

HEIGHT-DIAMETER MODELS IN FORESTRY WITH INCLUSION OF COVARIATES

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ABSTRACT: The main difficulty in selecting height-diameter relationships is the large number of variables involved. Techniques for decomposition of model parameters with inclusion of covariates relating to individual trees and to the stand collectively can improve model precision. This study aimed to evaluate quality improvement in the fit of height-diameter models by inclusion of covariates. The data in this study was obtained from commercial *Eucalyptus* sp. plantations in southern Bahia state. Firstly two reduced models were fitted, one linear and another nonlinear, considering the same trend of height variation as a function of diameter, for all genetic materials being studied. Between the two, the logistic model presented the best performance for the relevant database. After fitting parameters for the selected model, the complete formulation was fit with inclusion of variables relating to individual trees, which improved model precision. A reduction of 17% was observed in the residual standard error value when comparing reduced model and complete model, with inclusion of covariates.

Key words: *Eucalyptus*, height-diameter relationship, modeling.

MODELOS HIPSOMÉTRICOS FLORESTAIS COM A INCLUSÃO DE COVARIANTES

RESUMO: A principal dificuldade na modelagem da relação hipsométrica é o grande número de variáveis que a influenciam. Diante disso, técnicas de decomposição dos parâmetros do modelo, com a inclusão de covariantes relacionadas com árvores individuais e com o povoamento, podem melhorar a precisão do mesmo. Este estudo foi realizado com o objetivo de avaliar a melhoria da qualidade do ajuste de modelos hipsométricos pela inclusão de covariantes. Os dados do presente estudo são provenientes de plantios comerciais de *Eucalyptus* sp. situados na região sul do estado da Bahia. Inicialmente, foram ajustados dois modelos reduzidos, um linear e um não linear, considerando a mesma tendência de variação da altura em função do diâmetro, para todos os materiais genéticos estudados. Entre os dois modelos, o logístico foi o que apresentou melhor performance para a base de dados em questão. Após o ajuste dos parâmetros do modelo selecionado, a formulação completa foi ajustada com a inclusão das variáveis relativas à árvore individual, melhorando-se, com isso, a precisão do modelo. Houve uma redução de 17% no valor do erro padrão residual quando comparados o modelo reduzido e o modelo completo, com a inclusão das covariantes.

Palavras-chave: *Eucalyptus*, relação hipsométrica, modelagem.

1 INTRODUCTION

Forest inventory studies usually measure the diameter of all trees in a plot and the height of some. The aggregate data set is used for establishing a height to diameter relationship, which will then be used for estimating the height of the remaining trees in the plot on the basis of already measured diameters (MACHADO et al. 1993).

The use of height-diameter equations in forest inventory studies has been common practice and has rendered inventories more economical and quicker to make.

The height-diameter relationship describes the correlation between height and diameter of the trees in a stand on a given date (SCHMIDT 1977), and this relationship can be represented by a mathematical model. According to the author, height-diameter relationships

have been widely studied by several researchers through an array of mathematical models that are reasonably efficient, conditional on stand composition and site quality.

The modeling of forest phenomena has evolved considerably in recent decades, and among various methods of representing total height as a function of DBH are linear and nonlinear models.

Linear regression models can be applied to diverse fields of knowledge. Many a time the linear model is used only due to the ease in which the approximate relationship is described. The true relationship, however, between a dependent variable and one or more independent variables can be described by a nonlinear model, to be determined based on theoretical knowledge of the problem being addressed. Thus, in many situations linear models may be unsuitable. A typical example in the field of biological

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sciences is growth modeling, where it might be necessary to fit nonlinear functions to best explain the growth process. Here, the following references may be useful: Bates & Watts (1988), Calegario et al. (2005), Cordeiro & Paula (1989), Draper & Smith (1981), Gallant (1987), Khattree & Naik (1999), Myers (1990), Ratkowsky (1983) and Souza (1998), to name a few.

A major difficulty in modeling the height-diameter relationship, as cited by Batista et al. (2001), is the large number of variables influencing it and thus hindering the construction of generic models based on empirical methods such as linear and nonlinear regression. With that said, techniques to decompose parameters of a nonlinear model, with inclusion of covariates relating to individual trees and to the stand collectively can improve model precision. This study aimed to evaluate quality improvement in the fit of height-diameter models by inclusion of covariates.

