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Artificial Neural Networks for early prediction of eucalyptus stem diameter across climatic gradientes

Predição precoce do diâmetro de fuste de eucalipto em um gradiente climático utilizando Redes Neurais Artificiais

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ABSTRACT

Developing an artificial neural network (ANN) model for predicting eucalyptus growth where no plantations have been previously established is extremely important. Thus, this work aims to model the growth of a eucalypt clonal stand using ANN and to evaluate the model's ability to be applied to other sites with different genetic materials and edaphoclimatic conditions. The used data files were obtained from continuous forest inventories of 18 commercial *Eucalyptus* clones from 17 sites in different states of Brazil, that are part of the TECHS project (Tolerance of Clonal *Eucalyptus* to Water, Thermal and Biotic Stresses). The multilayer networks were tested using the error backpropagation learning algorithm and activation function of the hyperbolic tangent type. The quality of the selected models was assessed based on graphical analysis of residual dispersion, the correlation between observed and estimated values ($r_{y\hat{y}}$), mean error (ME) and root mean square error (RMSE%). The most efficient neural network for predicting DBH (diameter at breast height) growth uses the DBH parameter measured at approximately two years of age and their respective means as input variables. The model developed for predicting DBH of individual trees in a specific site provided good accuracy while maintaining a correlation above 0.90 and RMSE% below 10% in most places where it was applied, without needing to adjust the synaptic weights. In conclusion, the Artificial Neural Networks with a hidden layer that use only the parameter diameter at breast height (DBH) at an age close to two years and their respective mean as input variables, is promising, but their accuracy decreases when applied to environments with climatic conditions different from those of the network training site.

Keywords: *ANN, Artificial intelligence; Clonal test; Forest inventory; Modeling of forest growth.*

RESUMO

O desenvolvimento de um modelo de rede neural artificial (RNA) para prognose de crescimento de eucalipto em locais onde não há plantios já estabelecidos é de extrema importância. Assim, o objetivo deste trabalho foi modelar o crescimento em diâmetro do fuste de um povoamento clonal de eucalipto empregando redes neurais artificiais e avaliar a capacidade da aplicação do modelo em outros locais com diferentes materiais genéticos e condições edafoclimáticas. Os dados utilizados neste estudo foram obtidos a partir de inventários florestais contínuos de 18 clones comerciais de Eucalyptus spp. em 17 locais de diferentes estados do Brasil, ao longo de um gradiente climático, que faz parte do Projeto TECHS (Tolerância de Eucaliptos Clonais aos Estresses Hídrico, Térmico e Biótico). As redes testadas neste trabalho foram do tipo múltiplas camadas com o algoritmo de aprendizado de retropropagação do erro e função de ativação do tipo tangente hiperbólica. A qualidade dos modelos selecionados foi avaliada com base na análise gráfica da dispersão residual, na correlação entre os valores observados e estimados ($r_{y\hat{y}}$), no erro médio (EM) e na raiz quadrada do erro quadrático médio (RMSE%). A rede neural que utilizou o diâmetro à altura do peito (DAP), avaliado próximo aos dois anos de idade, e sua respectiva média como variáveis de entrada foi a que apresentou melhor desempenho na prognose do crescimento em DAP. O modelo desenvolvido para prognose do DAP de árvores individuais em um local foi capaz de manter boa acurácia, mantendo correlação acima de 0,90 e RMSE% abaixo de 10 na maioria dos locais em que foi aplicado, sem a necessidade de ajustes nos pesos sinápticos. Concluindo, as Redes Neurais Artificiais com camada oculta que utilizam apenas o parâmetro diâmetro à altura do peito (DAP) em idade próxima aos dois anos e sua respectiva média como variáveis de entrada são promissoras, mas sua precisão diminui ao ser aplicada a ambientes com condições climáticas distintas às do local de treinamento da rede.

