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COMPARATIVE ANALYSIS OF INDIVIDUAL GROWTH CURVES IN BROILER CHICKENS

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Abstract: In this study, growth curves for 62 individual broiler chickens were obtained by evaluating weekly live weight data collected over a six-week period, using several growth models, including Gompertz, Gamma, Logistic, Richards, Bertalanffy, Cubic, Cubic Piecewise, Wilmink, Wood, Exponential, Monomolecular, and McNally. In the comparison of these growth curves, various statistical criteria, such as mean square error, adjusted coefficient of determination, accuracy factor, bias factor, Durbin-Watson statistic, Akaike information criterion, adjusted Akaike information criterion, and Bayesian information criterion, were employed. The Gompertz model provided the best fit across all criteria, accurately representing the growth curve of broiler chickens ($\bar{R}^2 = 0.99$, AIC= 62.42, CAIC: 76.42, BIC: 57.50). Similar to other studies in the literature, this model has been shown to produce reliable results under varying environmental and genetic conditions. The obtained data provide significant contributions to decision support systems in growth monitoring, genetic analysis, and the development of production strategies.

Keywords: Growth curves, Broiler chickens, SAS

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1. Introduction

Poultry farming plays a critical role in meeting the increasing global demand for animal protein. Broiler chickens, in particular, have become one of the most preferred species in industrial production systems due to their rapid growth capacity, short production cycles, and high feed conversion ratios (Bessei, 2006; Akinsola et al., 2021). In this context, accurately monitoring and modeling the growth performance of broiler chickens is crucial not only for enhancing economic efficiency but also for improving genetic selection and feeding programs (Silambarasan et al., 2012).

Animal growth modeling is typically carried out through mathematical growth curves that describe the changes in live weight over time. These models define the biological stages of growth (initial, rapid growth, plateau phase) while also quantifying individual performance differences (Knízetová et al., 1991). However, most growth modeling is often done using aggregate data, overlooking the need to model individual weight changes. Individual modeling provides more accurate insights into the growth rate, genetic potential, and environmental influences on each bird, enabling more personalized and precise predictions. Therefore, individual-based modeling studies are critical for optimizing production systems and making more informed decisions (Buzala and Janicki, 2016; Akinsola et al., 2021).

This study presents a comparative analysis of twelve different growth models (Gompertz, Gamma, Logistic, Richards, Bertalanffy, Cubic, Piecewise Cubic, Wilmink, Wood, Exponential, Monomolecular, McNally) using individual live weight data to gain a more detailed understanding of broiler chicken growth. Each of these widely used models offers distinct parametric structures for different growth phases, and their performance in modeling individual data sets has been evaluated. The findings will facilitate more accurate modeling of the growth process in broiler chickens and demonstrate how individual based modeling can contribute to decision support processes in broiler chickens production.

2. Materials and Methods

The material of this study consists of live weight data of broiler chickens raised at the Poultry Farming Unit of the Research and Application Farm, Faculty of Agriculture, Çukurova University. A total of 62 broiler chickens were included in the study, with the live weight of each bird measured individually from week 0 (hatch) to week 6 on a weekly basis. The mean and standard deviation values of the obtained data set are presented in Table 1.

In the modeling of the growth process, twelve growth models, which are frequently used in the literature and possess different structural characteristics, were evaluated. These models include Gompertz, Gamma, Logistic, Richards, Bertalanffy, Cubic, Piecewise Cubic, Wilmink, Wood, Exponential, Monomolecular, and McNally models. The mathematical formulas for each model are provided in Table 2.

Table 1. Mean and standard deviation values for the broiler chickens

	Mean and Standard Deviation
1.Week	42.02±2.10
2.Week	223.91±18.21
3.Week	548.8±722.53
4.Week	1151.64±74.30
5.Week	1509.23±137.49
6.Week	2063.3±5124.35

