



**Bayesian inference describing statistical models based on the average daily gain of Nile Tilapia (*Oreochromis niloticus* "GIFT")**

***Modelagem estatística utilizando inferência Bayesiana para descrever o ganho em peso médio diário em Tilápias do Nilo (*Oreochromis niloticus* variedade "GIFT")***

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**Abstract:** The aim of the current study was to analyze four statistical models using Bayesian inference to describe the average daily gain (g) (ADG) during the genetic selection of the Nile Tilapia (*Oreochromis niloticus* "GIFT"). The data set had records from 2,615 fish collected from the fourth generation (G4) of the breeding programme in the Floriano Breeding Station of the Universidade Estadual de Maringá, Maringa County, Paraná State, Brazil. In these analyses, we considered an animal model where sex was the fixed effect, linear and quadratic effects of the fish age was covariates in days in conjunction with the additive genetic effects. The models were modified based on the available information from additive genetic effects and common environments of hatchery (c), nursery (w), or none of them. The heritability results were estimated for the models, M2=0.24 and M4=0.23 and high for M1=0.83 and M3=0.79. The criterion of selection in the DIC model was lower for the M1 with -282.59 and higher for M4 with 1754.57. Another criterion of selection was the marginal log density of the Bayer factor which corroborates with the DIC only for the lower value in which M1=585.29. Less computer efforts to achieve convergence was found using the M1 model with 15,000 chains, which was the best model to explain and predict the phenomenon.

**Keywords:** Bayes factor, genetic breeding, fish, model.

**Resumo:** O objetivo do estudo atual foi analisar quatro modelos estatísticos usando inferência Bayesiana para descrever o ganho diário médio (g) (ADG) durante a seleção genética da Tilapia do Nilo (*Oreochromis niloticus* "GIFT"). O conjunto de dados foi composto por informações de 2.615 peixes, pertencentes a quarta geração (G4) do programa de melhoramento de peixes na estação de experimental de Floriano da Universidade Estadual de Maringá, município de Maringá, Paraná, Brasil. Nessas análises, consideramos um modelo animal em que o sexo foi o efeito fixo, os efeitos lineares e quadráticos da idade do peixe foram covariáveis em dias e os efeitos genéticos aditivos. Os modelos foram modificados com base na informação disponível de efeitos genéticos aditivos e ambientes comuns de larvicultura (c), alevinagem (w), ou nenhum deles. Os resultados para herdabilidade estimados para os modelos, M2 = 0,24 e M4 = 0,23 foram considerados médios e altos para M1 = 0,83 e M3 = 0,79. O critério de seleção no modelo DIC foi menor para o M1 com -282,59 e superior para M4 com 1754,57. Outro critério de seleção foi a densidade de registro marginal do fator Bayer que corrobora com o DIC apenas para o valor mais baixo em que M1 = 585,29. Menos esforços de computador para alcançar a convergência foram encontrados utilizando o modelo M1 com 15 mil cadeias, sendo o melhor modelo para explicar e prever o fenômeno.

**Palavras chave:** Fator de Bayes, melhoramento genético, peixe, modelo

**Introduction**

In fish breeding, the foremost decision is to determine achievements to choose traits to improve

and, thus, decide strategies of selection straightforward to the objectives fixed in the programme. In animal production, the expectancy



is to find products of high quality, and the breeding or the selection have to act as an economic strategy to reach the standards of quality facing genetic gains in one or various traits necessary to obtain the produce. These traits have to be responsive to the selection and cost-effective to the fish grower, industry and consumers because breeding programmes increases the productivity of aquatic farming (Gjedrem, 2000; Hulata, 2001).

The choice of any characteristic as the criterion of selection requires strictness on both, the quantity and quality of information and know-how about genetic and phenotypic parameters of the productive trait. In Tilapias, the focus of the breeding programmes has been limited to growth rate (Ponzoni et al., 2005).

In 2005, the introduction of 30 families of Nile Tilapia variety GIFT started the fish breeding programme in the Floriano Experimental Station, at Maringá County, Paraná State, Brazil. This national background with Tilapia has been promising positive results because of the positive genetic gains. The average daily gain of 2.6% in the generation G2 rose to 8.1% in the G3 (Oliveira, 2011), and may achieve the level of 15% per generation under highlighted breeding programmes (Ponzoni et al., 2005).

In fish, the average daily gain (ADG) is relevant and important in breeding programmes because it is highly correlated with production and live weight (g) with estimates of a 0.95 and 0.89 for phenotypic and genetic characteristics (Oliveira, 2011). Easy to record, the ADG has motivated its use as the criterion of selection at the breeding programme with Tilapia in the Universidade Estadual de Maringá.