2 MATERIAL AND METHODS

2.1 Location and characterization of study site

To conduct this research, we used biometric data from commercial *Eucalyptus* sp. plantations in southern Bahia state (Figure 1). The region lies between 17°17'30" and 17°54'01" of south latitude and between 39°11'39" and 40°26'26" of west longitude.

The study site comprises areas with flat to slightly rugged topography and altitudes of 5-100 m above sea level, also known as 'Tabuleiros Costeiros'. Geologically, most areas correspond to 'Barreiras' formation, which is characterized by depositions of clayey sandy sediments predominantly from the tertiary period, interposed with laterite beds and pebble layers on crystalline bedrock.

The local climate ranges from Af (hot and humid with no dry season and rainfall above 1,300 mm/year) in coastal strips, to Aw (hot and humid with dry winter and rainfall above 750 mm) toward the interior.

The local predominant soils include cohesive argisols and spodosols, the latter being typically acid and low fertility soils with high aluminum saturation.

The original vegetation includes areas of Atlantic Forest tableland (Ombrophilous Dense Forest and Semi-evergreen Seasonal Tropical Forest), also known as 'Hiléia Sul-Bahiana'. In more recent patches of sandy sediment, typically boasting a shallower impervious layer or a more superficial water table, fragments occur of a vegetation known locally as 'muçununga' (predominance of shrub-tree stratum) and native flooded grasslands (predominance of herbaceous stratum).

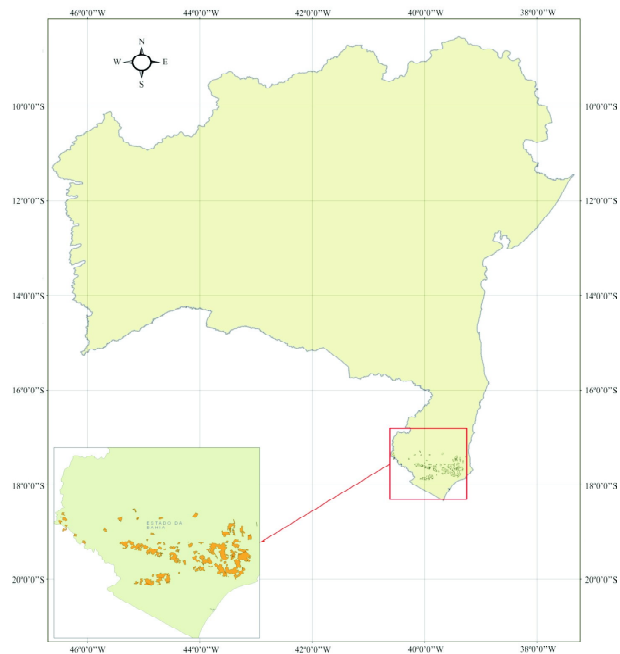


Figure 1 – Location of study site.

Figura 1 – Localização da região de estudo.

2.2 Data collection

Biometric data were obtained from 2,657 permanent plots installed according to a sample intensity of 1:5, with tree age ranging between 2 and 6 years.

Plots were defined as a function of a preset number of trees, which corresponds to 4 rows of 5 plants (20 plants) extending over approximately 180m².

In each plot we measured the diameter of all trees, the total height of five and the height of two dominant trees, besides the plot area and qualitative information about trees. Equipment used included an electronic caliper, a Suunto clinometer and a measuring tape, following a zigzag pattern of measurement.

All data were stored in the electronic caliper to be later downloaded and submitted to consistency analysis and processing.

2.3 Reduced model

To fit reduced models, in other words, without inclusion of covariates, the total height of trees was modeled as a function of the diameter of all individuals in the stand, ignoring the group structure.