Table 2. Equations used in modeling growth curves

Model Names	Equality
Gompertz	$\mathrm{Y_t = \beta_0 exp(-\beta_1 exp(-\beta_2 t))}$
Gamma	$\mathrm{Y_t = {\beta_0}^{\beta_1}(e^{-\beta_2 t})}$
Logistic	$\mathrm{Y_t = \beta_0(1+\beta_1 exp(-\beta_2 t))^{-1}}$
Richard	$\mathrm{Y_t = \beta_0(1+\beta_1 exp(-\beta_2 t))^{\beta_3}}$
Bertalanffy	$\mathrm{Y_t = \beta_0\left(1-\beta_1 exp(-\beta_2 t)\right)^3}$
Cubic	$Y_t=\beta_0+\beta_1 t+\beta_2 t^2+\beta_3 t^3$
Cubic Piecewise	$Y_t=\beta_0+\beta_1 t+\beta_2 t^2+\beta_3 t^3+\beta_4(t-a)^3$
Wilmink	$\mathrm{Y_t = \beta_0 + \beta_1 t + \beta_2 e^{-0.05t}}$
Wood	$\mathrm{Y_t = \beta_0 t^{\beta_1} * e^{-\beta_2}t}$
Exponential	$\mathrm{Y_t = \beta_0 * e^{\beta_1}t}$
Monomolecular	$\mathrm{Y_t = \beta_0(1-e^{-\beta_1 t})}$
McNally	$\mathrm{Y_t = \beta_0 t^{\beta_1} exp(-\beta_2 t + \beta_3 t^{1/2})}$

In the equations given in Table 2, β₀, β₁, β₂, β₃, and β₄, represent the parameters in the equations, t represents the time and Y_t represents the live weight gains at the t-th time (Şahin and Efe 2010; Yavuz et al., 2019; Yalçınöz and Şahin; 2020).

Table 3. Model comparison criterions

Criterion	Equality
Mean Square Error	$\mathrm{MSE = ESS/EDF}$
Adjusted Coefficient of Determination	$\mathrm{\overline{R}^2 = 1-(1-R^2)(n-1/(n-p-1))}$
Accuracy Factor	$\mathrm{AF = 10^{\sum_{i=1}^{n}\lvert log(\widehat{Y_i}/Y_i)\rvert/n}}$
Bias Factor	$\mathrm{BF = 10^{\sum_{i=1}^{n} log(\widehat{Y_i}/)/n}}$
Durbin-Watson Value	$\mathrm{DW = \dfrac{\sum_{i=2}^{n}(e_1-e_2)^2}{\sum_{i=1}^{n} e_1^2}}$
Akaike Information Criterion	$\mathrm{AIC = nxln\left(\dfrac{MSE}{n}\right) + 2k}$
Corrected Akaike Information Criterion	$\mathrm{CAIC = nxln\left(\dfrac{MSE}{n}\right) + \left(\dfrac{n(n+p)}{n-p-2}\right)}$
Bayesian Information Criterion	$\mathrm{BIC = nxln\left(\dfrac{MSE}{n}\right) + kln(n)}$

MSE: Mean Square Error, ESS: Error Sum of Squares, EDF: Error Degrees of Freedom, n: sample size, p: number of independent variables, $\widehat{Y_i}$: estimated value, Y_i: observation value, e_i: error term and k: number of parameters.

The goodness of fit of each model to the observed data was evaluated using various statistical comparison criterions, including mean square error, adjusted coefficient of determination, accuracy factor, bias factor, Durbin-Watson statistic, Akaike information criterion, adjusted Akaike information criterion, and Bayesian information criterion. Details of these comparison criterions are provided in Table 3 (Tolun et al., 2023; Tolun et al., 2024; Çetenak et al., 2024).

3. Results and Discussion

In this study, the arithmetic means and standard errors of the model comparison criteria are presented in Table 4, and the parameter estimate values are provided in Table 5. The growth predictions made by each model based on the mean values are graphically shown in Figure 1, allowing for a visual assessment of the models' fit to the observed data.

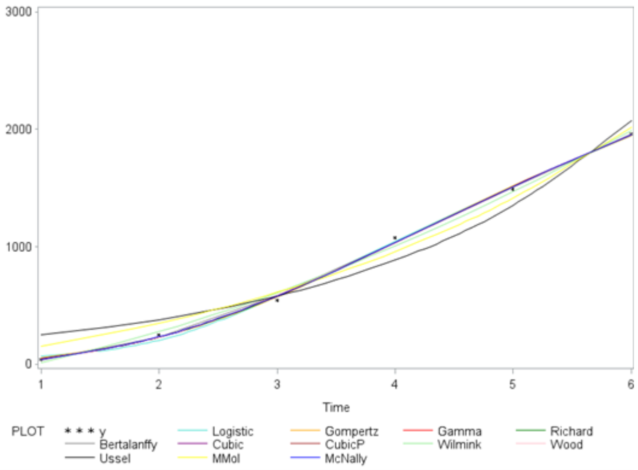

Figure 1. Growth curves obtained for all models.

