Brazilian Journal of Biometrics, **41**, 265-273 (2023)
doi:10.28951/bjb.v41i3.629

BRAZILIAN JOURNAL OF
BIOMΣTRICS
ISSN:2764-5290

ARTICLE

Spline functions and nonlinear models for modeling the growth of sheep in Northeast Brazil[1]

Diana Campos de Oliveira[1], Kaléo Dias Pereira[*2], Antônio Policarpo Souza Carneiro[2], Joel Augusto Muniz[3], Paulo Luiz Souza Carneiro[4], Carlos Henrique Mendes Malhado[4] and Antonio Alcyone Oliveira de Sousa Junior[5]

[1]Statistics Departament, Federal University of Ouro Preto, Ouro Preto-MG, Brazil
[2]Federal University of Viçosa, Viçosa-MG, Brazil
[3]Statistics Departament, Federal University of Lavras, Lavras-MG, Brazil
[4]Biology Sciences Departament, Stadual University of Bahia South-West, Jequie-BA, Brazil
[5]Federal Institute of Education, Science and Technology of Bahia, Santa Inês-BA, Brazil
*Corresponding author. Email: kaleo.pereira@ufv.br

(Received: August 8, 2022; Revised: December 13, 2022; Accepted: February 3, 2023; Published: September 25, 2023)

Abstract
Modeling animal growth is essential to manage quality meat production systems at a low cost. This study aimed to compare the linear-linear, linear-plateau, and linear-linear-linear spline functions with the nonlinear models Brody, Richards, and von Bertalanffy to model the growth of crossbred sheep in the Northeast of Brazil. Weighing data from the genetic groups of meat sheep Dorper x Morada Nova, Dorper x Rabo Largo, and Dorper x Santa Inês were used. Knots in the spline fitting were considered unknown and estimated under the segmented nonlinear regression approach. Overall, splines were more accurate than traditional nonlinear models in describing the growth of sheep of all genetic groups. The linear-plateau spline was superior in predicting weight as a function of the age of sheep. The linear-plateau function also resulted in estimates of parameters (growth rates, time for animals to reach adult weight, and adult weight) with easier biological interpretations, which can be used in practice for decision-making for herd management.

Keywords: animal growth modeling, biometric measurements, longitudinal data, meat production.

1. Introduction

Sheep farming in Brazil has a herd of 13.8 million animals distributed mainly in the Northeast (65.5%) and South (24.0%), and the rest in the other regions (IBGE, 2020). According to Malhado *et al.* (2009), one of the main obstacles in sheep farming is the fact that producers are not aware of the advantages of producing good quality meat, as animals are slaughtered at older ages and with a worse carcass quality.

According to Vidal *et al.* (2006), sheep play an important role in food supply and income generation in the Northeast. However, the low genetic potential of herds associated with the scarcity of pastures during the dry season, inadequate management practices, poor sanitary conditions, and other deficiencies contribute to low levels of productivity and profitability. The authors also commented on the need to use efficient methods of raising lambs to provide quality, low-cost meat to increase profitability.

Studies that relate weight with the age of sheep are characterized as a consistent way to assess the development and production efficiency of animals. Thus, these studies assist in defining the best age for slaughter and the most appropriate management to increase the productivity of herds (Hossein-Zadeh, 2017). In general, nonlinear models have been used in growth studies because they provide estimates of parameters with the possibility of biological interpretation, such as maturity rate and adult weight (Carneiro *et al.*, 2014;

Teixeira Neto *et al.*, 2016; Souza *et al.*, 2017). Also, the fact that nonlinear models are usually more efficient to describe the growth pattern of sheep and other animals is very consolidated, with debate only about which model is more efficient for studies with sheep (Sarmento *et al.*, 2006; Dilliwar *et al.*, 2016; Balan *et al.*, 2017; Mokhtari *et al.*, 2019).

Souza *et al.* (2011) evaluated the growth of Morada Nova sheep and observed that the models of Brody, Richards, and von Bertalanffy were adequate. Nimase *et al.* (2018) used six nonlinear models for modeling the growth of Madgyal sheep in India and found better results with the Brody model, as well as Simasiku *et al.* (2019), in research with animals of the Damara, Dorper, and Swakara breeds carried out in Namibia.