Two models were tested, one linear and one

nonlinear, respectively represented by a polynomial model of degree 2 (1) and a logistic model (2):

$$HT_i = \beta_0 + \beta_1 DBH_i + DBH_i^2 + \varepsilon_i \quad (1)$$

$$HT_i = \frac{A}{1 + \exp\left[\frac{C - DBH_i}{E}\right]} + \varepsilon_i \quad (2)$$

where:

- HT_i: total height of i-th tree (meters);
- DBH_i: diameter at breast height of i-th tree (centimeters);
- β₀, β₁, A, I and E: parameters to be estimated by regression;

ε_i: statistical error with normal distribution, zero mean and constant variance.

The polynomial model is widely used for modeling height as a function of diameter, considering that variation in the former variable is not linear as a function of the latter.

Likewise, the logistic model (2) was originally proposed for modeling growth in human populations and later became popular for studying plant growth (ZEIDE 1993). In this model, the generated curves show monotonic growth until they reach a point of inflection where maximum growth is achieved, after which point it declines and tends to zero in the upper horizontal asymptote.

Parameters A, C and E refer to asymptote, point of inflection and scale respectively. Asymptote is the maximum point reached by the curve and has the unit of y-axis. Point of inflection refers to mean response age and has the unit of x-axis. Scale refers to the point at about 0.73% of the asymptote and has the unit of x-axis.

2.4 Complete model

Based on the fact that variation in the total height of individual trees is not explained by diameter alone, the general model parameters were decomposed associating variables such as age and genetic material to them. The great flexibility of this method lies in the fact that the variables may be associated to one parameter and not to another, depending on significance.

The polynomial model of degree 2 (3) and the logistic model (4 and 5) are presented below, with inclusion of covariates:

$$HT_i = \left(\beta_0 + \sum_{i=1}^n I\beta_{0i}MG\right) + \left(\beta_1 + \sum_{i=1}^n I\beta_{1i}MG\right)DBH_i + \left(\beta_2 + \sum_{i=1}^n I\beta_{2i}MG\right)DBH_i^2 + \varepsilon_i \quad (3)$$

$$HT_i = \frac{A + \sum_{i=1}^n IA_iMG}{1 + e^{\left[\frac{\left(C + \sum_{i=1}^n IC_iMG\right) - DBH_i}{\left(E + \sum_{i=1}^n IE_iMG\right)}\right]}} + \varepsilon_i \quad (4)$$

$$HT_i = \frac{A + \sum_{i=1}^n IA_iMG + A_{n+1}Age}{1 + e^{\left[\frac{\left(C + \sum_{i=1}^n IC_iMG\right) - DBH_i}{\left(E + \sum_{i=1}^n IE_iMG\right)}\right]}} + \varepsilon_i \quad (5)$$

where:

- HT_i: total height of i-th tree (meters);
- DBH_i: diameter at breast height of i-th tree (centimeters);

β₀, β₁, A, C and E: fixed parameters;

∑ⁿ_{i=1} Iβ_j_iMG: refers to parameter associated to i-th genetic material and I is an indicator variable with value 1 for the i-th genetic material and 0 for other materials, for the j-th parameter;

∑ⁿ_{i=1} IA_iMG: refers to parameter associated to i-th genetic material and I is an indicator variable with value 1 for the i-th genetic material and 0 for other materials, for parameter asymptote;

∑ⁿ_{i=1} IC_iMG: refers to parameter associated to i-th genetic material and I is an indicator variable with value 1 for the i-th genetic material and 0 for other materials, for parameter inflection;

∑ⁿ_{i=1} IE_iMG: refers to parameter associated to i-th genetic material and I is an indicator variable with value 1 for the i-th genetic material and 0 for other materials, for parameter scale;

A_{n+1}: effect associated to age, for parameter asymptote;

ε_i: statistical error with normal distribution, zero mean and constant variance.

2.5 Fit method and statistical analysis

To fit the models application S-PLUS was used, looking to obtain comparative statistics, particularly the residual standard error.

After the reduced models were fitted and analyzed, parameters were decomposed and estimated with inclusion of covariate genetic material.

After the best complete model was selected, it was fitted with the additional effect of tree age, other than the already included genetic material.