Table 4. Model comparison and evaluation criterions

Models	MSE	CCD	AIC	CAIC
Gompertz	5533.27±1084.80	0.99±0.01	62.42±2.74	76.42±2.74
Gamma	14689.11±3535.81	0.99±0.001	63.41±2.11	77.41±2.11
Logistic	14094.11±3594.93	0.99±0.003	63.24±2.05	77.24±2.05
Richard	20282.83±5284.30	0.99±0.004	65.15± 2.09	111.82±2.09
Bertalanffy	19808.81±6831.76	0.99±0.002	66.28±2.26	112.95±2.26
Cubic	51392.75±31097.3	0.90±90.02	63.56±2.50	77.56 ±2.50
Cubic Piecewise	18059.42±4613.17	0.99±0.003	64.74±1.94	111.41±1.94
Wilmink	16782.94±2720.14	0.99±0.004	69.86±1.14	116.53±1.14
Wood	12409.94±3246.48	0.99±0.003	63.81± 1.97	77.81±1.97
Exponential	70797.88±18939.0	0.99±0.01	79.42±0.97	93.42±0.97
Monomolecular	33752.85±7410.72	0.99±0.003	74.50±0.98	88.50±0.98
McNally	172174.8±55500.3	0.99±0.04	73.07±3.21	87.07±3.21
	BIC	DW	AF	BF
Gompertz	57.50±2.11	2.01±0.1	1.03±0.08	1.05±0.04
Gamma	58.20±2.05	2.28±0.5	1.03±0.01	1.08±0.02
Logistic	58.02±2.03	1.98±0.4	1.03±0.01	1.09±0.01
Richard	57.91±2.14	1.88±0.4	1.03±0.02	1.01±0.02
Bertalanffy	59.04±2.26	2.12±0.2	1.05±0.10	1.06±0.05
Cubic	58.65±2.48	2.22±0.3	1.13±0.04	1.11±0.02
Cubic Piecewise	58.33±1.91	2.46±0.6	1.12±0.04	1.11±0.02
Wilmink	62.62±1.11	1.65±0.4	1.08±0.04	1.01±0.07
Wood	58.90±1.90	2.58±0.7	1.04±0.01	1.05±0.02
Exponential	74.51±0.94	2.10±0.2	1.08±0.01	1.06±0.01
Monomolecular	69.59±0.99	2.17±0.3	1.06±0.01	1.04±0.01
McNally	68.16±3.14	2.06±0.1	1.04±0.04	1.02±0.02

MSE: Mean Square Error, **CCD:** Corrected Coefficient of Determination, **AIC:** Akaike Information Criterion, C**AIC:** Corrected Akaike Information Criterion, **BIC:** Bayesian Information Criterion, **DW:** Durbin-Watson, **AF:** Accuracy Factor, **BF:** Bias Factor.

Table 5. Parameters estimates of growth curves

Models	a	b	c	d	e
Gompertz	3141.62±110.18	6.54±0.27	0.42±0.02	-	-
Gamma	12.20±3.26	1.31±0.35	0.17±0.04	-	-
Logistic	52.14±4.98	150.68±20.46	0.13±0.01	-	-
Richard	3156.92±114.53	0.28±0.13	0.45±0.03	0.15±0.04	-
Bertalanffy	3613.18±112.81	1.08±0.03	0.26±0.01	-	-
Cubic	98.27±47.79	-235.87±50.98	144.27±24.88	-11.61±2.12	-
Cubic Piecewise	96.12±45.1	-212.14±54.17	140.19±26.11	-10.13±2.15	0.001±0.008
Wilmink	2684.00± 7717.51	405.32±108.32	2923.40±781.31	-	-
Wood	48.19±2.55	3.02±0.208	0.31±0.03	-	-
Exponential	160.62±3.38	0.42±0.004	-	-	-
Monomolecular	-451.40±18.75	-0.28±0.007	-	-	-
McNally	120.55±31.06	2.64±0.51	0.48±0.13	1.59±1.17	-

According to the comparison criterions provided in Table 4, the models with the lowest mean square error values are Gompertz, Logistic, and Gamma, in that order. This result indicates that these models have higher predictive power compared to the others.

When evaluating the adjusted coefficient of determination, all models produced results at the 0.99 level. This suggests that the models have high explanatory power and exhibit a strong fit to the observed data.

The Durbin-Watson statistic yielded values close to 2 for all models. This finding indicates that there is no significant autocorrelation among the error terms, and the models meet the assumption of independent errors. The accuracy and bias factors of the models being close to 1 further support that the predictions are reliable and unbiased.

According to the evaluations of Akaike information criterion, adjusted Akaike information criterion, and Bayesian information criterion, the Gompertz, Logistic, and Gamma models obtained lower values compared to the other models.

When all metrics are considered together, it can be concluded that the Gompertz model best represents the live weight data of broiler chickens.

