



The Use of Some Nonlinear Functions to Explain Growth in Japanese Quails with Multivariate Adaptive Regression Splines Algorithm

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ABSTRACT

The study aimed was to determine the best nonlinear function describing the growth stages of the Japanese quail breed. To this aim, growth functions such as exponential, logistic, von Bertalanffy, Brody, and Gompertz were used as nonlinear functions is used in the description of the body weight-age relationship of male and female Japanese quails. The Multivariate Adaptive Regression Splines (MARS) data mining algorithm was applied to the individual growth parameters obtained from the determined as the best fit model, and the relationship between sex and growth parameters with it has been revealed. The study dataset was 1267 body weight-age records collected from the hatching to the 6th week of age of 181 Japanese quails consisting of 90 females and 91 males. Each model was applied separately for both males and females. Model fit criteria such as coefficient of determination (R^2), adjusted coefficient of determination (R^2_{adj}), Akaike's information criterion (AIC), and Bayes information criterion (BIC) were used to evaluate the performances of the growth functions used individually. All the statistical analyses were made by the R package program. The growth curve models were ranked in the form of Logistic > Gompertz > von Bertalanffy > Brody > Exponential according to the goodness of fit criteria. The most suitable model among the non-linear models in terms of performance was logistic. When the relationship between the growth curve parameters and body weight of the logistic model was explained with the MARS algorithm, the goodness of fit criteria showed that the obtained MARS model showed reliable performance. In addition, Pearson's correlation coefficient between real and estimated body weight was found quite strong for the MARS algorithm ($r=0.935$). The results showed that the MARS algorithm can be presented as a good reference for breeders to establish breed standards and selection strategies for Japanese quails in growth parameters for breeding purposes.

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Introduction

Quail breeding is a branch of animal husbandry that attracts great attention in many parts of the world due to its low energy and high protein in biologically important meat components. In addition to lean meat, eggs are lower in cholesterol than chicken eggs (Musa et al., 2008). Quail breeding is a vital production branch for eggs in Japan and Southeast Asia and meat in Europe (Minvielle, 1998).

Quail breeding is a breed that has been widely cultivated in recent years due to its advantages, such as resistance to diseases, high egg production per live weight of animals, and low feed consumption (Inci et al., 2016). In addition, it is extensively utilized in poultry breeding research due to its extreme fertility (Ayasan, 2013; Inci et

al., 2016). Compared to other poultry fields, quail breeding can adapt a massive number of animals without demanding extreme lodgement in the unit area (Alkan et al., 2008; Inci et al., 2016).

Japanese quails reach approximately 16 cm in size for males, while females reach approximately 18.5 cm (Inci et al., 2016). Commonly, quails are not marketed according to their weight, but at the age of 4-5 weeks, they are marketed per piece. However, consumers' wish to buy heavier quail has caused some organizations to cut quails at a late age which has caused problems with abdominal fat (Narinc et al., 2014). It is very important to know the growth in order to express this situation more effectively.

Growth is a critical issue in raising the economic revenue from animal breeding. The main idea of growth in farm animals is a procedure in which the physiological and morphological difference in both weight and volume takes place during the period from hatching to maturity (Topal et al., 2004; Topal and Bolukbasi, 2008; Rizzi et al., 2013; Kaplan and Gurcan, 2018). Following the growth of farm animals is vital for farm management (Do and Miar, 2020). In animal breeding, all periods of growth must allocate for effective and sustainable farm management. In this context, the breeders gave attention to body weight due to growth rates. Within the scope of animal breeding, various growth curves describe the changes in body weight or size over time (Do and Miar, 2020). Growth curve modeling is intended to examine longitudinal information on growth over time (Bahreini Behzadi, 2014). In the current environmental conditions, the ability to reach the maximum genetic potential for the grownup biological material can be explained with the help of growth curves (Setiaji et al., 2013). To understand the growth patterns well, it would be more suitable to benefit from the growth curves related to the increasing age of the farm animals. Growth curve models can also use in animal species in selection programs as the inherited growth parameters (Fitzhugh, 1976; Mignon-Grasteau, 1999; Do and Miar, 2020). For this reason, many scientists have reported that the proper management methods are determined effectively with non-linear models (Eyduran et al., 2008; Kucuk and Eyduran, 2009; Kum et al., 2010; Waheed et al., 2016; Sakar and Erisek, 2019).

