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Research Article
(Araştırma Makalesi)

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Modeling of different covariance structures with the Bayesian method in repeated measurements*

Tekrarlanan ölçümlerde farklı kovaryans yapılarının Bayes yöntemi ile modellenmesi

* This article is summarized from the 1st author's doctoral thesis.

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ABSTRACT

Objective: The objective of this study was to obtain solutions by modeling different covariance structures with Bayesian analysis methods in repeated measurement and to show its applicability to data in animal science.

Materials and Methods: This article focused on the analysis of the body weight data of 4154 weaned 8-month-old lambs. Repeated measurement analyses based on the mixed effect model were evaluated with Bayesian methods. Models were created for 12 different covariance structures. As the model comparison criterion, Deviation Information Criteria based on the relationship between the fit of the data to the model and the complexity of the model were used.

Result: Among 12 different covariance structures, the unstructured covariance structure was determined as a suitable structure for the data of this study.

Conclusions: It was concluded that various variance-covariance structures, such as body weight, can be easily modeled in repeated measurement data. Instead of PROC MCMC methods that require complex and computational difficulties and profound coding knowledge, it was presented a relatively user-friendly and fast procedure with its theoretical structure and demonstrated its feasibility. As a result of the literature review, this is the first study in which Bayesian methods solved a wide variety of variance-covariance structure models.

ÖZ

Amaç: Bu çalışma, tekrarlı ölçümlerde farklı kovaryans yapılarını Bayes analiz yöntemleriyle modelleyerek çözümler elde etmeyi ve bunun hayvan bilimindeki verilere uygulanabilirliğini göstermeyi amaçlamaktadır.

Materyal ve Yöntem: Bu makalede sütten kesilmiş 8 aylık 4154 kuzunun canlı ağırlık verileri analiz edilmiştir. Karma etki modeline dayalı tekrarlı ölçüm analizleri Bayes yöntemleri ile değerlendirilmiştir. 12 farklı kovaryans yapısı için modeller oluşturulmuştur. Model karşılaştırma kriteri olarak, verilerin modele uyumu ile modelin karmaşıklığı arasındaki ilişkiye dayalı Sapma Bilgi Kriterleri kullanılmıştır.

Araştırma Bulguları: 12 farklı kovaryans yapısı arasından yapılandırılmamış kovaryans yapısının bu çalışmanın verilerine uygun yapı olduğu belirlendi.

Sonuç: Tekrarlanan ölçüm verilerinde vücut ağırlığı gibi çeşitli varyans-kovaryans yapılarının kolaylıkla modellenebileceği gösterilmiştir. Karmaşık ve hesaplama zorlukları ve derin kodlama bilgisi gerektiren PROC MCMC yöntemleri yerine, nispeten kullanıcı dostu ve hızlı bir prosedür, teorik yapısıyla birlikte sunuldu ve uygulanabilirliği gösterildi. Literatür taraması sonucunda bu, Bayes yöntemlerin çok çeşitli varyans-kovaryans yapı modellerini çözdüğü ilk çalışmadır.

INTRODUCTION

Repeated measurement analysis is a widely used design in biological researches. The primary purpose of repeated measurement data is to examine simple factor effects (main effects) and their interaction effects. The strength of this method is that repeated measurement analysis is the only design form in which it is possible to obtain information on individual variations. Standard regression and variance analysis methods do not meet the appropriate assumptions for repeated measurements. The models and methods to analyze these data have to define the relationship between the observations obtained from the same unit. For this reason and because of their correlation structure, there is a need to represent the repeated measures data with special statistical models and their complementary analysis methods. Mixed models provide more flexibility in modeling covariance structures for repeated measurement data and adequately explain the time-dependent correlations of units (Eyduran & Akbaş, 2010; Littell et al., 1998). Verbeke and Molenberghs are pioneers in repeated measures, particularly with their work "Linear Mixed Models for Longitudinal Data," which is considered a classic in repeated measurement analysis (. The mixed model for repeated measures is popular for individually randomized trials with continuous longitudinal outcomes. The advantage of this method is that it does not have to take an equal number of measurements, observations with missing data are included in the analysis, and it is flexible in determining the covariance structure suitable for the data (Cnaan et al., 1997; Verbeke & Molenberghs, 2012). Bayesian Monte Carlo methods offer a more effective alternative to statistical methods such as Maximum Likelihood (ML). For instance, quantitative genetics has a historical record of relying on Bayesian statistics, especially in animal breeding, since Sorensen and Gianola's seminal work (de Villemereuil, 2019; Sorensen et al., 2002). Geneticists Daniel Gianola and Daniel Sorensen introduced MCMC procedures in the 1990s to solve animal breeding problems using Bayesian statistics, and its use has become more and more common. Instead of using the mathematical expression, MCMC provides a set of random sample numbers extracted from a probability density function (Blasco & Blasco, 2017). Unlike traditional approaches to estimating model parameters, a Bayesian paradigm treats model parameters as random variables, and Bayes' theorem is used to derive probability distributions for model parameters.

As with all statistical models, each measurement has a residual. Since repeated measures on the same individual are usually serially correlated, it is usual to have residuals that are not independently and identically distributed, meaning that the covariance structure of the residuals must be clearly modeled (McNeish, 2017). Correct determination of covariance structures for repeated measurements is essential for accurately estimating the standard errors of the coefficients of the mean profiles (Fitzmaurice et al., 2012). Although evaluating a suitable covariance structure for the data is complex, mixed model analysis is more sensitive. A complex situation becomes even more complicated when the covariance structure is unknown. In this case, the key to the data analysis strategy is to choose the covariance structure.

The expression of the general linear mixed model in matrix form is as follows:

$$\boldsymbol{Y} = \boldsymbol{X\beta} + \boldsymbol{Z\gamma} + \boldsymbol{\varepsilon}$$

In the equation here, $\boldsymbol{X}$ and $\boldsymbol{Z}$ are the design matrix for fixed and random effects, respectively, $\boldsymbol{\beta}$ and $\boldsymbol{\gamma}$ are the fixed and random effects vectors, respectively, and $\boldsymbol{\varepsilon}$ is the errors vector. It is assumed that $\boldsymbol{\gamma}$ and $\boldsymbol{\varepsilon}$ are $N(\mathbf{0}, \boldsymbol{G})$ and $N(\mathbf{0}, \boldsymbol{R})$ distributions and independent, respectively.

While the error vector is normally distributed with $e_i \sim N(0, R_i)$, it is $R_i = cov\,(e_i)$. Assuming that the random effects are normally distributed, the expected value and variance of the model are as follows:

$$E\begin{bmatrix}\gamma_i \\ e_i\end{bmatrix} = \begin{bmatrix}\mathbf{0} \\ \mathbf{0}\end{bmatrix} \text{ and } Var\begin{bmatrix}\boldsymbol{\gamma} \\ \boldsymbol{\varepsilon}\end{bmatrix} = \begin{bmatrix}\boldsymbol{G} & \mathbf{0} \\ \mathbf{0} & \boldsymbol{R}\end{bmatrix}.$$

The representation of the covariance matrix of $\boldsymbol{G}$ random effects and the covariance matrix of errors $\boldsymbol{R}$ are as follows:

$$\boldsymbol{G} = Var(\gamma_i) = \begin{bmatrix} var(\gamma_{1i}) & cov(\gamma_{1i},\gamma_{2i}) & \dots & cov(\gamma_{1i},\gamma_{qi}) \\ cov(\gamma_{1i},\gamma_{2i}) & var(\gamma_{2i}) & \dots & cov(\gamma_{2i},\gamma_{qi}) \\ \vdots & \vdots & \dots & \vdots \\ cov(\gamma_{1i},b_{qi}) & cov(\gamma_{2i},\gamma_{qi}) & \dots & var(\gamma_{qi}) \end{bmatrix}$$

$$\boldsymbol{R} = Var(e_i) = \begin{bmatrix} var(e_{1i}) & cov(e_{1i},e_{2i}) & \dots & cov(e_{1i},e_{ni}) \\ cov(e_{1i},e_{2i}) & var(e_{2i}) & \dots & cov(e_{2i},e_{ni}) \\ \vdots & \vdots & \dots & \vdots \\ cov(e_{1i},e_{ni}) & cov(e_{2i},e_{ni}) & \dots & var(e_{ni}) \end{bmatrix}$$

In the classical mixed model, $\boldsymbol{R} = \sigma^2\boldsymbol{I}$, where $\boldsymbol{I}$ is the $n \times n$ identity matrix, and $\boldsymbol{G}$ is the diagonal matrix containing variance components. The choice of the covariance structure is equivalent to the choice of structure for $\boldsymbol{G}$ and $\boldsymbol{R}$. The first step is to consider the study's design and the obstructive nature of the observations (Gomez et al., 2005).