Palavras-chave*:* *RNA; Inteligência artificial; Teste clonal; Inventário florestal; Modelagem do crescimento florestal.*

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1. INTRODUCTION

In Brazil, eucalyptus crops cover about 76% of the planted forest areas; in addition to the highest average productivity of 32.7 m^3/ha per year, these crops also have the lowest rotation in the world with approximately 6.7 years on average between planting and harvesting (IBÁ, 2024). Even so, time is a critical factor in eucalyptus production, hindering several essential processes for crop development, such as selecting new genotypes due to delayed selection cycles, as well as establishing adequate management plans. Therefore, searching for the most appropriate mathematical models to predict forest growth is usual and necessary since these models allow predicting yield over time while facilitating forest planning and management.

Among the main models, those predicting the growth of individual trees stand out for generating detailed information on the dynamics of the stand structure (Castro et al., 2013). However, compared to traditional regression models, numerous authors have proven the higher efficiency of artificial intelligence tools such as artificial neural networks (ANN) for predicting forest growth (Binoti et al., 2014; Campos et al., 2016; Cardoso-Silva et al., 2019; Dantas et al., 2024; Leal et al., 2020; Rocha et al., 2021a; Vieira et al., 2018), eucalyptus trunk tapering estimates (Cunha-Neto et al., 2019), basic wood density (Demertzis et al., 2017), the effect of defoliation and dieback on the decreasing yield of commercial eucalypt plantations (Rocha et al., 2021b), identification of eucalyptus species (Teodoro et al., 2024), among others. The ANN models have shown higler efficiency than regression models (Batista et al., 2022; Cardoso-Silva et al., 2019); they are based on a network of biological neurons that can quickly process large data files and approximate nonlinear functions, mapping input and output relationships based on their self-learning while also providing good generalization ability, and low susceptibility to noise and outliers, among other characteristics (Haykin, 2009).

Most research applying ANNs to predict forest yield uses a single dataset from a particular site or region, randomly dividing this set so that part of the data is destined for the training networks and another part for their validation. However, the ANN training, where weights are adjusted by the learning algorithm, and the ANN validation step, where the ability to produce adequate outputs is tested for inputs absent in the training step (Binoti et al., 2014), require a dataset obtained in older forests so that the network outputs can be compared with the values obtained from measuring the trees, thus attesting the model efficiency.

Currently, the forest sector tends to expand to areas with soil and climate different from those where breeding programs were implemented and conducted, a necessity to meet the growing demand for forest-based products that arise from population growth. To this end, developing an ANN model for predicting the growth of eucalyptus clonal forests for such locations would be, initially, impossible due to the lack of established plantations. Thus, this work aims to model the stem diameter growth of eucalyptus trees from clonal stands as a function of numerical variables using ANN and to evaluate the model's ability to be applied to other sites with different genotypes and climates, without adjusting the synaptic weights.

2. MATERIAL AND METHODS

The data files used were obtained from continuous forest inventories at 17 sites in different states of Brazil, with different climates according to the Köppen classification (Figure 1, Table 1).

The data refer to 18 commercial clones of *Eucalyptus* that are part of the TECHS project (Tolerance of Clonal Eucalyptus to Water, Thermal and Biotic Stresses). The clones were divided into three groups: plastic, tropical and subtropical (Table 2). Each site has 11 of the 18 clones (Table 1), of which 4 plastic clones are common to all sites and 7 clones are climate-specific according to site classification (Binkley et al., 2017), except for site 16, which has only 10 clones due to the lack of a specific one.