Various non-linear methods such as Exponential, Logistic, von Bertalanffy, Brody, and Gompertz have been suggested to determine the growth. Non-linear models are more effective than linear models in explaining growth due to their sigmoidal structure (Hojjati and Hossein-Zadeh, 2018). These non-linear models permit the interpretation of metabolic incidents in animals during growth periods (Fitzhugh, 1976; Do and Miar, 2020). Many kinds of research have been allocated to model the growth curve in quail.

The primary purpose of this present study was to define the best one among some non-linear functions such as Exponential, Logistic, von Bertalanffy, Brody, and Gompertz for a description of the growth of male and female Japanese quails. Afterward, the relationship between the best model parameters explaining growth, gender, and body weight at 6th was modeled with the MARS algorithm.

Material and Methods

Data Collection and Analysis Procedure

In the study, a data set containing a total of 1267 body weight-age records of the hatching to the 6th week of age of Japanese quails were used.

The hatched chicks are wing-banded and individually weighed from hatching to 6 weeks of age. The chicks were placed in controlled temperature battery incubators in an area of 130 cm² per quail. The temperature was 34°C in their first week of life and was lowered by 1.5°C per week until the quails were 5 weeks old, after which the warming was stopped. Quails were kept in the light for 23 hours and in the darkness for 1 hour. Sex determination in quails was made at the age of 3 weeks according to feather color. During the trial period, the quails were fed with a feed consisting of 11.7 MJ kg⁻¹ metabolic energy and 210 g crude protein kg⁻¹ ad libitum and were given unlimited water throughout the experiment.

In the quails subject to the research, the growth was defined by using five nonlinear models such as body weights, Brody, exponential, logistic, von Bertalanffy, Brody and Gompertz models. The mathematical explanation of the five selected growth models is given in Table 1.

The interpretation of the unknown parameters of each nonlinear equation can be done as follows. BW refers to the weight of quails weighed from hatching to 6 weeks of age. The first of the unknown parameters, the a parameter, is the live weight at maturity, which is the asymptotic limit of the live body weight for each age. As the second parameter, which is one of the unknown parameters, the b parameter is an integration constant adjusted for the situation that is different from the initial weight and time. This coefficient makes it possible to interpret the ratio of asymptotic mature live body weight obtained after birth. The parameter c, which is used in the models containing the estimations of the 3 parameters, which is the subject of the study, is a constant that is specific for each of the nonlinear equations and expresses the linear rate of change of the logarithmic function of live weight over time (Kopuzlu et al., 2014).

Goodness-of-fit criteria such as R², R²_{adj}, Akaike's information criterion (AIC), and Bayesian information criterion (BIC) were used to compare and explain growth curve model performances. The expressions of the goodness-of-fit criterion functions are given below, respectively.

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

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

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

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

where; SSE is sum of square error, SST is total sum of squares, log-likelihood is the maximum likelihood term, number of parameters is shown by k, n is the sample size of the study.

Table 1. Mathematical description of the selected growth curve models.

Model	Equation	Number of parameters	Reference
Exponential	$BW = a * \exp^{b*time}$	2	Arnhold 2017
Logistic	$BW = a * (1 + b * \exp^{-c*time})^{-1}$	3	Bahreini Behzadi et al. 2014
von Bertalanffy	$BW = a * (1 - b * \exp^{-c*time})^3$	3	von Bertalanffy 1957
Brody	$BW = a * (1 - b * \exp^{-c*time})$	3	Bahreini Behzadi et al. 2014
Gompertz	$BW = a * \exp^{(-b*\exp^{-c*time})}$	3	Gompertz 1825

The following fixed effects model was adopted to determine the environmental factors in the growth curves used to explain the growth of quails.

$$Y_{ijk} = \mu + S_i + T_j + e_{ijk}$$

where; μ is about the overall mean of the flock, S_i is about one of the fixed effects of the i^{th} sex ($i = \text{male, female}$) and Y_{ijk} is about the vector of estimated curve parameters i.e. a, b and c for the k^{th} Linda geese.