This article is about facilitating the modeling of different covariance structures. Growth data collected from lambs at different times were used to represent repeated measurement data commonly used in animal science. Generating 12 models with different covariance structures for body weight data and show how all models can fit in PROC BGLIMM because the procedure is relatively new. In the SAS package program, Bayesian solutions are implemented using not only the long-standing original and versatile Bayesian procedure, PROC MCMC, but also the new PROC BGLIMM procedure. PROC MCMC is a simulation-based general Bayesian approach that offers flexibility in model specification but requires more user programming knowledge. Mixing efficiency can sometimes be less than due to the general sampling (non-model-specific) algorithms that PROC MCMC uses (Chen et al., 2016). PROC MCMC also has certain limitations, such as the absence of automated support for a CLASS statement to manage categorical variables. PROC BGLIMM is a Bayesian procedure designed explicitly for fitting generalized linear mixed models using Markov chain Monte Carlo methods. It employs optimal parallelized sampling algorithms for improved performance, handles multilevel nested and non-nested random-effects models, and fits models to multivariate or longitudinal data that contain repeated measurements (Shi & Chen, 2019). The Bayesian approach to statistical modeling involves treating model parameters as random variables and estimating the joint distribution of all parameters in the model. This can be done using Markov chain Monte Carlo (MCMC) methods, which allow for sampling from the posterior distribution of the model parameters given the data. The random effects parameter **γ** adds an extra sampling step to the Gibbs algorithm, thus eliminating the need to integrate **γ** to make inferences about **β** numerically. MCMC methods generate estimates of the marginal distribution for all fixed-effects parameters, including the **G** and **R** covariance matrices.

MATERIALS and METHOD

Data set and descriptive statistics

The material of this study consists of the repeated measurements of body weight data of 4154 weaned 8-month-old lambs. The number of measurements is the same for each animal, and body weight measurements from 1 to 6 months were taken for each animal. The herd year (1 to 6), the number of days to weaning, and the sire were recorded for each animal. Data for analysis were prepared in longitudinal data format for 59 sires, with a record for the time of measurement in one column and a record for each time at which body weight was measured in another column. The change of the repeated measurement body weight data of lambs from the first month to the sixth month is depicted in Figure 1 with a boxplot.

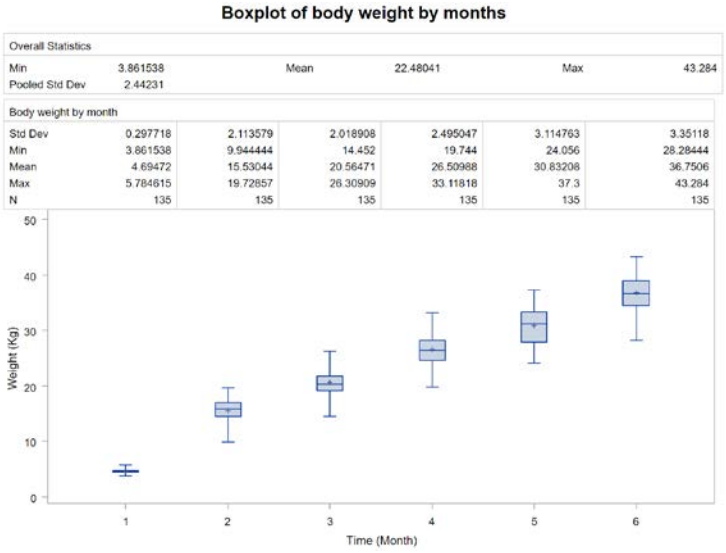

Figure 1. Boxplot of body weight by months.

Şekil 1. *Aylara göre vücut ağırlığı kutu grafiği.*

The profile graph showing the change of body weights over time (months) according to six different herd years is given in Figure 2. To have the correct standard errors of the estimated coefficients of the mean profile, it is necessary to have or know a good idea of the appropriate covariance structure of repeated measurements. In a Bayesian framework, the accurate covariance matrix will have appropriate standard deviations for the posterior distribution of the coefficients included in the mean profile of the repeated response over time. It should be noted that the covariance matrix of errors in the mean response depends on the mean response and vice versa, so these two items are related.

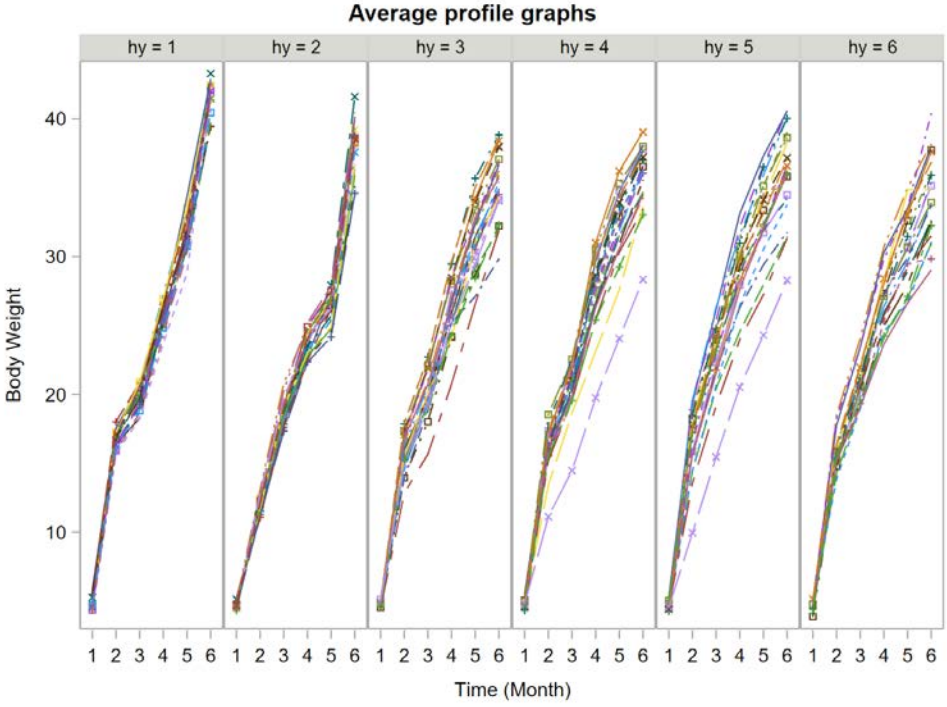

Figure 2. Average profile graphs for body weights (hy: herd year).