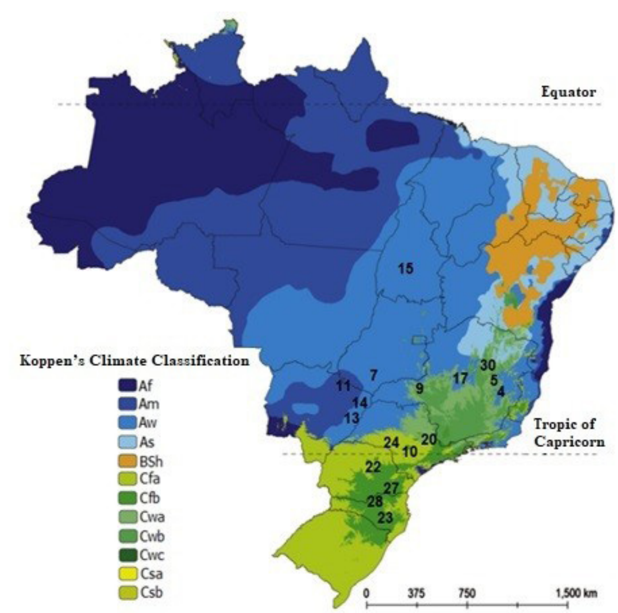

Figure 1. Climate classification (Alvares et al., 2013) and the 17 sites studied.

Table 1. Local climate, geographical location and clone sets from each studied site.

Site	Neighboring city	Rainfall	Temp	Clone sets
4	Belo Oriente - MG	1236	22.58	Plastic + Tropical
5	Guanhães - MG	1443	22.23	Plastic + Tropical
7	Rio Verde - GO	1472	22.58	Plastic + Tropical
9	Estrela do Sul - MG	1519	23.6	Plastic + Tropical
10	Botucatu - SP	1314	22.41	Plastic + Subtropical
11	Chapadão do Sul - MS	1665	24.22	Plastic + Tropical
13	Três Lagoas - MS	1179	25.09	Plastic + Tropical
14	Inocência - MS	1194	25.15	Plastic + Tropical
15	Brejinho de Nazaré - TO	1305	27.69	Plastic + Tropical
17	Três Marias - MG	1216	24.11	Plastic + Tropical
20	Mogi Guaçu - SP	1535	21.82	Plastic + Tropical
22	Telêmaco Borba - PR	1789	19.87	Plastic + Tropical
23	Otacílio Costa - SC	1666	16.66	Plastic + Subtropical
24	Borebi - SP	1706	22.75	Plastic + Tropical
27	Antônio Olinto - PR	1780	18.53	Plastic + Subtropical
28	Três Barras - SC	1902	17.46	Plastic + Subtropical
30	Bocaiúva - MG	938	24.43	Plastic + Tropical

Rainfall = annual rainfall (mm); Temp = annual average temperature (°C) based on 24 months after planting.

Table 2. Clone description, genotype identification and each clone set.

Clone	Genotype	Set
A1	*E. urophylla* x *sp.*	Plastic
C3	*E. grandis* x *E. camaldulensis*	Plastic
K2	*E. Saligna*	Plastic
Q8	*E. grandis* x sp	Plastic
F6	*E. benthamii*	Subtropical
I9	*E. dunni*	Subtropical
J1	*E. benthamii*	Subtropical
L3	*E. urophylla* x *E. globulus*	Subtropical
M4	*E. dunni*	Subtropical
N5	*E. dunni*	Subtropical
O6	*E. grandis*	Subtropical
B2	*E. urophylla* x *E. grandis*	Tropical
D4	*E. grandis* x *E. urophylla*	Tropical
E5	*E. urophylla*	Tropical
G7	*E. urophylla*	Tropical
H8	*E. grandis* x *E. urophylla*	Tropical
P7	*E. urophylla* x *E. brassiana*	Tropical
R9	*E. urophylla*	Tropical

Local 7 was chosen for developing the ANN model because it exhibited means temperature and precipitation values close to the overall mean of these variables across all studied sites. To this end, the following variables were considered: diameter at breast height (DBH) at first age (13 months, DBH_1, cm) and DBH at second age (27 months, DBH_2, cm) of individual trees; clone average at first age ($\overline{X}_1$, cm) and clone average at second age ($\overline{X}_2$, cm) on the site; and individual DBH at third age (50 months) of all living trees of the 11 clones (DBH_3, cm), totaling 1324 trees.

Data from site 7 were divided into two sets, one with about 80% of the data (1086 trees) for training the networks and another with approximately 20% of the data (238 trees) for the validation stage. This proportion was chosen because it has performed well previously when using large datasets for developing ANN models (Binoti et al., 2015; Cabacinha & Lafetá, 2017; Nascimento et al., 2013; Reis et al., 2016; Teodoro et al., 2015). To test the model's ability to predict the DBH of different genotypes, the dataset for training the networks had trees from 8 different clones (B2, C3, G7, H8, K2, P7, Q8 and R9), while the set used in the validation step contained only trees from the other 3 clones (A1, D4 and E5).

