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ARTICLE

Bayesian modeling of the Gompertz curve for meat quails growth data considering different error distributions

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Abstract

This study applied the Gompertz model to quail growth data, assuming symmetric and asymmetric homoscedastic and heteroscedastic error distributions (Normal, *t*-Student, Skew normal, and Skew *t*), under a Bayesian framework. Model selection criteria included the Bayesian Deviance Information Criterion (DIC) and the analysis of residual standard deviation (σ), as well as graphical assessment of the fit. For both homoscedastic error structures (males: DIC=7.186; σ=10.73) and (females: DIC=5.572; σ=11.88) as well as heteroscedastic structures (males: DIC=6.493; σ=0.795) and (females: DIC=4.405; σ=0.824), the best fits were obtained by considering the Skew t distribution for errors. In homoscedastic fits, significant residual asymmetry (λ) was observed only for female quails (CI(λ)=[-8.039;-0.340]), whereas in heteroscedastic fits, the parameter was not significant for both sexes. Additionally, heteroscedasticity (δ) captured in the fits was significant for both sexes (males: CI(δ)=[1.66;2.13] and females: CI(δ)=[1.80;2.26]). Understanding animal growth is crucial for optimizing management and feeding practices, reducing time and costs in production. In this case, the use of nonlinear models considering heteroscedastic and/or asymmetric residual structures contributes to greater accuracy in decision-making.

Keywords: Quail meat; Asymmetric distributions; Heteroscedasticity; Homoscedasticity.

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1. Introduction

Understanding the process of animal growth is of great importance for production systems, as it allows for the identification of moments in the animal's life when growth occurs more or less rapidly, and even when growth stops. This makes it possible to adopt different nutritional management strategies at various stages of animal growth. Studying this field involves summarizing information about the lives of animals using nonlinear regressions applied to a set of mathematical parameters with biological interpretations (Lopes *et al.,* 2016).

In the literature, there are several nonlinear models that describe animal growth, and particularly for quails, models such as Brody (B), Gompertz (G), Logistic (L), and Von Bertalanffy (V), among others, can be used (Ribeiro *et al.,* 2020; Rossi *et al.,* 2017). The choice of using nonlinear models is driven by the fact that the entire growth process can be described by a few parameters, which are biologically meaningful (Louzada *et al.,* 2014).

Assuming normality and independence of residuals for nonlinear regression models is a common practice because it makes the models easily applicable in widely used statistical software. However, the assumption of normality is quite restrictive and lacks robustness when data exhibits deviations from normality, particularly in the presence of skewness. For such situations, there are proposals in the literature, such as asymmetric distributions (Azzalini, 1985; Campos & Andrade, n.d.; Louzada *et al.,* 2014; Sahu *et al.,* 2003).

Frequentist approaches tend to encounter problems in parameter estimation and convergence, primarily due to the bounded parameter space for asymmetry coefficients. Alternatively, the Bayesian approach is more flexible and may provide better inferences (Campos, 2011; Gelman *et al.,* 2013). In this regard, the use of alternative methods, such as Bayesian methods, can lead to more consistent and parsimonious results.

The aim of this study was to analyze the fitting of the Gompertz growth curve to quail growth data, separated by sex, considering both symmetric and asymmetric distributions (Normal, t-Student, Skew normal, and Skew t) within homoscedastic and heteroscedastic error structures under a Bayesian framework.

2. Matherials and methods

2.1 Data

The data were collected through an experiment conducted in accordance with the regulations proposed by the Committee for Animal Experimentation Ethics of the State University of Maringá, Paraná (UEM) under protocol number 061/2012 (Grieser, 2012). A total of 400 broiler quails Japanese (*Coturnix Coturnix Coturnix*) were used, with 238 males and 162 females. The experimental period lasted from 1 to 42 days, with weekly weighings. Individual weight measurements were monitored using a precision balance (1500g x 0.01g). This process allowed for the empirical observation of growth curves for quails by sexes during the specified period.

2.2 Modeling

In the literature, various models and parameterizations are available to fit different animal growth curves. Some models provide a biological explanation for their parameters. It is also possible to assume different error distributions and adapt their dispersion over time. In this study, the Gompertz growth curve will be considered for modeling with different distributions for errors, as well as homoscedastic and heteroscedastic structures.

