson et al. (2011) indicated that their semi-parametric method had similar performance as a more traditional parametric approach for predicting whole-stem volume, merchantable volume, number of logs, small-end diameter of the first log, and volume of the first log, while Özçelik et al. (2010) suggested that the nonparametric neural network was superior to the parametric approach. To our knowledge, the semi-parametric approach of penalized splines has yet to be assessed for predicting stem taper.

Penalized splines, which are an evolution of the spline, are well known for avoiding under/over fitting and poorly behaved estimation in the tails (Harrell 2015). However, since weights for its smooth function is based on a penalization criteria, inference might be difficult. Pedan (2003) pointed out, however, that the penalized spline regression displays the same solution when using mixed effects modeling, since this technique is closed related to smoothing. Consequentially, the penalized mixed spline methodology might prove highly robust and flexible for predicting stem taper and volume.

Despite the importance of eucalyptus plantations in Brazil, comparisons of contrasting taper functions have been more limited. Therefore, this study aimed to develop and compare contrasting taper approaches applicable to four different and widely used eucalyptus genetic families. In particular, interest was in the approach that resulted in more stable predictions when estimating both stem taper and individual tree volume across a range of tree size classes. Taper functions were developed from the semi-parametric methodology of penalized mixed splines as well as several alternative commonly used parametric model forms including the 5th degree polynomial, the polynomial of integer and fractional powers, the segmented polynomial of Max and Burkhart (1976) and the variable exponent form of Kozak (2004). Specific research

objectives were to: (1) fit each of these methods to each genetic family; (2) evaluate predictions of both stem taper and volume; and (3) compare a family-specific approach to a generalized approach that treated genetic family as a random effect. Our expectations were that the penalized mixed spline would perform best for both stem taper and volume, while the generalized approach would be superior to the genetic family-specific approach.

2. Material and methods

2.1. Study area and database

The study was conducted on a population stratified with four different genetic families of eucalyptus with total planted area of 20,000 ha, located in the municipality of Água Clara, eastern Mato Grosso do Sul (MS) (Figure 1). The state of Mato Grosso do Sul is the sixth largest state in Brazil, with an area greater than England. In recent past, MS has dramatically increased its acreage in eucalyptus plantations. MS is now the second largest eucalyptus roundwood producer state in Brazil (Painel Florestal 2015). The location of Água Clara is at 20°26'53" S and 52°52'40" W, with average elevation of 303 m and Aw Köppen climate classification. The mean temperature is 26° C, while the average annual rainfall is 1,350 mm (Alvares et al. 2013).

The study area is in flat lands, where the soils are predominantly Quartz-sand dystrophic neosol, which are deep, excessively drained soils and presents low water retention capacity and fertility. The database was composed of four different genetic families of eucalyptus, each planted at 5.0 x 2.6 m spacing, where precommercial thinning was applied when the plantations were 2 years old. The plantations were different from the predominant status of Brazilian industrial forests as the focus was not pulpwood and energy production, but saw-timber production. A total of 590 trees, distributed in 117 stands and four genetic families, were bucked

and scaled during 2012 to 2016. An average of 5 trees per stand were selected, implying that the selection of trees was balanced across different genetic families.

The plantations ages where trees were bucked and scaled range from 3.9 to 6.6 years (Table 1). On each scaled tree, measurements of diameter at 1.30 m above ground (DBH), diameter inside bark (dib), diameter outside bark (dob), bark thickness, total height (H) and stump height were taken. Measurements representing the tree bole were also taken, where dob, dib and bark thickness were measured at the stump height, at the middle height between the stump and 1.3m, and after 1.3 m at every 2 m until the tree top.

Table 1 is here

Figure 1 is here

2.2. Taper functions

We developed and applied new taper functions using a penalized mixed spline methodology, which were compared to the taper functions of the 5th degree polynomial, polynomial of integer and fractional powers, Max and Burkhart (1976), and Kozak (2004).

The analysis was performed in the software R (R Core Team 2015) with the package nlme (Pinheiro et al., 2016) for fitting all the taper models. For all the approaches, within-stem correlation and variance heteroskedasticity were accounted for using a first-order continuous autocorrelation function (CAR1) and power variance function. Each of these approaches is described in more detail below.

2.2.1. 5th degree polynomial

The 5th degree polynomial is the most commonly applied taper function in Brazil for eucalyptus due to its model form simplicity and acceptable precision (Sanquetta et al. 2015). The polynomial is a flexible continuous function that is used to describe the shape of the tree bole. The 5th degree polynomial was first introduced by Schöepfer in 1966 (Sanquetta et al. 2015):

$$(1) \quad \frac{d_i}{DBH} = (\beta_1 + b_1) \left(1 - \frac{h_i}{H}\right) + (\beta_2 + b_2) \left(1 - \frac{h_i}{H}\right)^2 + \beta_3 \left(1 - \frac{h_i}{H}\right)^3 + \beta_4 \left(1 - \frac{h_i}{H}\right)^4 + \beta_5 \left(1 - \frac{h_i}{H}\right)^5$$

where β_{js} are the fixed coefficients to be estimated; b_1 and b_2 are the random coefficients based on each tree (stand) and stand, since the higher variability at the tree base; d_i is the dob; h_i is the stem height; other variables were already defined.

A single generalized function was fitted as well. This generalized function included genetic family as a random component so that b_1 and b_2 are the random coefficients based on each tree (stand), stand (genetic family) and genetic family.

While Equation (1) and its generalization are constrained to predict an upper-stem diameter $d = 0$ when $h = H$, most applications of the 5th degree polynomial in Brazil possess an intercept term b_0 and hence do not contain this logical constraint.