The model representing the artificial neuron, expressed in the equation below, has input signals (X_j) that represent the dendrites of a biological neuron, weights that simulate the synapses ($W_{k.j}$) connecting the inputs to the body of the artificial cell, a summation (Σ) for the input signals weighted by the respective synapses of the neuron, an activation function f(x) used to constrain the output amplitude of a neuron, and a bias (b_k) that either increase or decrease the net input of the activation function (Haykin, 2009):

$$Y=f\left(\sum_{j=1}^{m} w_{k.j}\ x_j + b_k\right) \quad (1)$$

The multilayer networks used had an error backpropagation learning algorithm, a hyperbolic tangent activation function, and the maximum number of iterations (or epochs) for each network equal to 1,000. The input variables were DBH_1, DBH_2, $\bar{X}_1$ and $\bar{X}_2$, and the network output was the variable DBH_3. Four models were considered according to the network inputs (Table 3). To prevent greater magnitude variables from having a greater influence on the results of the networks, the data were normalized in the 0 to 1 range using the following equation:

$$X_{norm}=\left(\frac{X_i - X_{min}}{X_{max} - X_{min}}\right) \quad (2)$$

where X_{norm} is the normalized value, X_i is the actual value to be normalized, X_{min} and X_{max} are the variable minimum and maximum values, respectively.

The number of neurons in the single hidden layer of each model was established according to the Fletcher-Gloss method (Silva et al., 2010) considering the number of input and output variables, as follows:

$$\left(2.\sqrt{n}+n_2\right) \le n_1 \le \left(2.n+1\right) \quad (3)$$

Where n is the number of network inputs, n_1 is the number of neurons in the hidden layer and n_2 is the number of neurons in the output layer.

A total of 400 ANNs were trained, 100 for each of the models, and from each model, only one was chosen based on the correlation between the values observed and those estimated by the networks, as used by Reis et al. (2018). The quality of the 4 selected models was assessed based on the following criteria: graphical analysis of residual dispersion, the correlation between observed and estimated values ($r_{y\hat{y}}$), mean error (ME) and root mean square error (RMSE%), as follows:

$$r_{y\hat{y}}=\frac{Cov\ (y,\hat{y})}{\sqrt{S^2(y).S^2(\hat{y})}} \quad (4)$$

where Cov is the covariance, S^2 is variance, y is the observed value, and $\hat{y}$ is the value estimated by the ANN.

$$ME=\frac{\sum_{i=1}^{n}\left(y_i-\hat{y}_i\right)}{n} \quad (5)$$

where: y_i is the observed value of the *i-th* variable; $\hat{y}_i$ is the estimated value of the *i-th* variable, and *n* is the sample size.

$$RSME(\%)=\frac{100}{\bar{y}}\sqrt{\frac{\sum_{i=j}^{n}(y_i-\hat{y}_i)^2}{n}} \quad (6)$$

where: y_i is the observed value of the *i-th* variable; $\hat{y}_i$ is the estimated value of the *i-th* variable, and *n* is the sample size.

The best ANN model was selected according to the evaluation criteria and applied, without adjusting the synaptic weights, to the data from the other 16 evaluated sites, following the same criteria ($r_{y\hat{y}}$, ME and RMSE%). The network input and output variables were obtained for an interval between 24 and 29 months for both DBH_2 and $\bar{X}_2$, and between 49 and 53 months for DBH_3. The analysis was performed using the Statistica software (StatSoft, 2004).

3. RESULTS AND DISCUSSION

Networks 1 and 4 had the best performance for predicting the DBH in the training stage, as evidenced by the lower data dispersion in the figures of the observed and estimated values (Figure 2). Furthermore, ANN 4 had a mean error value (ME) closer to zero, indicating a lower bias of this model compared to the others, whereas ANN 1 was the farthest value from zero among the models tested in this phase (Table 4).