Şekil 2*. Canlı ağırlık için ortalama profil grafikleri (sürü yılına göre).*

Bayesian formulation of repeated measures

In this study, a linear mixed model will be used. The linear mixed model is a generalized version of the linear model. In the general form, the linear mixed model is as follows: when the ith individual has n_i repeated measurements.

$$\boldsymbol{y}_i = \boldsymbol{X}_i\boldsymbol{\beta} + \boldsymbol{Z}_i\boldsymbol{\gamma}_i + \boldsymbol{\varepsilon}_i \qquad i = 1,2,\cdots,m \qquad (2.1)$$

where $\boldsymbol{y}_i$ is $(n_i \times 1)$ dimensional observation vector for ith individual and n_i is the number of measurements for the ith individual; $\boldsymbol{X}_i$ is $(n_i \times p)$ dimensional design matrix for the fixed effects; $\boldsymbol{\beta}$ is $(p \times 1)$ dimensional vector of unknown fixed regression coefficients; $\boldsymbol{Z}_i$ is $(n_i \times q)$ dimensional a matrix of covariates associated with the random effect; $\boldsymbol{\gamma}_i$ is $(q \times 1)$ dimensional vector of random effects parameters and $\boldsymbol{\gamma}_i \sim N(0, \boldsymbol{G}_i)$; and $\boldsymbol{\varepsilon}_i$ is $(n_i \times 1)$ dimensional a vector of error terms and $\boldsymbol{\varepsilon}_i \sim N(0, \boldsymbol{R}_i)$ and is independent of $\boldsymbol{\gamma}_i$.

When the sire effect is assumed to be a random effect, in this case, the effect of each sire on the response variable $\boldsymbol{y}_i$,is represented by a random effect vector $\boldsymbol{\gamma}_i$. Suppose the relationship between the effects of all sire is described by a normal distribution with a mean of 0 and a variance of σ_s^2.

Repeated measurements can be obtained either as multiple measurements taken from the same trial unit at the same time or as a single measurement taken from the same trial unit multiple times or as a combination of these two. In this case, suppose $\boldsymbol{\varepsilon}_i = \{\varepsilon_{i1}, \varepsilon_{i2}, \cdots, \varepsilon_{im}\}$ is a vector of measurements taken from m equal time interval. Each of the measurements comes from a normal distribution and has the following covariance matrix.

$$\boldsymbol{R}_i = Var(\boldsymbol{\varepsilon}_i) = \begin{bmatrix} \sigma_{11} & \sigma_{21} & \cdots & \sigma_{1m} \\ \sigma_{21} & \sigma_{22} & \cdots & \sigma_{2m} \\ \vdots & \vdots & \vdots & \vdots \\ \sigma_{m1} & \sigma_{m2} & \cdots & \sigma_{mm} \end{bmatrix}$$

Since all measurements were taken from the same experimental unit, they are related to each other. Here $\boldsymbol{R}_i$ is the covariance matrix of the errors for the ith individual. A linear mixed model extends the simple multiple regression model, $\boldsymbol{y} = \boldsymbol{X\beta} + \boldsymbol{\varepsilon}$, and allows the random effect $\boldsymbol{\gamma}_i$ to be added to the regression coefficients. In other words, the addition of random effects helps to distinguish between the conditional mean (individual-specific) $E(\boldsymbol{y}_i|\boldsymbol{\gamma}_i) = \boldsymbol{X}_i\boldsymbol{\beta} + \boldsymbol{Z}_i\boldsymbol{\gamma}_i$ and the marginal mean (population-mean) $E(\boldsymbol{y}_i) = \boldsymbol{X}_i\boldsymbol{\beta}$. Similarly, the individual-specific covariance $Cov(\boldsymbol{y}_i|\boldsymbol{\gamma}_i)$ and the population-mean covariance $Cov(\boldsymbol{y}_i)$ are:

$$Cov(\boldsymbol{y}_i|\boldsymbol{\gamma}_i) = Cov(\boldsymbol{\varepsilon}_i) = \boldsymbol{R}_i$$

$$Cov(\boldsymbol{y}_i) = Cov(\boldsymbol{Z}_i\boldsymbol{\gamma}_i) + Cov(\boldsymbol{\varepsilon}_i) = \boldsymbol{Z}_i\boldsymbol{G}_i\boldsymbol{Z}_i' + \boldsymbol{R}_i$$

Finally, $y_i \sim N(\boldsymbol{X}_i\boldsymbol{\beta},\ \boldsymbol{Z}_i\boldsymbol{G}_i\boldsymbol{Z}_i' + \boldsymbol{R}_i)$ can be written for each individual. Here, the variance of $\boldsymbol{y}_i$ is $\boldsymbol{V}_i = \boldsymbol{Z}_i\boldsymbol{G}_i\boldsymbol{Z}_i' + \boldsymbol{R}_i$. The random part of the model was fitted by identifying the terms describing the random pattern matrix $\boldsymbol{Z}_i$ and determining the variance-covariance structures of the matrices $\boldsymbol{G}_i$ and $\boldsymbol{R}_i$. Now, suppose we have matrix $\boldsymbol{Z}_{N\times m} = \text{block diagonal}[Z_i]$ where $\sum_{i=1}^{m} n_i$. We assume that $\boldsymbol{Y} = (y_1', y_2', \ldots, y_m')'$, $\boldsymbol{X} = (X_1', X_2', \ldots, X_m')'$, $\boldsymbol{\gamma} = (\gamma_1', \gamma_2', \ldots, \gamma_m')'$, $\boldsymbol{\varepsilon} = (\varepsilon_1', \varepsilon_2', \ldots, \varepsilon_m')'$, $\boldsymbol{G} = blockdiagonal[G_i]$, and $\boldsymbol{R} = blockdiagonal[R_i]$ for the sake of simplicity of notation. The linear mixed effects model in Equation (2.1) can be rewritten in full matrix notation.

$$\boldsymbol{Y} = \boldsymbol{X\beta} + \boldsymbol{Z\gamma} + \boldsymbol{\varepsilon} \qquad (2.2)$$

The marginal probability density function of $\boldsymbol{Y} \sim N(\boldsymbol{X\beta}, \boldsymbol{ZGZ'} + \boldsymbol{R})$ and given $\boldsymbol{\gamma}$, the conditional density function of $\boldsymbol{Y}$ can be written as $\boldsymbol{Y}|\boldsymbol{\gamma} \sim N(\boldsymbol{X\beta} + \boldsymbol{Z\gamma}, \boldsymbol{R})$. In addition to these assumptions, the $\boldsymbol{\gamma} \sim N(\boldsymbol{0}, \boldsymbol{G})$ and $\boldsymbol{\varepsilon} \sim N(\boldsymbol{0}, \boldsymbol{R})$ assumptions should be considered while constructing the mixed effects likelihood function.

Prior distribution

The most critical part of Bayesian analysis is to assign prior distributions to all unknown parameters $(\boldsymbol{\beta}, \boldsymbol{\gamma}, \boldsymbol{G}, \boldsymbol{R})$ in the model. In the case of the fixed effects vector **β**, the multivariate normal distribution representing sufficient a priori information about these parameters is determined as the a priori distribution and can be written as following.

$$\beta|b_0, B_0 \sim N(b_0, B_0).$$
$$f(\boldsymbol{\beta}|\boldsymbol{b_0}, \boldsymbol{B_0}) \propto |\boldsymbol{B_0}|^{-\frac{p}{2}} exp\left\{-\frac{1}{2}(\boldsymbol{\beta}-\boldsymbol{b_0})'\boldsymbol{B_0}^{-1}(\boldsymbol{\beta}-\boldsymbol{b_0})\right\} \quad (2.3)$$

The random effects vector **γ** can be determined as the normal distribution to a priori distribution.

$$\gamma|G \sim N(0, G)$$
$$f(\boldsymbol{\gamma}|\boldsymbol{G}) \propto |\boldsymbol{G}|^{-\frac{q}{2}} exp\left\{-\frac{1}{2}\boldsymbol{\gamma}'\boldsymbol{G}^{-1}\boldsymbol{\gamma}\right\} \quad (2.4)$$

