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# Advances in Animal Biosciences

## Proceedings of the 9th Workshop on Modelling Nutrient Digestion and Utilization in Farm Animals (MODNUT), 14-16 September 2019, Brazil

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*Advances in Animal Biosciences* is an associated publication to the journal *animal*. It aims to publish high-quality conference, symposium and workshop proceedings about animal-related aspects of the life sciences with emphasis on farmed and other managed animals. These can be in the form of a book of abstracts, summaries or complete papers. The format will highlight the title of the meeting and organisations involved but the publications will have the added advantage of forming a series under *Advances in Animal Biosciences.*

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Cover picture of chicks kindly provided by Bruno Biagioli (MODNUT committee)

# Proceedings

of the
9th Workshop on Modelling Nutrient Digestion
and Utilization in Farm Animals (MODNUT)

# 2019

## Advances in Animal Biosciences

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The Proceedings of the 9th Workshop on Modelling Nutrient Digestion and Utilization in Farm Animals (MODNUT) constitute summaries of papers presented at the 9th MODNUT held at the Itamambuca Eco Resort, Ubatuba, São Paulo, Brazil, 14-16 September 2019.

The summaries have been reviewed. Views expressed in all contributions are those of the authors and not those of the MODNUT Committee.

This publication contains all the summaries that were available at the time of going to press.

**Editors**

I A M A Teixeira
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# Assessing nutritional models: methods and issues

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**Application** The assessment of mathematical models require methods that explicitly recognize errors in the model and lead to statistics and tests that answer the question ‘Is the model satisfactory for a stated purpose?’.

**Introduction** Research in nutrition often leads to hypotheses and theories that must be expressed using mathematics. The mathematics involved can be a single function or take a much more complex form, resulting in what are known as mathematical models. Such models can be classified as dynamic or static, mechanistic or empirical, deterministic or stochastic. Deterministic models simply reflect the inability of the modeler to estimate the precision of the proposed model. Also, because models are abstractions and simplifications of the much more complex reality, they cannot fully characterize reality in its most intricate details: ultimately all models must be wrong. This leads to the inevitable need to assess the adequacy of a given model in representing sufficiently well the features of the real world relevant to a defined task or set of objectives. This is the essence of model assessment, which is different to model validation because models can never be valid (i.e., correct), but can be useful.

**Results** Many methods of model assessment have been proposed and have been reviewed by Tedeschi (2006). In general, methods fall into one of the following categories: linear regression, including orthogonal regression and modified regression, analyses of deviations, analyses of residuals, concordance correlation coefficient, mean square error of prediction, partitioning of MSEP into error in central tendency (i.e., mean bias), errors due to regression (i.e., linear bias), and errors due to disturbances (or random errors). All of these methods suffer from one or more deficiencies in that they either set an incorrect model, test an incorrect hypothesis, provide metrics that are not easily interpretable, or fail to answer the right question. An ideal assessment method should (1) account for the stochastic nature of both observations and model predictions, (2) set correct null hypotheses, (3) treat model predictions and observations interchangeably, and (4) provide quantitatively interpretable statistics relative to precision and accuracy. We have proposed a method based on linear structural relationships (St-Pierre, 2015). Unlike ordinary least-squares, where the projections from the observations to the regression line are parallel to the y-axis and inverse regression where they are parallel to the x-axis, the generalized projection regression method (GePReM) projects the observations on a regression line in a direction determined by the ratio of the precision of the observations to that of the mathematical model predictions. Estimation and testing issues arise when the model is expressed in the common slope-intercept format. A polar transformation circumvents issues related to estimation and testing. The parameter for the angle between the regression line and the horizontal axis has symmetrical confidence intervals and is equivariant to the exchange of observations and model predictions. The null hypothesis for the equivalence test is that the model predictions are not equivalent to the observations. Information size is calculated as the simple ratio of the variance of the true values of the observations and of the computer model predictions divided by their respective precision. This information size plays a critical role in determining the number of observations required and the size of the zone of practical tolerance for the equivalence tests. The terminology used in the comparison of measurement methods is adapted to that of model assessment based on the equivalence tests on the relative precision, regression slope, and mean bias. Further work is needed to expand GePReM to accommodate the general case where observations are gathered across many studies.

**Conclusion** Most methods currently used in model assessment do not answer the correct question, are incorrectly interpreted, or lead to incorrect tests. GePReM has a solid statistical foundation and leads to tests that answer the relevant question as to whether the model is adequate for a given application.

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# The Role of Mechanistic Models in the Era of Big Data and Intelligent Computing

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**Application** Empirical and mechanistic models have supported the agriculture sector for decades, but their role in the coming era of 'big data' and intelligent computing is unclear. This positional paper proposes that hybridization of modelling approaches represent a niche for agriculture where our cumulative biological knowledge (within mechanistic models) meets the emerging data collection and predictive potential of big data analytics using machine learning and deep learning methods.

**Introduction** Mechanistic models (MM) have served as 'decision-support' and 'opportunity analysis' tools within animal agriculture for decades. Such models define how a biological system works based on theory, and use that cumulative biological knowledge to generate predictions and recommendations (in practice) and provide causality and generate/evaluate hypotheses (in research). Their associated limitations, however, revolve around obtaining sufficiently accurate inputs, user training and accuracy/precision of predictions on-farm. The new wave in digitalization technologies may, however, augment some of these challenges. New data-driven (DD) modelling methods such as machine learning (ML) and deep learning (DL) examine patterns in data to find useful predictors of a given outcome. The deluge of sensor data and new 'intelligent' (self-learning) modelling techniques such as ML and DL may address some of the limitations of traditional MM approaches – access to input data (e.g. sensors) and on-farm calibration. At the same time, however, most of these new methods lack transparency in the reasoning behind predictions – something which is inherent within mechanistic models and has historically allowed one major functional use of models - to translate knowledge into wisdom. The objective of this paper is to propose that these two seemingly divergent methodologies could be hybridized to advance the models we use, our knowledge of biology and support movement towards true knowledge-based precision agriculture systems.

**Methods** In order to identify potential niches for models within animal agriculture of the future, a cross-species (dairy, swine, poultry) examination of the current state-of-the-art in (1) mechanistic modelling, (2) data availability (sensors & other on-farm data collection systems) and (3) new methodologies (DD, ML, DL analytics) is undertaken.

**Results** We hypothesize that there are several ways the two diverging approaches – DD modelling and MM – may be hybridized to advance both our predictive capabilities and system understanding: (1) Utilizing new data-streams (e.g. intake, rumination behaviour, activity sensors, environmental sensors, cameras, NIR) to apply MM in real-time and/or more accurately with new resolution and capabilities in input data; (2) Hybridization of MM and DD approaches where (for e.g.) a ML framework is supplemented/deepened by MM-generated parameters or predicted outcome; and (3) Hybridization of MM and DD approaches, where biological bounds are placed on parameters within a MM framework, and the DD system parameterizes the MM for (e.g.) individual animals, farms or integrations.

**Conclusions** As animal systems modellers we should examine potentially advantageous relationships between MM and DD, by expanding our tool box to explore the new DD analytical approaches to find opportunities to increase understanding of biological systems, find new patterns in data and move the field towards intelligent knowledge-based precision agriculture systems.

# Predicting clinical mastitis incidence and pathogen type: challenges and options for sparse datasets

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**Application** Prediction of clinical mastitis (CM) before a dairy cow becomes clinical aides the farmer in choosing a treatment and early treatment can save milk in current and future lactations. Utilizing outlier detection and data filling procedures to clean inline-milker data before training CM models can decrease error.

**Introduction** Mastitis costs farmers an estimated $2 billion in the US annually. Although mastitis' total cost is great, the prevalence is only about 15 CM cases per 100 cows per lactation, or 1 CM case per 2033 cow-days (~0.05%; (McDougall et al., 2007). When considering the costs of predicting a CM case, the cost of a false-negative is close to $0, because the cow will likely show signs of mastitis in the coming days. The costs of false-positives (FP) and true-positives (TP) are lost milk and medication. Additionally, TP cases incur costs on future performance, but also benefits from recovery and rejoining the herd. Using previous literature, the cost of an FP is estimated at $165 and the net benefit of treating a TP cow is a gain of $132 (Bar et al., 2008).

**Material and methods** Data used in this trial were collected from dairy farms at Virginia Tech (VT) and the University of Florida (UF). Two datasets were collated, a case-control dataset (PAIR, n = 268, CM% = 50%), and a longitudinal (LT, n = 136,107, CM% = 0.47%) dataset. Data were collected using in-line milk analyzers (AfiLab©, S.A.E. Afikim, Israel) and pedometers (Afi PedometerPlus or Afi Pedometer) for 14 d prior to and following a CM event. All data were scaled, outliers were removed, and missing data-handling techniques like using a cow's previous day's values or the herd average value were employed to improve future accuracy at the individual cow level. All models were built with CM as the binary response variable and explanatory variables were activity, fat, protein, lactose, MY, conductivity, lactation, and DIM. Gram-positive and -negative models were iterated 1,000 times and evaluated under binary classification error loss.

**Results** Models yielded average Sp and Se of 99.9% and 34.6% for GP models and 99.8% and 55.6% for GN models. When our derived cost equation per 100 cows was applied to the models, the weighted models produced an estimated net loss of only $0.29 per prediction made assuming a 0.05% incidence of CM.

**Conclusion** The current research shows potential pitfalls of training models without considering the applications of the model on-farm. A model with Sp/Se = 75/95 (CM incidence of 0.05%) would have an estimated net loss of $8.19 per cow-prediction. Clinical mastitis cases are costly to the farmer, but the costs or errors in mastitis detection models are not equal between the four classification outcomes. By attempting to properly assess the costs of predicting CM, not the CM case itself, more applicable models can be built.

**Acknowledgments** We wish to acknowledge farm staff at the Virginia Tech Dairy Center and the University of Florida Dairy Unit for assistance with data collection and Afimilk Ltd. for data extraction.

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# Molly at 32: What Works and What Does Not

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**Application** The Molly model is primarily a research tool used for knowledge integration and testing.

**Introduction** The dairy cow model Molly (Baldwin 1995) was developed by Baldwin and coworkers in 1987. That work encompassed a rewrite of an earlier model and was composed of equations containing parameters derived in isolation or were assumed. More than 30 manuscripts describing evaluations, structural changes, and parameter estimates have been published. The objective of this work is to summarize some components of the model that seem to represent the observed data well and other areas that do not.

**Results** Most work with Molly has been undertaken using only lactating cow data. Li et al. (2018) added meta data from beef animals resulting in much greater range in diet composition. Ruminal starch digestion was poorly represented with 60% RMSE for predictions of outflow. Non-ammonia, non-microbial nitrogen (N) is also not predicted well at 40% RMSE, and microbial N outflow had an RMSE of 30%. Both had substantial mean bias, but no slope bias suggesting a parameter estimation problem. Total N outflow had an RMSE of 19% with no bias suggesting offsetting bias in the 2 subflows. Fiber and lipid outflow were predicted with much greater accuracy.

Ruminal ammonia concentrations were predicted with an RMSE of 50% of which 44% was due to slope bias. Predictions of blood urea had an RMSE of 52% with 29 and 33% mean and slope bias, respectively. Although pH appeared precise at an RMSE of 5%, the CCC was 0 indicating the model was capturing none of the observed variation. These 3 entities were found to be correlated suggesting a link. Ruminal ammonia and pH problems also were suggested to contribute to the microbial growth problem. The ammonia and urea problems were associated with inadequate rates of exchange of the 2 across the rumen wall. The N cycling problem was addressed using data from double labelled urea experiments which has helped with microbial growth and ruminal pH. However, pH predictions remain a problem exhibiting much less range than in reality.

Ruminal volatile fatty acid (VFA) concentrations were predicted with reasonable precision and minimal bias suggesting the empirical approach to partitioning fermented carbohydrate works. However, VFA production rates were predicted very poorly (Ghimire et al., 2014), although data quality was poor. The highly empirical structure of this system needs to be more mechanistic, Ghimire et al. (2017) attempted to utilize thermodynamic state to influence carbon partitioning with no gain in precision suggesting it is not a major factor.

Predictions of blood concentrations of glucose and amino acids have moderate error, but the rise in fatty acids after calving is significantly underpredicted suggesting that adipose function during the transition period is inadequately described. Milk production and composition was predicted with reasonably good accuracy and precision after updates to the representations of mammary cells, activity per cell, and the hormonal framework. Body weight and condition score are fairly well predicted, however, weight gain in the growing state has not been adequately evaluated to date.

**Conclusions** Considerable progress has been made in updating the model, but much work remains.

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# Can artificial intelligence improve the prediction adequacy of mathematical modeling in ruminant nutrition?

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**Application**. Artificial intelligence methods might be able to increase the prediction accuracy of mathematical models by incorporating the big data collected by sensors.

**Introduction**. Mathematical modeling has enabled the development of decision support systems to assist in the feeding management of ruminants for about 50 years. The first technological wave in mathematical modeling was likely the evolution of digital computing and data analysis. Since then, substantial progress in mathematical modeling has been absent, almost reaching to a halt. Artificial intelligence (AI) might incentivize an avant-garde technological wave in predictive analytics (Tedeschi, 2019), but the scientific community has a long way to go. The objective of this study was to compare AI methods with least-squares regression to predict methane emission.

**Material and methods**. A database was developed from published studies that have measured methane emission of cattle and have reported characteristics of animal (body weight, dry matter intake) and diet (organic matter, crude protein, neutral detergent fiber, acid detergent fiber, ether extract, and starch content and digestibilities; and gross, digestible, and metabolizable energies), and measured methane emission using indirect calorimetry. Because there were many incomplete records, a synthetic database (n = 10,000) was created using @Risk 7.6 assuming random Latin hypercubic sampling, the best fit distribution of each variable, and the Spearman correlation among them. The synthetic database was used to compare the adequacy of predicting daily methane emission using three methods: the artificial neural network (ANN), machine learning (ML), and multiple linear regression (MLR) using R 3.4.4. The assessment of prediction adequacy was obtained from 100 simulations consisted of either the full synthetic dataset or randomly subsampling 2,000 records of the normalized synthetic database variables, using the normalization equation: $(x-\bar{x})/(\max(x)-\min(x))$. All independent variables of the subsample database (n = 2,000) was further randomly split into train database (n = 1,600; 80%) and test database (n = 400; 20%). The train database was used to train the ANN and ML algorithms and to develop the MLR equation, and the test database was used for prediction adequacy. The *neuralnet* package of R was used for the ANN learning, assuming five hidden layers. The *keras* package of R was used for the ML learning, assuming sequential model method, five hidden layers with rectified linear unit (*relu*) and sigmoidal activation functions, automatic dropout of layers, 30 epochs, batch size of 5, and automatic cross-validation (20%). The *lm* package of R was used for the MLR fitting. The root of the mean square error of the prediction (RMSEP), accuracy (Cb), and the determination coefficient ($r^2$) were used to assess prediction adequacy (Tedeschi, 2006).

**Results**. For the full synthetic dataset, the convergence/processing time needed by the ANN was highly variable but considerably greater than ML and MLR, the RMSEP and Cb were improved for ANN and MLR, and the precision ($R^2$) was least for ML (Table 1). The trend remained similar for the random synthetic, smaller datasets, except that the RMSEP was twice the value for ANN than ML and MLR (Table 1).

**Table 1.** Descriptive statistics of two learning and one fitting methods to predict methane emission (g/d)

| Type | n | Full Dataset (n = 100) | | | | Random Simulations (n = 100) | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | RMSEP | Cb | $R^2$ | Time | RMSEP | Cb | $R^2$ | Time |
| ANN | 25 | 42.2 | 0.84 | 0.30 | 566.5 | 102.7 | 0.87 | 0.12 | 18.7 |
| ML | 96 | 49.4 | 0.21 | 0.16 | 129.8 | 58.7 | 0.13 | 0.09 | 15.0 |
| MLR | 100 | 43.5 | 0.81 | 0.26 | 0.0 | 51.7 | 0.81 | 0.26 | 0.0 |

**Conclusion**. Our simulation suggests that AI methods have not been designed for precision, but accuracy, and requires larger dataset to perform adequately as well as the human element for judgment (i.e., knowledge and wisdom; Tedeschi, 2019). It seems that ML can accurately predict methane emission, but lacks precision compared to MLR. Future assessments should include more variables, improve the ML network by incorporating different layers and activation functions and improve overfitting and underfitting issues.

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## An improved algorithm for solving nonlinear profit maximizing animal diet problems

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**Application** We propose a method for solving nonlinear programming models (NLP) for profit maximization of animal diet to a precision of $\varepsilon$ by solving $O(\log \varepsilon^{-1})$ linear programming (LP) models.

**Introduction** Traditionally, diet optimization has the objective of minimizing the ration dry matter cost (MRC). Such a problem is solved through LP by fixing the level of animal performance and associated nutritional requirements. Maximum profit diet formulation for feedlots requires non-linear models, e.g. dry matter intake (DMI) and animal performance that are required to estimate costs and revenues (NRC 2016 [1]). We propose a method for solving an NLP for profit maximization that requires multiple LPs to be solved, each with different right-hand side and matrix coefficients.

**Material and methods** A simplified profit function (Z) is given by the nonlinear animal weight gain function $\Omega(\text{CNEm}, \mathbf{x})$ multiplied by the selling price $p$ (\$/kg), subtracting diet costs $C(\text{CNEm}, \mathbf{x})$ and fixed costs ($\alpha$), or: $Z(\text{CNEm}, \mathbf{x}) = p \,.\, \Omega(\text{CNEm}, \mathbf{x}) - C(\text{CNEm}, \mathbf{x}) - \alpha$ . Where $\text{CNEm} \in J = \{[lb, ub], lb, ub \in \mathbb{R}_0^+\}$ is the net energy for maintenance available in the diet, where $lb$ and $ub$ represent respectively the lower and upper bounds of CNEm; $\mathbf{x} \in \mathbb{R}^n$ is a vector variable representing daily feed intake of each diet ingredient. Profit Z is subject to a set of nutritional nonlinear constraints $\Phi(\text{CNEm}, \mathbf{x})$ and linear constraints $F(\text{CNEm}, \mathbf{x})$. For a given animal type and a fixed $\text{CNEm} = k_i$, the nonlinear function $\Omega$ becomes a constant value and $\Phi$ linear constraints. Thus maximizing the NPL $\{Z(k_i, \mathbf{x}): \Phi(k_i, \mathbf{x}), F(k_i, \mathbf{x})\}$ is equivalent to minimizing the LP $\{C(k_i, \mathbf{x}): \Phi(k_i, \mathbf{x}), F(k_i, \mathbf{x})\}$ and the optimal solution for $Z(\text{CNEm}, \mathbf{x})$ is given by:

$$Z^* = \max\{Z^*_i \mid Z^*_i = \max\{p \,.\, \Omega(k_i, \mathbf{x}) - C(k_i, \mathbf{x}) - \alpha, \text{ subject to: } \Phi(k_i, \mathbf{x})=0, F(k_i, \mathbf{x})=0, \mathbf{x} \in (\mathbb{R}_0^+)^n\}, \forall\, k_i \in J\}$$

We use the golden-section search method (GSS) [2] to solve for $k_i \in J$. The equations for $\Omega$, $\Phi$ and F are based on NRC 2016 [1]. We formulated a diet for typical Brazilian conditions: Nellore steers with shrunk bodyweight of 300kg at sales price of 1.44 US\$/kg, using 30 ingredients and nutritional values from NRC 2016 [1], including corn, sorghum and hay of soybean, cotton, wheat and rice. The LPs were solved using the CPLEX© solver [3] with a tolerance value $\varepsilon=10^{-2}$ for the GSS.

**Results** Figure 1 shows the proposed method converging to an optimal solution in 10 iterations with the GSS. Figure 2 shows how profit and animal performance vary for a 60 days diet as a function of CNEm for the whole linear space [lb, ub] with a step $\Delta=10^{-2}$.

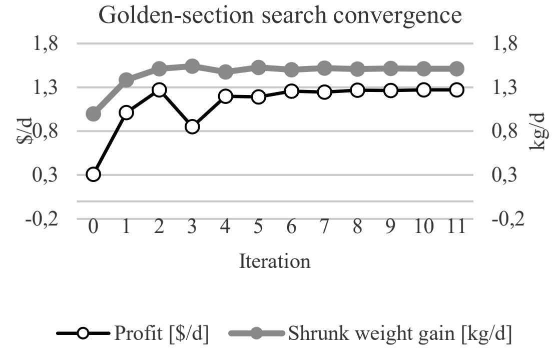

**Figure 1**. Golden-section search convergence for daily profit, with corresponding shrunk weight gain.

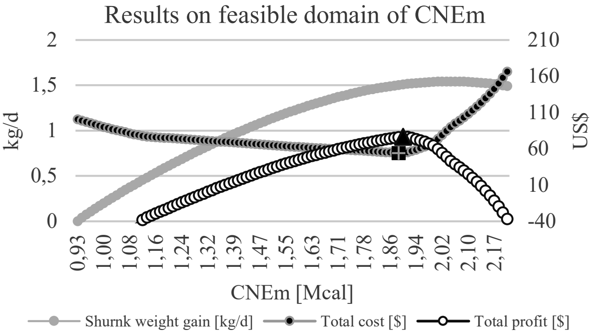

**Figure 2**. Profit and cost for 60 days diet and daily shrunk weight gain as a function of CNEm. The triangle and square highlights optimal solutions for maximum profit and minimum cost, respectively.

**Conclusion** Our approach introduces an efficient method for solving nonlinear profit maximizing animal diet formulation for beef cattle feedlot finishing systems. The method requires the solution of $O(\log \varepsilon^{-1})$ LPs, each of which can be solved in polynomial time, reducing the computational cost of solving the original NLP.

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# Modelling by meta-analysis enteric methane emissions from ruminants fed forages supplemented or not with tannins.

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**Application** Capturing the effect of tannin on methane emission by empirical equation, a tool for GHG inventory

**Introduction** Plant secondary compounds, such as tannins have been studied both for their nutritional effects (positive or negative) on animal productivity and health and for their anti-methanogenic properties. However, the mitigating effect of tannins on methane ($CH_4$) is inconsistent (Beauchemin et al., 2008; Makkar et al. 2003), due to the dose, the source and the structure of the tannins considered. The aims of this study was to apply a meta-analytic approach to compare the effects of different forages, with or without tannins, fed to ruminants on $CH_4$.

**Material and Methods** We collected published data (Web of Science, CAB) that reported, on the same treatment, dry matter intake (DMI), $CH_4$ emissions, digestibility parameters, forage chemical composition when available and reporting tannins effects. The main factors tested (Proc GLM, Minitab 16) were crude protein (CP), neutral detergent fibre (NDF), acid detergent fibre (ADF) contents of the forage, digestible organic matter (DOM), dry matter intake (DMI) expressed in % of live weight (DMI%LW) and tannins contents (condensed or hydrolysable) as covariates. Experiment and animal species, as qualitative factors were considered as fixed effects tested on inter-experiments-intra-factor variance. TAN content was log transformed because of non-normal distribution.

**Table 1**: Main descriptive parameters of the database

| | n | mean | sd | min | max |
|---|---|---|---|---|---|
| CP (g/kg DM) | 574 | 156 | 56.6 | 24 | 394 |
| NDF (g/kg DM) | 512 | 528 | 129.3 | 127 | 816 |
| ADF (g/kg DM) | 349 | 321 | 82.9 | 110 | 553 |
| DOM (g/kg DM) | 522 | 675 | 92.4 | 378 | 918 |
| DMI/LW (%) | 590 | 2.0 | 0.71 | 0.5 | 4.9 |
| $CH_4$ (g/kg DMI) | 586 | 21.3 | 5.45 | 6.7 | 37.5 |
| $CH_4$ (g/kg DOM) | 518 | 34.9 | 8.93 | 11.0 | 72.4 |

**Results** The database contained 103 publications, 204 experiments (nexp) and 554 treatments (ntrt). The main descriptive parameters of the database are given in table 1. Tannins contents, reported in 21 experiments and 398 treatments of the dataset, averaged TAN = 4.8 (sd= 22.85) g/kg DM and varied from 0 to 199 g/kg DM. There was around 20 different forage species containing either condensed tannins or hydrolysable tannins in the dataset. As previously observed by Eugène et al. (2014), methane production, expressed in g per kg of digestible OM (g/kg DOM) was significantly related to DMI%LW and NDF content of the forage. Moreover, tannins content (g/kg DM) have significant influences: **$CH_4$/DOM = 34.26 – 3.96 DMI%LW + 0.027 NDF – 1.72 Log10 (1+TAN)** (ntrt = 398, nexp = 147, RMSE = 3.1 g/kg, $P < 0.001$), where $CH_4$/DOM is the methane production in g per kg digested organic matter, NDF content (g/kgDM) and TAN is the tannin content (g/kgDM).

**Conclusion** Similarly to the study of Sauvant et al. (2011), we observed that DMI%LW decreased $CH_4$ emissions. Moreover, we observed that both NDF contents in forages increased significantly $CH_4$ emissions, whereas tannins contents decreased it. The decreasing effect of tannins on CH4 emission was in agreement with the *in vitro* study of Jayanegara et al. (2011) but in the present study the impacts of tannins were lower due to the significant contribution of DMI%LW and NDF effects. The effect of the source of tannins needs more research.

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# Digestible lysine requirement of broilers: Model evaluation and development of a Shiny online application in R

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**Application** The factorial model predicts the digestible Lysine (Lys) requirements of broilers by considering body weight and weight growth. Therefore, an interactive web application using Shiny in R was created to support simulations and data visualization by researchers and poultry nutritionists.

**Introduction** Prediction models can be used for simulations to support decision-making. Interactive visualization figures and codes are important to make data more accessible to researchers (Perkel, 2018). Currently, interactivity is a key to science communication. The objective of this study was to evaluate the Lys requirement model for broilers and to create an interactive web application for simulations.

**Material and methods** 1. Model Evaluation: Data from 6 independent studies (120 treatment means) were used to evaluate an equation (i.e., model) for estimating lysine (Lys) requirement for body weight gain (BWG) of broilers proposed by Sakomura et al. (2015). Data for line, sex, ambient temperature (°C), body weight (BW, kg), and BWG (g/d) were collected. The efficiency of digestible Lys utilization for growth (LysEff) was considered as 0.77. The equation evaluated was: Digestible Lys intake (mg/d) = $(45.1 \times BW^{0.75}) + [(-23.14 + 13.39 \times BWG) / LysEff]$ (1). The model was evaluated using root mean square errors (RMSE), mean bias, slope bias, concordance correlation coefficient (CCC), and goodness of fit ($R^2$). 2. Development of an interactive Poultry Science web application framework: Two R scripts (user-interface and server, R Core Team 2018) were written to control the layout, appearance, user-input, processing data, and model outputs. The R server code used equations for predicting the amino acid (AA) requirements of broiler chickens developed by Sakomura et al. (2015). The packages Shiny, rhandsontable, DT, ggplot2, plotly, and shinyjs were used.

**Results** The model predicted greater amounts of Lys requirement than observed values (1002 vs 967 mg/d) with a mean bias of –34.7 mg/d ($P < 0.05$) and slope bias of –0.03 ($P > 0.05$). The model explained about 96.3% of the variation in observed data and had an RMSE (% observed mean) of 11.76. Overall, the model accurately predicted the Lys requirement (CCC = 0.98) of broilers.

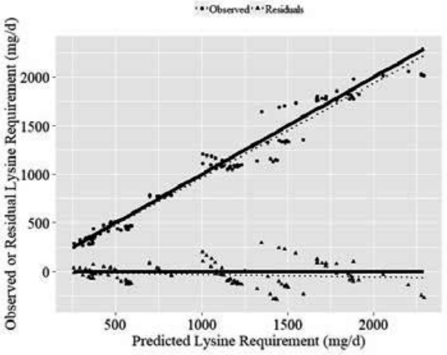
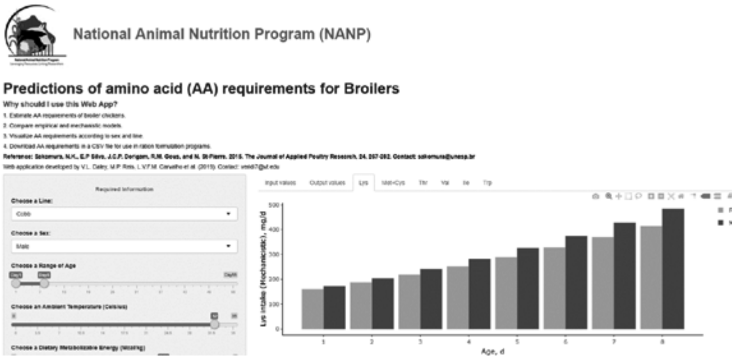


**Figure 1** Predictions of Lysine requirement of broilers, mg/d. Observed (●) or Residual (▲) values and regression lines (···) (n = 120)



Predictions of amino acid (AA) requirements for Broilers

Why should I use this Web App?

1. Estimate AA requirements of broiler chickens.
2. Compare empirical and mechanistic models.
3. Visualize AA requirements according to sex and line.
4. Download AA requirements in a CSV file for use in ration formulation programs.

Reference: Sakomura, N.K., E.P Silva, J.C.P. Dorigam, R.M. Gous, and N. St-Pierre. 2015. The Journal of Applied Poultry Research, 24, 267-282. Contact: sakomura@unesp.br

Web application developed by V.L. Daley, M.P. Reis, L.V.F.M. Carvalho et al. (2019). Contact: veridi7@vt.edu

Required Information

Choose a Line: Cobb

Choose a Sex: Male

Choose a Range of Age

Choose an Ambient Temperature (Celsius)

Choose a Dietary Metabolizable Energy (Mcal/kg)

**Figure 2** Interactive Poultry Science web application to estimate the amino acid requirements of broiler chickens.
Web app: https://veridianaldaley.shinyapps.io/NANP/
Short tutorial: https://is.gd/BrNANPApp

**Conclusion** The model that was evaluated can be used as a nutritional guide for predicting the digestible Lys requirement of broilers.

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# Challenges and headaches in modelling animal adaptive response

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**Application** This study highlights how modelling approaches in animal science have evolved due to the developments of data collecting methods. With the availability of new monitoring technologies, the use of hybrid models combining concept-driven and data driven approaches makes it possible to characterize and rank animals for their robustness. This characterization helps breeders to select for new criteria such as animal adaptive capacity faced with special perturbations, or more generally for their robustness faced to any perturbation.

**Introduction** In the current context of changing environments and an expanding human population, breeding for animal robustness and adaptive capacity becomes an important challenge to ensure that livestock production remains (or: becomes again) robust (Nguyen-Ba et al., submitted). Breeding for robustness is difficult because robustness is a complex trait to phenotype that requires knowledge of dynamically adaptive mechanisms at different levels within a living organism. Nowadays, new technologies make it possible to collect data at different levels of organisation at a high frequency and at a modest cost. For example, data at the animal level (e.g., feed intake or body weight) can be collected using automatic feeders while, at lower level, ruminal pH can be measured continuously using a pH bolus. This progress in collecting data will help animal scientists to better understand the animal's response when facing to environmental perturbations. Therefore, it will open new perspectives and horizons to quantify the adaptive response and, subsequently, rank and select animals based on their robustness. The objective of this article is to explain how mathematical models have adapted to the technological revolution of data collection. In this study, the focus is on data collected with novel monitoring technologies used in precision livestock farming, with the main objective to quantify the animal's adaptive capacity when it is facing environmental perturbations of known or unknown origin.

**Materials and Methods** Mathematical models are useful tools to decipher the relationship between data collected at different levels of time or space, to describe different animal functions, and to predict the animal's response to different perturbations. Since the seventies of the last century, several mechanistic models have been developed to study the effect of feed composition and frequency on animal performance. These models are typically based on concepts of nutrient partitioning and the efficiency of nutrient utilization (i.e., input-output relationships). Fewer models consider also environmental factors, which may be caused by the difficulty to characterize the environment (e.g., in the cases of health stressors) and/or the multiple traits with which the animal responds to changes in the environment (e.g., the response to heat stress). The common denominator of these mechanistic models is that they are concept-driven.

With the rapid progress in monitoring technologies, there is a move towards models analysing large amount of data, using statistical tools, with minimum information of the underlying mechanisms. Moreover, with technologies such as machine learning and data mining, processing huge datasets to detect periods of perturbations has become possible (Liako et al., 2018). This data-driven approach has become an alternative to the mechanistic concept-driven approach and the question arises to which extend these approaches can be or become complementary.

**Results** Two cases of data recording and possible models associated to quantify animal's adaptive response will be presented to demonstrate that the frequency of data collection and the diversity of data recording at different levels of organisation will guide the modelling approach.

**Conclusion** The results showed the necessity of concept driven approach, of data driven approach and also of combining these approaches to quantify the animal's adaptive response.

**Acknowledgment** This study received financial supports from the European Union's H2020 project Feed-a-Gene (grant agreement no. 633531).

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# Are actual animal growth models adequate to predict growth and estimate amino acid and other nutrient requirements?

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**Application** Actual animal growth models need to be revised to precisely estimate individual animal amino acids requirements

**Introduction** Energy, amino acids (AA), minerals, vitamins and water are essential nutrients that must be provided to animals in adequate amount to live (maintenance), grow, and produce (reproduction, lactation, etc.) (NRC, 2012). Feeding animals with diets providing the required amount of nutrients reduces energy expenditure (i.e., urinary energy losses and heat production), increases nutrient utilization efficiency, reduces nutrient excretion and feeding costs (NRC, 2012). Reducing nutrient supply require to 1) precisely estimate the amount of available nutrients in feed ingredients, 2) precisely estimate nutrient requirements, 3) formulate balanced diets that minimize excess nutrients, and 4) concomitantly adjust the dietary supply of nutrients to match the animals estimated requirements (Pomar et al, 2009). The estimation of nutrient requirements is an essential element to minimize nutrient supply. Mathematical models have been proposed to estimate nutrient requirements and to represent the animal responses in different nutritional, genetic and environmental contexts. The first models were based on average empirical laws relating animal responses to nutrient intake (Whittemore and Fawcett, 1976). These models have since evolved becoming more mechanistic (less empirical), considering other influencing factors and having the parameters better characterized (Oltjen et al., 1986; van Milgen et al., 2008). However, the majority of these models use comprehensible nutritional principles to represent the biological phenomena of a single average animal.

**Discussion** The success of feeding growing animals with low protein diets is limited by the inaccuracy of the principles used to estimate AA and other nutrient requirements. One of these principles states that for AA, growing animals need nutrients for maintenance and growth. Maintenance requirements can be assumed related to BW while AA efficiency (e.g., 72% for Lys) and body protein AA concentration are constant (e.g., 7% for Lys) (van Milgen et al., 2008). These parameters are, however, affected by nutrient restriction while pigs may respond differently to these modulating factors (Remus et al., 2019). Also, pigs are raised in groups and fed with a unique feed for long periods. Individual pigs within a given population differ in terms of BW, ADG, health, etc. and therefore, differ in the amount of AA they each need. Therefore, when feeding a group of pigs, the concept of maintenance and growth requirements may not be appropriate. In this situation, nutrient requirements should be seen as the optimal balance between the proportion of animals that needs to be overfed and underfed. Furthermore, there is a large variation in animal responses to AA intake which together with the observed AA interactions (Jansman et al., 2018) highlights the weakness of the ideal protein concept when applied to conventional and unconventional production systems (i.e., low protein diets, personalize feeding, etc.) (Remus et al., 2019).

**Conclusion** The inaccuracy of actual models estimating AA and other nutrient requirements, both for individual animals and populations, limits our ability to reduce dietary nutrient supply in growing animals. New mathematical models are needed to precisely estimate nutrient requirements accounting for the changes that occur over time and for the variation that exists among animals. These new models should review many of the principles actually used to represent the animals metabolism and to estimate AA and other nutrient requirements. They also have to integrate in the estimation of nutrient requirements not only the role in production, but also other essential metabolic functions while ensuring that other functional nutrients (e.g., fermentable carbohydrates) are supplied to maximize the integrity of the intestinal morphology and microbiota, immune system, etc.

