TR SİİRT UNIVERSITY GRADUATE SCHOOL OF NATURAL AND APPLIED SCIENCES

NONLINEAR REGRESSION MODELS AND APPLICATIONS IN ANIMAL SCIENCE

MS THESIS

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The thesis study entitled "Nonlinear Regression Models and Applications in Animal Science" prepared by Nabeel Taher Abdulazeez ALGAILANI has been accepted as a Master Degree thesis with unanimity of votes by the following jury on the date of 15/05/2018 at Siirt University, Graduate School of Natural and Applied Sciences, Department of Mathematics.

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PREFACE

Praise be to God, and above all, to the one God, almighty for accomplishing this research and completing it to the satisfaction of the professors at the University. I would like to thank my professor Dr. Nazire Mikail, who supervised this research, and gave me valuable observations and guidance in the reasons to complete this thesis and ask God to reward them for their great efforts and I am pleased to extend my thanks and gratitude to Dr. Abdulkadir Karakaş, from the Mathematics Department, who had the credit to help me as I would like to thank my friends and colleagues at the Zakho Institute to help me complete my thesis and thank my family for helping me so much, especially my wife and children.

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LIST OF ABBREVIATIONSANDSYMBOLS

Abbreviation		<u>Statement</u>
AIC	:	Akaike Information Criteria
MSE	:	Mean Squared Error
ME	:	Modeling Efficiency
MR	:	Mean Residual
DW	:	Durbin-Watson Statistics
LEG	:	Legendre Polynomials
RSD	:	Residual Standard Deviations
BIC	:	BayesianInformation Criteria
D	:	WellmotAgreement Criteria

<u>Symbol</u>		<u>Statement</u>
e	:	Natural logarithm base
λ	:	Langrange multiplier
ε _t	:	Random error
F(t)	:	Function
S	:	Persistency
r	:	Correlation coefficient
\mathbf{R}^2	: /	Coefficient of determination
R ² _{adj}	:	Adjusted coefficient of determination
Yt	:	Observed value in t th time
Т	:	time
a	:	intercept
Yi	:	Observed value in i th time
\overline{Y}	:	Arithmetic mean of observed value
$\widetilde{\mathbf{Y}}_{i}$:	Predicted value
$\overline{\mathcal{E}}$:	Absolute percentage error
n	:	Number of observation
p	:	Number of parameters in the model

ÖZET

YÜKSEK LİSANS TEZİ

DOĞRUSAL OLMAYAN REGRESYON MODELLERİ VE ZOOTEKNİDE UYGULAMALARI

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Hayvancılıkta zamana bağlı olarak değişen büyüme, verim ve üretim verileri çoğunlukla doğrusal olmayan modellerle ifade edilmektedir. Bu nedenle, doğrusal olmayan regresyon modelleri hayvancılıkta önemli yer tutmaktadır.

Bu çalışmada doğrusal olmayan regresyon modelleri hakkında genel bilgi verilerek, hayvancılıkta uygulanma alanları ile ilgili örneklere değinilmiştir. Süt veriminin zamana göre değişimini gösteren laktasyon eğrileri, canlıların büyüme eğrileri, yumurta ağırlığı ve üretimi eğrilerini en iyi şekilde tanımlayan doğrusal olmayan modeller araştırılmıştır. Farklı modellerin uygulanması sonucunda doğru modelin seçimi için belirleme katsayısı, düzeltilmiş belirleme katsayısı, hata kareler ortalaması, Wellmot uzlaşma kriteri, mutlak yüzde hata, Akaike bilgi kriteri, Bayes bilgi kriteri gibi ölçütler tanıtılmıştır. Bunun yanı sıra modellerin, SAS, STATISTICA, SPSS, MINITAB istatistik paket programlarında çözümleri için adımlar gösterilmiştir.

Sonuç olarak, en çok kullanılan modeller seçilerek, hayvancılıkta uygulanan doğrusal olmayan modeller tabanı oluşturulmuştur.

Anahtar Kelimeler: Laktasyon eğrileri, büyüme eğrileri, matematiksel modelleme, regresyon

ABSTRACT

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NONLINEAR REGRESSION MODELS AND APPLICATIONS IN ANIMAL SCIENCES

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Time dependent data, such as growth, yield and production in animal husbandry, are often expressed in nonlinear models. For this reason, nonlinear regression models take an important role in animal science.

In this study, general information about nonlinear regression models was given and examples related to application areas in animal husbandry were referred. Nonlinear models that best describe the lactation curves, which show the change of milk yield with time, the growth curves of the animals, the egg weight and the production curves, were investigated. For correct model selection, after application of different models, criteria such as determination coefficient, adjusted determination coefficient, mean square error, Wellmot agreement criterion, absolute percentage error, Akaike information criterion, Bayesian information criterion were introduced. In addition, the steps for solving the models in SAS, STATISTICA, SPSS, MINITAB statistical package programs have been shown.

As a result, the most used models were selected and a base of nonlinear models applied in animal science was created.

Keywords: Lactation curves, growth curves, mathematical modeling, regression

INTRODUCTION

In data analysis, the best model for describing the data, the best statistical index to judge the goodness of fit, choosing appropriate model among competing models is a general task. In this study it was attempt to provide animal science researches with a general framework on how to approach these tasks.

Nonlinear regression models are important tools because many growth, yield and production processes are better represented by nonlinear than linear models. Fitting nonlinear models is not a single-step procedure but an involved process that requires careful examination of each individual step. Depending on the objective and the application domain, different priorities are set when fitting nonlinear models; these include obtaining acceptable parameter estimates and a good model fit while meeting standard assumptions of statistical models. It was propose steps in fitting nonlinear models: choose candidate models, set starting values, fit models, check convergence and parameter estimates, find the "best" model among competing models, check model assumptions (residual analysis), and calculate statistical descriptors and confidence intervals (Archontoulis and Miguez, 2015).

Traditionally, mathematical models have been applied to describe growth-age relationship in animals. One important feature of these models is their ability to describe the weight gain and evaluate some interesting biological parameters, such as the mature weight, the rate of maturing and the rate of gain. These parameters are useful tools to provide estimates of the daily feed requirements or to evaluate the influence of the environmental conditions on the weight gain of the animal. Growth models are also used to predict the optimum slaughter age. Therefore, mathematical models applied for animal growth can be considered as being important control and optimization (Teleken et al, 2017). Studying beef cattle growth curves is essential because it supplies relevant information to establish strategic plans to obtain subsidies for the areas of nutrition and genetic breeding such as improved management, nutritional requirement determination, knowledge of the genetic variability of the characteristics linked to growth and assessment of the genetic potential of the animals for growth, contributing to the process of decision making to adopt a certain technology (Marinho et al., 2013).

Animal growth does not follow a linear pattern, being explained mathematically by functions that have parameters with biological meaning (Selvaggi et al., 2017). Research on the characteristics of livestock growth provides useful and practical information for breeding purposes. Two important parameters of growth are the genetic potential for growth and the time to reach maturity. When animal growth is described by a growth curve, these parameters can be presented as biologically interpretable constants in a mathematical equation. Classical growth models such as Gompertz, Logistic, von Bertalanffy and Richard's equations are still widely and frequently used to describe various biological processes.

Determination of various growth parameters (weight at different ages, daily weight gain, rate of maturity, time of inflection or the point on the growth curve when the rate of growth is maximal and weight at inflection) are quite important for selection of animals at early phases of growth by using predicted parameters. Manipulation of selection due to these parameters helps to determine suitable management and feeding regimens and to decide optimal age at which animals can be used for production purposes. Some authors reported that growth curve parameters can be used as direct breeding criteria in improving some of the growth associated traits in addition to describing growth in animals. Type of growth curves changes depend on fixed and random effects. Hence, growth curves should be presented based on the species, environmental conditions and the growth characteristics studied. Growth rate is not same in every life period in animals and, therefore, linear models are not suitable. For describing growth in animals during the main growth phase nonlinear models should be used which are more complex than linear models. Many growth phenomena in nature show an "S" shaped pattern (sigmoidal) with initially slow growth speeding up before slowing down to approach a limit (Ersoy et al., 2007).

The main advantages of nonlinear models are parsimony, interpretability, and prediction (Bates and Watts, 2007). In general, nonlinear models are capable of accommodating a vast variety of mean functions, although each individual nonlinear model can be less flexible than linear models (i.e., polynomials) in terms of the variety of data they can describe; however, nonlinear models appropriate for a given application can be more parsimonious (i.e., there will be fewer parameters involved) and more easily interpretable. Interpretability comes from the fact that the parameters can be associated with a biologically meaningful process.

By using illustrative examples that include published mathematical models describing lactation in cattle, we show how structural identifiability analysis can contribute to advancing mathematical modeling in animal science towards the production of useful models and highly informative experiments. Rather than attempting to impose a systematic identifiability analysis to the modeling community during model developments, we wish to open a window towards the discovery of a powerful tool for model construction and experiment design.

The computations required for nonlinear regression analyses are not flexible without the use of a computer, and almost every statistical packages have routines for nonlinear regression. It was explained the use of the computer for nonlinear regression analyses.

The aim of this study is to provide an overview of nonlinear models and to develop a guideline to understand the family of functions used in animal husbandry applications, to discuss key methodological issues on parameter estimation, model performance, and comparison, and to demonstrate step-by-step analysis of experimental data using a nonlinear regression model.

LITERATURE REVIEW

2.1. Growth models

In the study of Santos et al.(1999) the monthly measured height at withers data from birth to 36 months of age of 26 Pantaneiro horses were used to fit Brody, Richards, Gompertz, Logistic, Weibull and Morgan-Mercer-Flodin nonlinear response functions. Based on measures of average curvature and combined mean square error, the Weibull model was chosen. The asymptote of this curve, representing the average height at maturity was higher for males than females. The maturity index, however, was more elevated for females than males. There was indication of a negative association between the maturity index and height at maturity only for females. These results indicate that females mature earlier.

In the study of Hassen et al. (2004) were described body weight (BW) changes of purebred Angus bulls and heifer and was evaluated bias in the adjustment of weaning weight measures to a 205-d age. Linear and non-linear growth functions were used to evaluate changes in BW. Models used were a simple linear regression model fitting cubic polynomial of age at measurement (model I) and a Logistic model (model II). Predicted mature weight for bulls was 763 kg (1,678.6 lbs.) as compared to 541.9 kg (1192.2 lbs.) for heifers. Bulls attained a maximum average daily weight gain (ADG) of 1.75 kg/d (3.85 lbs/d) at a mean age of 296 d. The maximum ADG attained by heifers was 1.24 lb/d (2.73 lb/d) at a mean age of 261 d.

Şengül and Kiraz (2005) in their study tried to model the growth curves of male and female turkeys with respect to their live weight-age relationships and to determine a non-linear model explaining their growth curve better. For this purpose four different non-linear models were used to define growth curves of turkeys, namely Gompertz, Logistic, Morgan-Mercer-Flodin (MMF), and Richards. The coefficients of determination for these models were 0.9975, 0.9937, 0.9993 and 0.9966 for females and 0.9974, 0.9933, 0.9993 and 0.9969 for males, respectively. Considering model selection criteria, Gompertz, Logistic and Richards models seen to be suitable models for explaining Large White turkey growth. The main objective of the study of Ersoy et al. (2007) was to estimate growth parameters of California turkeys at early phases of growth by using linear and nonlinear growth models for regulation of growth intensity for attaining adequate growth and development in California turkeys.

In the study of Vitezica et al. (2010), were compared models for growth (BW) before overfeeding period for male mule duck data from 7 families of a QTL experimental design. Four nonlinear models (Gompertz, Logistic, Richards, and Weibull) and a spline linear regression model were used. The Akaike information criterion was used to evaluate these alternative models. Among the nonlinear models, the mixed effects Weibull model had the best overall fit. Two parameters, the asymptotic weight and the inflexion point age, were considered random variables associated with individuals in the mixed models. In this study, asymptotic weight had a greater effect in Akaike's information criterion reduction than inflexion point age. In this data set, the between-ducks variability was mostly explained by asymptotic BW. Comparing fixed with mixed effects models, the residual SD was reduced in about 55% in the latter, pointing out the improvement in the accuracy of estimated parameters. The mixed effects spline regression model was the second best model. Given the piecewise nature of growth, this model is able to capture different growth patterns, even with data collected beyond the asymptotic BW.