An alternative to these nonlinear models aiming to describe the relationship between weight and age is to define a model composed of parts of linear segments, called segmented regression or spline (Zhang & Goh, 2016). According to Hernandez (2010), the spline is a statistical technique to model phenomena in transition and changes. In this case, the functional form of the response variable is changed at specific points, the knots, which are generally of practical interest because they represent major changes in the pattern of the response variable as a function of the independent variable.

The advantage in using spline functions is related to possible gains in accuracy in modeling and the estimation of parameters whose biological interpretation is simpler than the parameters of the usual nonlinear models. Aggrey (2002) affirms that the use of spline functions can be a alternative to high order polynomials or complex nonlinear models. During a research about mule duck growth curves using spline mixed effects functions, Vitezica *et al.* (2010) obtained results of fit quality similar to Weibull function and better the results of other nonlinear models adjusted.

Pre-defined knots in spline functions become a constant and the estimation is performed by the theory of linear models using the least-squares method. However, knots estimated based on the data lead to the nonlinear regression, in which estimates are obtained through iterative methods, as described by Rezende *et al.* (2007).

Therefore, this study aimed to compare the fitting of the linear-linear, linear-plateau, and linear-linear-linear spline functions with the nonlinear models Brody, Richards, and von Bertalanffy to model the growth of crossbred sheep in the Northeast region of Brazil.

2. Material and methods

The data used to fit the models were obtained from an experiment carried out at the Experimental Station of Jaguaquara by Universidade Estadual do Sudoeste da Bahia researches in Jaguaquara, administrative micro-region of Jequié, BA. The data came from three genetic groups of sheep obtained by crossing Dorper x Morada Nova (DMN), Dorper x Rabo Largo (DRL), and Dorper x Santa Inês (DSI) breeds with 151, 195, and 208 weighings, respectively, per genetic group from 2003 to 2005 with 15 days of interval between weighings. A total of 36 DMN (26 males and 10 females), 61 DRL (36 males and 25 females), and 59 DSI animals (31 males and 28 females) were used. After weaning, the animals were left out to graze in the daytime, also receiving mineral salt, and stabled in the late afternoon.

The linear-plateau (LP), linear-linear (LL), and linear-linear-linear (LLL) splines are given by equations (1), (2), and (3), respectively:

$$(\mathrm{LP})y_i = \begin{cases} \beta_{00} + \beta_{01}x_i + e_i, \text{ if } x_i < t_1 \\ \beta_{00} + \beta_{01}t_1 + e_i, \text{ if } x_i \geq t_1 \end{cases} \tag{1}$$

$$(\mathrm{LL})y_i = \begin{cases} \beta_{00} + \beta_{01}x_i + e_i, \text{ if } x_i < t_1 \\ \beta_{00} + \beta_{01}x_i + \beta_1(x_i - t_1) + e_i, \text{ if } x_i \geq t_1 \end{cases} \tag{2}$$

$$(\mathrm{LLL})y_i = \begin{cases} \beta_{00} + \beta_{01}x_i + e_i, \text{ if } x_i < t_1 \\ \beta_{00} + \beta_{01}x_i + \beta_1(x_i - t_1) + e_i, \text{ if } t_1 \leq x_i < t_2 \\ \beta_{00} + \beta_{01}x_i + \beta_1(x_i - t_1) + \beta_2(x_i - t_2) + e_i, \text{ if } x_i \geq t_2 \end{cases} \tag{3}$$

In the equations, y_i is the weight of sheep at age x_i, β_{00} is the weight at birth, and β_{01} is the average daily weight gain (ADWG) of the sheep at the first growth phase, that is, it defines the first segment of the spline function, whereas β_1 and β_2 are interpreted as variations in ADWG between the growth phases. Thus, negative values for β_1 and β_2 indicate a reduction in the growth rate from one phase to another. The parameters t_1 and t_2 are the knots that delimit the limits between the segments of the spline function, which are interpreted as the ages in which the sheep undergo substantial changes in growth, and e_i is the random error, assuming independence, normal distribution, and homogeneity of variances. The growth rates or ADWG of each phase are obtained by the parametric functions (β_{01}), $(\beta_{01} + \beta_1)$, and $(\beta_{01} + \beta_1 + \beta_2)$ for the first, second, and third growth phases, respectively.