To complete the prior distribution definitions, the variance-covariance matrices $\boldsymbol{G}$ and $\boldsymbol{R}$ need to be determined. It is possible to specify a prior probability expression for the parameters $\boldsymbol{G}$ and $\boldsymbol{R}$. It will be assumed that these parameters have an inverse-Wishart distribution. Given V_g and v_g, the prior distribution of $\boldsymbol{G}$ can be written as;

$$G \sim W_m(v_g + m, V_g)$$
$$f(\boldsymbol{G}|v_g, V_g) \propto |\boldsymbol{G}|^{-\frac{1}{2}(v_g+m+1)} exp\left\{-\frac{1}{2}tr\,(v_g\boldsymbol{G}^{-1}V_g)\right\} \quad (2.5)$$

Similarly, given V_r ve v_r, the density function of the prior distribution of $\boldsymbol{R}$ is the inverse-Wishart distribution given below.

$$\boldsymbol{R} \sim W_m(v_r + m, \boldsymbol{V}_r)$$
$$f(\boldsymbol{R}|v_r, \boldsymbol{V}_r) \propto |\boldsymbol{R}|^{-\frac{1}{2}(v_r+m+1)} exp\left\{-\frac{1}{2}tr\,(v_r\boldsymbol{R}^{-1}\boldsymbol{V}_r)\right\} \quad (2.6)$$

Here, $\boldsymbol{V}_g$ and $\boldsymbol{V}_r$ are hyperparameters of $(m \times m)$ dimensional and can be interpreted as initial values of prior distributions of variance-covariance parameters $\boldsymbol{G}$ and $\boldsymbol{R}$, respectively. v_g and v_r are also hyperparameters of the prior distribution of the variance-covariance matrix, and these are as a measure of the degree of belief in $\boldsymbol{V}_g$ and $\boldsymbol{V}_r$ or as integer values that can be interpreted as degrees of freedom. When $\boldsymbol{V}_g = 0$ and $\boldsymbol{V}_r = 0$, in the absence of a priori information, the priori distributions of $\boldsymbol{G}$ and $\boldsymbol{R}$ given in equations (2.5) and (2.6) will be noninformative as follows.

$$f(\boldsymbol{G}) \propto |\boldsymbol{G}|^{-\frac{1}{2}(m+1)}$$
$$f(\boldsymbol{R}) \propto |\boldsymbol{R}|^{-\frac{1}{2}(m+1)}$$

Likelihood function

Model (2.2) states that given $\boldsymbol{\beta}, \boldsymbol{\gamma}, \boldsymbol{G}$, and $\boldsymbol{R}$, the observation vector $\boldsymbol{Y}$ has the following likelihood function.

$$f(\boldsymbol{Y}|\boldsymbol{\beta}, \boldsymbol{\gamma}, \boldsymbol{G}, \boldsymbol{R}) = (2\pi)^{-N/2}\,|\boldsymbol{R}|^{-N/2}\,exp\left\{-\frac{1}{2}(\boldsymbol{Y}-\boldsymbol{X\beta}-\boldsymbol{Z\,\gamma})'\boldsymbol{R}^{-1}(\boldsymbol{Y}-\boldsymbol{X\beta}-\boldsymbol{Z\,\gamma})\right\} \quad (2.7)$$

Joint posterior density function

The prior distributions given in equations (2.3), (2.4), (2.5) and (2.6) for $\boldsymbol{\beta}, \boldsymbol{\gamma}, \boldsymbol{G}$ and $\boldsymbol{R}$, respectively, are multiplied by the likelihood function given in (2.7) for the model in (2.2). Given $\boldsymbol{Y}$ according to Bayes' rule, the joint posterior density function of the parameters can be obtained as follows.

$$\begin{aligned} f(\boldsymbol{\beta}, \boldsymbol{\gamma}, \boldsymbol{G}, \boldsymbol{R}|\boldsymbol{Y}) &= f(\boldsymbol{\beta}|b_0, B_0) \times f(\boldsymbol{\gamma}|\boldsymbol{G}) \times f\big(\boldsymbol{G}|v_g, V_g\big) \times f(\boldsymbol{R}|v_r, V_r) \times f(\boldsymbol{Y}|\boldsymbol{\beta}, \boldsymbol{\gamma}, \boldsymbol{G}, \boldsymbol{R}) \\ &\propto |\boldsymbol{B_0}|^{-\frac{p}{2}} \exp\left\{-\frac{1}{2}(\boldsymbol{\beta} - \boldsymbol{b_0})' \boldsymbol{B_0}^{-1} (\boldsymbol{\beta} - \boldsymbol{b_0})\right\} \times |\boldsymbol{G}|^{-\frac{q}{2}} \exp\left\{-\frac{1}{2}\boldsymbol{\gamma}' \boldsymbol{G}^{-1} \boldsymbol{\gamma}\right\} \\ &\times |\boldsymbol{G}|^{-\frac{1}{2}(v_g + m + 1)} \exp\left\{-\frac{1}{2} tr\big(v_g \boldsymbol{G}^{-1} V_g\big)\right\} \times |\boldsymbol{R}|^{-\frac{1}{2}(v_r + m + 1)} \exp\left\{-\frac{1}{2} tr(v_r \boldsymbol{R}^{-1} V_r)\right\} \\ &\times |\boldsymbol{R}|^{-N/2} \exp\left\{-\frac{1}{2}(\boldsymbol{Y} - \boldsymbol{X\beta} - \boldsymbol{Z\,\gamma})' \boldsymbol{R}^{-1} (\boldsymbol{Y} - \boldsymbol{X\beta} - \boldsymbol{Z\,\gamma})\right\} \end{aligned}$$

which can be rewritten as

$$\begin{aligned} f(\boldsymbol{\beta}, \boldsymbol{\gamma}, \boldsymbol{G}, \boldsymbol{R}|\boldsymbol{Y}) \propto\ & |\boldsymbol{B_0}|^{-\frac{p}{2}} |\boldsymbol{G}|^{-\frac{1}{2}(q + v_g + m + 1)} |\boldsymbol{R}|^{-\frac{1}{2}(N + v_r + m + 1)} \\ & \times \exp\left\{-\frac{1}{2}(\boldsymbol{\beta} - \boldsymbol{b_0})' \boldsymbol{B_0}^{-1} (\boldsymbol{\beta} - \boldsymbol{b_0})\right\} \exp\left\{-\frac{1}{2} tr\big[\boldsymbol{G}^{-1}\big(v_g V_g + \boldsymbol{\gamma}'\boldsymbol{\gamma}\big)\big]\right\} \\ & \times \exp\left\{-\tfrac{1}{2} tr\big[\boldsymbol{R}^{-1}\big(v_r V_r + (\boldsymbol{Y} - \boldsymbol{X\beta} - \boldsymbol{Z\,\gamma})'(\boldsymbol{Y} - \boldsymbol{X\beta} - \boldsymbol{Z\,\gamma})\big)\big]\right\} \end{aligned} \tag{2.8}$$

Let's denote all parameters $\boldsymbol{\beta}, \boldsymbol{\gamma}, \boldsymbol{G}$ and $\boldsymbol{R}$, with θ and let $\pi(\theta)$ be the function of interest. Bayesian interpretation aims to obtain the expected mean under the posterior density function.

$$E[\pi(\theta)] = \int f(Y|\theta) f(\theta) d\theta \tag{2.9}$$

Where $f(\boldsymbol{\theta}) = f(\boldsymbol{\beta}|b_0, B_0) \times f(\boldsymbol{\gamma}|\boldsymbol{G}) \times f\big(\boldsymbol{G}|v_g, V_g\big) \times f(\boldsymbol{R}|v_r, V_r)$, $f(\boldsymbol{Y}|\boldsymbol{\theta})$ is the conditional density function of $\boldsymbol{Y}$ given the parameters or the likelihood function given in (2.7). There are at least two difficulties in obtaining this. In particular, (2.9) is analytically challenging to obtain. Second, although the standard Monte Carlo approach can be a solution for such a high-dimensional integral problem, it is not easy to apply. Because the marginal posterior density function may be of an unknown form and it is not easy to draw a sample from such a density function. Fortunately, the Gibbs sampling approach can be applied to overcome this problem, which allows the user to draw samples from the joint distribution using the conditional posterior distribution of each parameter, given the other parameters.