ANN 4 also provides a better generalization capacity, as evidenced by the lower RMSE% and ME values in the validation stage, in addition to a higher correlation between the observed and estimated values. The other ANN yielded less accurate estimates and a lower correlation between observed and estimated values (Table 4). This result shows a greater correlation among the variables involved in ANN 4, which uses as input variables only variables obtained in the second age, compared to the other networks, which use at least one variable obtained in the first age (Table 3).

Massaro et al. (2010) obtained an excellent correlation between DBH measured in trees nearly two years old and 50 months old when investigating the feasibility of applying early selection in clonal tests of *Eucalyptus* spp. Li et al. (2017) analyzed the correlation between growth traits in eucalyptus of different ages and reported a good correlation between DBH at two years and more advanced ages, but this correlation is considerably reduced for trees younger than two years old. Thus, the input variables in the first age may have affected negatively the correlations and accuracy of networks 1, 2 and 3, especially in the validation stage. Additionally, ANN 4 has a simpler configuration with a smaller number of neurons, thus facilitating its application and favoring its choice to be applied to other sites.

Applying the ANN 4 model to the other sites showed the same trend for the estimated and observed DBH values (Figure 3), with positive correlations ranging from 0.78 to 0.96, and remaining above 0.90 in 11 of the 16 sites (Table 5). The model also shows good

Table 3. Architecture, input and output variables of artificial neural networks selected in the training phase.

ANN	Architecture	Input	Output
1	4-5-1	DBH_1, DBH_2, $\bar{X}_1$, $\bar{X}_2$	DBH_3
2	2-3-1	DBH_1, DBH_2	DBH_3
3	2-3-1	DBH_1, $\bar{X}_1$	DBH_3
4	2-3-1	DBH_2, $\bar{X}_2$	DBH_3

ANN = Artificial Neural Networks; DBH_1 = Diameter at breast height (cm) at first age (13 months); DBH_2 = Diameter at breast height at second age (27 months); $\bar{X}_1$ = Clone average on site at first age; $\bar{X}_2$ = Clone average on site at second age; DBH_3 = Diameter at breast height (cm) at third age (50 months).

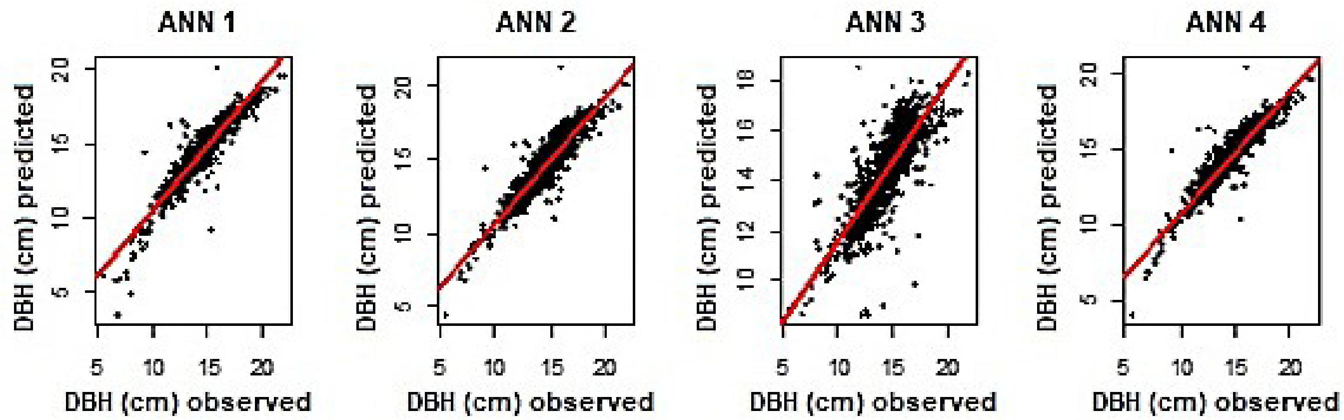

Figure 2. Graphical analysis of predicted vs. observed diameter at breast height (DBH, cm) of individual eucalyptus trees in the training phase of artificial neural networks.