The usual nonlinear models Brody (1945), Richards (1959), and von Bertalanffy (1957) were selected to describe the growth of sheep due the satisfactory performance presented in previors researchs with the same genetic materials. The models Brody (4), Richards (5), and von Bertalanffy (6) are, respectively:

$$y_i = \beta_1(1 - \beta_2 e^{-\beta_3 x_i}) + e_i \tag{4}$$

$$y_i = \frac{\beta_1}{\left(1+e^{(\beta_2-\beta_3 x_i)}\right)^{\frac{1}{\beta_4}}} + e_i \tag{5}$$

$$y_i = \beta_1(1 - \beta_2 e^{-\beta_3 x_i})^3 + e_i \tag{6}$$

In the models, y_i is the weight of sheep at age x_i, β_1 is the adult weight or asymptotic weight of the animal, β_2 is an integration constant and has no interpretation in this case, β_3 is the maturity rate and is characterized as an indicator of the speed with which the animal approaches adult weight, β_4 is the inflection parameter and refers to the point at which the animal moves from an accelerated growth phase to an inhibitory growth phase, x_i the age of sheep, and e_i is the experimental error with a normal distribution of zero mean and σ^2 variance. The growth rate or ADWG is estimated in the nonlinear models by the first derivative of each model relative to age, being a parametric function that depends on age and variable throughout the growth phase. Moreover, growth rates are constant within each phase in the spline functions, facilitating the interpretation of parameters and the practical use of this information to describe the behavior of animal growth.

The estimates of parameters for all models were performed using the generalized least squares method for nonlinear regression models, whose solutions were obtained using the Gauss-Newton iterative process via PROC NLIN from the software SAS® (SAS, 2014). The asymptotic matrix of variances and covariances of the parameter estimators can be generated once the convergence is verified, according to Equation (7):

$$\widehat{\mathrm{var}}(\hat{\theta}) = (\mathbf{X}'\mathbf{X})^{-1}\hat{\sigma}^2 = (\mathbf{X}'\mathbf{X})^{-1}\mathrm{MSE}, \tag{7}$$

where $\mathbf{X}$ is the matrix of partial derivatives relative to each parameter and MSE is the mean square of the experimental error.

The comparison between models considers the zootechnical interpretation of the parameter estimates and the fit quality. The latter was evaluated according to the Akaike information criterion (AIC), the Schwarz Bayesian criterion (BIC), the coefficient of determination (R^2), and the mean absolute error (MAE), following Equations (8), (9), (10), and (11).

$$\mathrm{AIC} = -2\mathrm{loglike} + 2p \tag{8}$$

$$\mathrm{BIC} = -2\mathrm{loglike} + p\ln(\mathrm{n}) \tag{9}$$

$$R^2 = \hat{\rho}^2 \tag{10}$$

$$\mathrm{MAE} = n^{-1} \textstyle\sum_i^n |y_i - \hat{y}_i|, \tag{11}$$

where loglike is the value of the natural logarithm of the maximized likelihood function, p is the number of parameters, n is the number of observations, $\hat{\rho}$ is the estimated correlation between observed and predicted values, y_i is the observed value, and $\hat{y}_i$ is the predicted value of the weight of animals.

3. Results and discussion

The linear-plateau spline showed the best fit quality for the genetic group DMN, as the AIC and BIC estimates showed the lowest values for this model and the highest R^2 among all models (Table 1). A slightly better fit for this genetic group was observed with the Brody model than the other nonlinear models, as this model showed betther results for all fit quality evaluators.

Table 1. Akaike information criterion (AIC), Bayesian information criterion (BIC), and coefficient of determination (R^2) of the linear-plateau (LP), linear-linear (LL), and linear-linear-linear (LLL) splines and the Brody, von Bertalanffy, and Richards nonlinear models for sheep of the genetic groups Dorper x Morada Nova (DMN), Dorper x Santa Inês (DSI), and Dorper x Rabo Largo (DRL)