Liu et al. (2011) in their study estimated and compared the growth curve parameters for live weight of standard black, brown, mahogany, Hedlund white and sapphire minks. The data were collected from five colour types in the period from seven days to 24 weeks of age. Three hundred mink (about 60 of each colour types) were used. Six different non-linear models, namely Logistic, Gompertz, Brody, Richards, Bridges, and Janoschek were used to define the growth curves of the mink. Models were compared using coefficients of determination (R^2 values), the Akaike's information criterion (AIC) and the Bayesian information criterion (BIC). The R^2 were high for all models, ranging from 0.923 to 0.985 for different breeds of mink. Comparing the models by AIC, BIC values and the residuals showed the following results. Three of the models fitted the growth curves very well. Colour type differences were observed in the growth parameters of mink. The brown, mahogany and sapphire was observed to be late maturing and lighter at maturity, while the standard black and Hedlund white had a higher growth rate, reached maturity earlier and attained a heavier mature weight.

Araujo et al. (2012) were published study with the objective of to adjust nonlinear models for the growth curves for a buffaloes herd raised in floodable lands in Rio Grande do Sul State, monthly records measured from birth to two years-old of 64 males and 63 females born between 1982 and 1989 were used. The models used were: Von Bertalanffy, Brody, Gompertz and Logistic. The parameters were estimated by NLIN procedure and the criteria used to evaluate the adjustment given by the models were: asymptotic standard deviation; coefficient of determination; average absolute deviation of residues and asymptotic index. Von Bertalanffy and Brody models overestimated the male asymptotic weight (A) in 15.9 and 171.3 kg, respectively, and the Gompertz and Logistic models underestimated it in 4.5 and 13.4 kg, respectively. For females, the Logistic model underestimated the asymptotic weight (-2.09kg), and Gompertz, Von Bertalanffy and Brody overestimated this parameter in8.04, 17.7, and 280.33kg, respectively. The biggest average deviation was estimated by Brody model for both sexes, characterizing the biggest index. Considering the criteria, it is recommended the Gompertz and Logistic models for adjust females and males Murrah buffaloes breed growth curves.

In the study of Marinho et al.(2013) growth curves of Nellore cows were estimated by comparing six nonlinear models: Brody, Logistic, two alternatives by Gompertz, Richards and Von Bertalanffy. The models were fitted to weight – age data, from birth to750 days of age of 29221 cows, born between 1976 and 2006 in the Brazilian states of Acre, Amapá, Amazonas, Pará, Rondônia, Roraima and Tocantins. The models were fitted by the Gauss-Newton method. The goodness of fit of the models was evaluated by using mean square error, adjusted coefficient of determination, prediction error and mean absolute error. Biological interpretation of parameters was accomplished by plotting estimated weights versus the observed weight means, instantaneous growth rate, absolute maturity rate, relative instantaneous growth rate, inflection point and magnitude of the parameters A (asymptotic weight) and k (maturing rate). The Brody and Von Bertalanffy models fitted the weight-age data but the other models did not. The average weight (A) and growth rate (K) were: 384.6±1.63 kg and

0.0022±0.00002 (Brody) and 313.40±0.70 kg and 0.0045±0.00002 (Von Bertalanffy). The Brody model provides better goodness of fit than the Von Bertalanffy model.

Galeano-Vasco et al.(2014), in their study, were compared Von Bertalanffy, Richards, Gompertz, Brody, and Logistics nonlinear regression models for their ability to estimate the growth curve in commercial laying hens. Data were obtained from 100 Lohmann LSL layers. The animals were identified and then weighed weekly from day 20 after hatch until they were 553 days of age. All the nonlinear models used were transformed into mixed models by the inclusion of random parameters. Accuracy of the models was determined by the Akaike and Bayesian information criteria (AIC and BIC, respectively), and the correlation values. According to AIC, BIC, and correlation values, the best fit for modeling the growth curve of the birds was obtained with Gompertz, followed by Richards, and then by Von Bertalanffy models. The Brody and Logistic models did not fit the data.

In the study of Raji et al.(2014) seven growth models using body weight measurements from 300 progeny obtained from unselected random bred parents were compared. The study which lasted for 20 weeks was carried out at the University of Maiduguri Livestock Teaching and Research farm. R^2 values for the Asymptote regression, Exponential, Gompertz, Logistic, Monomolecular, Richards and Weibull models were 0.994, 0.935, 0.997, 0.997, 0.998, 0.998, 0.998 and 0.999 respectively. The Weibull model had the highest coefficient of determination (R^2) value (0.999) and Exponential (0.935) least. In contrast, the exponential model had the highest MSE (Mean Square Error), SD (Standard Deviation) and AIC (Akaike Information Criterion) values while Weibull model had the least. The Exponential had the poorest fit (higher MSE, SD and AIC values and lower R^2) while the Weibull, Gompertz and Richards models best described the data in that order (lower MSE, SD and AIC values and higher R^2). In order words, the nonlinear models described the data better than linear. Therefore, based on goodness of fit criteria; R^2 , MSE, SD and AIC values, the Weibull model best described live weight data of the Japanese quail in Nigeria.

In the study of Salako (2014) nonlinear functions of body weight at different age intervals were used to estimate the mature weight (A), shape of response (B) and maturing rate (k) parameters of asymptotic growth models for Nigeria White Fulani and N'dama cattle. Records obtained from flocks kept at the University of Ibadan teaching and research farm in Ibadan were used. Mitsherlich, Gompertz and Richard functions were fitted to the data in addition to the linear function. Age-weight records of White Fulani from birth to 4 years and from N'dama monitored to 30 months of age was used to estimate the average growth curve for each breed. Predicted A and k values for weight at fixed ages in the iterative processes indicated that Richard's function was inadequate for both breeds. Mature weight was attained at approximately 4 years of age in N'dama from both Mitscherlich and Gompertz model but was yet to be reached at that age in the White Fulani. Mitscherlich function gave better estimates of weight at maturity, but the asymptotic residual variances were higher in N'dama because the birth weight was overestimated. Linear and nonlinear regression analyses of weight-age data and comparisons of degree of maturity at different premature ages showed that the differences in the growth patterns of the two breeds agreed with late rather than early predicted values of A and k.

In the study of Sahin et al.(2014) was detected the best model to explain the variation of live weight of Anatolian buffaloes using the nonlinear models. For this purpose, in the production period of 2011-2012, live weight records of 640 heads Anatolian buffalo calves including 309 male and 331 female reared in different farm conditions of Tokat were used. To achieve the objective of the study, the non-linear models of Logistic, Richards, Gompertz and Brody function were used. To decide which one is the best model, the coefficient of determination (R2) and the mean square error (MSE) statistics were used. The coefficient of determination (R2) for Logistic, Brody, Gompertz and Richards models were found as 0.96, 0.92, 0.96 and 0.98 for female calves and 0.94, 0.93, 0.95 and 0.97 for male calves, respectively. And mean squared errors (MSE) were found as 682.32, 703.51, 548.66 and 498.63 for females and 637.48, 688.32, 598.12 and 528.74 for male Anatolian buffaloes, respectively. As a result, the best fitted model based on MSE and R² criterias was Richards model. Also, the growth and development traits such as sexual maturity age, breeding age, appropriate slaughter age in male and female Anatolian buffalo calves can be estimated using the Richards model.

Bahashwan et al.(2015) in their study estimated Dhofari cattle growth curve and fitted using non-linear function models of Gompertz, Von Bertalanffy and Logistic. Data of 2540 weight performances of 617 Dhofari cattle from birth to 228 months of

age were used in this study. Analysis revealed an initial average live birth weight of 17.8 ± 0.99 kg and of 360 ± 23.6 kg at an average age of 228 months. The estimated values of a (mature body weight) parameter ranged from 316 to 321 kg at ages ranged from 36 to 48 months. Parameters of b and k were estimated to be 2.11 ± 0.021 and, 0.106 ± 0.002 , 0.522 ± 0.004 and, 0.087 ± 0.001 , and 20.5 ± 0.001 and, 0.127 ± 0.002 , for Gompertz, Von Bertalanffy, and Logistic models respectively. Inflection weights and time were found to range from 95 to 158 kg, and 5 to 9 months of age respectively. Degree of maturity (U_t) at birth was 5.59, 8.99, 12.8%, and at puberty was 36.8, 26.6, and 44.0% for Gompertz, Von Bertalanffy, and Logistic, respectively. Models used to fit the growth curve had high determination coefficients above 92% with the highest was for Von Bertalanffy (93.6%) for goodness of fit.

Hossein-Zadeh and Golshani (2016) in their study tried to describe the growth pattern in Guilan sheep using non-linear models. Six non-linear mathematical equations (Brody, Negative exponential, Logistic, Gompertz, Von Bertalanffy and Richards) were used to describe the growth curves in Guilan sheep. The dataset included 42,257 weight records of lambs from birth to 240 days of age during years 1994 to 2014. Each model was separately fitted to body weight records of all lambs, males and females, using the NLIN and MODEL procedures of SAS. The models were tested for goodness of fit using adjusted coefficient of determination, root means square error (RMSE), Durbin-Watson statistic, Akaike's information criterion (AIC) and Bayesian information criterion (BIC). Richards model provided the best fit to the growth curve in females and all lambs, with the lowest RMSE, AIC, and BIC values compared to the other models. The Brody model provided the best fit of growth in male lambs due to the lower values of AIC and BIC compared to the other models. The Negative Exponential model provided the worst fit of growth for males, females and all lambs.

Kaplan and Gürcan (2016) in their study was conducted to determine the goodness of fit of Gompertz, Logistic, Von Bertalanffy, Richards, Levakovich and Janoschek growth models in Japanese quail. Therefore, weekly live-weight data obtained from 372 females and 339 males were fitted. Females' live weights were found to be higher than that of males, and the first divergence in the growth of female and male birds occurred in 21–28 days, and it survived until the experiment (p<0.001). The

coefficient of determination (\mathbb{R}^2), adjusted coefficient of determination (adj. \mathbb{R}^2), mean square error (MSE), Akaike's information criteria (AIC) and Bayesian information criterion (BIC) were used to determine the best growth model. \mathbb{R}^2 and adjusted \mathbb{R}^2 values of the growth models were similar and close to 1, indicating that all models perform well in describing age-related changes in live weight in quail. Based on the MSE, AIC and BIC values, Richards model was determined to be the best fitting model to the growth data of both sexes. Consequently, it has been demonstrated that Richards function which has a flexible structure in terms of inflection point is the most appropriate growth function for both female and male birds.

In the study of Cak et al.(2017) was investigated the growth characteristics of Colored Mohair goat using four nonlinear growth models. Thirty (n=22 males and n=8 females) Colored Mohair kids were used. The kids were weighed at 2-week intervals from birth to 150 days. The Monomolecular, Gompertz, Richards and Three Parameter Logistic models were used. The best model was determined by considering the root mean square error (RMSE), R^2 (%) and asymptotic correlation coefficient criteria. It was concluded that the Gompertz and Richards models were favourable for singletons and that the Richards model was favorable for determining twin Colored Mohair goat growth characteristics. Birth type should be considered in subsequent genetic evaluations. Furthermore, producing heavier carcasses (13-17 kg) in < 150 days may increase productivity and efficiency of the goat farming system.

Hossein-Zadeh (2017) in his study tried to describe the growth curves in Iranian Moghani sheep, five non-linear mixed mathematical equations (Brody, Negative exponential, Logistic, Gompertz and Von Bertalanffy) were compared. After selecting the best-fitted model based on purely statistical criteria, variance components and genetic parameters for growth curve characteristics were estimated. The data set and pedigree information used in the current study were obtained from the breeding station of Moghani sheep and included 7905 weight records of 1581 lambs from birth to 400 days of age between the years 1994 and 2012 inclusive. Each model was fitted to body weight records for all lambs, males, females, single and twin lambs using the NLMIXED procedure in SAS and the parameters were estimated. Animal was considered as subject in the models. The non-linear mixed models were examined for goodness of fit using Akaike's information criterion (AIC) and residual variance. In

general, evaluation of different growth equations used in the current study indicated the potential of the non-linear functions to fit body weight records of Moghani sheep. Also, the results of the current study showed that improvement of growth curve parameters of Moghani sheep could be possible in selection programmes. Therefore, development of an optimal selection strategy to achieve a desired shape of growth curve through changing genetically the parameters of model would be very important.