Full conditional posterior densities

To apply Gibbs sampling for the model given in Equation (2.2), fully conditional posterior distributions of $\boldsymbol{\beta}, \boldsymbol{\gamma}, \boldsymbol{G}$ and $\boldsymbol{R}$ are required, given the remaining parameters. Considering the conditional posterior distribution gives an idea about the structure of the posterior distribution and provides the basis for an effective calculation. The full conditional posterior distributions of $\boldsymbol{\beta}, \boldsymbol{\gamma}, \boldsymbol{G}$, and $\boldsymbol{R}$ are obtained from the joint posterior probability density function given in (2.8). To obtain the full conditional distributions of $\boldsymbol{\beta}, \boldsymbol{\gamma}$, the following rule is used. Let the probability density function of the vector $\boldsymbol{\theta}$ be proportional to the following exponential expression;

$$\exp\left\{-\frac{1}{2\sigma^2}(\boldsymbol{\theta}' \boldsymbol{A\theta} - 2\boldsymbol{\theta}' a)\right\}$$

Where $\boldsymbol{A}$ is a positive definite matrix, the distribution of $\boldsymbol{\theta}$ is $N(\boldsymbol{A}^{-1}a, \boldsymbol{A}^{-1})$ in this case.

Conditional posterior distribution of $\boldsymbol{\beta}$: The conditional posterior probability density function of $\boldsymbol{\beta}$ is proportional to the following exponential expression.

$$\exp\left\{-\frac{1}{2}\big[\boldsymbol{\beta}'\big(\boldsymbol{X}'\boldsymbol{R}^{-1}\boldsymbol{X} + \boldsymbol{B_0}^{-1}\big)\boldsymbol{\beta} - 2\boldsymbol{\beta}'\big(\boldsymbol{X}'\boldsymbol{R}^{-1}(\boldsymbol{Y} - \boldsymbol{Z\gamma}) + \boldsymbol{B_0}^{-1} b_0\big)\big]\right\}$$

Thus, the conditional posterior distribution of $\boldsymbol{\beta}$ is as follows.

$$[\boldsymbol{\beta}|\boldsymbol{\gamma},\boldsymbol{G},\boldsymbol{R},\boldsymbol{Y}]\sim N\left(\left(\boldsymbol{X}'\boldsymbol{R}^{-1}\boldsymbol{X}+\boldsymbol{B_0}^{-1}\right)^{-1}\left(\boldsymbol{X}'\boldsymbol{R}^{-1}(\boldsymbol{Y}-\boldsymbol{Z}\boldsymbol{\gamma})+\boldsymbol{B_0}^{-1}b_0\right),\left(\boldsymbol{X}'\boldsymbol{R}^{-1}\boldsymbol{X}+\boldsymbol{B_0}^{-1}\right)^{-1}\right) \quad (2.10)$$

Conditional posterior distribution of $\boldsymbol{\gamma}$: The conditional posterior probability density function of $\boldsymbol{\gamma}$ is proportional to the following exponential expression.

$$\exp\left\{-\frac{1}{2}\left[\boldsymbol{\gamma}'(\boldsymbol{G}+\boldsymbol{Z}'\boldsymbol{R}^{-1}\boldsymbol{Z})\boldsymbol{\gamma}-\boldsymbol{2\gamma}'\left(\boldsymbol{Z}'\boldsymbol{R}^{-1}(\boldsymbol{Y}-\boldsymbol{X}\boldsymbol{\beta})\right)\right]\right\}$$

Thus, the conditional posterior distribution of $\boldsymbol{\gamma}$ is as follows.

$$[\boldsymbol{\gamma}|\boldsymbol{\beta},\boldsymbol{G},\boldsymbol{R},\boldsymbol{Y}]\sim N\left((\boldsymbol{G}+\boldsymbol{Z}'\boldsymbol{R}^{-1}\boldsymbol{Z})^{-1}\left(\boldsymbol{Z}'\boldsymbol{R}^{-1}(\boldsymbol{Y}-\boldsymbol{X}\boldsymbol{\beta})\right),(\boldsymbol{G}+\boldsymbol{Z}'\boldsymbol{R}^{-1}\boldsymbol{Z})^{-1}\right) \quad (2.11)$$

Conditional posterior distribution of $\boldsymbol{G}$: The posterior probability density function of $\boldsymbol{G}$ is proportional to the following expression.

$$|\boldsymbol{G}|^{-\frac{1}{2}(v_g+m+1)}exp\left\{-\frac{1}{2}tr\left[\boldsymbol{G}^{-1}\left(v_gV_g+\boldsymbol{\gamma}'\boldsymbol{\gamma}\right)\right]\right\}$$

Thus, the conditional posterior distribution of $\boldsymbol{G}$ is as follows.

$$[\boldsymbol{G}|\boldsymbol{\beta},\boldsymbol{\gamma},\boldsymbol{R},\boldsymbol{Y}]\sim W^{-1}\left(q+v_g,\boldsymbol{\gamma}'\boldsymbol{\gamma}+v_gV_g\right) \quad (2.12)$$

Conditional posterior distribution of **R**: The posterior probability density function of **R** is proportional to the following expression.

$$|\boldsymbol{R}|^{-\frac{1}{2}(N+v_r+m+1)}\exp\left\{-\frac{1}{2}tr\left[\boldsymbol{R}^{-1}\left(v_rV_r+(\boldsymbol{Y}-\boldsymbol{X}\boldsymbol{\beta}-\boldsymbol{Z}\,\boldsymbol{\gamma})'(\boldsymbol{Y}-\boldsymbol{X}\boldsymbol{\beta}-\boldsymbol{Z}\,\boldsymbol{\gamma})\right)\right]\right\}$$

Thus, the full conditional posterior distribution of **R** is obtained as follows.

$$[\boldsymbol{R}|\boldsymbol{\beta},\boldsymbol{\gamma},\boldsymbol{G},\boldsymbol{Y}]\sim W^{-1}(N+v_r,(\boldsymbol{Y}-\boldsymbol{X}\boldsymbol{\beta}-\boldsymbol{Z}\,\boldsymbol{\gamma})'(\boldsymbol{Y}-\boldsymbol{X}\boldsymbol{\beta}-\boldsymbol{Z}\,\boldsymbol{\gamma})+v_rV_r) \quad (2.13)$$

The $\boldsymbol{W}^{-1}$ in (2.12) and (2.13) shows the inverse Wishart distribution with m variables. The Wishart distribution is parameterized according to the degrees of freedom (v_g and v_r) and the precision matrix ($\boldsymbol{V}_g$ and $\boldsymbol{V}_r$). The inverse-Wishart distribution is a conjugate prior for the covariance matrix of the multivariate normally distributed variables. This means that when combined with the likelihood function, it will result in a posterior distribution belonging to the same family of distributions. Another significant advantage of the inverse Wishart distribution is that it provides positive precision of the covariance matrix (Schuurman et al., 2016).