		Evaluator			
Genetic group	Model	AIC	BIC	R^2 (%)	MAE
DMN	LP	649.81	658.86	99.73	2.95
	LL	773.69	785.76	97.63	2.89
	LLL	774.46	792.57	97.34	2.91
	Brody	772.58	781.63	74.88	2.89
	Richards	794.45	806.52	74.47	2.91
	von Bertalanffy	773.79	782.84	74.72	2.92
DSI	LP	1184.99	1195.01	88.42	3.53
	LL	1185.22	1198.57	86.92	3.53
	LLL	1177.42	1197.45	86.83	3.50
	Brody	1206.96	1216.96	72.30	3.78
	Richards	1192.83	1206.18	73.45	3.61
	von Bertalanffy	1197.79	1207.80	73.25	3.62
DRL	LP	1026.60	1036.42	93.60	3.39
	LL	1028.59	1041.68	92.72	3.38
	LLL	1031.56	1051.19	92.74	3.36
	Brody	1043.30	1053.12	71.48	3.42
	Richards	1034.60	1047.69	71.52	3.47
	von Bertalanffy	1037.76	1047.57	67.62	3.39

The linear-linear-linear spline had the better fit for the weight-age data for the genetic group DSI when considering the AIC and MAE estimates. In the other hand, the linear-plateau spline produced the lower value for BIC and higher R^2, in addition to an MAE practically equal to that of the linear-linear-linear spline. Thus, the linear-plateau spline also presented an adequate fit for the genetic group DSI. Moreover, the Richards model presented the best fit for the genetic group DSI among the nonlinear models, with lower values for AIC, BIC, and MAE and higher for R^2.

The comparison of the estimates of the fit quality evaluators showed that the linear-plateau spline had the best fit for the data of the genetic group DRL, with the lowest AIC and BIC values and an R^2 of 93.60% (Table 1). The Richards model showed the best fit for the genetic group DRL among the nonlinear models. In general, splines provided a better fit than the nonlinear models, with better results for AIC, BIC, R^2, and MAE. The linear-plateau function demonstrated a certain superiority over other spline functions and nonlinear models. Therefore, linear-plateau curves best represented the growth trend of genetic groups (Figure 1). The LP curves show that the genetic group DSI is easily identified as the earliest and DMN as the most delayed.