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# Predicting the weights of the physical components of broilers and turkeys using allometry

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**Application** Using allometry, the weights of body components such as breast, thigh, drum and wing meat can be accurately predicted without making use of a growth function for each component.

**Introduction** In broiler and turkey rearing revenue is generated by selling different body components in diverse markets. Thus whole birds, modified whole birds or different body components may be sold according to market demand. The increasing consumer demand for breast meat has resulted in a search for ways of producing broilers and turkeys that yield a greater amount of this desirable body component. Knowledge about the yield of different body components under different conditions, and the development of methods to predict these yields, is therefore of considerable value.

These issues raise a general problem in growth analysis, which is to be able to predict the effects of genotype, feed and environment on the yield of body components such as breast, thigh, drum and wing meat. Such predictions may be accomplished directly, using a growth function specific to each component or indirectly, by predicting the growth of the component as a proportion of body protein growth. A general case can be made for using feather-free body protein as a predictor. What is needed for each genotype is a description of the weights of body protein and of the different components of the body at different stages of growth so that the allometric relationships between the components and body protein can be determined. Differences in the allometric relationships between genotypes, or those brought about through nutritional or environmental manipulation, would enable these effects to be modelled.

**Evidence** Evidence from a number of trials with broilers (Danisman & Gous, 2011; 2013) and turkeys (Gous *et al.*, 2019) indicates that no differences exist in these allometric relationships between strains or sexes, and that only in cases where a significant amount of lipid is deposited in the tissues, such as occurs on low protein feeds, is there any change in the intercept but not in the slope of each allometric relationship.

**Implications** The implications of these findings are of considerable interest: the weights of these important components can be accurately predicted without making use of a growth function for each component, and it casts doubt on claims that genetic selection has changed the relative proportions of breast, thigh and drum meat in broilers and turkeys.

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# Economic valuation of gene expression in sustainable agricultural systems

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**Application** The integration of genetic, market and systems description through modeling may offer a new method for the economic valuation of gene expression (EVGE) of sires.

**Introduction** Livestock producers and geneticists lack and available quantitative methodology to carry out a holistic economic valuation of the sire gene expression. Through this study, we developed a methodology for the valuation of sires, which takes into account the influence of the market, the genetic evaluations of the breeding stock, and its impact on the livestock production system, using México as a reference. This can be used as a decision-making tool to select the attributes of the animal, with more genetic-based efficiency, to improve the market-related-production parameters.

**Materials and methods** Price information of 202 zebu sires and 26 of their attributes, included genetic evaluation, were collected at four livestock fairs in México. The information collected was filtered and evaluated for his feasibility to be used in hedonic methodology, to determine the partial price of the attributes (Tejeda, *et al.*, 2018, Terfa, *et al.*, 2013). Subsequently, the information was integrated into a bovine production system model, developed to describe the behavior of a system type in a specific region of México. Finally, the integrated model (IM) solution was used as the base to construct several economic indices of EVGE.

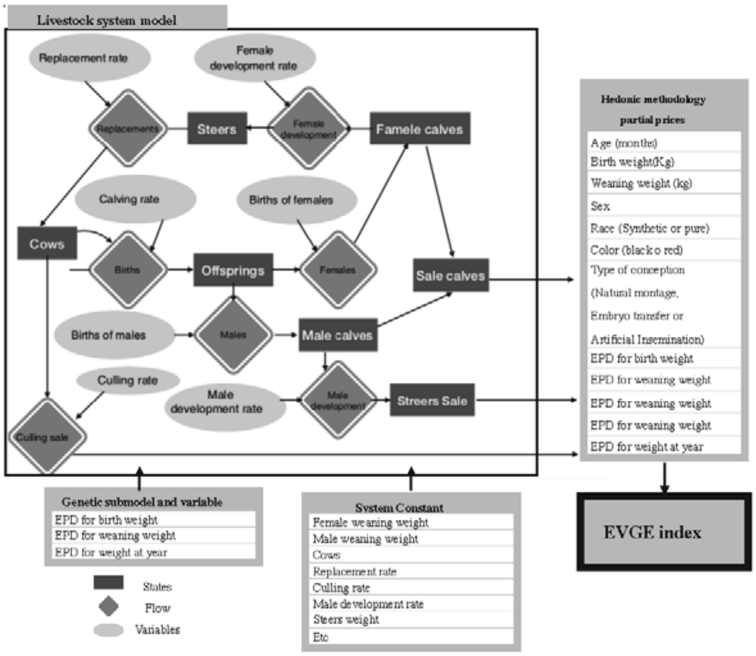

**Figure 1.** Scheme of EVGE model.

**Results** The developed IM was integrated into a general index (iEVGE, US Dollars /EPD*y), that describes the rate of change between the production and Expected Progeny Differences (EPD)(*). Four specific indices were derived from the general index, $\text{iEVGE}_{\text{Equal}}$, $\text{iEVGES}_{\text{Non-equal}}$, $\text{iEVGES}_{\text{Multiple}}$, and $\text{iEVGES}_{\text{Progeny}}$, for the evaluation of unique equal (same EPD), unique non-equal (different EPD), whole animal, or progeny-related pair of EPD.

**Conclusions** The proposed methodology appears as the basis for the construction of a new set of indices for the EVGE, that can be used for the valuation of livestock or other animal systems. It is necessary, however, to test its feasibility and efficiency to improve the production in the long term.

**Acknowledgements** We thank FMVZ, UACH and, especially, Dr. Joel Dominguez Viveros for their support.

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# Initial evaluation of the use of the inverse problem in the study of the partition of energy in pregnant sheep

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**Application** The inverse problem may offer a heuristic understanding of the energy partitioning in pregnant sheep.

**Introduction** Complex models are developed to predict the performance of animal science systems and simple models to estimate few key parameter values (Tedeschi and Fox, 2018). However, it is possible to fit multiple curves to multi-parameter models to deep in the heuristic understanding of biological systems that in another way where not possible (Vargas-Villamil and Tedeschi 2014). The inverse problem (IP) methodology was used to explore its potential to study the energy partitioning in pregnant sheep with nutritional restriction (NR).

**Material and methods** An inverse dynamic multi-parameter model (IMM) was developed and multi-fitted to data curves obtained from production behavior and body composition data of pregnant (16 animals) and non-pregnant sheep (16 animals) datasets. Every dataset where arranged in four groups, TT (without NR), TR (NR for 50 d post-breeding), RR (with NR) and RT (NR for 30 d pre-breeding) for the evaluation of voluntary feed intake (VFI), liveweight, body composition, metabolic (carcass, fat, head, tail, skin and foot), physiological (viscera, intestine, and blood) and reproductive changes (udder, uterus and fetus). Then, the IMM where extended to evaluate the partition and energy balance in the metabolic, physiologic and reproductive subsystems through algebraic equations and a solution was obtained.

**Results** The data suggested an effect of the previous nutritional state on the metabolic and physiological changes carried out during the feeding except by those related to the reproduction (Table 1). The body adjustments to nutritional restriction allowed an improvement of the energetic balance in restricted and non-restricted diets. The energetic adjustments were apparently led by a selective reduction of the carcasses size in 0.05, 0.18, 0.065 and 0.0050, and the required energy was supply by the fat degradation in 0.30, 0.30, 0.33 and 0.16 Mcal/d, for TT, TR, RR and RT, respectively.

**Table 1.** Partitioning of the energy in sheep in the first third of gestation with restricted and non-restricted diets.

| | Groups | | | |
|---|---|---|---|---|
| | TT | TR | RR | RT |
| VFI (Mcal/d) | 2.78 | 1.55 | 1.44 | 1.44 |
| Heat loss (Mcal/d) | 2.98 | 2.00 | 1.72 | 1.50 |
| Energy balance (EB) (Mcal/d) | 0.10 | -0.45 | -0.28 | 0.029 |
| Metabolic EB (Mcal/d) | -0.26 | -0.46 | -0.35 | -0.12 |
| Physiological EB (Mcal/d) | 0.064 | 0.0065 | 0.069 | 0.052 |
| Reproductive EB (Mcal/d) | 0.0040 | 0.0031 | -0.0011 | -6.03E-05 |
| Error | 3.99627 | 2.88446 | 1.58492 | 2.81503 |

**Conclusions** The IMM integral evaluation allowed a detailed heuristic description of the energy balance and partition in a complex system as the restricted pregnant sheep. The mass-balanced model allowed not only to identify the energetic response of the ewes to restricted diets, but also to quantify these changes. The successful implementation of the IP methodology requires to expand the experiment and the model design to focus on the obtention of specific biological information than in statistic differences. Otherwise, the benefit will be limited.

**Acknowledgements** We thank CONACYT for the master's degree student support.

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# A novel multi-inverse approach for a holistic understanding of applied animal science systems

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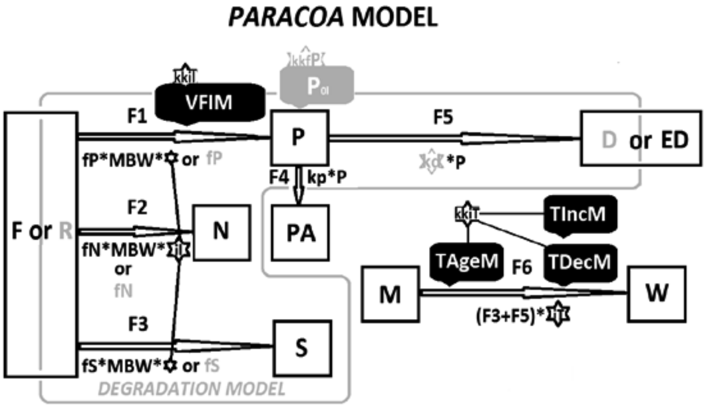
**Application** The deterministic multi-inverse approach is an alternative approach that provides new possibilities for the construction of useful models and offers valuable insight into understanding the research process.

**Introduction** Advances in technology and mathematical methods have provided opportunities to investigate new approaches for the holistic quantification of complex biological systems. One objective of these approaches (Vargas-Villamil and Tedeschi, 2014), including the novel, multi-inverse deterministic approach (MIA) proposed in this work, is to deepen the understanding of biological systems through the structural development of a useful, best-fitted inverse mechanistic model. The objective of this work was to evaluate the capacity of MIA to obtain meaningful quantitative nutritional information from a previous experiment on sheep feeding saccharina (a sugarcane by-product).

**Material and methods** A mechanistic frame multi-parameter and degradation model were developed based on the concept of mass balance. To develop and construct a best-fit inverse model set to improve the structural description of the biological system, different theories regarding the relation between model structure and system behavior were investigated. The effects of the treatments, model structure, parameter type, parameter value, and objective function value were studied. Finally, a best-fitted model was chosen and evaluated.



***PARACOA* MODEL: Optimized *Parameters:*** iI, VFI index; iT, transformation Index; kkiI, increase of iI; kkiT, increase or decrease of iT. ***Variables***: kd, degradation fractional rate; kkfP, increase of potentially degradable fraction, kp, Passage fractional rate; MBW, Metabolic body weight. ***State Variable***: F, feed; P, potential degradable biomass; N, non- degradable fraction; S, soluble biomass; M, mass; W, body weight; ED, effective degraded biomass; PA, non- degraded biomass that pass to posterior tract. ***Fluxes:*** F1 = IntakeP, VFI of potentially degradable biomass or Potentially degradable fraction; F2 = IntakeN, VFI of Non- degradable biomass; F3 = IntakeS, VFI of soluble biomass; F4 = Pas, Passage of biomass. F5 = Deg, Degradation of biomass; F6 = Gain, Body weight gain. ***Model modification:*** VFIM, increase of VFI; TAgeM, post-degradation dry matter transformation related to animal age; TIncM, increase of iT parameter values as a consequence of the level of corn treatment; TDecM, decrease of iT parameter values as a consequence of the level of corn treatment.

**DEGRADATION MODEL: *Optimized parameters:*** kd; kkfP. ***State Variable***: R, biomass in the nylon bag in the rumen; P; N; S; D, degraded biomass. ***Fluxes:*** F1 = fP, potentially degradable fraction; F2 = fN, non-degradable fraction; F3 = fS, soluble fraction; F5 = Dege, effective degradation of biomass; F6 = Gain, Body weight gain. ***Extended equation:*** $P_{0.l.}$ P, potential degradable biomass at 0 % of corn level.

**Figure 1**. Paracoa and degradation models.

**Results** The MIA successfully revealed an increase in the final weight of sheep with an increase in the percentage of corn in the diet, and although the soluble fraction also increased, the effective non-soluble degradation increased four-fold, indicating that the increased weight gain resulted from the non-soluble substrate. A profile likelihood analysis showed that the potential best-fitted model had identifiable parameters and that their relationships were affected by the type of data, a number of parameters, and model structure.

**Conclusions** The MIA was able to significantly reduce the objective function values by improving the biological description of the system. It is necessary to apply the MIA to larger and more complex datasets to obtain a clearer understanding of its potential.

**Acknowledgments** We thank CONACYT for the master's degree student support.

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# An empirical model to determine optimum energy density at different balanced protein levels in broilers

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**Application** Response surface model equations are useful to determine broiler response to energy density at different balanced protein levels so that optimal energy and nutrient levels can be determined for a given set of economic conditions.

**Introduction** Increasing energy density (ED) could improve broiler production response (Waldroup et al. 1976). Also, an application of ideal protein concept is to vary whole balanced amino acids profiles (Lemme et al. 2006), so that broiler responses to balanced protein (BP) can be increased even to levels far higher than currently recommended. Models combining ED and BP to predict broiler response are not available in the literature. The aim of this study was to adjust response surface model (RSM) equations to predict broiler response to ED at different BP levels.

**Material and methods** An experiment with 240 1-day-old Cobb 500 male broiler chicks up to 42 days old was performed to assess four ED each at four BP. Diets were formulated on an amino acid basis to meet or exceed a given set of specified nutrient levels based on NRC (1994) nutrient requirements with the starter lysine requirement corrected to 1.21% instead of 1.10% (Vazquez and Pesti, 1997). For ideal protein ratios, lysine was used as reference. ED of 3000, 3100, 3200, and 3300 kcal ME/kg were obtained maintaining constant nutrient weight per megacalorie. On each ED, lysine levels corresponding to each ED were considered to be the 100% BP level. Levels of 90, 110, and 120% BP were calculated for each ED so that the ideal protein profile was held constant, totalizing 16 nutrient profiles. Diets were formulated based on these nutrient profiles using corn, soybean meal, full fat soybean meal, fish meal, wheat middling, and mineral feedstuffs. The experimental data of body weight (BW), feed intake (FI), feed conversion rate (FCR), and margin over feeding cost (MOFC) were fitted using the RSREG procedure of SAS software. The broiler price assumed per kilogram of BW was 1.138 dollar. A ridge analysis from SAS software was used to compute de optimum response levels for BW, FI, FCR, and MOFC to search for the region of optimum response.

**Results** The estimated equations are as follows:

BW (kg/bird) = -65.44772 + 0.040219*ED + 0.067613*BP - 0.000006169*ED2 - 0.00000841*ED*BP - 0.000134*BP2

FI (kg/bird) = -103.681150 + 0.067707*ED + 0.050573*BP - 0.000010763*ED$^2$ - 0.0000054*ED*BP - 0.000144*BP$^2$

FCR (kg/kg) = 5.947385 - 0.000509*ED - 0.04256*BP - 0.000000125*ED$^2$ + 0.00000708*ED*BP + 0.00006375*BP$^2$

MOFC ($/bird) = -60.36318 + 0.034696*ED + 0.151485*BP - 0.000005069*ED$^2$ - 0.00003409*ED*BP - 0.000199*BP$^2$

The R$^2$ values for BW, BWG, FI, FCR, and MOFC indicated that 93.85, 93.87, 83.54, 93.62, and 86.43% of variability in the responses can be explained by RSM. Optimum ED and BP levels were calculated for BW (ED 3155.7 kcal/kg at BP 152.8%), FI (ED 3116.2 kcal/kg at BP 117.0%), FCR (ED 2883.3 kcal/kg at BP 173.7), and MOFC (ED 3010.6 kcal/kg at BP 122.5) at 42 days. These results indicate that optimum ED and BP levels for MOFC are different from the levels that maximized BW since optimum MOFC is influenced by economic conditions.

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# Feed and animal uncertainties: the confidence of metabolizable protein requirements and supplies estimated with National Research Council (2001) in 15 commercial dairy farms

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**Application** The applications of the method used here are: 1) exploration of a methodology to evaluate global output uncertainty of a nutrition model in a specific context; 2) knowledge of the confidence interval between metabolizable protein (**MP**) supply and estimated milk protein yield (**MPY**) to better define a safety margin when formulating.

**Introduction** On commercial dairy farms, feed and milk composition are often analysed by near infrared spectrometry (**NIRS**) and body weight (**BW**) often estimated using the thoracic circumference, which come with uncertainties linked to the equations used to estimate them. This creates uncertainties on estimations of MP supplies (**MPsupp**) and requirements (**MPrqt**) calculated using these parameters. In addition, selecting the wrong forage maturity or botanical composition in the National Research Council (NRC, 2001) model may also alter MPsupp. The goal of the project was to evaluate the uncertainties of MPsupp and MPrqt in commercial farms related to the uncertainties of animal and feed characteristics inputs in the model, and to establish confidence intervals (**CI**) in the prediction of the relationship with **milk MP** (MPY/0.67) and available MP (**MPav**) [(**MPsupp – MPrqt** for maintenance)].

**Material and methods** The NRC (2001) model was first programed in R environment (R Core Team, 2017) to automatize the process. Uncertainties were assigned to NIRS analyses (4 to 10% depending on the nutrient), BW (8%), dry matter intake (6%), milk yield (2%) and forage composition shifted one "category of maturity or legume content". Animals data and feed samples were collected on one test-day from 547 cows in 15 farms under dairy herd improvement. Factor uncertainties were assumed to be normally distributed around 100, the standard deviation set as the uncertainties. Global uncertainties were obtained with 3500 simulations for each cow with combined random correction factors for the selected variables uncertainties altogether, as uncertainties are assumed to be uncorrelated. Results were analysed as the percentage of difference of simulation values with the original value to centered differences.

**Results and discussion** As uncertainties can be positive or negative, and the probability of selection are normally distributed, means of difference percentage of 0% were first expected. However, high skewness (<-2 for microbial MP, MPsupp and MPav) indicates a mean possibly different from 0%. Because of this skewness, microbial MP 5th and 95th percentiles are unevenly distributed around the mean at -4.21 and 1.46%: this translates to a -5.63% to 4.90% and -9.59% to 8.31% CI to MPsupp and MPav, respectively. Milk MP 90% CI was between -7.22% and 7.57% of the original value, without skewness (0.06). Assuming a 1:1 relationship of MPav with milk MP, the CI was calculated as:*(1+milk MP $Q^{th}$ percentile)/(1+MPav 100-$Q^{th}$ percentile)*, where Q is the value of selected percentile. Thus, the 90th CI is estimated between 119 and 86% of possible values for the relationship of MPav and milk MP. This means that a predicted value of MPav estimated at 1500 g could represent between 1290 and 1785g of milk MP.

**Conclusion** Although this method is a fastidious process to estimate uncertainties, it was useful to deal with the non-linearity in the NRC model, which caused non normal distribution of uncertainties. The uncertainties' translated in an expected -14 to 19% CI on MPav and milk MP relationship with the NRC (2001) model in commercial conditions.

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# Modelling of feather growth in broilers

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**Application:** The study of the growth of feathers by tracts aims to better understand the dynamism of growth and moulting and use this information to predict the amino acid requirements for broilers.

**Introduction:** Feather growth in broilers has not been studied as for whole body. A few research has provided some information about feathers (Lucas and Stettenheim, 1972; Fisher, 2016). The objective of this work was to describe the growth of feathers from various tracts of broilers.

**Material and Methods:** Two hundred chicks of each sex x strain (Cobb and Ross) were randomly assigned to ten pens of 20 chicks each and fed according to requirement, a four-phase feeding programme. One bird per pen (10 birds per genotype) was sampled and euthanized at 14, 28, 42, 56, 70, 84, 98 and 112 d of age. All feathers were dry-plucked from each of seven tracts (capital-cervical, dorsopelvic, interscapular, pectoral, femoral, dorsocaudal and humeral-alar) and measured the weight (g) for each tract. The weight of feathers was adjusted to a Gompertz equation.

**Results:** No significant differences were observed between strain ($p>0.05$), on the other hand, there are differences among sex ($p<0.05$). The parameters A (weight maturity), B (maturity rate) and t * (inflection point) of total feathers and for each of the seven tracts are shown in table 1. For each tract, the strains were similar in feather growth, however the mature weight of feather was higher for male chickens, while the rate of maturing was higher for female.

**Table 1.** Mean of Gompertz parameters[1] describing the growth of feathers total and in seven tracts of male and female Cobb and Ross broilers

| Tract | Males | | | | Females | | | |
|---|---|---|---|---|---|---|---|---|
| | A, g | B, /d | t*, d | $R^2$ | A, g | B, /d | t*, d | $R^2$ |
| Total feather | 266 | 0.0398 | 40.1 | 0.930 | 205 | 0,0526 | 34.0 | 0.940 |
| Capital-cervical | 38.2 | 0.0294 | 46.9 | 0.857 | 20.0 | 0.0539 | 31.1 | 0.862 |
| Dorsocaudal | 19.9 | 0.0289 | 54.2 | 0.816 | 15.9 | 0.0389 | 48.1 | 0.762 |
| Dorsopelvic | 17.5 | 0.0492 | 38.0 | 0.809 | 15.3 | 0.0536 | 33.2 | 0.873 |
| Femoral | 47.1 | 0.0571 | 42.6 | 0.911 | 34.2 | 0.0765 | 36.6 | 0.920 |
| Humeral-alar | 52.2 | 0.0385 | 33.4 | 0.893 | 42.5 | 0.0437 | 32.6 | 0.946 |
| Interscapular | 13.4 | 0.0565 | 40.73 | 0.863 | 9.66 | 0.0653 | 32.2 | 0.808 |
| Pectoral | 36.0 | 0.0299 | 48.4 | 0.849 | 23.5 | 0.0506 | 34.1 | 0.826 |

[1] Gompertz equation of the form A*exp (-exp (-B*(X-t*))) where X is age, d

**Conclusion:** The study concludes that the growth rate of feathers in each tracts is different. Thus, it is possible to better understand the dynamism of growth and moult of feathers in order to better meet the amino acid requirements for broilers.

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# Models to predict feed intake: evaluation of predictions in dairy cattle

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**Application** Given an adequate description of the animal and the diets consumed the use of mathematical models can aid in planning feeding regimes to maximise performance in practical commercial situations

**Introduction** Mathematical modelling allows the simulation of feeding regimes and consequent performance of livestock. These models can aid to devise feeding strategies that minimise feed cost, maximising animal performance and reducing environmental impact. To achieve this, accurate prediction of feed intake (FI) is paramount. The aim of the present study was to evaluate four models in their prediction of FI in dairy cows fed total mixed rations (TMR): BSM-Milk (BioSimetrics Ltd.) a dynamic mechanistic whole cow model, the FI equation part of the CNCPS (Fox et al., 2004), the equation included in the Feed Into Milk model (FiM, Thomas 2004) and that in the NRC (2001). A trial was carried out at SRUC's Dairy Research Centre, Scotland UK. Two contrasting TMR were offered to two groups of forty five Holstein Friesian cows. The diets were: forage (g/kg/DM Grass silage 0.40, maize silage 0.23, crimped wheat 0.11, beans 0.25 and min 0.01) and concentrate based (Wholecrop 0.40, Megalac 0.02, whey 0.08, min 0.01 and a concentrate 0.50). Using electronic feeders (HOKO, Insentec, The Netherlands) individual FI were recorded daily. Details of the animals and the TMR were used as inputs. FI predictions obtained were compared to those obtained on-farm. To evaluate the predictions regression analysis, the limits of agreement (LoA) method and the concordance correlation coefficient (CCC) were used. All statistical analyses were carried out using the software R (2018).

**Results** The evaluated models predicted FI with different levels of success. Table 1 shows the results obtained. $R^2$ values were: 0.78 BSM-Milk, 0.48 CNCPS, 0.42 NRC and 0.47 FiM. The CCC were 0.88 BSM-Milk, 0.58 CNCPS, 0.61 NRC and 0.53 FiM. The LoA showed that BSM-Milk predicted FI in average 0.19 higher than observed (limits -3.80 to 4.19) but not tendency to over or under predict FI. Similarly CNCPS predicted FI 0.98 higher than observed (limits -5.06 to 7.03) and no tendency or over or under predictions. The NRC predictions were -0.41 lower than observed (limits -6.80 to 5.98) and predictions made with FiM were 4.19 higher than observed (limits 0.28 to 8.85) and results showed a slight tendency to over predict FI.

Table 1 Analyses of the relationship between feed intake observed and predicted with BSM-Milk, CNCPS (2004), Feed Into Milk (2004) and NRC (2001).

| | $R^2$ | CCC | Limits of Agreement method | | |
|---|---|---|---|---|---|
| | | | Average | Higher | Lower |
| BSM-Milk | 0.78 | 0.88 | 0.19 | 4.19 | -3.80 |
| CNCPS | 0.48 | 0.58 | 0.98 | 7.03 | -5.06 |
| FiM | 0.47 | 0.53 | 4.19 | 0.28 | 8.85 |
| NRC | 0.42 | 0.61 | -0.41 | 5.98 | -6.80 |

**Conclusion** Given an adequate description of the animal and the rations consumed BSM-Milk was the model with the best performance when compared with the rest of the evaluated models. Future research should compare BSM-Milk predictions to those obtained with models that use a more mechanistic approach to FI prediction.

**Acknowledgements** This research was supported by Innovate UK via Knowledge Transfer Partnership and Biosimetrics Ltd.

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# Modelling the feed intake response of growing pigs to diets contaminated with mycotoxins

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**Application** The procedure quantifies resistance and resilience traits in pigs, with the potential to be used in breeding programs.

**Introduction** Quantifying robustness of farm animals is essential for breeding and management strategies. Elements of the response of animals to perturbations, an important element of robustness (Friggens et al., 2017), can nowadays be measured by technologies such as automatic feeding stations. A novel data analysis and modelling procedure was developed to quantify feed intake response of growing pigs to perturbations (Nguyen-Ba et al, submitted). The procedure estimates the target trajectory of cumulative feed intake (**target CFI**) as a benchmark from which the impact of a perturbation on the animal (i.e. resistance) and its subsequent response through compensatory feed intake (i.e. resilience) can be quantified. The objective of this study was to use this procedure to quantify resistance and resilience of pigs from an experiment where they received diets with or without mycotoxin-contaminated cereals.

**Material and methods** The procedure was applied to data from a published study about the effects of mycotoxin (deoxynivalenol) on the feed intake of growing pigs (Serviento et al., 2018). Experimented pigs (n=155) were divided among a control group (CC) and three challenged groups. Pigs in each of the challenged groups received a diet contaminated with mycotoxins from day 113 to day 119 of age (DC group), from day 134 to day 140 of age (CD group), or twice during both periods (DD group).

**Results and discussion** No significant difference between parameters of the target CFI was found among the four groups. Moreover, the estimated average daily feed intake of group CC was very close to the observation (2.86 vs. 2.87 kg/ d). This means that the target CFI of each pig could be estimated independently of the challenge. Applying to pigs in three challenged groups, the procedure estimated precisely the start and end times of the perturbations (Table 1).

Table 1. Estimated start and end times mycotoxin perturbations had on the pigs

| Challenged period | Times | Median | Mean ± SD |
|---|---|---|---|
| Beginning (DC and 1st time DD) | Start | 112 | 112 ± 2.0 |
| | End | 123 | 123 ± 3.7 |
| End (CD and 2nd time DD) | Start | 133 | 131 ± 5.8 |
| | End | 142 | 142 ± 1.9 |

Correlation between resistance and resilience were low (-0.07, -0.13, -0.00, -0.33 for groups DC, CD, and for the 1st and 2nd challenge in the DD group, respectively), indicating that the two traits represent different phenomena. Results from the quantification of the response of pigs in different groups indicated that pigs at different ages or body weights responded differently to the mycotoxin challenge. Those receiving the mycotoxin-contaminated diet later on in life had a more important immediate reduction in feed intake compared with those receiving the challenge early on. However, the older or heavier pigs recovered faster from the challenge.

**Conclusion** The data analysis procedure using feed intake as a response trait proved its capacity to detect and quantify the response of animals to a mycotoxin-contaminate diet.

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# Estimation of the optimal economic intake of lysine for broilers

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**Application** The Reading model allows establishing strategies of nutritional management to meet productive and economic aspects. By simulation, this model allows a nutritionist to estimate the level of a given amino acid that produce the maximum economic return, considering the variation of the broiler nutrition flock.

**Introduction** The Reading model describes the response of a flock to a nutrient limiting by integrating the responses of the individuals making up the population. The model also estimates the optimal economic amino acids intake of a population. The objective of the study is to estimate the optimal economic intake of digestible lysine (dLys) for broiler chickens.

**Material and methods** Three trials were conducted using male broiler chickens (Cobb 500), one for each phase, initial (1-14 days old), grower (15-28 days old), and finisher (29-42 days old). A total of 640 birds were used, with treatments randomly distributed in 32 experimental units of 20 birds each, totaling 8 treatments of 4 replications each. The experimental diets were formulated based on the dilution technique (Fisher and Morris, 1970) by mixing two isoenergetic feeds, high protein (HP) and nitrogen free (NF), obtaining feeds with the same amino acid profile. Levels of dLys ranged from 0.87% to 1.60%, 0.78% to 1.75%, and 0.64 to 1.28% for starter, grower and finish phases, respectively. To prepare a counter proof and confirm that dLys were the first limiting nutrient in the feed, the diet with the lower level of dLys were replicated with the addition of L-lysine, to achieve the second level of dLys used. The Reading Model was adjusted to estimate the average lysine intake and the optimum lysine intake ($A_{opt}$), according to the response variables. The Reading model is described as follows: $A_{opt}$ (mg/day)=$a.BWG_{max} + b.BW+\sqrt{(a^2.\sigma^2BWG_{max} + b^2.\sigma^2BW)}.z$ where, BWGmax is the maximum body weight gain, BW is the mean body weight of birds, a is the requirement of amino acids pe unit of BWG, b per unit of BW and z is the index that suggests how many times the deviation from the requirement must be added to the average requirement of the population. The z represents the economic index of the equation, z = a*k, where, k is the ratio of the marginal cost of the amino acid to the cost of the gram of the product. The Reading Model parameters were determined using the EFG software.

**Results** The results of counter proof demonstrate that dLys was the first limiting nutrient in the feed ($p<0.05$).

Table 1. Reading model parameters,lysine intake(mg/bird/day) and %dLys estimates for broiler chickens.

| Phase | a | b | Average Lys Intake | %dlys | Optimum economic Lys Intake | %dlys |
|---|---|---|---|---|---|---|
| 1-14 days | 12.13 | 29.64 | 405 | 1.02 | 541 | 1.37 |
| 15-28 days | 13.21 | 189.98 | 1419 | 1.19 | 1586 | 1.33 |
| 29-42 days | 10.00 | 256.61 | 1765 | 0.89 | 2076 | 1.05 |

%dlys calculated according to feed intake recommendations by Rostagno et.al (2017): initial 39.6, grower 118.6 and finisher 197.5g/bird/day.

**Conclusion** The digestible lysine intake of 546, 1586 and 2076 mg/bird/day for the initial, growth and finisher phases allows the maximum economic return of broilers, according to the variability of the population, these values account for 98% of the population.

**Acknowledgements** We would like to thank the FAPESP and CNPq for financial support.

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# Modelling feed intake of broilers under pathogen challenge

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**Application** The use of a mechanistic model to predict the actual feed intake of broilers under sanitary challenge may help poultry nutritionists to adjust the feeding program. Furthermore, it allows to know about the impact of the sanitary challenge on feed intake and body weight.

## Introduction

Growth models have been used for simulations in order to predict performance in production system by considering different scenarios in poultry industry. These models provide important information that could help producer and nutritionist in decision-making process such as the best age for harvesting where the profit is highest or deciding nutritional programs. In these models it is essential to predict actual feed intake (AFI) accurately. Sandberg et al., (2006) reported that based on relative feed intake (RFI) it is possible to model the AFI of broiler under pathogen challenge. This study aimed to develop a model for predicting the RFI of broilers challenged with *Eimeria maxima* and *Clostridium perfringens*; integrate this model into a mechanist simulation model (Broiler Growth Model, BGM); to evaluate the simulation outcomes and certify whether the inclusion of this model into the BGM allows to predict broilers performance under a pathogen challenge condition.

**Material and methods** The model was built using the feed intake of broilers submitted to challenge sanitary and broilers raised under unchallenged condition. All data was obtained from a previous field trial (Oliveira et al., 2019). The RFI was daily calculated during the whole experimental period dividing the AFI of challenged broilers by the AFI of unchallenged broilers. The RFI was fitted into broken line function (linear and quadratic) resulting in a segmented model (SM). This model was integrated into the BGM and used to correct the AFI output when broilers are in sanitary challenge. The simulation outputs were compared with observed data of the file trial. Outcomes were analysed by residual analysis.

**Results** The figure 1 (a) and (b) shows the outcomes of the simulation and observed data. After 42 days, the accumulated AFI observed in the trial (AFIa) was 4581 g and the value estimated in the software (AFIn) was 5% lower. The estimated values for body weight (BW) at 0, 14, 21, 28, 35 d were 50, 502, 956, 1419 and 2126 g, wich was 1%, 4%, 8%, 5% and 2% lower than observed BW, respectively. On the other hand, estimated BW at 42 d (2781 g) was higher than observed BW in 5%, with no mean bias of prediction ($p > 0.05$).

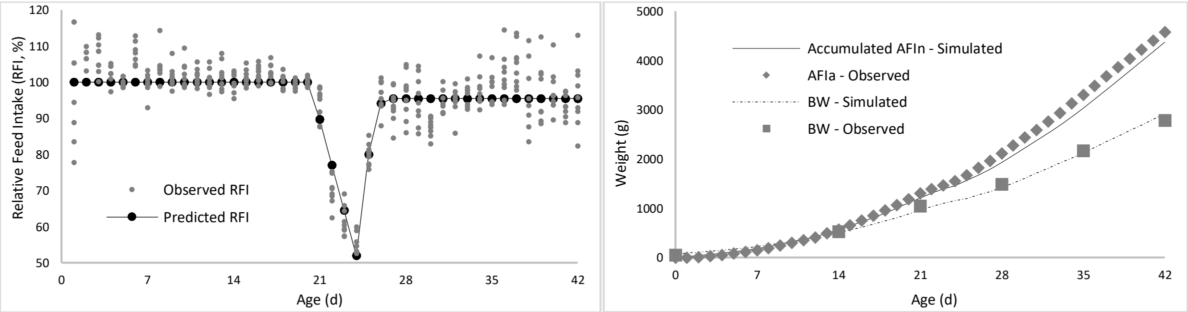

Figure 1 (a) Representation of observed and estimated relative feed intake (RFI) by age. (b) Observed (AFIa) and estimated (AFIn) actual feed intake accumulated and body weight (BW) of challenged broilers from 1 to 42 d-old.

**Conclusion** The results indicate that the SM for predicting the RFI of broilers under pathogen challenge can be included into BGM, allowing to make a realistic simulation, as confirmed by observed data of a field trial.

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# Modelling the maximum feed intake of laying hens based on bulk capacity

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**Application** To consider the bulk capacity of birds to predict actual feed intake in laying hens.

**Introduction** The physical filling of the gastrointestinal tract in poultry seems to be the main control factor of the food intake (Ferket & Gernat, 2006). This filling would be related to some physical properties of the feed and to some scaled measure of the size of the bird. As a result, the animal will increase its feed intake in an attempt to satisfy its physiological needs. This experiment was designed with two purposes: (1) to identify a physic property of 'bulky' feeds, responsible for limiting their intake, (2) describe the maximum capacity of gastrointestinal tract of birds.