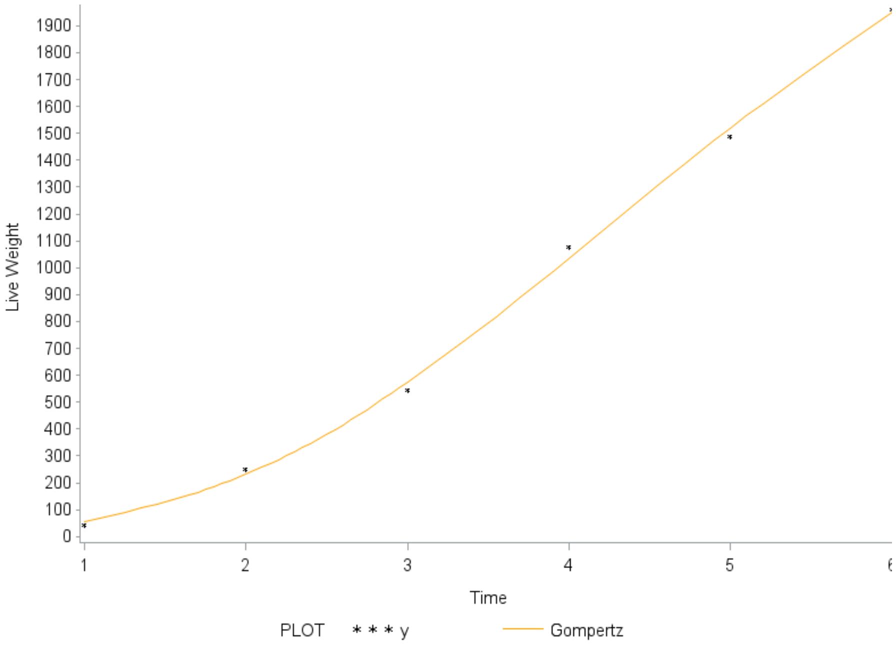

Figure 2. Growth curve obtained for the Gompertz model.

The predicted growth curve for this model is shown in Figure 2, and its high fit to the observed data is visually confirmed.

The results obtained indicate that the Gompertz model demonstrated stronger performance in terms of statistical fit compared to the other models. This is attributed to the model's flexible structure, which allows it to effectively represent the different growth phases (initial, rapid growth, and plateau phase).

The use of various statistical criteria, including mean square error, adjusted coefficient of determination, Durbin-Watson statistic, accuracy and bias factors, as well as Akaike, adjusted Akaike, and Bayesian information criteria, has enabled a comprehensive evaluation of both the statistical adequacy and predictive power of the models.

The Gompertz model emerging as the most suitable model in this study is consistent with findings from previous research. Ricklefs (1967), Tzeng and Becker (1981), Anthony et al. (1986), Anthony et al. (1991), Barbato (1991), Marayuma (1998), Şengül and Kiraz (2005), Nooris et al. (2007), Demuner et al. (2017), and Şengül et al. (2024) have all reported that the Gompertz model is frequently used to represent poultry growth data.

4. Conclusion

The findings of this study reveal that the Gompertz model outperforms the other models in terms of overall fit and predictive success. In criteria such as mean square error, adjusted coefficient of determination, accuracy factor, bias factor, Durbin-Watson statistic, and information criteria, the Gompertz model was identified as the statistically most suitable model. Its low error rate and high explanatory power indicate that it effectively represents the growth process of broiler chickens.

The results emphasize that model selection is of great importance not only for biological relevance but also for statistical validity. The Gompertz model's ability to balance different growth phases, its simple structure, and high predictive accuracy make it a valuable tool for applied animal science research and production planning. In this context, its use as a decision support tool in areas such as feeding strategies, determining slaughter times, and economic efficiency analysis is considered to be beneficial.

Future research should focus on testing the performance of the Gompertz model in different genetic lines, environmental conditions, and production systems to assess its generalizability. Additionally, comparing parametric models with modern approaches such as machine learning and Bayesian methods could contribute to the development of more flexible and effective solutions in growth modeling.

Author Contributions

The percentages of author' contributions are presented below. The author reviewed and approved the final version of the manuscript.

	İ.G.
C	100
D	100
S	100
DCP	100
DAI	100
L	100
W	100
CR	100
SR	100
PM	100
FA	100

C=Concept, D= design, S= supervision, DCP= data collection and/or processing, DAI= data analysis and/or interpretation, L= literature search, W= writing, CR= critical review, SR= submission and revision, PM= project management, FA= funding acquisition.

Conflict of Interest

The author declare that there is no conflict of interest.

Ethical Consideration

Ethics committee approval was not required for this study because of there was no study on animals or humans.

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