The presence of homogeneity of variances was verified by Levene test (Almeida *et al.,* 2008).

The Gompertz (1825) model, is given by

$$y_i = \beta_1 e^{-\beta_2 e^{-\beta_3 x_i}} + \epsilon_i \tag{1}$$

where β_1 is the parameter representing the asymptotic weight value of the response variable, β_2 is a constant representing the initially observed value, and β_3 is the growth rate of the response variable, indicating the speed at which the value approaches the maximum observed value, thereby determining the efficiency of growth.

2.3 Asymmetric Errors

The asymmetric *t*-Student distribution is an extension of the *t*-Student distribution (T) and is used in cases where, in addition to residual asymmetry, there are extreme values present, that is, data with asymmetric and/or heavy-tailed structures. It is more effective than the asymmetric normal distribution Azzalini (1985) because it is more robust in such cases (De La Cruz & Branco, 2009; Mangueira *et al.*, 2016).

Godoi (2007) shows that if a random variable Z is referred to as the standard asymmetric *t*-Student or Skew *t* (ST) with skewness parameter λ and kurtosis ν, its probability density function is given by:

$$f_z(Z) = 2t_\nu(z)T_{\nu+1}\left(\lambda_z\sqrt{\frac{1+\nu}{\nu+z^2}}\right) \tag{2}$$

in which t_ν is the probability density function of a standard *t*-Student distribution with ν degrees of freedom, $T_{\nu+1}$ is the cumulative distribution function of a standard *t*-Student distribution with $\nu + 1$ degrees of freedom, and $-\infty < z < +\infty$.

The parameter λ represents the shape of the distribution. If $\lambda < 0$, there is negative skewness; if $\lambda > 0$, there is positive skewness, and if $\lambda = 0$, the distribution is symmetric and equivalent to the *t*-Student distribution and for $n \to \infty$, the normal or gaussian distribution (N).

2.4 Homoscedastic Errors

The Gompertz model adjustments were carried out considering homoscedastic error distributions: Normal (N), *t*-Student (T), Skew normal (SN), and Skew *t* (ST) for each of the models (Amaral, 2009; Azzalini, 1985; Cancho *et al.*, 2010; De La Cruz & Branco, 2009; Freitas, 2005; Louzada *et al.*, 2014; Rossi *et al.*, 2017; Rossi & Santos, 2014; Sahu *et al.*, 2003).

2.5 Heteroscedastic Errors

In this stage, the best fit from the previous step was considered, but now with a multiplicative heteroscedastic structure (Guler *et al.*, 2022; Rossi *et al.*, 2017), where the variance of errors is proportional to an unknown power (δ) of one of the explanatory variables:

$$Var(\epsilon_i) = \sigma_i^2 = \sigma^2 x_i^\delta \tag{3}$$

where δ is the degree of heteroscedasticity and σ^2 is a common standard among all error variances (Buzolin, 2005; Mazucheli *et al.*, 2011).

2.6 Estimation

All inferential procedures were conducted using Bayesian methods, and for this purpose, the data were analyzed in the *R* software (R Development Core Team, 2023) through the *BRugs* package (Ligges, 2006) linked to *OpenBUGS* (Spiegelhalter *et al.,* 2007). The Gibbs Sampler algorithm was employed within the MCMC (Markov Chain Monte Carlo) framework for simulations.

The modeling used was proposed by De La Cruz & Branco (2009), which makes the Skew normal (SN) distribution a particular case of the Skew *t* (ST) (Rossi & Santos, 2014).

For the implementation, the following hierarchical structure is employed in the models:

$$y_{ij}|x_{ij}, \beta, \sigma^2, \lambda, \nu, \delta_{ij}, z_{ij} \sim N\left(f(x_{ij}, \beta) - \mu_{\epsilon_{ij}} + \lambda z_{ij}, \delta_{ij}^{-1}\sigma^2\right) \tag{4}$$

where $Z_{ij} \sim N(0, \delta_{ij}^{-1})I_{(z_{ij}>0)}$ and $\delta_{ij} \sim Gamma\left(\frac{\nu}{2}, \frac{\nu}{2}\right)$, and assuming $\beta \sim T(0, 10^{-2}, 2)$, $\sigma \sim U(0, 100)$, $\lambda \sim T(0, 10^{-2}, 2)$, and $\nu \sim Exp(10^{-1})I_{(2.5,\infty)}$ as prior distributions.