**Material and methods** Two trials were carried out to study the gastrointestinal bulky capacities of pullets and laying hens, one for each phase (Pre-laying: 14 to 18 wk. old and Laying: 26 to 30 wk old). For each trial, 225 birds of Hyline W36® strain were housed into individual cages performing the experimental unit. A balanced diet (B) was formulated to meet or exceed the requirement of all nutrients. The treatment diets were made diluting B with 0%, 2.5%; 5%; 10% and 15% of cellulose fibre, rice husk, sand, vermiculite and sawdust. The feed intake (g/d) were divided per kg of body weight, to determine the scale feed intake (SFI, g/kg/d). The measurements of 'bulkiness' of feeds were density, water-holding capacity (WHC), cation-exchange capacity (CEC), and oil holding capacity (OHC). To evaluate which measurement had the higher correlation with the SFI, multivariate exploratory analysis was used. To estimate the maximum feed intake capacity, a linear broken line (Robbins et al., 2006) was adjusted using SFI in function of 'bulkiness' measurement. All statistics were performed in RStudio©, (version 1.0.143; R Core Team, 2018).

**Results** The results from multivariate analysis demonstrate that WHC was the 'bulkiness' measurement most related with bulk capacity. Intakes from all treatment feeds increase linearly with the dilution of the feeds, until a breaking point where the feed intake starts to decrease. The WHC of 3.59 in the feed was estimated to be the maximum value that could be consumed by the pullets and laying hen.

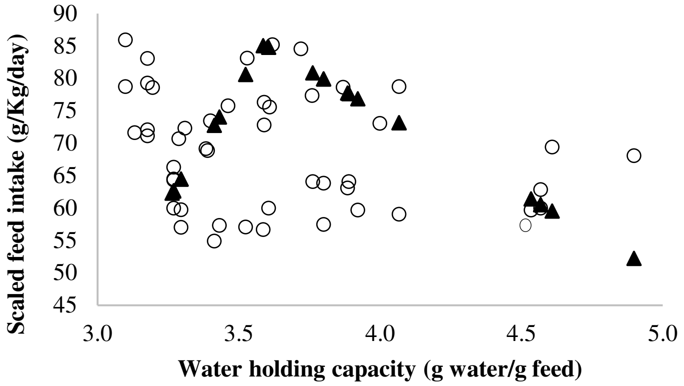

Figure 1. The scaled feed intake (SFI; g/kg per d) on the experimental feeds v. their water- holding capacity estimated (WHC; g water/g dry feed). SFI = 85.13 + 25.19*(3.59 - WHC) + 70.54*(WHC - 3.59). Observed dataset is represented by (o) and predicted dataset is represented by (▲).

**Conclusion** In conclusion, the WHC content is the physic measure of feed bulky that can be used to predict SFI in pullets and laying hens from 14 to 30 weeks of age. This physical property provides the threshold value marking the breaking point were feed intake is reduced due to gut fill.

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# Maintenance lysine, methionine + cystine and threonine requirements for quails (Coturnix coturnix japonica)

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**Application** Values of these amino acids maintenance requirements for quails are used to make more precise diets with consequent reduction in the cost of it.

**Introduction** Different levels of amino acids for laying quails have been recommended over the decades. This is due to the type of method used and units in which these recommendations are expressed. However, the use of a methodology capable of meeting these deficiencies can contribute to the accuracy of the recommendations. This work aimed to determine the requirement for the maintenance of lysine, methionine + cystine and threonine using nitrogen balance with diets formulated by the dilution method and values relativized with the metabolic weight of the animal.

**Material and methods** The trial was carry in São Paulo State University (UNESP), School of Agricultural and Veterinarian Sciences, Jaboticabal. Fifty - six adult male quails, individually housed, were used in metabolic cages, with trough - style feeder, nipple - type drinking fountain and collection trays. Eight treatments were used, the latter being the control group, with seven replications with one bird. A concentrated protein and protein-free diet was formulated according to the recommendations of the Japanese and European quail's tables (Silva and Costa 2009). The established levels were 0.052, 0.103, 0.155, 0.207, 0.310, 0.414 and 0.620%, obtained by the dilution technique (Fisher and Morris 1970). A nitrogen-free diet was provided for 24 hours. During the following 72 hours the birds were fed the experimental rations. The excreta were collected daily, frozen and at the end of the test were pre-dried in an oven (55°C for 72 hours). Dry matter and total nitrogen from diets and excreta were analyzed. The variables collected were ingestion (NI) and nitrogen excretion (NEX). Nitrogen balance (BN) was obtained by difference between NI-NEX. The requirement for those amino acids maintenance was obtained by linear regression between amino acids and BN consumption, and the maintenance requirement was defined as the amount of amino acid required to maintain BN = 0.

**Results** All of amino acids that have been studied had significant values for a (intercept) and b (slope) parameters.

**Table 1.** Maintenance requirements for digestible lysine, methionine + cystine and threonine estimated from linear regression equation, based on metabolic weight (mg/$BW_{kg}^{0.67}$).

| Amino acids | Intercept | Slope | Pr > F | $R^2$ | mg/$BW_{kg}^{0.67}$ |
|---|---|---|---|---|---|
| Lysine | -345.5 | 2.24 | < 0.001 | 0.71 | 154 |
| Methionine + Cystine | -340.0 | 2.63 | < 0.001 | 0.92 | 129 |
| Threonine | -470.8 | 3.26 | < 0.001 | 0.94 | 144 |

**Conclusion** Considering the degree of maturity of the animal. the amounts of lysine, methionine + cystine and threonine required for maintenance were calculated to be 154, 129 and 144 mg per unit of metabolic weight per day.

**Acknowledgements** The first author acknowledges the scholarship by the CAPES Foundation.

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# The response of laying hens to leucine intake

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**Application** Understand the response of laying hens to a given amino acid is useful, since it will enable nutritionists formulate feeds with lower levels of nitrogen, and offer the right amount of nutrients to meet the genetic potential of an specific percentage of the population of birds. If the response to a given nutrient is known, this can be used to simulate different scenarios, which could be used as a decision tool by nutritionists.

**Introduction** Amongst the essential amino acids, leucine (Leu) has the protein anabolism as the main function which promotes the growth and the egg production. Regardless its benefits, the excessive inclusion in diets can stimulates the hepatic catabolism of isoleucine and valine, leading to a deficiency of both amino acids (D'Mello; Lewis, 1970). Despite this knowledge, few is known about the response of laying hens crescent levels of Leu. A study was conducted with the objective to evaluate the response of laying hens to digestible Leu (dLeu) intake, adjusting the reading model to predict the intake of dLeu according to egg output (EO) and body weight (BW), considering the variability of the population.

**Material and methods** One hundred and twenty laying hens of 63 weeks-old (Lohmann LSL) were used to evaluate the response on EO given crescent levels of dLeu. A total of 8 treatments (7 levels of dLeu and 1 counter-proof) were randomly distributed in 120 experimental units of one laying hen each, performing 15 replicates per treatment. The diets were formulated using the dilution technique, producing increasing levels of dLeu (6.0, 7.0, 8.0, 9.0, 10.0, 11.0, 12.0 g/kg of dLeu) and a counter-proof with 7.0 g/kg to verify if Leu was the limiting amino acid. The study lasted 10 weeks (6-wk of adaptation and 4-wk for data collection). The BW (kg) was measured at the first, sixth and tenth week. The variables collected were: egg production (EP, %); feed intake (FI, mg/bird/d), and egg weight (EW, g of egg). The EO was obtained by multiplying the EP by EW. Amino acid intake, EO, and BW were analyzed as One-way ANOVA. The amino acid intake (mg/bird/d) was adjusted in function of EO and BW, using the Reading Model, according to procedures available in the EFG software (2006). The Reading model equation is: $Iaa = a * EO_{max} + b * BW + \sqrt{(a^2 * \sigma^2_{EOmax} + b^2 * \sigma^2_{BW})}$; where, Iaa is the intake of dLeu estimated (mg/bird/day); a is the mg amino acid per g egg output (mg/g); b is the maintenance requirement, i.e., mg amino acid per unit body weight (mg/kg); $EO_{max}$ is the maximum egg output estimated (g/day); σ is the deviation observed for $EO_{max}$ and BW.

**Results** Laying Hens fed a counter-proof diet have an improvement of EO compared with laying hens ($P<0.05$), confirming that dLeu was the first limiting nutrient in the feed. The parameters estimated by the Reading Model was 11.6 (a) for egg output and 43.4 (b) for maintenance. The efficiency of Leu utilization (EU), was determined dividing the estimated coefficient a (11.6) by the first derivative of the model (0.0862), given the value of 74%. Based on the first part of the equation, dLeu (mg/bird/d) = 11.6 * EOmax + 43.4 * BW and using a BW of 1.61 kg and an EOmax of 68g, dLeu intake estimated was 858 mg/bird/d, that represents 50% of the population of birds. Considering that both BW and EO has normal distribution, and using values that represents the distance of one standard deviation from the mean, the equation adjusted was: Leu (mg/bird/d) = 11.6 * EOmax + 43.4 * BW + $\sqrt{(11.62^2 * 3.0^2 + 43.4\ 2^2 * 0.22^2)}$, thus, to supply the genetic potential of the average individual plus one standard deviation from the mean, is necessary add 35.8 mg/bird of dLeu to the amount estimated to meet the genetic potential of average bird, totaling 894 mg/bird/d of dLeu intake, which imply to fulfill the genetic potential of 84.1% of the population. In addition, when two standard deviation from the mean are used, is necessary to add 71.7 mg/bird/d of dLeu to the average, which means a 930 mg/bird/d of dLeu to meet the genetic potential of 97.7% of the population.

**Conclusion** The observed data was successful adjusted to Reading Model. The efficiency of utilization estimated for dLeu was 74%. Knowing the response of a laying hen to a given egg output, could be useful to modelers and nutritionists, helping in a decision-making process.

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# Evaluation of remote monitoring units for estimating live weight and supplement intake of grazing cattle

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**Application** Remote monitoring units for estimating live weight and supplementary intake of grazing cattle to assist producers (ranchers) make informed management decisions.

**Introduction** Production of grazing cattle is mainly constrained by limited quantity and quality of available forages. Deficiencies in metabolisable energy, CP, and minerals (P, S, and Na) can restrain the performance of cattle in grazing systems. Supplementary feeding can rectify inadequacies and maintain production. However, strategic supplementation in grazing ruminants is often imprecise due to large variation in intake between-animals (Neave et al., 2018). Therefore, measuring supplement intake (SI) has the potential to optimise and improve SI efficiency. Remote walk over weighing (WoW) units are currently available to collect individual animal information on live weight (LW) with minimal interference (González et al., 2014) but a remote automatic supplement weighing (ASW) unit to estimate SI is not yet commercially available. The objectives of this study were to evaluate both a commercial WoW and a purpose built ASW unit to estimate SI of individual cattle.

**Material and methods** Evaluation of WoW and ASW units was conducted at the University of New England Beef Cattle Research Station, NSW, Australia. Mature Angus cows (n = 55; LW 629 ± 50 kg) and calves (n = 57; LW 284 ± 33 kg) 6-7 months of age, grazed a drought affected pasture of newly germinated subterranean clover (*Trifolium subterraneum L.*) and senescent grasses on a 32.5 ha paddock for 41 days in early autumn. Each animal was fitted with a unique radio-frequency identification tag enclosing a passive transponder. Cattle had *ad libitum* access to pasture, silage, a lick-block supplement and water. The molasses-based 40 kg lick blocks contained 4.7% CP and incorporated fenbendazole ($C_{15}H_{13}N_2O_3S$; FBZ) as an intake marker. A fenced quadrangle area of 625m$^2$ with a commercial WoW unit and a purpose built ASW unit was established. A water trough along with the lick-blocks were attractants for cattle to walk across the WoW unit and enter the enclosure. The ASW was designed to calculate the total time spent by cattle at the lick-blocks. Two complementary experiments were conducted. Experiment 1 evaluated the accuracy, precision and repeatability of static *versus* WoW LW. To conduct the repeatability analysis 90 pairs of data derived from consecutive measurements of static and WoW LW were made on 9 cattle within 120 minutes with 10 replicates per individual. Experiment 2 evaluated the relationship between lick block intake (g/day) and total time spent at the ASW unit (hits/day), with one hit recorded for every 600 mS of attendance. All cattle were tail-bled 6 times and 52 plasma samples were selected for analysis. Data were analysed using customised statistical techniques and the lm function in R.

**Results** Model evaluation of static *versus* WoW LW indicated that WoW over-estimated LW by 16 and 32 kg (calves and cows), where 38% and 9% of error (bias and slope components) was associated for both calves and cows. The repeatability study of WoW established that using a rolling average (5 consecutive weights) improves the accuracy of the WoW LW estimate. There was a significant relationship between total time spent by cattle at ASW unit and block intake ($r^2$=0.92; $P$<0.01). A positive linear relationship ($P$<0.01) existed between total time spent by cattle at the ASW unit and blood concentration of FBZ and its derivatives oxfendazole and oxfendazole sulfone ($P$<0.01), with $r^2$ of 0.54, 0.73, and 0.75, respectively, across individual animals.

**Conclusion** The WoW over-estimated static LW. However, there was very little bias in the slope indicating that a linear regression model could be developed to adjust the WoW LW to reduce the mean bias and improve the estimate of WoW LW. Total time spent by cattle at the ASW unit as well as individaul blood FBZ data indicated that the ASW unit has useful capability in estimating SI by grazing cattle.

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# Empirical modelling grazing ingestive behaviour based on meta-analyses, comparison between cattle and small ruminants

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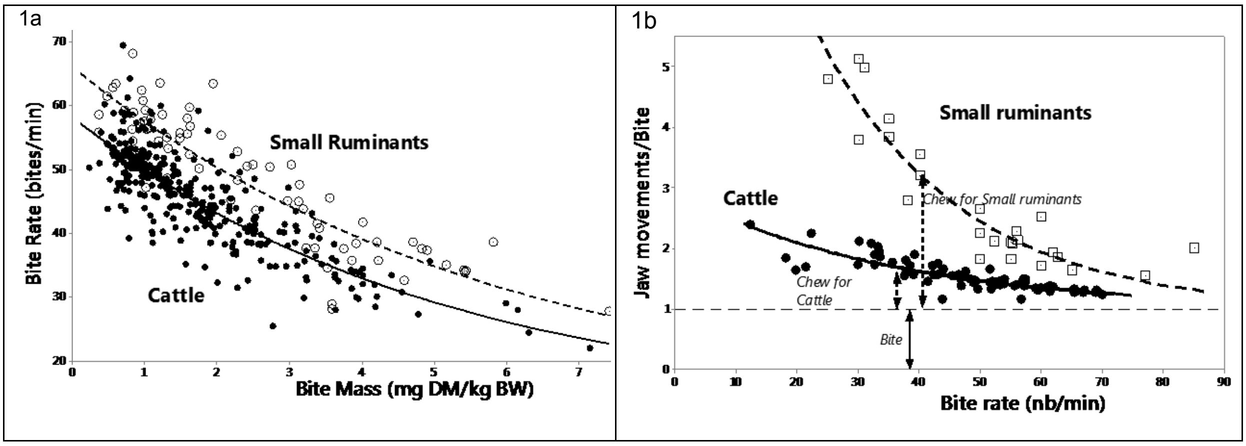
**Implication** A meta-analytic approach was performed to highliht grazing behaviour specificities of different animal species, usable for modelling mixed grazing systems

**Introduction** Numerous studies have been published on ingestive behaviour (IB) of grazing ruminants. However data and studied factors are largely dispersed through the literature and there is no specific studies of differences between animal species. Therefore the present target is to use a meta-analyse to compare IB between cattle (C) and small ruminants (SR).

**Material and Methods** Published results on IB of grazing ruminants (114 papers, 921 treatments, and 275 experiments) were pooled and coded. This database was already used for a quantitative study of components of Bite Mass (Boval and Sauvant, 2009), it contains 79% of treatments with cattle.

**Results** When the data for both species are pooled, the scaling of Bite Mass on Body Weight (BM, mg DM/kg BW) is 1. In contrast, for similar BW, SR graze more deeply in the sward than C, thus a common equation between Bite Depht (BD) and sward height has been obtained with a scaling of $BW^{0,20}$ (Boval and Sauvant, 2019). Otherwise, for a same Bite Mass (BM), Bite Rate (BR) is significantly higher for SR, the mean difference being of almost 10 Bites/min (Figure 1a). Moreover for similar level of BR, the number of Jaw Movements (JM) per bite is higher for SR, the difference becoming larger at lower values of BR (Figure 1b). As shown in this later figure, the difference between both species is due to the number of chews/bite, most important for SR with their moving lips, while C mainly use their tongue. The outcome of all these differences is that for a same BM, Intake Rate (IR, min/kg BW) is slightly higher for SR than C: **IR = 145 (1-exp(- a BM)**. Indeed in this equation the parameter a is respectively for C and SR, of 0.444 (n=331, RMSE=9.7) and of 0.543 (n=72, RMSE=10.8).

Figure 1: Intra species and intra-experiment regressions between (1a) Bite Rate and Bite Mass and (1b)Jaw Movements and Bite Rate.



**Conclusions.** The comparative harvesting process suggest that, compared with a pure grazer (C) a grazer-browser (SR), grazing deeper with much more JM, could need more energy to harvest the same Bite Mass (g/kg BW). These comparative results, enabled by a meta-analytic approach, provide a better understanding of which sward can be better exploited by which ruminant and can be used notably in modelling mixed grazing system (d'Alexis et al., 2014).

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# Forbes' minimal total discomfort model offers novel insights into modelling intake

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**Application** This provides a way to examine integration of mechanisms known to control intake.

**Introduction** Forbes (2007) proposed a novel way to understand the regulation of intake based on minimal total discomfort. This used a concept whereby the deviation of the current from the optimal state of a resource use (eg energy) was mathematically transformed into a discomfort parameter which could be plotted as intake increased for a particular feed. In that way a minimal total discomfort could be calculated and this would be the predicted intake around which the animal hovered on a daily basis to achieve an average daily intake. This concept was used here with some changes as to how discomfort is derived mathematically and how minimal total discomfort is estimated.

**Materials and methods** Data of intake, digestibility and retention time of steers consuming eight forages varying in intake from 5.5 to 18.9 g DM/kgW.d was taken from Prior et al (1998) and Panjaitan et al (2010). Maximum net energy requirement for a 300kg steer to grow at 2kg/d was calculated. Current net energy supply was calculated from intake, estimated ME content and efficiency of use of energy based on standard equations. Discomfort was expressed as:

Discomfort NE = (Genetic Maximal NE use – Current NE supply)/Genetic Maximal NE use.

Thus the declining change in discomfort as intake of a particular feed increased could be plotted. Similarly as intake increases, rumen fill would increase and distension discomfort increases. Rumen fill at any intake can be calculated from retention time of DM.

Discomfort from rumen fill = (current rumen fill/maximal rumen fill)$^2$ where maximal rumen fill was set at 23.6g DM/kg W.

Minimal total discomfort was calculated as the point of intersection of the discomfort function associated with NE (hunger discomfort) and that of the function associated with rumen fill (satiety discomfort). This represents the intake at which hunger signals (hunger discomfort) arising from the lateral hypothalamus become less than satiety signals (satiety discomfort) arising from the ventro-medial hypothalamus. It is the point of switch from the dominance of the LH to the VMH.

**Results** The relationship between observed and predicted intake was:

Observed DM intake (g/d) = 348 + 1.08 Predicted DM intake (g/d) $R^2 = 0.94$ RSD = 360

**Conclusion** The model shows good agreement with observed data but more importantly provides a means of integrating physical and metabolic signals. Forbes' concept provides a novel and important way forward to mathematically examine intake regulation. The current work proposes a different mathematical way to examine discomfort signals arising from forage intake and how they might be integrated but supports the concept of a minimal total discomfort as a useful way forward in modelling intake regulation.

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# Empirical modelling non productive expenditures and requirements in ruminants

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**Application** Non productive expenditures and requirements can impair feed efficiency in ruminants, a set of empirical models updating the older ones is proposed.

**Introduction** The efficiency of the transformation of feed resources by farm animals, ruminants in particular, has become a major challenge at the scale of animals, farms and animal chains. Numerous articles have evoked this question, to be able to correctly analyze this problem it is necessary to model more accurately nonproductive expenditures and requirements. Indeed, these are often linked to the level of performance and therefore reduce the gains of efficiency which can be expected if they are ignored. The overall efficiency of feed resource processing by farm animals is the product of digestive and metabolic efficiencies. In this paper we focused on the empirical models dealing with energy (E) and protein (P), most of them were published in the INRA feed system (INRA, 2018). In this work we are seeking on the one hand to provide simplified models and on the other hand to bring some useful explanatory relations still little known.

**Material and methods** Three databases "Bovidig", "Rumener" and "Mosarco" presented in INRA (2018) were studied by meta-analyses to split inter- and intra-experiment variations to perform this work. The major basic equations were presented in chapters 3, 4 and 6 of this book, the other ones which are more synthetic are now presented.

**Results** Non-productive digestive losses of energy are mainly related to digestive interactions which increase losses of Fecal E (FE). These are related to 3 factors, the Feeding Level (FL = Dry Matter Intake, DMI%Body Weight, Eq3.4), the proportion of concentrate in diet DM (PCO, Eq 3.5) and the rumen protein balance (RPB, Eq.3.9). These interactions decrease diet values compared to values calculated by additivity from Feed Tables. They are partly compensated through lower losses as E of methane in % of Gross E (ECH4%GE, Eq3.12 and 3.13) and urine (EU%GE, Eq 3.14). For instance, in Rumener with experiments only focused on influence of FL, an increase of 10 points of FE%GE (32.3±8.2) relies to a decrease of about 4 points of ECH4±EU (10.6±2.5 %GE) [**ECH4+EU%GE = 23.25-0.408 FE%GE** (n = 317, nexp = 114, RMSE = 1.21)]. The outcome is that, in MoSARCO with experiments focused on influence of PCO, the dietary Milk Net Energy (NEL = 1636±103 kcal/kg DM) can be explained by PCO (0.46±0.15) and DMI (20.9±3.4 kg/d) centred intra-experiment: [**NEL = 1635 - 6.52 DMI -376 PCO + 790 PCO$^2$** (n = 405, nexp = 184, RMSE = 31.5)]. It appears that impact of PCO is first slightly negative and become positive beyond the threshold of around 0.24.

At the level of protein digestion there are also losses of endogenous proteins. In INRA 2018 this loss is predicted from non digestible organic matter intake (Eq 7.3). Expressed in terms of gCP/kg BW (0.94±0.33) it can be more globally estimated from DMI (29.2±8.7g/kgBW)in "Bovidig" [**EndCP = 0.045 + 0.031 DMI** (n=1915, nexp=685, RMSE=0.049)]. In dairy cows with "Mosarco", there is also a close relationship between Milk Protein Yield (MPY = 990±206 g/d) and total non productive CP losses (npCP = 500±65 g/d) [**npCP = 312.7 + 0.191 MPY** (n=1294, nexp=306, RMSE=17.7)]. This illustrates that npCP losses are not negligible compared with MPY.

The heat production (HP), that is the difference between Metabolisable and Net Energy, is the most important non-productive expenditure of energy (HP%GE = 46.9±12.8). It can be predicted for all types of ruminants from $BW^{0.95}$ and FL (Eq 6.34). Beyond the maintenance expenditure, a large part of the HP comes from ingestive and digestive activities which are globally proportional to DMI. Thus, in "Rumener" the HP (37.9±12.9 kcal/kgBW) is closely explained by level of DMI (20.1±3.9 g/kg BW) [**HP = 17.7 + 1.03 DMI** (n=822, nexp=267, RMSE=2.2)], the slope (1.03±0.2) being not different from 1.0 kcal HP/g DMI.

**Conclusions** Thanks to meta-analyses of databases the non productive expenditures can be predicted both at the level of basic mechanistic factors and more globally at the level of the whole animal from simple criteria.

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# Evaluation of Molly cow model predictions of ryegrass digestion in dairy cows

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**Application** The Molly model is a tool with great potential for the study of diets of grazing cows.

**Introduction** Molly is a deterministic, mechanistic, dynamic model designed to represent the underlying key biological aspects of digestion, metabolism, and production of a dairy cow (Baldwin *et al*., 1987). Although the model has been revised and updated in the last three decades, and its predictions have been improved, its ability to predict temperate pasture-based diets is still unclear. Temperate pasture diets support dairy production systems in different parts of the world, and are characterized by the use of ryegrass (*Lolium* sp.) as a predominant species. The aim of this study was to evaluate predictions by the Molly model of ruminal fermentation, digestion, and production for animals fed diets predominant in ryegrass.

**Material and methods:** This work was carried out using a version of Molly containing updated digestion and metabolism parameters and an improved representation of ruminal digesta outflow (Li *et al*., 2018). Model simulations were conducted using ACSLX (3.1.4.2, Aegis Technologies Group Inc., Huntsville, AL). The model was set to simulate 14 days to ensure the simulated fermentation had reached steady state. Data used for model evaluation were collected from 27 publications with 115 treatments conducted with lactating dairy cattle. The inclusion criteria were studies in which pasture intake represented from 45 to 100% (mean 77%) of the total diet, and botanical composition over 85% of ryegrass (*Lolium multiflorum* or *Lolium perenne*). Predicted values from day 14 of the simulations were compared with observed data using the model as described by Li *et al.* (2018) (initial) or after refitting selected digestion parameters to the data (final). Selected parameters were slope and intercept for protein (*slpP* and *intP)* and cellulose (*slpCe* and *intCe)* degradation rate, ammonia (*kAm*) and volatile fatty acid absorption rate ($d^{-1}$), intercept for pH, and microbial biomass (g DM basis) per mole of ATP (*miAtp).*

**Results** As evidenced by RMSE values, milk production (MP) and composition and body reserves are moderately well represented, however, MP was slightly overestimated in the refitting. The refitting resulted in an improved estimation of fecal outflows (about 50% decrease in RMSE than previous values), associated with a better representation of fiber digestion (higher final *slpCe*, 4.47 vs 3.15 $mol^{-1}$). Refitting *slpP*, *intP*, *kAm* values decreased RMSE of blood urea, milk N and rumen ammonia concentrations, but increased RMSE for microbial N (*miAtp* 0.19 vs 0.08 g $mol^{-1}$ of ATP). Volatile fatty acids concentrations and pH were accurately estimated in both cases.

**Table 1** Residual error analyses for Molly predictions, comparing observed and predicted data using the settings of Li *et al.* (2018) (I) or after refitting digestion parameters to the data (F)

| Variable | Obs | -Predicted- | | - RMSE - | | Variable | Obs | -Predicted- | | - RMSE - | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | I | F | I | F | | | I | F | I | F |
| BW, kg | 567 | 614 | 626 | 8.9 | 11.0 | pH | 6.13 | 6.04 | 6.09 | 3.0 | 2.7 |
| BCS | 2.66 | 2.50 | 2.56 | 7.3 | 6.1 | Ammonia$^4$ | 10.5 | 7.9 | 11.4 | 49.4 | 42.7 |
| Milk, kg/d | 24.5 | 25.9 | 27.5 | 23 | 25.6 | TVFA$^4$ | 0.115 | 0.104 | 0.111 | 17.5 | 16.1 |
| Milk fat$^1$ | 4.08 | 4.88 | 4.59 | 23.3 | 18.4 | Acetate$^4$ | 0.076 | 0.068 | 0.069 | 15.7 | 16.5 |
| Milk protein$^1$ | 3.27 | 3.44 | 3.44 | 7.6 | 7.7 | Propionate$^4$ | 0.026 | 0.024 | 0.025 | 13.3 | 10.0 |
| Milk lactose$^1$ | 4.61 | 4.63 | 4.63 | 3.2 | 3.2 | Butyrate$^4$ | 0.016 | 0.012 | 0.016 | 28.4 | 14.4 |
| Outflow NDF$^2$ | 2.13 | 3.6 | 2.53 | 78.3 | 44.2 | Fecal DM$^5$ | 3.44 | 4.23 | 3.43 | 30.1 | 15.8 |
| Microbial N$^2$ | 0.24 | 0.24 | 0.40 | 24.4 | 75.3 | Fecal OM$^5$ | 3.10 | 3.88 | 3.02 | 31.9 | 18.8 |
| Blood Urea$^3$ | 18.3 | 23.8 | 20.4 | 38.8 | 22.7 | Fecal NDF$^5$ | 1.75 | 2.9 | 2.05 | 76.1 | 41.1 |
| Milk N, kg/d | 0.11 | 0.16 | 0.13 | 80.1 | 61.0 | Fecal ADF$^5$ | 1.08 | 1.66 | 1.08 | 58.8 | 25.5 |

$^1$%, $^2$ruminal outflow kg/d, $^3$mg/dL,$^4$mmol/L, $^5$kg/d, RMSE: Root Mean Squared Error, Obs: Mean Observed, BW: Body weight, BCS: Body condition score, TVFA: Total volatile fatty acids, OM: Organic matter.

**Conclusion** The Molly model as parameterized by Li *et al.* (2018) underpredicted ruminal and total tract NDF digestion, but predicted ruminal microbial N outflow without mean bias. Molly adequately represents the digestion and consequent production from cows grazing temperate forages; however, further adjustments must be made in the representation of the rumen fermentation and digestion of protein and fiber and adjusting energy expenditure.

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# Evaluation of predicted ration nutritional values by NRC (2001) and INRA (2018) feed unit systems

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## Application

Quantitative knowledge on the prediction accuracy of OM digestibility (OMD) and duodenal non-ammonia N (NAN) flow by NRC (2001) and INRA (2018) gives insight in their ability to predict overall nutritive values of rations.

## Introduction

Feed unit systems offer the possibility to formulate rations by matching feed values with animal requirements. The accuracy of this approach relies heavily on the quantification of various animal digestive responses to dietary changes. One important aspect is the prediction accuracy of metabolizable protein and net energy for lactation which are often used to characterize the overall nutritive values of a ration. A possibility for evaluating the quality of these nutritional values is to compare elements predicted by these feeding systems for which numerous measurements are available in literature. Therefore, the aim of this study was to compare measured total tract OMD and duodenal flow of NAN, reported from a literature dataset, with their respective predictions by two feeding systems: the recently updated INRA (2018) and the older, yet widely used, NRC (2001) system.

## Material and methods

A dataset from the literature was compiled. In total, 761 treatment means (from 188 experiments) had measured OMD and 229 treatments (from 59 experiments) had measured duodenal flow of NAN. Feed values, including OMD and duodenal NAN flow, were predicted for both systems according to the list of equations published in NRC (2001) and INRA (2018) using the same chemical analysis for all forages and ingredients. As the objective was to evaluate the ability of both feed unit systems to predict responses of duodenal NAN flow and OMD to dietary changes, and not absolute values per se, the comparison with measured values was adjusted for the fixed effect of experiment, using Proc Mixed of SAS (SAS Institute Inc., Cary, NC, USA). The slope of the relationship, concordance correlation coefficient (CCC) and the root mean square prediction error (RMSPE; in % of observed mean) were used to evaluate the quality of the independent predictions.

## Results

The OMD response to dietary changes had greater slope and CCC, and lower RMSPE, by INRA (2018) compared with NRC (2001) (Figure 1). The duodenal NAN flow response was similar between INRA (2018) and NRC (2001).

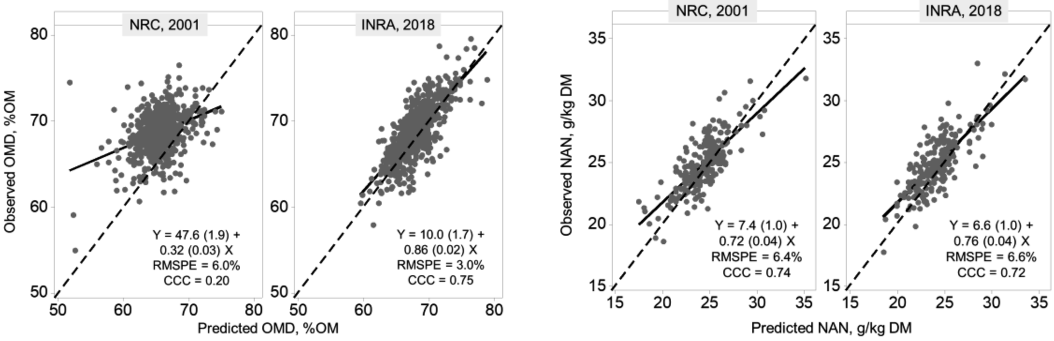

**Figure 1.** Comparison between observed and predicted values of OMD and NAN by NRC (2001) and INRA (2018).

## Conclusion

Overall, OMD response to dietary changes had lowest RMSPE and highest CCC for INRA (2018) model. In the case of duodenal NAN flow, the accuracy of the prediction was similar between the two feeding systems.

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# SIMON: Modelling digestion and growth in calves fed milk replacer and solid feed

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**Application** For conventional calves and veal calves reared in Europe, intake of milk replacer is combined with provision of solid feed. SIMON, a growth simulation model for veal calves used in practice, was revised to consider performance in response to solid feed as well as the impact of milk replacer feeding frequency on efficiency.

**Introduction** Modelling the impact of solid feed (SF) on growth and N efficiency in calves requires consideration of multiple factors including rumen wall, motility, and microbial population development. In addition, while it is well known that milk replacer (MR) feeding frequency affects N efficiency, it was not considered in the original iteration of the SIMON growth model for veal calves (Gerrits et al. 1997). It was therefore the objective of this paper to revise the SIMON model to (1) simulate the effect of SF inclusion on nutrient digestibility and delivery to the animal and (2) predict the effects of within day MR feeding frequency on N efficiency to improve model predictions and relevance.

**Materials and methods** An existing rumen fermentation model for beef (Ellis et al., 2014) was further adapted to simulate fermentation and digestion in growing calves and linked with the SIMON veal growth model (Gerrits et al. 1997). Intake of SF was modelled as continuous, while MR intake was modelled as a pulse dose (e.g., 1, 2 or 4 meals per day). The evaluation database (41 treatments from 7 studies) contained calves with an average BW of 143 (± 9.3) kg and DMI of 1.1 (± 0.15) kg/d SF. Modifications to the rumen model included equations specifying the prediction of rumen volume ($V_{\mathrm{Ru}}$), rumen fractional passage rate ($k_p$), pH, the development of the rumen microbial population upon initiation of solid feeding and the development of the rumen wall. In order to adequately model the postprandial appearance of nutrients (e.g. glucose) in the blood, an abomasal and two small intestine pools were added to regulate absorption and appearance of MR nutrients in the blood. Model predictions were evaluated by concordance correlation coefficient (**CCC**) analysis and visual plots of predictions and residuals.

**Results** Modifications allowed the model to predict the directional change in total tract NDF digestibility observed in the evaluation dataset (46% at 108 kg and 56% at 164 kg BW), although the magnitude of change was less (47% and 50%, respectively). The variable $V_{Ru}$ was predicted with a CCC of 0.69, $k_p$(forage) with a CCC of 0.49 and $k_p$(concentrate) with a CCC of 0.61. Digestible N efficiency (dNeff, %) was predicted with a CCC of 0.66 and followed the pattern of observed dNeff across differences in MR feeding frequency.

**Conclusions** Overall, the model performed reasonably well with respect to digestibility, dNeff and nutrient appearance in the blood, but results also highlight areas for further development.

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# Inhibited methanogenesis in the bovine rumen: dynamic modeling of microbial metabolism in response to 3-nitrooxypropanol and nitrate supplementation

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**Application** 3-nitrooxypropanol (3-NOP) and nitrate ($NO_3^-$) have been shown to effectively decrease enteric methane ($CH_4$) emissions from ruminants. Dynamic model simulations explain the response of $CH_4$ emissions to the intake of feed supplemented with 3-NOP and $NO_3^-$.