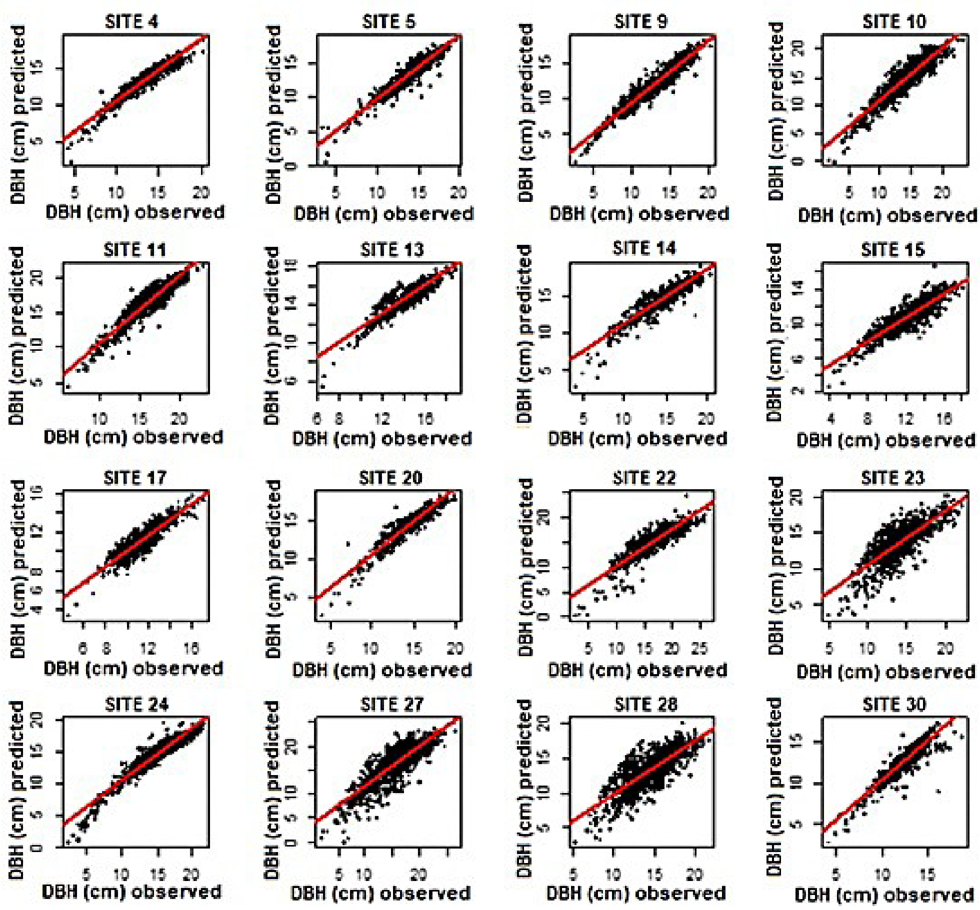

Figure 3. Graphical analysis of DBH (cm) predicted by an ANN model vs. observed DBH (cm) of individual eucalyptus trees at 16 sites in different states of Brazil.

Table 4. Performance of selected neural networks in the training and validation phases.

ANN	Training			Validation		
	$r_{y\hat{y}}$	*ME*	*RMSE%*	$r_{y\hat{y}}$	*ME*	*RMSE%*
1	0.93	0.081	4.75	0.89	0.226	7.18
2	0.91	0.064	5.93	0.81	0.921	9.51
3	0.81	0.068	8.63	0.72	0.818	14.23
4	0.94	-0.024	4.94	0.95	0.064	4.66

$r_{y\hat{y}}$ = Correlation between observed and predicted values; *ME* = mean error; *RMSE%* = Root mean square error.

Table 5. Performance of the selected ANN at site 7 when applied to another 16 sites in different regions of Brazil.