Hojjati and Hossein-Zadeh (2017) in their study were used five non-linear mathematical equations (Brody, Negative exponential, Logistic, Gompertz and Von Bertalanffy) in order to describe the growth curves in Iranian Mehraban sheep. The data set used in this study was obtained from the Agricultural Organization of Hamedan province and comprised 35,414 weight records of lambs which were collected from birth to 365 days of age during 1991–2011. Each model was fitted separately to body weight records of all lambs, male and female lambs and single and twin lambs using the NLIN and MODEL procedures in SAS. The models were tested for goodness of fit using adjusted coefficient of determination (adj. R²), root mean square error (RMSE), Durbin-Watson statistic (DW), Akaike's information criterion (AIC) and Bayesian information criterion (BIC). The Brody model provided the best fit of growth curve in all lambs, male and female lambs and single and twin lambs due to the lower values of AIC and BIC than other models. The Logistic model provided the worst fit of growth curve for all lambs, male and female lambs and single and twin lambs. Evaluation of different growth equations used in this study indicated the potential of the non-linear functions for fitting body weight records of Mehraban sheep.

Masoudi and Azarfar (2017) in their study compared four nonlinear models to describe growth parameters of broiler chicken fed on different levels of corn bran. Two experiments were designed for this purpose. In the first experiment, 80 chickens (308 Ross strain) that had been fed on the same diet and weighed separately were used to determine the best model. Indicators of R^2 , ACI and the number of circulation of the model were used to confirm the best model. In the second experiment, 300 one-day-old Ross 308 broiler chickens were used in a completely randomized design with four treatments and five replicates. The treatments included control and diets contained 2.5, 5 and 7.5% corn bran. Results showed that the Gompertz function had the highest R2 and the lowest AIC and number of iterations. So, the Gompertz model best described

the broiler growth curves. R^2 , AIC values and number of iterations of the Gompertz model were 0.9970, 648 and 5, respectively. Overall, the results showed that the Gompertz model described the biological curves of broiler fed on corn bran better than other models. Also, growth parameters were affected by corn bran.

Segura-Correa et al. (2017) in their study selected the best non-linear model that fits the growth curve of turkeys managed under the tropical conditions of Southern Mexico. Data from 481 Hybrid converter turkeys (236 females and 245 males) reared under commercial conditions typical of that region were used. Turkeys were given ad libitum access to feed and water. Body weight was weekly recorded from 1 day to 23 weeks of age. Five non-linear mathematical models (Brody, Gompertz, Logistic, Von Bertalanffy and Richards) were chosen to describe the age-weight relationship. The Brody and Richards' models fail to converge. The best fitting model was chosen based on the average prediction error (APE); the multiple determination coefficient R^2 and the Akaike information criterion (AIC). In both sexes, Von Bertalanffy and Gompertz were the best models. The highest estimates of parameter A (mature weight) for both females and males were obtained with the von Bertalanffy model followed by the Gompertz and Logistic. The estimates of A were higher for males than for females. The highest estimates of parameter k (rate of maturity) for both females and males were, in decreasing order for the Logistic, Gompertz, and von Bertalanffy models. k values for female turkeys was higher than for males. The best models to describe turkey growth were the Von Bertalanffy and Gompertz models.

Selvaggi et al.(2017) in their study was aimed to estimate the parameters of Logistic, Gompertz, Richards and Von Bertalanffy growth curve models in a sample of Podolica young bulls to determine the goodness of fit. Animals were weighed every 3 months from birth to 810 days of age. The results indicate that all the growth models used were easily fitted to the observed data with Gompertz and Logistic functions presenting less computational difficulty in terms of number of iteration to achieve convergence. Moreover, Logistic and Richards equations provided the best overall fit being useful to describe the growth of Podolica bulls. Considering that the literature lacks information on growth curves in Podolica breed, the study of a mathematical model for growth describing the developmental pattern of a specific population within a peculiar environment is a useful tool to improve Podolica breed production.

In the study of Teleken et al.(2017) was compared the goodness of fit of five non-linear growth models, i.e. Brody, Gompertz, Logistic, Richards and von Bertalanffy in different animals. It also aimed to evaluate the influence of the shape parameter on the growth curve. To accomplish this task, published growth data of 14 different groups of animals were used and four goodness of fit statistics were adopted: coefficient of determination (\mathbb{R}^2), root mean square error (RMSE), Akaike information criterion (AIC) and Bayesian information criterion (BIC). In general, the Richards growth equation provided better fits to experimental data than the other models. However, for some animals, different models exhibited better performance. It was obtained a possible interpretation for the shape parameter, in such a way that can provide useful insights to predict animal growth behavior.

2.2. Milk production

Orman and Yıldırım (1998) in their study were estimated the parameters of the regression models for the lactation curve. A total of 45 standard milk yield records obtained from the first, the second and the third lactations of Jersey breed in Karaköy State Farm were used. Milk production records were corrected for the ages of cows and the numbers of lactation. The parameters were estimated in two stages. In the first stage, the data were applied to the five nonlinear models, developed by different authors. The best fitting model is chosen according to the advantages and disadvantages of these models. In the second stage, five different estimation methods were compared. Among the five methods studied, the MRT (Marquardt) method was seen to be more practical and required less computing time than the others. The best fit model was used with MRT method for the estimated and the lactation curves were obtained for each of the three lactation groups. The curves of the three lactation groups were discussed in regard to the animal breeding and statistics.

Rekaya et al. (2001) in their study were used Wood's function, to describe the shape of the lactation curve in the first three lactations of Holstein cows. Wood's function was reparameterized to include the logarithm of persistency as a parameter. The data consisted of 65 677 test-day records of 2875 cows. All cows were required to have first lactation test-day milk yield records. A three-stage Bayesian hierarchical

nonlinear model was implemented. The first stage described within-cow variation and the second stage accounted for between-animal variation. The third stage consisted of the priors used. Negative genetic correlations between the first (measure of yield) and second (related to the increasing yield phase of lactation) parameters of Wood's function were found for all three lactations: -0.59, -0.55 and -0.39 for first, second and third lactations, respectively. The genetic correlation between the first parameter of Wood's function and log-persistency was negative in each of the three lactations (-0.20, -0.31 and -0.31). The genetic correlation between the second parameter and log-persistency was low (0.06, 0.09, 0.03 for each of the lactation). Heritabilities of all parameters tended to decrease with parity, mainly due to an increase in residual variance. Heritabilities of persistency were 0.17, 0.16 and 0.14 for first, second and third lactations was 0.26 (first and second), 0.32 (second and third) and 0.23 (first and third). Residual correlations followed a similar pattern but tended to be larger in absolute value than genetic correlations.

Cunha et al.(2010) in their study selected models of lactation curves with a better adjustment to the observed data in models of milk production simulation systems. A data base on 6,459 recordings of daily milk production was used. These data were obtained from monthly and fortnightly controls of milk between 2004 and 2007, from 472 lactations of animals from ten different milking cow herd farms. Based on rolling averages of milk production (MP-L/day) per cow, the ten herd farms were divided into low (L < 15), medium (15 <M < 20) and high (H > 20). Data were also divided according to the lactation numbers in first, second, third or greater. Eight lactation curve models commonly used in literature were compared. The models were individually adjusted for each lactation. The goodness of fit used for comparison of those models was the coefficient of determination, mean square error, mean square prediction error and the Bayesian information criterion. The values for the goodness of fit obtained in each model were compared by using 95% probability confidence interval. Wilmink model showed a better adjustment for cows of the first lactation numbers, whereas the Wood model showed a better adjustment for cows of the third or greater lactations numbers for the low milk production groups. Wood model showed a better adjustment for all the lactation numbers for the medium milk production group. Dijkstra model showed a better adjustment for all lactation numbers for the high milk production group. Despite of being more recent, the model by Pollott, mechanist based and with a higher number of parameters, showed a good convergence for the used data.

Küçük and Eyduran(2010) in their study tried to determine the most appropriate nonlinear model for describing complete lactation of Akkaraman and German Blackheaded Mutton x Akkaraman B₁ Crossbreed Sheep. The data were consisted of milk production records collected from 25 Akkaraman (Genotype I) and 23 German Blackheaded Mutton x Akkaraman B₁ Crossbreed Sheep (Genotype II) with 2 year of age. Daily milk yields of all ewes were recorded fortnightly from 15^{th} days to 150^{th} days of lactation. Quadratic, Cubic model, and Wood models were fitted to daily milk yield – time data in order to explain daily milk yield-time relationship of these ewes. These models were fitted to averages of daily milk yield of all ewes at each period for two genotypes. It was concluded that the best nonlinear model for describing complete lactation of Akkaraman breed and German Blackheaded Mutton x Akkaraman B₁ Crossbreed Sheep Was found to be Cubic model.

Korkmaz et al.(2011) in their study tried to determine a suitable nonlinear model explaining the lactation season curve of Simmental cows. Monthly milk yield records representing the test days milk yield of 777 Simmental cows were used to estimate lactation curve parameters by using Wood, Gaines, Parabolic, Hayashi, Dhanno and (second degree) polynomial models and to compare the shape of lactation season curves resulted from fitting all of these models. These models were given in explanation of the parameters and according to the lactation season, the parameters a, b and c for these models at all the periods was estimated. Secondly, the formula of some criteria, such as time to peak, peak production, turning point time and turning point production, are presented in mathematical procedure and then t the criteria values are calculated for all of the examined models. Furthermore, partial derivatives of the models according to the parameters were given in mathematical procedure. For the season, winter, spring, summer, fall and without season the lactation curve graphs for all the nonlinear models were drawn, respectively. Moreover, the best nonlinear model was used to determine the adjusted coefficient determination (R^2 adj), mean square prediction error (MSPE) and Bayesian Information Criteria (BIC). The runs test was used for determining whether data different systematically according theoretical curves. Generally, polynomial model gave the best nonlinear model to the data compared to the other models.

In the study of Mao et al.(2012) revealed the variations of daily milk yield, milk fat percentage, milk protein percentage and somatic cell score (SCS), and to establish the prediction models for these parameters in the lactation period for Chinese Holstein in Southern China. A 33194-test-day dairy herd complete data from 5 Chinese Holstein dairy farms were collected in the southern China from first lactation to third lactation between 2008 to 2010 years and fitted to nonlinear curve of test-day milk yield, milk fat percentage, milk protein percentage and SCS with the Wood's incomplete gamma function model. The curve of test-day milk yield for Chinese Holstein was the standard lactation curve, and the curves of milk fat percentage, milk protein percentage and SCS were the reversed standard lactation curve. The best fitness of the Wood's model occurred for milk protein percentage and daily milk yield with the lowest residual mean square, then following for milk fat percentage. The poor model fitness ($R^2 \le 0.7$) was observed for SCS which residual mean square was highest. Daily milk yield peak day was accompanied with occurrences of minimal milk protein and SCS in the estimated lactation model. The minimal milk fat percentage came at the latest time of 18th week to 21th week in lactation curve. The peak milk yield was 30.4 kg·d⁻¹ for first-parity cows, but the persistence for maintaining high milk yield and low SCS were greater than those of second- and third- parity cows in the latter lactation period, and the maximal milk yields for second- and third-parity dairy cows were 35.9 and 36.2 kg \cdot d⁻¹, respectively. The persistence for keeping high milk fat percentage and milk protein percentage was greater for second-parity cows than those of first- and third-parity cows in the latter lactation period. The Wood's incomplete gamma function model was appropriate to predict the variation for test-day milk yield, milk fat percentage, milk protein percentage, and was not appropriate for SCS for Chinese Holstein dairy cows in Southern China.

In the study of Hossein-Zadeh(2016) in order to describe the lactation curves of milk yield (MY) and composition in buffaloes, seven non-linear mathematical equations (Wood, Dhanoa, Sikka, Nelder, Brody, Dijkstra and Rook) were used. Data were 116,117 test-day records for MY, fat (FP) and protein (PP) percentages of milk from the first three lactations of buffaloes which were collected from 893 herds in the period

from 1992 to 2012 by the Animal Breeding Center of Iran. Each model was fitted to monthly production records of dairy buffaloes using the NLIN and MODEL procedures in SAS and the parameters were estimated. The models were tested for goodness of fit using adjusted coefficient of determination (R²adj), root means square error (RMSE), Durbin-Watson statistic and Akaike's information criterion (AIC). The Dijkstra model provided the best fit of MY and PP of milk for the first three parities of buffaloes due to the lower values of RMSE and AIC than other models. For the first-parity buffaloes, Sikka and Brody models provided the best fit of FP, but for the second- and third-parity buffaloes, Sikka model and Brody equation provided the best fit of lactation curve for FP, respectively. The results of this study showed that the Wood and Dhanoa equations were able to estimate the time to the peak MY more accurately than the other equations. In addition, Nelder and Dijkstra equations were able to estimate the peak time at second and third parities more accurately than other equations, respectively. Brody function provided more accurate predictions of peak MY over the first three parities of buffaloes. There was generally a positive relationship between 305-day MY and persistency measures and also between peak yield and 305-day MY, calculated by different models, within each lactation in the current study. Overall, evaluation of the different equations used in the current study indicated the potential of the non-linear models for fitting monthly productive records of buffaloes.