**Introduction** 3NOP supplementation to dairy cattle diets effectively mitigated enteric $CH_4$ production. Although the mode of action of 3-NOP was elucidated to be the inhibition of the archaeal methyl-coenzyme M reductase (MCR), it was indicated that 3-NOP is at least partly reduced to nitrite ($NO_2^-$), which also inactivates MCR (Duin et al., 2016). Furthermore, $NO_2^-$ was suggested to contribute to the $CH_4$ inhibiting effect of $NO_3^-$ supplementation as well (Latham et al., 2016), although the mechanism of inhibition is still unclarified. The aim is to model the response of the fermentative and methanogenic metabolism in the rumen to 3-NOP, $NO_3^-$ and their derivatives using a dynamic mechanistic approach.

**Materials and methods** An extant mechanistic rumen fermentation model with state variables for ruminal carbohydrate substrates, bacteria and protozoa, gaseous and dissolved fermentation end products and methanogens (Van Lingen et al., personal communication) was extended with a state variable of either 3-NOP or $NO_3^-$. Both of these new models also comprised a $NO_2^-$ state variable. Feed composition and intake rate (twice daily feeding regime), and supplement inclusion level were used as model inputs. Model parameters were estimated to experimental data that were collected from the literature.

**Results** The 3NOP and $NO_3^-$ models both predicted a marked peak in hydrogen ($H_2$) emission shortly after feeding, the magnitude of which increased with higher doses of the supplement administration. A decreased $CH_4$ emission rate was associated with 3-NOP and $NO_3^-$ supplementation. Omission of the $NO_2^-$ state variable from the 3-NOP model did not change the overall dynamics of $H_2$ and $CH_4$ emission and other metabolites. However, omitting the $NO_2^-$ state variable from the $NO_3^-$ model did substantially change the dynamics of $H_2$ and $CH_4$ emissions indicated by a decrease in both $H_2$ and $CH_4$ emission after feeding.

**Conclusion** This model evaluated the underlying mechanisms of the rumen microbial metabolism in response to 3-NOP and $NO_3^-$ supplementation. Simulations do not point to substantial methanogenic inhibition by $NO_2^-$ upon 3-NOP supplementation, whereas the metabolic response to $NO_3^-$ supplementation may largely depend on archaeal inhibition by $NO_2^-$.

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## Determining the appropriate inclusion of physically effective fiber for finishing beef cattle diets

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**Application.** Rumination time can be used to calculate physically effective fiber for finishing beef cattle.

**Introduction.** Coarse roughages, high in neutral detergent fiber (NDF), are included in the diets of finishing feedlot steers to stimulate rumination, aid in maintaining ruminal health, and decrease incidence of acidosis. Increasing levels of dietary roughage can increase rumen fill, thus diluting energy intake. The threshold at which dietary roughage provides the appropriate level of physically effective NDF (peNDF) without compromising growth remains unclear. The objective of this research was to calculate peNDF from rumination in beef steers consuming finishing diets with various levels of corn stalks.

**Materials and methods.** Rumination and daily dry matter intake (DMI) were compiled from five finishing experiments ($n$ = 507; average BW = 333 ± 23 kg) to calculate peNDF of finishing feedlot diets. Of the five experiments, corn stalks were included from 5 to 15% (DM basis) in steam-flaked or dry-rolled corn-based diets. Steers were equipped with a sensory ear tag or collar (Allflex Livestock Intelligence; Madison, WI) to measure rumination (min/d). Rumination was recorded in 2-h intervals and summed daily to calculate daily rumination. To compare intake and rumination, a mixed model was used with pen or animal as the experimental unit, trial as the random effect, and corn stalk inclusion rate as the main effect. The method was based on Mertens (2002) to calculate peNDF. To establish a constant for physical effect factor (pef), a zero-intercept linear model was used to regress rumination min on NDF intake. Then, daily rumination time was divided by this slope (average rumination time per kilogram of NDF) to compute the pef for each corn stalk inclusion rate. The pef of each inclusion rate was multiplied by the NDF intake to compute peNDF intake (kg/d). Then, the peNDF intake was divided by the DMI to compute peNDF (% of diet DM). Finally, a regression between the peNDF (%) and rumination time of each corn stalk inclusion rate was developed to estimate the ideal peNDF of the average rumination time per kilogram of NDF.

**Results.** Table 1 has the DMI, NDF, rumination time, and peNDF values for each corn stalk inclusion rate. The average rumination time per kilogram of NDF was 159 min/kg NDF. The regression between peNDF and rumination time was $peNDF = 0.0008 \times Rumination\ Time - 0.0505$. Thus, assuming the average rumination time, the ideal peNDF is 7.67% (DM basis).

**Table 1**. Effects of corn stalks inclusion rate (% DM basis) on dietary physically effective NDF (peNDF)

| | Corn Stalk Inclusion Rate | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| Item | 5.00 | 5.10 | 5.56 | 6.40 | 6.56 | 9.75 | 9.96 | 14.95 | 15.00 | SE |
| DMI, kg | $7.7^{h}$ | $8.9^{e}$ | $12.8^{a}$ | $10.5^{c}$ | $10.7^{b}$ | $10.2^{d}$ | $8.2^{f}$ | $8.1^{g,f}$ | $8.1^{g,f}$ | 0.2 |
| Rumination | | | | | | | | | | |
| min/d | $332^{e}$ | $290^{g}$ | $394^{b}$ | $223^{i}$ | $242^{h}$ | $311^{f}$ | $342^{d}$ | $357^{c}$ | $500^{a}$ | 6.2 |
| min/kg | | | | | | | | | | |
| DM | $45^{b}$ | $36^{c}$ | $30^{d}$ | $21^{f}$ | $26^{e}$ | $31^{d}$ | $45^{b}$ | $46^{b}$ | $65^{a}$ | 0.9 |
| NDF | $251^{b}$ | $183^{d}$ | $157^{e}$ | $131^{f}$ | $116^{f}$ | $154^{e}$ | $207^{c}$ | $197^{c}$ | $282^{a}$ | 4.7 |
| peNDF | $637^{b}$ | $463^{d}$ | $398^{e}$ | $332^{f}$ | $294^{f}$ | $389^{e}$ | $525^{c}$ | $499^{c}$ | $714^{a}$ | 11.9 |
| NDF, % | 18.0 | 19.4 | 19.4 | 16.3 | 22.6 | 20.0 | 22.0 | 23.4 | 23.0 | — |
| NDF, kg/d | $1.38^{g}$ | $1.71^{f}$ | $2.49^{a}$ | $1.71^{f}$ | $2.41^{b}$ | $2.03^{c}$ | $1.81^{e}$ | $1.89^{d}$ | $1.87^{d}$ | 0.03 |
| pef | 1.49 | 1.06 | 1.01 | 0.82 | 0.59 | 0.99 | 1.18 | 1.19 | 1.65 | |
| peNDF, kg/d | 2.06 | 1.81 | 2.52 | 1.40 | 1.41 | 2.01 | 2.14 | 2.25 | 3.09 | 0.01 |
| peNDF, % | 26.8 | 20.4 | 19.7 | 13.3 | 13.2 | 19.7 | 26.0 | 27.7 | 38.1 | 0.10 |

**Conclusion.** Our value of 159 min/kg NDF was similar to Mertens' (2002) 150 minutes/kg NDF, but a full linear regression indicated a significant intercept of 174 minutes and a slope of 69.4 min/kg NDF. The ideal peNDF of the finishing diets was 7.67, coinciding with Fox and Tedeschi (2002) recommendation of high-energy diets to be between 7 to 10% of the diet. Based on these recommendations, corn stalk inclusion between 5 to 15% provided adequate peNDF for finishing beef cattle.

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# Mechanistic model of metabolic use of dietary phosphorus and calcium and dynamics of body ash deposition in growing pigs: version 2.0

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**Application** A more precise estimation of phosphorus and calcium requirements in growing pigs will reduce these minerals utilization and excretion and increase the sustainability of the current phase-feeding systems.

**Introduction** Precision feeding may reduce phosphorus (P) and calcium (Ca) excretion and enhance sustainability but requires an accurate estimate of P and Ca requirements. Given the complexity of P metabolism because of multiple interactions, response criteria, and production objectives, mathematical modeling has been chosen to represent it. The aim of this paper is to update an existing model and evaluate its accuracy to predict growing pig body Ca and P repartition with the purpose of giving recommendations.

**Material and methods** Data (diet, body composition) of 4 experiments (Pomar *et al.*, 2006; Langlois *et al.*, 2016a and 2016b; Gonzalo *et al.*, 2018) were used to build an equation of the bone ash deposition potential independent of protein deposition. This has been done by using dietary treatments that exceeds the most Ca and P requirements (1 out of 17 treatments). In the remaining treatments, animals received 1) excess (control group), 2) deficient or imbalance (deficient group), and 3) deficient followed by control (depletion-repletion group) dietary Ca and P. The model prediction accuracy was assessed using mean squared prediction error (MSPE) and its decomposition into error of central tendency (ECT), regression (ER) and disturbance (ED).

**Results and discussion** The deposition dynamics is not the same for the different body tissues. In fact, there is no relationship between ash and protein deposition (Figure 1) as currently assumed in actual growth models (e.g., InraPorc, van Milgen et al., 2008 and NRC, 2012). With the new equation of the potential of Ca deposition into bone in relationship to bodyweight (BW, kg) ($Y = 6.46 + 4.49 \times 10^{-4} \times BW^2$; $R^2=0.76$), the model offers good prediction accuracy with MSPE of 6.7 and 7.8 % for P and Ca, respectively, which are mainly associated to disturbance error using the entire database (90 and 84 % for P and Ca respectively). However, in control group pigs it slightly underestimates body Ca and P (respectively, MPSE, 6.4 and 4.4%; ECT, 53 and 8 % for P and Ca). Conversely, Ca is overestimated in pigs fed deficient (MPSE, 8.7 %, ECT, 32 %) and depletion-repletion diets (MPSE, 7.3 %, ECT, 19.91). This overestimation is particularly important for body Ca in heavier body weight pigs (ER, 40.43 %) from deficient group. These results seem to be related to the lack of regulation of Ca and P metabolism especially bone resorption.

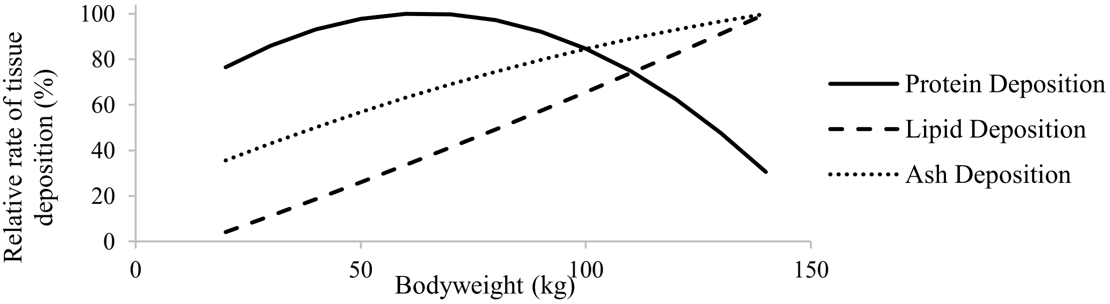

**Figure 1** Relative rate of tissue deposition in relation to pig bodyweight

**Conclusion** The independency of bone ash deposition potential to protein deposition permits to obtain accurate prediction of body P and Ca in control group pigs, although a slightly underestimate remains. Next steps will be to improve accuracy of prediction in low Ca diets.

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# Prediction models of reticulorumen kinetics of particles and solutes in growing goats

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**Application** DMI might be used as predictors in models for estimating passage rate and sex must be considered in the models.

**Introduction** Predictions of reticulorumen (RR) passage rate ($k_p$) of large particles ($k_{plp}$), small particles ($k_{psp}$), and solutes ($k_{ps}$) are essential to optimize the use of ingested feed by ruminants as they account for methane loses, microbial protein yield, and fiber digestion (Grandl et al., 2017; Müller, et al., 2013). Additionally, few prediction models of $k_p$ of particles and solutes have been developed for goats. Variables related to animal growth (i.e., sex, body weight (BW) (Almeida et al., 2016), feed intake, and GIT capacity (Müller, et al., 2013)) have been considered the driver force of RR kp (Grandl et al., 2017). The objective of this study was to develop prediction models of RR $k_{plp}$, $k_{psp}$, and $k_{ps}$ for growing Saanen goats.

**Material and methods** Our dataset involved 175 individual records of castrated males (C, n = 61), females (F, n = 57), and intact males (I, n = 57) growing Saanen goats from two studies. In the first study, goats were slaughtered at 15, 22, and 30 kg BW, and in the second study at 30, 37, and 45 kg BW. Goats slaughtered at the last BW of each study were fed at three levels of feed restriction (0%, 25%, and 50% ad libitum) of same diets. Our candidate's predictor variables were individual goat's BW (kg), sex, DM intake (DMI, g/day), diet composition (OM, NDF, and indigestible NDF (iNDF); % of DM), RR digesta pH, and total NDF digestibility (NDFd). The $k_p$ was assessed by using the method of emptying the RR segment in slaughtered animals, adopting iNDF, Yb, and Cr-EDTA as makers for $k_{plp}$, $k_{psp}$, and $k_{ps}$, respectively. NDFd was calculated as (1 – [(iNDF:NDF ratio of ingested diet)/(iNDF:NDF ratio of colon-rectum digesta)]). The $k_{ps}$ was also included as candidate predictor variable for $k_{psp}$ (Seo et al., 2009). The predictor variables for $k_{plp}$, $k_{psp}$, and $k_{ps}$ models were selected by fitting models that had all possible combinations of predictor variables. Linear mixed effects models were fitted using lmer function from lme4 package (version 1.1-17) of R (R Core Team), considering a random effect of study $s \overset{i.i.d.}{\sim} N(0, \sigma^2_s)$ and $\varepsilon \overset{i.i.d.}{\sim} N(0, \sigma^2_\varepsilon)$. The model that minimized the Akaike's information criterion was selected as the best model for each RR $k_p$. Variance inflation factor (VIF) was used as multicollinearity index for the predictor variables in the models, RMSE (defined as positive square root of the average squared differences between observations and predictions from the fixed effect part of the model only) and the Lin's concordance correlation coefficient (CCC) were used as a measure of goodness of fit and agreement between observations and predictions.

**Results** The best fitted model for each RR $k_p$ was:

$$k_{plp\ /h} = 0.0043 - 0.00048 \times BW_{(kg)} + 0.000010 \times DMI_{(g)} - 0.026 \times NDFd + 0.00085 \times iNDF_{(\%\ DM)} + 0.0055 \times pH \quad [1]$$

$$k_{psp\ /h} = -\ 0.24 - 0.000012 \times DMI_{(g)} - 0.00063 \times NDF_{(\%\ DM)} + 0.0030 \times OM_{(\%\ DM)} - 0.021 \times NDFd + 0.0049 \times pH + 0.057 \times k_{ps(/h)} \quad [2]$$

$$k_{ps\ /h} = 1.79 - 0.0053 \times BW_{(kg)} + 0.00014 \times DMI_{(g)} + 0.0032 \times NDF_{(\%\ DM)} - 0.016 \times OM_{(\%\ DM)} - 0.20 \times NDFd - 0.019 \times iNDF_{(\%\ DM)} + 0.0204 \times pH + 0.047 \times F + 0.028 \times I \quad [3]$$

All VIF were smaller than 4.4. The RMSE of $k_{plp}$, $k_{psp}$, and $k_{ps}$ models were 0.00769, 0.00910, and 0.0489 /h, respectively. The CCC was lower for $k_{plp}$ and $k_{psp}$ models (0.37 and 0.46, respectively) than for $k_{ps}$ model (0.74).

**Conclusion** DMI, as a predictor variable on all models, demonstrates its direct effect on RR $k_p$ of growing goats. Moreover, the RR $k_p$ of solutes has an important role on RR $k_p$ of small particles in growing goats. Predicting RR $k_p$ of particles is more difficult than RR $k_p$ of solutes for growing goats. As a further step, cross-validation should be performed to evaluate the predictive ability of the models.

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# Assessing the predictive capabilities of a dynamic mechanistic model of *in vitro* rumen fermentation and methane production

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**Application** Mathematical modelling of rumen *in vitro* fermentation offers a potential tool for the design of methane mitigation strategies.

**Introduction** We have previously developed a mechanistic dynamic model of *in vitro* rumen fermentation (Muñoz-Tamayo *et al*., 2016). The model was efficient to represent calibration data from experiments using rumen inocula from goats. The objective of this work was to assess further the robustness of the model by challenging the model against an independent data set.

**Material and methods** The experimental data set was obtained using rumen inocula sampled from the rumen of two cannulated dry cows fed at maintenance. Five total mixed rations (TMR) were collected from different dairy farms and characterized for chemical parameters, along with NDF, crude protein and starch degradability rates determined by previously developed enzymatic based methods (Gallo et al. 2018). Each TMR was incubated in diluted rumen fluid. The dynamics of fermentation were tracked at six sampling times (2, 5, 9, 24, 36, and 48 h) by measuring gas production and composition, as well as the concentrations of acetate, butyrate, propionate, and ammonia. The developed mathematical model (Muñoz-Tamayo *et al*., 2016) was calibrated using volatile fatty acids (VFA) and $CH_4$ data. Model calibration was performed with the IDEAS Matlab toolbox (Muñoz-Tamayo *et al*., 2009) using a maximum likelihood estimator.

**Results** The figure 1 shows the experimental data for one TMR compared against the model predicted variables. The model represented satisfactorily VFA concentrations and $CH_4$ production with Lin's concordance correlation coefficient (CCC) of 0.93 in average. We further assessed whether the hydrolysis rate constants of dietary carbohydrates and proteins determined enzymatically could be used as known parameters in the model while keeping satisfactory predictions. When using the enzymatically determined hydrolysis rate constants, the CCC was in average of 0.89, indicating the need of further improvements.

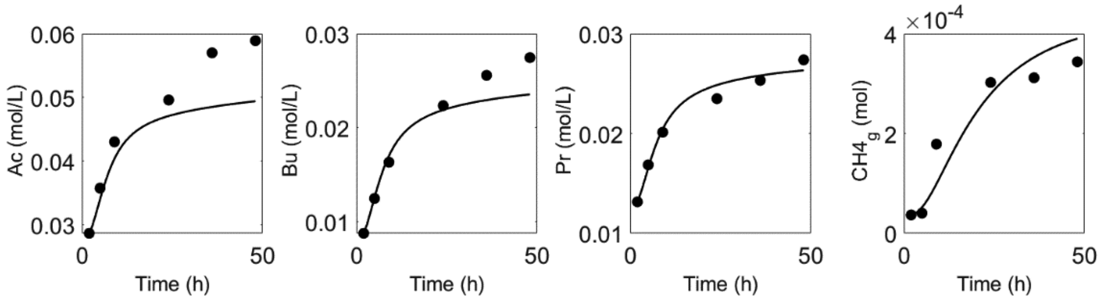

**Figure 1**. Experimental data of rumen fermentation (•) are compared against model predicted responses (-). Ac = Acetate; Bu = butyrate; Pr = Propionate.

**Conclusion** The model evaluation performed in this work strengthen the capabilities of our model structure to predict the *in vitro* fermentation pattern and $CH_4$ production from rumen microbiota. Further model extensions are currently undertaken to enhance the model capabilities for the assessment of strategies for methane mitigation.

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# Statistical Methods to Compare the Efficacy of Methionine Sources in Broilers

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**Application** This study recommends statistical methods to determine the bio-efficacy of methionine sources in commercial broiler feeds.

**Introduction** Methionine (Met) is available under different forms: DL-Methionine (DL-Met), L-Methionine (L-Met) and DL-Hydroxy-Methionine (OH-Met). For decades, there has been debate regarding the efficacy but only few studies emphasized on methodological aspects of this comparison (e.g. Vazquez-Anon et al. 2006; Kratzer and Littell 2006). This work aims to determine the appropriate statistical method to compare the efficacy of Met sources.

**Materials and methods** Two experiments were performed using male Ross PM3 broiler chickens that were reared for 36 days, divided into three feeding phases: 0-10 d, 11-24 d and 25-35 d. Experimental treatments consisted of a basal deficient diet in sulfur amino acids and diets supplemented at three equimolar doses with either L-Met or DL-Met (Trial 1) and L-Met or OH-Met (Trial 2). Body weight gain from each feeding phase in each of the two experiments were fitted to different models: (i) linear plateau, (ii) quadratic plateau and (iii) exponential models. Three explanatory variables were used in each model: the theoretical Met doses, the analyzed Met doses and the analyzed Met intake. The effect of the Met sources was tested on the different parameters of the models. The best models were selected using the Bayesian Information Criteria (BIC).

**Results** In the two trials, there was no effect of the Met sources on the different parameters for all models, which indicated no difference between the efficacies of the Met sources. The BIC values were similar between statistical models when using the same explanatory variables. However, the lowest BIC were obtained with the models based on Met intake (Table 1). In the starter phase of the second trial, the use of theoretical and analyzed doses did not allow convergence of the models. This was possibly due to the lack of data on the curve, before the maximum performance was reached.

Table 1. Parameters of the best performing models (1 = exponential plateau; 2= quadratic plateau; 3 = linear plateau) applied on the body weight gain of broilers fed L-Met, DL-Met, or OH-Met

| Age, d | Eq. | Trial 1: L-Met vs. OH-Met | | | Trial 2: L-Met vs. DL-Met | | |
|---|---|---|---|---|---|---|---|
| | | Theoretical Met | Analyzed Met | Met intake | Theoretical Met | Analyzed Met | Met intake |
| 0-10 | 1 | 226; 53; 14.7; BIC = 378.3 | 226; 54; 17.8; BIC = 375.7 | -1220; 1502; 3.96; BIC = 351.6 | No convergence | No convergence | -7853; 8123; 6.25; BIC = 371.1 |
| 11-24 | 2 | 515; 3457; 0.22; BIC = 482.4 | 515; 4002; 0.19; BIC = 478.6 | -183; 318 6.81; BIC = 461.5 | 521; 3919; 0.18; BIC = 485.1 | 521; 4314; 0.16; BIC = 484.5 | -226; 353; 6.21; BIC = 472.3 |
| 25-35 | 3 | 745; 5040; 0.09; BIC = 492.8 | 748; 5334; 0.08; BIC = 503.1 | 264; 140; 6.62; BIC = 492.0 | 701; 5479; 0.08; BIC = 519.1 | 701; 5479; 0.08; BIC = 519.1 | 217; 147; 6.44; BIC = 505.2 |
| 25-35 | 1 | 745; 449; 21.6; BIC = 491.4 | 746; 447; 23.6; BIC = 494.7 | -1532; 2748; 0.51; BIC = 484.1 | 701; 464; 33; BIC = 519.3 | 701; 465; 25; BIC = 519.4 | -2049; 3233; 0.58; BIC = 507.5 |

Linear-plateau: $y = ax + b$ if $x < x_0$; $y = y_{max}$ if $x \geq x_0$; Quadratic-plateau: $y = y_0 + ax + bx^2$ if $x < x_0$; $y = y_{max}$ for $x \geq x_0$; Exponential plateau: $y = a + b_1(1-e^{-c_1 x_1}) + b_2(1-e^{-c_2 x_2})$

**Conclusion** This work demonstrates that if appropriate explanatory variables are used, the choice of statistical models have little impact in estimating the bio-efficacy of methionine sources. The best explanatory variable allowing to compare Met sources is the Met intake. In most of the cases, the best performing model is the exponential model.

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# Digestibility of neutral detergent fiber of forages estimated *in vivo* with sheep or from chemical composition

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**Application** The *in vivo* digestibility of neutral fiber detergent by sheep is poorly estimated by equation of Weiss *et al.* (1992), which is based on forage lignin content.

**Introduction** Weiss *et al.* (1992) proposed an improve and expand the prediction equation developed by Conrad *et al.* (1984) and this model was validated with animals fed mixed diets (forage and concentrate). The objective of the present study was compare the digestibility of the NDF in *in vivo* tests with lambs fed on a forage, with the digestibility of neutral fiber detergent (dNDF) through the equation proposed by Weiss *et al.*, 1992.

**Material and methods** The experiments were conducted with male sheep fed diets of only forage, housed in metabolism cages through periods of 10 to 14 days of adaptation and 5 to 7 days of total collection of faeces. Data from fifteen experiments conducted with 370 lambs and 7 types of forages were evaluated. The diets consisted of different types of forages at variable maturity stages. The forage species used were *Lolium multiforum* (n = 160), *Echinochloa sp* (n = 32), *Pennisetum purpureum Schum. Cv. Mott* (n = 32), *Cynodon dactylon var. Dactylon sp* (n = 32), *Pennisetum clandestinum* (n = 18), *Arachis pintoi* (n = 32), *Pennisetum glaucum* (n = 64). The average ± standard deviation values of NDF and lignin content (% on dry matter), as well as of *in vivo* dNDF, were respectively: 53.5 ± 8.03, 71.2 ± 0.96, 62.7 ± 2.40, 69.5 ± 6.56, 65.2 ± 1.21, 65.1 ± 3.43, 54.5 ± 2.65 and 3.66 ± 1.63, 5.40 ± 0.82, 2.96 ± 0.13, 7.54 ± 1.98, 4.91 ± 0.54, 4.48 ± 0.53, 5.63 ± 3.22. The average *in vivo* dNDF values of each trial were then compared to those estimated through the Weiss *et al.* (1992) equation as follow: 0.75 (NDF - Lig) x [1- (Lig / NDF) 0.667], through simple linear regression.

**Results** There was a poor and not significant relationship between the dNDF values obtained *in vivo* with those estimated through the equation based on lignin content in forages (Figure 1).

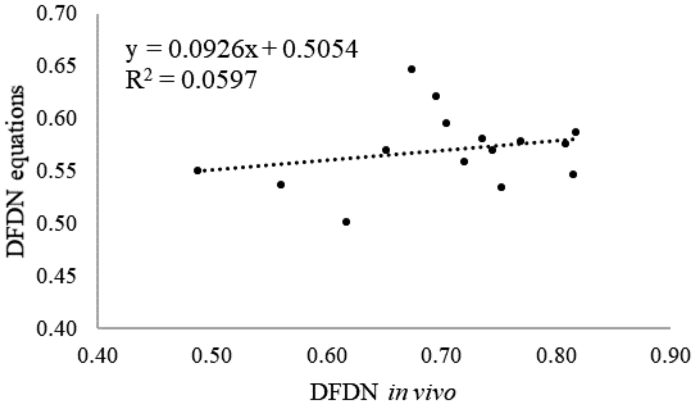

Figure 1. Relationship between values of digestibility of neutral detergent fiber (dNDF) estimated *in vivo* with those estimated from an equation based on the chemical composition of forage (Weiss *et al.*, 1992).

**Conclusion** The *in vivo* nNDF by sheep is poorly estimated by equation of Weiss *et al.* (1992).

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# Spline regression assessment of accuracy of hydrogen and methane emission measurements from dairy cattle using various sampling schemes

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**Application** Sampling scheme of emitted gases from cattle severely affects predicted daily $H_2$ emission.

**Introduction** Enteric $H_2$ and $CH_4$ emissions from cattle are measured using equipment such as the GreenFeed system and climate respiration chambers (CRC). GreenFeed systems are developed for spot sampling, whereas gases are sampled continuously in CRC. Sampling schemes for gas collection relative to diurnal patterns of $CH_4$ emission are considered important (Hammond et al., 2016). Given the greater diurnal variation in $H_2$ emission compared to $CH_4$ emission (Van Lingen et al., 2017), the appropriateness of sampling schemes may apply even more to $H_2$ emissions. The aim of the present study is to assess the accuracy of daily $H_2$ and $CH_4$ emission from dairy cattle using various sampling schemes of collection of emitted gases.

**Materials and Methods** Gas emission data measured in CRC from a 2 × 2 crossover in vivo experiment with 4 dairy cows were available (Van Lingen et al., 2017). Gases were sampled every 12 min for three consecutive days. Cows were fed at 95% of the ad libitum dry matter intake, with the feed fed in two portions per day. Spline regression, a technique for which the data determines the shape of the curve rather than a specific forcing function, was applied to predict diurnal $H_2$ and $CH_4$ emission rates. Predictions corresponded to sampling performed every 0.5, 1 and 2 h which started at 0 or 0.5 h after feeding, and to a scheme with samples taken at 2, 6 and 10 h after feeding.

**Preliminary results** Less frequent sampling starting at 0 h from feeding numerically under-predicted the continuously measured $H_2$ emission in CRC up to 46% (Table 1), whereas hourly and bihourly sampling starting at 0.5 h resulted in numerical over-prediction of $H_2$ emissions. Predicted $CH_4$ emissions ranged from 96 to 103% of the measured mean for all sampling schemes.

**Conclusion** Less frequent sampling can have a major impact on predicted daily $H_2$ emissions resulting in both numerical under- and over-prediction, whereas sampling schemes had a relatively minor effect on predicted daily $CH_4$ emissions.

Table 1 – $H_2$ and $CH_4$ emission from dairy cattle (mean ± SD) continuously measured in climate respiration chambers and spline regression predictions using various sampling schemes with respect to feeding time.

| | Continuous sampling | Every 0.5 h from 0 h | Every 1 h from 0 h | Every 2 h from 0 h | Every 1 h from 0.5 h | Every 2 h from 0.5 h | At 2, 6 and 10 h |
|---|---|---|---|---|---|---|---|
| $H_2$ (g/d) | 1.49 (0.64) | 1.44 (0.64) | 1.24 (0.55) | 0.69 (0.29) | 1.33 (0.75) | 2.66 (1.43) | 0.88 (0.62) |
| $CH_4$ (g/d) | 408 (17) | 408 (20) | 404 (19) | 392 (21) | 421 (20) | 418 (23) | 404 (35) |

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# Feed efficiency of growing pigs under heat stress conditions is influenced by lipid but not by protein deposition in conventional and precision feeding strategies

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**Application** Differently from nutritional strategies, the feed efficiency effects from lipid deposition may be an important factor to select pigs with adequate body composition under heat stress conditions.

**Introduction** Pigs under heat stress conditions may affects the partitioning of protein and fat deposition (Le Bellego et al., 2002). Moreover, high protein or lipid deposition is expected in pigs with greater or lesser feed efficiency, respectively, under thermoneutral conditions (Patience, 2012). In this study, we evaluate the lipid and protein deposition impacts on the feed efficiency of pigs raised under thermoneutral and heat stress conditions.

**Material and methods** Forty-eight barrow pigs from the same genetic line (Agroceres, AGPIC 337, averaging 41 ± 0.98 kg) were assigned to treatments: T1 – Precision feeding (IPF) under thermoneutral (TN: 23 °C) condition; T2 – Conventional 2-phase feeding (CON) under TN condition; T3 – IPF under heat stress (HS: 30 °C) condition; T4 – CON feeding under HS condition. The experiment lasted 55 days (phase 1 from d 0 to 27 and phase 2 from d 28 to 55). Conventional-fed pigs received within each phase a constant blend of diets A (high nutrient density) and B (low nutrient density) supplying the estimated nutrient requirements of the group, while pigs fed the precision feeding strategy received daily a personalized blend providing the estimated amount of nutrients. Body protein and lipid content were assessed by a dual-energy X-ray absorptiometry at the beginning and at the end of each phase. Data from phase 1 and 2 were analyzed using the CORR procedure of SAS including feed efficiency during each phase, protein and lipid deposition by kg of body gain for each treatment.

**Results** The correlation between feed efficiency and protein or lipid deposition for each treatment are presented in figure 1. Except for pigs under HS conditions, protein deposition has a strong positive correlation with feed efficiency for growing pigs. However, lipid deposition had a strong negative correlation with feed efficiency, even when pigs were exposed to HS. CON and IPF pigs presented similar results regarding protein and lipid deposition.

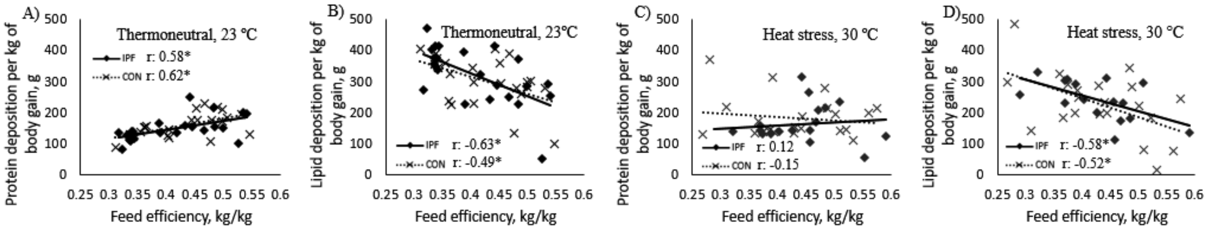

**Figure 1** Pearson correlation between feed efficiency and: Protein deposition for IPF and CON pigs under TN conditions (A); Lipid deposition for IPF and CON pigs under TN conditions (B); Protein deposition for IPF and CON pigs under HS conditions (C); Lipid deposition for IPF and CON pigs under HS conditions (D). * represents a significant Pearson correlation P<0.05

**Conclusion** Under HS conditions, the lipid deposition influences the feed efficiency of growing pigs negatively, suggesting that this variable may be of great interest to select pigs for tropical conditions.

**Acknowledgements** The authors thank the financial support received from the São Paulo Research Foundation (FAPESP, grant 2018/15559-7 and 2015/05241-1, Brazil).

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# Modelling of heat production in adult birds

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**Application** Heat production partitioning in fasting heat production (FHP), heat production due to physical activity (AHP), and thermic effect of feeding (TEF) could improve the accuracy of models to predict energy requirement.

**Introduction** The net energy (NE) system was suggested as more accurate system to express the energy metabolism and requirements on animals (Noblet, 2007). Although research with NE system has been widely developed in swine, in poultry there is a lack of study. A better understanding of energy utilization for FHP, AHP, and TEF may contribute to improve the efficiency of nutrient and energy utilization (Rivera-Torres *et al.*, 2010). Furthermore, could be help to determine NE maintenance. Therefore, the objective of the present study was to quantify the FHP, TEF, and AHP on adult birds.

**Material and methods** A assay was carried on using 18 Hy Line Brown roosters of 54 weeks-old (2.916±0.15 kg) to measure $O_2$ consumption (L/kg$^{0.75}$/d) and $CO_2$ production (L/kg$^{0.75}$/d). The heat production (HP) was calculated using Brouwer equation: HP (kJ/kg$^{0.75}$/d) = $16.15*VO_2 + 5.016*VCO_2$. The birds were housed in open-circuit respirometry chambers with environmental controller. The days of measurement was divided in: adaptation (3 days), and measurements of heat production on fed (HP, 1 day), and fasted (FHP, 1 day) birds. The physical activity (PA) was measured using a vibration sensor (m/s$^2$). To estimate HP and FHP at linear regression was fitted: $Y = \beta_0 + \beta_1*X$; where $Y$ is HP or FHP, $X$ is PA, $\beta_1$ is HP rate by PA unit, and $\beta_0$ is HP at zero PA. The TEF was calculated as the difference between HP and FHP.

**Results** According to linear equation (**Figure 1**), for each PA unit, the HP increase 59.61 and FHP increase 104.87 kJ/kg$^{0.75}$/d for feeding and fasting birds, respectively. The FHP and TEF at zero PA was 319 and 232 kJ/kg$^{0.75}$/d, respectively (**Figure 2**). These values are in agreement with O`Neil *et al.* (1971) and Liu *et al.* (2017).

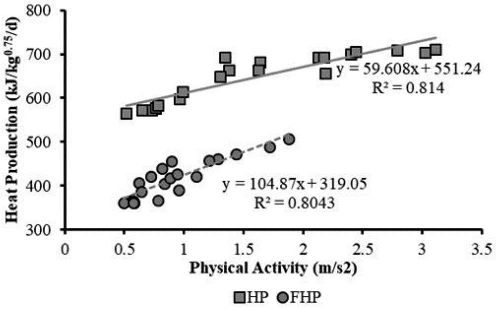

**Figure 1**. Linear regression of heat production (HP) and fasting heat production (FHP) at different rates of physical activity (PA).

