



## Comparison of Nonlinear Functions to Define the Growth in Intensive Feedlot System with XGBoost Algorithm

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### ABSTRACT

The aim of this study was to define the growth by using nonlinear functions in intensive feedlot system with XGBoost algorithm. To achieve this aim, five nonlinear functions were implemented. To implementation of the study, Brown Swiss (n=41) and Simmental (n=95) breed were used. Each nonlinear functions were examined for each breed. According to the results of the nonlinear functions, logistic model was the best prediction model for defining the growth of each breed. In this study, the parameters in the best prediction model were calculated individually and the relationship of these parameters with body weight was evaluated with the XGBoost algorithm. Model comparison criteria such as standard deviation ratio (SD<sub>ratio</sub>), Pearson's correlation coefficient (PC), determination of coefficient (R<sup>2</sup>) and Akaike's information criteria (AIC) were used to evaluate the XGBoost algorithm. In conclusion, the XGBoost algorithm can be an effective and optional approach that allows breeders to estimate live weight from growth parameters. This algorithm can operate on large data sets with high accuracy and speed, leading to significant improvements in agricultural productivity and animal health management. XGBoost enables more accurate predictions by analyzing the effects of various characteristics (e.g., nutritional level, breed, age). Therefore, this method can be used to determine critical parameters such as body weight in animal breeding practices, serving as a powerful support tool for operational decisions.

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## Introduction

As the world population increases, the nutritional needs of people also increase in linear. In this context, the need for protein, which forms the basis of quality nutritional needs, is also increasing. The need for protein of animal origin, which is one of the quality protein sources, is increasing in parallel with these. The day-to-day increase in the world population has led to overuse of global resources, with a positive correlation between the need for animal food and the standard of living associated with animal food production (Cardoso, 2012). This situation raises concerns about the environmental sustainability of production chains connected to the livestock sector (Roma et al., 2017a). The entire livestock sector, and especially beef production, is now placed under a special focus (Gerber et al., 2015). In this context, there are many sources of heterogeneity in the stages of high yield from an animal in terms of the area studied. Because the yield level at the level allowed by the genotype changes with breeding

studies, and the maximum yield that the genotype can give varies depending on environmental factors. There are many applications in increasing the efficiency of beef cattle. Some of these are pasture system, intensive system and semi-intensive system practices. The intensification of beef cattle systems consists of a process that aims to increase the yield relatively by eliminating the aged animals or insufficiently productive animals from the herd (Vaz et al., 2020). With the implementation of these systems, both the efficiency to be obtained from livestock will increase for the consumer and the income from livestock will increase for the breeder. In this regard, it is very important to define the growth in increasing the yield obtained from livestock.

Growth term is a main factor in increasing both the financial revenue from livestock and the animal product available to the consumer. The perception of growth for livestock consists of a process in which morphological and

physiological changes occur in both weight and body mass from birth to mature age (Topal and Bolukbasi, 2008; Kaplan and Gürcan, 2018). In addition to all these, monitoring of growth in animals is very important in herd management (Do and Miar, 2019). For an efficient and sustainable livestock, all stages of growth should be addressed. In this way, it will be simpler to breeders to predict growth term and determine the amount of feed, applicable drug dose and time to market required inside the herd. In this context, breeders paid consideration to live weights as a result of body mass changes. Many methods entitled growth curves can be used in animal breeding to describe changes in body mass index and weight over time (Do and Miar, 2019). In this context, some nonlinear growth curve models were proposed to examine data on growth over time for biological systems (Bahreini et al., 2014). The ability of growing biological material over time to reach its maximum level of superior genetic potential under recent environmental situations can be clarified by growth curves. In order to understand the growth more clearly, in livestock studies, growth will be more effectively described by using growth curves to express the growth depending on the age of the animals. Although the pattern of growth differs for each animal species, the use of growth curve models in selection programs will be more useful in expressing growth since initial parameters of the growth curves are heritable (Do and Miar, 2019). For this purpose, many researchers have explained the growth with nonlinear models and reported that selection practices can be done effectively in determining herd management (Sakar and Erisek, 2019; Yavuz et al. 2019).

The expression of growth can vary from species to species and from breed to breed. In this context, growth curve models that are highly explanatory for each species or even for each breed will differ. For this reason, researchers have proposed different growth curve models such as Exponential, Brody, Gompertz, Logistic and von Bertalanffy in describing growth.