Bangar and Verma (2017) in their study tried to determine the suitable nonlinear model which most accurately fitted to lactation curves of five lactations in 134 Gir crossbred cows reared in Research-Cum-Development Project (RCDP) on Cattle farm, MPKV (Maharashtra). Four models viz. gamma-type function, quadratic model, mixed log function and Wilmink model were fitted to each lactation separately and then compared on the basis of goodness of fit measures viz. adjusted R², root mean square error (RMSE), Akaike's Informaion Criteria (AIC) and Bayesian Information Criteria (BIC). As there was significant difference in milk yield in different lactations, nonlinear modelling showed varied fitting of lactation curve in first lactation and other lactations. Among the four models studied, mixed log function provided best fit of the lactation curve of primiparous cows, due to lower values of RMSE, AIC and BIC. However, in multiparous cows, gamma-type function described most appropriately the lactation curve as compared to other model. Quadratic model gave least fit to lactation curve in almost all lactations. Peak yield was highest in fourth lactation and least in first lactation. The persistency was higher in first lactation of Gir crossbred. It was suggested that lactation curve models may be helpful to setting the management strategies at farm level, however, modelling must be optimized regularly before implementing them to enhance productivity in Gir crossbred cows.

Piccardi et al.(2017) in their work fitted and compared three non-linear models (Wood, Milkbot and Diphasic) to model lactation curves from two approaches: with and without cow random effect. Knowing the behaviour of lactation curves is critical for decision-making in a dairy farm. Knowledge of the model of milk production progress along each lactation is necessary not only at the mean population level (dairy farm), but also at individual level (cow-lactation). The fits were made in a group of high production and reproduction dairy farms; in first and third lactations in cool seasons. A total of 2167 complete lactations were involved, of which 984 were first-lactations and the remaining ones, third lactations (19 382 milk yield tests). PROC NLMIXED in SAS was used to make the fits and estimate the model parameters. The Diphasic model resulted to be computationally complex and barely practical. Regarding the classical Wood and MilkBot models, although the information criteria suggest the selection of MilkBot, the differences in the estimation of production indicators did not show a significant improvement. The Wood model was found to be a good option for fitting the expected value of lactation curves. Furthermore, the three models fitted better when the subject (cow) random effect was considered, which is related to magnitude of production. The random effect improved the predictive potential of the models, but it did not have a significant effect on the production indicators derived from the lactation curves, such as milk yield and days in milk to peak.

2.3. Egg production

Four mathematical models (Compartmental, Modified compartmental, Wood, and Adams-Bell were fitted to different patterns of egg production data in laying hens to compare the fits of these models in the study of Miyoshi et al.(1996).

The egg production data were obtained from the two lines which were founded on a basis of divergent selection for egg quality traits. Egg production data of individual hens were classified in six patterns. The average hen-day rates of lay were calculated for every 10days from the first egg for each pattern. The comparison of fits was based on the R²adjusted for degrees of freedom and Akaike's Information Criterion (AIC). The fits of models were similar for the egg production data showing a general pattern of curve. However, the model parameters could not be estimated by these three models for the data whose patterns showed abrupt decreases after the peak of egg production. The data in which the period from the first egg to the peak of egg production was short and linearly decreased after reaching the peak showed poor fits of the models. The parameters of all patterns could be estimated by the Wood model, but the fits were lower than those of the others.

Savegnago et al.(2012) in their study fitted the weekly egg production rate of selected and non-selected lines of a White Leghorn hen population, using nonlinear and segmented polynomial models, and to study how the selection process changed the egglaying patterns between these 2 lines. Weekly egg production rates over 54 wk of egg production (from 17 to 70 wk of age) were measured from 1,693 and 282 laying hens from one selected and one non-selected (control) genetic line, respectively. Six nonlinear and one segmented polynomial models were gathered from the literature to investigate whether they could be used to fit curves for the weekly egg production rate. The goodness of fit of the models was measured using Akaike's information criterion, mean square error, coefficient of determination, graphical analysis of the fitted curves, and the deviations of the fitted curves. The Logistic, Yang, Segmented Polynomial, and Grossman models presented the best goodness of fit. In this population, there were significant differences between the parameter estimates of the curves fitted for the selected and non-selected lines, thus indicating that the effect of selection changed the shape of the egg production curves. The selection for egg production was efficient in modifying the birds' egg production curve in this population, thus resulting in genetic gain from the 5th to the 54th week of egg laying and improved the peak egg production and the persistence of egg laying.

In the study of France et al.(2013) models based on linear systems of differential equations were contrasted with those based on nonlinear systems. Regression equations arising from analytical solutions to linear compartmental schemes are considered as candidate functions for describing egg production curves, together with aspects of parameter estimation. Extant candidate functions are reviewed, a role for growth

functions such as the Gompertz equation suggested, and a function based on a simple new model outlined. Structurally, the new model comprises a single pool with an inflow and an outflow. Compartmental simulation models based on nonlinear systems of differentia equations, and thus requiring numerical solution, are next discussed, and aspects of parameter estimation considered. This type of model is illustrated in relation to development and evaluation of a dynamic model of calcium and phosphorus flows in layers. The model consists of 8 state variables representing calcium and phosphorus pools in the crop, stomachs, plasma, and bone. The flow equations are described by Michaelis-Menten or mass action forms. Experiments that measure Ca and P uptake in layers fed different calcium concentrations during shell-forming days are used to evaluate the model. In addition to providing a useful management tool, such a simulation model also provides a means to evaluate feeding strategies aimed at reducing excretion of potential pollutants in poultry manure to the environment.

Narinc et al. (2013) in their study, tried to detect some traits with respect to egg production, to determine the cumulative hen-housed egg numbers, and to compare goodness of fit of different nonlinear models for the percentage of hen-day egg production. The mean age at first egg was 38.9 d and the age at 50% egg production was 45.3 d. The quail reached peak production at 15 wk of age (wk 9 of egg production period) when the percentage of hen-day egg production was found to be 94%. The cumulative hen-housed egg number for 52 wk as of the age of sexual maturity was 253.08. The Monomolecular function, a Nonsigmoid model, was used in the nonlinear regression analysis of the cumulative egg numbers. Parameters a, b, and c of the monomolecular model were estimated to be 461.70, 473.31, and 0.065, respectively. Gamma, McNally, Adams-Bell, and Modified compartmental models, widely used in hens previously, were used in the nonlinear regression analysis of the percentages of hen-day egg production. The goodness of fit for these models was compared using the values of R², Akaike's information criterion, and Bayesian information criterion. It was determined that all the models are adequate but that the Adams-Bell model displayed a slightly better fit for the percentage of hen-day egg production in Japanese quail than others.

Narinc et al.(2014) in their review covers the egg production models used in poultry. Similarities and discrepancies among the models are illustrated using a real data

obtained from a layer breeder flock. Some of the functions were developed for this purpose, such as nonlinear regression equations (Gamma, McNally, McMillan, Adams-Bell, Compartmental, Modified Compartmental, Logistic-curvilinear, Gloor, Lokhorst, Narushin-Takma) and some multiphasic (Segmented Polynomial, Persistency, Individual). Almost all of these functions have been developed to allow modeling on the basis of flock averages. Most models having empirical structure and a small number of parameters are considered biologically meaningful. New models are currently required to be useful for both individual egg yields and to contain biologically relevant parameters.

Broiler breeders hens (meat-type hens) have lower reproductive potential than laying-type hens. Statistical models for predicting potential laying pattern are important for economically optimal breeding strategy of egg production in a poultry flock. Otwinowska-Mindur et al. (2016) in their study tried to find the most suitable function for describing the egg-laying rate and egg weight during the broiler breeders' production period and to characterize laying pattern in groups of hens with different egg production. The following four mathematical models were used: Gamma, Narushin-Takma, Logistic-curvilinear, and Compartmental. The daily recorded egg production data from 100 broiler breeder hens were used. Hen-weekly egg production was described using laying rate during successive weeks after reaching sexual maturity (26 weeks of age) and daily recorded egg weight. On the basis of the total number of eggs laid, groups of hens with low (21%), intermediate (52%), and high (27%) egg production were created. The differences between the goodness-of-fit criteria values (AIC, R^2 , MSE) were small, with all the examined models having the same quality of curve fitting for egg-laying rate and egg weight. The logistic-curvilinear model was able to fit well both egg-laying rate and egg weight of the whole broiler breeder hens' flock, and also when hens were divided into three egg production groups. This model could be considered in a long-term prediction of the reproductive potential in the commercial management. Moreover, the presented model could be useful in the research on different reproduction parameters of individual hens.

Nogueira et al.(2016) in their study estimated the weight increase in the laying hens' egg based on diet protein intake, using two models and compare both. It was used the Gompertz function and Sigmoidal function $y=p+q/(1+e^{((r+(s*x)))})$ where

y=egg weight; p=bottom asymptote; p+q=upper asymptote; r=constant; s=constant; x=poultry body weight, to estimate body weight and egg weight respectively. Two models were adjusted to describe the increase in egg weight on the basis of diet protein intake. The first, used the saturation kinetics equation and the second, used a quadratic polynomial equation, IEW=a-(b(*(c-CP))^2), where IEW=increase in egg weight; a=constant; b=intercept on ordinate axis; c=diet protein intake value which is maximum increase and CP=crude protein(%). These models were adjusted and evaluated using database from studies conducted in the Poultry Science Laboratory. The statistical criteria used MSE (Mean square error), ED (Error due to deviation from regression slope) and R^2 (Coefficient of determination) to evaluate the fit of curves using NLINMIXED and REG procedures of SAS. The evaluation of models that they estimate the egg weight increase in function of the diet protein intake had for saturation kinetics model, 2.94, 0.30 and 0.91 for MSE, ED and R²whereas for the quadratic polynomial model, the values were 16.85, 1.01 and -0.07. According to statistic made, the model based on the saturation kinetics(non-linear) equation had lower values of MSE and ED then higher R²that explain a better fit than the other model(linear). These results shown that is possible to estimate the increase in egg weight using the proposed non-linear model, however other parameters will be adding to improve the accuracy of estimation.

3. MATERIAL AND METHODS

3.1. Material

Material of the study was the research articles on nonlinear regression models applied in animal husbandry. 38 articles concerning lactation curves, growth curves and egg weight and production were investigated, nonlinear models used in these articles collected and the base of nonlinear models used in animal science was created.

3.2. Method

Regression studies the relationship between a variable of interest Y and one or more explanatory or predictor variables $x^{(j)}$. The general model is $Y_i = h(x^{(1)}_i, x^{(2)}_i, \dots, x^{(m)}_i; \theta_1, \theta_2, \dots, \theta_p) + E_i$.

Here, h is an appropriate function that depends on the explanatory variables and parameters, that we want to summarize with vectors $\mathbf{x} = [\mathbf{x}^{(1)}_{i}, \mathbf{x}^{(2)}_{i}, \dots, \mathbf{x}^{(m)}_{i}]^{T}$ and $\boldsymbol{\theta} = [\theta_{1}, \theta_{2}, \dots, \theta_{p}]^{T}$.

The unstructured deviations from the function h are described via the random errors E_i . The normal distribution is assumed for the distribution of this random error, so $E_i \sim N(0, \sigma^2)$, independent.

In (multiple) linear regression, functions h are considered that are linear in the parameters θ_i ,

 $Y_{i} = h(x_{i}^{(1)}, x_{i}^{(2)}, \dots, x_{i}^{(m)}; \theta_{1}, \theta_{2}, \dots, \theta_{p}) = \theta_{1}x_{i}^{(1)} + \theta_{2}x_{i}^{(2)} + \dots + \theta_{p}x_{i}^{(p)},$

Where, the x $_{(j)}$ can be arbitrary functions of the original explanatory variables $x_{(j)}$. (Here the parameters are usually denoted as β_i instead of θ_i .)