Multivariate Adaptive Regression Splines (MARS) Algorithm

The Multivariate Adaptive Regression Splines (MARS) algorithm, developed by Friedman (1991) as a modified version of the CART algorithm, is a nonparametric regression technique that provides a more efficient description of the nonlinear and interaction effects between response and explanatory variables to solve the problems within the scope of classification and regression. The MARS algorithm does not need any assumptions about the functional relationships between the response and the explanatory variables (Aksoy et al. 2019; Altay, 2022). The MARS algorithm is a regression procedure that purposes to separate several slopes into separate splines for the training dataset (Aksoy et al. 2019). Splines are connected to each other and the connection points between these parts are called “knot”. At this stage, candidate knots are positioned at random places within the range of each estimator (Aksoy et al. 2019). In the MARS algorithm, it works according to two-stage processes, including forward and backward stages (Arthur et al. 2020). In the first phase, MARS starts with an intersection in the first model during the forward selection phase and iteratively includes pairs of basis functions with the fewest training errors to improve the model. The forward pass stage characteristically produces an overfitted model that reaches maximum complexity (Friedman 1991; Eyduran et al. 2019). The model created in the forward transition phase provides a particularly good fit. However, the generalization ability of the constructed model may be poor for a previously unknown data set, which means an overfitting problem. To deal with this problem, the key functions that contribute the least to the MARS prediction model are eliminated in what is also known as the backward stage (Zaborski et al 2019; Arthur et al 2020).

The formula of the MARS algorithm used to estimate the BW through parameters such as a, b, and c obtained from the growth functions and effective predictors such as the sex factor can be written as follows:

$$\hat{y} = \beta_0 + \sum_{m=1}^M \beta_m \prod_{k=1}^{K_m} h_{km}(X_{v(k,m)}) \quad (1)$$

where: \hat{y} is the predicted response variable (BW), β_0 is an intercept, β_m is the coefficient of basis functions, $h_{km}(X_{v(k,m)})$ is the basis function, in which $v(k,m)$ is an index of the response variable in the m^{th} component of the k^{th} product, K_m is the parameter limiting the order of interaction. Due to the following generalized cross-validation error (GCV) among extremely complex candidate MARS models in the forward pass stage, the pruning procedure is passed in the backward pass, and the

basic functions that reduce the model performance obtained at this stage are eliminated (Eyduran et al. 2019; Zaborski et al. 2019):

$$GCV(\lambda) = \frac{\sum_{i=1}^n (y_i - y_{ip})^2}{\left[1 - \frac{M(\lambda)}{n}\right]^2} \quad (2)$$

where: n is the sample size for training data, y_i is the detected value of the response variable (BW), y_{ip} is the estimated value of the response variable (BW), $M(\lambda)$ is the penalty function for the complexity of the model including λ terms.

The quail data set for the Japanese breed was divided into two data sets such as training and test set as 70%-30%. In the training set, a tenfold cross-validation resampling technique was utilized to decide on the finest MARS model from inside the 72 MARS models (degree = 1:4 and nprune=2:20) within the scope of BW estimation.

The prediction performance of the optimal MARS model was evaluated using the following goodness-of-fit criteria (Grzesiak and Zaborski 2012; Eyduran et al. 2019; Zaborski et al. 2019):

1. Pearson correlation coefficient (r) between the observed and predicted LW values,

$$r_{y_i y_{ip}} = \frac{cov(y_i, y_{ip})}{s_{y_i} s_{y_{ip}}} \quad (3)$$

2. Akaike information criterion (AIC):

$$\begin{cases} AIC = n \cdot \ln \left[\frac{1}{n} \sum_{i=1}^n (y_i - y_{ip})^2 \right] + 2k, & \text{if } n/k > 40 \\ AIC_c = AIC + \frac{2k(k+1)}{n-k-1} & \text{otherwise} \end{cases} \quad (4)$$

3. Root-mean-square error (RMSE):

$$RMSE = \sqrt{\frac{1}{n} \sum_{i=1}^n (y_i - y_{ip})^2} \quad (5)$$

4. Relative Root Mean Square Error (rRMSE)

$$rRMSE = \frac{\sqrt{\frac{1}{n} \sum_{i=1}^n (y_i - y_{ip})^2}}{\bar{y}} * 100 \quad (6)$$

