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# Bayesian comparison of models for precision feeding and management in growing-finishing pigs

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## Abstract

Precision feeding and management of growing-finishing pigs typically require mathematical models to forecast individual pig performance from past data. The current approaches, namely double exponential smoothing (DES) and dynamic linear regression are likely to have some limitations in their applicability since they: (1) assume that responses can be forecasted linearly, which only holds in the short-term, and (2) often take insufficient account of uncertainty and correlations in the estimated traits. We developed and evaluated alternative approaches to forecasting individual growth or intake responses based on nonlinear models (allometric, monomolecular, rational) and Bayesian methodology to fit models to the data and generate probabilistic forecasts. We applied these approaches to individual data from two distinct pig populations, to parameterise the models (fitting based on a training dataset) and forecast performance (forecast horizons: 1-30 d tested on a validation dataset). We found that good fitting did not guarantee accurate forecasting, which is quantitatively relevant in the medium-to-long term. Forecasts from nonlinear models were more accurate compared to those from benchmark linear models, with the allometric model being more accurate for most pigs across considered forecast horizons. While DES was the best model at fitting, it was also the least accurate at forecasting for all forecast horizons. These results enhance the understanding of how underlying biological growth responses could be approximated using straightforward mathematical relationships. The approach could be utilised to formulate optimised feeding strategies and inform management decisions, including pen allocation or end-weight prediction.

Keywords: Precision feeding; Forecasting; Bayesian modelling

## 1. Introduction

Precision feeding and management strategies (Berckmans, 2006; Wathes, Kristensen, Aerts, & Berckmans, 2008; Filipe, Knol, Vogelzang, & Kyriazakis, 2018) that account for variation in the requirements and growth trajectories of individual animals could substantially improve resource utilisation and reduce environmental impacts of livestock systems, as well as increase profitability of these operations (Cerosaletti, Fox, & Chase, 2004; Andretta, Pomar, Rivest, Pomar, & Radünz, 2016; Zuidhof, 2020). It is possible that such strategies may also enhance animal welfare (D'Eath, Tolkamp, Kyriazakis, & Lawrence, 2009).

The implementation of precision feeding and management strategies typically require mathematical models to forecast performance of individual animals from past data. Successful forecasting of individual growth or feed intake responses in the context of precision feeding and management is conditional on: (1) how well the mathematical model approximates the underlying biological process; (2) how accurately the parameter values of the model can be estimated from the information on past performance of the animals; and (3) whether the estimates are accompanied by a quantification of uncertainty to inform the extent to which they can be relied upon. While previous precision feeding and management studies in pigs (Hauschild, Lovatto, Pomar, & Pomar, 2012; Brossard, Taoussi, Van Milgen, & Dourmad, 2017; Quiniou, Brossard, & Marcon, 2017; Peña Fernández et al., 2019) often provide assessments of different forecasting approaches, the aforementioned three conditions are rarely taken into full consideration, which may limit the conclusions about the applicability of these approaches. Here, we compare the most frequently utilised approaches in the literature with alternatives aimed at addressing some of the identified main limitations.

The previously developed precision feeding and management systems in growing-finishing pigs tackle the problem of forecasting individual growth responses based on previous feed consumption and bodyweight (BW) data typically using either: (i) double exponential smoothing (DES) (Hauschild et al., 2012; Brossard et al., 2017; Quiniou et al., 2017), a type of weighted moving average of past observations (Holt, 1957; Brown, 1959); or (ii) dynamic linear regression (DLR) (Peña Fernández et al., 2019), where the regression parameters can vary over time (Petris, Petrone, & Campagnoli, 2009). Both approaches assume that growth responses to nutrient intakes are linear in relation to the explanatory variables, time (age) or feed intake respectively, despite considerable evidence suggesting that these processes are nonlinear, at least in monogastric livestock species (Kuhi, Kebreab, Lopez, & France, 2004;

Van Buggenhout, Aerts, Vranken, & Berckmans, 2004; Schulin-Zeuthen et al., 2008; Demmers et al., 2018). Most responses can be approximated by a linear relationship within a short-term window and this is the implicit basis on which linear models are then applied. The length of this window is often unknown in advance but is necessarily limited because the responses change nonlinearly during the course of growth, as growth slows down and eventually stops (Fitzhugh & Taylor, 1971; Blaxter, Fowler, & Gill, 1982; Filipe, Leinonen, & Kyriazakis, 2018). Thus, in forecasting growth, the confidence in a linear relationship is expected to decrease, as the forecast horizon increases, from e.g., one day to three or to seven days, and so on. Consequently, the key question concerns which nonlinear relationship should be used for longer forecasts. Currently, the answer to this question is unknown and is the main reason why we test several nonlinear deterministic relationships between the two traits of interest (i.e., feed consumption and BW), which are associated with the conversion of feed into biomass.