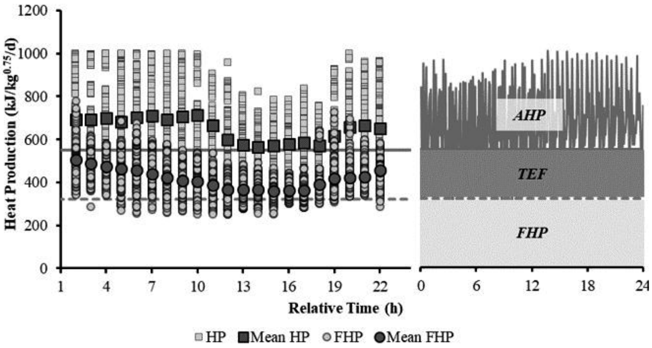

**Figure 2**. Heat production partitioning in fasting heat production (FHP), thermic effect of feeding (TEF) and thermic effect of physical activity (AHP).

**Conclusion** The heat production partitioning into a FHP, TEF and considering the physical activity effect (AHP) for each component, improve the interpretation data of energy utilization in adult birds.

**Acknowledgments** The authors thank CAPES for scholarship process N° 88882.330298/2019-01

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# Modeling the rate of feed passage in Japanese quails

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**Application** A better understanding of the dynamics of feed through the digestive tract in quails.

**Introduction** The rate of feed passage in the digestive tract influences on the dynamics of the digestive and absorptive processes, and consequently, in the use of nutrients. Dietary factors such as physicochemical composition of the ingredients may affect the rate of feed passage. Although the understanding of the rate of feed passage is relevant, no studies have investigated this issue in Japanese quails. Therefore, the aim of this work was to evaluate the rate of feed passage of Japanese quails fed diets with different AMEn contents.

**Material and methods** Thirty-two Japanese quails from VICAMI® Company were housed in a conventional facility, distributed in eight battery cages with four birds per replicate. Birds were fed with two diets: a low apparent metabolizable energy N-corrected (AMEn) of 8.84 MJ/Kg or a high AMEn content of 14.07 MJ/Kg. In order to measure the rate of feed passage, an external indicator ($TiO_2$) was added to the diets. The trial started at 07h:00min when birds were fed with the experimental diets containing 0.5% of (TiO2) for two hours. At 09h:00min, both experimental diets were replaced with identical ones, except for the addition of the indicator, until the end of the trial. All excreta started to be collected at 08h:00min, every hour, for 12 hours. Subsequently, excreta samples were weighed, processed and analyzed to determine the dry matter and (TiO2) contents. The (TiO2) recovered in each collection was expressed as a cumulative percentage of the total (TiO2) recovery for each treatment. The mean retention time (MRT) was calculated using the equations described by Coombe and Kay (1965). The time required to reach 1% (T1) and 50% (T50) of (TiO2) excretion (Ferrando et al., 1987) were estimated from the cumulative excretion curves using a modified Weibull model (Murthy et al., 2004): $Ti_{Ex}=1-exp[-(T/a)^b]$, where $T$ represents the time, in hours (h), to reach a specific proportion of excreted (TiO2) ($Ti_{Ex}$) (e.g. 1% and 50% represented by T1 and T50, respectively); $a$ is the scale parameter, and $b$ is the shape parameter. The diets were compared by model identity analysis and test of equality of parameters.

**Results** The adjusted models were: $T = 2.6\times[-\ln(1-Ti_{Ex})]^{1/3.4}$ using a low AMEn diet and $T = 2.56\times[-\ln(1- Ti_{Ex})]^{1/2.89}$ for the diet with high AMEn content. The result of the model identity analysis revealed that the diets are different, thus they do not have the same identity. However, parameter equality is acceptable when considering the average value of 2.58 (2.60 vs 2.56) and the equation may be rewritten considering only the differences in the exponent, from 3.4 for low AMEn diet and 2.89 for high AMEn diet. Therefore, there was a statistical difference ($P<0.05$) between 1% Ti excretion times, (low AMEn 0.67 vs high AMEn 0.52) and 50% (low AMEn 2.34 vs high AMEn 2.26). The MRT for the low AMEn diet was 6.67 h, whereas for the high AMEn diet was 6.59 h. The MRT was 6.63h, which is higher than values found by Shires et al. (1987) for broiler (5.63h) and laying hens (5.98h).

**Table 1** Rate of feed passage and mean retention time of Japanese quails fed with low and high EMAn diets

| AMEn (MJ/Kg) | T1 (h) | T50 (h) | MRT (h) |
|---|---|---|---|
| 8.84 | 0.67 | 2.34 | 6.67 |
| 14.07 | 0.52 | 2.26 | 6.59 |

**Conclusion** The dynamics of feed passage in the digestive tract of Japanese quails presented specific characteristics, which differs from other production birds. This outcome indicates that caution is necessary when changing diet composition.

**Acknowledgments** The first author thanks the scholarship provided by CNPq.

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# Optimum proportion of sulfur amino acids for broiler chickens

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**Application** The conversion of Methionine (Met) to Cystine (Cys) may be considered to determine an optimum Met:Cys/SAA ratio for broiler chickens in order to optimize animal performance.

**Introduction** Although Met and Cys have been considered together as Sulfur Amino Acids (SAA) in broiler diets, these two amino acids play different roles in protein metabolism. Once Met can be converted to Cys by the transsulfuration pathway, this biological reaction can balance the proportion of these amino acids when there is Met excess and Cys deficiency. However, the transsulfuration pathway could be insufficient depending on the imbalance of these amino acids, even when an adequate SAA is supplied. Therefore, the present study investigates how Met conversion is affected by different Met:Cys/SAA ratios.

**Material and Methods** Twelve one-d-old male chicks were fed by four diets formulated to supply 48:52; 50:50; 52:48; and 56:44 of Met:Cys/SAA ratio and the SAA level was kept the same for all diets. Diets were supplied with L-($^{15}N_2$) Cys (35 mmol.kg$^{-1}$) for 14 days and birds were raised until 56d of age. Samples of whole body were collected and analyzed for $^{15}$N and Cys content by stable isotope and aminogram analyses to determine the conversion from Met to Cys, as described by Pacheco *et al.* (2018). A broken-line regression model was fitted to the data according to Robbins *et al.* (2006).

**Results** The maximum Met conversion was 43% and it would be reached in chicks fed a diet with 52.3% of Met/SAA, which may maximize the animal performance. This outcome corroborates with other studies that reported a maximum performance when 52% of SAA was Met (Baker *et al.*, 1996; Pacheco *et al.*, 2018).

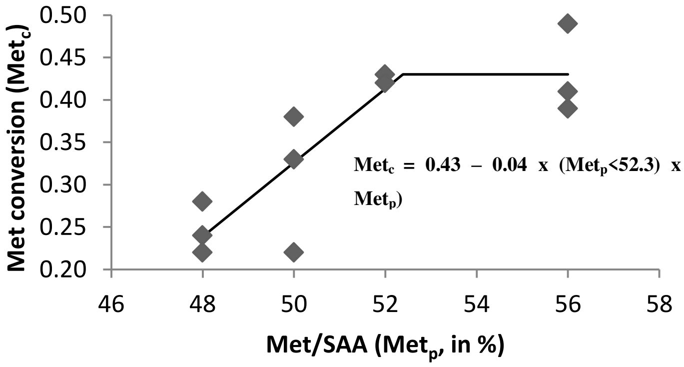

**Figure 1.** Met conversion in broiler chickens fed different Met/SAA ratio diets

**Conclusion** A 52.3:47.7 of Met:Cys/SAA ratio diet results in a maximum Met conversion of 43% in broiler chickens. Above 52%, the transsulfuration pathway could be insufficient to balance the SAA proportion.

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# Genotype effects on energy and protein requirements in growing goats

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**Application** Genotype influences energy requirements, but not protein requirements of growing goats. Protein requirements is not affected by goat genotype. These results may be useful for improving robustness of feeding systems for goats.

**Introduction** Goats of different genotypes have different growth pattern and body composition in a given body weight (McGregor, 1985; Mpairwe et al., 2014). We hypothesized that such differences due to genotype will result in different energy and protein requirements for maintenance (**$NE_m$** and **$NP_m$**, respectively) and weight gain (**$NE_g$** and **$NP_g$**, respectively) among dairy (Saanen), meat (50% or more of Boer), and indigenous (local breeds) goat types. This study was designed to investigate the genotype effect on energy and protein requirements of dairy, meat, and indigenous goats, as well as provide estimates of $NE_m$, $NP_m$, $NE_g$ and $NP_g$.

**Material and methods** Individual animal data from eleven comparative slaughter studies were gathered and a meta-analytical approach was used. Two distinct databases were used as follows. Linear and non-linear equations were fitted using 227 individual records of meat (n=75), dairy (n=97), and indigenous (n=55) male goats, to depict $NP_m$ and $NE_{m,}$ respectively. Allometric equations of energy and protein content against empty body weight (EBW) were fitted using 240 individual records of meat (n=74), dairy (n=99), and indigenous (n=67) male goats, to depict $NE_g$ and $NP_g$. All parameters of fitted equations were obtained and tested for genotype fixed effect using the MIXED procedure of SAS (SAS Inst. Inc., Cary, NC; version 9.4).

**Results** Our findings showed that $NE_m$ of meat goats was 8.5% greater (80.3 kcal/kg$^{0.75}$ EBW) than dairy and indigenous goats (74.0 kcal/kg$^{0.75}$ EBW; $P<0.05$). Whereas, $NP_g$ was not affected by genotype (1.92±0.239 g/kg EBW; P=0.91). Irrespective of goat type, $NP_g$ did not change as goats grew from 5 to 45 kg BW (P=0.12; ranging from 185.1 ± 1.82 to 192.5 ± 4.33 g/kg of EBW gain). On the other hand, $NE_g$ increased from 1,699 ± 65.8 to 3,450 ± 219 kcal/kg of EBW, from 1,732 ± 52.2 to 2,899 ± 133 kcal/kg of EBW, and from 1,785 ± 44.8 to 4,119 ± 198 kcal/kg of EBW for meat, dairy, and indigenous goats between 5 and 45 kg BW, respectively ($P<0.01$).

Table 1. Net protein and energy requirements in growing goats

| Requirement[1] | Meat | Dairy | Indigenous |
|---|---|---|---|
| $NP_m$, g/kg EBW | 1.92±0.239 | 1.92±0.239 | 1.92±0.239 |
| $NE_m$, kcal/kg$^{0.75}$ EBW | 80.3±2.58 | 74.0± 1.96 | 74.0± 1.96 |
| $NP_g$, g/kg of EBW gain | 185±1.82 to 193±4.33 | 185±1.82 to 193±4.33 | 185±1.82 to 193±4.33 |
| $NE_g$, Mcal/kg of EBW gain | 1.67±0.658 to 3.45±0.219 | 1.73±0.522 to 2.90±0.133 | 1.79±0.448 to 4.12±0.198 |

[1] NPg and NEg from 5 to 45 kg BW, respectively; Monte Carlo method was used to estimate standard deviations.

**Conclusion** Protein requirements is not affected by goat genotype. The genotype alters goat body composition, thus the requirements for $NE_g$ in meat, dairy, and indigenous goats. Future research should evaluate the maturity degree effect on $NE_g$.

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# Impact of buffer turnover rate on outflow of N compounds in a semi-continuous culture fermenter (RUSITEC)

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**Application** Models to estimate ruminal protein degradation.

**Introduction** The degradation rate (kd) is a key parameter for estimating the rumen degradable protein (RDP) fraction of feedstuffs, as by using the equation: A + B(kd/kd+kp), where A and B are the soluble and insoluble protein fractions, respectively, and kp is the passage rate from rumen (NRC, 2001). The values of Kd reported in most nutritional systems were conventionally estimated through the *in situ* technique (Orskov and McDonald, 1979). This method, however, is based on the determination of disappearance of N compounds from bags, which may occur by the leakage from sample through the bag pores, not necessarily implying degradation by ruminal bacteria. This leakage of sample can involve in an overestimation of the RDP fraction of the crude protein (Bach et al., 2008), which could be exacerbated by an increased passage rate (kp). Thus, we aimed to evaluate the effect of the liquid fraction kp on N compounds profile outflow in semi-continuous culture fermenters.

**Materials and methods** Five semi-continuous culture fermenters were used in an incomplete 3 x 3 Latin square design. The three runs trials were carried out on 9 days each, with 4 days of adaptation and 5 days of sample collection. Each fermenter received daily 10g of the diet in nylon bags with porosity of 50μm. The incubated diet was composed by corn silage (0.60), corn grain (0.21) and soybean meal (0.19). The liquid effluent was removed daily and sampled for N, α-amino-N, peptide-N and ammonia-N analysis. Statistical analysis was carried out using the MIXED procedure of SAS, and linear effects of treatments were analyzed by regression.

**Results** Increasing the passage rate of the liquid fraction did not affect the N degradation or ammonia-N flow, however, increased linearly the peptide-N flow, the total N flow and the total N flow to disappeared N ratio, and decreased linearly the α-amino-N flow.

Table 1. Effect of buffer infusion rate on outflow of N compounds in a RUSITEC system.

| | Kp (%/h) | | | | |
|---|---|---|---|---|---|
| | 3 | 5 | 7 | SEM[1] | p-value[2] |
| Incubated N (mg) | 245 | 245 | 245 | 0.82 | ns |
| N degradation (%) | 53.5 | 54.6 | 53.7 | 1.16 | ns |
| N flow (mg/d) | | | | | |
| Peptide-N | 22.9 | 48.3 | 56.7 | 5.14 | <0.01 |
| α-amino-N | 1.98 | 1.39 | 1.29 | 0.202 | 0.01 |
| Ammonia-N | 15.4 | 12.0 | 13.8 | 1.65 | ns |
| Total N (TN) | 40.3 | 61.7 | 71.7 | 4.93 | <0.01 |
| TN/disappeared N | 0.36 | 0.55 | 0.63 | 0.050 | <0.01 |

[1]Standart error of the mean; n= 5 per treatment. [2]Probability of treatment effect by linear regression analysis.

**Conclusion** The outflow of soluble peptides, as proportion of the N which disappeared from sample, increased linearly at increased buffer infusion rate in the semi-continuous fermenter. This result indicate that the in situ technique overestimate the degradable and underestimate the undegradable protein fraction of feedstuffs.

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# Assessing essential amino acid availability and metabolism in lactating dairy cows infused with methionine, lysine, and histidine or leucine and isoleucine.

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**Application** Knowledge of AA uptake and metabolism in mammary gland will help optimizing post absorption AA utilization, thus improve nitrogen (N) efficiency.

**Introduction** It is well recognized that further improvements in AA efficiency of utilization in mammary tissue are due to changes in protein accretion and partition. A better knowledge of AA metabolism within the mammary gland will help optimize the milk protein production under reduce N intake (Dijkstra et al., 2013). By coupling isotope tracers with arterio-venous difference technique and compartmental modelling, Crompton et al. (2014) quantified Phe and Tyr metabolism in mammary glands of dairy cows. However, studies on AA metabolism in mammary gland with infused EAA were lacked. The objective of this study was to evaluate the effects of jugular infusion of 2 groups of AA on essential AA (EAA) availability and utilization by the mammary glands.

**Material and Methods** Four cows (78 ±10 DIM) were assigned to 4 jugular infusion treatments: saline (CON), methionine plus lysine plus histidine (MKH), isoleucine plus leucine (IL), or MKH plus IL (MKH-IL) in a 4 x 4 Latin square design. Each period was 16 d in length with 8 d of adaption followed by 8 d of jugular AA infusion. Infusion rates were 10 g of methionine, 38 g of lysine, 20 g of histidine, 50 g of leucine and 22 g of isoleucine per day. On last day of each period, a $^{13}$C labeled AA mix was infused into the jugular vein over a 6 h period, and blood samples were collected hourly and assessed for AA enrichment. Total plasma AA entry rates and AA metabolism in mammary glands were estimated for each EAA by fitting a 10-pool, dynamic model to observed plasma and milk, $^{13}$C AA enrichment.

**Results** Milk production increased significantly with infused IL ($p=0.04$), but did not change in response to MKH ($p=0.44$). Milk protein concentration and yield increased for the MKH infusion ($p<0.01$) whereas milk protein yield tended to increase for IL ($p=0.08$). The blood Ile entry rates were 352, 294, 453, and 286 g/d for CON, MKH, IL and MKH-IL respectively. The MKH infusion significantly decreased Ile entry ($p=0.01$) while IL infusion had no effect on Ile entry. The increase in Ile entry with MKH infusion reflected decreased Ile availability from the diet or decreased recycling of Ile in the body. The Ile uptake rate in mammary gland were 1.43, 1.27, 1.05, and 1.28 ($\text{min}^{-1}$) for CON, MKH, IL and MKH-IL respectively. The IL infusion significantly decreased the Ile uptake rate in the mammary gland ($p=0.05$) while the MKH infusion had no significant effect. The AA efflux and oxidation rates in the mammary gland was not affected by treatments.

**Conclusion** The Ile and Leu infusion decreased the mammary uptake rate of Ile, thus increased the recycling Ile. Other essential AA uptake and metabolism by the mammary glands will be reported.

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# Model of phosphorus flux and excretion in growing lambs

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**Application** The model is useful to adjust dietary P intake and supplementation, reducing excretion losses, and consequently, reducing environmental damages.

**Introduction** Small ruminant producers provide supplemental dietary phosphorus (P) as dietary supplements for animals due to its importance in maintaining metabolic functions. However, providing more P than the animal requires can negatively impact the environment (Tamminga, 1996). Isotope ($^{32}$P) dilution is an accurate technique to determine animal P metabolism and fluxes between tissues. Models of P metabolism in animals are necessary to allow dietary P manipulation to achieve reduced P excretion while maintaining animal health and productivity. The study aimed to adapt a multicompartmental model to predict P fluxes in lambs.

**Methods** Eighteen Santa Ines male lambs (age = 6 months, body weight = 31.8 ± 4.6 kg) were randomly divided into two groups and fed 50 or 100% of their P requirements based on the National Research Council (2007) recommendations. All animals were given a bolus infusion of $^{32}$P, and a 6-pool model was used to derive P fluxes. Modeled pools were the rumen, small intestine, large intestine, plasma, bone, and soft tissues. Daily intake and excretion of P in feces and urine and the specific activity of P and mass of stable P in each pool were determined and used as inputs to the model. The model was evaluated using mean squared prediction error (MSE), root mean squared error (RMSE) expressed as a proportion of the observed mean, and concordance correlation coefficients (CCC) to evaluate the precision and accuracy of model fits.

**Results and discussion** Daily P fluxes through the rumen, SI, LI, and plasma were greater for animals fed the adequate-P diet as compared to those fed the low-P diet (Table 4, $P < 0.001$). Surprisingly, fluxes between plasma and bone ($P = 0.896$), and plasma and ST ($P = 0.416$) were not different between treatments, however, there were numerical differences in the balance of P between plasma and bone where the balance was more negative for animals fed the P-restricted treatment (- 0.74 g/day; $P = 0.011$) than animals fed adequate P-diets (-0.35 g/d). Similar results were observed for the balance of P between ST and plasma ($P = 0.004$) where animals fed the adequate-P diet had positive P balance (0.0046) representing retention of P in tissues, and the low-P diet had negative values (-0.0769) which indicated P resorption from tissues. Regarding the low-P treatment, the P-balance between bone and plasma was 0.701 g/day ($P = 0.005$), and between ST and plasma was 0.064 g/day ($P = 0.011$), which indicated reabsorption from the combined tissues. The fact that both treatments had negative P balance may indicate some bias in the measurements of P intake or P excretion. As this is an accumulator for measurement errors, it is not uncommon to have bias in the balance measurement.

**Conclusion** The model can be used for predicting P fluxes in lambs fed different diets, and thus can be used as a nutritional tool to reduce the excretion of P in feces.

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# Sensitivity of microbial crude protein methods in estimating the total fecal nitrogen of tropical cattle

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**Application:** Direct and indirect methods of estimating microbial crude protein synthesis (MCP) can be used to accurately predict total fecal-nitrogen (N) excretion.

**Introduction:** The ruminant feeding system of the French Institute for Agricultural Research (INRA, 2018) estimates the fecal-N excretion of cattle in warm climates using rumen-undegradable crude protein (RUP), MCP synthesis, and non-digestible neutral detergent fiber (NDNDF). However, different methods exist to predict duodenal MCP flow, which may affect the estimation of fecal-N excretion. This study aimed at (a) evaluating the sensitivity of fecal-N predictions, (b) comparing estimates of fecal-N excretion using various methods to predict rumen MCP synthesis, and (c) assessing the accuracy and precision of predicted fecal-N excretion in cattle under typical tropical feeding conditions.

**Methods:** A dataset was compiled from three feeding trials conducted with cattle under typical tropical feeding situations that included 17 dietary treatments and 163 observations. Total fecal-N excretion in these trials was quantified using the external fecal marker titanium dioxide (Glindemann et al., 2009). The database included information (arithmetical mean±standard deviation) on RUP (368±126.2 g/kg crude protein), NDNDF (169±14.7 g/kg dry matter {DM}), and fecal-N excretion (65±53.4 g/day). Rumen MCP synthesis (g/kg DM) was estimated using four methods. Firstly, MCP flow was estimated from fermented organic matter using equation 4.15 of the INRA feeding system (INRA, 2018). Due to a lack of information, it was assumed that fermented organic matter was equal to digested organic matter minus truly digestible dietary protein and the NDNDF in the animals' diets. Secondly, MCP synthesis was derived from estimates of the total duodenal flow of microbial and feed crude protein (i.e., utilizable crude protein; GfE 2001) determined by the *in vitro* Hohenheim gas test (HGT) method (Steingaβ et al., 2001). Hence, MCP flow was calculated by subtracting RUP from utilizable crude protein (g/kg DM). Thirdly, a constant MCP yield of 10.1 g MCP/MJ of metabolizable energy (MJ/kg DM) (GfE, 2001) was assumed to derive rumen MCP synthesis. Lastly, duodenal MCP flow was predicted from urinary purine derivatives (PD) excretion according to Chen and Gomez (1992). Subsequently, fecal-N excretion was calculated according to INRA (2018; equation 13.1). A Montecarlo analysis was used to assess the sensitivity of estimates of fecal-N excretion. Accuracy and precision of fecal-N predictions were evaluated using the concordance correlation coefficient (CCC). Statistical analyses were done by Minitab Companion (2019) software.

**Results:** Estimates of total fecal-N excretion are most sensitive to changes in RUP and duodenal MCP synthesis. Differences ($p < 0.01$) in MCP synthesis were found between the different approaches used to estimate rumen MCP synthesis with (arithmetical mean±standard deviation) 83±11.6 g, 68±32.1 g, 77±17.8 g, and 50±25.6 g/kg DM for INRA, HGT, GfE, and PD, respectively. No differences (p=0.85) in total fecal-N excretion were observed between INRA (64±42.5 g/d), HGT (64±43.1 g/d), GfE (64±43.2 g/d), and PD (60±38.7 g/d) methods. Predictions of fecal-N excretion were more accurate when derived from estimates of rumen MCP synthesis by HGT (CCC=0.95), INRA (CCC=0.95), and GfE (CCC=0.95) than by PD (CCC=0.92). The lower CCC of fecal-N predictions when MCP flow was derived from urinary PD excretion may at least partly be related to inaccuracies in the PD method (Wassie et al., 2019).

**Conclusions:** Predictions of fecal-N excretion according to INRA (2018) are sensitive to changes in RUP and MCP. Nevertheless, equations by INRA (2018) can accurately predict total fecal-N excretion of cattle under typical tropical feeding conditions, irrespective of the method used to estimate rumen MCP synthesis.

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# Modelling broiler requirements for methionine and cystine considering sulfur amino acids conversion

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**Application:** Handling stable isotopes to understand how amino acids are partitioned into body and feather has been in these tissues a potential tool to estimate efficiency of amino acid utilization and optimize the factorial models to help nutritionists to formulate diets with a higher accuracy.

**Introduction:** Since methionine (Met) is converted into cystine (Cys); and that controversies still surround such conversion rates; poultry diets are conventionally formulated to meet bird requirements for total sulfur amino acid (SAA) and supply excessive amounts of Met to necessary dietary Cys supply. In a previous study, was determined the rate with which Met is converted into Cys (Pacheco, 2018). This study was conducted in order to develop factorial models, which predict Met and Cys requirements in separately and as total SAA.

**Material and Methods:** Twenty-one broiler cobb chickens from 14 to 28d of age were fed experimental diets containing different Met:Cys ratios (44:56, 50:50 and 56:44). Birds were given diets daily supplemented with L-($^{15}$N) Met (60 mmol.kg$^{-1}$) or L-($^{15}N_2$) Cys (35 mmol.kg$^{-1}$) throughout the entire experimental period. Excreta were daily collected and at the end of the trial, birds were euthanized in order to collect feather-free body and feathers. Samples were analyzed for $^{15}$N and $^{15}$N-Met content to determine the conversion from Met to Cys.

**Results:** The efficiencies of Met, Cys and Met+Cys utilization determined for feather-free body were 51, 75, and 59%, whereas for feathers the efficiencies for these amino acids were estimated in 93, 78 and 83%, respectively. Maintenance coefficients considered to develop the factorial models were 200 mg.kg$^{-1}$ body protein weight for Met, 75.4 mg/kg body protein weight for Cys, and 275 mg/kg body protein weight for Met + Cys. Analyzed Met, Cys, and Met + Cys in feather-free body were equivalent to 25, 11, and 36 mg/g, and 6, 70 and 76 mg/g in feathers, respectively. Feather loss was considered as 0.01g/g. Taking into account a four-phase feeding program (1 to 7d, 8 to 21d, 22 to 33d, and 34 to 42d of age) broiler requirements for Met+Cys in each phase were 194, 603, 1166 and 1398 mg/bird.day$^{-1}$; Met in 125, 386, 755 and 918 mg/bird.day$^{-1}$; and Cys in 78, 244, 463 and 543 mg/bird.day$^{-1}$ considering the broiler requirements in the pre-starter, starter, grower, and finisher phases, respectively. Our estimates were similar to those described by the Brazilian Tables for Poultry and Swine (BTPS)(Rostagno et al., 2017) and genetic strain guideline (GL) (Table 1).

Table 1. Comparison among the requirements (mg.d$^{-1}$) estimated by factorial models of this study and recommend by Brazilian Tables (BTPS) and Guideline (GL).

| Age (days) | Met | | | Cys | | | Met+Cys | | |
|---|---|---|---|---|---|---|---|---|---|
| | mg.d$^{-1}$ | | | | | | | | |
| | Model[1] | BTPS | GL | Model[2] | BTPS | GL | Model[3] | BTPS | GL |
| 1-7 | 112 | 125 | 107 | 80 | 101 | 103 | 192 | 226 | 210 |
| 8-21 | 346 | 381 | 321 | 250 | 307 | 293 | 596 | 688 | 614 |
| 22-33 | 678 | 723 | 615 | 475 | 582 | 552 | 1153 | 1305 | 1167 |
| 34-42 | 823 | 863 | 850 | 558 | 695 | 763 | 1382 | 1558 | 1613 |

[1] $M_{MET} = [(200.2 x BP_m{}^{0.73} x\ u) + (0.01\ x\ FP\ x\ 6)] + [(25\ x\ BPD)/0.57 + (6\ x\ FPD)/0.94]$

[2] $M_{CYS} = [(75.4 x BP_m{}^{0.73} x\ u) + (0.01\ x\ FP\ x\ 70)] + [(11\ x\ BPD)/0.71 + (70\ x\ FPD)/0.78]$

[3] $M_{M+C} = [(275.6 x\ BP_m{}^{0.73}\ x\ u) + (0.01\ x\ FP\ x\ 76)] + [(36\ x\ BPD)/0.60 + (76\ x\ FPD)/0.82]$

**Conclusion:** Handling stable isotopes to understand how amino acids are partitioned into body and feather has been in these tissues a potential tool to estimate efficiency of amino acid utilization. The factorial models developed in current research may help nutritionists to formulate diets with a higher accuracy. In possess of such information and understanding the dynamic between production cost and broiler selling price, the nutritionist could guide broiler production process towards higher efficiency and profitability.

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# Mechanistic model of metabolic use of dietary phosphorus and calcium and dynamics of body ash deposition in growing broilers

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**Application** This model allows the prediction of bird responses to various dietary P and Ca strategies.

**Introduction** Several phosphorus (P) response criteria can be used depending on the objective of production (*e.g.* profitability, welfare and environment) challenging the utilization of a single value of requirement. A robust multi-criteria model aiming to simulate actual calcium (Ca) and P retention within the different anatomical fractions and body ash of the broiler according to animal growth potential and dietary Ca and P intake has been developed.

**Material and methods** The model was built with a mechanistic approach using experimental data of body tissue composition and literature data analyzed with meta-analysis. It includes two submodules integrating respectively the growth of bird tissues and the metabolic fate of P and Ca. For the growth aspect, weight gain was calculated as the sum of daily depositions of protein, water, fat and ash. The daily "ideal" protein deposition (feathers and body) is estimated as a function of body weight using allometric equations recalculated from Silva *et al.* (2015). Ideal protein deposition is then modulated according to the actual daily intake of lysine. Daily lipid deposition is then quantified by the difference between metabolizable energy intake and losses (heat production) and deposition in the form of proteins. Based on a meta-analysis (Hedli *et al.*, 2019), feed intake is modulated by dietary Ca and P supply. The second submodule predicts ash deposition depending on dietary Ca, P, and phytase levels. In this submodule, absorption equations of P and Ca from a meta-analysis using ileal digestibility data (Couture *et al.*, 2018), as well as P and Ca levels in tissues are used to estimate P, Ca and ash depositions in bone, soft tissues and feathers.

**Results and discussion** Feeding a 21-days old broiler with a reference diet fulfilling requirements, showed that 62% of P was deposited into bones, followed by 33% in proteins, 2% in feathers and 3% in lipids while Ca deposition was deposited at 95% into bones, 4% into proteins, 1% into feathers, and 0.5% into lipids. When simulating diets with contrasted Ca and P levels, the model adequately represent critical aspects of P and Ca metabolism in growing broilers. For instance increased P supplementation with adequate Ca intake results in increased Ca retention and reduced urinary losses because these minerals are deposited together (Figure 1a). Besides, in a well-supplied P diet, the increase in Ca intake from 5.0 to 10 g/kg results in an improvement in P retention with a reduction in urinary losses (Figure 1b). It also showed a reduced feed intake in low P and high dietary Ca diet and priority for P soft tissues P deposition at the expense of bones.

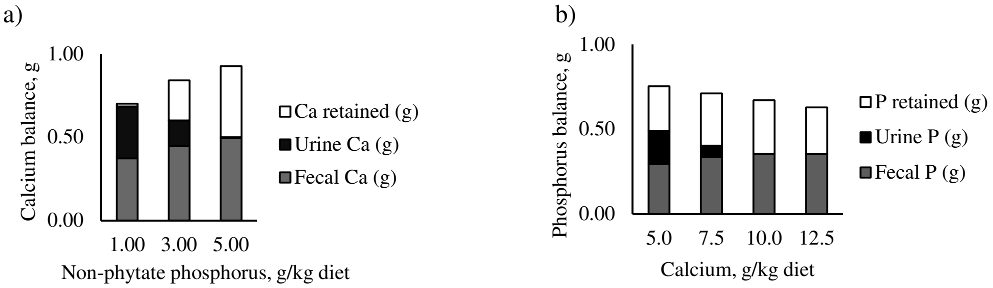

Figure 1. Calcium balance (a) and phosphorus balance (b) in function of dietary calcium and phosphorus supply.

**Conclusion** The proposed model simulates the metabolic fate of dietary P and Ca in growing broilers and the dynamics of body ash integrating the most relevant physiological processes involved in broiler P metabolism. The next steps will be the validation of the model using data from a trial specifically designed for that. Then the model could be reversed to estimate P requirements according to production objectives.

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## Threonine requirements of growing pigs: a meta-analysis

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**Application** Precise estimations of threonine (Thr) requirements can maximize nitrogen efficiency of utilization in growing pigs.

**Introduction** Threonine is considered the second limiting amino acid in corn-soybean meal diets for pigs. Although several studies have been conducted to study Thr requirements, still there is no consensus regarding the ideal recommendation. Therefore, this study aimed to quantify Thr requirements for pig populations and acquire information to further model Thr requirements in individual pigs.

**Material and methods** The database contained 29 Thr dose-response scientific communications published between 1987 and 2018. In the selected communications, lysine was provided at 90%, and all other amino acids at 110%, of their requirements. A categorical code was used to analyze data from the initial, growing, and finishing phases. Average daily gain (ADG) responses were expressed relative (ADG%) to the greatest response in the study (i.e., greatest ADG in each study was considered 100%). Relative Thr intake ($Thr_{int}$) was expressed in relation to NRC (2012) recommendations (i.e. NRC recommendation was considered 100%). Non-linear regressions were fitted by NLIN procedure of SAS for each dose-response study using the linear-plateau (LRP) model $Y = U \times (X<R) \times (R-X) + L$ (where, U is the slope coefficient when $X<R$, L is the break point in the Y-axis, and R represents the break point in the X-axis). The breaking-point in the LRP was interpreted as the relative $Thr_{int}$, required to maximize ADG%. The LRP models were then sequentially fitted by NLMIXED procedure to obtain a model in which all the parameters (U, R, and L) were randomized. This step was performed to combine the models generated for each trial and to obtain a model that considered the variability among studies.

**Results** Considering the studies individually, the $Thr_{int}$ requirements to maximize ADG% varied from 73% to 143% of the estimated by the NRC (2012). In three experiments, pigs did not respond to $Thr_{int}$ levels. In the initial phase, $Thr_{int}$ required to maximize ADG% was 15% above the NRC (2012) recommendations, whereas during the growing phase ADG% was maximized at 100% of NRC (2012) recommendations. Finishing pigs required 3% less $Thr_{int}$ than the recommended by the NRC (2012).

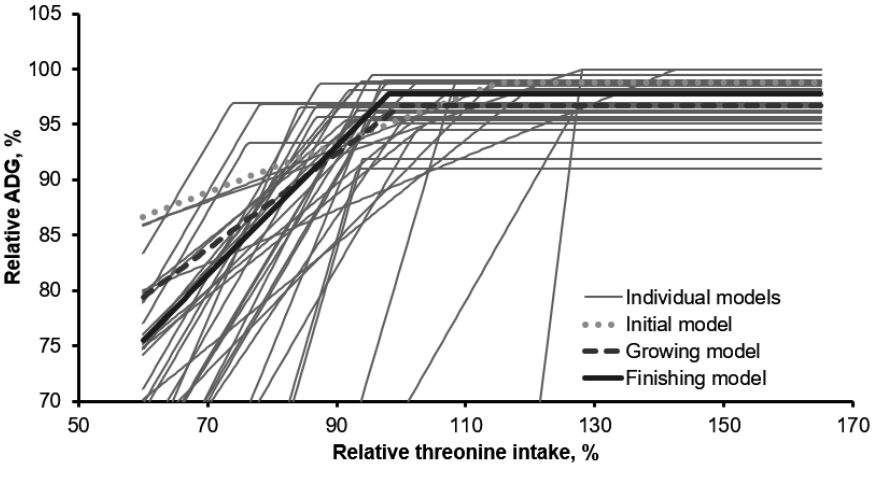

**Figure 1.** Threonine intake requirement relative to the NRC (2012) to maximize weight gain of pigs.

**Conclusion** A large variance in Thr requirements is observed among studies. Still, the LRP shows that, with exception of the initial period, providing pigs with Thr according to NRC recommendations may maximize ADG% response. However, these data should be interpreted with caution, once the linear-plateau model might represent the average pig response rather than the population response, which is curvilinear. Maximal population growth rate is obtained at higher dietary amino acid levels than the average pig of the population (Pomar *et al.*, 2003).

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# Metabolizable energy partition for japanese quails

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**Application** Knowing the energy intake partition for maintenance, growth and egg production makes it possible to structure models and recommend energy intake considering the differences of birds in body weight, weight gain and egg production in commercial lots.