5. Mean error (ME):

$$ME = \frac{1}{n} \sum_{i=1}^n (y_i - y_{ip}) \quad (7)$$

6. Mean absolute deviation (MAD):

$$MAD = \frac{1}{n} \sum_{i=1}^n |y_i - y_{ip}| \quad (8)$$

7. Standard deviation ratio (SD_{ratio}):

$$SD_{ratio} = \frac{s_m}{s_d} \quad (9)$$

8. Performance Index (PI)

$$PI = \frac{rRMSE}{1+r} \quad (10)$$

9. Global relative approximation error (RAE):

$$RAE = \sqrt{\frac{\sum_{i=1}^n (y_i - y_{ip})^2}{\sum_{i=1}^n y_i^2}} \quad (11)$$

10. Mean absolute percentage error (MAPE):

$$MAPE = \frac{1}{n} \sum_{i=1}^n \left| \frac{y_i - y_{ip}}{y_i} \right| * 100 \quad (12)$$

where, n is sample size for training set in the data, k is the number of model parameters, y_i is the actual value of the BW, y_{ip} is the estimated value of the BW, s_m is the standard deviation of the model errors, s_d is the standard deviation of the BW.

All the statistical evaluations were made using R package (R Core Team, 2020). Descriptive statistics of the quantitative characteristics were estimated by using “psych” package in R package (Revelle, 2020). For performing the growth curve models “easynls” and “nlstools” packages were used (Arnhold, 2017; Baty et al., 2015). To perform the MARS algorithm, “caret” package were used in R software (Kuhn, 2020). To display the predictive performances of the MARS algorithms, “ehaGoF” package (version 0.1.1) developed by Eyduran (2020) was employed.

Results and Discussion

To describe the data set, the descriptive statistics from hatching week to 6th week body weight are given in Table 2 for male and female Japanese quails. For male and female Japanese quails, the highest body weight was identified at 6th week of age (177.18±16.33 g and 205.84±21.35 g), respectively.

The expected growth parameters obtained for each growth curve model of male Japanese quail are shown in Table 3. The predicted live body weight (a) varied between models and genders. The greatest predicted body weight at the 6th week of age was observed 427.800 g for male Japanese quail in Brody growth curve model. The exponential growth curve model was the lowest 6th weeks of age body weight with values of 39.024 g for male breed. The parameter of c varied between the models from 0.096 ± 0.012 (Brody growth curve model) to 1.113± 0.026 (Logistic growth curve model) for males.

The expected growth parameters obtained for each growth curve model of female Japanese quail are shown in Table 4. The predicted live body weight (a) varied between models and genders. The greatest predicted body weight at the 6th week of age were observed 1085 g for female Japanese quail in Brody growth curve model. The exponential growth curve model was the lowest 6th weeks of age body weight with values of 40.008 g for female breed. The parameter of c varied between the models from 0.037 ± 0.011 (Brody growth curve model) to 0.999± 0.024 (Logistic growth curve model) for males.

In Table 5, to compare the different nonlinear growth curve model functions, the goodness of fit criteria were computed for exponential, logistic, von Bertalanffy, Brody and Gompertz models in each gender. The highest R² and R²_{adj} values were determined for von Bertalanffy growth model for each sex. Also, the lowest AIC and BIC values were computed for the von Bertalanffy growth model. According to the lowest AIC and BIC and the highest R² and R²_{adj} was determined for von Bertalanffy growth model. Therefore, von Bertalanffy growth model was to best fitting model for Linda geese breeds of each sex.

When the growth curve models used in this study are examined according to the criteria of goodness of fit, the models are ranked in the order of Logistic > Gompertz > von Bertalanffy > Brody > Exponential (Table 5). Therefore, the Logistic growth curve model was selected as the finest model in describing the relationship between BW and weeks in Japanese quails.

Table 2. Descriptive statistics of body weight of Japanese quails from hatching week to 6th weeks

Week	Male BW (Mean±SD)	Female BW (Mean±SD)
Hatching	8.23±0.95	8.37±0.85
1	24.56±4.59	25.69±3.99
2	64.74±8.76	68.67±8.91
3	106.32±11.35	111.34±12.08
4	151.94±19.10	161.78±21.73
5	164.11±13.37	190.21±17.69
6	177.18±16.33	205.84±21.35

BW: Body weight; SD:Standard Deviation

Table 3. Estimated parameters for the selected growth curve models and their 95% confidence interval for male Linda geese breed.