Predicting genetic values with excellence during the selection requires reliable estimates of the variance components. Furthermore, the choice of the statistical model is the foremost step to analyze the data by choosing a model with less parameters but highly efficient in describing the response through affordable, safe and precise statistical inference (Bozdangan, 1987). Since 1986 (Gianola & Fernando, 1986), the Bayesian inference has been strategically recommended to solve animal breeding problems but only in decade of 1990 it became a routine in animal breeding (Gianola & Foulley, 1990; Jensen et al., 1994; Rekaya, 1997).

The Bayesian theory is underlined in the conjunct distribution of sample data named

likelihood function and *a priori* distribution about the parameters to determine the *a posteriori* distribution based on the product likelihood x priori, where is did inferences (Silva et al., 2005). In Brazil, it has been largely recommend in animal breeding (Magnobosco, 1997; Rosa, 1999).

In general, the animal model  $y = X\beta + Za + e$  accounts for genetic additive and residual effects for every individual, although the analyses may range according to the data set and the available information, i.e. maternal genetic effects, common environment, or permanently modification in the results and in the genetic merit of the animals. Thus, the relevance of the information included in the animal model is truly important. Misztal (2008) stated that the model have to contain the foremost effects or those that change the parameters when they are missing, and not necessarily because they are statistically significant.

The model selection obey the criterion (Bozdongan, 1987; Wolfinger, 1993; Littell et al., 2002) based on the maximum likelihood function highlighting the likelihood ratio, the Akaike criterion (Akaike, 1974) useful for testing two models when both are a reparametrization (nestle or framed). This criterion admits a real model for describing unknown data and choosing among a group the model that minimize the divergence of Kullback-Leibler (K-L). The best goodness of fit is found based on the lower AIC values. The DIC - *Deviance Information Criterion* (Spiegelhalter et al., 2002) is similar to the AIC when the fixed models are investigated. Furthermore, another criterion is the Bayesian from Schwarz (BIC) (Schwarz, 1978), when the best fit has the lower AIC. The *Deviance Information Criterion* (DIC) (Spiegelhalter et al., 2002) is relatively similar to AIC when the model has only fixed effects. Another criterion is the (BIC) Bayesian of Schwarz (Schwarz, 1978) which assumes the existence of true model to describe the relation of the dependent with the explanatory variables. This model is defined as the statistics that maximize the probability of identify the true model among other under evaluation. The lower BIC indicates the best goodness of fit.

The model choice can be done by the relative density of the data applying the log-score on the Bayes Factor (FB). The method consists in applying the log of marginal probabilities from every variate  $y$ , conditioned to the other records.



The result is a predictive score, or the estimate of the data prediction. The Bayes Factor is similar to the likelihood test from the frequentist inference and can be applied to compare models. Mathematically, it is summarized as the following deviance,  $-2\log\text{Likelihood}$  (Gelman et al., 2004) or  $D(y|\theta) = -2 \log [p(y|\theta)]$ . In the BUGS software for Bayesian Inference (Gilks, Thomas & Spiegelhalter, 1994) this deviance is different of the frequentist inference in which the D of the reduced is compared to the complete model. In the Bayesian inference, the lower expected deviance (DIC) is the one with the higher probability a posteriori (Gelman et al., 2004).

The aim of this experiment was to apply the Bayesian inference on statistical models to discriminate which one allows better goodness of fit of parameters to improve the accuracy in the GIFT Tilapia selection with genetic outstanding.

### Material and methods

Information from 2,615 fish in the data bank of the fourth generation in the breeding programme of the Universidade Estadual de Maringá (UEM), Paraná State, Brazil were analysed in this experiment. The fish had an average daily gain of  $1.37 \pm 0.477$  g.

The experiment started in Fish Station of the UEM, mating animals of the third generation (G3) to obtain the fourth generation (G4). They generated clusters of siblings and half-siblings individualized by *Passive Integrated Transponder (PIT) tags* (Oliveira, 2011). Soon after the recovering period, they were transferred into pond nets in Diamante do Norte County, Parana State where the average annual temperature in the Corvo River was about 24 °C. The animal density was 150 fish m<sup>3</sup> using some animals with no microchips to make up the population. The ponds were genetically connected with siblings and half-siblings.

The data sets were monitored by SAS® (Statistical Analysis System) to guarantee the information quality through eliminating inconsistent records. Thus, the data set had information from 2,615 animals in grams.

Estimates of the covariance components were carried out by Gibbs sampling using Bayesian inference from the GIBBS1f90 software (Misztal et al., 2002). The animal model included the fixed effects of sex, linear and quadratic effects of the covariate age (d) for the last biometric record (5<sup>a</sup>).