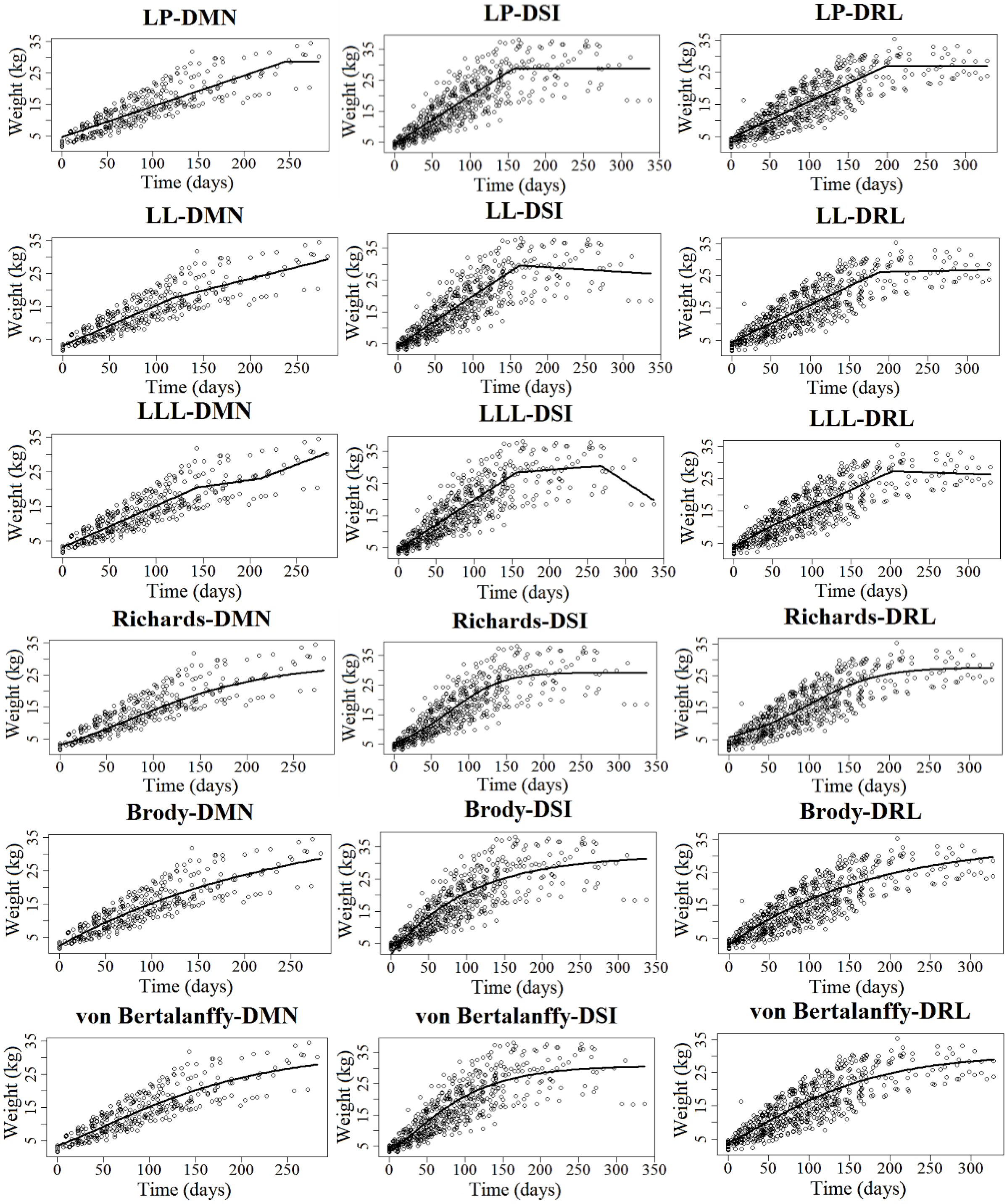

Figure 1. Growth curves generated by the linear-plateau (LP), linear-linear (LL), and linear-linear-linear (LLL) spline functions and the Richards, Brody, and von Bertalanffy nonlinear models for sheep of the genetic groups Dorper x Morada Nova (DMN), Dorper x Santa Inês (DSI), and Dorper x Rabo Largo (DRL).

Table 2 shows that the average daily weight gain (ADWG) estimated for the first segment ranged from 0.10 to 0.16, 0.12 to 0.16, 0.12 to 0.15 kg day^{-1} for the linear-plateau, linear-linear, and linear-linear-linear spline functions, respectively. In this case, the genetic group DSI showed the highest estimate of weight gain in this first growth phase for these first two spline functions.

Table 2. Parameter estimates of the linear-plateau (LP), linear-linear (LL), and linear-linear-linear (LLL) spline functions for sheep of the genetic groups Dorper x Morada Nova (DMN), Dorper x Santa Inês (DSI), and Dorper x Rabo Largo (DRL) with their respective asymptotic standard errors

		Spline functions		
Genetic group	Parameter	LP	LL	LLL
DMN	β_{00}*	4.61±0.53	2.96±0.72	3.11±0.64
	β_{01}	0.10±0.01	0.12±0.01	0.12±0.01
	β_1	–	−0.05±0.01	−0.08±0.03
	β_2	–	–	0.07±0.04
	t_1	246±13	118±17.52	144±14.9
	t_2	–	–	211±26.55
DSI	β_{00}	4.49±0.69	4.45±0.68	4.55±0.67
	β_{01}	0.16±0.01	0.16±0.01	0.15±0.01
	β_1	–	−0.17±0.01	−0.14±0.02
	β_2	–	–	−0.17±0.05
	t_1	157.1±5.77	162±6.77	156±9.33
	t_2	–	–	267.5±12.44
DRL	β_{00}	4.57±0.52	4.37±0.53	3.92±1.04
	β_{01}	0.11±0.01	0.12±0.01	0.13±0.03
	β_1	–	−0.11±0.01	−0.02±0.03
	β_2	–	–	−0.12±0.01
	t_1	197.9±7.48	188±10.68	49±51.24
	t_2	–	–	202.9±11.19

*β_{00} corresponds to the weight at birth; β_{01} is the average daily weight gain (ADWG); β_1 and β_2 represent the variations in ADWG between growth phases; t_1 and t_2 are the ages at which sheep undergo substantial changes in growth.

Similar results were found by Piola Júnior *et al.* (2009), who evaluated the influence of different energy levels in the feed on the performance and characteristics of sheep carcasses. The ADWG estimated by the authors ranged from 0.12 to 0.208 kg day^{-1}. On the other hand, the values were lower than those observed by Carvalho *et al.* (2008), who evaluated nutrient intake, weight gain, and feed conversion of intact male lambs fed diets in the feedlot containing different energy levels, obtaining estimated ADWG values of 0.236, 0.220, 0.212, and 0.257 kg day^{-1}.