SITES	r_{yy}	*ME*	*RMSE%*
4	0.95	-0.087	5.41
5	0.94	0.478	5.95
9	0.96	0.886	9.08
10	0.93	-0.610	9.57
11	0.93	-0.403	5.77
13	0.90	-0.512	6.35
14	0.91	0.019	7.32
15	0.88	1.425	14.35
17	0.90	0.210	6.81
20	0.94	-0.009	5.07
22	0.89	1.607	12.53
23	0.78	0.395	11.78
24	0.95	0.480	6.72
27	0.84	-0.675	14.52
28	0.80	1.234	14.02
30	0.90	-0.258	7.37

$r_{y\hat{y}}$ = Correlation between observed and predicted values; *ME* = Mean error; *RMSE%* = Root mean square error.

accuracy, with RMSE% ranging between 5.07 and 14.52 between sites while remaining below 10 in most (Table 5). Binoti et al. (2015) analyzed different ANN configurations in the projection of the volume of eucalyptus clones in a single site and selected networks with RMSE% ranging from 10.89 to 15.49, while Reis et al. (2018) tested ANN on diametric distribution prognosis in a forest stand in the Amazon area and selected 5 network architectures with RMSE% above 15.30 in the training phase. Batista et al. (2022) found correlations between 0.88 and 0.97 with RSME% between 4.30 and 21.39% in the training phase, correlations between 0.68 and 0.96 and RSME% between 10.79 and 27.23% in the validation phase, and correlations between 0.68 and 0.92 with RSME% between 10.98 and 23.17 in the utilisations/application phase for volume prediction in different eucalyptus species/genetic material. They also found that the accuracy of the estimates provided by ANN was higher than that obtained with nonlinear regression when evaluating all eucalyptus species. Thus, the error values (RMSE%) obtained here using ANN, even when higher than 10%, can be considered adequate when compared to other growth prognosis studies, such as those mentioned previously.

The correlation was less than 0.90 in the same five sites where the model proved to be less accurate, with RMSE% values above 10. Four of these sites are located below the Tropic of Capricorn (Figure 1) and have the lowest average annual temperatures (Table 1). The further south in Brazil the sites are located the lower the average annual temperature while the data shows that the correlation between observed and estimated data was also lower. A correlation value of less than 0.90 with RMSE% above 10 was observed in another site located further north in Brazil (Figure 1), the local with the highest average annual temperature among all the evaluated sites (Table 1). Binkley et al. (2017) investigated the interaction of the same clones evaluated in this work in 36 environments throughout Brazil and Uruguay and reported that wood yield decreased by up to 40% for a variation in the average annual temperature of only 4 ºC. However, the yield difference between the different sites does not necessarily explain the decrease in the correlation and accuracy of the model, which may be associated with the different effects of environments on genotypes, that is, the genotype by environment interaction (GEI), as reported by Araujo et al. (2019) and Binkley et al. (2017), working with other datasets from the TECHS project.

The GEI may cause different yields among sites in different levels for each genotype over time, which may result in changing rankings of clones in different environments. This interaction effect on the phenotypic manifestation in eucalyptus is commonly reported in the literature (Araujo et al., 2019; Castro et al., 2018; Nunes et al., 2002; Pupin et al., 2015; Santos et al., 2015; Silva et al., 2019a; Silva et al., 2019b; Silva et al., 2022). According to Araujo et al. (2019), climatic pressure affects the gene expression of genotypes and, consequently, the phenotypic pattern in each growing environment. Therefore, there will always be a risk associated with forest productivity when planting occurs in new environments, due to the unpredictable nature of genotype-environment interactions. This is due to the very nature of climatic variation and pressure on genotypes, as the phenotype results from the combination of genotypic and environmental effects, which are determined by the individual's gene pool.

Several factors contribute to the existence of genotype-environment interaction in eucalyptus, such as differences in altitudes (Reis et al., 2025), temperatures and precipitation (Araujo et al., 2019, Binkley et al., 2017), as well as management and silvicultural practices (Gonçalves et al., 2013; Stape et al., 2010), such as planting spacing, fertilization, weed control, among others.