Body weight estimation based on parameters used as starting parameters in growth curve models is also an important consideration. The purpose of this study, which will help in defining the growth that differs from species to species, is to define the growth in beef cattle as well as to estimate the end-fattening body weight from the initial parameters of the growth curve model that makes the strongest prediction with different breeds factor by the XGBoost algorithm.

## Material and Methods

### Animal Material

Brown Swiss (n=41) and Simental (n=95) breeds were used as a data for this study in Niğde province of Türkiye. The animals used in the study were fed on average 35.82% for roughage and 64.18% for concentrate. This directional feeding continued throughout the experiment. The roughage and concentrate feed raw materials given to the animals during the trial (6 months) are given in Table 1. The experiment was published in 2014 and was based on the dollar exchange rate of that year (\$1 = 2.19 TL). The last procedure of the experiment, the animals were sold the carcass for kg with an average of 12.10 \$.

Table 1. The information about the ration of the used animals in experiment

Feeds	Ration (kg/day)	Price (\$/kg)	RCA
Barley mash	2	0.59	1.19
Corn mash	2	0.55	1.10
Urea	0.5	0.91	0.46
Premix	0.25	1.37	0.34
Corn silage	4	0.16	0.64
PSWM	2	0.16	0.32
Fattening feed	4	0.62	2.48
Beet pulp	2	0.14	0.27
Total	16.75	4.50	6.80

PSWM: Peanut stalk, wheat stalk mixed; RCA: Ration cost of per animal (\$)

### Methodology

Body weights taken from animals periodically for 5 months were selected five growth curve models. These models were Exponential, Brody, Gompertz, Logistic and von Bertalanffy models. The equations for each selected growth model are given in Table 2 (Gompertz, 1827; Von Bertalanffy, 1957; Bahreini et al., 2014; Arnhold, 2022).

Table 2. The description of the selected five nonlinear models

Model	Equation	NP
Exponential	$BW = a * \exp^{b*t}$	2
Logistic	$BW = a * (1 + b * \exp^{-c*t})^{-1}$	3
VonBertalanffy	$BW = a * (1 - b * \exp^{-c*t})^3$	3
Brody	$BW = a * (1 - b * \exp^{-c*t})$	3
Gompertz	$BW = a * \exp^{(-b*\exp^{-c*t})}$	3

NP: Number of parameters

BW is noted body weight for each of t<sup>th</sup> month of age. The first unknown initial parameter is a which is a live body weight at the period of maturity, which is asymptotic boundary of the body weight for several ages of time (t). The second unknown initial factor of b is an additional constant set consistent with the condition that it varies from the time and personal weight. By the coefficient it is imaginable to understand the percentage for asymptotic live weight to be gotten after the birth. The parameter of c is a factor which states the linear variation amount of a logarithmic function of body weight over the time, which is certain for all of the nonlinear equations (Kopuzlu et al., 2014).

To evaluate and describe the growth with nonlinear functions, several criteria such as R<sup>2</sup>, R<sup>2</sup><sub>adj</sub>, Bayesian information criterion (BIC) and Akaike's information criterion (AIC) were used. The model comparison functions are given below, respectively.

$$R^2 = 1 - \frac{SSE}{SST} \tag{1}$$

$$R^2_{adj} = R^2 - \left(\frac{k-1}{n-k}\right) (1 - R^2) \tag{2}$$

$$AIC = n \ln \left(\frac{SSE}{n}\right) + 2k \tag{3}$$

$$BIC = n \ln \left(\frac{SSE}{n}\right) + k \ln(n) \tag{4}$$

where, k is the number of parameters, n is the number of sample size of the study, SST is total sum of squares, SSE is sum of square error. To decide the major effects of environmental factors on the nonlinear functions of the animals, the next fixed effect model is accepted:

$$Y_{ij} = \mu + S_i + e_{ij} \quad (5)$$

where,  $\mu$  is about the general mean of the herd,  $S_i$  is about fixed effects of the  $i$ th breed ( $i$ =Simmental or Brown Swiss) and  $Y_{ij}$  is about the vector of projected starting parameters.