2.2.2. Polynomial of integer and fractional powers

Hradetzky (1976) studied the best powers when describing the shape of the tree bole and suggested a polynomial with exponents ranging from 0.005 to 25 would be more suitable to describe stem taper than instead of the fixed 5th degree polynomial (Assis et al. 2001). Exponents closer to zero were better at describing the tree base, while exponents of 20 and 25 were better for the top portion of the tree. The stepwise selection of the best exponents resulted from a

combination of a maximum six coefficients that presented the highest F-test. The fitted Hradetzky (1976) presents the general form:

$$(2) \frac{d_i}{DBH} = (\beta_1 + b_1) \left(1 - \frac{h_i}{H}\right)^{p_1} + (\beta_2 + b_2) \left(1 - \frac{h_i}{H}\right)^{p_2} + \beta_3 \left(1 - \frac{h_i}{H}\right)^{p_3} + \beta_4 \left(1 - \frac{h_i}{H}\right)^{p_4} + \beta_5 \left(1 - \frac{h_i}{H}\right)^{p_5} + \beta_6 \left(1 - \frac{h_i}{H}\right)^{p_6}$$

where β_{js} are the fixed coefficients to be estimated; b_1 and b_2 are the random coefficients based on each tree (stand) and stand. Since the highest variability is at the tree base; p_n are the exponents ranging from 0.005 to 25.

A generalized function that included genetic family as a random component was fitted, where b_1 and b_2 are the random coefficients based on each tree (stand), stand (genetic family) and genetic family. The selection of the best exponents was previously explained, however, a maximum of seven coefficients was employed in the generalized function.

2.2.3. Max and Burkhart (1976)

A very widely used taper function was developed by Max and Burkhart (1976), which models the transition from the frustum of neiloid to frustum of paraboloid at the lower part of the stem, and once again the transition of the frustum of paraboloid to cone in the upper part of the stem with one smooth continuous function. The points of transition from one solid form to another are called knots, and the lower knot associated with the change from frustum of neiloid to frustum of paraboloid generally occurs in the lower 12% of relative height or where $h_i/H < 0.12$. The transition from frustum paraboloid to cone generally occurs in the upper 25% of relative height or when the knot of h_i/H exceeds 0.75. The Max and Burkhart (1976) segmented taper function can be expressed as:

$$(3) \left(\frac{d_i}{DBH} \right)^2 = \beta_1 \left(\frac{h_i}{H} - 1 \right) + \beta_2 \left(\left(\frac{h_i}{H} \right)^2 - 1 \right) + (\beta_3 + b_3) \left(\alpha_1 - \frac{h_i}{H} \right)^2 I_1 + (\beta_4 + b_4) \left(\alpha_2 - \frac{h_i}{H} \right)^2 I_2$$

where α_1 is the knot value of h_i/H or point of transition between the frustum of paraboloid and cone in the upper part of the stem (75 - 85% of total height) to be estimated; α_2 is the knot value of h_i/H or point of transition between the frustum of neiloid and frustum of paraboloid in the lower part of the stem (10-15% of total height) to be estimated; I_1 is 1 if $h_i/H < \alpha_1$, otherwise I_1 is 0; I_2 is 1 if $h_i/H < \alpha_2$, otherwise I_2 is 0; β_1, β_2 are the other fixed coefficients to be estimated; b_3 and b_4 are the random coefficients based on each tree (stand) and stand following Cao and Wang (2011).

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A generalized segmented taper function was fitted by including the genetic family as one of the random components, where b_3 and b_4 are the random coefficients based on each tree (stand), stand (genetic family) and genetic family.

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2.2.4. Kozak (2004)

A widely used variable exponent taper function was developed by Kozak (2004). He proposed a flexible taper function that continuously describes the shape of the bole. Since this is a continuous taper function, the transition from the frustum of neiloid to frustum of paraboloid, and from the frustum of paraboloid to cone are compensated by the exponent changes. The Kozak taper function can be expressed as:

$$(4) \quad d_i = (\alpha_0 + a_0) DBH^{\alpha_1} H^{\alpha_2} X^{[\beta_1 z^4 + \beta_2 (1/\exp(DBH/H)) + (\beta_3 + b_3) X^{0.1} + \beta_4 (1/DBH) + \beta_5 H^Q + \beta_6 X]}$$

where $X = \left(1 - \left(\frac{h_i}{H}\right)^{1/3}\right) / (1 - p^{1/3})$, $Q = (1 - z^{1/3})$, $p = 1.3 / H$ and $Z = \frac{h_i}{H}$; $\alpha - \alpha_2$, β_1, β_6 are the fixed coefficients to be estimated; a_0 and b_3 are the random coefficients based on each tree (stand) and stand following Li et al. (2012); p is the relative height where trees change from a neiloid to a paraboloid, or the inflection point.

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The generalized variable exponent taper function of Kozak (2004) was also fitted and a_0 and b_3 are the random coefficients based on each tree (stand), stand (genetic family) and genetic family.

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2.2.5. Penalized Mixed Spline

The Max and Burkhardt (1976) taper function has five restrictions or constraints and the derivation is quite challenging. Following the Max and Burkhardt (1976) concept, we wanted to add another knot that includes the bottom portion of the stem. However, we employed a flexible and more efficient way to express that, which is based on splined polynomial taper functions.

In a splined polynomial function a sequence of knots are employed to separate these functions and a smoothness function is applied in order to ensure a smoothly join between these functions at each knot (Pedan 2003). Smoothness, as suggested by Pedan (2003), is attained in our application by using quadratic polynomials where we used $k = 4$ empirical knots ($k_1 = 0.10$, $k_2 = 0.34$, $k_3 = 0.75$, $k_4 = 0.97$). In addition, we decided to add a tree size variable used in previous work by McTague (1992):

$$(5) \quad \frac{d_i}{DBH} = \beta_1 \left(1 - \frac{h_i}{H}\right) + \beta_2 \left(1 - \frac{h_i}{H}\right)^2 + \beta_3 S + \sum_{k=1}^K u_k \left(\left(1 - \frac{h_i}{H}\right) - k_1 \right)_+^2$$

where $\beta_1 - \beta_3$ are the coefficients to be estimated; $S = \frac{DBH^2 H}{10000} \ln\left(2 - \frac{h_i}{H}\right)$; u_k are the knots coefficients to be estimated; the + subscript operator infers that the function is only computed if $1 - (h_i/H)$ is larger than the knot value inside the parenthesis, otherwise the value is zero (hence replacing the dummy variable used in the Max-Burkhardt taper function).