Among the sites studied, there are significant differences in temperature and precipitation (Table 1), which reinforces the robustness of ANN for predicting the growth of eucalyptus clones for different locations and/or sets of cultivated clones. In addition to the different environmental conditions and changes in some of the clones cultivated from one location to another, we must also consider that the ANN tested involves growth projections at different ages, which makes the scenario more complex, as there are changes in the growth rate between clones over time, also reducing the correlation of performance between ages (Li et al., 2024; Massaro et al., 2010).

GEI studies allow checking different genotype performances across sites while determining adaptability and stability over time

(Araujo et al., 2019; Silva et al., 2022). Adaptability is the ability of a genotype to respond favorably to its environment, while stability is the predictability of its behavior. Thus, to ensure greater confidence in recommending clones for planting, it is necessary to select genotypes with greater productive stability and adaptability, as highlighted by Araujo et al. (2019), Silva et al. (2019a), and Silva et al. (2022).

Similarly, as reported by some authors, the GEI requires a detailed study of the behavior of individuals and environments through adaptability and stability analyses (Araujo et al., 2019; Van Eeuwijk et al., 2016), the scope of which is not part of the present study. Further details on GEI with eucalyptus can be obtained from studies conducted by Araujo et al. (2019), Silva et al. (2019a), Silva et al. (2019b), and Silva et al. (2022).

For the same set of genotypes, a comparison between sites 10 and 23 shows that mean annual precipitation and mean annual temperature varied more than 300 mm and 5 ºC, respectively, between sites (Table 1), with a difference of 15 p.p. in the correlation between observed and estimated data and inversion of the model predictive trend. Compared to the observed data, the values predicted for sites 10 and 23 were, respectively, overestimated and slightly underestimated (Table 5). Likewise, for the same set of genotypes again, the difference between the annual average temperatures of sites 4 and 15 was greater than 5 ºC while the correlations differed by 7 p.p. and the RMSE% by almost 9 p.p. (Table 5). This result indicates that clone yields did not change in the same proportion at different locations over time, thus supporting the conclusion that the genotype by environment interaction (GEI) affected the correlation and accuracy of the model on the different sites studied.

On the other hand, except for site 23, the other sites showed a correlation between the observed and estimated data greater than 0.80 while model accuracy remained close to values reported by other authors that investigated and proved the ANN efficiency for predicting growth traits in tree species (Batista et al., 2022; Binoti et al., 2015; Cordeiro et al., 2022; Lacerda et al., 2017; Vieira et al., 2018). Furthermore, sites 10 and 11 located in regions with contrasting climates, according to the Köppen classification (Figure 1), and planted with different genotype groups, exhibited similar correlations and accuracies (Table 5). Using genotypes specific to each environment is a way to minimize the effects of the genotype x environment interaction (Cruz et al., 2004). Therefore, despite the considerable environmental differences between the studied locations, using clone sets more suitable for different types of climate, reduced the effect of the genotype by environment interaction, allowing the model to perform well when applied to different sites.

Thus, the importance of this study is evident because, even in places where the results were not so satisfactory, forest growth can still be predicted with a certain degree of reliability under different soil and climatic conditions and sets of clones.

4. CONCLUSIONS

Neural networks with a hidden layer that use only the parameter diameter at breast height (DBH) at an age close to two years and their respective mean as input variables is promising for predicting the growth of individual trees, however, its accuracy decreases for climatic conditions contrasting with those used for training the ANN. Furthermore, ANN can make a great contribution when applied as auxiliary tools in breeding programs for early selection and in studies on the choice and adaptation of genotype to cutivation in different conditions, whether due to climate variations or forest expansion into new areas. The ANN is promising to forest management and inventory practices, for predicting growth.

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AUTHOR CONTRIBUTIONS

WMS: conceptualization, data curation, formal analysis, methodology, investigation, validation, writing; MJA: data curation, formal analysis, methodology, validation, writing; OCC: data curation, formal analysis, validation, writing; RCP: conceptualization, supervision, data curations, formal analysis, methodology, investigation, validation, writing. All authors revised the manuscript and approved the final version.