**Introduction** Energy is often used in feed formulations as a reference base to express the requirements of other nutrients (Rivera-Torres et al., 2010), in addition, energy utilization efficiency is the key point to develop models capable to predict intake based on its partition. Therefore, the aim of this study was to evaluate the energy partition for Japanese quails in the egg production phase.

**Material and methods** Two hundred and seventy Japanese quail of the VICAMI® line, 16 weeks old were housed in a climatic chamber, with room temperature control. Ten treatments (metabolizable energy levels) were distributed in completely randomized, with six replicates of five quails per experimental unit. The variables, metabolizable energy intake (MEI), egg mass (EM), retained energy (RE) were expressed in kcal/kg$^{0.67}$. The utilization efficiency ($k_t$) was estimated by the relation between RE and MEI. The metabolizable energy for maintenance ($ME_m$) was obtained by solving the equation RE = 0. The net energy requirement for WG was obtained by the relationship between ER in the feather free body (FFB) as a function of the FFB. The utilization efficiency for egg production ($k_o$) was obtained by the relationship between RE in EM and corrected MEI for maintenance and weight gain (WG). Based on the efficiencies, the requirements for WG and EM were calculated.

**Results** The metabolizable energy for maintenance ($ME_m$) found was 135.12 kcal/kg$^{0.67}$ per day. The metabolizable energy requirement for WG ($ME_g$) obtained was 5.25 kcal per gram WG. Based on this efficiency, was the metabolizable energy requirement for the egg production MEe was calculated, of 3.1 kcal per gram of egg mass.

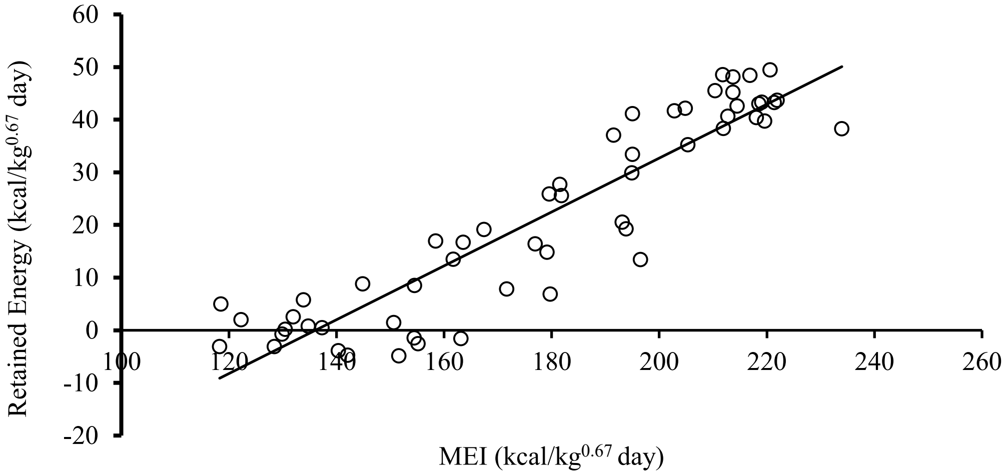

**Figure 1**. Retained energy (RE) as a function of the metabolizable energy intake (MEI) of 16 to 26 weeks of age Japanese quails. RE = -68.91 + 0.51 × MEI, $R^2$ = 83%.

**Conclusion** The energy intake by Japanese quails partitioned according to the model: IEM = 135.12 × BW$^{0.67}$ + 5.25 × WG + 3.1 × EM. The current study provides procedures and methods designed for quails as well as a simple and flexible model that can be quickly adopted by technicians and poultry companies.

**Acknowledgements** We would like to thank the VICAMI®, Loureiro Farm, the first projects program of the research Pro-rectory/UNESP for financial support.

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# Predictions from live animal assessment of total denuded beef yield and marbling score: model development and evaluation

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**Application** Predicting total denuded beef lean meat yield (**LMY**, %), marbling score and Meat Standards Australia (**MSA**) index from live animal assessments will provided an opportunity for producers (ranchers) to make informed management decisions.

**Introduction** Until recently, a beef carcass grid consisting of weight and fatness categories (i.e., grid-based system) with some adjustment for age (number of adult teeth) determined the price paid to Southern beef producers for Australian slaughter cattle. With the introduction of the MSA grading system (Watson *et al.* 2008) the beef industry is moving towards payments that account for MSA grades and traits such as LMY, marbling [i.e., intramuscular fat (**IMF**)] score and MSA index (a weighted average over 39 MSA primal cuts - a single number ranging from 30 to 80). BeefSpecs tools have been developed to assist producers meet market specifications and in particular, the BeefSpecs drafting tool (Walmsley *et al.*, 2010; http://beefspecs.agriculture.nsw.gov.au/drafting) predicts carcass compliance rates and graphically displays a grid-based system of P8 fat (mm) *versus* hot standard carcass weight (kg). The development of BeefSpecs is based on the study of Keele *et al.* (1992) that explicitly describes fat and fat free mass (**FFM**) of the empty body. We have developed a procedure to separate fat and FFM into carcass and non-carcass components and therefore predict LMY. With these new additional equations and inputs from live animal assessments BeefSpecs can now predict MSA Index, an Australian standard measure of predicting eating quality and the potential merit of a carcass. This study reports on the development of BeefSpecs carcass component equations to predict LMY; the development and evaluation of predicting MSA marbling score from chemical IMF; the evaluation of BeefSpecs predictions of carcass weight (**CW**, kg), bone weight (kg), FFM (kg), and chemical IMF (%) with independent datasets and BeefSpecs predictions of LMY. We further describe how these BeefSpecs outputs can be used to estimate the potential MSA index.

**Material and methods** Data from literature on the chemical composition of carcass and non-carcass components over a wide range of cattle weights published by Haecker (1920) was used as the primary source of information in this study. Additional data from Moulton *et al.* (1922) was used to provide a means of converting some of Haecker's (1920) classifications into contemporary carcass components. Four serial slaughters on low and high muscling Angus cattle (heifers and steers) covering three pasture (n=94) and one feedlot grain (n=31) endpoint were used in the development (unpublished). Model evaluation was conducted using two independent datasets.

**Results** Model evaluation indicated that the mean differences between observed and predicted were biased in CW but very little mean or slope bias were detected for bone and FFM equations. Only results on Angus steers are reported here – the mean±SD of CW and LMY were 204±22kg and 68.9±2.40% (n=100) and 271±46kg and 61.7±3.15% (n=180) for grass and grain, respectively.

**Conclusion** Modelling LMY is challenging! Data to develop models comes from controlled experiements and comparisons are made with industry data with associated errors from plants (abattoir/slaughter house) and large variation between plants. Nevertheless the new LMY predictions in BeefSpecs provides producers information on factors which affect growth rate before slaughter to achieve cost savings in feed consumption and breeding decisions to improve profitability.

**Acknowledgements** We acknowledge funding support from Meat and Livestock Australia.

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# The effect of the precision of dry matter intake estimation on the predicted marginal yield of milk and milk components using a response model

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## Application

Variation in predicted milk yield response based on simulated variation in DMI is less than 1% of total milk yield, which seems small enough to move towards practical application of response curves.

## Introduction

The ability to predict milk production and milk components response in cows can improve nutrient use efficiency and economic success. Daniel *et al.* (2016) developed equations that predict milk components response to simultaneous changes in dietary supply of net energy ($NE_L$) and metabolisable protein (MP). For these equations to work on farm, both milk outputs and intakes of $NE_L$ and MP, and therefore dry matter intake (DMI), have to be known. Current models of DMI prediction for individual cows can reach a prediction error of around 2 kg/d DMI (Zom *et al.*, 2012). This paper evaluates the effect of DMI prediction error on the variation in predicted response of milk and components yield, to a change in nutrient supply. Because the marginal milk response changes depending on the efficiency of $NE_L$ and MP utilisation (Daniel *et al.*, 2016), a low, medium, and high efficiency scenario was evaluated.

## Material and methods

Milk, milk protein and milk fat yield response equations were calibrated on $NE_L$ and MP supply, based on the dataset and methodology of Daniel *et al.* (2016). From this dataset, a real measured treatment was selected with cows with an efficiency of use of maintenance corrected $NE_L$=100% (energy balance = 0) and MP =67%. In this "pivot" scenario, cows consumed 21.7 kg/d DM and produced 31.2 kg/d milk, 1151 g/d fat and 1023 g/d protein. From this scenario (1), the intake of $NE_L$ and MP for a less (Scenario 2) and a more efficient (Scenario 3) cow was calculated by increasing or decreasing efficiency with 1 standard deviation, whilst maintaining the same dry matter intake and milk performance. For each scenarios, the variation in milk response to an increase of 1.5 kg/d of DMI (150 g/d MP and 8.9 MJ/d $NE_L$) was predicted for simulated errors of 2, 1 and 0.5 kg/d DMI for the starting situation (1000 simulations for each scenario x DMI error combination, with the RAND statement in SAS).

## Results

Absolute milk (component) response did not change with the level of variation in DMI prediction and is presented as one value (M) (Table 1). For scenario 1, standard deviations of the response in milk yield were 0.80%, 0.43% and 0.19% relative to predicted total milk production, with simulated errors for DMI of 2, 1 and 0.5 kg/d. The predicted response is smallest for less efficient cows (Scenario 2) and largest for most efficient cows (Scenario 3), which is in line with the curvilinear nature of the response equations.

**Table 1.** Starting milk production, mean (M) and standard deviation (S) for predicted milk (component) response to increasing $NE_L$ and MP supply (8.9 MJ $NE_L$ and 150 g MP per day), in three efficiency scenarios, simulating three levels of DMI prediction error (S2, S1, S0.5: 2 kg/d, 1 kg/d, and 0.5 kg/d).

| | | | Scenario 1:med.efficiency | | | | Scenario 2: low efficiency | | | | Scenario 3: high efficiency | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | start | M | S2 | S1 | S0.5 | M | S2 | S1 | S0.5 | M | S2 | S1 | S0.5 |
| Milk | kg/d | 31.2 | 1.1 | 0.26 | 0.14 | 0.06 | 0.7 | 0.23 | 0.12 | 0.06 | 1.4 | 0.25 | 0.18 | 0.09 |
| Protein | g/d | 1023 | 42 | 11.3 | 6.0 | 2.8 | 27 | 10.0 | 5.0 | 2.4 | 56 | 11.0 | 7.9 | 3.9 |
| Fat | g/d | 1151 | 20 | 13.8 | 7.3 | 3.4 | 2 | 12.2 | 6.1 | 2.9 | 37 | 13.4 | 9.6 | 4.8 |

## Conclusions

At a prediction error of DMI in the starting situation of 2 kg/d DMI or smaller, the effect on variation in predicted milk response of a 1.5 kg change in DMI is modest when compared to total milk production.

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# Evaluation of predicted milk response to changes in dietary $NE_L$ and MP supply based on either the NRC (2001) or INRA (2018) feed unit systems

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**Application** Response equations calibrated on NRC (2001) and INRA (2018) net energy for lactation ($NE_L$) and metabolizable protein (MP) supply, are similar in their capability to predict milk responses to $NE_L$ and MP changes.

**Introduction** Recently for the INRA (2018) feed unit system, equations that predict milk performance response to change in $NE_L$ and MP supply, have been developed by calibrating response to supply (Daniel et al., 2016). In the present conference, Daniel et al. (2019) compared measured total tract digestibility for OM and duodenal flow of NAN, reported in a literature dataset, with the predictions by two feeding systems: the INRA (2018) and the NRC (2001) system. The current abstract reports the development of production response equations for NRC, which did not previously exist, by calibrating milk response to $NE_L$ and MP supply on the dataset of Daniel et al. (2016) and compares the predictive capacity of this new calibration for NRC, with existing INRA response equations.

**Material and methods** The dataset (825 treatments in 282 studies) and methods of Daniel et al. (2016) were used to calculate $NE_L$ and MP supply from diets for the NRC (2001) feed unit system. Nutrient supply for each study was centered relative to a pivot situation where conversion efficiency of $NE_L$ supply above maintenance into milk energy is 1.0, and MP efficiency is 0.67. Within study, milk energy and component yields were regressed to the delta ($\Delta$) of supply relative to centered pivot, for linear, squared and interaction of $\Delta$MP and $\Delta NE_L$. For evaluating the new response equations calibrated for NRC and existing INRA equations, one treatment of each study in the dataset was randomly selected to calculate pivot supply for MP and $NE_L$ with equations of both systems, as in Daniel et al. (2017). Next, we used the response equations to predict milk energy and component yields for the other treatments in the experiment. Predictions were assessed through RMSPE, its decomposition to ECT, ER and ED, and CCC.

**Results** The RMSPE (relative to observed mean) was on average 5.5% (milk energy yield), 7.8% (milk fat yield) and 5.9% (milk protein yield), and CCC was at least 0.93 (Table 1).

**Table 1.** Summary of observed vs predicted milk production parameters, as predicted by response equations that have been calibrated on MP and $NE_L$ supply from the same dataset, for two feed unit systems.

| | Model | N | Observed[1] | Predicted[1] | RMSPE | ECT | ER | ED | CCC | Slope (SE) |
|---|---|---|---|---|---|---|---|---|---|---|
| Milk energy yield (MJ/day) | NRC | 543 | 93.1 ± 18.6 | 93.3 ± 19.4 | 5.5 | 0.3 | 7.4 | 92.3 | 0.96 | 0.93 (0.011) |
| | INRA | | | 93.2 ± 19.4 | 5.5 | 0.1 | 7.9 | 92.0 | 0.96 | 0.93 (0.011) |
| Milk fat yield (g/day) | NRC | 543 | 1135 ± 239 | 1135 ± 250 | 7.7 | 0.0 | 8.7 | 91.3 | 0.94 | 0.89 (0.015) |
| | INRA | | | 1135 ± 252 | 7.9 | 0.0 | 9.9 | 90.1 | 0.93 | 0.89 (0.015) |
| Milk protein yield (g/day) | NRC | 543 | 973 ± 198 | 979 ± 203 | 6.1 | 1.2 | 5.4 | 93.3 | 0.96 | 0.93 (0.012) |
| | INRA | | | 976 ± 204 | 5.7 | 0.5 | 5.9 | 93.6 | 0.96 | 0.93 (0.011) |

[1]Mean± SD; RMSPE: Root mean square prediction error (% of observed mean); ECT: Error due to intercept bias (% of MSPE); ER: Error due to slope bias (% of MSPE); ED: Error due to disturbance (% of MSPE); CCC: Concordance correlation coefficient (scale from -1 to 1); Slope: Slope of predicted vs. observed regression.

**Conclusion** The prediction of milk energy, protein and fat yield using response equations calibrated on $NE_L$ and MP supply from either the NRC (2001) or INRA (2018) system has similar RMSPE, ECT, ER, ED and CCC.

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NRC 2001. Nutrient Requirements of Dairy Cattle. 7th rev. ed. Natl. Acad. Press, Washington, DC.
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# Genetic parameters for a new frame score system for Nelore cattle

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**Application** New frame score system for Nellore cattle is useful for modeling growth and genetic improvement.

**Introduction** The size that an animal will achieve at maturity is determined primarily by genetics, and in turn determines many aspects of growth and reproduction. Most equations that represent growth of an organism produce sigmoidal curves that have an asymptotic maximum (mature size) and a point of inflection Larger mature size animals grow more rapidly, and at similar weights are leaner than smaller mature size animals (Sainz and Baldwin, 2003).. For meat animals, market demands determine ideal degrees of carcass fatness, so that there are also ideal end weights that vary according to each animal's mature size. Therefore, we may conclude that mature size is an indispensable parameter in modeling growth of an organism.

**Material and methods** Data were obtained from the Nellore breeding program (ANCP) for 1853 males and 1371 females raised on pasture in Brazil, and included age, body weight (BW), hip height (HH), and subcutaneous backfat (BF, by ultrasound). Those data were used to estimate the carcass weight (CW) of each animal, and then CW was regressed on age and backfat to generate an equation that allowed prediction of CW at a constant BF = 6 mm for each animal. Predicted CW were stratified into a table that classifies Frame scores according to predicted CW on a scale of 1 to 12, with each score corresponding to ±15 kg of CW. Estimated FS were subjected to bivariate genetic analyses using average-information restricted maximum likelihood (airemlf90; Gilmour *et al.*, 1995, 2009).

**Results** By design, the mean FS were 6.5 for Nellore bulls and heifers (Figure 1), corresponding to mean CW of 309 and 208 kg, respectively. The heritability of FS was estimated to be 0.20. Moreover, FS was genetically correlated to Longissimus muscle area (0.51), Backfat (-0.10), Age at first calving (-0.11), BW at 450 d (0.75), and CW (0.95).

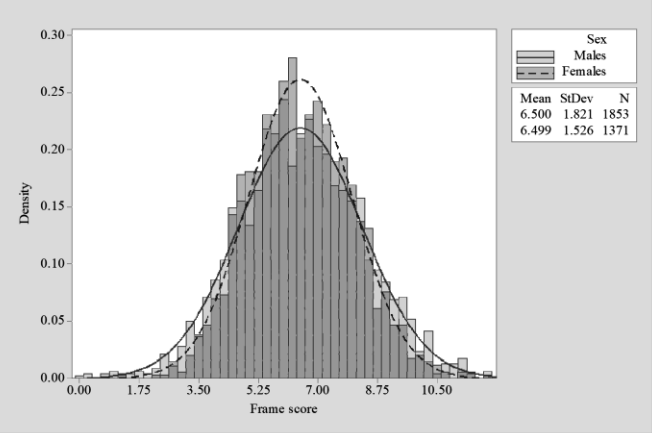

Figure 1. Distribution of estimated frame scores for male and female Nellore cattle.

**Conclusion** A novel frame score system was developed for Nellore cattle based on height, weight and composition. It allows estimation of ideal carcass endpoint, is moderately heritable, and is genetically correlated with other traits of economic importance.

**Acknowledgements** We would like to thank the Brazilian Association of Breeders and Researchers for access to the data, and Dr. Fernando B. Lopes for his assistance with the initial genetic modeling.

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# Efficiency of energy deposition in growing-pigs fed high-fat / low-protein diets under daily cyclic high ambient temperature conditions

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## Application

High-fat and low-protein diets are differently metabolized and used in terms of fat deposition. These differences should be considered according to ambient temperature and pork market.

## Introduction

Nutritional strategies, which include feeding pigs with low crude protein and/or high energy content diet have been suggested to attenuate the effects of high ambient temperatures. However, the use of these techniques may result in fatter carcass because the energetic efficiency for lipid deposition is greater than protein. Modelling energy metabolism based on net energy (NE) allows a more precise expression of available energy for production purposes (protein and fat deposition) by considering the differences in the metabolic utilization among nutrients. This study was performed to evaluate the efficiency of energy retention as fat of high-fat and low-crude protein diet in pigs under daily high ambient temperature conditions.

## Material and methods

Thirty-two castrated male pigs (22 kg BW) were randomly assigned to control (CON) or high-fat/low-crude protein diet (HF/LP). Cyclic high ambient temperature was induced by exposing pigs to 22 ºC from 1800 to 1000 h and to 30 ºC from 1001 to 1759 h, characterizing the ambient temperature variation in tropical areas. Body composition was measured at the beginning and end of the experiment (days 0 and 70) through dual-energy X-ray absorptiometry. Lean mass was converted to body protein according to Pomar and Rivest (1996). Energy retained as fat and protein were calculated assuming that fat mass contained 39.6 MJ/kg (Sainz and Wolff, 1988) and protein 23.8 MJ/kg (Kleiber, 1961). Net energy requirement for maintenance (NEm) was estimated by InraPorc® model. Thus, NE intake partitioned to fat deposition was estimated (NE fat = NE intake – NEm – NE retained as protein). Finally, the efficiency of energy utilization for fat deposition (Kf) was also calculated (NE retained as fat/ NE fat). The results were considered statistically significant if $P < 0.05$.

## Results

The efficiency of energy deposition as fat in HF/LP-pigs was 17% higher than CON ($P < 0.05$; Table 1). Our results demonstrate the applicability of the NE system in the partitioning of energy intake.

Table 1. Body composition of pigs under daily cyclic high ambient temperature (n=16/diet)

| Itens | CON[1] | HF/LP[2] | RSD | *P*-value |
|---|---|---|---|---|
| NE intake, MJ/day | 13.89 | 16.29 | 4.74 | < 0.01 |
| NEm, MJ/day [3] | 0.809 | 0.875 | 4.36 | 0.86 |
| Energy retained as protein, MJ/day | 2.87 | 3.42 | 1.01 | 0.74 |
| Energy retained as fat mass, MJ/day | 7.32 | 10.89 | 3.36 | < 0.01 |
| NE intake partitioned to fat, MJ/day | 9.98 | 12.13 | 4.02 | < 0.01 |
| Kf [4] | 0.73 | 0.88 | 4.25 | 0.02 |

[1]CON = Control diet; [2]HF/LP = High-fat/low-crude protein diet; [3]NEm = Net energy requirement for maintenance; [4]Kf = Efficiency of energy deposition as fat.

## Conclusion

Pigs fed with high-fat/low-crude protein diet have a greater efficiency to retain energy as fat.

## Acknowledgements

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# Energy and protein requirements of crossbred Holstein × Gyr heifers

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**Application:** Provide equations to estimate energy and protein requirements of Holstein × Gyr dairy heifers.

**Introduction:** Proper estimates of nutrient requirements for cattle empowers nutritionists to formulate efficient diets which meet requirements for maintenance and production. The crossbreed Holstein × Gyr is widely used for dairy production in the tropics. However, data for estimating energy and protein requirements for Holstein × Gyr heifers raised under tropical conditions are scarce. Thus, we aimed to estimate the energy and protein requirements for maintenance and growth of crossbreed Holstein × Gyr heifers raised in tropical conditions.

**Material and Methods**: Twenty-two crossbred Holstein × Gyr heifers averaging 102.2 ± 3.4 kg of initial body weight were used, with four animals slaughtered at the beginning of the experiment as reference. The remaining animals were then assigned to three treatments, which were rates body weight gains: high (1.0 kg/d), low (0.5 kg/d) and maintenance (0.1 kg/d). At the end of the experiment, all animals were slaughtered to determine final empty body weight (EBW) and composition. The net energy requirements for maintenance ($NE_m$) were estimated using an exponential regression between heat production (HP) and the metabolizable energy intake (MEI) ($Mcal/EBW^{0.75}/d$), $HP = \beta_0 \times e^{\beta 1 \times MEI}$, where $\beta_0$ represents the net energy required for maintenance. The point where MEI equals HP was considered the metabolizable energy requirements for maintenance ($ME_m$). The efficiency of use of metabolizable energy for maintenance ($k_m$) was obtained from the ratio between $NE_m$ and $ME_m$. The net energy requirements for growth ($NE_g$) were estimated from the model $RE = \beta_0 \times EBW^{0.75} \times EBG^{\beta 1}$, where RE is the retained energy (Mcal/d) and EBG is the empty body gain (kg/d). The efficiency of use of metabolizable energy for gain ($k_g$) was estimated as the slope of the regression between RE and MEI for gain ($Mcal/EBW^{0.75}/d$). The metabolizable protein requirements for maintenance ($MP_m$, $g/kg\ BW^{0.75}$) were estimated by the ratio between the intercept ($\beta_0$) of the regression between the MPI (kg/d) and EBG (kg/d), $MPI = \beta_0 + \beta_1 \times EBG$, and the average metabolic BW ($BW_m^{0.75}$), where MPI is the metabolizable protein intake. The net protein requirements for gain were estimated as the first derivative of the allometric equation of the body protein content (BPC, kg) in the EBW (kg). The efficiency of use of metabolizable protein for gain ($k$) was calculated as the slope of the regression between retained protein and MPI (both in $g/EBW^{0.75}/d$).

**Results:** The $NE_m$ and $ME_m$ were 70.0 and 110.0 $kcal/EBW^{0.75}/d$, respectively. The $k_m$ was 0.64. The estimated equation to predict $NE_g$ was: $NE_g\ (Mcal/d) = 0.072 \times EBW^{0.75} \times EBG^{0.601}$. The $k_g$ was 0.32. The $MP_m$ was 3.82 $g/EBW^{0.75}$ per day. The equation to predict $NP_g$ was: $NP_g\ (g/d) = 243.65 \times EBW^{-0.091} \times EBG$. The $k$ obtained was 0.48. The requirements of metabolizable energy and protein were greater than estimates by BR-CORTE (2016) or NRC (2001) for animals heavier than 110 kg (Figure 1). The animals used in NRC (2001) and BRCORTE (2006) had a greater BW than the heifers used in the present study. Thus, the energy and protein requirements proposed by these studies may underestimate those of young Holstein × Gyr dairy heifers raised in tropical conditions.

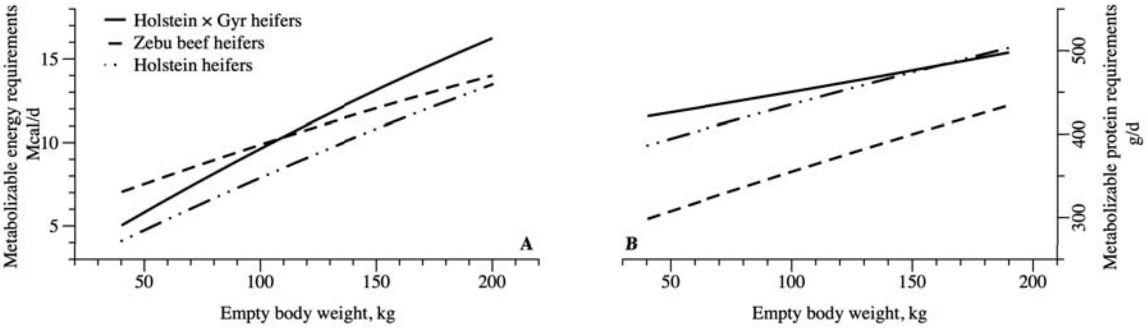

Figure 1. Metabolizable energy (A) and protein (B) requirements for Holstein × Gyr heifers (this study), Holstein heifers (NRC, 2001) or zebu beef heifers (BR-CORTE, 2016). EBG = 1.0 kg/d was used in all equations

**Conclusion:** We recommend the equations generated in this study to estimate the energy and protein requirements for maintenance and growth for crossbred Holstein × Gyr dairy heifers raised in tropical conditions.

**Acknowledgements:** The authors thank FAPEMIG for funding this research.

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# Systematic review on genetic potential characterization of the Japanese quail growth

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**Application** Our findings support reflections and decision on development specialized Japanese quail lines for egg production.

**Introduction** Currently, large Brazilian farms house more than 100,000 quails in automated production systems that provide a regular supply of eggs with good quality to the market (Silva *et al.,* 2019). The prediction of potential performance it is the first step towards the prediction of the nutrient requirements (Gous *et al.,*1999). The objective of this research was to characterize the genetic potential of Japanese quail growth through a systematic review.

**Material and methods** The review of literature was performed by codifying the publications in electronic spreadsheet that presented the following information: subspecies (*Coturnix coturnix japonica*), body weight (***W***), age (***t***), experimentation place (country). The experiments of the same article they received the study code ($S_1$, $S_2$ $S_3$...$S_n$). It was considered that the experiments were delineated adequately to describe the genetic potential. The studies were interpreted through the function parameters Gompertz. The values of W and t were used to estimate the parameters of the function Gompertz, $W = Wm\times e\{[-e^{((ln\ (-ln(Wi/Wm)))-B\times t}]\}$, in which $W$ is the body weight (g); $Wm$ is the body weight during maturity (g); $Wi$ is the body weight during birth (g); B is the maturity rate (day $^{-1}$); $t$ is the age of the bird (in days). For each study were generated the parameters $Wm$, $Wi$ and $B$, in which t* is the age of maximum growth rate. The variables $Wm$, $Wi$, $B$ and $t^*$ were analyzed using comparative techniques of non-linear models to prove possible differences in the Gompertz parameters adjusted with information of studies conducted in Brazil *versus* other countries. To interpret the correlation of the parameters with the year of the publication, were used exploratory techniques, grouping analysis (single linkag), and main components.

**Results** Information from 50 essays from 23 published papers between 1960 and 2019 were used to describe the genetic growth potential of Japanese quails. The most distant studies on date and adjusted values to $Wi$ (8,6 and 11,6), $Wm$ (116 and 342), $B$ (0,1039 and 0,0453) and $t^*$ (9 and 27) were the studies of Wilson *et al.* (1960) and Aljumaily *et al.* (2019), respectively. The comparison between the adjusted Gompertz parameters for Brazilian studies *versus* other countries, showed that the Brazilian studies differ in growth potential ($Wi$ *5.9*, $Wm$ *155*, $B$ *0.071*, and $t^*$ *17*) in relation to the other studies in the database ($Wi$ *3*, $Wm$ *180*, $B$ *0.088*, and $t^*$ *16*). Cluster analysis revealed differences in grouped variables between Brazilian studies versus other countries. The variable B showed a greater Euclidean distance in relation to the other variables ($Wi$, $Wm$ and $t^*$), while for the other countries the variable Wm was isolated, with a greater Euclidean distance of the other variables ($Wi$, $B$ and $t^*$). By the main component analysis (PCA) it was possible to detect the directions that the values of $Wi$, $Wm$, $B$ and $t^*$ assumed over time. The PCA 1 for Brazilian studies explains 84% of the information and presented the following correlations $Wi$ *-0.96*, $Wm$ *0.89*, $B$ *-0.81*, $t^*$ *0.98* and year -0.29. The PCA 1 for the other countries explains 77% of the information and the correlations are $Wi$ *0.17*, $Wm$ *0.64*, $B$ *-0.93*, $t^*$ *0.96* and year 0.61. In relation to year, it is possible to infer only for the other countries, in which there was a reduction in the precocity of the birds. This result is also present in Brazilian studies, but it is not possible to relate to the year due to the low correlation.

**Conclusion** Japanese quails show considerable diversity in the genetic potential. The genetic improvement of Japanese quails had different objectives.

**Acknowledgements** The first author acknowledges the scholarship by the CAPES Foundation.

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# Empirical modeling of the proportion of fines in pelleted feeds

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**Application** Mathematical models can be used to identify the main influencing factors and quantify their effect on pelleting process.

**Introduction** Fines are the portion that is disaggregated from the pellet's initial form, which can occur at any stage of pelletization, transporting, and handling processes from the feed factory to the farm (Pucci *et al*., 2010). Many factors may interfere in pellet quality, but quantitative information on this topic is still scarce in the literature. Thus, this study was developed to identify influential factors in an industrial pelleting process that affect the fine proportion in feeds for broilers and pigs.

**Material and Methods** Two independent databases were used to calibrate and validate the models. Each column of the spreadsheet represented a descriptive variable of the manufacturing process (industrial yield; amperage; pressure in the conditioner; and temperatures of environment, conditioner, and cooler), feed characteristics (inclusion of the ingredients in the feed formula and chemical composition of the main ingredients), and pellet quality (percentage of fines). Formulas for finishing pigs and initial-to-final broilers were included in the database. Each row of the spreadsheet represented one observation, or the equivalent of a lot of produced feed. The data were submitted to graphical analysis, descriptive statistics, and regression analysis by stepwise procedure (forward selection procedure, $\alpha = 0.15$). Three models were developed for the response variable (percentage of fines): Model I, including characteristics of the manufacturing process and inclusion of the ingredients in the formula; Model II, characteristics of the manufacturing process and weighted chemical composition; and Model III, characteristics of the manufacturing process, inclusion of the ingredients in the formula, and weighted chemical composition. The accuracy of the models (validation) was evaluated by the mean square of the predicted error (MSPE).

**Results** The models obtained in this studydiffered from each other in the number of selected predictors. However, the main factors have been found repeatedly in the models. Model I ($R^2$: 51.58%) included 10 predictors (amperage$^*$; temperature of cooler$^*$, environment$^*$, and conditioner$^*$; inclusion of semi-integral soybean meal$^*$, rice bran$^*$, feather meal$^*$, soybean oil$^*$, liquid methionine, and liquid lysine$^*$; factors indicated by $^*$ are significant at $P<0.05$). Model II ($R^2$: 53.34%) included 12 predictors (amperage$^*$; temperature of cooler$^*$, environment$^*$, and conditioner; mineral matter of calcitic limestone, maize$^*$, semi-integral soybean meal$^*$, and rice bran$^*$; ethereal extract of soybean oil$^*$ and feather meal$^*$, dry matter of soybean meal$^*$; and crude protein of feather meal). The model to predict fines from the complete set of variables (Model III, $R^2$: 53.61%) included 16 predictors (amperage*; temperature of cooler*, environment*, and conditioner; inclusion of semi-integral soybean meal*, feather meal*, and soybean oil*; mineral matter of maize*, feather meal*, and rice bran*; dry matter of soybean meal* and feather meal*; crude protein of semi-integral soybean meal*; and ethereal extract of semi-integral soybean meal*, meal meal, and feather meal*). The factors that most contributed to explain the total variance were amperage (at least 25% in the Model II), followed by cooler temperature (at least 3% in the Model II) and inclusion of soybean oil (at least 2% in the Model III). The models obtained in this study were able to explain an important portion of the variation. However, even considering relevant factors, part of the variance remained unaccounted for, which indicated that critical factors in the pelletizing process were not included in this study and may also have being frequently ignored during quality control inspection in feed mills. The model that considered characteristics of the manufacturing process and the inclusion of the ingredients in the formula (Model I) was the most accurate (MSPE=14.05) when compared to the models II (MSPE=356.93) and III (MSPE=603.80), indicating that this set of factors should be well monitored in the feed mills.

**Conclusion** The amperage, the temperature of the cooler, and the inclusion of soybean oil in the feed formulas are the main factors influencing the fine proportion in pelleted feed. Still, further improvements on pellet quality depend on identifying other potential factors influencing the pelleting process.

**Acknowledgements** We would like to thank Cooperativa Languiru for the support to this project.

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# Optimizer use in a commercial ration balancing software can reduce diet costs as compared to those of dairy nutritionists in the mid-Atlantic region

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**Application** Optimizing diets according to least-cost formulation has the potential to save dairy producers money without sacrificing milk production.

**Introduction** In recent years, non-linear optimizers have been adopted in several commercially-available ration balancing software programs. These programs allow the user to create cost-conscious rations that meet animal nutrient requirements with relative ease thanks to built-in NRC (2001) or CNCPS models. However, it is unclear if nutritionists are using built-in optimizers to reduce dietary price, or if reducing ration cost is their primary concern at all. The objective of this study was to evaluate the effectiveness of a nonlinear optimizer resident in a commercially-available ration-balancing software, and determine if mid-Atlantic region dairy nutritionists who use the software take advantage of the available optimizers to develop cost-effective rations.

**Materials and methods** Nutritionists servicing the mid-Atlantic region were invited via email to complete two ration balancing scenarios: 1) a ration balanced according to their preferred methods (**NUTR**, n=5), and 2) a ration that maximized N efficiency (**NUTRN**, n=5). They were asked to balance these rations for a 726 kg cow consuming 26 kg DMI/d and producing 45 kg of milk/d. They were also instructed to use a feed library we provided which contained a broad range of ingredients populated with regional feed mill prices. In the present study, only participants who used Nutritional Dynamic Software (NDS) compatible software were used in analysis (n=5 participants). PROC MEANS was used to summarize the metabolizable protein content (MP; g), lysine %MP, methionine %MP, and average cost/cow/d of nutritionists' rations (USD). These means were compared to two rations we balanced using the non-linear optimizer resident in NDS with the same feed library, prices, and animal specifications given to the nutritionists: one that did (**OPTAA**) and one that did not (**OPT**) account for Met and Lys requirements. When balancing OPTAA with consideration of Met and Lys, requirements were set as a %MP (Rulquin et al 2007). A minimum of 0.91 kg of alfalfa hay was specified as the sole ingredient constraint in OPT and OPTAA.

**Results** Table 1 summarizes selected parameters for both optimized and nutritionist-developed rations. When compared to OPTAA (the ration optimized for requirement of Met and Lys as a percentage of MP) nutritionist rations cost at least $1.17 more per cow per day. The predicted cost of OPTAA was greater than OPT due to increased post-ruminal Lys inclusion.