Eight models for uni-characteristics from which the most complete -- the number eight (M8) -- have the following matrix shape:

$$y = X\beta + Z_1a + Z_2c + Z_3w + e;$$

where:

$y$  is the observation vector;

$X$ ,  $Z_1$ ,  $Z_2$  e  $Z_3$ , are incidence matrices of the environment effects, genetic direct effects and common environment of hatchery and nursery, respectively;

$\beta$  is the vector of sex effects, raising site and age;

$a$ ,  $c$ ,  $w$  and  $e$  are, respectively, the vectors of additive genetic effects, common environment of hatchery, nursery and residual.

All the models accounted for the additive genetic effects and the residual. The model 1 (M1) accounted just for the additive genetic effect, the M2 for common effect of hatchery (c), the M3 for common effect of nursery (w), the M4 for common effect of nursery (c) and hatchery (w). The number of fish in the parentage matrix ( $A^{-1}$ ) was 10,301.

The following Gibbs chains to achieve convergence were M1: 15,000; M2: 30,000, M3: 25,001, M4: 30,000 after burn-in 10% of the initial iterative calculation.

The analyses account for additive genetic effects, common effects of hatchery and nursery environment and residual as obeying the normal distribution and the *a priori* distribution as non-informative. Convergence was tested and verified by the POSTGIBBSf90 software (Misztal et al., 2002) through the diagnose test of Geweke (1992) and Heidelberg & Welch (1983), in the CODA Library (Convergence Diagnosis and Output Analysis) version 0.4, developed by Cowles et al. (1995) and embed in the R programme (version 2.8.1 (2008-12-22)).

In Bayesian inference, the most common method to evaluate the merit of a statistical model is to generalize the frequentist method, the Akaike information criterion (AIC). Spiegelhalter et al. (2002), however, developed an information criterion in which the effective number of parameter is given by:

$$pD = D^* - D(\theta^{**});$$

where  $D(\theta) = -2\ln p(y|\theta)$  is the deviance function,  $\theta^{**} = E(\theta|y)$  e  $D^* = E(D(\theta^{**})|y)$

The information criterion is the DIC (*Deviance Information Criterion*), given by:



$$DIC = -2 \log p(y|\theta'') + 2pD.$$

D\* estimate the model goodness of fit and pD gage its complexity. The DIC generalize the AIC and small values of the DIC are more adequate because they have a weighed fit according to the complexity degree. Based on the authors, the following criterion may be used:

$D = |DIC_A - DIC_B|$  (for comparing two models):

- Whether  $D < 5$ : non-significant;
- Whether  $5 \leq D \leq 10$ : significant;
- Whether  $D > 10$ : highly significant.

The GIBBS1f90 software have the DIC and the Bayes Factor (FB), which is used to select models and can be calculated by computational methods as the Monte Carlo or numeric method in every situation as the Laplace approximation method. This factor is related to likelihood ratio test where the parameters are maximized rather than integrated (Missão, 2007). The FB is the measure from data favoring the statistical model. In 1961, Jeffreys suggested interpret the Factor in four intervals. Kass and Raftery (1995) made a motion to use two times the log of the FB to achieve precision in the intervals. Thus, the value has the same scale of likelihood ratio test by using:

$2\log_e(B_{10})$	B10	
0 – 2	1 – 3 =	Nonsignificant
2 – 6	3 – 20 =	Significant
6 -10	20 – 150 =	Strong
> 10	> 150 =	Stronger

Based on the DIC and the log of the marginal density for FB, we discriminate the

statistics among the current models. In computational terms, the DIC is more attractive than the Bayes Factor because the terms can be attached in the MCMC routines (Zhu and Carlin, 2000; Berg, Meyer and Yu (2002). In the current study, we made the option by both criteria based on the (GIBBS1f90) software.

**Results and discussions**

The models M1 (0.17) and M3 (0.16) unlike the M2 (0.04) and M4 (0.04) were the best explanation for the additive genetic variation. The M1 was different about the inclusion of the common effect of nursery in the M3 indicating that the inclusion of ( $w^2$ ) has little modification in the additive genetic variation. M2 and M4 are similar about the common effect of nursery ( $c^2$ ) indicating that the presence of this effect there is a little contribution to understand the additive genetic effect. The M4 also has the  $w^2$  effect. The decrease in the genetic variation in this model is significantly lower than in the M3, but nonsignificant in comparison with the M2. This result indicates harmful interference of the  $c^2$  during the additive genetic variation (Table 1).

Estimates from the variances in common nursery environment ( $c^2$ ) and hatchery ( $w^2$ ) ranged from 0.004 to 0.09. The lower residual variances was estimate for the models M1 (0.03) and M3 (0.04) (Table 1). This response in the additive genetic variation in the several models about the inclusion of the  $c^2$  and  $w^2$ , or both effects may be explained by the content and the figure of every variable because these results were estimates from the last biometry, the fifty one, where the fish had an average age of 294 days when the common effects of nursery ( $c^2$ ) were far away in time unlike the common effect of the hatchery.