For $\delta = 0$ and excluding the prior distribution for ν, the errors follow a Skew normal (SN) distribution.

Frequentist estimates were used as initial values for the model parameters. A total of 110,000 iterations were generated, with 10,000 discarded to avoid initial effects. To eliminate autocorrelation between iterations, a spacing of 10 points was used. Thus, a final chain with 10,000 observations was obtained for each parameter. The *coda* package (Plummer *et al.,* 2006) was used to assess the convergence of chains, considering the criteria of Heidelberger & Welch (1983) (1983) and Geweke (1992).

The model selection criterion used was the Bayesian Deviance Information Criterion (DIC), in which lower values indicate higher plausibility for the model, that is, a better fit to the data (Spiegelhalter *et al.,* 2002).

Checking the proper fit of the model to the data was performed using probability quantile-quantile (QQ-Plot) graphs, in which linear patterns are expected (Fernandes, 2019).

The significance testing of all model parameters, particularly skewness (λ) and heteroscedasticity (δ), is determined by examining whether or not the zero value falls within the corresponding Credibility Interval (CI) of the parameters (95% CI=$[P_{2.5\%}; P_{97.5\%}]$). In other words, if CI(λ) contains zero, the distribution is considered symmetric; otherwise, it is considered asymmetric. Similarly, for heteroscedasticity, if CI(δ) contains zero, then homoscedastic adjustment is sufficient, whereas if it does not contain zero, it suggests a heteroscedastic adjustment.

3. Results and Discussion

A descriptive summary of the mean weight and standard deviation of observations in the analyzed quails, at each age by sex, is presented in Table 1.

The Levene's test ($p < 0.01$) supports the presence of heteroscedasticity in the data for both sexes.

Table 1. Mean weight (g) and standard deviation (SD) at different ages (days) of the quails

Sex		Age						
		1	7	14	21	28	35	42
Male	weight	8.86	31.36	78.19	131.41	182.20	216.10	238.10
	SD	0.68	6.56	11.50	16.10	19.90	19.37	23.49
Female	weight	8.80	32.61	81.60	137.67	190.40	236.60	282.80
	SD	0.73	6.31	12.30	17.24	27.19	28.16	34.38

It is possible to observe an increasing trend in the standard deviation as age increases in both sex, indicating a potential presence of heteroscedasticity in the data.

Female quails exhibit a greater variation in growth rate compared to male quails, showing a higher standard deviation in six out of seven measurements taken (Figure 1)

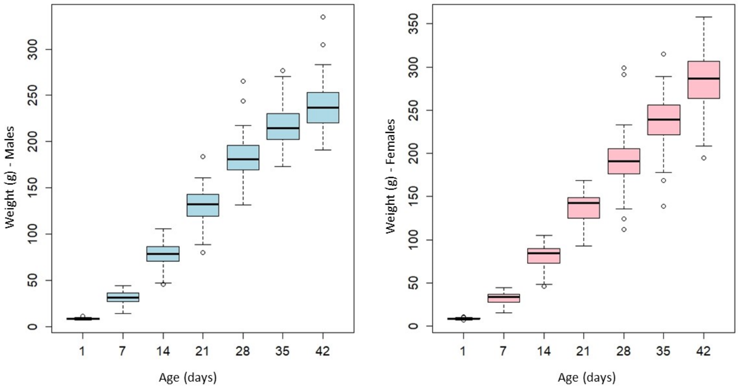

Figure 1. Boxplot of quail weights (g) by sexes.

All chains of the posterior distributions of parameters in the assumed models were assessed using the criteria of Heidelberger & Welch (1983) and Geweke (1992).

In Tables 2 and 3, parameter estimates of the considered models and DIC values are presented for both sexes, considering homoscedastic and heteroscedastic error structures, respectively.