Table 1 Predicted analyses of researcher-optimized vs nutritionist-developed rations.

| | Researcher rations | | Nutritionist rations[1] | |
|---|---|---|---|---|
| Parameter | OPT | OPTAA | NUTR | NUTRN |
| MP, g/d | 2964 | 3022 | 3123 ± 54.55 | 3095 ± 48.71 |
| Met, % MP | 2.51 | 2.16 | 2.50 ± 0.05 | 2.44 ± 0.12 |
| Lys, %MP | 6.38 | 6.99 | 6.80 ± 0.05 | 6.91 ± 0.04 |
| Cost, USD/head/d | 5.03 | 5.27 | 6.46 ± 0.16 | 6.44 ± 0.07 |
| Cost difference, USD/head/d[2] | -- | -- | 1.19 ± 0.16 | 1.17 ± 0.07 |

[1]Means and SEMs of nutritionists' final diet analyses (n=5 participants).
[2]Mean difference between diets formulated by researchers and OPTAA.

**Conclusion** Results from nutritionist-submitted rations give a better understanding of the cost-consciousness of the decisions they make for their clients. This shows an advantage to optimizer use by nutritionists who have access to this feature. Further, accounting for true requirements of all essential amino acids (AA, g/d) would allow more tailored optimization that reflects the true cost of meeting postruminal AA needs.

**Acknowledgements** Special thanks goes to Virginia Agricultural Council for providing grant funds for this project, and to both the Virginia Feed Association and Virginia Cooperative Extension for providing the resources needed to reach out to regional nutritionists.

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# Weight gain response of laying-type pullets to the intake of methionine+cystine

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**Application** Curvilinear models are best suited to represent the response of animals to nutrient supply and, consequently, to estimate nutrient requirements.

**Introduction** In dose-response experiments, requirements of nutrients are estimated by assessing the response of groups of animals submitted to different intakes of a given nutrient for a certain period of time. The objective of this study are to model the responses of weight gain (WG) according to the methionine+cysteine (Met+Cys) intake using nonlinear mathematical functions and derive equations for the gain and maintenance requirements for each function and determine the Met+Cys requirements that maximize the WG.

**Material and methods** Three trials were performed using 1,448 laying-type pullets. The trials utilized a completely randomized design, with eight treatments and six replications. In the first phase (2-6 weeks) it was used 15 pullets per experimental unit. In the second and third phase (8-12 and 14-18 weeks) it was used eight pullets per replication. The levels of Met+Cys were obtained by the dilution technique. The mathematical functions used to describe WG responses to Met+Cys supply were the broken line, broken line with curvilinear ascendancy, Michaelis-Menten, saturation kinetics, logistic and exponential. Models were selected with the Bayesian information criterion and evaluated by residual analysis.

**Results** The requirements of Met+Cys for the $WG_{max}$ in the phases (2-6, 8-12 and 14-18 weeks) were estimated at 313, 381 and 318 mg/day, respectively. The partitioning of Met+Cys requirements for WG were estimated at 20, 22 and 27 mg/g of gain for the phases 2-6, 8-12 and 14-18 weeks, respectively, and 214, 53 and 30 mg/kgBW$^{0.75}$ for the maintenance in the referred phases.

**Table 1**. Estimates of Met+Cys requirements for a 99% $WG_{max}$ and partitioning of growth and maintenance.

| Models | a, requirement for growth | | | | | | | | | m, requirement for maintenance | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | 2-6 weeks | | | 8-12 weeks | | | 14-18 weeks | | | 2-6 weeks | | 8-12 weeks | | 14-18 weeks | |
| | $a_1$ | $a_2$ | $a_3$ | $a_1$ | $a_2$ | $a_3$ | $a_1$ | $a_2$ | $a_3$ | $m_1$ | $m_2$ | $m_1$ | $m_2$ | $m_1$ | $m_2$ |
| BL | 216 | 205 | 19 | 268 | 249 | 22 | 268 | 266 | 25 | 3 | 14 | 35 | 51 | 8 | 8 |
| BLQ | 266 | 223 | 21 | 330 | 261 | 23 | 318 | 293 | 27 | 30 | 120 | 28 | 41 | 30 | 30 |
| M&M | 758 | 246 | 23 | 571 | 286 | 26 | 692 | 277 | 26 | | | | | | |
| SK | 488 | 223 | 21 | 523 | 259 | 23 | 480 | 308 | 28 | 75 | 299 | 131 | 193 | 128 | 128 |
| LOGI | 311 | 218 | 20 | 410 | 244 | 22 | 378 | 297 | 27 | 53 | 210 | 36 | 53 | 37 | 37 |
| LOGII | 311 | 218 | 20 | 408 | 243 | 22 | 378 | 297 | 27 | 54 | 215 | 36 | 53 | 37 | 37 |
| Sig | 313 | 222 | 20 | 412 | 242 | 22 | 378 | 301 | 28 | 54 | 214 | 36 | 53 | 37 | 37 |
| MITS | 1100 | 218 | 20 | 982 | 259 | 23 | 1123 | 301 | 28 | | | | | | |
| MONO I | 591 | 237 | 22 | 564 | 262 | 23 | 554 | 314 | 29 | 32 | 126 | 52 | 77 | 64 | 64 |
| MONO II | 591 | 237 | 22 | 562 | 261 | 23 | 554 | 314 | 29 | 32 | 126 | 52 | 77 | 52 | 52 |
| Mean | 495 | 225 | 21 | 500 | 257 | 23 | 512 | 297 | 27 | 42 | 165 | 51 | 75 | 49 | 49 |

Broken line (BL); Broken line with curvilinear ascendancy (BLQ), Michaelis-Menten (M&M), saturation kinetics (SK); Logistics I (LOGI); Logistics II (LOGII). Sigmoid (Sig), Mitscherlich (MITS) Monomolecular II (MONOI) and Monomolecular II (MONOII). Phase 1, 2-4 weeks old, Phase 2, 8-12 weeks old; Phase 3 14-18 weeks old; a, requirement for growth, $a_1$, mg/day for 99% of $WG_{max}$, $a_2$, mg/day to obtain 10.8 g/day of gain; $a_3$, mg/g to obtain 10.8 g/d of gain ; m, requirement for maintenance; $m_1$, mg /bird, $m_2$, mg/$_{kg}$BW$^{0,75}$; BW, mean body weight 0.160 kg for Phase 1; 0.597 kg for Phase 2; 1.003 kg for Phase 3.

**Conclusion** Based on statistics and biological interpretability of model parameters, the selected functions were: Sig for the 2-6 and 8-12 weeks, BLQ for the 14-18 weeks. We point out that the methodology of future studies should be designed to allow the successful estimation of parameters of interest that describe the growth at different body weights.

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# A virtual experiment to investigate effects of feeding practices and animal health status on the technical, economic and environmental performances of a pig-fattening unit

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## Application

An individual-based model of a pig-fattening unit was used to compare the effects of pig management strategies in different sanitary context on unit performance. It is included in a decision support tool for on-farm application.

## Introduction

Profitability and environmental impacts of pig fattening are mainly associated to animal performance, which is the result of interactions between pig genotype, feeding programs, animal management, and health status. Models and tools can help farmers understanding the effects of different options on the performances of their production system. However, most models considered so far animals in healthy conditions. Therefore, it is unknown whether the best scenarios identified with healthy pigs are also best ones for animals of impaired health. This study aimed at quantifying how feeding practices and animal management modify performance of the unit in healthy or impaired health conditions using an individual-based model of the pig-fattening unit.

## Material and methods

The model of the pig fattening unit considers individual variability in performance among pigs, farmers' feeding practices and animal management, and estimates environmental impacts (through Life Cycle Assessment) and economic results of the unit (Cadero et al., 2018a). This model provides reliable estimates of the fattening unit performance (Cadero et al., 2018b). A virtual experiment was designed with 96 scenarios, resulting from different options for batch interval (7 vs. 35 days), management of lightest pigs (use or no use of a buffer room), feed rationing (*ad libitum*, restriction to 2.5 kg/d) and sequence plans (two-phase, daily-phase), scale of application of the feeding programs (i.e. room, pen, individual), and health status of the pig herd (i.e. healthy vs. impaired). The effects of the factors were tested through variance analysis, and a typology was built from multivariate data analyses.

## Results and Discussion

Health status, batch interval and feed sequence plan explained the greatest part of the variance of model outputs. Healthy population induced higher gross margin (11.2 *vs.* 1.5 €/pig on average) and lower environmental impacts (2.24 *vs.* 2.38 kg $CO_2$-eq/ kg pig live weight gain) than the impaired health population. Restricted, daily-phase, and individual feedings improved economic and environmental performance in both health statuses. For same feeding practices, 35-days batch interval resulted in higher gross margin and lower environmental impacts than 7-days batch interval in the healthy context, and conversely, resulted in the impaired context in lower gross margin but also lower environmental impacts than 35-days batch interval. Indeed, 7-days batch interval allows extending fattening duration relatively to 35-days and consequently increases in the impaired context the average slaughter weight and the proportion of pigs with slaughter weight in the range of the payment grid.

## Conclusion

Impaired health of the pig herd has major effect on the economic and environmental performances of the unit, but feeding practices can significantly reduce this degradation. In our study, providing feed supply close to the requirements compensates to some extent the loss of performance of impaired health population. This study also demonstrates that batch interval for best gross margin and environmental impacts of the pig-fattening unit depends on the health status of the pig herd.

## Acknowledgements

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## Human edible feed conversions of United States beef production

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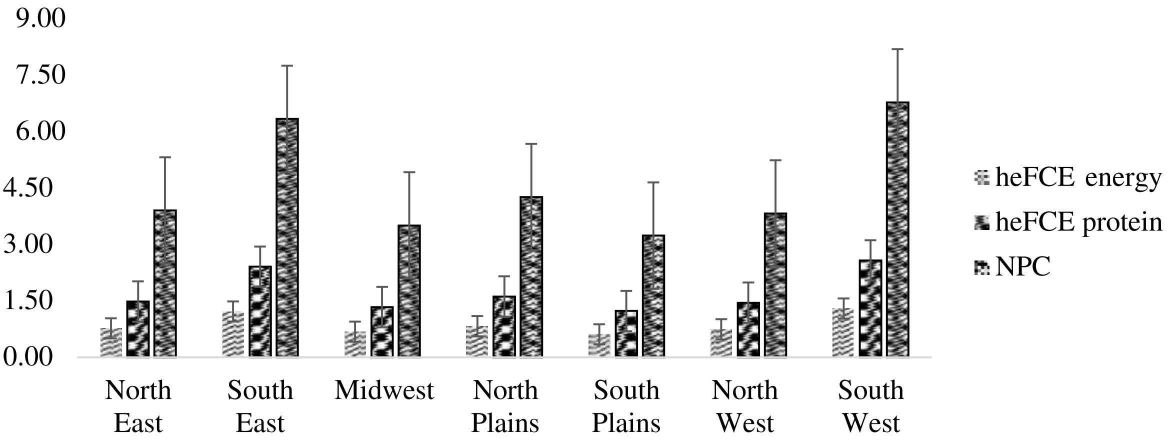
**Application** Regional human edible feed conversion efficiencies and net protein contribution values of beef production in the US indicate whether cattle contribute toward, or compete with, human nutrient requirements.

**Introduction** Multiple factors need to be considered in assessing the sustainability of ruminant livestock production, such as the valuable role ruminants serve in the conversion of feeds grown on non-arable lands and by-products into products suitable for human consumption (Oltjen and Beckett, 1996). The use of intensive systems, where ruminants are fed large quantities of potentially human edible crops, such as cereal grains, poses a debate about the competition between livestock and humans for grains that could be consumed directly by humans. The inclusion of animal products in human diets provides an important source of energy and protein, which often have higher digestibility and superior amino acid compositions (Ertl et al., 2016).

**Material and methods** This analysis was conducted for seven U.S. regions in order to determine the human edible feed conversion efficiency (heFCE) of energy and protein and the net protein contribution (NPC) of U.S. beef production using data collected by the National Cattlemen's Beef Association. Efficiency and NPC values above 1 indicate that beef production is contributing more to meeting human protein or energy requirements than the cattle are consuming, and values below 1 indicate beef is competing for those nutrients.

**Results** The Southwest and Southeast regions returned heFCE values for energy above 1, while the average of all regions was 0.88 ± 0.27 SD. All regions had heFCE values for protein above 1 with an average of 1.73 ± 0.54 SD. The NPC of all US regions were greater than 3; averaging 4.55 ± 1.41 SD, which illustrates beef's contribution of high quality protein to human diets.

Figure 1 Human edible feed conversion efficiencies and net protein contributions of US beef production.



**Conclusion** Incorporating a detailed evaluation of different production system efficiencies in converting potentially human edible feeds into human edible animal products of higher quality broadens the discussion for beef's place in the diet.

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# Applying a mechanistic fermentation and digestion model for emissions accounting on dairy farms

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**Application** A process-based model currently used as Tier 3 method in Dutch national inventory since 2005 (Bannink et al., 2011) was used to derive emission factors applied in a farm accounting tool for Dutch dairy farmers and the dairy sector.

**Introduction** Enteric $CH_4$ is the largest contributor to on-farm GHG emissions, followed by $CH_4$ emission in case manure is stored. The use of generic estimates, such as the fixed % of gross energy intake with feed being emitted as enteric $CH_4$ or fixed values for digestibility, volatile solids and the methane conversion factor to calculate $CH_4$ from stored manure, ignores variation caused by nutritional factors. To let farm accounting tools become more specific and conclusive on consequences of nutritional or farm management on GHG emissions, the concept of using generic estimates was abandoned.

**Materials and methods** An existing process-based Tier 3 model (Bannink et al., 2018) was used to perform model simulations and derive new emission factors and associated calculation rules to account for variation in enteric $CH_4$ emission and fecal N digestibility in an existing farm accounting tool (Annual Nutrient Cycling Assessment; unpublished) adopting Emission Factors (EF) that express $CH_4$ or N emissions per kg dietary or manure DM or per kg N excreted). Also variation in apparent faecal N digestibility, manure and urine composition (Dijkstra et al., 2018) and excreted volatile solids (VS; simulated excretion of organic matter) were quantified with the process-based model. the unit of g $CH_4$/kg DM.

**Results** Using the process-based model, an EF value was estimated for every feedstuff in the Dutch feeding tables. When evaluating the impact of the diet type on EF estimates, a minimum of three EF appeared necessary (for 0, 40 and 80% maize silage in roughage DM) to let the weighed EF value for diets in the complete range of 0-80% maize silage in roughage DM match the Tier 3 predicted EF value. Tier 3 simulations indicated an almost linear decline in EF value with increase in feed intake from 14 to 24 kg DM/d. This decline was very similar for the different diet types with -0.2 g $CH_4$/kg DM per 1 kg DM/d increase in feed intake. Also EF values were estimated for roughages based on a comparison of modelling as well as recent experimental work. Number of days of regrowth was estimated to affect grass silage EF values with a maximum change of 4 g $CH_4$/kg grass silage DM. Maize silage EF value was estimated to decrease with 0.5 g $CH_4$/kg maize silage DM per 10 g increase in starch in maize silage DM. Estimates of excreted VS were lower compared to IPCC Tier 2, due to the high dietary quality of the diet. Calculations on $CH_4$ emission form excreted VS appear more accurate than estimates based on sampled manure or the IPCC Tier 2 approach adopting a constant diet digestibility.

**Conclusions** Translating mechanistic modelling results towards a farm accounting methodology in order to capture variation in EF for enteric $CH_4$ and apparent N digestibility (to estimate N emission) in particular, but also towards $CH_4$ emission from excreted VS, appears promising. Application of the adapted farm accounting tool appears more realistic as it handles variation in various on-farm emission sources instead of using generic values.

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# Sustainable precision livestock farming: calibrating the real-time estimation of daily protein gain in growing-finishing pigs

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**Application** Prediction of real-time individual body protein (BP) mass is required for precision feeding to further improve nutrient requirements estimations.

**Introduction** To feed individual pigs with daily tailored diets individual daily lysine requirements have to be estimated in real-time using mathematical models as the proposed by Hauschild et al. (2012). Still this model assume that the proportion of protein (PD) in body weight gain (PD/BWG) is constant (e.g. 16 %). However, PD/BWG varies over time and among animals. Therefore the aim of this study was to predict individual BP over time to further obtain individual PD/BWG.

**Material and methods** Data from 56 pigs (35-135 kg BW) were used. Individual BP obtained by dual X-ray absorptiometry (DXA) was regressed over body weight (BW) assuming a null intercept and quadratic response. Individual pig BP estimations were obtained using the MIXED procedure of SAS, considering within pigs repeated measures in time (Figure 1, a). Coefficients of concordance and determination were both 0.99, and the root mean square error was 0.19. This general model ($\mathrm{BP} = 0 + \beta 1 \times \mathrm{BW} - \beta 2 \times BW^2$; where β1=0.22138, and β2= -0.000421) was applied to individuals assuming that pigs have a common population β1 but a specific β2 parameter value. Individual β2 estimates were obtained by NLIN procedure of SAS, based on observed BP. In sequence, β2 was associated to daily cumulative gain:feed and used to estimate a β2 for each pig daily. A Gompertz curve was used to fit the data (a=28.97, b=0.041 and c=0.0166) as means of comparison.

**Results** Validation of the general model in an independent dataset (488 observations; 21-126 kg BW) showed good model accuracy (mean absolute error of prediction= 2.5%; bias= 0.9). This model was chosen over the Gompertz model (mean absolute error of prediction= 4.5%; bias= -0.6), due the better fit (Figure 1, b). The gain:feed presented high correlation with observed PD/BWG (r= 0.91, P<.0001) and β2 (r= 0.76, P<.0001) during the first growing period. Still, the use of cumulative gain:feed to predict BP yielded poor estimates.

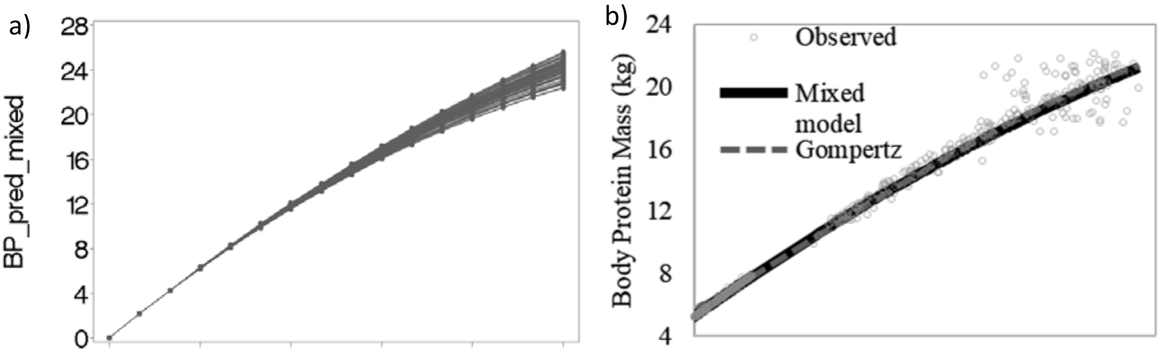

**Figure 1**. Model calibration (a) of body protein mass (BP_pred_mixed) as a function of body weight using individual β2 estimated from observed BP and general model validation (b).

**Conclusion**. The proposed model is able to predict in real-time BP with good accuracy. Although not all of the observed individual variation can be explained with the available data (e.g. comulative gain:feed), representing the dynamics of BP in actual real-time models represents a major improvement in estimating individual animal daily nutrient requirements and will contribute to further improve the efficiency of precision feeding systems.

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# Modeling broiler production in the Chesapeake Bay area: Effects of management decisions on N and P outputs

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**Application** The models described herein allow stakeholders to explore the effects of different management strategies on productivity and excretion of N and P into the environment. These models represent a more flexible, realistic representation of animal management than those currently used in policy-making tools like the Chesapeake Bay model and could scale to inform more flexible policy that accurately represents livestock management options.

**Introduction** The Chesapeake Bay Watershed (CBW) is the largest estuary and has the greatest watershed land area per volume of water in the United States. Runoff of N and P from farms represents a major non-point source contributor of nutrients entering a watershed. Agriculture accounts for 42% of N pollution in the CBW, with goals to decrease N 32% from 2017 levels, and P levels 12%, by 2025 (U.S. Environmental Protection Agency; EPA, 2018).

**Material and methods** The SWAT model (Arnold et al., 2012) was supplemented with a dynamic, mechanistic animal systems model parameterized to represent U.S. broiler production, including inputs for management, feed, and genetics. In turn, excreted N and P from broilers was introduced through SWAT routines as applied manure available for runoff and the implications for watershed N and P could be evaluated. All equations for N and P production from animals were derived from past research. To demonstrate model use and effects on the greater watershed, a series of simulations were generated representing broiler systems with different rates of phytase usage (0 vs 1000 U/kg fed) or dietary N levels (19% vs 16% CP). The simulation lasted until chicks would be harvested at 44 days, with a switch to a finishing diet at 22 days.

**Results** The total amount of P excreted by the simulated broiler flocks decreased by 41.3% when using phytase at 1000 U/kg fed. This excretion decrease is similar to that estimated in the original paper from which our equation was derived (Kornegay et al., 1996). By decreasing the finisher diet CP content from 19 to 16%, resulting total N excretion decreased by 20.1%. The final BW calculated was not affected by this change, however, it has been shown that total DMI would increase in lesser CP diets (Belloir et al., 2017).

**Conclusion** Phytase and decreased CP diets present two management practices that could potentially lower the environmental impact of the poultry industry in eutrophication-prone watersheds. Models such as this extension to the SWAT model provide stakeholders tools to better evaluate strategies to decrease N and P excretion into waterways.

**Acknowledgments** Support for this work was provided by the John Lee Pratt Foundation.

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# Dairy systems characteristics and sustainability in Paraná State, Brazil

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**Application** Structural and productive characteristics of dairy farms are related to sustainability indicators

**Introduction** Food production has recently faced the challenge of adapting to new institutional and market demands, characterized by large-scale production, high-quality products, and processes of low social and environmental impact (Dervillé and Allaire 2014). These new demands, driven by sustainability principles, are an important issue for agricultural producers (Sakané et al. 2013). The challenge of achieving sustainability in dairy production systems - DPS has been present in several parts of the world (Dervillé and Allaire 2014). In Brazil, this new demand brought a significant decrease in milk production for medium and small-scale farmers (Souza and Buainain 2013). Therefore, we must seek solutions for dairy farmers to remain in the activity in a more competitive way, especially considering the social and economic importance of them to the State of Paraná, Brazil, which are the focus on this research. In this context, we aimed to measure the sustainability performance in dairy farms located in Paraná State, Brazil, and compare the typologies of those systems, considering structural and productive variables.

**Material and methods** Semi-structured forms were administered to 75 dairy production systems located in Paraná State, Brazil. Structural and production variables were used to analyze the typology of dairy production systems. Dairy farmers have answered questions considering their actions toward sustainability. These questions were used in Exploratory Factor Analysis – EFA, in order to generate sustainability indicators (SI). SI were applied in hierarchical cluster analysis - HCA. Lastly, we compare the groups of dairy production systems and their typology considering structural and productive variables, by the use of Kruskal-wallis Test ($P<0.05$).

**Results** Milk production systems were heterogeneous in terms of structural and production characteristics. EFA has generated three sustainability indicators - SI-1 "economic performance,", SI-2 "environmental performance" and SI-3 "social performance". HCA has generated three groups of dairy systems - G1, G2 and G3. G1 can be considered as reference in sustainability performance. G2 had an intermediate sustainability performance, and G3 presented the worst sustainability performance (Table 1). Considering the typology, G1, G2, and G3 dairy farms had no differences in total farm area. G1 had the best results for milk production (L/day), number of cows, number of lactating cows, milk production per cow (L/cow/day), and milk production per area (L/ha/day). No differences were observed between G2 and G3 regarding these production variables.

**Table 1** Sustainability levels of each dairy farm group

| Group | SI-1 | SI-2 | SI-3 |
|---|---|---|---|
| Group 1- high sustainability | $0.712^{a}$ | $0.810^{a}$ | $0.751^{a}$ |
| Group 2- intermediate sustainability | $-0.094^{b}$ | $0.156^{a}$ | $-0.303^{b}$ |
| Group 3- low sustainability | $-1.313^{c}$ | $-1.656^{b}$ | $-0.107^{a}$ |

SI= Economic Performance; SI-2= Environmental Performance and SI-3= Social Performance. Different letters in the same column indicate that the values differ significantly according to Kruskal-wallis Test ($P<0.05$).

**Conclusion** Results indicate a relationship among production scale, milk productivity and sustainability indicators in Paraná dairy systems. Dairy systems with better sustainability performance presented highest structural and production scores.

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# Optimization models to evaluate feeding strategies and mitigate methane emissions

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**Application** The methane emissions of feeding strategies were minimized using three linear programming models.

**Introduction** In recent years, several authors have developed mathematical models to estimate or reduce greenhouse gas emissions in dairy production when variables like food composition, growth phase, enteric fermentation and manure management are considered (Chun-Youl et al, 2014). Therefore, the objective of this research was to develop three optimization models to simulate feeding strategies that mitigate the emission of methane in dairy cattle.

**Material and methods** In the present study, an optimization model previously developed was modified (Castelan-Ortega et al., 2018), subsequently three linear programming models were developed. The first optimization model (LP1) considered the requirements of a dairy cow producing 15 L day$^{-1}$, an intake of 11 kg of dry matter (DM), weight loss of -0.5 kg day$^{-1}$, 125 MJ day$^{-1}$, 0.95 kg day$^{-1}$ of metabolizable protein. In the second optimization model (LP2), four plant species and a mixture that showed a methane mitigation potential in vitro were considered as activities, therefore the model selected the specie with the highest potential. The optimization model 3 (LP3) considered the output of LP1 and LP2 to mitigate methane emissions. An empirical linear regression model was developed in this project based in four models already published to estimate methane production (L cow$^{-1}$day$^{-1}$) and it was considered in LP1 and LP3 to estimate the methane production of selected ingredients. The optimization models and the regression models were implemented in a demo version of Lingo software (Release 17.0.78).

**Results** The LP1 model selected five out of seven ingredients available in small-scale dairy systems of central Mexico and the estimated methane production was 369 (L cow$^{-1}$ day$^{-1}$), the LP2 model selected Pine tree leaves as a species with the highest potential for methane mitigation when used up to 3% of the DM requirement. The LP3 model selected maize silage (MS), Maize grain (MG) and bakery waste (Bw) when the output of LP2 model was used and a reduction of 38% in methane production was obtained.

Table 1. Outputs of the optimization models LP1, LP2 and LP3

| LP1 | | | LP2 | | LP3 | | |
|---|---|---|---|---|---|---|---|
| DIn (kg DM) | | $CH_4$ of diet L cow$^{-1}$ day$^{-1}$ | Species with methane mitigation potential | | DIn (kg DM) | | $CH_4$ of diet L cow$^{-1}$ day$^{-1}$ |
| Oats | 0.56 | | Ruta 3% | 0.0 | MS | 5.5 | |
| MS | 5.5 | | Fig 3% | 0.0 | MG | 2.7 | |
| MG | 2.2 | 369 | Pine 3% | 1.0 | Bw | 2.7 | 229 |
| Bw | 2.8 | | Piper 3% | 0.0 | | | |
| | | | Mixsp 3% | 0.0 | | | |

**Conclusion** the results indicated that pine tree leaves used up to 3% of the DM requirement can reduce up to 38% of methane emissions.

**Acknowledgements** We would like to thank to Consejo Nacional de Ciencia y Tecnología (CONACyT), México por el financiamiento de la presente investigación (proyecto numero 247825).

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# Broiler Growth Model: optimizing a feeding program to maximise economic returns

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**Application** The Broiler Growth Model (BGM) estimates growth, feed intake, energy and amino acid requirements of broilers and by integrating this information with the feed formulator will determine the feeding program that maximizes economic returns for the enterprise.

**Introduction** Simulations models that have been developed to predict the growth of broilers provide the opportunity to understand nutrient utilization and estimate nutrient requirements. Such models could be more useful if they could optimize production, since poultry producers should be attempting to maximise productivity at minimal cost. The economic optimum can be achieved using a growth model integrated to a feed formulator such as that used in the broiler optimizer described by EFG Software (2010). The aim of this study was to demonstrate how the BGM could be used to perform an economic optimization of a given feeding program.

**Materials and methods** The Broiler Growth Model (BGM) is a mechanistic model, based on theories developed by Emmans and colleagues (Hauschild et al., 2015). The model predicts growth and nutrient requirements of broilers, accounting for several factors that may prevent the bird from eating the desired amount of food which would then reduce the intake of energy and essential nutrients required for body growth. These constraining factors include certain environment conditions and the bulkiness of the feed. Recently, two tools were incorporated into BGM, a feed formulator and a tool for economic optimization, which enables the program to predict a feed program that will optimize the economic return, based on feeding cost and revenue. Using BGM software, the maximum broiler performance and profit can be predicted, based on different feeding programs.
In this simulation, the feed program was composed of two diets (initial, 1 to 21 d, and grower, 22 to 42 d). The model predicted the rate of growth and hence the nutrient requirements of the broiler, and the feeds designed to meet these requirements were formulated using the formulation tool. The cost per kg of each ingredient was set according to prices obtained from Avisite (2018) and converted to US dollar. The economic optimization tool tested 40 levels of balanced protein (BP) for each diet, performing a combination of 3,600 feeding programs. In each of the two diets an interval of 0.010% digestible lysine (Lys) was set between simulations. To maintain the balanced protein, the ratio of all amino acids with Lys were kept constant. In the initial phase, Lys ranged from 1.174 to 1.564 %, and in the final phase, from 1.045 to 1.435 %. The feed cost (US$/kg of feed) ranged from 0.770 to 1.032 in the starter phase and from 0.705 to 0.879 in the finisher phase. A population of broilers was generated producing 25 different growth potentials. The variables evaluated were feed intake, body weight (BW) and parts, being breast, thigh, drum, and wing weight, whose market selling prices (US$/kg of part) were set at 0.675, 2.75, 2.00, 2.00, 2.50 US$, respectively.

**Results** In total, 90,000 simulations were performed (3,600 feeding programs x 25 individuals) using the economic optimization tool from BGM. To maximize BW, the levels of Lys were 1.35 and 1.05 % in the two phases. To maximize economic returns based on live weight or carcass, the levels were 1.07 and 0.95 % of Lys. Finally, to maximize the profit based on selling parts of the bird, the Lys content was predicted to be 1.60 and 1.31 % for the starter and finisher phases, respectively.

**Conclusion** The BGM is a mechanistic model that enables different economic scenarios to be simulated considering the feeding cost and the revenue of broilers thereby permitting the optimization of the feeds in a given feeding program.

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# How complex does a mathematical model need to be to describe the dynamics of methane production in cattle?

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**Application** A simple dynamic model of methane production using only dry matter intake as predictor is a promising solution for predicting individual methane emissions in a large-scale context.

**Introduction** The production of methane by the rumen microbiota is a complex biological process. When tackling the modelling of methane production, the modeler decides what complexity is needed to answer the scientific question for which the model is intended. Such a choice results in a diversity of models spanning both empirical and mechanistic approaches. In this work, our objective was to provide a simple model-based solution for monitoring individual methane emissions in cattle.

**Material and methods** The experimental data set for the model calibration was obtained from the study of (Moate et al., 2018) with eight rumen-fistulated Holstein dairy cows in late lactation fed with either wheat or corn-based diets. Dry matter intake (DMI) and methane emissions were simultaneously measured in respiration chambers during two days. DMI data were smoothed using a Gaussian model (Boston et al., 2008). We used the mathematical model developed by (Munoz-Tamayo et al., 2018) to represent the dynamics of methane flux $y$ (g/min). The model has two parameters following the ordinary differential equation $\frac{\mathrm{d}y(t)}{\mathrm{d}t} = a \cdot DMI(t) - b \cdot y(t)$.

**Results** Figure 1 displays the model calibration for an individual cow fed either corn or wheat based diets. The model captured the dynamics of methane flux with an average Lin's concordance correlation coefficient of 0.72.

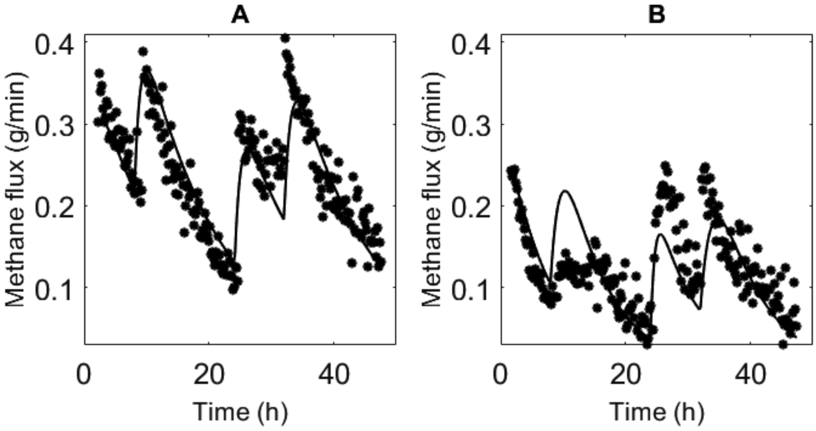

**Figure 1**. Experimental data of individual methane flux (*) are compared against model predicted responses (-) for the corn (A) and wheat (B) diets. For the corn diet, the parameter estimates were $a = 2.10*10^{-5}$ gCH4/(g × DM × min), $b = 1.30*10^{-3}$ min$^{-1}$. For the wheat diet, $a = 2.0*10^{-5}$ gCH4/(g × DM × min), $b = 2.40*10^{-3}$ min$^{-1}$.

**Conclusion** Despite methane production being a complex process, a simple model is able to describe the dynamic pattern of methane production in dairy cows from the pattern of DMI which is a major driving force. This model integrated with a sensor of DMI, is a potential tool for predicting methane emissions at an individual level.

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# Assessing differences in livestock sustainability and efficiency in arid, temperate and sub-tropical environments using a dynamic beef water footprint model

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**Application** Estimation of beef cattle water demands using meta-modeling and dynamic modeling provides insight for producers to develop strategies to improve production and advances current beef water footprint methodology.

**Introduction** Anticipated growth in the demand for beef products driven by increased protein consumption, brings into question the sustainability and efficiency of water use for U.S. beef production (Tedeschi *et al.*, 2015). Current assessment of the U.S. beef production industry provides a wide range of water footprint (WF) measurements (695 to 14,191 L water/kg of boneless meat) of green (rainfed), blue (ground or surface), and grey (waste treatment) water use, and lacks clearly defined region-specific estimates (Doreau *et al.*, 2012; Mekonnen and Hoekstra, 2012). The objective of this study was to evaluate differences in the Texas Beef WF ($WF_B$) in ten unique climate regions using three scenarios with the Texas Beef Water Footprint model (TXWFB) and provide policy recommendations for achieving a sustainable $WF_B$.

**Material and methods** The TXWFB model was developed using Vensim DSS™ and evaluated with the Model Evaluation System and accounted for ten unique climate regions that overlay 12 ecoregions with arid, temperate, and subtropical conditions. The $TXWF_B$ employed meta-modeling by incorporating equations from existing dynamic agricultural and mechanistic, Ruminant Nutrition System (RNS; Tedeschi and Fox, 2018), models to account for regional climate, forage specific water demand ($m^3$/t biomass), cattle population (head of cattle), growth (body weight, kg), and water use ($m^3$) dynamics. Three scenarios were tested to assess the differences in average L water per kg of boneless meat of a 589 kg live weight (LW) feedlot animal (boneless meat = 41.7% LW): 1) Base case (BC) of typical Texas beef cattle production; 2) removal of the water cost (30 $m^3$/ton) of dried distillers grain (DDG) in the feedlot phase (25% of diet); 3) a 50% reduction in evapotranspiration (ET) water footprint costs from pasture and hay production. Simulations were estimated for Texas cattle production from 2004 to 2017 and accounted for a 23-month lifespan from calving to obtaining mature weight. Differences between regions for each scenario were analyzed using a linear mixed model in Program R (*lmreTest*; *lme4*) to perform a repeated measure ANOVA.