The weights at maturity (Table 2), estimated using linear-plateau spline functions, were 29.21, 29.63, and 26.34 kg for the genetic groups DMN, DSI, and DRL, respectively, showing a higher similarity between the adult weight of the groups DMN and DSI. Carneiro *et al.* (2007) found similar results for the adult weight of the genetic groups DMN, DSI, and DRL using traditional nonlinear models, with values of 27.14, 28.68, and 26.09 kg, respectively. Zapata *et al.* (2001) studied the yield and composition characteristics of meat sheep carcasses in the Northeast of Brazil and observed live weights of up to 30 kg, with an average usually lower than that of animals of breeds from temperate climate raised in the South region.

The ages at which the animals reached adult weight, that is, the ages on the plateau (parameter t_1 of the linear-plateau splines), were 246, 157, and 198 days for the genetic groups DMN, DSI, and DRL, respectively (Table 2). Thus, the group DSI showed a higher precocity for weight gain, while the group DMN was the latest. These results are similar to those observed by Sarmento *et al.* (2006), who found, through the absolute growth rate for traditional nonlinear models, that animals around six months of age practically did not gain more weight.

Changes in growth behavior, estimated by the linear-linear spline, happened when the animals were aged 118, 162, and 188 days (parameter t_1) for the genetic groups DMN, DSI, and DRL, respectively. After these ages, the animals showed lower gains than at the initial ages. Negative estimates for the parameter β_1 indicate a delayed growth in the second phase. The genetic group DMN had a reduction in ADWG from 0.12 to 0.07 kg day^{-1}, while the other two groups had a marked reduction in the growth rate, with an estimated ADWG of −0.01 and 0.01 kg day^{-1} for the groups DSI and DRL, respectively (Table 2).

The linear-linear-linear spline showed that the estimated ADWG for the second segment ranged from 0.01 to 0.11 kg day^{-1} between the three genetic groups. The ADWG estimated in the third segment showed negative values of −0.16 and −0.01 kg day^{-1} for DSI and DRL, respectively, while the genetic group DMN had an estimated value of 0.11 kg day^{-1}. Carneiro et al. (2007) analyzed the same genetic groups and observed that DSI had a higher growth rate than DMN and DRL after 30 days of age. Theoretically, negative ADWG values indicate weight loss, but it is inconsistent in practice. In this case, a negative ADWG may be the consequence of problems in adjusting the model.

Estimates for the adult weight (β_1) obtained by nonlinear models ranged from 27.58 to 41.01 kg (Table 3). Iqbal al. (2019) estimated the adult weight of Mengali sheep from Balochistan by the von Bertalanffy model and found a value of 42.82 kg.

Table 3. Parameter estimates of the Richards, Brody, and von Bertalanffy nonlinear models for sheep of the genetic groups Dorper x Morada Nova (DMN), Dorper x Santa Inês (DSI), and Dorper x Rabo Largo (DRL)

Model	Parameter	DMN	DSI	DRL
Richards	β_1*	28.99±3.87	29.29±0.80	27.58±1.02
	β_2	4.00±1.71	2.94±1.74	3.31±1.77
	β_3	0.01±0.006	0.03±0.01	0.03±0.01
	β_4	0.81±0.008	1.77±1.12	2.1±1.21
Brody	β_1	41.01±6.21	32.49±1.40	34.47±2.65
	β_2	0.94±0.02	0.95±0.03	0.92±0.02
	β_3	0.004±0.001	0.010±0.0012	0.006±0.0009
von Bertalanffy	β_1	32.18±2.43	30.80±0.97	30.68±1.48
	β_2	0.53±0.02	0.54±0.03	0.50±0.02
	β_3	0.009±0.001	0.015±0.001	0.010±0.01

*β_1 represents the adult weight, β_2 is an integration constant; β_3 corresponds to the maturity rate; β_4 refers to the point at which the animal moves from an accelerated growth phase to a growth stabilization phase.

The estimated maturation rate (β_3), that is, the speed at which the animal reaches adult weight, ranged from 0.004 to 0.030 (Table 3). Sarmento et al. (2006) analyzed the growth of Santa Inês sheep using the von Bertalanffy, Brody, Gompertz, Logistic, and Richards nonlinear models and obtained results similar to those of the present study, with values between 0.0094 and 0.0287 for the maturation rate. The estimates of the parameter β_4, which defines the inflection point in the Richards model, ranged from 0.81 to 2.1. Balan et al. (2017) analyzed nonlinear models to describe the growth of Mecheri sheep in southern India and obtained a value of 1.56 as the general estimate for this parameter.