Comparison between complete models with and without the age effect was done using the likelihood ratio test (LRT) which compares the differences among the linearized maximum likelihood functions of each model to the value obtained of a chi-square distribution, with number of degrees of freedom equal to the difference in number of parameters between models 1 and 2, given by:

$$\left\{ \left[\frac{ka_1(ka_{1+2})}{2} \right] + \left[\frac{kap_1(kap_{1+2})}{2} \right] + e_{i_1} \right\} - \left\{ \left[\frac{ka_2(ka_{2+1})}{2} \right] + \left[\frac{kap_2(kap_{2+1})}{2} \right] + e_{i_2} \right\}$$

where: $e(i)$ represents the number of residual variances considered in each model.

Besides the MLRT, the Akaike information criterion (AIC) and Schwarz Bayesian information criterion (BIC) were also used as references. Both tests allow comparison between non-nested models and penalize models with a greater number of parameters. In the case of BIC the penalty is more stringent, tending to favor more parsimonious models (NUNEZ-ANTÓN & ZIMMERMAN 2000; WOLFINGER 1993). In the case of AIC, the comparison value is given by:

$$AIC = -2 \log L + 2p$$

and in the case of BIC, comparison is given by:

$$BIC = -2 \log L + p \log(N - r)$$

where: p refers to the number of model parameters, N is the total number of observations and r is the rank of matrix X , which is the incidence matrix for fixed effects.

Lower AIC and BIC values indicate better fit.

3 RESULTS AND DISCUSSION

3.1 Analysis of data

The relationship between DBH (cm) and HT(m) in the materials studied is illustrated in Figure 2. We noted a consistent increment in HT with increase in diameter, yet with variations in the intercept and/or inclination of curves, for each genetic material.

3.2 Reduced models fit

The first step was to fit reduced equations based on linear and nonlinear models, relating HT as response and DBH as covariate for all materials, ignoring the group structure.

As is verified in Table 1 data, the two models used for explaining height variation as a function of DBH had

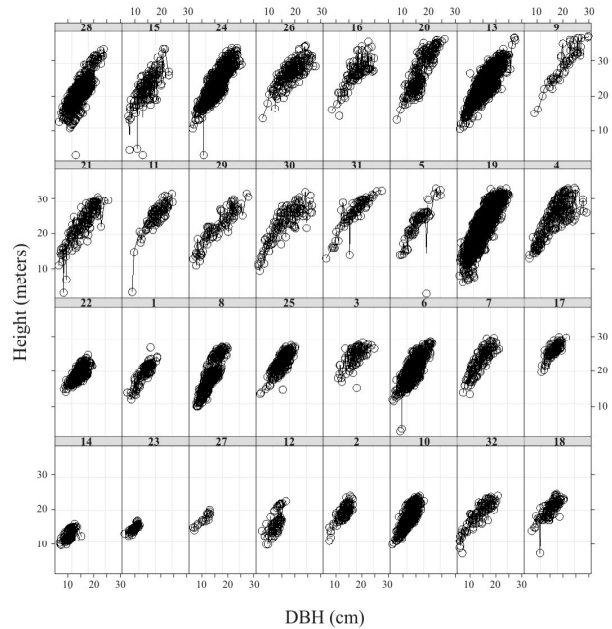


Figure 2 – Linear relationship between total height (meters) and diameter at breast height (cm), for 32 clones.

Figura 2 – Relação linear entre a altura total (metros) e o diâmetro à altura do peito (cm), para 32 clones.

significance on the parameters. Therefore, considering this criterion alone, either of the two models could be used for estimating height as a function of DBH. Yet, based on other criteria, the nonlinear model proves superior. Observing the standard error of each model, the logistic model presents lower values, generating narrower confidence intervals and higher t-values associated to parameters. Another positive characteristic of the logistic model is associated with the correlations between parameters. Table 1 data also reveals that the correlations between pairs of parameters were lower, indicating that the presence of parameters is necessary and that the model does not have an excessive number of parameters. Another important characteristic of the logistic model, as mentioned previously, is its interpretability for the three parameters, which facilitates the algorithm convergence process to estimate them.

3.3 Complete models fit

To verify differences between genetic materials, complete equations were fitted, generating a model more practical to use. Thus, the parameters of the polynomial model of degree 2 and logistic model were decomposed and estimated with inclusion of genetic material (Table 2).