**Table 1.** Estimates of variance components ( $\sigma^2$ ) and the covariance for additive genetic effect ( $\sigma_a^2$ ), common effect of hatchery environment ( $\sigma_c^2$ ), common effect of nursery environment ( $\sigma_w^2$ ), residual ( $\sigma_e^2$ ) and phenotypic effect ( $\sigma_y^2$ ), for models M1, M2, M3 and M4.

Models	$\sigma_a^2$	COV <sub>AM</sub>	$\sigma_m^2$	$\sigma_c^2$	$\sigma_w^2$	$\sigma_e^2$	$\sigma_y^2$
<b>M1</b>	0.17	-	-	-	-	0.03	0.20
<b>M2</b>	0.04	-	-	0.04	-	0.09	0.18
<b>M3</b>	0.16	-	-	-	0.004	0.04	0.20
<b>M4</b>	0.04	-	-	0.04	0.003	0.09	0.18

The heritability illustrates the relative proportion of the genetic and environmental influences on genotypic manifestation of the traits

and indicates the easy or difficult degree to improve some traits, from which higher heritability means higher facility. Higher herdabilities are





presented by M1 with 0.83 and M3 with 0.79 unlike M2 with 0.24 and M4 with 0.23 (Table 2) This result indicate the M1 with capacity to help the breeder the best understanding of the genotype expression through the phenotype, offering more accuracy in the fish selection, and highlighting the individual genetic value rather than the family values.

Based on Lush (1936), when the  $h^2$  of some trait is high, it is possible highlight the massal selection or discriminate the animals by their phenotype values or apparent merit. In contrast, as soon as the value is reduced, the individual have to be choosing by their intrinsic value, evaluated from the family responses.

Table 2. Heritability estimates ( $h^2$ ), common effects of hatchery environment ( $c^2$ ) and common effect of nursery environment ( $w^2$ ).

Modelo	$h^2$	$c^2$	$w^2$
M1	0.83	-	-
M2	0.24	0.23	-
M3	0.79	-	0.02
M4	0.23	0.21	0.02

Models: M1;M2;M3 and M4.

Selecting animals with high heritability, the genetic gain will be emphasized, but under high  $h^2$  in which the individual response is the emphasis rather than families, the risk is to lose the variability that is very important for breeding programmes. This fact did not occur in Tilapia because all the families are maintained through selection generation by representative progenies. In this case, the best animals from all the families in the breeding population are selected to guarantee the variability and consequently the programme longevity. Thus the M1 model with the best explanation of the phenotypic variation because the genetic differences in individuals and higher  $h^2$  may be used without losses in the genetic variability in next generations. The M1 have the best estimates with higher explanation of the additive genetic variation (Table 1) and higher heritability (Table 2). The environmental variance depends on the farming and management e higher variations of the conditions reduce the heritability while higher uniformity increases it (Falconer, 1987). However, the environmental information (hatchery and nursery) available can be ignored because of the low participation in phenotype expression of the ADG, based on the current results.

Based on the DIC, the best model is the M1 because it aggregated only additive genetic values and residual effects in its estimates with *Deviance Information Criterion* of -282,59, in contrast with the worst goodness of fit for the M4 with 1754,57 (Table 3). Negative values of DIC are possible, as we found in the current experiment (DIC M1:-282.59), under some circumstances such as sampling distributions log- nonconcave (for example, the t-Student) when there is substantial conflict in the data a priori, when the distribution a posteriori for a parameter is highly asymmetric or symmetric bimodal, or the mean a posteriori is statistically poor which induce a large bias (available in: The Bugs Projec < <http://www.mrc-bsu.cam.ac.uk/bugs/winbugs/dicpage.shtml#q7>> outubro, 2013). In parameters of the M1, the a posteriori was asymmetric which justifies the negative value.

The model M1 with the lower DIC has lower deviance, because the best model has the lower deviance (Gelman et al., 2004) where  $-2\log(p)$  for FB=585.29 (Table 3).

The less computational effort was found fitting the M1 model with 15,000 chains to achieve convergence of parameters (Table 3).

Table 3. DIC estimates, logarithm of the marginal density For the Bayes Factor, and chain number to convergence

Models	DIC	$-2\log(p)$ for Bayes Factor	Chain number
M1	-282.59	585.29	15,000



M2	1,710.51	1,823.79	30,000
M3	81.19	912.26	25,001
M4	1,754.57	1,782.47	30,000

### Conclusion

The most reliable model with lower number of effects to explain and predict the efficacy the ADG of the Nile Tilapias was the M1. It was the best model in explaining the additive

genetic variation, had higher heritability and better values of goodness of fit for DIC and marginal density for BF in conjunction with less computational effort.

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