Equation (6), which we defined as the penalized mixed spline approach (PMS), is a normal linear mixed model, where the quadratic expression and S are fixed and the expression for the knots are declared random based on each tree (stand) and stand. It is suggested that the mixed-effects model then resolves the smoothing spline regression, which turns it into penalized regression spline (Pedan 2003):

$$(6) \quad y = X\beta + Zu + \varepsilon, [u, \varepsilon]^T \sim N(0, \text{diag}(\sigma_u^2 I, \sigma_\varepsilon^2 I))$$

$$\text{where } X = \begin{bmatrix} \left(1 - \frac{h_1}{H_1}\right) & \left(1 - \frac{h_1}{H_1}\right)^2 & DBH^2 H \ln\left(2 - \frac{h_1}{H_1}\right) \\ \vdots & \vdots & \vdots \\ \left(1 - \frac{h_n}{H_n}\right) & \left(1 - \frac{h_n}{H_n}\right)^2 & DBH^2 H \ln\left(2 - \frac{h_n}{H_n}\right) \end{bmatrix} \quad Z = \begin{bmatrix} \left(\left(1 - \frac{h_1}{H_1}\right) - k_1\right)_+^2 & \dots & \left(\left(1 - \frac{h_1}{H_1}\right) - k_k\right)_+^2 \\ \vdots & \ddots & \vdots \\ \left(\left(1 - \frac{h_n}{H_n}\right) - k_1\right)_+^2 & \dots & \left(\left(1 - \frac{h_n}{H_n}\right) - k_k\right)_+^2 \end{bmatrix}$$

Finally, an expanded PMS taper function, which was a single generalized equation with genetic family as the random component, was fit as well, where $b_1 - b_2$ are the random coefficients associated with genetic family.

The penalized mixed spline methodology displays a closed-form integral, however, its use for volume estimation is extremely tedious, which makes its use inconvenient and susceptible to error. We suggest instead, the numerical integration of the taper function with small intervals and the use of Smalian's formula for volume estimation.

2.3. Goodness of fit

Prior to fitting any taper function, the dataset was stratified by tree size class (every 10th quantile). Thus, 30% of the dataset were randomly removed from each tree size class for each genetic family. The removed datasets for each genetic family were used for predictive validation. For the predictive validation, the statistics of Mean Absolute Error (MAE), Mean Error (T) and Root Mean Square Error (RMSE) were calculated for each of the four genetic families for each taper approach. These three statistics were calculated when predicting stem taper (dob at any stem height) and individual tree volume (cumulative individual tree merchantable volume).

$$(7) \quad MAE(\%) = \frac{\sum_{i=1}^n \left(\frac{|O_i - P_i|}{O_i} \right)}{n} 100$$

$$(8) \quad T(\%) = \frac{\sum_{i=1}^n \left(\frac{O_i - P_i}{O_i} \right)}{n} 100$$

$$(9) \quad RMSE = \sqrt{\frac{\sum_{i=1}^n (O_i - P_i)^2}{n}}$$

where n is the number of observation; O_i is the observed variable; P_i is the estimated variable.

Smaller MAE and RMSE indicate better fit. T statistics closer to zero indicates less biased estimates. We fitted five taper functions to each of the four genetic families as well as five generalized taper functions, and we then used the three different statistics to determine the best approach. Therefore, to simplify the analysis, we simply ranked the performance of each taper function and then decided the best one when estimating stem taper and individual tree volume.

For all approaches, stem volume estimation was based on numerical integration of Smalian's formula. The different section lengths coincided with the exact locations where observed measurements of the tree bole were taken. Graphical analysis for volume prediction along the stem was also conducted to ensure the stability of each taper function. The R package ggplot2 (Wickham 2009) was used to produce the graphical analysis.

3. Results

3.1. Performance of the taper functions for each genetic family

Since we fit a total of 25 equations, the fitted coefficients are presented in Supplemental Materials. The retained coefficients were all significant at the $p = 0.05$ level and were judge to be important in describing the shape of the tree bole. When coefficients were not significant, they were removed and the function was refitted to maintain parsimony.

High accuracy was achieved when estimating stem taper and individual tree volume using all taper functions (Table 2). Estimates were generally accurate with low bias and the taper functions were well behaved in describing the shape of the tree bole (Figure 2). Irrespective of the genetic family and taper approach, the RMSE was never greater than 0.86 cm for dob estimation and 0.019 m³ for individual tree volume estimation. In addition, T and MAE were never greater than 6.5% and 10%, regardless dob or volume estimation.

Table 2 is here

Figure 2 is here

The statistics of Table 2 indicated similar estimates for all examined taper approaches. Thus, we decided to rank the three statistics across the different taper approaches to determine the one that performed better when predicting both stem taper and individual tree volume (Table 3). Overall, when estimating dob and individual tree volume, PMS and generalized PMS taper functions performed slightly better, although all the approaches, particularly Kozak (2004) for dob estimation, performed well. The generalized functions behaved worse than the functions fitted to each genetic family, although in the PMS approach this behavior was not detected. PMS and generalized PMS taper functions performed similarly, which is an indication of the better behavior of this approach when compared to others.

Table 3 is here

3.2. Performance of the taper functions when stratifying the dataset according to tree size

Although PMS and generalized PMS taper functions performed better when predicting stem taper and individual tree volume, a further investigation was needed to assess how the taper functions performed across a range tree size classes, particularly for volume. When stratified by three size classes (33th quantile, 33th to 67th quantile, and 67th to 100th quantile of DBH), the results indicated low bias and high accuracy of all taper functions across the diameter size classes (Table 4).