Model	Parameters	Estimate	Standard error	Confidence interval (95%)
				(Lower bound-Upper bound)
Exponential	a	39.024	1.216	36.637-41.411
	b	0.273	0.006	0.260-0.285
Logistic	a	179.273	1.352	176.618-181.926
	b	17.813	1.023	15.804-19.821
	c	1.113	0.026	1.062-1.163
von Bertalanffy	a	201.753	3.033	195.796-207.710
	b	0.868	0.025	0.820-0.916
	c	0.521	0.018	0.485-0.557
Brody	a	427.800	39.790	349.682-505.953
	b	1.004	0.004	0.997-1.011
	c	0.096	0.012	0.073-0.119
Gompertz	a	193.193	2.255	188.765-197.620
	b	3.993	0.132	3.733-4.252
	c	0.655	0.019	0.618-0.692

Table 4. Estimated parameters for the selected growth curve models and their 95% confidence interval for female Linda geese breed

Model	Parameters	Estimate	Standard error	Confidence interval (95%)	
				(Lower bound-Upper bound)	
Exponential	a	40.008	1.234	37.584-42.430	
	b	0.292	0.006	0.280-0.304	
Logistic	a	213.831	2.030	209.844-2017.817	
	b	17.584	0.978	15.663-19.504	
	c	0.999	0.024	0.952-1.047	
von Bertalanffy	a	257.604	5.587	246.633-268.575	
	b	0.815	0.019	0.777-0.853	
	c	0.418	0.017	0.385-0.450	
Brody	a	1085	289.200	517.019-1652.659	
	b	1.002	0.001	0.998-1.005	
	c	0.037	0.011	0.015-0.059	
Gompertz	a	238.091	3.747	230.732-245.450	
	b	3.859	0.116	3.631-4.088	
	c	0.560	0.018	0.525-0.595	

Table 5. Goodness of fit criteria for the selected growth curve models

Model	AIC		BIC		R ²		R ² _{adj}	
	Male	Female	Male	Female	Male	Female	Male	Female
Exponential	5995.407	5996.647	6008.777	6009.984	0.830	0.858	0.830	0.857
Logistic	5027.848	5187.014	5045.675	5204.797	0.963	0.961	0.962	0.961
von Bertalanffy	5091.193	5214.087	5109.020	5231.870	0.960	0.960	0.959	0.959
Brody	5327.788	5391.339	5345.615	5409.122	0.940	0.946	0.940	0.946
Gompertz	5053.102	5187.923	55070.929	5205.706	0.961	0.960	0.961	0.960

Table 6. Results of performances for MARS algorithm in the training and test set

Goodness-of-fit criteria	Train set	Test set
Root mean square error (RMSE)	7.976	8.253
Relative root mean square error (rRMSE)	4.161	4.325
Standard deviation ratio (SD _{ratio})	0.334	0.354
Coefficient of variation (CV)	4.18	4.36
Mean absolute percentage error (MAPE)	3.342	3.697
Coefficient of determination (R ²)	0.888	0.875
Akaike's information criterion (AIC)	543.705	227.498

Numerous growth curve models have been used to describe different types of growth in farm animals; however, there is no information in the literature about the estimation of live weight from growth parameters for quails yet. In this context, in this study, the relationship between the growth curve parameters and body weight of the best selected model according to the goodness of fit criteria is explained with the MARS algorithm.

The optimum MARS model was determined as degree:1 and nprune:4 from among the 108 candidate MARS models. The MARS model obtained with 4 terms was given below:

$$BW = 187.5068 - 0.6181486 * \max(0, a - 91.36) - 7.510232 * \max(0, 26.73 - b) + 8.875301 * \max(0, b - 26.73)$$

where, the first term of the optimum MARS model has the coefficient of 187.5068 as named the intercept. The second term is $\max(0, a - 91.36)$ which cut-off point is 91.36 with the coefficient of -0.6181486. The third term is $\max(0, 26.73 - b)$ which has the coefficient of -7.510232.

The last term is $\max(0, b - 26.73)$ with a coefficient of 8.875301. According to the obtained MARS model, sex and one of the growth parameter c is not significant variables to predict the BW for Japanese quails.

The results of the MARS algorithm, which was evaluated within the scope of goodness of fit criteria, were given in Table 6.