Bayesian analysis of data set using proc BGLIMM

The mixed-effects model used for the dataset is as follows.

$$y_{ijk}=\beta_0+\beta_1hy_i+\beta_2x_{ijk}+s_k+e_{ijk}$$

Where, y_{ijk}: monthly body weights; hy_i: herd year; β_0, β_1, β_2: regression coefficients; x_{ijk}: days to weaning; s_k: sire; and e_{ijk}: error. The effect of the sire, which is a random effect, follows a normal distribution $s_k\sim N\left(0_q,\sigma_b^2I_q\right)$.

For all regression coefficients, β_j $(j=1,2)$, fixed effect herd year hy_i, and weaning days x_{ijk} were determined as a noninformative prior distribution with large variance Normal (0; var=1e4). These noninformative prior distributions were solved by the Proc BGLIMM procedure. A single chain of size 10,000 iterations was run. The initial 500 iterations were discarded as a burn-in, and every second sample was recorded to reduce autocorrelation. In total, 5,000 samples were recorded for each parameter, and the means of the sample values were used as an estimate of the parameters. Basically, 12 different models were created for 12 different variance-covariance structures. These 12 models are

modeled with noninformative prior selection. In addition, variance components and unstructured variance-covariance structures from these models were remodeled with informative priors. To compare models, a Bayesian comparison criterion Deviance Information Criteria (DIC) was used, based on the relationship between the fit of the data to the model and the complexity of the model. The Deviance Information Criteria (DIC) (Spiegelhalter et al., 2002) is a model comparison tool similar to the well-known probability-based information criterion Akaike Information Criterion (AIC) (Akaike, 1973), and Bayesian Information Criteria (BIC) (Schwarz, 1978). This criterion, which uses the posterior distributions of the models obtained by the MCMC method, is useful in Bayesian model selection and has been used in many studies (Fikse et al., 2003; Rekaya et al., 2003; Legarra et al., 2005; François & Laval, 2011; Holand et al., 2013). DIC is defined as $DIC = \bar{D}(\theta) + p_D$, where $p_D = \bar{D}(\theta) - D(\bar{\theta})$. And $\bar{D}(\theta)$ is the mean of the deviation in iterations. It measures how well the data fit the model using the likelihood function $\left(-2logL(D|\theta)\right)$ and sampled parameter values at each iteration.

RESULTS

For all models, the posterior distributions of the parameters were calculated one by one, and convergence was checked. A special care should be given while interpreting the results when the chain does not have MCMC convergence of posterior distribution. In this study, there was a general convergence in the posterior distributions of all parameters, and different diagnostic tests, such as the Geweke test, Monte Carlo standard errors, and effective sample size, were evaluated together with trace charts. Therefore, reliable posterior statistics of parameters for body weight data have been obtained and can be interpreted.

The twelve models using different variance-covariance structures with informative prior and two models with noninformative prior specification were created in this study, and the results were evaluated. The DIC values of the models are given in Table 1. These values are calculated using the equation $DIC = Dbar + pD = Dhat + 2pD$. Where pD is the number of effective parameters that should be included in the model, the mean of the posterior distribution of the deviation $Dbar,$ and the log-likelihoods calculated from the Gibbs sampling iteration. Assuming the unknown parameters of the model is θ, the deviation from the posterior mean of θ is $Dhat$.

Table 1. Summary of DIC comparison values of models

Çizelge 1. *Modellerin DIC karşılaştırma değerlerinin özeti*

	Model	DIC	Dbar	Dhat	pD
Noninformative	**VC**	3320.31	3269.89	3219.47	50.42
	CS	3327.76	3280.51	3233.27	47.25
	CSH	3014.26	2966.70	2919.13	47.57
	HF	2895.96	2891.27	2886.59	4.68
	AR (1)	3290.40	3249.74	3209.08	40.66
	ARH (1)	2965.02	2913.68	2862.34	51.34
	FA (1)	2551.29	2481.55	2411.80	69.74
	ANTE	2533.23	2475.89	2418.55	57.34
	TOEP	3214.28	3163.33	3112.38	50.95
	TOEPH	2910.90	2872.92	2834.93	37.98
	UN	2499.38	2460.82	2422.27	38.55
	ARMA	3278.50	3234.29	3190.08	44.21
Informative	**VC**	3320.20	3270.73	3221.27	49.47
	UN	2482.95	2459.34	2435.74	23.60

The model with the smallest DIC value is accepted to be the most suitable model. When the models with noninformative prior distributions are evaluated, the model with the lowest DIC value among 12 different models is the unstructured (UN) variance-covariance structure. The variance-covariance matrix of the model with the unstructured structure determined as the most suitable model is tabulated in Table 2.

Table 2. $\boldsymbol{R}$ variance-covariance matrix for the unstructured model

Çizelge 2. *Yapılandırılmamış model için* $\boldsymbol{R}$ *varyans-kovaryans matrisi*

R Matrix						
Row	**Column 1**	**Column 2**	**Column 3**	**Column 4**	**Column 5**	**Column 6**
1	0.18840	-0.0684	0.0177	0.0201	-0.0416	-0.1385
2	-0.06837	4.1512	3.1752	4.0258	5.4634	1.5813
3	0.01771	3.1752	3.9813	4.4706	4.7099	1.2691
4	0.02012	4.0258	4.4706	5.9967	6.5966	1.8482
5	-0.04155	5.4634	4.7099	6.5966	9.1552	3.4360
6	-0.13850	1.5813	1.2691	1.8482	3.4360	10.4639

The rows and columns of the variance-covariance matrix $\boldsymbol{R}$ represent the repeated measurement time value. The diagonal elements of the matrix in Table 2 are variance components, and it can be easily seen that this matrix has a heterogeneous covariance structure. It can easily be seen that the variance of the body weight data increases from the first month to the sixth month. While the body weight variability in the first month was 0.1884, the body weight variability in the sixth month was 10.4639. It is expected that the variability will increase as the body weights increase over the months. The correlation matrix for the model in the unstructured variance-covariance structure is given in Table 3.

Table 3. $\boldsymbol{R}$ correlation matrix for the unstructured model

Çizelge 3. *Yapılandırılmamış model için* $\boldsymbol{R}$ *korelasyon matrisi*

R Correlation Matrix						
Row	**Column 1**	**Column 2**	**Column 3**	**Column 4**	**Column 5**	**Column 6**
1	1.00000	-0.0773	0.0205	0.0189	-0.0316	-0.0986
2	-0.07730	1.0000	0.7810	0.8069	0.8862	0.2399
3	0.02045	0.7810	1.0000	0.9150	0.7801	0.1966
4	0.01892	0.8069	0.9150	1.0000	0.8903	0.2333
5	-0.03164	0.8862	0.7801	0.8903	1.0000	0.3510
6	-0.09865	0.2399	0.1966	0.2333	0.3510	1.0000

It can easily be seen from Table 3 that the correlation is generally higher between pairs of observations close to each other and lower between pairs of observations far from each other. It is clear from Table 1 that the unstructured model DIC value is also smaller in two covariance structures examined in the informative prior specifications. Therefore, the unstructured model was determined as the most appropriate covariance structure for the body weight data used in this study for informative and noninformative prior specifications. For the model whose covariance structure is unstructured, the parameters and the mean, standard deviations, and highest posterior density (HPD) of the posterior distributions are given in Table 4.

The HPD intervals can be examined to determine if the model parameters have a significant effect. As can be seen from Table 4, no significant effect of all herd years was found on monthly body weights since their HPD intervals include 0 value. Likewise, the days to weaning do not have a statistically significant effect on body weight. However, the measurement months have statistically significant effects. Trace, autocorrelation, and posterior density graphs of each parameter are given in Appendix. It is understood from these graphs that the Markov chain converges successfully for all parameters, as there is no autocorrelation, and the posterior distributions are almost normally distributed.