Table 4 is here

When ranking the taper functions, it was observed that their behavior were quite different across the different size classes (Table 5). For instance, the taper functions of Hradetzky (1976), Max and Burkhardt (1976), and Kozak (2004) performed well for average-sized and larger trees, while the generalized Kozak (2004) performed well for smaller and larger trees. In contrast, the 5th degree polynomial taper function was never observed as one of the best taper functions for any tree size class. The generalized PMS and PMS models were consistently ranked as the best or second best approaches for the evaluated statistics. In particular, the total for each approach indicated that generalized PMS and PMS were the best taper approaches to describe individual tree volume with PMS ranked higher for small and average trees and the generalized PMS for larger trees. Since the generalized PMS and PMS were always high ranked across the examined tree size classes, this demonstrated the greater flexibility of the PMS methodology when compared to other taper approaches.

Table 5 is here

Finally, an examination of the performance of the taper models when estimating volume along the stem was conducted. Generalized PMS and PMS were observed to perform better when estimating the volume from stump to tree top (Figure 3). The generalized PMS behaved especially better along the stem profile, which can be highlighted by its accurate and stable estimates especially when predicting the volume of the first (lower) 40% of the tree height. This behavior indicates that this taper approach produces accurate estimates for the portion of the tree where volume is higher. The other taper functions also presented realistic behavior, although the 5th degree polynomial, Hradetzky (1976) Kozak (2004), Max and Burkhardt (1976) and their generalized functions displayed overall more unstable predictions.

The higher estimation errors noticed for genetic family four might be more indicative of a lack of a suitable sample size to capture its variability, since this genetic family presents the highest variation according to tree size (Table 1) and fewer trees were bucked and scaled to represent such variability when compared to the other genetic families.

Figure 3 is here

3.3. Sampling distribution of the error statistics and testing of the inclusion of the variable tree size in the PMS approach

Since the PMS approach as a generalized function had the overall best results, this section focused on the analysis of the robustness of this approach. Robustness is inspected with respect to error distributions and the precision gain by including a tree size variable in the taper function.

First, a total of 10,000 random samples using the non-parametric bootstrap technique were generated. These random samples allowed the estimation of the sampling distribution of the T, MAE and RMSE statistics when applied to evaluate the cumulative individual tree volume (Figure 4 and Table 6). Overall, the approach gave high accuracy and low bias associated with the estimates. Confidence intervals for T, MAE and RMSE at a 95% confidence level displayed short interval lengths, which reinforced the accuracy of the predictions generated from the PMS approach. Differently from the previous analysis, however, the overall statistics accounted for all genetic families instead of the specific genetic family evaluation.

Table 6 is here

Figure 4 is here

For the PMS approach, we have proposed the inclusion of a variable related to the tree size to better estimate stem taper and tree volume. It was hypothesized that this variable reflects the stand density effect in plantations with same spacing and allow increasing the accuracy of the volume predictions. It is obvious how the inclusion of such variable allow better predictions for each genetic family, especially of the first (lower) 40% of the tree height (Figure5). This is a critical factor that validates the use of such a variable, since this is the most valuable part of the tree. The exception is the genetic family 4. However, the lack of ideal sample size, previously mentioned, circumvents a better fit for this genetic family.

Figure 5 is here

Testing the Full PMS approach over different genetic families also indicated better results by using the specific coefficients for the genetic families in the quadratic expression instead of the average fitted coefficients. The specific coefficients for the quadratic expression are presented in Supplemental Materials.

4. Discussion

The accurate description of the shape of the tree bole is critical for assessing multiple products generated by a specific forest and it is quite challenging for eucalyptus species where stem taper is constantly changing (Gomat et al. 2011). In this study, we applied 10 different approaches to modeling taper with an extensive database containing four genetic families widely

planted in a region of great forestry expansion in recent years (Painel Florestal 2015). The analysis highlighted the PMS methodology (in both family-specific and generalized form) as capable to effectively describe the shape of the tree bole, since PMS and generalized PMS approaches displayed greater flexibility and stability when estimating stem taper and individual tree volume across the range of tree size classes.

To our knowledge, this is the first application of a PMS methodology for predicting stem taper, although some studies have already used other spline methodologies (Kublin et al. 2013; Kuželka and Marušák 2014a; Kuželka and Marušák 2014b). Kuželka and Marušák (2014a), for instance, applied several spline approaches for stem profile studies with Norway spruce (*Picea abies* (L.) Karst.), and the authors found the best results when applying the local interpolation spline known as Catmull-Rom. Compared to these other spline approaches, we believe PMS offers several advantages, particularly ease of estimation and prediction.

Accurate and low biased estimates are desirable for the selected taper function when estimating total volume and dob (Li et al. 2012). However, a close examination in the behavior of the volume predictions along the stem is critical (Li and Weiskittel 2010), especially for the first (lower) portion of the tree, where the most valuable tree products originate. The PMS and generalized PMS approaches displayed stable predictions along the stem profile, except for genetic material 4. However, the generalized PMS performed best for this genetic family when compared to other approaches. We highlight the overall high stability of generalized PMS predictions. Since the addition of the genetic family as random effect provided improved stability for volume predictions, this result indicates that a single generalized model for eucalyptus can be used, which is similar to the findings of Trincado and Burkhart (2006).

Given the noteworthy characteristics and performance of the generalized PMS model, we suggest how the results can be generalized for other genetic families. Both Lynch et al. (2005) and Trincado and Burkhart (2006) have proposed calibration methods for new observations using a reduced sample size of 5-6 trees. Their methodology works well for linear mixed models with one class (cluster) type variable. The generalized PMS model presented here has two class or cluster type variables; namely genetic family and knots. The inverted variance-covariance matrix in this case is complex, leading to a tedious calibration procedure. We suggest that when a new genetic family is deployed, even with only 5-6 sample trees, that the entire generalized PMS model be refitted. In this way, it is possible to preserve the shrinkage properties of the knots and penalty function, while calibrating the taper model to the new genetic family.