**Results** Average $WF_B$ estimates indicated distinct differences between Texas regions and that water reducing scenarios increased water use efficiency measurements across all regions compared to the BC.

**Table 1** Texas beef water footprint simulation results across ten unique climate regions.

| Locations | BC | | DDG | | ET | |
|---|---|---|---|---|---|---|
| | Mean range | SD | Mean range | SD | Mean range | SD |
| Regions 1,2,8 | 8,788-8,808$^{b}$ | 295 | 8,599-8,620$^{b}$ | 294 | 4,588-4,595$^{b}$ | 154 |
| Region 3 | 8,135$^{d}$ | 238 | 7,946$^{d}$ | 242 | 4,233$^{d}$ | 129 |
| Regions 4 and 9 | 7,708-7,782$^{e}$ | 174 | 7,519-7,594$^{e}$ | 170 | 4,004-4,043$^{e}$ | 99 |
| Region 5 | 9,122$^{a}$ | 250 | 8,933$^{a}$ | 248 | 4,767$^{a}$ | 134 |
| Regions 6,7,10 | 8,370-8,530$^{c}$ | 243 | 8,181-8,341$^{c}$ | 242 | 4,361-4,447$^{c}$ | 128 |

SD; Stand Deviation. $^{a,b,c,d,e}$ Different letters in the same row indicate Tukey post hoc difference $P<0.05$

**Conclusion** The variation among the average $WF_B$ estimates confirmed that water demands differ among ecosystems and are greater in more arid environments compared to temperate and subtropical regions, which provides essential baseline estimates for sustainability initiatives. Standardization in the assessment of WF is needed given their predictive discrepancies. Thus, strategies that reduced the $WF_B$ warrant clarification of $WF_B$ accounting for byproducts and ET to more adequately describe appropriate levels of sustainable beef cattle water use per region.

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# Dynamic monitoring and real-time estimation of individual lysine requirements of growing-finishing pigs with deviation from its typical feeding patterns

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**Application** A framework development to monitor feed intake and to estimate lysine requirements for pigs with atypical feed intake patterns will allow moving toward a sustainable pig production.

**Introduction** Economic and environmental benefits were achieved by feeding individual pigs with daily tailored diets. The development of a framework to identify and estimate nutrient requirements for pigs with atypical feed intake patterns will allow moving toward a more efficient approach for its implementation in commercial swine farms. Accordingly, the purpose of this study was developing a framework to monitor feed intake and to estimate lysine requirements for pigs with atypical feed intake patterns.

**Material and methods** First, a dynamic linear model (DLM) was proposed to model the typical daily feed intake (DFI) and daily gain (DG) pattern of pigs. A standardized tabular cumulative sum control chart was applied to the forecast errors generated by DLM to give warnings when pigs showed deviations of its typical feeding pattern. The forecast individual DFI estimates are expressed as its higher DFI relative to that non-challenged period, termed relative feed intake (RFI). Finally, DLM and RFI approaches were integrated into an existing mathematical model (original model) to estimating real-time individual nutrient requirements for pigs with atypical feeding patterns. This general approach was evaluated with data from two studies that investigated the effect of precision feeding systems for growing-finishing pigs. The proposed general approach to estimate real-time individual nutrient requirements (update model) was evaluated by comparing its estimates with those generated by the original model (Hauschild et al., 2012).

**Results** For 11 individuals from 130, the DLM did not fit well the observed data in a determined period. This implied in an increase of the sum of standardized forecast error and in the number of times steps the model needed to adapt to the new patterns. Lastly, the results of this study showed that the updated model allowed to reduce inter and intra-individual variation for the estimated lysine requirements compared to the original model (Figure 1).

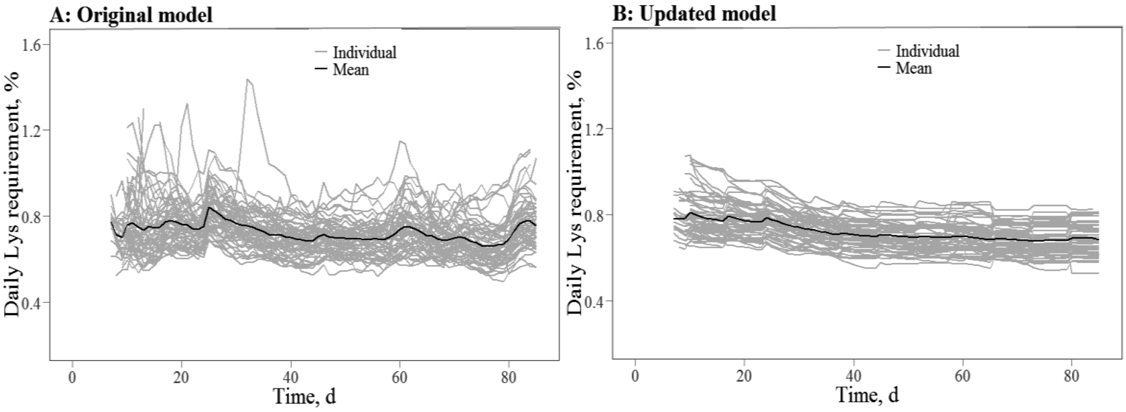

**Figure 1** Daily optimal lysine concentration estimated for each pig by the original (A) and updated model (B)

**Conclusion** The empirical approach proposed is presented as a tool for on-line monitoring daily feed intake and allows estimating real-time lysine requirements for growing-finishing pigs accounting the reduced feed intake and growth potential for pigs with atypical feeding patterns.

**Acknowledgements** Financial support FAPESP projects No. 2018/15559-7 and 2016/25157-8.

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# Evaluation of an Egg Production Model and introducing an economic optimizer

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**Application** The Egg Production Model (EPM) estimates egg production and feed intake of laying hens, accounting for factors that may prevent the bird from achieving its genetic potential. The values predicted in the EPM can be used to perform simulations using different scenarios, which could be used as a decision tool.

**Introduction** Very few models have been designed to predict egg production in laying hens whilst accounting for factors that may constrain feed intake. This is possibly because models designed to predict egg production are more complex than growth models. The objective of this work was to evaluate a method to predict feed intake and egg output (Gous, 2014) and to demonstrate how the model could be used to maximise economic returns in an egg production enterprise.

**Material and methods** The EPM was developed at the poultry science laboratory, located at FCAV – Unesp, Jaboticabal – Brazil. Rate of lay, and egg weight and composition, considering yolk, albumen and shell, were predicted using the method of Johnston and Gous (2003; 2007). With this information, and accounting for the efficiency of utilization of nutrients, it is possible to predict the daily intake of energy and amino acids necessary to achieve the genetic potential. The environment, bulkiness of the feed and the maximum rate of lipid deposition in the body were included as constraining effects, enabling the prediction of actual feed intake (AFI) and the impact of a change in feed composition on egg production. Furthermore, two tools were developed and added into the model, a feed formulator and a feeding program optimization, which enable the prediction of the feed composition or the feeding program that will maximize economic returns. To evaluate the model, a database was constructed using five published papers, in which laying hens were fed a diet containing increasing levels of digestible lysine (ranging from 0.58 to 0.90 % dLys) as the first limiting nutrient. Feed intake (FI, kg) and egg output (EO, g) were the response variables evaluated. The concordance correlation coefficient (CCC) was calculated to verify the accuracy and precision of the EPM, using R scripts provided by the National Animal Nutrition Program (NANP, 2019) for R statistical software (version 1.0.143; R Core Team, 2018). In a separate exercise an economic optimization was performed in order to obtain the level of dLys in the feed that maximized the economic returns of laying hens at 24 weeks of age. The simulation was set with a feed formulated to contain 0.89% of dLys and all nutrients necessary to meet the requirement of the laying hen. The cost per kg of each ingredient and the cost of egg was set according to prices available from Avisite (2018) and converted to US dollar. The price of feed was US$ 1.18 and the price of 30 dozen eggs was US$ 17.5. The economic optimization tool was used to test 20 levels of dLys, ranging from 0.38 to 1.38 %, with a difference of 0.05% of dLys between diets.

**Results** The reduction of dLys in the feed below 0.70 % resulted in a reduction of both FI and EO. However, at levels above this, only FI was reduced, indicating that the laying hen adjusted FI according to the first limiting nutrient. When these simulated results were compared with the published papers the CCC values obtained for FI and EO were 0.39 and 0.69, respectively. The feed containing 0.83 % dLys (US$1.17) was estimated to maximize economic returns since the price of feed declined with no impact on egg production, resulting in an increase in profit of approximately 4 % in comparison with the profit obtained with hens consuming 0.89 % dLys.

**Conclusion** The results obtained with the Egg Production Model indicate that both egg output and feed intake may be predicted with relative precision and accuracy. The economic optimization tool could be used to make nutritional decisions and maximize economic returns in an egg production system.

**Acknowledgements** This study was financed by the Sao Paulo State Foundation (Fapesp), Process: 2013/25761-4 and 2016/11172-5.

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# Modeling $N_2O$ emission from beef cattle supplemented with phytogenic additives

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**Application** Modeling environmental impacts (emissions) of nutritional strategies

**Introduction** Nitrous oxide ($N_2O$) is a potent greenhouse gas, being 300 times more effective in the global warming than carbon dioxide ($CO_2$). In the livestock production is emitted from urine and dung. Nitrogen is mainly excreted in urine by the animals, and the correct protein supplementation is essential to optimize N efficiency usage, and avoid N losses to the environment (Histrov et al., 2013).

Phytogenic additive like condensed tannins may act on the urine N compound and soil microorganism, mitigating $N_2O$ emissions. We aimed to model $N_2O$ fluxes from urine treated with condensed tanins with phytogenic additives using multiple linear regression and regression tree to identify the key driving variables involved in $N_2O$ production.

**Material and Methods** We used a data set of $N_2O$ emissions from urine that was treated with different amount of condensed tannins (zero, moderate -0.5% dry mass bases and, high 1%). The data set complies 240 observation. To model $N_2O$ fluxes the explanatory variables were temperature, ammonium, nitrate and carbon dioxide. Multiple linear regression and regression tree were carried out using R (3.2.3).

**Results** The multiple linear regression estimated the parameter adequately. Using step wise option, the variable $CO_2$ was chosen by the model. This variable explained the 35% of variation in $N_2O$ fluxes.

The regression tree identified two branches. The first one was temperature and the second one $CO_2$ fluxes. When temperature was higher than 25 ºC the highest fluxes of $N_2O$ was observed and when $CO_2$ was lower than 4.27µg $CO_2$ $m^{-2}$ $h^{-1}$ $N_2O$ fluxes was close to zero.

**Conclusion** The two approaches can be used to model $N_2O$ emissions from experiments of strategies of animal supplementation. While multiple linear regression identified the which variable explain $N_2O$ production the regressions tree classified two variables that better explain $N_2O$ production.

**Acknowledgements** We would like to thanks Fundação de Amparo a Pesquisa de São Paulo (FAPESP grant 2015/16631-5) and Coordenação de Aperfeiçoamento do Pessoal de Nível Superior (CAPES) for the scholarship.

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# Modeling $N_2O$ emission from animal feeding pasture using single and multiple linear regression

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**Application** Modeling greenhouse gas emissions from animal in pastures

**Introduction** Nitrous oxide ($N_2O$) is a potent greenhouse gas, in Brazil its accounts 15% of greenhouse gas emission. In the beef cattle production is emitted from urine and dung. The form of nitrogen, dose, period of application and temperature affect its production (Cardoso et al., 2017).

In grassland variables such as sward heights, soil temperature and moisture, $NO_3^-$ and $NH_4^+$ content affect $N_2O$ production. We aimed to model $N_2O$ fluxes from an intensive managed grassland using single and multiple linear regression and to identify the key driving variables involved in $N_2O$ production.

**Material and Methods** We used a data set of $N_2O$ emissions from grassland managed at 3 grazing intensity: swards heights 15, 25 and 35 cm. The data set from Cardoso et al. (2017) has 4800 observation. To model $N_2O$ fluxes the explanatory variables were rainfall, soil moisture, temperature, ammonium, nitrate and carbon dioxide. Single and multiple linear regression were carried out using R (3.2.3).

**Results** Multiple linear regression was significative with sward height in summer, 3 variables during spring (soil moisture, $NH_4^+$ and $NO_3^-$ ) and, 4 in the autumn ($CO_2$, soil moisture, temperature and $NH_4^+$). However, the $R^2$ of the model was relatively low 0.24, 0.39 and 0.41 for the summer, spring and, autumn. When the $R^2$ are lower than 0.5 the prediction of a dependent variable by the explanatory variables is weak. After running the single linear regression with the significant variables identified in the multiple regressions separately, only $NH_4^+$ ($R^2$=0.66; $p<0.001$) during the spring and soil moisture ($R^2$=0.75; $p<0.001$) during the autumn presented significative correlation with $N_2O$ emissions.

**Conclusion** The two types of regression can be used to model $N_2O$ emissions from animal excreta feeding grass. While multiple linear regression identified the which variables explain $N_2O$ production the single linear regression better modelled $N_2O$ emissions.

**Acknowledgements** We would like to thanks Fundação de Amparo à Pesquisa de São Paulo (FAPESP grant 2017/11274-5) and Coordenação de Aperfeiçoamento do Pessoal de Nível Superior (CAPES) for the scholarship.

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# Determination of Marandu palisadegrass biomass under continuous stocking using satellite images

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## Application

Estimative of pasture biomass using satellite-derivable vegetation indices

## Introduction

In pastoral systems, constant production of forage is a key factor to assure pasture perenniality and animal performance, as well as it is an important ecological variable for understanding the responses to the climate system. Traditional techniques for measuring the amount of pasture biomass are based on field data destructive collection that are accurate, but time and labor intensive, often difficult to implement and only practicable for small areas. Alternatively, satellite-derivable vegetation indices (VI) are a promise technique to estimate pasture biomass that deserve investigation. Indeed, a commercial program in Brazil has been released and provides estimation of pasture production by means of remote sensing. Therefore, the objectives of this study are: (1) To establish the relationship between satellite-derivable VI and Marandu palisadegrass forage mass under continuous stocking rate during the growing season; (2) To validate commercial algorithms from Sigfarm® to estimate forage mass using satellite-derivable VI.

## Material and methods

The experimental area comprised of two adjacent areas of Marandu palisadegrass pasture (*Brachiaria brizantha* 'Marandu'), summing 33 paddocks (experimental units), receiving or not N fertilization. Pasture were managed under continuous stocking to maintain grazing height fixed at 25 cm during the growing season, using the put-and-take methodology with young beef bulls. Field dataset collection (total forage mass and morphological composition) and satellite images were assessed from Dec/2015 to Mar/2016; Jan/2017 to Apr/2017, Jan/2018 to Apr/2018 and Dec/2018 to Mar/2019 during growing or wet season. The satellites images were downloaded from US Geological Survey (USGS, http://earthexplorer.usgs.gov). Orthorectified reflectance values of spectral bands were used to calculate the VI: normalized difference vegetation index (NDVI), green normalized difference vegetation index (GNDVI), simple ratio index (SRI) and modified simple ratio (MSR). Linear regressions and their adequacy were performed using 10-fold cross-validation technique. Additionally, the model adequacy of commercial algorithms from Sigfarm platafform (https://sigfarm.com.br) based on the observed values in dataset was assessed by using the model evaluation system (http://nutritionmodels.com/mes.html).

## Results

Correlation coefficients for dry forage mass showed weak relationship with VI in general ($r < 0.40$). Conversely, fresh forage mass, dry leaf+stem and dry leaf mass were positively correlated to VI ranging from 0.52 to 0.76. Due the poor correlation of a single VI, the best model to predict dry forage mass input GNDVI and SR, explaining only 33% of the variation in the observed paddock average pasture mass ($r^2 = 0.33$, root of mean square error (RMSE) = 1.14). The best predictor of fresh forage mass was GNDVI ($r^2 = 0.49$, RMSE = 1.14). The NDVI was the best predictor of total dry leaf+stem mass ($r^2 = 0.39$, RMSE = 0.92) and the best estimate of dry leaf mass was obtained using SRI ($r^2 = 0.59$, RMSE = 0.45).

The model evaluation of the Sigfarm® algorithm for predicting leaf mass revealed that model precision ($r^2 = 0.75$, RMSE = 0.43) was moderate, and the accuracy (i.e, Cb) of the prediction was high (> 0.99), suggesting that, on average, predicted and observed values were very close. The mean square error of prediction (MSEP) decomposition of leaf mass indicated that most of the errors associated with the prediction are related to random errors (92.2% of MSEP).

## Conclusion

Satellite-derivable vegetation indices are suitable to estimate leaf mass with moderate precision. Sigfarm® algorithm to estimate pasture leaf mass is precise and accurate.

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Sigfarm Intelligence Ltda

# Identifying key driving variables on enteric methane emissions using regression tree

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**Application** Modeling environmental impacts (emissions) of nutritional strategies.

**Introduction** Enteric methane ($CH_4$) production by ruminants is a fundamental process for the appropriate functioning of the digestive system of these animals, but, from the nutritional point of view, it results in loss of raw energy intake and consequently reduces animal performance (Johnson & Johnson, 1995). $CH_4$ production is directly related to the dry matter intake and diet quality. Nitrogen (N) is the nutrient that most limits pasture productivity, and influences forage nutritive value.

Nitrogen fertilization or the legume consortium with tropical grasses play an important function in the productive performance of pastures and may also affect $CH_4$ production by ruminants, in order to reduce the negative contribution of livestock to global warming and increase the animal and productive efficiency. We aimed to model $CH_4$ emissions from crossbred dairy heifers kept in marandu grass pastures fertilized with N or mixed with forage peanut using regression tree to identify the explanatory variables of $CH_4$ emissions and to develop pasture management strategies using the variables identified in the modeling process.

**Material and Methods** We used a data set of $CH_4$ emissions from crossbred dairy heifers kept in marandu grass pastures fertilized with N or mixed with forage peanut to model $CH_4$ production. The data set complies 84 observations. To model $CH_4$ emissions, the explanatory variables were body weight (BW), forage quality attributes represented by dry matter intake (DMI), neutral detergent fiber (NDF), crude protein (CP) and dry matter digestibility (Dig). Regression tree was carried out using R (3.2.3).

**Results** The regression tree identified three branches. The most important variable determining $CH_4$ production is Dig that was split in two levels. When Dig is lower than 56% the $CH_4$ emissions is controlled by NDF content that is higher than 61%, the prediction of $CH_4$ emission is 202 g animal$^{-1}$ day, otherwise it was 139 g animal$^{-1}$ day. If the Dig is higher than 56% the BW is the second variable driving $CH_4$ production, e.g. when the animal has lower than 319 and NDF was lower than 60%, the predicted $CH_4$ emissions is 110 g animal$^{-1}$ day, otherwise it was 159 g animal$^{-1}$ day.

**Conclusion** The regression tree can be used to model $CH_4$ emissions from experiments of strategies of animal feeding on pasture. This statistical modelling classified three variables that better explain $CH_4$ emissions by ruminants (digestibility, neutral detergent fiber content and body weight).

**Acknowledgements** We would like to thank National Council for Scientific and Technological Development (CNPq) for financing the project and Coordination of Improvement of Higher Education Personnel (CAPES) for the scholarship.

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# Potential of Ctx(Ile$^{21}$)-Ha antimicrobial peptide as additive modulator of rumen fermentation: an *in vitro* approach

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**Application** The development of a new natural additive can reduce the microbial resistance caused by the antibiotics used in animal production.

**Introduction** Considering the antibiotic resistance that many microorganisms have presented, the antimicrobial peptides (AMP) have been used in the last years against pathogenic microorganisms in several areas. The Ctx(Ile$^{21}$)-Ha antimicrobial peptide (Vicente et al., 2013) appears as an alternative to the zootechnical additives already used. It acts by optimizing the use of available nutrients by reducing the methane production and the number of Gram-positive bacteria in the rumen. This study estimate the gas production potential of bovine ruminal fluid supplemented with the antimicrobial peptide Ctx(Ile$^{21}$)-Ha.

**Material and *methods*** *In vitro* studies were performed using rumen fluid collected directly from ruminally cannulated steers. The treatments used were the combination of three different substrates: Total diet (60% of *Urochloa brizantha* cv. Marandu and 40% of concentrate), *Urochloa brizantha* cv. Marandu and corn silage with five additives, as follow: without additive (NO), 5 mg/L of monensin (MON) (Quinn et al., 2009), 2.5 mg/L of Ctx(Ile$^{21}$)-Ha (AMP 2.5), 5 mg/L of Ctx(Ile$^{21}$)-Ha (AMP 5.0), and 7.5 mg/L of Ctx(Ile$^{21}$)-Ha (AMP 7.5). The additive levels were based on mg/L of buffered ruminal fluid. The experiment was conducted following the procedures described by Mauricio et al. (1999). The buffered ruminal fluid (30 mL) was placed in bottles with 0.2 g of substrate (dry matter – DM basis) plus the additive, and the bottles were immediately sealed. The gas production was recorded at 3, 6, 9, 12, 24 and 48 hours after the bottles were sealed. The final volume of gas (FV; mL/g of organic matter – OM), degradation rate (S; $h^{-1}$), and lag time (L; $h^{-1}$) was calculated using the equation proposed by Schofield et al. (1994): $Y_t$ (mL/g of OM) = FV*(1+exp(2-(4*S*(GASTIME-L))))$^{-1}$, where: $Y_t$ = volume of gas produced until time *t* (mL/g OM).

**Results** The results are shown in table 1. We observed no effect of interaction substrate*additive and substrate on FV, S, and L ($P \geq 0.25$). AMP had higher or equal FV than MON, which supports the use of AMP as a feed additive. On the other hand, AMP had slower S than MON ($P \leq 0.02$). We observed no effect of additive on L ($P = 0.15$).

Table 1: Potential of gas production, degradation time and lag time

| | Substrate[1] | | | Additive[2] | | | | | | *P*-value | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | Ctx(Ile$^{21}$)-Ha AMP | | | | | |
| | TD | MAR | CS | NO | MON | 2.5 | 5.0 | 7.5 | SEM | Substrate | Additive |
| FV[3] | 116 | 116 | 111 | $109.8^{ab}$ | $90.8^{b}$ | $122.9^{ab}$ | $105.3^{b}$ | $143.8^{a}$ | 11.49 | 0.9 | 0.02 |
| S[4] | 0.049 | 0.050 | 0.048 | $0.044^{b}$ | $0.072^{a}$ | $0.038^{b}$ | $0.056^{ab}$ | $0.036^{b}$ | 0.0071 | 0.96 | <0.01 |
| L[5] | 2.08 | 2.85 | 3.14 | 3.01 | 1.91 | 3.16 | 1.94 | 3.42 | 0.52 | 0.25 | 0.15 |

[1]TD = total diet, MAR = Marandu, and CS = Corn silage; [2]NO = no additive; MON = Monensin, 2.5 = 2.5 mg of Ctx(Ile$^{21}$)-Ha/kg DM, 5.0 = 5.0 mg of Ctx(Ile$^{21}$)-Ha /kg DM, and 7.5 mg of Ctx(Ile$^{21}$)-Ha /kg DM; [3]Final volume of gas, ml/g OM; [4]Degradation rate, $h^{-1}$; [5]Lag time, $h^{-1}$.

**Conclusion** These are preliminary studies and we are carrying out new approaches to have a better understanding of this data. Partial results showed that monensin can be replaced by 2.5 and 7.5 mg of the peptide/kg DM without significant increase in gas production.

**Acknowledgements** We thank to FAPESP for financial support for the development of the project (process nº 2016/00446-7). We thank CAPES and CNPq for granting the scholarships.

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# Prediction of beef cattle performance on tropical pastures receiving supplementation during the wet and dry seasons

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**Application** The same level of supplementation can provide different beef cattle performance at different seasons in Brazilian grazing systems.

**Introduction** During dry season, supplementation has been used to minimize the negative scenario of beef cattle performance due to feed shortage (Reis *et al*., 2009). However, supplementation has also been used during the wet season as a strategy to improving the individual animal performance and to decrease the time needed for slaughter, resulting in higher productivity per area (Reis *et al*., 2009). There still not an overall recommendation of which level of supplementation is more suitable throughout the different seasons of the year. Therefore, our objective was to identify the impact of supplementation on average daily gain (ADG) and gain per hectare (GPH) in tropical beef cattle systems during the dry season and wet season using a meta-analytical approach.

**Material and Methods** Database was built with level of supplementation ranging from 0 to 16 g/kg body weight (BW) and the effect of supplementation level was examined during both dry and wet season. The effect of season and type of supplement (energetic and protein) on the regressions of ADG and GPH against the level of supplementation was determined using the MIXED procedure of SAS (v. 9.4). Regressions were analyzed by including the study as a random effect and by weighting for the number of replicates per treatment (St-Pierre, 2001); also, cattle age and average BW were tested as covariates. When season was significant, the intercepts and slopes were compared using the CONTRAST statement. The slopes and intercepts of each equation were estimated using the ESTIMATE statement. Unless otherwise indicated, $P < 0.05$ was considered statistically significant.

**Results** The intercept of the regression between ADG and supplement intake was different between seasons ($P < 0.05$) whereas the slope was similar for both seasons (Eq. 1 and 2). The equation slopes revealed that, on average of both seasons, the ADG increased by 0.308 g/d for each 1.0% of increase in the supplement intake. Both the intercept and slope of the regressions between GPH and supplement intake (Eq. 3 and 4) were different between seasons ($P < 0.05$). The GPH increased by 4.90 kg/d/ha for each 1.0% of increase in the supplement intake during the wet season, whereas during the dry season it increased at a rate of only 1.15 kg/d/ha. There was no effect of supplement type on the slope of regressions.

$\text{ADG (DS)} = 0.0811\ (\pm 0.0245) + 0.308\ (\pm 0.0182)\ \text{LS} - 0.00039\ (\pm 0.00013)\ \text{Age} + 0.00139\ (\pm 0.00030)\ \text{BW}$ (Eq.1)
$\text{ADG (WS)} = 0.221\ (\pm 0.0285) + 0.308\ (\pm 0.0182)\ \text{LS} - 0.00039\ (\pm 0.00013)\ \text{Age} + 0.00139\ (\pm 0.00030)\ \text{BW}$ (Eq.2)
$\text{GPH (DS)} = 0.417\ (\pm 0.166) + 1.15\ (\pm 0.213)\ \text{LS} - 0.0022\ (\pm 0.00087)\ \text{Age} + 0.0050\ (\pm 0.0019)\ \text{BW}$ (Eq.3)
$\text{GPH (WS)} = 0.764\ (\pm 0.192) + 4.90\ (\pm 0.104)\ \text{LS} - 0.0022\ (\pm 0.00087)\ \text{Age} + 0.0050\ (\pm 0.0019)\ \text{BW}$ (Eq.4)
where, ADG = average daily gain; GPH = gain per hectare; DS = dry season; WS = wet season; LS = level of supplementation; Age = cattle's age; BW = body weight.

**Conclusion** Beef cattle had similar increases in ADG following supplementation, regardless of season. A previous research showed that over tropical pastures the GPH may increase due to increasing the stocking rate (Boval *et al*., 2015). However, probably due to the low quality of forage at dry season, the supplementation *per se* is not able to guarantee the increase of stocking rate at dry season in similar levels to the wet season. Therefore, even using supplementation the GPH at dry season will always be lower than that obtained at wet season.

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# Optimum biological and economic balanced digestible protein levels for pacu (*Piaractus mesopotamicus*) juveniles

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**Application** Evaluation of dietary protein requirements of fish by taking into account both biological and economic responses is a significant factor in profitable and sustainable aquaculture practices

**Introduction** Due to increasing feed costs and high nitrogen excretions, protein requirements should be determined by taking into account both biological and economic outputs (Eits et al., 2005a, b; Khan, 2019). This study aimed to calculate optimum biological and economic balanced digestible protein (BDP) levels for pacu juveniles.

**Materials and methods** Two basal diets, one with high protein and the other with low protein content, were formulated according to the diet-dilution approach. Both the diets were provided with an essential amino acid balance and equal amounts of optimum digestible energy and other supplements. Then these two diets were mixed up in proper proportions in order to achieve six experimental diets containing different levels of balanced digestible protein (BDP) at the rate of 163, 201, 238, 272, 315 and 348 g kg$^{-1}$ (dry matter basis), respectively. A total of 432 healthy fish with average initial body weight of 10.82 ± 0.14 g were distributed among 18 fiber tanks (24 fish per tank/replicate) of 1000-L capacity each, being connected to a closed re-circulation aquaculture system (RAS). The experimental design was completely randomized which consisted of 6 treatments and 3 replicates, each. Fish were fed with respective diets three times a day at 09:00, 12:00 and 17:00 h until apparent satiation.

**Results** The quadratic regression model calculated the optimum biological level of 326 g DBP kg$^{-1}$ (dry matter) and the optimum digestible protein to energy (DP: DE) ratio was calculated to be 22.13 g MJ$^{-1}$ (dry matter) for gaining maximum performance of juvenile pacu. The economic model calculated the optimum economic level of 311 g DBP kg$^{-1}$ (dry matter) and the optimum DP: DE ratio was calculated to be 21.11 g MJ$^{-1}$ (dry matter) for pacu that will be sold as whole body fish. For pacu that will be sold as cut-up portions i.e., eviscerated and sliced fish, the economic model calculated the optimum economic levels of 316 and 319 g kg$^{-1}$ and the optimum DP: DE ratio was calculated to be 21.47, and 21.67 g MJ$^{-1}$, respectively.

**Conclusion** Optimum economic protein requirements of fish should be calculated and adjusted according to the fluctuations in the selling price of fish, protein rich ingredients and the way fish is marketed such as whole body or in cut-up portions.

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# Dynamic model for methane emission and milk production from dairy goats based on energy balance measures

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**Application** The dynamic model should be valuable for preparing methane ($CH_4$) emission inventories in goats by different countries.

**Introduction** Although a major quantity of the methane emission arises from cattle (74%) and buffalo (11%), the world goat population (1.01 billion) produces around 4.6 million tons of enteric $CH_4$, representing 5% of total $CH_4$ emissions from livestock (FAOSTAT, 2018; Patra 2014). Feed efficiency is non linear and not constant (Kebreab *et al.*, 2003; Jørgensen 2015), and a poor efficiency has implications for environmental concerns. The goat requires energy (E) that can do work and some E is transferred to milk, other is excreted and certain heat (maintenance and $CH_4$ emissions) is lost during every E transformation. The aim of this study was to develop, represent and assess a dynamic mathematical model for dairy goats based on flow of the E intake though the body, quantifying $CH_4$ emissions and total amount of milk produced.

**Material and methods** A dynamic and model was developed by representing major body-E kinetics. Food contains chemical E, so mass balance was converted to E balance. E and time units to the model were expressed in kJ/kg $BW^{0.75}$ and days, respectively. Dry matter intake (DMI), dietary gross energy (GE) and BW were input variables. The model includes 3 E pools; utilized E from feed (Q_I), E assimilated (Q_A) and E in reserves (Q_R, Figure 1). All fluxes were represented by mass action equations with exception of milk-E that was of Michaelis-Menten type. Fractional rate of assimilated-E flux to the $CH_4$ was adjusted for DMI and assimilated-E to heat production was adjusted for BW. To develop the model, data from literature and experimental E balance obtained from 8 dairy goats at mid lactation (16 weeks) was used. The model was optimized by solving for all the parameters simultaneously and externally evaluated using 123 measured of E intake, fecal, urinary, $CH_4$, heat production and milk E output observations from mid-lactating Murciano-Granadina dairy goats fed total mixed rations (forage, 40%; GE, 16-18 kJ/g DM; DMI, 1294-2199 g/day; BW, 33-61 kg). The model consisted of a dynamic system of differential equations coded in R (R Core Team, 2016).

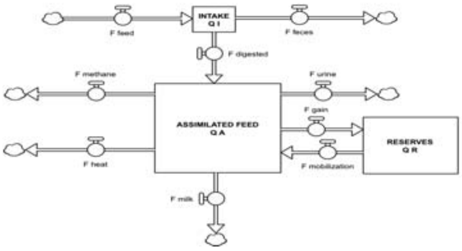

**Fig. 1**. Schematic representation of Energy dynamic model

**Results** The optimized model predicted milk E with root mean square prediction error (RMSPE) of 6.8% of the average observed values. The E-$CH_4$ lost was predicted with acceptable RMSPE (< 30%) of the average observed values. The slope bias of 14% for E-$CH_4$ suggested systematic error probably associated to the assumption expended to predict $CH_4$. Milk-E random bias was <1% indicating good representation and parameterization of E transfer in the model. So, simulations for DMI of 1.4, 1.7 and 2.0 kg/d showed non-linear $CH_4$ emissions [20, 31and 45 g/d, respectively] and milk production [2001, 2074 and 2127 g/d, respectively].

**Conclusion** The goat model was set up to simulate indoor facilities in which the goat was fed mixed rations. Integration of information generated from other experiments and literature into the simulation model will contribute to a more dynamic understanding of the energy transfer and conversions in this system.

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# Combining a bioclimatic and a growth model to assess the effect of management practices and building ambiance on growing pig performances at the batch level

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## Application

The combination of a bioclimatic and a growth model is performed to allow the assessment of pig performances and energy consumption at the batch level depending on pen characteristics, feeding strategy, management of building ambiance and climate conditions.

## Introduction

Most pigs in the EU are reared in controlled environment rooms, combining direct and indirect consumption of energy. The indirect energy consumption depends on the amount and quality of the feed delivered to each pig, the number of pigs and growth performance level. Bioclimatic models represent and predict the energy balance and direct energy consumption at the room level, based on characteristics of the building, management of the climate control tool and average performance of pigs. Available growth models usually simulate performance of pigs in a dynamic way depending on the feeding strategy but only under thermoneutral conditions. In the present study, a model was developed within the EraNet PigSys project to connect a bioclimatic model (Thermisim) and a growth model (InraPorc) to evaluate growing pig performance and energy consumption at the batch level in a dynamic way, depending on pen characteristics, feeding strategy, management of building ambiance and outdoor climate conditions.

## Materials and method

The model is of a multi-object type, mechanistic, dynamic, determinist and pig centred. It was written in Python language. The growth model is an individual-based model adapted from the InraPorc model, combined with a generator of the within-room pig population and additional tools dealing with management issues such as mortality rate or delivery to slaughterhouse (Cadero *et al.*, 2018). At the room level, the bioclimatic model allows for the calculation of the rate of ventilation and the input of heat required to achieve the expected ambient temperature. It accounts for the interaction between room characteristics (size, insulation), equipment (fans, heater), parameters of the climate control box and the average characteristics of the group of pigs (number, weight, performance, heat production) (Marcon *et al.*, 2016). Main model developments were related to i) an hour-time step accommodating for those of Thermisim (second) and InraPorc (day); ii) the influence of ambient conditions at day D on feed intake at day D+1; iii) the circadian partition of feed intake; iv) the dynamic partition of the thermic effect of digestion; v) the definition of the lower and upper critical temperature based on individual daily body weight. The model was evaluated from a French database elaborated from a batch of pigs whose average growth profile was known as well as details on diets and rooms, and indoor and outdoor temperature both measured every 15 minutes.

## Results

Based on simulation, *in silico* growth performance were similar to *in vivo* values (i.e., relative RMSEP below 2.6% for average daily gain, feed intake and feed conversion ratio). The simulated ambient temperature differed from measured values by less than 0.5°C, which is below the measurement accuracy. Given this high precision level and accounting for the major contribution of ventilation rate to temperature regulation, the prediction of ventilation rate was considered sufficiently reliable for further investigations.

## Conclusion

The model obtained from the combination of Thermisim and InraPorc allows for a good prediction of performance and ambient temperature. The next step is to use this model to evaluate the performance of pigs under different climatic conditions and in different building or feeding conditions.

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