In nonlinear regression, functions h are considered that cannot be written as linear in the parameters. Often such a function is derived from theory. In principle, there are unlimited possibilities for describing the deterministic part of the model. As we will see, this flexibility often means a greater effort to make statistical statements.

3.2.1. Some commonly used families of nonlinear regression functions

While simple and multiple linear regression functions are adequate for modeling a wide variety of relationships between response variables and predictor variables, many situations require nonlinear functions. Certain types of nonlinear regression functions have served, and will continue to serve, as useful models for describing various physical and biological systems. A few of these situations for the case of a single predictor variable was listed below.

 The following functions have been considered in modeling the relationship between crop yield Y and the spacing between rows of plants, concentration Y of a drug in the bloodstream and time X after the drug is injected when this concentration is measured, the rate Y of a chemical reaction and the amount X of catalyst used, and many other relationships.

$$\mu_{y}(x) = \frac{1}{(\beta_{1} + \beta_{2} x)^{\beta_{3}}}$$
(1)

$$\mu_{y}(x) = \frac{1}{(\beta_{1} + \beta_{2}x + \beta_{3}x^{2})}$$
(2)

$$\mu_{y}(\mathbf{x}) = \frac{1}{\beta_{1} + \beta_{2} \mathbf{x}^{\beta_{3}}} \tag{3}$$

Typical members of the families of curves (1)-(3) are displayed in Fig. (3.1) -(3.3), respectively.



Figure 3.1. Three members of the family of curves (1). Where, (a) $\beta_1 = 0.6$, $\beta_2 = 1$, $\beta_3 = -1$; (b) $\beta_1 = 0.1$, $\beta_2 = 1$, $\beta_3 = 0.3$; (c) $\beta_1 = 0.2$, $\beta_2 = 1$, $\beta_3 = 2$.



Figure 3.2. Three members of the family of curves (2).



Where, (a) β_1 = 1, β_2 =3, β_3 =-0.2; (b) β_1 =8.94, β_2 =-22.4, β_3 =16; (c) β_1 =8, β_2 =-8, β_3 =1.

2. S-shaped curves, often referred to as sigmoidal curves, arise in various applications, including bioassay, signal detection theory, engineering, and economics. Various types of growth data often conform to sigmoidal curves. Some of the nonlinear regression function that have been used in such situations include:

$$\mu_{y}(x) = \beta_{1} e^{-e^{-(\beta_{2}+\beta_{3}x)}}$$
(4)

$$\mu_{y}(x) = \frac{\beta_{1}}{1 + e^{-(\beta_{2} + \beta_{3}x)}}$$
(5)

$$\mu_Y(x) = \frac{\beta_1}{[1 + e^{-(\beta_2 + \beta_3 x)}]^{\beta_4}} \tag{6}$$

The model in (4) is often called the Gompertz model, the model in (5) is usually referred to as a logistic regression model, and the model in (6) is called Richard's model. Typical curves belonging to the families (4)-(6) are shown in Fig.(3.4) -(3.6), respectively.



Figure 3.4. Three members of the family of curves (4). Where, (a) $\beta_1 = 1$, $\beta_2 = -1.5$, $\beta_3 = 3$; (b) $\beta_1 = 1$, $\beta_2 = -3.5$, $\beta_3 = 7$; (c) $\beta_1 = 1$, $\beta_2 = -5$, $\beta_3 = 9$.



Figure 3.5. Three members of the family of curves (5). Where, (a) $\beta_1 = 1$, $\beta_2 = -3.22$, $\beta_3 = 8$; (b) $\beta_1 = 0.95$, $\beta_2 = -4.61$, $\beta_3 = 10$; (c) $\beta_1 = 1$, $\beta_2 = -2.3$, $\beta_3 = 4$.



Figure 3.6. Three members of the family of curves (6). Where, (a) $\beta_1 = 1$, $\beta_2 = -3.22$, $\beta_3 = 8$, $\beta_4 = 3.33$; (b) $\beta_1 = 0.95$, $\beta_2 = -4.61$, $\beta_3 = 10$, $\beta_4 = 0.33$; (c) $\beta_1 = 1$, $\beta_2 = -2.3$, $\beta_3 = 4$, $\beta_4 = 1.25$.

3. When the response variable Y steadily increases (decreases) with the independent variable X but the magnitude of the rate of increase (decrease) becomes smaller and smaller, with the response variable ultimately approaching a constant value called the asymptote, the family of curves defined by

$$\mu_{y}(x) = \beta_{1} + \beta_{2} e^{-\beta_{3} x} \tag{7}$$

has been found to provide useful nonlinear regression models. Three members of the family in (7) are displayed in Fig.3.7. Typical applications where such models are useful include the study of yield as a function of rate of application of fertilizer, mortality rate as a function of time, amount of chemical converted in a reaction as a function of time, etc.



Figure 3.7. Three members of the family of curves (7). Where, (a) $\beta_1 = 1$, $\beta_2 = -0.9$, $\beta_3 = 4$; (b) $\beta_1 = 1$, $\beta_2 = -0.8$, $\beta_3 = 2$; (c) $\beta_1 = 1$, $\beta_2 = -1$, $\beta_3 = 0.9$.

Numerous other useful families of nonlinear regression functions exist. Here it was presented some of the simplest and the most commonly used functions. Although all the application just discussed involves only a single predictor variable, the models can be extended to the case of multiple predictor variables in a variety of ways.

3.2.2. Statistical assumptions and inferences for nonlinear regression

The most commonly used set of assumptions for nonlinear regression is the same as assumptions for linear regression. The complete set of assumptions is given below:

3.2.2.1. Assumptions for Nonlinear Regression

The (k + 1) variable population $[(Y, X_1, \dots, X_k)]$ is the study population under investigation.

Assumption 1: The mean of the subpopulation of Y values determined by $X_1=x_1, ..., X_k=x_k$ is denoted by $\mu_y(x_1, ..., x_k)$, and is a nonlinear function of unknown parameters. At times we find it useful to write $\mu_y(x_1, ..., x_k; \beta_1, ..., \beta_p)$ for the regression function to emphasize the fact that it depends on the parameters $\beta_1, ..., \beta_p$. Assumption 2: The standard deviations of the Y values are the same for each subpopulation determined by specified values of the predictor variables X_1, \ldots, X_k . This common standard deviation of all the subpopulations is denoted by $\sigma_{Y|X_{1,\ldots},X_k}$.

Assumption 3: Each subpopulation of Y values, determined by specified values of the predictor variables $X_1, ..., X_k$ is Gaussian.

Assumption 4: The sample (of size n)is selected either by simple random sampling or by sampling with preselected values of $X_1, ..., X_k$.

Assumption 5: All sample values y_i , $x_{i,1}$,..., $x_{i,k}$ for i=1,...,n are observed without error.

3.2.2.2.Parameter Estimation

A popular method for estimating the unknown parameters in a nonlinear regression function is the method of least squares. According to this method, the estimates of $\beta_1, ..., \beta_p$ are obtained by minimizing the quantity $\sum_{i=1}^{n} e_i^2$, the sum of squares of errors of prediction, where e_i is given by

$$e_i = y_i - \mu_y(x_{i,1}, \dots, x_{i,k})$$

As usual, the least squares estimates of $\beta_1, ..., \beta_p$ are denoted by $\hat{\beta}_1, ..., \hat{\beta}_p$. The estimated value of the subpopulation mean $\mu_y(x_1, ..., x_k)$ is denoted by $\hat{\mu}_y(x_1, ..., x_k)$. It is referred to as the fitted value corresponding to $x_1, ..., x_k$, and is obtained by substituting the least squares estimates of the parameters into the regression function. This is algebraically expressed by the equation

$$\hat{\mu}_{y}(x_{1}, \dots, x_{k}) = \mu_{y}(x_{1}, \dots, x_{k}; \hat{\beta}_{1} \dots, \hat{\beta}_{p})$$
(8)

The quantity \hat{e}_l defined by

$$\hat{e}_i = y_i - \hat{\mu}_y(x_{i,1}, \dots, x_{i,k})$$
(9)

is called the residual corresponding to sample item i.

The minimum value for the sum of squares of errors of prediction corresponding to the least squares estimates $\hat{\beta}_1 \dots, \hat{\beta}_p$ is denoted by SSE, an abbreviation for the more complete notation SSE(X_1, \dots, X_k).Thus

$$SSE = \sum_{i=1}^{n} \hat{e}_{i}^{2} = \sum_{i=1}^{n} [y_{i} - \hat{\mu}_{y} (x_{i,1}, \dots, x_{i,k})]^{2}$$
(10)

and as in linear regression, it will referred to SSE as the sum of squared errors. The quantity MSE, which is an abbreviation for the more complete notation $MSE(X_1,...,X_k)$, is given by

$$MSE = \frac{SSE}{(n-p)} \tag{11}$$

and is called the mean squared error, and it is an unbiased estimate of σ^2 . The corresponding estimate of σ is given by

$$\hat{\sigma} = \sqrt{\frac{SSE}{n-p}} = \sqrt{MSE} \tag{12}$$

In the case of multiple linear regression, the least squares estimates of the parameters $\beta_1, ..., \beta_p$ can be computed quite easily. However, the estimation of parameters in nonlinear regression models usually requires the use of iterative methods on digital computers, and explicit formulas for the estimates are generally not available. Most commonly available statistical software packages provide routines for calculating $\hat{\beta}_1 ..., \hat{\beta}_p$. To use any of these nonlinear regression programs, it must be supplied, in addition to the data, a set of starting values or initial guesses for $\beta_1, ..., \beta_p$. It is often helpful if the starting values are close to the actual least squares estimates $\hat{\beta}_i$. However, you may not have such initial guesses. Sometimes you can obtain good initial estimates of $\hat{\beta}_i$, or at least the signs of $\hat{\beta}_i$, based on theoretical considerations or by plotting the sample data.

3.2.2.3. Confidence Intervals and Tests of Hypotheses

Exact confidence interval procedures or exact hypothesis tests are generally not available for parameters in nonlinear regression models. However, approximate inference procedures are available. In practice, the computations required for carrying out approximate hypothesis tests or obtaining approximate confidence intervals are best performed using a suitable computer program. Any computer program for calculating the estimates of parameters in a nonlinear regression function usually outputs an approximate standard error (ASE), sometimes also referred to as an asymptotic standard error, for each parameter estimate. The approximation is usually quite good if the number of observations in the sample is large. Confidence intervals for $\beta_1,...,\beta_p$ may be computed, and tests may be carried out, with approximate standard errors in place of exact standard errors. Confidence intervals and tests for $\sigma = \sigma_{Y|X_1,...,X_k}$ can be computed, without any modification. The degrees of freedom to use for table-values are, as usual, equal to

n-p = n-(number of β parameters in the model)

The details are as follows. Suppose $\beta_1, ..., \beta_p$ are unknown parameters in a nonlinear regression function. An approximate 100(1- α) % confidence interval for β_j is given by the confidence statement

$$\mathbb{C}[\hat{\beta}_{j} - t_{1 - \frac{\alpha}{2}; n-p} ASE(\hat{\beta}_{j}) \leq \beta_{j} \leq \hat{\beta}_{j} + t_{1 - \frac{\alpha}{2}; n-p} ASE(\hat{\beta}_{j})] \approx 1 - \alpha$$
(13)

Where ASE($\hat{\beta}_j$) is the approximate standard error for $\hat{\beta}_j$. An approximate level α test of the hypothesis

 $NH:\beta_j = q \qquad \text{versus} \qquad AH:\beta_j \neq q \qquad (14)$

(where q is a specified number) is conducted as follows :

Compute
$$t_C = \frac{\hat{\beta}_j - q}{ASE(\hat{\beta}_j)}$$
. Reject NH if $|t_C| > t_{1 - \frac{\alpha}{2}; n - p}$ (15)

In general, due to the approximate nature of the inference procedures for nonlinear regression problems, the actual confidence coefficients associated with the confidence interval and P-values for tests discussed above may be quite different from the stated values. If critical decisions have to be made, the investigator should consult a professional statistician (Graybill and Iyer, 1994).