Combining the advantages mentioned above, including the good accuracy and low bias when individually estimating the cumulative volume and stem taper, and the great stability when predicting volume along the stem, the generalized PMS model can efficiently describe the shape of the tree bole for ages 4-7 and for all genetic families. This is an innovative result of significant importance as individual taper functions are customarily fit for every forest compartment and for each one-year age class in Brazil (Kohler et al. 2016). Additionally, including a tree size variable in the PMS approach predicts the stand density effect in plantations which contributes to the increase of precision.

The inclusion of S or size independent variable in the generalized PMS equation, where $S = \frac{DBH^2 H}{10000} \ln\left(2 - \frac{h}{H}\right)$, serves as a proxy for the age variable as well. While the effect of size or age is strongest at the base of the tree, larger trees at a given relative height, display more taper. While the fitting data set of this study, contained only a single spacing, namely 5.0 x 2.6 m, it is safe to state that stand of higher stem density will contain trees of smaller breast height diameters

and smaller live crown ratios, resulting in better stem profile. The recession of the live crown however, can be attenuated by intensive silvicultural practices such as fertilization.

The accurate and stable predictions along the tree stem elucidate the potential validity of using the PMS approach for any other commercial tree species. The flexibility of such approach for accurately predicting stem taper and individual tree volume of eucalypts of varying genetics merits attention. Eucalypts face dramatic annual change in tree size due to their high growth rate (Scolforo et al. 2017). To our knowledge this rapid change in the stem taper is not observed for other tree commercial species. Since PMS displays the ability to accurately model the change of eucalyptus stem taper, this approach is likely suitable for any other commercial tree species. Gomat et al. (2011) discussed the necessity of developing taper functions that can display unbiased results if fitted for any tree species and it is possible to infer that the PMS approach presents this capability.

The other taper functions displayed a suitable behavior as well. The 5th degree polynomial and Hradezky (1976) are the most widely applied taper functions for eucalyptus forest in Brazil, since they display simplicity and ease of estimation (Assis et al. 2001). A closer examination of these approaches indicated relatively accurate and low biased estimates, however, unstable volume predictions along the stem were observed either using the generalized functions or specific fits to each genetic family. Ribeiro and Andrade (2016) compared the performance of different stem taper functions for eucalyptus in the state of Tocantins in Brazil and indicated more reliable estimates for the taper functions of the 5th degree polynomial and Hradetzky (1976). Although these two taper functions displayed the best fit results, the authors reported, however, a high degree of uncertainty when estimating volume along the stem.

Several studies have reported the performance of the Kozak (1969) taper function for eucalyptus in Brazil, such as exemplified by Figueiredo-Filho and Schaaf (1999). It is interesting to note, however, that even Kozak (2004) being perhaps the most popular variable exponent taper function in the world, this taper function has never published for eucalyptus plantations in Brazil. In order to bridge the scarcity of studies with taper approaches comparison, the Kozak (2004) and generalized Kozak (2004) taper functions were fitted for the first time for eucalyptus forests in Brazil. The innovative results suggested accurate and low biased estimates of the Kozak (2004) especially for average and larger trees, while the generalized Kozak (2004) performed best for smaller and larger trees. These taper functions, however, displayed unstable volume predictions along the stem for some genetic families, which can compromise the quality of predictions when assessing the multiple product potentials of a forest. Schröder et al. (2014) noticed similar behavior when applying the Kozak (2004) taper function to slash pine (*Pinus elliottii*) in Brazil.

Finally, the segmented taper function of the Max and Burkhart (1976) approach, which was high ranked for averaged and larger trees, seemed to display unstable predictions of volume along the stem. Similar unstable predictions were observed when applying the generalized taper function. These results were already observed by Souza et al. (2008), where the authors applied the Max and Burkhart (1976) taper function to eucalyptus plantations in Brazil.

Future studies using the PMS approach developed in this study should provide additional evaluation with different species, management regimes, and tree spacing in order to reinforce the flexible nature of the PMS approach.

5. Conclusions

The 5th degree polynomial, generalized 5th degree polynomial, Hradetzky (1976), generalized Hradetzky (1976), Kozak (2004), generalized Kozak (2004), Max and Burkhart (1976), generalized Max and Burkhart (1976), PMS and generalized PMS approaches performed well when predicting stem taper and individual tree volume. The PMS and generalized PMS approaches however, displayed the best performance among all the tested approaches. These models were best for accurately predicting volume for all tree size classes, which is indicative of the flexible behavior of the PMS methodology. In particular, the generalized PMS displayed the greatest stability for volume estimation along the stem as opposed to the other generalized functions. In addition, this taper approach enabled the use of a single generalized model to describe the shape of the tree bole for any genetic family regardless age class and allows calibration using relatively few observations for a new genetic family. Finally, the PMS methodology presented in this study was highly efficient for describing both stem form and volume, while being relatively easy to fit. Consequently, its application in future studies is recommended.

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Table 1. Descriptive statistics and number of scaled trees in each age-class for each genetic family of the eucalyptus plantations.