The quality of the variables' estimates and subsequent forecasts can be considerably impacted by the choice of the estimation method for fitting to the data, irrespective of the model used (Wagenmakers, Lee, Lodewyckx, & Iverson, 2008). The current precision feeding and management systems in pigs rely predominantly on maximum likelihood (Myung, 2003) to obtain estimates from the data. However, this methodology generates single point estimates and gives insufficient information about the uncertainty and correlations in the estimated variables (Babtie & Stumpf, 2017), which could mislead the decision-making process and could lead to a suboptimal formulation of feeds. Alternative estimation methods based on the Bayesian framework, which outputs distributions of possible values of the variables (Gelman et al., 2013), may yield more reliable point estimates and measures of uncertainty (Beerli, 2005; Filipe & Kyriazakis, 2019).

Considering the above limitations of the current approaches to the problem of forecasting individual pig growth and intake responses based on past performance, the objectives of this paper were to develop and evaluate quantitatively alternative approaches to this problem. We hypothesised that non-linear approaches would perform better than the current approaches, which assume linearity. These alternative approaches were selected with the following criteria in mind: (a) models should describe the relationship between feed consumption and consequent BW gain rather than the relationships of these traits to time; (b) fewer and interpretable model parameters are preferred; (c) estimation methods should give sufficient information on uncertainty and correlations in estimated variables. The results of this study were expected to enhance the understanding of how underlying biological growth responses of growing-finishing pigs could be approximated using straightforward mathematical relationships and could be used to deliver more optimised precision feeding and management strategies.

## 2. Materials and methods

There was no requirement for ethical approval, since the data originated from previous experiments, which were granted ethical approval on behalf of the original trial investigators.

### 2.1. Data

Empirical data, at age $t$ (d), on daily feed intake, $DFI_t$ (kg/d), and bodyweight, $BW_t$ (kg), of individual pigs from two distinct pig populations were obtained from two independent experiments conducted by: (1) INRAE at the UE3P unit (Pig Physiology and Phenotyping Experimental Facility, https://doi.org/10.15454/1.5573932732039927E12), Saint Gilles, France (Population A) and (2) Topigs Norsvin at their commercial testing facilities (Population B). Data from these two populations (Population A: $n = 32$ pigs; Population B: $n = 30$ pigs) covered the growth period from a typical post-nursery weight (approximately 35 kg) to a typical slaughter weight (approximately 110-120 kg). In each of the two experiments, pigs were kept in nearly commercial conditions (*ad-libitum* access to water, group housing, ambient room temperature of 20-24°C) and were offered two feeds successively, formulated to meet or exceed the expected population-average nutritional requirements prevailing at the time of the experiment (National Research Council, 1998). The change in feeds occurred when animals from each population reached approximately 65 kg. A detailed description of the experimental conditions utilised in the two aforementioned experimental trials could be found in Serviento, Brossard, and Renaudeau (2018) and Brossard et al. (2017). Descriptive statistics summarising both datasets are given in Table 1.

### 2.2. Model structure and candidate functions

To relate feed intake to $BW_t$ rather than to time (Whittemore & Green, 2001; Black, 2009), and to reflect the fact that the feed consumed over a period of time should relate to changes in $BW_t$ and other unobserved mass flows (that is, excretion of solids and fluids, water consumption, etc.) over the same period (Filipe, Piles, Rauw, & Kyriazakis, 2019), we focused on the relationship between the cumulative $BW_t$ gain and cumulative feed intake. For each animal we define period cumulative feed intake $(CFI_t)$:

$$CFI_t = \sum_{i=1}^{n(t)} DFI_{\tau(i)} \text{ (kg)} \tag{1}$$

and period cumulative $BW_t$ gain, $(CG_t)$:

$$CG_t = \sum_{i=1}^{n(t)} \left(BW_{\tau(i)} - BW_{\tau(i-1)}\right) = BW_t - BW_{t_0} \text{ (kg)}, \tag{2}$$

where $n(t)$ is the number of observations by time $t$, and $\tau(i), \left(i = 0,1,\dots,n(t)\right)$ are the specific ages, which we will call time points, when observations took place for a given animal; at $t_0 = \tau(0)$, BW was measured, but the feed consumption was not (note also that $\tau\left(n(t)\right) = t$).