XGBoost (eXtreme Gradient Boosting) was first proposed by Tianqi Chen and Carlos Guestrin in 2011 and is a model that can be modified by many scientists in solving regression and classification type problems (Chen and Guestrin, 2016). XGBoost algorithm is one of the most effective algorithms proposed in machine learning algorithms in latest times (Ma et al., 2018). The XGBoost procedure is a tree-based algorithm with the similar decision directions as the decision tree, in addition to being depended on the gradient tree boosting method (Zhong et al., 2018). Boosting algorithms are one of the machine learning algorithms that may use classification and regression type problems. At each step of the boosting algorithm, it produces a weak learner to predict or classify and accumulates the learned learner in the total model. If the weak learner obtained at each step depends on the gradient way of the loss task, it can be termed as Gradient Boosting Machines (GBM) (Friedman, 2001). In addition, XGBoost can be able to operate sparsity and to knock out the overfitting difficulty of the data set by employing the regularization and shrinkage approaches (Chen and Guestrin, 2016; Gertz et al., 2020). First of all, the XGBoost algorithm proceeds the explanatory variables that can improve the efficiency of depend on the decision tree model rules to recognize between the two groups. Moreover, useless explanatory variables are consistently built at the speed of the computation time of the CPU (Gertz et al., 2020). This process includes the key idea is to construct a cluster which has a low bias and high variance decision trees (Chen and Guestrin, 2016).

To evaluate the model prediction performance for the XGBoost tree structure, the following criteria were used (Zaborski 2019; Eyduran 2019) [19,20]:

1. Akaike information criterion (AIC):

$$\begin{cases} AIC = n \cdot \ln \left[ \frac{1}{n} \sum_{i=1}^n (y_i - y_{ip})^2 \right] + 2k, & \text{if } \frac{n}{k} > 40; \\ AIC_c = AIC + \frac{2k(k+1)}{n-k-1} & \text{otherwise} \end{cases} \quad (6)$$

2. Standard deviation ratio (SDR):

$$SD_{ratio} = \frac{S_m}{S_d} \quad (7)$$

where, n is the number of sample size of the data set, number of explanatory variables is presented by using the k parameter,  $y_i$  is the actual observation of the response variable (BW),  $y_{ip}$  is the predicted observation of the response variable (BW),  $s_m$  represents the standard deviation of the model's error,  $s_d$  represents the standard deviation of the response variable (BW).

All the statistical process were carried out by applying R software (R Core Team, 2021). Descriptive statistics of all features were predicted by using “psych” package in R software (Revelle, 2022). The selected nonlinear functions were performed and compare by using “nlstools” and “easynls” packages (Arnhold, 2022; Baty et al., 2015). To complete the XGBoost procedure, “caret” package were utilized (Kuhn, 2022). The last process of this study was visualized to presentation of the performances for XGBoost algorithm by using “chaGoF” package (Eyduran, 2022).

## Results

To define of the data set, in Table 3, the descriptive statistics are given. For Simmental and Brown Swiss cattle, the body weight was compared by performing the analysis of variance for each breed. Differences between groups were evaluated with the Duncan multiple comparison test. A statistical difference was determined between the monthly average live weights of the animals fed during the 6-month period ( $p < 0.05$ ).

Table 3. Descriptive statistics for each breed and age.

Age (month)	Simmental BW (M± SE)	Brown Swiss BW (M± SE)
0	295.73±4.04	297±8.25
1	340.19±4.67	341±8.52
2	380.76±5.01	377.79±9.85
3	422.83±5.33	417.96±9.97
4	453.46±5.93	442.42±10.17
5	481.02±6.02	469.79±12.4

M± SE: Mean± Standard Error

The predictable growth parameters for all nonlinear model for Simmental cattle breed are presented in Table 4. The estimated body weight (a) wide-ranging among the nonlinear models and breeds. The highest estimated body weight in 5th months of intensive period were observed 720.030 kg for Simmental breed in Brody nonlinear model. The exponential nonlinear model was determined as the lowest 6th month of live weight with values of 309.776 kg for Simmental breed. For the parameter of b as initial parameters, Logistic nonlinear model made the greatest rate, which varied from 0.093 to 0.947. The initial parameter of c shows for the 6th month of the feeding period which wide-ranging between the nonlinear models from 0.116±0.046 (for Brody model) to 0.316 ± 0.049 (for Logistic model) for Simmental breed.

For Brown Swiss breed, the predictable growth parameters for all nonlinear models are shown in Table 5. The predicted body weight (a) wide-ranging among the models and breeds. The greatest estimated body weight in 6th month were detected 647.587 kg in Brody nonlinear model. The exponential nonlinear model had the lowest 6th month live weight with values of 311.308 kg. Logistic nonlinear model made the peak amount for b parameter, which varied from 0.086 to 0.843 with other nonlinear models. The one of initial parameters c implies the 6th month of growth amount which assorted between the used nonlinear models from 0.136 ± 0.094 (Brody model) to 0.323 ± 0.100 (Logistic model) for Brown Swiss breed.