Table 2. Parameter estimates of the Gompertz model considering distribution Normal, *t*-Student, Skew normal and *t*-Skew for errors homoscedastic

Homoscedastic					
Error	Parameter	Male		Female	
		Mean (SD)	$P_{2.5\%} - P_{97.5\%}$	Mean (SD)	$P_{2.5\%} - P_{97.5\%}$
	β_1	274.293 (3.560)	(267.819 ; 281.898)	368.436 (10.658)	(348.792 ; 391.356)
	β_2	3.786 (0.086)	(3.626 ; 3.963)	3.648 (0.087)	(3.488 ; 3.826)
N	β_3	0.0788 (0.0019)	(0.0747 ; 0.0826)	0.0615 (0.0024)	(0.0567 ; 0.0665)
	τ	0.0039 (0.0001)	(0.0036 ; 0.0043)	0.0021 (0.0001)	(0.0019 ; 0.0024)
	σ	15.854 (0.375)	(15.145 ; 16.609)	21.560 (0.604)	(20.431 ; 22.793)
	DIC	7,381		5,841	
6*T	β_1	269.602 (3.134)	(263.902 ; 275.972)	358.057 (7.880)	(343.521 ; 375.219)
	β_2	3.754 (0.059)	(3.641 ; 3.876)	3.726 (0.052)	(3.625 ; 3.827)
	β_3	0.0797 (0.0015)	(0.0766 ; 0.0827)	0.0652 (0.0017)	(0.0614 ; 0.0686)
T	ν	3.300 (0.487)	(2.493 ; 4.387)	2.230 (0.190)	(2.008 ; 2.713)
	τ	0.0087 (0.0009)	(0.0071 ; 0.0107)	0.0076 (0.0008)	(0.0060 ; 0.0093)
	σ	17.696 (1.984)	(15.282 ; 22.348)	54.834 (86.468)	(23.954 ; 173.716)
	DIC	7,260		5,674	
6*SN	β_1	274.390 (3.503)	(267.570 ; 281.615)	369.906 (9.645)	(351.815 ; 390.011)
	β_2	3.634 (0.087)	(3.466 ; 3.811)	3.793 (0.107)	(3.594 ; 4.013)
	β_3	0.076 (0.0019)	(0.073 ; 0.080)	0.0629 (0.0024)	(0.0583 ; 0.0677)
SN	λ	16.175 (1.685)	(12.591 ; 19.128)	-20.858 (4.133)	(-25.820 ; -11.847)
	τ	0.0066 (0.0008)	(0.0051 ; 0.0083)	0.0034 (0.0005)	(0.0024 ; 0.0044)
	σ	12.343 (0.748)	(10.966 ; 13.879)	17.071 (1.288)	(14.922 ; 20.243)
	DIC	7,249		5,744	
6*ST	β_1	270.182 (3.259)	(263.884 ; 276.759)	355.707 (7.346)	(342.061 ; 370.845)
	β_2	3.720 (0.085)	(3.560 ; 3.894)	3.856 (0.086)	(3.690 ; 4.034)
	β_3	0.0792 (0.0018)	(0.0756 ; 0.0829)	0.0666 (0.0019)	(0.0630 ; 0.0703)
ST	λ	1.116 (1.977)	(-2.773 ; 5.003)	-4.247 (1.968)	(-8.039 ; -0.340)
	ν	3.403 (0.504)	(2.615 ; 4.557)	2.694 (0.176)	(2.505 ; 3.159)
	τ	0.0087 (0.0008)	(0.0071 ; 0.0106)	0.0071 (0.0008)	(0.0057 ; 0.0087)
	σ	10.727 (0.544)	(9.692 ; 11.832)	11.885 (0.644)	(10.673 ; 13.176)
	DIC	**7,186**		**5,572**	

Table 3. Parameter estimates of the Gompertz model considering distribution Normal, *t*-Student, Skew normal and *t*-Skew for errors heteroscedastic