3.2.3. Linearizable models

In some situation it may be possible to transform a nonlinear regression function $\mu_y(x)$ using appropriate transformations of the response variable, the predictor variables, the parameters, or any combination of these, such that the transformed function is linear in the unknown parameters. If the transformed variables satisfy assumptions for multiple linear regression, then the transformed problem can be solved as linear regression. Using the results for the transformed problem, it can be often obtained results for the original problem, as an example, consider the model

$$\mu_{\nu}(x) = \beta_1^* e^{-\beta_2^* x} \tag{16}$$

where, β_1^* is positive. This model is a special case of the model given in (7) with the β_1 term set to zero. By taking the logarithm to the base e of both sides, we get the transformed function $\ln[\mu_Y(x)] = \ln(\beta_1^*) - \beta_2^* x$. Now let $\ln(\beta_1^*) = \beta_0$ and $-\beta_2^* = \beta_1$. We thus have $\ln[\mu_Y(x)] = \beta_0 + \beta_1 x$ which, is linear in the unknown parameters. This suggests that if we set Z=ln(Y), the regression function of Z on X will be approximately linear and will be given by

$$\mu_z(x) \approx \beta_0 + \beta_1 x \tag{17}$$

This regression function of Z on X make approximate inference about the parameters $\beta_0 = \ln(\beta_1^*)$ and $\beta_1 = -\beta_2^*$. This in turn will lead to inferences about β_1^* and β_2^* , the parameters of interest in the original problem.

More specifically, if the data are (y_1, x_1) , ..., (y_n, x_n) , we let $z_i=\ln(y_i)$ and get at the transformed data (z_1, x_1) , ..., (z_n, x_n) . If the transformed data satisfy assumptions for straight line regression (at least approximately), then can be drawn inferences about $\mu_Z(x)$ in (17). Thus the estimates of β_0 and β_1 in (17) will calculated by the formulas given below:

$$\hat{\beta}_{1} = \frac{\sum (z_{i} - \bar{z})(x_{i} - \bar{x})}{\sum (x_{i} - \bar{x})^{2}}$$
(18)

and

$$\hat{\beta}_0 = \bar{z} - \hat{\beta}_1 \bar{x} \tag{19}$$

where, $\bar{z} = \frac{1}{n} \sum_{i=1}^{n} z_i$. So we get

$$\hat{\beta}_{2}^{*} = -\hat{\beta}_{1}$$
 (20)

and

$$\hat{\beta}_{1}^{*} = \exp(\bar{z} - \hat{\beta}_{1}\bar{x})$$
 (21)

Some examples of linearizable models and their linear representations are given in Table 3.1. In some cases an investigator is not confident that assumptions hold(even approximately) for the transformed variables. In these cases, the parameter estimates obtained by performing a linear regression analysis on the transformed data may be useful as starting values for nonlinear regression programs. This is a commonly used strategy.

Table 3.1. Exampl	es of linearizable	models and their	linear representation
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Original regression function	Linearizing transformation	Suggested transformation
		01 1
$\mu_Y^*(x) = \beta_1^* e^{\beta_2^* x}$	$\ln[\mu_Y^*(x)] = \ln(\beta_1^*) + \beta_2^* x = \beta_0 + \beta_1 x$ where $\beta_0 = \ln(\beta_1^*)$ and $\beta_1 = \beta_2^*$	Z=ln(Y), for $Y > 0$

$\mu_Y^*(x) = (\beta_1^*)^x$	$\ln[\mu_y^*(x)] = x \ln(\beta_1^*) = \beta_1 x \text{where } \beta_1 = \ln(\beta_1^*)$	Z = ln(Y), for $Y > 0$
$\mu_Y^*(x) = \frac{1}{\beta_1^* - \beta_2^* x}$	$\frac{1}{\mu_Y^*(x)} = \beta_1^* - \beta_2^* x = \beta_0 + \beta_1 x \text{ where } \beta_0 = \beta_1^* \text{ and } \beta_1 = -\beta_2^*$	$Z = \frac{1}{Y}$, for $Y \neq 0$
$\mu_Y^*(x) = \frac{1}{1 + e^{-(\beta_1^* + \beta_2^* x)}}$	$\ln\left(\frac{\mu_Y^*(x)}{1-\mu_Y^*(x)}\right) = \beta_1^* + \beta_2^* x = \beta_0 + \beta_1 x$ where $\beta_0 = \beta_1^*$ and $\beta_1 = \beta_2^*$	$Z=ln\left(\frac{Y}{1-Y}\right), \text{ for } 0 < Y < 1$

3.2.4. Model selection criteria

For selection of appropriate model following criteria can be used: (Burnham and Anderson, 2002).

a) Coefficient of determination

$$R^{2} = 1 - \sum_{i=1}^{n} \left(y_{i} - \mathcal{G}_{p} \right)^{2} / \sum_{i=1}^{n} \left(y_{i} - \overline{y} \right)^{2}$$
(22)

b) Adjusted coefficient of determination,

$$R_{adj}^{2} = 1 - \left(1 - R^{2}\right) \frac{n - 1}{n - p}$$
(23)

c) Mean square error (MSE)

$$MSE = \sqrt{\frac{1}{n-p} \sum_{i=1}^{n} (y_i - y_i)}$$
(24)

d) Wellmot agreement criteria

$$\mathbf{D} = 1 - \frac{\sum (y_i - \hat{y}_i)^2}{\sum \{|y_i - \bar{y}| + |\hat{y}_i - \bar{y}|\}^2}$$
(25)

e) Absolute percentage error

$$\overline{\varepsilon} = \frac{100\%}{n} \sum_{i=1}^{n} \left| \frac{y_i - \frac{y_i}{p_i}}{y_i} \right|$$
(26)

f) Akaike information criteria (AIC)

$$\mathbf{AIC} = \ln\left[\frac{1}{n}\sum_{i=1}^{n} \left(y_{i} - \mathcal{Y}_{i}^{p}\right)^{2}\right] + \frac{2p}{n - \left(p + 1\right)}, \left(\frac{\mathbf{n}}{\mathbf{p}} < 40\right)$$
(27)

g) Bayesian information criteria (BIC)

$$\mathbf{BIC} = \ln\left[\frac{1}{n}\sum_{i=1}^{n} \left(y_i - \mathcal{G}_i\right)^2\right] + \frac{p}{n}\ln n \tag{28}$$

In the equations (22)-(28);

- n is the number of observation,
- p-is the number of parameters in the model,
- y_i –is a yield in the time i,
- \overline{y} is an arithmetical mean of yield,
- $\oint -is$ the predicted yield.

For the selection of the best model; Coefficient of determination, Adjusted coefficient of determination and Wellmot agreement criteria must be highest, but other criteria must be the least.

4. RESULTS AND DISCUSSIONS

4.1. Growth models base

In animals, the plot of live weight against age or time results in a characteristic sigmoidal growth curve, consisting of three differentiated parts: an initial self-accelerating phase, an intermediate linear phase and a final self-decelerating phase which fades out as the animal reaches maturity (Fig. 4.1). Growth rate (weight gain per unit of time, usually in g or kg day⁻¹) varies with age, increasing during the self-accelerating phase until reaching a maximum in the intermediate phase, when it is relatively constant. In the last phase, the growth rate decreases progressively to zero, reaching a final plateau when the animal achieves mature or asymptotic body weight, maintaining a relatively stable weight with changes attributed to the availability of feed, the demands of the reproductive cycle and the season of the year (Lopes, 2008).



Figure 4.1. Different growth curves of different breeds of cattle (Lopes, 2008)

A large number of growth equations or functions have been reported trying to describe the growth curve of animals (Table 4.1) best in terms of a few parameters that can be interpreted biologically and used to derive other relevant growth traits.

Name	Equation	Parameter meaning
Bridges	$Y_t = Y_0 + Y_f \{1 - exp[-(kt^n)]\}$	Parameter k define the scale and shape of the curve
Brody	$\begin{split} Y_t &= Y_0 e^{k_1 t}, \qquad 0 \leq t \leq t^*, \\ Y_t &= Y_f - (Y_f - Y^*) e^{-k_2 (t - t^*)}, t \geq t^* \end{split}$	Parameters k_1 and k_2 define the scale and shape of the curve

Table 4.1. Equations	used	to	describe	the	growth	curves
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$$Y_t = \frac{v_t v_t}{v_t (w - v_t) v_t} \left[\frac{v_t (w^{-1} k_t)}{V_t (w^{-1} k_t - 1)} \right]$$
, whereParameters and k
define the scale and
shape of the curveCount $Y_t = Y_0 + bt + cln(t + 1)$ Parameters b and c
define the scale and
shape of the curveExponential $Y_t = Y_0 e^{kt}$, $0 \le t \le t_f$
 $Y_t = Y_0 e^{kt}$, $0 \le t \le t_f$ Parameters b, $b_1 > \dots$,
b, define the scale and shape of the curveExponential polynomials $Y_1 = Y_0 exp(b_1t + b_2t^2 + ... + b_4t^0)$ Parameters b, $b_1 > \dots$,
b, define the scale and shape of the curveExponential quadratic $Y_1 = Y_0 exp(b_1t + b_2t^2 + ... + b_4t^0)$ Parameters k and a
define the scale and
shape of the curveFrance $Y_1 = Y_0 exp([k(t - \frac{et^2}{2})])$ $t < T$
Parameters k and a
define the scale and
shape of the curveGaussian $Y_t = Y_0 + (Y_t - Y_0)exp[-k(t - T) + 2c(\sqrt{t} - \sqrt{T})], t \ge T$ Parameters k and c
define the scale and
shape of the curveGompertz $Y_t = Y_0 + (Y_t - Y_0)(1 - e^{-kt^2})$ Parameters k and k
define the scale and
shape of the curveJolicoeur's generalized
Gompertz $Y_t = Y_0 + kt^r$ $Y_t = Y_0 + kt^r$ Kucchi $Y_t = Y_t \left[\frac{t^n}{k^t + t^n} \right]^t$ Parameters b, k_1, k_2
define the scale and
shape of the curveLevakovic $Y_t = Y_t \left[\frac{t^n}{k^r + t^n} \right]^t$ Parameters k and c
define the scale and
shape of the curveLog-logistic $Y_t = Y_t - \frac{Y_t - Y_0}{k^r + t^n} e^{kt}$ Parameters k define
the scale and shape of the curveLopez $Y_t = \frac{Y_0 K + Y_t t}{K^n + t^n}$ Parameter K define
the scale and shape
of the curve

Mitscherlich
$$Y_t = Y_f (1 - e^{-kt})$$
, if $Y_0 = 0$ Parameter k define
the scale and shape
of the curveModified Von
Bertalanffy $Y_t = Y_0 + (Y_f - Y_0)(1 - e^{-kt})^{1/n}$ Parameter k define
the scale and shape
of the curveMonomolecular $Y_t = Y_f - (Y_f - Y_0)e^{-kt}$ Parameter k define
the scale and shape
of the curvePolynomials $Y_t = Y_0 + b_1 t + b_2 t^2 + ... + b_4 t^2$ Parameter k define
the scale and shape
of the curveRatio of polynomials $Y_t = \frac{Y_0 + b_1 t + b_2 t^2 + ... + b_4 t^4}{Y_0 + b_1 t + b_2 t^2 + ... + b_4 t^n}$ Parameters b_t, b_s
..., b_s define the scale
and shape of the curveReed $Y_t = \frac{Y_f}{1 + be^{-(k_1 + k_2 t^2 + k_3 t^3)}}$ Parameters b_t, k_2
and k_1 define the
scale and shape of
the curveRichards $Y_t = \frac{Y_0 + bt + cln(t + 1) + \frac{d}{t + 1} + \frac{e}{(t + 1)^2}$ Parameters b_t define
the scale and
shape of the
curveRobertson $Y_t = \frac{Y_0 Y_f}{[Y_0^n + (Y_f - Y_0)e^{-kt}]^{1/n}}$ Parameter k define
the scale and shape
of the curveSchumacher $Y_t = \frac{Y_0 exp \left[\frac{k_1 et_0}{k_1 + t_0} \ln \left(\frac{Y_0}{Y_0}\right)\right]$ Parameter k define
the scale and shape
of the curveSchumacher $Y_t = Y_0 exp \left[\frac{k_1 et_0}{k_1 + t_0} \ln \left(\frac{Y_0}{Y_0}\right)\right]$ Parameter k define
the scale and shape
of the curveSchumacher $Y_t = Y_0 exp \left[\frac{k_1 et_0}{k_1 + t_0} \ln \left(\frac{Y_0}{Y_0}\right)\right]$ Parameter k define
the scale and shape
of the curveSchumacher $Y_t = Y_0 exp \left[\frac{k_1 et_0}{k_1 + t_0} \ln \left(\frac{Y_0}{Y_0}\right)\right]$ Parameter k define
the scale and shape
of the curveSchumacher $Y_t = Y_0 exp$

Wan's generalized monomolecular	$Y_{t} = Y_{f} - \frac{1}{\frac{b}{Y_{f}} + \left(\frac{1}{Y_{f} - Y_{0}} - \frac{b}{Y_{f}}\right) \exp(kt)}$	Parameters b and k define the scale and shape of the curve
Weibull	$Y_{t} = Y_{f} - (Y_{f} - Y_{0}) \exp[-(kt)^{n}]$	Parameter k define the scale and shape of the curve
Wingerd	$Y_t = Y_0 + bt + c\sqrt{t}$	Parameters b and c define the scale and shape of the curve

 Y_t is body weight (kg), t is age, Y_0 and Y_f are initial and asymptotic weights

Fitting a curve with sufficient data for each individual would be expected to smooth out the random deviations. Parameters estimated after fitting growth functions can be useful to understand how genetic and environmental factors affect growth attributes, to identify alternative strategies to improve the efficiency of meat production, to assess the genetic merit and growth potential of meat animals, to estimate nutrient requirements of animals based on their expected daily weight gain or to make management, husbandry and marketing decisions.