Table 1 – Estimates and correlations for two reduced models used in the representation of variation in height as a function of DBH.**Tabela 1** – Estimativas e correlações para os dois modelos reduzidos utilizados na representação da variação da altura em função do DAP.

Param.	Estimates					Correlations	
	Value	Standard error	D.F.	t-value	p-value	β_1	β_2
Quadratic model (RSE=2.214 m)							
β_0	-0.2686	0.2825	17018	-0.951	0.341	-0.98	0.95
β_1	1.7880	0.0364	17018	49.055	<0.0001	X	-0.98
β_2	-0.0201	0.0012	17018	-17.37	<0.0001	X	X
Logistic model (RSE=2.208 m)							
				C	E		
A	36.2981	0.3468	17018	104.64	<0.0001	0.98	0.94
C	11.9641	0.1325	17018	90.241	<0.0001	X	0.90
E	7.0140	0.1160	17018	60.437	<0.0001	X	X

Table 2 – Estimates and correlations for complete models used in the representation of variation in height as a function of DBH and genetic material.**Tabela 2** – Estimativas e correlações para os modelos completos utilizados na representação da variação da altura em função do DAP e material genético.

Parameters	Estimates					Correlations	
	Value	Standard error	D.F.	t-value	p-value	β_1	β_2
Quadratic model (RSE=1.944 m)							
β_0	2.3541	0.9663	17018	2.4361	0.0149	-0.94	0.88
β_1	1.6198	0.1528	17018	10.600	<0.0001	X	-0.97
β_2	-0.0207	0.0052	17018	-3.965	<0.0001	X	X
Logistic model (RSE=1.947 m)							
				C	E		
A	32.5438	0.9486	17018	34.305	<0.0001	0.21	0.24
C	9.9173	0.4395	17018	22.562	<0.0001	X	0.17
E	6.9400	0.3810	17018	18.214	<0.0001	X	X

As can be noted, the inclusion of genetic material in both models reduced the residual standard error by around 10% (from 2.14 to 1.94), allowing better fit and consequently more accurate estimates of the total height of trees.

Both the polynomial and the logistic model could be used to estimate the total height of trees within each group. However, the logistic model not only presented a desirable biological response but was also slightly superior in relation to correlations between parameters. For this reason it was used in the other analyses.

Results of the effect of genetic material are illustrated in Table 3. All interactions had a significant probability

value, indicating different growth patterns.

Figures 3 and 4 illustrate different total height growth patterns as a function of diameter at breast height in individual trees per group of material, using the polynomial and the logistic models, respectively, for estimation. In both models we can clearly notice a difference in behavior when they are applied to each group separately (dotted line).

After selecting the logistic model as the best complete height-diameter model, the next step was to include the effect of age in the asymptote so as to obtain yet more accurate estimates, the results of which are illustrated in Table 4.

Table 3 – Estimated parameters of complete models.**Tabela 3** – Parâmetros estimados para os modelos completos.