Table 4. Predicted initial parameters for the chosen nonlinear models and confidence interval (95%) for Simmental breed.

	Parameters	Estimate	Standard error	Confidence interval (95%)	
				Lower bound	Upper bound
Exponential	a	309.776	3.487	302.927	316.625
	b	0.093	0.003	0.087	0.099
Logistic	a	575.129	37.251	501.961	648.297
	b	0.947	0.113	0.725	1.170
	c	0.316	0.049	0.220	0.412
von Bertalanffy	a	643.385	72.309	501.358	785.411
	b	0.228	0.026	0.176	0.282
	c	0.182	0.046	0.090	0.274
Brody	a	720.030	127.607	469.389	970.670
	b	0.591	0.069	0.454	0.727
	c	0.116	0.046	0.025	0.206
Gompertz	a	619.913	58.859	504.306	735.521
	b	0.742	0.088	0.570	0.915
	c	0.216	0.047	0.123	0.308

Table 5. Predicted initial parameters for the chosen nonlinear models and their confidence interval (95%) for Brown Swiss breed.

Model	Parameters	Estimate	Standard error	Confidence interval (95%)	
				Lower bound	Upper bound
Exponential	a	311.308	6.640	298.182	324.435
	b	0.086	0.006	0.074	0.099
Logistic	a	547.761	63.096	423.023	672.498
	b	0.843	0.191	0.466	1.220
	c	0.323	0.100	0.125	0.521
Von Bertalanffy	a	597.714	112.060	376.179	819.250
	b	0.208	0.045	0.117	0.298
	c	0.198	0.096	0.008	0.388
Brody	a	647.587	177.037	297.595	997.578
	b	0.542	0.118	0.307	0.776
	c	0.136	0.094	0.050	0.323
Gompertz	a	581.144	94.149	395.017	767.270
	b	0.672	0.149	0.377	0.966
	c	0.229	0.097	0.037	0.421

Table 6. Pearson’s correlations among the parameters for Simmental breed

	Parameters	a	b	c
Exponential	b	-0.878		-
Logistic	b	0.972		
	c	-0.972	-0.903	
von Bertalanffy	b	0.991		
	c	-0.990	-0.968	
Brody	b	0.997		
	c	-0.996	-0.987	
Gompertz	b	0.987		
	c	-0.986	-0.955	

The relationship between the initial parameters of the nonlinear models fixed to body weight from the several months of the data set are displayed in Table 6 (for Brown Swiss breed) and Table 7 (for Simmental breed) by using Pearson’s correlation coefficient, respectively. Table 6 showed that the correlation coefficient among the a and b parameters were calculated -0.878 (exponential), 0.972 (logistic), 0.991 (von Bertalanffy), 0.997 (Brody), 0.987 (Gompertz). The whole correlation coefficient among a and c parameters are negative and strong which have -0.972, -0.990, -0.996 and -0.986 for Brody, von Bertalanffy, logistic and Gompertz, respectively. The

correlation between b and c parameters are also strong and negative coefficients which have -0.903, -0.968, -0.987 and -0.955 for Brody, von Bertalanffy, logistic and Gompertz nonlinear models, respectively.

Table 7 showed the relationship between a, b and c parameters for each model. The obtained correlation coefficient among the a and b parameters were determined as -0.874, 0.582, -0.988, 0.994, 0.984, respectively. The obtained correlation coefficient among the a and c parameters is negative values. The negative correlation coefficients were determined as -0.873, -0.989, -0.994 and -0.985 for logistic, von Bertalanffy, Brody and Gompertz,

respectively. The correlation coefficients among the b and c parameters are negative and the coefficients were determined as -0.947, -0.981, -0.960 and -0.262, for Gompertz, Brody, von Bertalanffy and logistic respectively.

Table 7 showed that model comparison criteria were calculated for the logistic, exponential, Brody, Gompertz and von Bertalanffy models for each sex to comparison several nonlinear models. For examining the comparison of the models, the model comparison criteria should be the highest R<sup>2</sup> and R<sup>2</sup><sub>adj</sub> values and the smallest AIC and BIC values. In this context, Table 8 presented that the best results have given by logistic growth curve model inside the selected growth curve models for each breed.