4. Conclusions

The spline functions were more adequate than the usual nonlinear models to describe growth curves of the three genetic groups of crossed sheep, with the linear-plateau spline showing the best fit.

The parameter estimates of the spline functions (growth rates, time for animals to reach adult weight, and adult weight) were easy to interpret and can be used to assist decision-making in the management of herds.

Acknowledgments

To the Fundação de Amparo à Pesquisa do Estado da Bahia – FAPESB, Banco do Nordeste, Conselho Nacional de Desenvolvimento Científico e Tecnológico – CNPq, and Empresa Baiana de Desenvolvimento Agrícola – EBDA. Also, *in memorian* of Professor and Researcher Fabyano Fonseca e Silva, acknowledgments for all his great contribution at brazilian scientific research and in the formation of new professionals along his honorable carrier.

Conflict of interest

The authors declare no conflict of interest.

References

1. Aggrey, S. Comparison of three nonlinear and spline regression models for describing chicken growth curves. *Poultry Science* **81**(12), 1782–1788 (2002).
2. Balan, C., Kathiravan, G., Thirunavukkarasu, M., Jeichitra, V. Non-linear growth modelling in Mecheri breed of sheep**.** *Journal of Entomology and Zoology Studies* **5** (5), 2005-2008 (2017).
3. Brody, S. *Bioenergetics and Growth*. Rheinhold Publishing, New York. (1945).
4. Carneiro, P. L. S., Malhado, C. H. M., Souza Júnior, A. A. O., Silva, A. G. S., Santos, F. N., Santos, P. F., Paiva, S. R. Desenvolvimento ponderal e diversidade fenotípica entre cruzamentos de ovinos Dorper com raças locais. *Pesquisa Agropecuária Brasileira* **42** (7), 991-998 (2007).
5. Carneiro, A. P. S., Muniz, J. A., Carneiro, P. L. S., Malhado, C. H. M., Martins Filho, R., Silva, F. F. e. Identidade de modelos não lineares para comparar curvas de crescimento de bovinos da raça Tabapuã. *Pesquisa Agropecuária Brasileira* **49** (1), 57-62 (2014).
6. Carvalho, S., Vargas, T. D., Daltrozo, F. D., Kieling, R. Consumo de nutrientes, ganho de peso e conversão alimentar de cordeiros terminados em confinamento com dietas contendo diferentes níveis de energia. *Revista Brasileira de Agrociência* **14** (4), 86-90 (2008).
7. Dilliwar, L.; Verma, M. R.; Singh, Y. P.; Sharma, V. B.; Kumar, S.; Shukla, A. Nonlinear modelling of sheep and goat populations in India. *Journal of Applied and Natural Science* **8** (4), 1766-1769 (2016).
8. Hernandez, E.L. *Parameter Estimation in Linear-Linear Segmented Regression*. Dissertação (Mestrado em Ciência) – Faculty of Brigham Young University, Prova (2010).
9. Hossein-Zadeh, N. G. Modelling growth curve in Moghani sheep: comparison of non-linear mixed growth models and estimation of genetic relationship between growth curve parameters. *Journal of Agricultural Science* **155** (7), 1150-1159 (2017).
10. IBGE. *Censo Agropecuário 2017*. Available in: < https://censoagro2017.ibge.gov.br/templates/censo_agro/resultadosagro/pecuaria.html?localidade=0&tema=75674> Acessed in: March 31 2020.
11. Iqbal, F., Tariq, M. M., Eyduran, E., Huma, Zil-E, Waheed, A., Abbas, F., Ali, M., Rashid, N., Rafeeq, M., Mustafa, M. Z. Fitting Nonlinear Growth Models on Weight in Mengali Sheep through Bayesian Inference. *Pakistan J. Zool*. **51** (2), 459-466 (2019).
12. Malhado, C. H. M., Carneiro, P. L. S., Affonso, P. R. A. M., Souza Jr., A. A. O., Sarmento, J. L. R. Growth curves in Dorper sheep crossed with the local Brazilian breeds, Morada Nova, Rabo Largo, and Santa Inês. *Small Ruminant Research* **84**, 16-21 (2009).
13. Mokhtari, M. S., Borzi, N. K., Fozi, M. A., Behzadi, M. R. B. Evaluation of non-linear models for genetic parameters estimation of growth curve traits in Kermani sheep. Tropical *Animal Health and Production* **51**, 2203–2212 (2019).
14. Nimase, R. G., Kandalkar, Y. B., Bangar, Y. C. Non-linear modeling for estimation of growth curve parameters in Madgyal sheep. *Journal of Entomology and Zoology Studies* **6** (2), 463-465 (2018).
15. Piola junior, W., Ribeiro, E. L. de A., Mizubuti, I. Y., Silva, L. D. F., Rocha, M. A., Barbosa, M. A. A. F., Souza, C. L., Paiva, F. H. P. Weight gain and carcass characteristics of lambs receiving different levels of energy in the ration. *Ciências Agrárias* **30** (4), 935-944 (2009).
16. Rezende, D. M. L. C., Muniz, J. A., Ferreira, D. F., Silva, F. F. E., Aquino, L. H. Ajuste de modelos de platô de resposta para a exigência de zinco em frangos de corte. *Ciência e Agrotecnologia* **31** (2), 468-478 (2007).
17. Richards, F.J. A flexible growth function for empirical use. *Journal of Experimental Botany* **10**, 290-300 (1959).