Term added to parameter	Polynomial model of degree 2			Logistic model		
	β_0	β_1	β_2	Asymptote	Inflection	Scale
Genmat 1*	-1.387533	0.145001	-0.007510	-2.768895	-0.666884	-0.46322
Genmat 2	1.419338	-0.171932	0.001220	-1.796034	-0.853857	0.635241
Genmat 3	-1.536684	0.508234	-0.022902	-3.453299	-2.979254	-0.76589
Genmat 4	-9.364346	1.417943	-0.043698	-2.816172	-0.917199	-2.86373
Genmat 5	-1.066129	0.129979	-0.002245	0.676386	0.227467	-0.31008
Genmat 6	4.515481	-0.757154	0.027755	4.990816	2.591431	1.662648
Genmat 7	-3.390931	0.828903	-0.030030	-1.476943	-2.016944	-1.34294
Genmat 8	-3.184220	-0.137648	0.017246	2.409503	2.822493	-0.90043
Genmat 9	-1.401787	0.178514	0.000420	5.697664	1.980222	0.045287
Genmat 10	0.288910	-0.285287	0.010584	-1.547723	0.573953	-0.04808
Genmat 11	-8.095052	0.943041	-0.025766	-3.365577	0.751660	-3.24154
Genmat 12	4.200140	-1.151040	0.043364	-1.762910	2.045218	0.064740
Genmat 13	2.225429	-0.242288	0.008817	5.601214	1.817448	1.896370
Genmat 14	5.613368	-1.413012	0.045675	-6.486923	0.7565803	1.572661
Genmat 15	-0.959787	0.254911	-0.008730	0.185332	-0.640303	-0.15555
Genmat 16	-5.791261	1.012260	-0.030918	-0.941573	-0.938106	-2.02674
Genmat 17	-4.037008	0.989139	-0.034714	-0.153696	-2.537345	-0.65407
Genmat 18	3.101626	-0.438779	0.006638	-3.137611	-1.186931	1.368292
Genmat 19	-3.455746	0.261506	-0.001144	3.024837	1.741143	-0.36573
Genmat 20	1.441996	-0.180542	0.015956	10.505499	3.068576	0.629944
Genmat 21	-1.916961	0.317467	-0.009964	-0.384725	-0.362023	-0.58545
Genmat 22	4.204586	-0.546755	0.008113	-3.825357	-1.942785	1.818998
Genmat 23	5.479937	-1.044091	0.033444	-2.854937	0.059101	1.488464
Genmat 24	3.997329	-0.542935	0.020658	8.837047	3.425569	2.288988
Genmat 25	0.527090	0.152515	-0.008906	-0.721545	-1.591112	0.273073
Genmat 26	-0.607897	0.462507	-0.017532	-0.785994	-2.301772	-0.81619
Genmat 27	5.276994	-0.733804	0.020898	-1.175605	-0.838053	1.556080
Genmat 28	7.928571	-1.210781	0.042286	9.226472	4.575269	2.894405
Genmat 29	1.437360	-0.181150	0.002348	-0.617851	-0.235401	0.778310
Genmat 30	-4.054545	0.844014	-0.031793	-4.816947	-2.227449	-2.78976
Genmat 31	-0.830386	0.457961	-0.015433	0.530314	-1.660629	-0.62769
Genmat 32	-0.577881	0.133302	-0.014139	-6.794767	-2.540083	-0.01635

* Genmat = genetic material

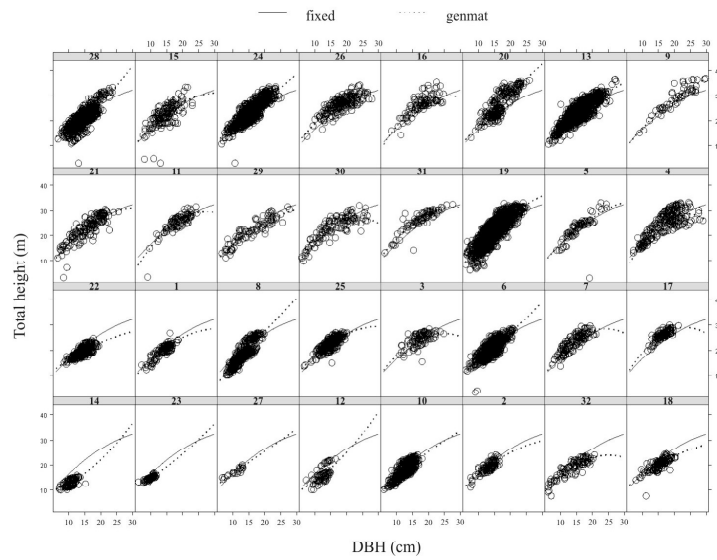


Figure 3 – Height growth patterns as a function of diameter at breast height per genetic material (Genmat), as obtained by complete fit of the polynomial model of degree 2.

Figura 3 – Padrões de crescimento da altura, em função do diâmetro à altura do peito, para cada material genético (Genmat), obtidos pelo ajuste completo do modelo polinomial de grau 2.