Genetic Family	Data	Age of bucked and scaled trees (years)					DBH (cm)				H (m)				V (m ³)			
		4	5	6	7	Total	Mean	SD	Min.	Max.	Mean	SD	Min.	Max.	Mean	SD	Min.	Max.
1	Fit.	2	21	96	2	121	19.1	3.2	13.1	25.6	26.8	2.7	20.1	32.2	0.37	0.14	0.12	0.72
	Val.	1	7	32	1	41	19.6	3.4	13.4	27.4	27	2.6	21.6	30.4	0.39	0.13	0.14	0.78
2	Fit.	-	23	114	2	139	18.8	3.4	13.1	27.9	25.5	3.2	16.4	31.7	0.34	0.15	0.10	0.80
	Val.	-	8	37	1	46	18.8	3.2	13.6	24.4	25.3	2.9	16.4	32.1	0.34	0.14	0.11	0.62
3	Fit.	-	30	88	24	142	19.2	3.5	12.4	27.4	25.4	2.6	18.3	31.8	0.34	0.14	0.07	0.72
	Val.	-	10	29	8	47	19	3.4	11.2	26.8	25.3	2.5	18.7	29.5	0.33	0.13	0.06	0.64
4	Fit.	-	-	10	30	40	18.3	5.1	10	26.5	21.9	4.2	13.8	28.5	0.27	0.17	0.05	0.65
	Val.	-	-	4	10	14	18.6	5.1	11	26.6	22.3	3.3	15.4	28	0.28	0.15	0.07	0.65

SD: standard deviation; Min.: minimum; Max.: maximum; V: total volume outside bark; Fit.: fitting dataset; and Val.: validation dataset. Genetic Family: 1 (*E. urograndis*), 2 (*E. urograndis*), 3 (*E. urograndis*), 4 (*E. urograndis*).

Table 2. Accuracy statistics (T, MAE, and RMSE) applied to evaluate the dob (cm) and individual tree volume (m^3) estimation for the taper functions.

Genetic family	Taper functions	Validation - dob (cm)			Validation - volume (m^3)		
		T (%)	MAE (%)	RMSE (cm)	T (%)	MAE (%)	RMSE (m^3)
1	5 th degree Polynomial	-1.22	6.46	0.71	-1.58	4.56	0.018
	G. 5 th degree Polynomial	0.56	6.59	0.73	0.04	4.61	0.016
	Hradetzky (1976)	-1.16	7.14	0.73	-1.24	4.51	0.018
	G. Hradetzky (1976)	-0.45	6.99	0.71	0.21	4.48	0.016
	Kozak (2004)	-1.57	6.76	0.65	-0.94	4.23	0.015
	G. Kozak (2004)	-1.16	6.86	0.69	-0.06	4.25	0.015
	Max and Burkhardt (1976)	-2.98	7.61	0.70	-0.91	4.37	0.018
	G. Max and Burkhardt (1976)	-1.83	7.69	0.73	0.18	4.59	0.017
	PMS	-0.81	6.22	0.66	-0.91	4.26	0.015
	G. PMS	-0.17	6.19	0.69	-1.09	4.30	0.014
2	5 th degree Polynomial	1.44	6.72	0.79	0.05	4.46	0.015
	G. 5 th degree Polynomial	2.56	6.88	0.81	1.62	4.69	0.016
	Hradetzky (1976)	1.18	7.39	0.77	0.29	4.44	0.015
	G. Hradetzky (1976)	1.83	7.11	0.76	1.83	4.64	0.016
	Kozak (2004)	0.07	6.46	0.73	-0.14	4.40	0.015
	G. Kozak (2004)	1.94	6.65	0.75	1.24	4.31	0.016
	Max and Burkhardt (1976)	-1.38	7.41	0.78	0.22	4.46	0.016
	G. Max and Burkhardt (1976)	0.55	7.24	0.79	1.55	4.71	0.016
	PMS	1.53	6.41	0.73	-0.07	4.25	0.014
	G. PMS	1.46	6.40	0.72	-0.78	4.27	0.014
3	5 th degree Polynomial	-2.97	7.52	0.84	-1.17	4.91	0.018
	G. 5 th degree Polynomial	-3.98	7.84	0.86	-1.56	4.94	0.019
	Hradetzky (1976)	-1.61	7.49	0.82	-0.96	4.85	0.018
	G. Hradetzky (1976)	-4.30	7.71	0.80	-1.35	4.88	0.019
	Kozak (2004)	-2.63	6.88	0.72	-1.49	4.83	0.015
	G. Kozak (2004)	-4.05	7.59	0.71	-1.69	4.82	0.015
	Max and Burkhardt (1976)	-4.64	8.85	0.82	-0.92	4.81	0.017
	G. Max and Burkhardt (1976)	-6.43	9.85	0.85	-1.58	4.92	0.018
	PMS	-2.53	6.83	0.72	-1.19	4.73	0.015
	G. PMS	-2.76	6.92	0.72	-1.59	4.82	0.015
4	5 th degree Polynomial	0.08	7.80	0.77	2.39	4.81	0.013
	G. 5 th degree Polynomial	-3.97	7.84	0.85	-4.91	6.46	0.017
	Hradetzky (1976)	1.68	9.37	0.80	2.37	4.87	0.013
	G. Hradetzky (1976)	-4.30	7.71	0.80	-4.64	6.26	0.017
	Kozak (2004)	0.80	6.61	0.76	2.06	5.22	0.018
	G. Kozak (2004)	-4.05	7.59	0.71	-4.85	6.61	0.016
	Max and Burkhardt (1976)	-1.26	7.95	0.76	2.11	4.94	0.013
	G. Max and Burkhardt (1976)	-6.43	9.85	0.85	-5.11	6.54	0.014
	PMS	0.33	7.64	0.77	2.15	5.13	0.016
	G. PMS	-0.76	7.66	0.76	-0.42	5.01	0.012

G.: Generalized

Table 3. Rank of each the taper models examined in this analysis based on T (%), MAE (%), and RMSE. These were calculated for dob (cm) at multiple stem heights and individual tree volume (m³) for the four genetic families.