Many studies have been done on modeling growth curves for different species in farm animals by means of different nonlinear functions. However, there is no information about body weight estimation from individual growth parameters gained from nonlinear models for beef cattle in the literature yet. In this context, we aimed to

explain the body weight from individual growth curve parameters with XGBoost algorithm.

The XGBoost algorithm was interpreted within the scope of the model comparison criteria. In this context, we used four model comparison criteria such as standard deviation ratio (SD<sub>ratio</sub>), Pearson's correlation coefficients (PC), coefficient of determination (R<sup>2</sup>) and Akaike's information criterion (AIC). To explain the model performance, the succeed model should be the highest PC and R<sup>2</sup> values and the lowest SD<sub>ratio</sub> and AIC values. In this context, Table 9 was given for explaining the success of the model performance within the scope of model comparison criteria. Table 9 showed that the XGBoost algorithm was a reliable model for estimating the body weight from individual growth curve parameters obtained from the logistic growth curve model. The obtained correlation coefficient among actual and predicted 5th month of weight was so strong and significant for the XGBoost algorithm (p<0.01).

Table 7. Pearson's correlations between the parameters for Brown Swiss breeds

	Parameters	a	b	c
Exponential	b	-0.874		-
Logistic	b	0.582		
	c	-0.873	-0.262	
von Bertalanffy	b	0.988		
	c	-0.989	-0.960	
Brody	b	0.994		
	c	-0.994	-0.981	
Gompertz	b	0.984		
	c	-0.985	-0.947	

Table 8. Model comparison criteria for the selected nonlinear models

Model	AIC		BIC		R <sup>2</sup> (%)		R <sup>2</sup> <sub>adj</sub> (%)	
	Simmental	Brown Swiss	Simmental	Brown Swiss	Simmental	Brown Swiss	Simmental	Brown Swiss
Exponential	6117.349	1533.825	6130.386	1542.734	60.17	59.02	60.10	58.74
Logistic	6097.786	1530.070	6115.169	1541.949	61.65	60.64	61.51	60.08
von Bertalanffy	6097.986	1530.078	6115.369	1541.958	61.63	60.63	61.50	60.07
Brody	6098.137	1530.095	6115.520	1541.974	61.62	60.62	61.49	60.06
Gompertz	6097.923	1530.073	6115.306	1541.952	61.64	60.63	61.50	60.07

Table 9. Results of performances for XGBoost algorithms in the training and test set

Model comparison criteria	XGBoost	
	Train	Test
Standard deviation ratio (SD <sub>ratio</sub> )	0.04	0.358
Pearson's correlation coefficients (PC)	0.999	0.938
Coefficient of determination (R <sup>2</sup> )	0.998	0.868
Akaike's information criterion (AIC)	140.820	213.120

In the XGBoost algorithm, in which live weight is estimated from the individual parameters gotten from the growth curve model and the breed factor, the variables affecting the live weight were evaluated with sensitivity analysis (Figure 1). According to Figure 1, it was determined that the variable that affected the live weight the least was the Swiss Brown breed, while the variable that affected the most was the parameter.

The variables such as a, b and c was express in the Figure 1 that a parameter is a live body weight at the period of maturity, b is an additional constant set consistent with the condition that it differs from the time and personal weight and c parameter is a factor that states the linear variation amount of a logarithmic function of body weight over the time.

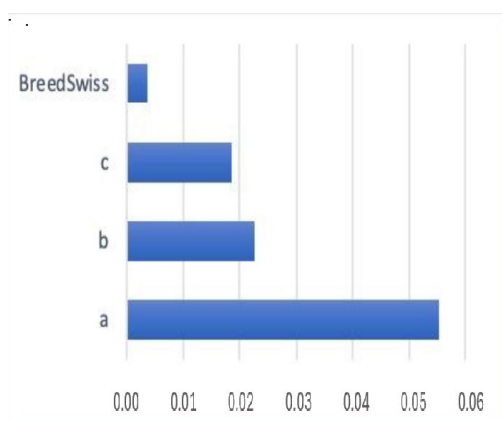


Figure 1. Sensitivity analysis for XGBoost algorithm

## Discussion

Understanding and estimating the growth procedures in animal husbandry, especially in rural areas that make a living from animal husbandry, is very important for a sustainable livestock. Nonlinear models called as growth curve models, which is widely used in defining growth, is a beneficial method for biological estimation, research and explaining growth associations (Ramos et al., 2013; Ibtisham, 2017).