Different polynomial functions have been suggested to fit growth data, but the growth functions most extensively used are non-linear and belong to two main groups: exponential polynomials and asymptotic functions (Lopez, 2008). The simplest sigmoidal functions are characterized by a fixed inflection point (occurring at a fixed proportion of asymptotic weight), such as the logistic function or the Gompertz model. More complex and flexible sigmoidal functions are capable of describing either diminishing returns or sigmoidal patterns and, in this latter case, the inflexion point may be variable, occurring at any weight or time. A classical example is the Richards function, which, for some given values of its parameters, may result in the Mono-molecular, Logistic, Gompertz or Von Bertalanffy equations (Table 4.1).

4.2. Milk yield models base

A classical nonlinear curve is the representation of the time course of lactation. The lactation curve of the dairy cow shows a rapid increase in yield after parturition to a peak a few weeks later, followed by a gradual decline until the cow is dried off about 10 months after calving, giving a dry period of about 8 weeks (Fig.4.2).



Figure 4.2. Lactation curve in a dairy cow (fitted and observed data), (Lopez, 2008)

A similar trend has been observed in sheep and goats, although the shape of the curve may be slightly different, with a less sharp profile (a lower peak) and a faster or slower decline in the descending part of the curve. A number of mathematical equations have been proposed to describe the lactation curve, with the aim to fit them to milk yield data and to obtain estimates of some important performance features, such as initial yield after parturition, time to peak and production at that peak (maximum yield), duration of the lactation, total yield per lactation and persistency, defined either as extent to which peak yield is maintained or rate of decline in milk production after peak (Thornley and France, 2007; Lopez, 2008). Thus, accurate description of lactation curves has an important relevance to the dairy livestock industry for research, breeding and management, providing interesting information for determining nutrient allowances for lactating animals, estimating total yield per lactation from incomplete records and forecasting herd performance. Lactation equations represent a useful tool for developing and evaluating mechanistic models, aimed at explaining the main features of the milk production pattern in terms of known biology of the mammary gland during pregnancy and lactation.

An account of some time-dependent functions proposed to describe the lactation curve in dairy cows, sheep and goats is given in Table 4.2.

Name	Equation	Parameter meaning
Ali and Schaeffer	$Y_{t} = a + bt + ct^{2} - dlog(t) - k[log(t)]^{2}$	Parameters a, b, c, d, k define the scale and shape of the curve

Table 4.2. Equations used to describe the lactation curve

Cobby and Le Du	$Y_t = a(1 - e^{-ct}) - bt$	Parameters a, b and c define the scale and shape of the curve
Cobby and Le Du (double exponential)	$Y_t = a(1 - e^{-dt})e^{-bt} = a(e^{-bt} - e^{-ct});$ c=b+d	Parameters a, b, c and d define the scale and shape of the curve
Dhanoa	$Y_t = at^{kc}e^{-ct}$	Parameters a, k, c define the scale and shape of the curve
Dijkstra	$Y_{t} = \operatorname{aexp}\left[\frac{b}{c}(1 - e^{-ct}) - dt\right]$	Parameters a, b, c and d define the scale and shape of the curve
Emmans and Fisher	$Y_{t} = \operatorname{aexp}[-e^{d-bt}]e^{-ct}$	Parameters a, b, c, d define the scale and shape of the curve
Gaines of Brody (declining exponential)	$Y_t = ae^{-ct}$	Parameters a and c define the scale and shape of the curve
Guo and Swalve	$Y_t = a + b\sqrt{t} + clog(t)$	Parameters a, b and c define the scale and shape of the curve
Hyperbolic	$Y_t = a + b/t$	Parameters a and b define the scale and shape of the curve
Jenkins and Ferrell	$Y_t = ate^{-ct}$	Parameters a and c define the scale and shape of the curve
Morant and Gnanasakthy	$Y_{t} = \operatorname{aexp}\left(-\operatorname{bt} + \operatorname{ct}^{2} + \frac{d}{t}\right)$	Parameters a, b, c and d define the scale and shape of the curve
Nelder	$Y_t = \frac{t}{a + bt + ct^2}$	Parameters a, b, c define the scale and shape of the curve
Quadratic	$Y_t = a + bt - ct^2$	Parameters a, b, c define the scale and shape of the curve
Pollott	$Y_{t} = \left[a_{1} / \left(1 + \frac{1-b}{b} e^{-ct} \right) - a_{2} / \left(1 + \frac{1-d}{d} e^{-gt} \right) \right] (1 - e^{-ht})$	Parameters a_1 , a_2 , b, c, d, h and g define the scale and shape of the curve
Ratio of polynomials	$Y_{t} = \frac{a(t+b)}{(t+b)^{2} + c^{2}}$	Parameters a, b and c define the scale and shape of the curve
Sauvant and Fehr	$Y_t = d + at^b e^{-ct}$	Parameters a, b, c, d define the scale and shape of the curve
Scheeberger	$Y_t = a(t - t_0)^b e^{-c(t - t_0)}$	Parameters a, b, c define the scale and shape of the curve
Sikka	$Y_t = ae^{(bt-ct^2)}$	Parameters a, b, c define the scale and shape of the curve

Singh and Gopal	$Y_t = a - bt + d \ln(t)$ $Y_t = a + bt + ct^2 + d \ln(t)$	Parameters a, b, c and d define the scale and shape of the curve
Wilmink	$Y_t = a + be^{-kt} + ct$	Parameters a, b, c and k define the scale and shape of the curve
Wood	$Y_t = at^b e^{-ct}$	Parameters a, b, c define the scale and shape of the curve

 Y_t is a milk yield, t is time of lactation (day, week, month)

A large number of equations have been reported, ranging from simple linear functions (to fit only the declining phase of the lactation) to complex multiphasic models with a large number of parameters. Equations are presented attempting to group them according to their functional form. Most of the equations are empirical models, based on the similarity between observed lactation profiles and the fitted curves achieved with each equation. For instance, growth functions, such as logistic and Gompertz, written in their differential form and expressed as a function of time, have potential application as lactation equations, because the lactation curve is similar to the plot of growth rate (daily weight gain) against time (Thornley and France, 2007; Lopez, 2008).

4.2. Egg production models base

Another classical nonlinear curve is the time course of egg production in laying poultry, particularly in commercial laying hens. Typically, the curve is a representation of the average production rate of a flock of birds (Fig. 4.3), plotting the average percentage of birds in the flock laying an egg on a daily basis; where *eggs* is the total number of eggs laid in the flock each week and birds is the total number of hens in the flock) against time (either in weeks of age or in weeks after onset of laying). The curve is very similar to the lactation curve and several equations have been used to describe it, some of them similar to those used to fit lactation data (Thornley and France, 2007; Lopez, 2008).



Figure 4.3. Egg production curve for a commercial laying hen (Lopez, 2008)

Some of the models have been derived to represent the production cycle of each individual hen. Although the general pattern of this curve is similar, the discrete nature of the variable (number of eggs laid by a given hen weekly) results in a decreasing part of the curve with several successive descending steps or phases (Grossman and Koops, 2001). Table 4.3 shows nonlinear models used in egg production.

Name	Equation	Parameter meaning
Adams and Bell	$Y_t = \frac{a}{1+bc^t} - d(t-g)$	Parameters a, b, c, d, g define the scale and shape of the curve
Fialho and Ledur (piecewise or segmented model)	$\begin{split} \mathbf{Y}_{t} &= \mathbf{a} - 3\mathbf{a} [\frac{t_{p-t}}{t_{p}}]^{2} + 2\mathbf{a} [\frac{t_{p-t}}{t_{p}}]^{3}, \ 0 \leq \mathbf{t} \leq t_{p} \\ \mathbf{Y}_{t} &= \mathbf{a} - \mathbf{c} (\mathbf{t} - t_{p}), \qquad \mathbf{t} \geq t_{p} \end{split}$	Parameters a and c define the scale and shape of the curve
Grossman and Koops, 2001	$Y_t = a(\frac{1 - e^{-t}}{1 + e^{-t}}) - b(\frac{1 - e^{-t}}{1 + e^{-(t-c)}})$	Parameters a, b, c define the scale and shape of the curve
Grossman et at., 2000 (simplified egg production persistency model for the flock)	$ Y_{t} = a \left(\frac{b}{t_{2} - t_{1}}\right) \left[ln \left(\frac{e^{t/a} + e^{t_{1}/a}}{1 + e^{t_{1}/a}}\right) - ln \left(\frac{e^{t/a} + e^{t_{2}/a}}{1 + e^{t_{2}/a}}\right) \right] + acln \left(\frac{e^{t/a} + e^{(t_{2} + p)/a}}{1 + e^{(t_{2} + p)/a}}\right) $	Parameters a, b, c define the scale and shape of the curve
Grossman et at., 2000 (simplified egg production persistency model for an individual bird)	$Y_{t} = \frac{b}{t_{2}} t - a \frac{b}{t_{2}} \ln(\frac{e^{t/a} + e^{t_{2}/a}}{1 + e^{t_{2}/a}}) + acln(\frac{e^{t/a} + e^{(t_{2}+p)/a}}{1 + e^{(t_{2}+p)/a}})$	Parameters a and b define the scale and shape of the curve
Kovalonko and Tribat (exponential of a 2 nd , or 3 rd order polynomial)	$Y_{\rm T} = \exp(a + bt + ct^2 + dt^3)$	Parameters a, b, c, d define the scale and shape of the curve
Lokhorst	$Y_{t} = \frac{100}{1+ab^{t}} - (ct^{2} + dt + f)$	Parameters a, b, c, d, f define the scale and shape of the

Table 4.3. Equations used to describe the egg production curve

McMillan et at.1970 (compartmental model)	$Y_t = a(1 - be^{-ct}) e^{-kt}$	Parameters a, b, c, k define the scale and shape of the curve
McMillan, 1981 (double exponential)	$Y_t = a(e^{-bt} - e^{-ct})$	Parameters a, b, c define the scale and shape of the curve
McNally	$Y_t = at^b e^{-ct+d\sqrt{t}}$	Parameters a, b, c, d define the scale and shape of the curve
Minder and McMillan	$Y_t = a \frac{(1 - e^{-ct})}{c} e^{-kt}$	Parameters a, c, k define the scale and shape of the curve
Modified Compartmental	$Y_t = a(e^{-bt})/[1 + e^{-c(t-d)}]$	Parameters a, b, c and d define the scale and shape of the curve
Modified Gamma function	$Y_t = a (t - t_0)^b e^{-c(t - t_0)}$	Parameters a, b, c define the scale and shape of the curve
Narushin and Takma (ratio of polynomials)	$Y_t = \frac{at^3 + bt^2 + ct + d}{t^2 + ft + g}$	Parameters a, b, c, d, f, g define the scale and shape of the curve
Polynomials (3 rd or 4 th order)	$Y_t = a + bt + ct^2 + dt^3 + gt^4$	Parameters a, b, c, d, g define the scale and shape of the curve
Wood or Gamma function	$Y_t = at^b e^{-ct}$	Parameters a, b, c define the scale and shape of the curve
Yang (logistic – curvilinear)	$Y_t = \frac{ae^{-ct}}{1 + e^{-k(t-b)}}$	Parameters a, b, c, k define the scale and shape of the curve

curve

 Y_t is a measure of laying performance for a flock (egg production rate) or for an individual bird (eggs per week, perclutch or per month), t is time (bird's age or time from onset of laying)

Different comparative studies have concluded that performance of most of these equations fitting egg production data is satisfactory, attaining a similar goodnessof-fit with all functions.