Heteroscedastic					
Error	Parameter	Male		Female	
		Mean (SD)	$P_{2.5\%} - P_{97.5\%}$	Mean (SD)	$P_{2.5\%} - P_{97.5\%}$
N	β_1	278.312 (3.374)	(271.827 ; 284.967)	327.339 (6.183)	(315.820 ; 339.773)
	β_2	3.722 (0.012)	(3.698 ; 3.747)	3.881 (0.018)	(3.847 ;3.917)
	β_3	0.0767 (0.0008)	(0.0750 ; 0.0784)	0.0722 (0.0011)	(0.0701 ; 0.0744)
	δ	1.875 (0.046)	(1.781 ; 1.965)	2.076 (0.048)	(1.980 ; 2.169)
	σ	0.857 (0.056)	(0.755 ; 0.977)	0.782 (0.054)	(0.682 ; 0.897)
	DIC	6,537		5,044	
T	β_1	276.101 (3.191)	(269.914 ; 282.508)	326.890 (5.945)	(315.487 ; 338.608)
	β_2	3.716 (0.012)	(3.692 ; 3.741)	3.880 (0.016)	(3.848 ;3.914)
	β_3	0.0773 (0.0008)	(0.0756 ; 0.0789)	0.0726 (0.0011)	(0.0705 ; 0.0753)
	δ	16.978 (0.207)	(16.577 ; 17.396)	18.673 (0.332)	(17.973 ; 19.321)
	ν	1.870 (0.050)	(1.769 ; 1.970)	2.064 (0.053)	(1.956 ; 2.166)
	σ	12.951 (5.162)	(6.851 ; 26.656)	14.037 (6.804)	(6.611 ; 32...078)
	DIC	6,524		5,037	
SN	β_1	275.896 (5.4828)	(265.463 ; 287.471)	358.920 (13.850)	(333.099 ; 388.452)
	β_2	3.775 (0.088)	(3.617 ; 3.960)	3.537 (0.107)	(3.326 ;3.764)
	β_3	0.0778 (0.0777)	(0.0366 ; 0.0823)	0.0636 (0.0029)	(0.0577 ; 0.0697)
	λ	0.171 (8.643)	(-15.384 ; 17.124)	12.627 (16.503)	(2.795 ; 49.879)
	δ	1.884 (0.048)	(1.785 ; 1.976)	2.062 (0.051)	(1.964 ; 2.159)
	σ	0.848 (0.057)	(0.746 ; 0.972)	0.789 (0.058)	(0.685 ; 0.907)
	DIC	6,579		5,580	
ST	β_1	275.922 (4.656)	(265.162 ; 284.369)	355.475 (18.437)	(353.426 ; 397.560)
	β_2	3.752 (0.070)	(3.636 ; 3.942)	3.714 (0.167)	(3.438 ;4.147)
	β_3	0.0778 (0.0020)	(0.0744 ; 0.0828)	0.0647 (0.0044)	(0.0561 ; 0.0741)
	λ	-0.273 (1.721)	(-4.105 ; 3.103)	1.048 (6.379)	(-11.691 ; 11.381)
	δ	1.907 (0.119)	(1.664 ; 2.133)	2.028 (0.111)	(1.801 ; 2.258)
	ν	14.024 (7.553)	(3.981 ; 32.261)	24.968 (13.890)	(5.967 ; 59.295)
	σ	0.795 (0.142)	(0.550 ; 1.108)	0.824 (0.132)	(0.583 ; 1.118)
	DIC	6,493		4,405	

Among the fits considering different distributions, as well as different error structures (N, T, SN, and ST), in both cases, it was found that the fits considering the Skew *t* distribution (ST) for errors were the best-fitting to the data, exhibiting the lowest DIC values as well as the smallest standard deviations (σ).

In the homoscedastic structure, it was observed that there is no significant asymmetry (λ) of errors for male quails (CI(λ)=[-2.8;5.0]), but it is significant for females (CI(λ)=[-8.0;-0.3]). However, in the heteroscedastic structure, it was observed that there was no significant asymmetry (λ) in both sexes (CI(λ)=[-4.105;3.103] and CI(λ)=[-11.691;11.381], for males and females, respectively).

In the heteroscedastic structure, the significance of the heteroscedasticity parameter in errors (δ)

was observed for both sexes (CI(δ)=[1.664;2.133] and CI(δ)=[1.801;2.258], for males and females, respectively), indicating a more parsimonious model with biological reality.

The plot of standardized residuals and theoretical quantiles for Gompertz fit with homoscedastic errors (Figures 2 and 3) support the presence of positive and negative skewness for male and female quails, respectively, and suggest a potential lack of fit for the homoscedastic models indicated by these criteria. To enhance the precision of inferences about the parameters in models fitted to the data and achieve significant time and cost savings in production, an alternative could be to consider heteroscedastic errors.