Genetic family	Statistic	5 th degree Polynomial		G. 5 th degree Polynomial		Hradetzky (1976)		G. Hradetzky (1976)		Kozak (2004)		G. Kozak (2004)		Max and Burkhart (1976)		G. Max and Burkhart (1976)		PMS		G. PMS	
		dob	vol	dob	vol	dob	vol	dob	vol	dob	vol	dob	vol	dob	vol	dob	vol	dob	vol	dob	vol
1	T (%)	7	10	3	1	5	9	2	4	8	7	5	2	10	5	9	3	4	5	1	8
	MAE (%)	3	8	4	10	8	7	7	6	5	1	6	2	9	5	10	9	2	3	1	4
	RMSE	6	8	8	5	8	8	6	5	1	2	3	2	5	8	8	7	2	2	3	1
2	T (%)	5	1	10	9	3	5	8	10	1	3	9	7	4	4	2	8	7	2	6	6
	MAE (%)	5	6	6	9	9	5	7	8	3	4	4	3	10	6	8	10	2	1	1	2
	RMSE	8	3	10	6	6	3	5	6	2	3	4	6	7	6	8	6	2	1	1	1
3	T (%)	5	3	6	7	1	2	8	5	3	6	7	10	9	1	10	8	2	4	4	9
	MAE (%)	5	8	8	10	4	6	7	7	2	5	6	3	9	2	10	9	1	1	3	3
	RMSE	8	6	10	9	6	6	5	9	2	1	1	1	6	5	9	6	2	1	2	1
4	T (%)	1	6	7	9	6	5	9	7	4	2	8	8	5	3	10	10	2	4	3	1
	MAE (%)	6	1	7	8	9	2	5	7	1	6	2	10	8	3	10	9	3	5	4	4
	RMSE	5	2	9	8	7	2	7	8	2	10	1	6	2	2	9	5	5	6	2	1
Total		64	62	88	91	72	60	76	82	34	50	56	60	84	50	103	90	34	35	31	41

Vol: individual tree volume (m³); G.: Generalized

Table 4. Accuracy statistics (T, MAE and RMSE) applied to evaluate the individual tree volume (m^3) estimation for the taper functions with the dataset stratified (trees with DBH < 33th quantile; trees with DBH > 33th and < 67th quantile; trees with DBH > 67th quantile).

Genetic family	Taper functions	DBH < 33th quantile			33th < DBH < 67th quantile			DBH > 67th quantile		
		T (%)	MAE (%)	RMSE (m^3)	T (%)	MAE (%)	RMSE (m^3)	T (%)	MAE (%)	RMSE (m^3)
1	5 th degree Polynomial	-2.32	5.09	0.019	-1.23	4.13	0.019	-1.32	4.61	0.017
	G. 5 th degree Polynomial	-1.21	5.28	0.017	0.24	4.35	0.017	0.88	4.34	0.015
	Hradetzky (1976)	-2.13	5.06	0.018	-1.01	4.13	0.018	-0.74	4.47	0.016
	G. Hradetzky (1976)	-0.75	5.00	0.017	0.46	4.19	0.017	0.74	4.34	0.016
	Kozak (2004)	-1.53	4.46	0.014	-0.54	3.86	0.015	-0.91	4.47	0.015
	G. Kozak (2004)	-0.97	4.65	0.014	0.19	3.89	0.015	0.44	4.32	0.015
	Max and Burkhardt (1976)	-1.67	4.78	0.019	-0.63	4.01	0.019	-0.57	4.43	0.016
	G. Max and Burkhardt (1976)	-1.04	5.19	0.018	0.34	4.36	0.018	1.03	4.35	0.015
	PMS	-1.40	4.42	0.015	-0.46	3.94	0.015	-0.99	4.48	0.015
	Full PMS	-1.77	4.64	0.014	-0.65	3.88	0.015	-0.99	4.50	0.015
2	5 th degree Polynomial	-0.85	4.97	0.017	0.66	4.19	0.014	0.08	4.34	0.014
	G. 5 th degree Polynomial	0.83	4.94	0.017	2.20	4.54	0.015	1.59	4.66	0.015
	Hradetzky (1976)	-0.66	4.88	0.017	0.91	4.17	0.014	0.35	4.36	0.014
	G. Hradetzky (1976)	1.13	4.88	0.017	2.35	4.46	0.015	1.83	4.67	0.015
	Kozak (2004)	-1.13	4.62	0.015	0.50	4.32	0.015	-0.05	4.30	0.014
	G. Kozak (2004)	0.41	4.22	0.016	1.85	4.43	0.016	1.24	4.27	0.016
	Max and Burkhardt (1976)	-0.72	4.93	0.018	0.87	4.22	0.015	0.26	4.33	0.015
	G. Max and Burkhardt (1976)	0.73	4.97	0.018	2.16	4.57	0.016	1.52	4.66	0.016
	PMS	-1.08	4.59	0.016	0.58	4.14	0.014	0.03	4.09	0.014
	Full PMS	-1.08	4.76	0.016	-0.16	4.12	0.013	-0.66	4.06	0.013
3	5 th degree Polynomial	-1.54	5.13	0.017	-1.77	4.67	0.022	-0.22	4.91	0.015
	G. 5 th degree Polynomial	-1.78	5.06	0.018	-2.24	4.90	0.023	-0.67	4.84	0.015
	Hradetzky (1976)	-1.33	5.05	0.017	-1.58	4.62	0.022	0.01	4.84	0.015
	G. Hradetzky (1976)	-1.63	4.98	0.018	-1.99	4.91	0.023	-0.44	4.74	0.015
	Kozak (2004)	-1.61	5.01	0.015	-2.11	4.83	0.017	-0.76	4.63	0.015
	G. Kozak (2004)	-1.71	4.90	0.015	-2.39	5.01	0.018	-0.99	4.54	0.013
	Max and Burkhardt (1976)	-1.18	4.96	0.016	-1.57	4.61	0.021	-0.04	4.86	0.015
	G. Max and Burkhardt (1976)	-1.73	4.96	0.017	-2.31	4.95	0.022	-0.72	4.86	0.015
	PMS	-1.33	4.89	0.015	-1.63	4.59	0.017	-0.61	4.69	0.014
	G. PMS	-1.68	4.95	0.015	-2.02	4.74	0.018	-1.04	4.77	0.014
4	5 th degree Polynomial	2.31	5.19	0.015	2.07	4.44	0.012	3.22	4.43	0.011
	G. 5 th degree Polynomial	-5.56	7.02	0.018	-4.94	6.41	0.017	-3.42	5.24	0.012
	Hradetzky (1976)	2.26	5.23	0.015	1.75	4.42	0.012	3.15	4.43	0.011
	G. Hradetzky (1976)	-5.27	6.78	0.018	-4.20	5.96	0.017	-3.61	5.34	0.012
	Kozak (2004)	1.99	5.64	0.020	1.71	4.69	0.017	2.55	4.73	0.014
	G. Kozak (2004)	-5.03	7.02	0.015	-4.79	6.39	0.013	-4.47	5.89	0.010
	Max and Burkhardt (1976)	2.01	5.34	0.014	1.74	4.42	0.012	2.66	4.50	0.010
	G. Max and Burkhardt (1976)	-5.65	7.03	0.018	-5.06	6.51	0.017	-3.89	5.45	0.011
	PMS	2.06	5.44	0.018	1.69	4.61	0.015	2.62	4.77	0.013
	G. PMS	1.46	5.39	0.014	-0.67	4.69	0.012	-0.21	4.39	0.009