Although there are many methods for describing growth, the methods that best describe growth may differ between species and will vary from breed to breed. In this context, the method that defines the best growth for beef cattle is the logistic growth curve. By means of various model comparison criteria, it is aimed to find the most suitable model for Brown Swiss and Simmental breeds and with the logistic growth curve model selected on the basis of individually calculated growth parameters. For this aim, XGBoost algorithm was used, and the XGBoost algorithm was fitted reliable according to the goodness of fit criteria. The study of the growth curve of fattening cattle during the fattening period is dearth. In addition, there are some studies to describe the association among separately obtained growth curve parameters and body weight for various species. In this content, CART and MARS algorithms were performed for sheep, XGBoost and CART algorithms were performed for goose within the scope of explain the association among body weight, sex and growth parameters. However, there is no study for beef cattle species.

Putra et al., (2020) was performed the growth curves such as Gompertz, Logistic, Richards and Morgan Mercer-Flodin for Limousine and Simmental candidate bulls within the scope of early selection criterion. For this aim, 13 animals (6 Simmental and 7 Limousine) were used. The data were taken from birth to 8th month of age. The obtained  $R^2$  values were so high from our study. However, this difference is thought to be due to the fact that the data were taken from the birth.

Duan et al., (2021) was performed the Genome-Wide Association Analysis for Gompertz, logistic and Brody growth curve models in Chinese Simmental beef cattle. The period evaluated in the study is from birth to 18 months (0, 6, 12 and 18). For this aim, 808 Chinese Simmental beef cattle were used. For variable a, which seems to be the most effective variable in this study, close

values were obtained, except for Brody. In addition, the  $R^2$  values we obtained in our study are lower than those of Duan et al., (2021). However, this difference is thought to be due to the fact that Duan et al., (2021) started the study from birth to 18th month.

Hartati and Putra (2021) were performed the growth curve parameters such as logistic, Brody and von Bertalanffy for male and female Madura cattle. To explain the growth, the data were taken from birth to 20th month of age. For this aim, 186 animals (95 male, 91 female) were used. As a result of this study, logistic growth curve modeling was so close values with our study within the scope of  $R^2$ .

Hengweia et al., (2022) were performed the growth curves such as logistic, Brody, Gompertz, and Bertalanffy for the Qinchuan bull population. The data were taken from birth to 24th month of age. For this aim, 95 Qinchuan bull were used. As a result of the study, all growth curve models has higher than our study within the scope of  $R^2$ . However, this difference is thought to be due to the fact that they started the study from birth to 24th month.

Tırnk et al., (2022) were performed the growth parameters for goose species. In addition, the obtained individual growth parameters were used to explain of the relationship between nonlinear models' parameters, body weight and sex. Although the von Bertalanffy growth curve seems to be a more effective estimation model in this study, the XGBoost model is the best model for estimating body weight from individually obtained growth parameters and sex. The fact that the von Bertalanffy model is more reliable as a growth curve model is thought to be due to inter-species differences.

## Conclusion

In terms of the continuity of flock management in animal creation, it is a so vital mission for the breeder to chase the developmental periods in the herd. In this content, growth curve modeling will ensure a supportable and well-organized management mechanism. In this study was carried out, various nonlinear growth functions (exponential, logistic, Brody, Gompertz and von Bertalanffy) were assessed to describe the body weight-age association for Simmental and Brown Swiss beef cattle breed. In this context, it was specified that logistic model was the best fit among the other non-linear models such as Brody, Gompertz, von Bertalanffy and exponential compared in the sense of performance. The XGBoost algorithm could be useful separate parameters gotten from the specified the logistic model, and it was aimed to explain the association among the breed, body weight and growth parameters. In this way, it also exhibits the possible for XGBoost algorithm to find the body weight-breed-growth parameters association.

In the light of all this information, growth curve models and XGBoost algorithm may help to increase of the revenue from livestock and so it will be valuable to many flocks' organization features such as deciding the best non-linear model, proper feed consumption for animals and the optimum slaughter period of the animal.

## Declarations

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The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

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No financial support was received for conducting this study.

### Conflict of Interest

The authors declared that there is no conflict of interest.

### Author Contributions

DÇB and CT analyzed data and wrote the manuscript. MB revised the manuscript. All authors read and approved the final manuscript.

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