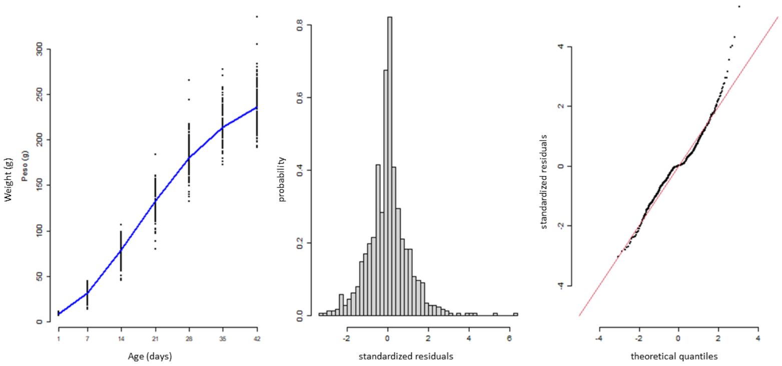

Figure 2. The Gompertz fit considering homoscedastic Skew *t* errors for male quails.

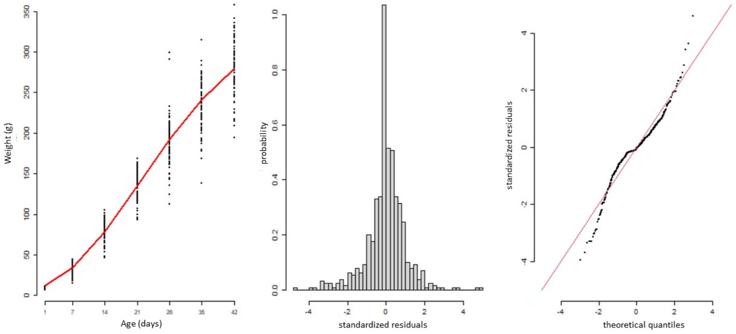

Figure 3. The Gompertz fit considering homoscedastic Skew *t* errors for female quails.

In Figures 4 and 5, the fits, standardized residuals, and theoretical quantiles of the Gompertz fits considering ST errors for heteroscedastic structures, respectively, for males and females are presented. A significant decrease in DIC values was observed among all models fitted considering a heteroscedastic error structure (Table 2).

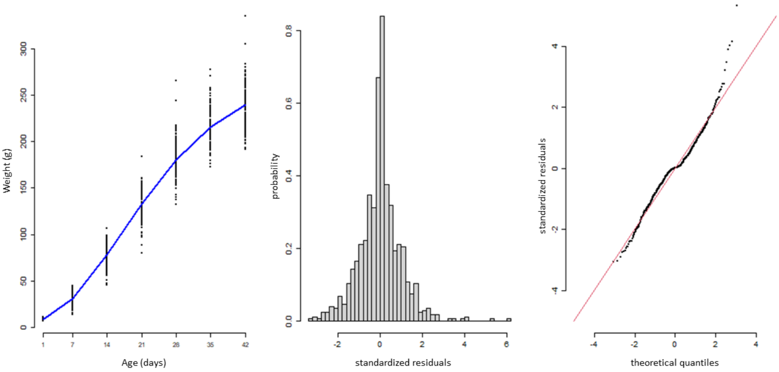

Figure 4. The Gompertz fit considering heteroscedastic Skew *t* errors for male quails.

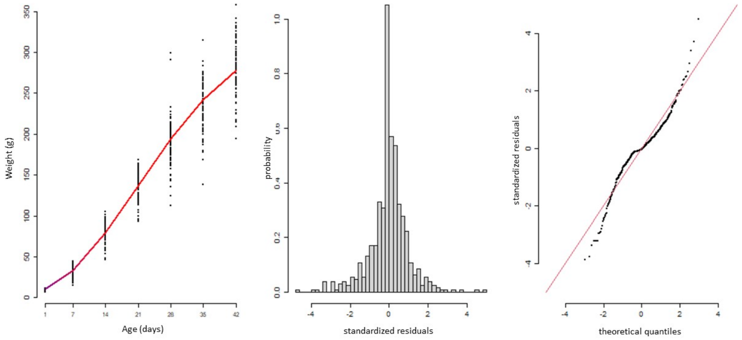

Figure 5. The Gompertz fit considering heteroscedastic Skew *t* errors for female quails.