G.: Generalized

Table 5. Ranking of various approaches examined to evaluate the taper function that best described individual tree volume (m³) for all the genetic families with the dataset stratified.

GF	Stat.	Pol	G. Pol	Hra	G. Hra	Koz	G. Koz	MB	G. MB	PMS	G. PMS
DBH < 33th quantile											
1	T	10	4	9	1	6	2	7	3	5	8
	MAE	8	10	7	6	2	4	5	9	1	3
	RMSE	9	5	7	5	1	1	9	7	4	1
2	T	6	5	2	9	9	1	3	4	7	7
	MAE	9	8	5	5	3	1	7	9	2	4
	RMSE	5	5	5	5	1	2	9	9	2	2
3	T	4	10	2	6	5	8	1	9	2	7
	MAE	10	9	8	6	7	2	4	4	1	3
	RMSE	6	9	6	9	1	1	5	6	1	1
4	T	6	9	5	8	2	7	3	10	4	1
	MAE	1	8	2	7	6	8	3	10	5	4
	RMSE	3	6	3	6	10	3	1	6	6	1
Total		77	88	61	73	53	40	57	86	40	42
33th < DBH < 67th quantile											
1	T	10	2	9	4	6	1	7	3	4	8
	MAE	6	9	6	8	1	3	5	10	4	2
	RMSE	9	5	7	5	1	1	9	7	1	1
2	T	4	9	6	10	2	7	5	8	3	1
	MAE	4	9	3	8	6	7	5	10	2	1
	RMSE	2	5	2	5	5	9	5	9	2	1
3	T	4	8	2	5	7	10	1	9	3	6
	MAE	4	7	3	8	6	10	2	9	1	5
	RMSE	6	9	6	9	1	3	5	6	1	3
4	T	6	9	5	7	3	8	4	10	2	1
	MAE	3	9	1	7	5	8	1	10	4	5
	RMSE	1	7	1	7	7	5	1	7	6	1
Total		59	88	51	83	50	72	50	98	33	35
DBH > 67th quantile											
1	T	10	5	3	3	6	1	2	9	7	7
	MAE	10	2	6	2	6	1	5	4	8	9
	RMSE	10	1	7	7	1	1	7	1	1	1
2	T	3	9	5	10	2	7	4	8	1	6
	MAE	6	8	7	10	4	3	5	8	2	1
	RMSE	2	6	2	6	2	9	6	9	2	1
3	T	3	6	1	4	8	9	2	7	5	10
	MAE	10	6	6	4	2	1	8	8	3	5
	RMSE	4	4	4	4	4	1	4	4	2	2
4	T	6	7	5	8	2	10	4	9	3	1
	MAE	2	7	2	8	5	10	4	9	6	1
	RMSE	4	7	4	7	10	2	2	4	9	1
Total		70	68	52	73	52	55	53	80	49	45

GF: Genetic Family; Stat.: Statistics; G: Generalized; Pol: 5th degree polynomial; F Pol: Full 5th degree polynomial; Hra: Hradetzky (1976); F Hra: Full Hradetzky (1976); Koz: Kozak (2004); F Koz: Full Kozak (2004); MB: Max and Burkhardt (1976); F MB: Full Max and Burkhardt (1976); F PMS: Full PMS.

Table 6. Average accuracy statistics (T, MAE and RMSE) and their confidence intervals at 95% confidence level applied to evaluate the individual tree volume (m^3).

Statistics	Mean	Confidence Interval (95 %)	
		Lower	Upper
T (%)	-1.09	-1.32	-0.85
MAE (%)	4.53	4.32	4.68
RMSE (m^3)	0.015	0.014	0.016

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Figure 1. Location of sampled Eucalyptus stands in Água Clara, MS.

Figure 2. Comparison of examined taper approaches for predicting stem taper of genetic family 1.

Figure 3. Residual plot with lowess trendlines to verify performances of various approaches for predicted volume across stem height for genetic families.

Figure 4. Overall sampling distribution of the accuracy statistics T, MAE and RMSE.

Figure 5. Residual plot with lowess trendlines to verify performances of PMS approaches with and without the variable tree size.

Figure 1. Location of sampled Eucalyptus stands in Água Clara, MS.

297x210mm (300 x 300 DPI)

Figure 2. Comparison of examined taper approaches for predicting stem taper of genetic family 1.
259x259mm (300 x 300 DPI)

Figure 3. Residual plot with lowess trendlines to verify performances of various approaches for predicted volume across stem height for genetic families.

259x259mm (300 x 300 DPI)

Figure 4. Overall sampling distribution of the accuracy statistics T, MAE and RMSE.

176x239mm (72 x 72 DPI)

Figure 5. Residual plot with lowess trendlines to verify performances of PMS approaches with and without the variable tree size.

259x259mm (300 x 300 DPI)