According to the goodness of fit criteria given in Table 6, it is possible to make a "good fit" comment about the model if the root mean square error (RMSE), relative root mean square error (rRMSE), standard deviation ratio (SD_{ratio}), coefficient of variation (CV), mean absolute percentage error (MAPE), Akaike's information criterion (AIC) values are low as well as the high Pearson's correlation coefficients (PC), coefficient of determination (R²). In this context, the examined MARS model showed the reliable performance. In addition, the Pearson's correlation coefficients between real and estimated BW is quite strong for MARS algorithm with the coefficient of 0.935. MARS algorithm created a more trustworthy model that has the highest performance with two predictors such as a and b growth parameters.

Defining growth and estimating growth processes are extremely important in terms of herd management in livestock. It is a useful method for evaluating and investigating the growth curve from a biological perspective, which is one of the methods used for this purpose, and for explaining the growth relationships (Ramos et al., 2013; Ibtisham et al., 2017). Logistic growth curve model was chosen as the model that gives the best results from the growth curves applied in this study. In addition, it was aimed to find the most suitable MARS model to determine which parameter has an effect on BW in Japanese quails, based on growth parameters calculated individually from the logistic growth curve model and various goodness-of-fit criteria as well as sex. When the goodness of fit criteria of the MARS model obtained in this context is evaluated, it can be said that it has a good fit.

There are many studies on Japanese quails within the scope of nonlinear growth curve models. However, there is no study describing the relationship between body weight using individually calculated growth curve parameters and gender. In this context, the data mining algorithms such as MARS and CART were used for several species, i.e. sheep, but the MARS algorithm was not used in quails to explain the relationship between body weight, sex and growth parameters. Only the MARS model was used by the Koskan et al. (2022) to predict the partial egg production of quails.

In addition to the nonlinear models used in this study, many studies are using different nonlinear models in Japanese quails. Sezer and Tarhan (2005) performed Richards, Gompertz and Logistic growth curve models for 3 lines of Japanese quails such as wild, white and brown. mean percentage error (MPE), mean bias error (MBE), root mean square error (RMSE), and confidence interval test (CIT) were used as a goodness of fit criteria for describing the growth. According to the results of this study, Richards function was chosen as the best fit model. Raji et al. (2014a) performed Gompertz function for describing the growth for Japanese quails. The coefficient of determination (R^2) was determined as 0.98 for male and female Japanese quails. According to our results, these differences may be due to the fact that management were not the same. Raji et al. (2014b) were performed Asymptote regression, Exponential, Gompertz, Logistic, Monomolecular, Richards and Weibull models for Japanese quails. According to the results, logistic growth curve model had the 0.998 within the scope of R^2 . This result is in agreement with the present study. Anang et al. (2017) performed Gompertz, Logistic, Richards, and MMF model for describing the growth of black and brown Japanese quail lines. Although the Gompertz model is the most suitable model, other models showed similar results. The R^2 value obtained in the present study and the results of the study are close to each other. Haqani et al. (2021) were performed Weibull, Logistic, Gompertz, Richards, and Brody growth curve models for determining the growth male and female Japanese quails. In the study, R^2 , R^2_{adj} , AIC, BIC, and RMSE were used as goodness-of-fit criteria. As a result of the study carried out in this context, the logistic growth curve model has an R^2 of 0.99. In this case, it is consistent with the results of our study.

Conclusion

It is very important to follow the developmental stages of the animals in the herd in order to ensure stability in herd management in animal production. In this context, the developmental stages of the herd will be followed with growth curve modeling, and a sustainable and efficient management mechanism will be provided. In this study, different nonlinear growth functions (Brody, exponential, logistic, von Bertalanffy, Brody, and Gompertz) were evaluated to define the relationship between body weight and age in the Japanese quail breed. According to the criteria of goodness of fit, it was determined that the most suitable model among the non-linear models in terms of performance was logistic. The MARS algorithm was applied to the individual growth parameters obtained from the determined Logistic model and it was aimed to express the relationship between sex and growth parameters. In this way, it will also demonstrate the potential of the MARS algorithm to determine the relationship between body weight-growth parameters and age in Japanese quail.

In conclusion, determining the best growth curve in quails, determining the optimum feed consumption of the animals that make up the herd management, and determining the best slaughter time of the animal will be beneficial for many factors, as well as help to increase the income from animal husbandry.

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