It can be seen that female quails have a significantly higher asymptotic weight, since their respective credibility interval do not intersect ($\hat{\beta}_1 = 275.92$; CI= [265.16; 284.37] and $\hat{\beta}_1 = 355.48$; CI= [353.43; 397.56], respectively, males and females). The analysis is analogous for the other parameters (Table 2 and Figure 6).

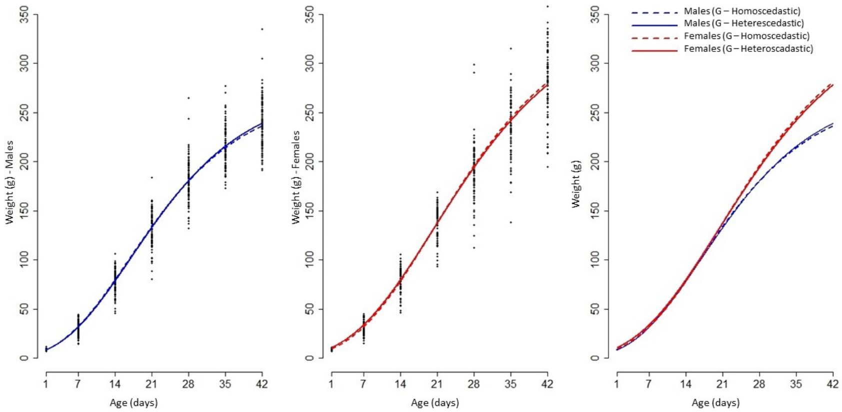

Figure 6. Gompertz fits with homoscedastic and heteroscedastic Skew *t* errors for male and female quails, respectively.

Rossi *et al.* (2017) fit the same models analyzed in this study to the weight of quails from three different lineages, one for meat production and two for egg-laying, separated by sexes, using a Bayesian approach to find the best model that described the data and compared the parameters among different quail lineages. They reported that the Gompertz model, in general, is considered the best fit for quail growth data (Guler *et al.,* 2022; Mazucheli *et al.,* 2011; Rossi & Santos, 2014). However, they mention that depending on the data structure and factors, such as the animal species, other models may provide better fits (Flinn & Midway, 2021).

Ribeiro *et al.* (2020) fitted the Brody, Von Bertalanffy, Richards, Logistic, and Gompertz models to the weight of meat quails from different lineages, using frequentist cluster analysis (centroid method). They assessed the similarities between the models based on the mean parameter estimates. They stated that the Richards model was the most suitable for describing the growth curves for the analyzed data and added that the Logistic model yielded similar results in the analysis without distinguishing between lineages.

Guler *et al.* (2022) employed a frequentist approach to fit and compare the Gompertz, Logistic, Von Bertalanffy, and Richards curves for two quail lineages (yellow and brown). They presented similar results regarding the asymptotic weights of the quails for the analyzed lineages.

Mazucheli *et al.* (2011) fitted the Gompertz model to quail weight data as a function of age, considering assumptions of homoscedasticity and multiplicative heteroscedasticity of variances, from both frequentist and Bayesian perspectives. They found that the heteroscedastic model provided the best fit to the data, as it did not overestimate the parameters of the birds' asymptotic mean weight.

Diniz *et al.* (2012) employed the Von Bertalanffy model to fit growth data of female Kubbard chickens under a Bayesian framework. They compared homoscedastic and multiplicative heteroscedasticity models of variances and concluded that accounting for the presence of heteroscedasticity significantly impacted the credibility intervals of the parameters, reducing them and leading to a decrease in the slaughter age of the chickens.

Louzada *et al.* (2014) proposed growth models considering heteroscedasticity and different error distributions (Normal and Skew normal) applied to chicken growth data. They demonstrated that the Skew normal distribution is a viable option for modeling growth curves with heteroscedasticity, allowing capturing the asymmetry and non-constant variability in the observed data.

4. Conclusions

The Gompertz model with heteroscedastic Skew t errors was the best fit for the weight data in relation to the ages of meat quails.

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