Table 4. Posterior statistics and intervals for model parameters

Çizelge 4*. Model parametreleri için sonsal istatistikler ve aralıklar*

Parametre	N	Mean	Standard Deviation	95% HPD[1] intervals	
Intercept	5000	36.1302	0.9449	34.2900	37.9510
hy 1	5000	0.1255	0.5489	-0.9809	1.1454
hy 2	5000	0.0515	0.3336	-0.6091	0.7105
hy 3	5000	0.0673	0.1288	-0.1846	0.3186
hy 4	5000	0.0498	0.1294	-0.2018	0.3039
hy 5	5000	0.0709	0.1284	-0.1790	0.3234
M 1	5000	-32.0588	0.2823	-32.6451	-31.5284
M 2	5000	-21.2220	0.2908	-21.7861	-20.6364
M 3	5000	-16.1885	0.2956	-16.7883	-15.6217
M 4	5000	-10.2416	0.3064	-10.8593	-9.6554
M 5	5000	-5.9175	0.3088	-6.5463	-5.3426
iDW[2]	5000	0.0103	0.0185	-0.0257	0.0464
Residual UN (1,1)	5000	0.1884	0.0467	0.1148	0.2837
Residual UN (2,1)	5000	-0.0684	0.2352	-0.5124	0.3892
Residual UN (2,2)	5000	4.1512	0.6856	2.9183	5.5409
Residual UN (3,1)	5000	0.0177	0.1988	-0.3649	0.4043
Residual UN (3,2)	5000	3.1752	0.5996	2.0616	4.3649
Residual UN (3,3)	5000	3.9813	0.6122	2.8819	5.1980
Residual UN (4,1)	5000	0.0201	0.2541	-0.4623	0.5307
Residual UN (4,2)	5000	4.0258	0.7194	2.7390	5.4758
Residual UN (4,3)	5000	4.4706	0.7123	3.1413	5.8562
Residual UN (4,4)	5000	5.9967	0.8755	4.3278	7.6887
Residual UN (5,1)	5000	-0.0416	0.3308	-0.6591	0.6392
Residual UN (5,2)	5000	5.4634	0.8971	3.8913	7.3130
Residual UN (5,3)	5000	4.7099	0.8224	3.1916	6.3807
Residual UN (5,4)	5000	6.5966	1.0159	4.7490	8.6818
Residual UN (5,5)	5000	9.1552	1.2841	6.8359	11.7349
Residual UN (6,1)	5000	-0.1385	0.3007	-0.7204	0.4517
Residual UN (6,2)	5000	1.5813	0.6737	0.2997	2.9111
Residual UN (6,3)	5000	1.2691	0.6302	0.0680	2.5371
Residual UN (6,4)	5000	1.8482	0.7606	0.4526	3.4623
Residual UN (6,5)	5000	3.4360	0.9687	1.6401	5.3816
Residual UN (6,6)	5000	10.4639	1.3865	7.8027	13.1404
Random Var	5000	0.1402	0.0307	0.0866	0.1993

[1] HPD: Highest Posterior Density; [2]iDW: days to weaning; hy: herd year; M: Months

Geweke test, Monte Carlo standard errors and effective sample size, autocorrelation time, and efficiency are reported in Table 5 to evaluate the convergence of the Markov Chain. At a probability level of 95% ($p \leq 0.05$) significance level, the Geweke diagnostic rejects the null hypothesis that the means from the beginning and end parts of each chain are equal only for the model parameters hy2, hy3, hy4, and Residual UN (6,6). All the other chains pass Gweke's test for stationary. The standard error of the mean, also known as the Monte Carlo standard error (MCSE) provides the accuracy of the posterior estimates of the parameters. The Monte Carlo standard errors of each parameter in Table 5 are significantly small relative to the posterior standard deviations (MCSE/SD), indicating that the Markov chain has stabilized and the mean estimates do not vary much over time. As a result of the examination of both autocorrelation graphs and diagnostic tests for each parameter, it was concluded that although some parameters show that there may be slight problems with convergence as a result of the diagnostic tests, the values are very close to the desired results, and the trace plots also confirm the convergence of the Markov chain for all parameters.

Table 5. Diagnostic tests of model parameters

Çizelge 5. *Model parametrelerinin teşhis testleri*

Parametre	Geweke		Monta Carlo Standard Error			Effective Sample Size		
	z	Pr > |z|	MCSE[1]	Standard Deviation	MCSE/SD	ESS[2]	Auto-correlation time	Efficiency
Intercept	0.7386	0.4601	0.036800	0.9449	0.0389	660.4	7.5707	0.1321
hy 1	2.1697	0.0300	0.028000	0.5489	0.0509	385.3	12.9761	0.0771
hy 2	1.0568	0.2906	0.018000	0.3336	0.0540	342.5	14.5970	0.0685
hy 3	0.4737	0.6357	0.002990	0.1288	0.0232	1852.2	2.6995	0.3704
hy 4	0.2222	0.8242	0.002820	0.1294	0.0218	2105.5	2.3748	0.4211
hy 5	-2.3034	0.0213	0.003160	0.1284	0.0246	1648.4	3.0332	0.3297
M 1	0.9224	0.3563	0.003860	0.2823	0.0137	5338.8	0.9365	1.0678
M 2	0.4914	0.6232	0.004040	0.2908	0.0139	5175.3	0.9661	1.0351
M 3	1.0284	0.3038	0.004100	0.2956	0.0139	5209.2	0.9598	1.0418
M 4	0.4652	0.6418	0.004260	0.3064	0.0139	5177.5	0.9657	1.0355
apM 5	-0.4156	0.6777	0.004290	0.3088	0.0139	5193.6	0.9627	1.0387
iDW	-0.9838	0.3252	0.000788	0.0185	0.0426	550.3	9.0865	0.1101
Residual UN (1,1)	0.9388	0.3478	0.001760	0.0467	0.0377	701.8	7.1245	0.1404
Residual UN (2,1)	1.2021	0.2293	0.015000	0.2352	0.0637	246.2	20.3062	0.0492
Residual UN (2,2)	0.8443	0.3985	0.032400	0.6856	0.0472	448.3	11.1533	0.0897
Residual UN (3,1)	1.9431	0.0520	0.011500	0.1988	0.0578	299.8	16.6754	0.0600
Residual UN (3,2)	1.1207	0.2624	0.027300	0.5996	0.0455	483.0	10.3518	0.0966
Residual UN (3,3)	1.4806	0.1387	0.023900	0.6122	0.0390	657.4	7.6058	0.1315
Residual UN (4,1)	1.7864	0.0740	0.015400	0.2541	0.0605	273.2	18.3042	0.0546
Residual UN (4,2)	1.0768	0.2816	0.031700	0.7194	0.0441	514.3	9.7213	0.1029
Residual UN (4,3)	1.2615	0.2071	0.027900	0.7123	0.0392	650.0	7.6923	0.1300
Residual UN (4,4)	1.1345	0.2566	0.030600	0.8755	0.0349	819.2	6.1038	0.1638
Residual UN (5,1)	1.2450	0.2131	0.020500	0.3308	0.0621	259.6	19.2584	0.0519
Residual UN (5,2)	0.8187	0.4129	0.038300	0.8971	0.0426	550.0	9.0903	0.1100
Residual UN (5,3)	0.9584	0.3378	0.033900	0.8224	0.0412	589.8	8.4768	0.1180
Residual UN (5,4)	0.8988	0.3687	0.039000	1.0159	0.0384	679.4	7.3591	0.1359
Residual UN (5,5)	0.5851	0.5585	0.042300	1.2841	0.0330	920.7	5.4305	0.1841
Residual UN (6,1)	-1.6937	0.0903	0.013600	0.3007	0.0451	491.7	10.1681	0.0983
Residual UN (6,2)	-1.5670	0.1171	0.017200	0.6737	0.0256	1530.8	3.2662	0.3062
Residual UN (6,3)	-1.4985	0.1340	0.014200	0.6302	0.0226	1965.7	2.5436	0.3931
Residual UN (6,4)	-1.4446	0.1486	0.016900	0.7606	0.0222	2029.2	2.4641	0.4058
Residual UN (6,5)	-1.5982	0.1100	0.022500	0.9687	0.0232	1851.2	2.7010	0.3702
Residual UN (6,6)	-2.2862	0.0222	0.030300	1.3865	0.0219	2093.4	2.3884	0.4187
Random Var	-0.8471	0.3969	0.000470	0.0307	0.0153	4262.9	1.1729	0.8526

[1]MCSE: Monta Carlo Standard Error; [2]ESS: Effective Sample Size; hy: herd year; M: Monthly body weights.