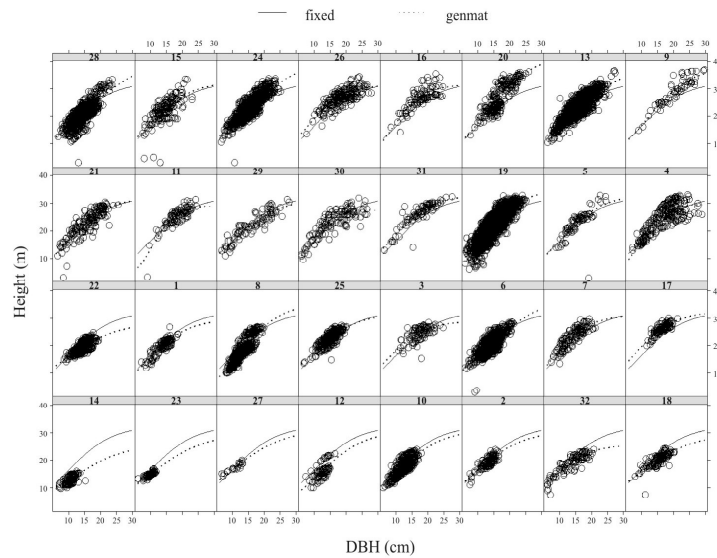


Figure 4 – Height growth patterns as a function of diameter at breast height per genetic material (Genmat), as obtained by complete fit of the logistic model.

Figura 4 – Padrões de crescimento da altura em função do diâmetro à altura do peito, para cada material genético (Genmat), obtidos pelo ajuste completo do modelo logística.

All parameters were found to be highly significant, indicating that a variation exists in the growth pattern among clones and among ages. Table 5 confirms this assumption by the maximum likelihood ratio test (MLRT) and the values of Akaike information criterion (AIC) and Schwarz Bayesian information criterion (BIC).

We noted significant changes ($P < 0.0001$) for the MLRT and also lower AIC and BIC values, with inclusion of the age effect in the asymptote, rendering this model more suitable for describing the data. Another important point was a reduction by 10% in the residual standard error (from 1.94 to 1.76), contributing significantly to obtaining more accurate estimates.

4 CONCLUSIONS

Out of the two tested models ignoring the group structure (linear polynomial of degree 2 and nonlinear logistic model), the model with best performance for the relevant database was the logistic model for presenting lower residual standard error and lower correlations

between the estimated parameters, indicating that there is no excess parameters in the model. Additionally, the important biological interpretability of parameters by this model significantly facilitates choosing initial values for the iterative process of the algorithm used for estimating the parameters;

The inclusion of covariates in the selected model, associated individually to the parameters, significantly improved model precision;

The complete model fit with inclusion of desired covariates presents more practical usability, as the sources of influence on the height growth pattern can be included in the relevant model, thus eliminating the need to stratify the stand which would entail a large number of equations and coefficients being registered in forest inventory systems.

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Table 4 – Estimated parameters and respective statistics for the complete logistic model, taking genetic material and tree age as covariate.

Tabela 4 – Parâmetros estimados e respectivas estatísticas para o modelo logístico completo, tomando-se como co-variável o material genético e a idade das árvores.

Parameter	Term added to parameter	Value	Standard error	D.F.	t-value	Probability
Asymptote	Intercept	21.4977	0.3851	17017	55.826	<0.0001
	Age	1.41354	0.0196	17017	72.025	<0.0001
Inflection	Intercept	8.20658	0.2254	17017	36.413	<0.0001
Scale	Intercept	5.09140	0.0833	17017	61.110	<0.0001

Residual standard error = 1.764528

Table 5 – Comparison between the complete logistic model without the age effect and the complete logistic model with the age effect on the asymptote.

Tabela 5 – Comparação entre o modelo logístico completo sem o efeito da idade e o modelo logístico completo com o efeito da idade na assíntota.

Model	DF	AIC	BIC	LogML	MLRT	p-value
1 – Complete logistic model (without age)	6	71615	71661	-35801		
2 – Complete logistic model (with age)	7	68016	68070	-34001	1vs2=3601	<0.0001

DF = degrees of freedom; AIC = Akaike information criterion; BIC = Bayesian information criterion; LogML = maximum likelihood algorithm; MLRT = maximum likelihood ratio test; p-value = value of probability above the calculated chi-square value.

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