4.4. Computer applications for nonlinear regression

There are many functions that are used to describe growth, lactation or changes in concentration of some substance over time. Parameters of nonlinear functions can be estimated using various numerical iterative methods.

4.4.1. SAS Example for Nonlinear Regression

The NLIN procedure of SAS will be used to estimate parameters describing growth by fitting a Brody curve to weights of an Angus cow (Kaps and Lamberson, 2004). The SAS program for nonlinear regression is as follows. Data represent weights of an Angus cow at ages from 8 to 108 months:

Weight, kg:	280	340	430	480	550	580	590	600	590 600
Age,months:	8	12	24	36	48	60	72	84	96 108

The Brody curve was fitted to the data:

$$Weight_i = A - (A - B)e^{-k(Age_i - 8)}$$

where:

A = the asymptotic (mature) weight

B = the estimated initial weight at Age₀ = 8 months

k = the maturing rate index

SAS program:

DATA Growth;

INPUT Age Weight @@;

DATALINES;

8	280	12	340	24	430	36	480	48	550
60	580	72	590	84	600	96	590	108	600

;

PROC NLIN;

PARMS A=600 B=280 k=0.05; MODEL Weight=A-(A-B)*exp(-k*(Age-8)); RUN

procedure is used. The PARMS statement defines parameters with their priors. Priors are guesses of the values of the parameters that are needed to start the iterative numerical computation. The MODEL statement defines the model: *Weight* is the dependent and *Age* is an independent variable, and *A*, *B*, and *k* are the parameters to be estimated.

Dependent Variable weight

Method: Gauss-Newton

Iterative Phase

				Sum of
Iter	А	В	k	Squares
0	600.0	280.0	0.0500	2540.5
1	610.2	285.8	0.0355	1388.7
2	612.2	283.7	0.0381	966.9
3	612.9	283.9	0.0379	965.9
4	612.9	283.9	0.0380	965.9
5	612.9	283.9	0.0380	965.9

NOTE: Convergence criterion met.

		Sum of	Mean		Approx
Source	DF	Squares	Square	F Value	Pr > F
Regression	3	2663434	887811	446.69	<.0001
Residual	7	965.9	138.0		
Uncorrected Total	10	2664400			
Corrected Total	9	124240			

Approx

Parameter	Estimate	Std Error	Approximate	95% Confidence Limi
А	612.9	9.2683	590.9	634.8
В	283.9	9.4866	261.5	306.3
k	0.0380	0.00383	0.0289	0.0470

Approximate Correlation Matrix

	А	В	k	
А	1.0000000	0.2607907	-0.8276063	
В	0.2607907	1.0000000	-0.4940824	
k	-0.8276063	-0.4940824	1.0000000	

Explanation: The title of the output indicates that the numerical method of estimation is by default Gauss-Newton. The first table describes iterations with

the current estimates together with residual sums of squares. At the end the program tells us that computation was successful (NOTE: Convergence criterion met). The next table presents an analysis of variance table including sources of variation (*Regression, Residual, Uncorrected Total, Corrected Total*), degrees of freedom (*DF*) Sums of Squares, Mean Squares, F Value and approximated P value (*Approx* Pr > F). The word 'approx' warns that for a nonlinear model the F test is approximate, but asymptotically valid. It can be concluded that the model explains the growth of the cow. The next table shows the parameter estimates together with their approximate Standard Errors and Confidence Intervals. The last table presents approximate correlations among the parameter estimates. The estimated curve is:

 $Weight_i = 612.9 - (612.9 - 283.9)e^{-0.038(Age_i - 8)}$

Fig. 4.4 presents a graph of the function with observed and estimated weights.



Figure 4.4. Weights over time of an Angus cow fitted to a Brody function (drawn by SAS); the linear presents estimated values and the points (•) observed weights.

4.4.2.STATISTICA Example for Nonlinear Regression

Statistics – Advanced Models – Nonlinear Estimation procedure will be used to estimate parameters describing growth by fitting a Brody curve to weights of an Angus cow given above. Nonlinear Estimation spreadsheet will be open as follow (Fig. 4.5):

Nonlinear Estimation: Spreadsheet1	8 23
Quick	ОК
User-specified regression, least squares	Cancel
User-specified regression, custom loss function	Ontions ▼
Quick Logit regression	
Quick Probit regression	🔁 Open Data
Exponential growth regression	SELECT
Piecewise linear regression	
You can also use the GLZ module to analyze continuous, binomial, dependent variables (e.g., for Logit or Probit regression).	or multi-nomial

Figure 4.5. Nonlinear Estimation Window in STATISTICA

It doesn't matter selecting 'User-specified regression, least squares' or 'Userspecified regression, custom loss function'. In second version also least squares will be given as default loss function. But you have chance to change it. Then typing function to be estimated we can realize the nonlinear estimation (Fig. 4.6).

Estimated function:	OK
Weight=A-(A-B)*EXP(-K*(Age-8))	Cano
	- 12 0
Loss function:	

Figure 4.6. Estimated and loss functions window

Output of the STATISTICA Package was given below:

```
Model is: Weight=A-(A-B) *EXP(-K*(Age-8))
Dependent variable: Weight
                                     Independent variables:
                                                                     1
Loss function: (OBS-PRED) **2
Final value: 965,89329887
                                                                              ,996105208
Proportion of variance accounted for:
                                                    ,992225585
                                                                      R =
                               Model: Weight=A-(A-B)*Exp((-k)*(Age-8)) (Spreadsheet1)
Dep. var: Weight Loss: (OBS-PRED)**2
                                Final loss: 965,89329887 R= ,99611 Variance explained: 99,223%
                      N=10
                                   Α
                                             В
                                                        k
                                 612,8654
                                           283,8943 0,037958
                      Estimate
```

Fig. 4.7 presents a graph of the function applied to the data.



Figure 4.7. Weights over time of an Angus cow fitted to a Brody function; points present estimated values

4.4.3. SPSS Example for Nonlinear Regression

Analyze – Regression – Nonlinear procedure will beused to estimate parameters describing growth by fitting a Brody curve to weights of an Angus cow given above. Nonlinear Regression spreadsheet is as follow (Fig. 4.8):

ta Nonlinear Regression		— X
Ø Age Ø Weight	Dependent	Loss Constraints Save Options
Pgrameters A(600) B(280) K(0.05)		

Figure 4.8. Nonlinear Regression Window in SPSS

Here we will add 'Weight' variable to the Dependent section, and type model to the Model Expression section. Then typing estimated function we can solve the nonlinear function.

SPSS output:

Nonlinear Regression Analysis

Iteration History [®]					
Iteration Number ^a	Residual Sum of		Parameter		
	Squares	А	В	k	
1.0	2540,499	600,000	280,000	,050	
1.1	1388,695	610,153	285,827	,036	
2.0	1388,695	610,153	285,827	,036	
2.1	966,891	612,152	283,717	,038	
3.0	966,891	612,152	283,717	,038	
3.1	965,895	612,891	283,911	,038	
4.0	965,895	612,891	283,911	,038	
4.1	965,893	612,863	283,893	,038	
5.0	965,893	612,863	283,893	,038	
5.1	965,893	612,866	283,894	,038	
6.0	965,893	612,866	283,894	,038	
6.1	965,893	612,865	283,894	,038	

Derivatives are calculated numerically.^b

a. Major iteration number is displayed to the left of the decimal, and minor iteration number is to the right of the decimal.

b. Run stopped after 12 model evaluations and 6 derivative evaluations because the relative reduction between successive residual sums of squares is at most SSCON = 1,000E-008.

Parameter Es	stimates
--------------	----------

Parameter	Estimate	Std. Error	95% Confidence Interval	
			Lower Bound	Upper Bound
А	612,865	9,268	590,949	634,781
В	283,894	9,487	261,462	306,326
k	,038	,004	,029	,047

Correlations of Parameter Estimates

	А	В	k
А	1,000	,261	-,828

B	,261 828	1,000		-,494 1.000		
<u>K -,828 -,494 1,000</u> ANOVA ^a						
Source		Sum of Squ	ares	df		Mean Squares
Regress	ion	2663434,107			3	887811,369
Residua	I	965,893			7	137,985
Uncorre	cted Total	2664400,000			10	
Correcte	ed Total	124240	,000		9	

Dependent variable: Weight^a

a. R squared = 1 - (Residual Sum of Squares) / (Corrected Sum of Squares) = ,992.

4.4.4. MINITAB Example for Nonlinear Regression

Stat – Regression – Nonlinear Regression procedure will be used to estimate parameters describing growth by fitting a Brody curve to weights of an Angus cow given above. Nonlinear Regression spreadsheet is as follow (Fig. 4.9):

Nonlinear Regression		X
C1 Age C2 Weight	Response: Weight Expectation Function Use Calculator Use Catalog Use Calculator Egit directly: A-(A-B)*exp(-k*(Age-8)) A-(A-B)*exp(-k*(Age-8)) Perdiction Parameters Options Prediction Graphs Results Storage	*
Help	<u>ō</u> k c	ancel

Figure 4.9. Nonlinear Regression Window in MINITAB

Here we will add Weight variable to the 'Response' section, and type model to the 'Edit directly' section. Using Parameter button we have to assign starting values for parameters (Fig. 4.10). Then typing estimated function we can solve the nonlinear function.

onlinear Regressio	on: Parameters			×
Function				
A-(A-B)*exp(-k*	(Age-8))			
equired starting va	lues:	Lockod		
A	values	500	-	
B		280	-	
k	0	.05	-	
ptional <u>c</u> onstraints Parameter A	Lower Bound	Upper Bound	-	
В				
k				

Figure 4.10. Starting values assignment for model parameters

MINITAB Output:

Nonlinear I Method	Regression	: Weight = $A - ($	(A - B) * exp(-B)	k * (Age - 8))	
Algorithm	Ga	uss-Newton			
Max iterati	ons	200			
Tolerance Starting Va	llues for Pa	0,00001 arameters			
Parameter	Value				
А	600				
В	280				
k Equation Weight = 6 Parameter 1	0,05 12,865 - (6 Estimates	512,865 - 283,89	14) * exp(-0,03	79581 * (Age -	8))
Parameter	Estimate	SE Estimate			
А	612,865	9,26823			
В	283,894	9,48661			
k	0,038	0,00383			

Summary	
Iterations	7
Final SSE	965,893
DFE	7
MSE	137,985
S	11,7467



Fig. 4.11 presents a graph of the function with observed and estimated weights.

Figure 4.11. Weights over time of an Angus cow fitted to a Brody function (drawn by MINITAB); the linear presents estimated values and the points (•) observed weights

5. CONCLUSION AND RECOMMENDATIONS

5.1. Conclusions

In this study, general information of nonlinear regression models, commonly used families of nonlinear regression functions, statistical assumptions and inferences for nonlinear regression and parameter estimation in these models was given and growth models, lactation curves and egg weight and production models were investigated in the frame of this information.

Selection of appropriate model with minimum parameters is very important in various model applications to the same data. It was given a range of model selection criteria in this study for this purpose. Also, computer applications for nonlinear models were introduced and step-by-step solving process was illustrated.

In the end of the study it was given the base of nonlinear regression models with parameters and specific application areas in animal science.

5.2. Recommendations

Distinction of nonlinear models from linear models is that the choice of the main function is critical and this can be difficult without wide knowledge of regression analysis.

This review of nonlinear models applied in animal science will make the task of choosing candidate models easier.

The created base of nonlinear regression models used in animal science will be widening by the researches in the future.

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Certificates	Name. City. Country	Graduation year
High school		
University	BachcesehirMustansiriya University/Baghdad	1980
Graduate School		

WORK EXPERIENCE

Year	Organization	Job

AREA OF SPECIALIZATION

FOREIGN LANGUAGES

Arabic-Kurdish-English

OTHER FEATURES YOU WANT TO SPECIFY

PUBLICATIONS