DISCUSSION and CONCLUSION

The distinguishing feature of the repeated measure analysis model from other models is its assumptions about error variance and covariance structure. Therefore, repeated measurement data analysis relies on appropriately calculating the correlations between observations within the same unit and the potential heterogeneous variances over time within the same unit. Based on this assumption, it was aimed for a wide range of covariance selections to make more accurate calculations, hence facilitating the selection of the most suitable model. As per the literature reviews, the GLM was chosen to analyze body weight data, considering that general linear mixed models that allow for covariance structures are appropriate for repeated measurement data. In determining the variance-covariance structure, it is effective whether it is homogeneous or heterogeneous, whether there is data with missing observations or not, whether the time intervals are equal or not, and whether the number of repeated measurements is more or less. Therefore, it cannot be directly stated that a particular variance-covariance structure is appropriate. Selecting the most suitable model for repeated measurement models containing complicated dynamics is more accurate by trying different covariance structures. The number of parameters for different covariance structures differs. It has been shown in this study that the convergence problem can be solved for a complex covariance structure when the number of data is large enough.

Bayes Monte Carlo methods offer an attractive alternative as compared to other statistical methods. Some advantages of the Bayesian approach are greater flexibility in model specification, incorporation of prior information, and straightforward interpretation of uncertainty. Many academic studies have adopted Bayesian methods in various research fields (e.g., (Calus et al., 2018; Gevrekçi & Akbaş, 2014; Lemoine, 2019; Milkevych et al., 2021; Theobald et al., 1997)). In order to interpret Bayesian analysis correctly, the researcher should have sufficient knowledge about MCMC. In cases where MCMC convergence of the posterior distribution does not occur, care should be taken when interpreting the results. Convergence can be achieved, and analysis accuracy can be increased by creating longer chains or choosing different priors. Trace plots are the most efficient convergence test used in the literature for convergence diagnosis. However, different diagnostic tests will give more accurate results instead of relying on only one convergence tool. In this study, different diagnostic tests, the Geweke test, Monte Carlo standard errors, and effective sample size, were evaluated together with trace charts. There was a general convergence in the posterior distributions of all parameters for the study data. Thus, reliable posterior statistics of parameters for body weight data were obtained, and their interpretations were given.

The Bayesian approach has some advantages. For example, there is no negative estimation problem of the variance components, and the sample size is increased by the simulation method in data sets with small sample sizes. Başar and Fırat (Başar & Fırat, 2016) emphasized that the Bayesian estimation method using the Gibbs sampling approach is suitable for estimating variance components under a balanced two-way nested design, especially for small sample datasets, compared to traditional methods. Yomi-Owojori et al. (Yomi-Owojori et al.,2020.) argued that the Bayesian approach is suitable for small sample-size experiments, which are common for repeated measurement designs. They indicate that the differences for different covariance structures are more than when the sample size is small but converge to the same results when the sample sizes are large. However, while Bayesian methods are better equipped to model data with small sample sizes, the estimates are susceptible to the properties of the a priori distribution. McNeish (McNeish, 2016) emphasized that Bayesian estimations may be worse than classical methods if this aspect is not considered.

Despite the many advantages of Bayesian analysis, there is an ongoing debate about its application in practice. The two main disadvantages of Bayesian analysis are assumed subjectivity in selecting informative priors and computational difficulties in applying Bayesian methods. A sufficiently large sample selection can relatively eliminate the subjectivity of an informative prior selection. The new

procedure of the SAS program, PROC BGLIMM, allows Bayesian analysis to be calculated more easily, easing the computational difficulties relatively. The fact that this new procedure is more user-friendly than PROC MCMC, which requires more programming knowledge, indicates that Bayesian analysis will be preferred by more researchers. PROC BGLIMM uses efficient sampling parallelized algorithms for performance, resulting in good mixing and faster computation (SAS Institute, 2019).

It was observed that the DIC values of the models created for the 12 different variance-covariance structures determined were relatively close to each other for UN (DIC: 2499.38), ANTE (DIC: 2533.23), and FA (DIC: 2551.29), with significant differences, compared to other models. Lunn et al. (Lunn et al., 2012) discussed “approximate” rules for interpreting differences in DIC value when choosing a preferred model. They concluded that while choosing the model according to the difference between the DIC values of the compared models, the model with higher DIC should be excluded if there are more than 10 differences between them. They also concluded that differences between 5 and 10 reflect “significant” differences in favor of the smaller DIC value model, and choosing a preferred model for discrepancies between models less than 5 may have misleading results. Because the difference of 33.85 between the models in the UN and ANTE variance-covariance structures with the closest DIC values to each other is greater than 10, it was found to be appropriate to prefer the model with the smallest DIC value, which is UN (see Table 1). This study proved that the Bayesian approach is suitable for repeated measurement designs of different variance-covariance structures and can easily model repeated data in animal science, such as body weight. As a result of the literature review, no variance-covariance structure model was found in this diversity, which was solved by Bayesian methods. In the case of the UN structure, this is a heterogeneous variance covariances structure with no assumptions. It can also be a good choice for the researcher when the number of repeated measurements is low. However, as with traditional regression, the best model is parsimonious with as few parameters as possible. The larger the number of parameters, the more complex the model, and the more specific the data and, therefore, less generalizable. The decision should be made with the belief that we should prefer the simpler model whenever possible. As a result, the UN covariance structure was considered preferable and suitable for biological data in repeated measurement analyses. Having few repeated measures and balanced data with equal time intervals led to choosing this model. In this study, the UN model also has a smaller DIC value for the two covariance structures examined in the informative prior selection. The results of noninformative and informative prior selections have been observed to be very similar. Therefore, the UN model was determined as the most appropriate covariance structure for the body weight data used in this study in selecting both informative prior and noninformative prior. This is the conclusion that if the sample size is large enough, the posterior distribution will not be affected much by informative or noninformative prior specifications. Although there are studies on modeling variance-covariance structures with classical methods in the literature, there are limited number of studies that involve modeling variance-covariance structures with Bayesian methods. This study presents the most comprehensive variety among the studies on modeling the variance-covariance structure whose parameter estimation method is Bayesian. It was proved that the complex formulations can be analyzed using Markov chain Monte Carlo approaches for any variance-covariance structure.

Twelve different covariance structures were modeled with PROC BGLIMM, and this new procedure was introduced. It was concluded that the PROC BGLIMM procedure is an effective and suitable method for repeated measurement analysis of Bayesian solutions. Based on the logic that progress in scientific research is based on accumulated knowledge, it is believed that the Bayesian solutions will find more place in many fields.

Acknowledgment/Disclaimers/Conflict of interest

The authors declare that no conflict of interest could be perceived as prejudicing the impartiality of the research reported.

Data Availability Statement

All data used for this article is available upon request.

Software

Data analysis was performed with SAS® Ondemand for Academics.

https://welcome.oda.sas.com/home (04.03.2023)

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