18. Sarmento, J. L. R., Regazzi, A. J., Sousa, W. H., Torres, R. A., Breda, F. C., Menezes, G. R. de O. Estudo da curva de crescimento de ovinos Santa Inês. *Revista Brasileira de Zootecnia* **35** (2), 435-442 (2006).
19. SAS Institute Inc. *Statistical Analysis System user's guide*. Version 9.4 ed. Cary: SAS Institute, USA (2014).
20. Simasiku, L., Charamba, V., Lutaaya, E. Modeling and comparison of the maturing rates of Damara, Dorper and Swakara sheep at Neudamm Farm. *Welwitschia International Journal of Agricultural Sciences* **1**, 41-48 (2019).
21. Souza, F. A. C., Fernandes, T. J., Moura, R. S., Meirelles, S. L. C., Ribeiro, R. A., Cunha, F. O., Muniz, J. A. Nonlinear modeling growth body weight of Mangalarga Marchador horses. *Ciência Rural* **47** (4), 2017.
22. Souza, L.A., Carneiro, P. L. S., Malhado, C. H. M., Paiva, S. R., Caires, D. N., Barreto, D. L. F. Curvas de crescimento em ovinos da raça morada nova criados no estado da Bahia. *Revista Brasileira de Zootecnia* **40** (8), 1700-1705 (2011).
23. Teixeira Neto, M. R., Cruz, J. F., Faria, H. H. N., Souza, E. S., Carneiro, P. L. S., Malhado, C. H. M. Descrição do crescimento de ovinos Santa Inês utilizando modelos não-lineares selecionados por análise multivariada. *Rev. Bras. Saúde Prod. Anim.* **17** (1), 26-36 (2016).
24. Vidal, M.F., Silva, R. G., Neiva, J. N. M., Cândido, M. J. D., Silva, D. S., Peixoto, M. J. A. Análise econômica da produção de ovinos em lotação rotativa em pastagem de capim tanzânia (Panicum maximum (Jacq)). Revista de Economia e Sociologia Rural **44** (4), 801-818 (2006).
25. Vitezica, Z. G., Marie-Etancelin, C., Bernadet, M. D., Fernandez, X., Robert-Granie, C. Comparison of nonlinear and spline regression models for describing mule duck growth curves. *Poultry Science* **89**(8), 1778–1784 (2010).
26. Von Bertalanffy, L. Quantitative laws for metabolism and growth. *Q. Rev. Biol.* 32, 217−231 (1957).
27. Zapata, J. F. F., Seabra, L. M. A. J., Nogueira, C. M., Bezerra, L. C., Beserra, F. J. Características de carcaça de pequenos ruminantes do Nordeste do Brasil. *Revista Ciência Animal* **11** (2), 79-86 (2001).
28. Zhang, W., Goh, A. T.C. Multivariate adaptive regression splines and neural network models for prediction of pile drivability. *Geoscience Frontiers* **7**, 45-52 (2016).