For each animal, an animal-specific total number of observations, *N*, was collected at animal-specific successive time points $\tau(i)$. We denote the time point of the last observation in the dataset as $T = \tau(N) = \tau\left(n(T)\right)$. Most observations were daily, $dt = \tau(i+1) - \tau(i) = 1$ d, but in rare instances the lags were greater than one d. In addition to the biological motivation above, the use of cumulative data was intended to reduce the effects of longitudinal random variation on the estimation and to lead to a better identification of a suitable mathematical representation of the feed intake-BW gain relationship.

Next, we assumed that the relationship between $CG_t$ and $CFI_t$ has the general form:

$$CG_t = f(CFI_t, \boldsymbol{\theta}) + \epsilon_t, \tag{3}$$

where $f(CFI_t, \boldsymbol{\theta})$ is a trend function of $CFI_t$ that depends upon a vector of unknown parameters $\boldsymbol{\theta}$, and $\epsilon_t$ is an ‘error’, or ‘residual’ term representing random deviations from the deterministic temporal trend. These deviations could be due to e.g., changes in the environmental conditions, or health status, or measurement error. In the case of the DES model, the relationships are:

$$CG_t = g_1\left(t, \boldsymbol{\theta_{1,t}}\right) + \epsilon_{1,t} \text{ and } CFI_t = g_2\left(t, \boldsymbol{\theta_{2,t}}\right) + \epsilon_{2,t} \tag{4}$$

As is common practice, we chose the error term to be a stochastic process that assumes independence from one observation time to another, additivity to the trend and homoscedasticity; specifically, the error was assumed to be normally distributed, i.e.

$$\epsilon_t \sim N(0, \sigma^2), \tag{5}$$

with zero mean and constant variance, $\sigma^2$, with $\sigma^2$ estimated from the data. This simplified error term could be modified if there was *a priori* belief or evidence supporting alternative assumptions.

For the trend functions, we considered (Table 2) the linear model (Cangar, Aerts, Vranken, & Berckmans, 2006) and three candidate nonlinear models, namely: allometric (Filipe et al., 2019), monomolecular (Spillman, 1924; France, Dijkstra, & Dhanoa, 1996; Schulin-Zeuthen et al., 2008) and rational (Powell et al., 2017). These models were chosen to capture the concavity of the empirical growth response to feed intake within the observed data range. The following sets of functions were rejected and not considered further: (i) polynomials of degree greater than one, since their parameters would not be biologically meaningful (Yin, Goudriaan, Lantinga, Vos, & Spiertz, 2003); (ii) piecewise functions due to complexities associated with identification and interpretation of switch points (Bolker, 2008); (iii) S-shaped functions, since the relationship between cumulative BW gain and cumulative feed intake does not appear to follow a sigmoidal pattern during growth (Schulin-Zeuthen et al., 2008; Kuhi et al., 2010); (iv) functions that are not monotonically increasing, since under normal conditions feed consumption should lead to an overall increase in body size during the growth period.

## 2.3. Benchmark model: double exponential smoothing

Double exponential smoothing is typically expressed as an iterative process involving the observed variable and latent (unobserved) states (Hyndman, Koehler, Snyder, & Grose, 2002), which for $CG_t$ is:

$$CG_t = l_{t-1} + b_{t-1} + \epsilon_t \tag{6}$$

$$l_t = l_{t-1} + b_{t-1} + \phi_1 \epsilon_t \tag{7}$$

$$b_t = b_{t-1} + \phi_2 \epsilon_t \, , \tag{8}$$

where $l_t$ and $b_t$ are the level (i.e. the moving average values) and the change (i.e. either increasing or decreasing value) of the trend (Hyndman & Athanasopoulos, 2018) at time $t$, respectively, and were initialised as follows: $l_0 = CG_{t_0}$, $b_0 = CG_{t_1} - CG_{t_0}$ (Wheelwright, Makridakis, & Hyndman, 1998).

A similar process with its own specific parameters is assumed for $CFI_t$. Traditionally, $\epsilon_t$ is assumed to have the same distributional form as in equation (3). Note that the models in equations (4, 6-8) are specified with time as independent variable, as opposed to the generic model from equation (3) which is specified in relation to $CFI_t$.

## 2.4. Fitting models to the data

The model in equation (3) for each candidate trend function (Table 2) and the benchmark model (equations (4, 6-8) and section 2.3), were fitted to the data of individual animals from each of the two distinct pig populations (section 2.1); inferences were made on an individual basis (i.e. separately for each pig in each population as in Filipe and Kyriazakis (2019)).

To account for the uncertainty and correlations between the parameter estimates for each candidate model, we utilised a Bayesian inference approach, which outputs estimated distributions rather than point estimates of the parameters (Gelman et al., 2013). Sample parameter distributions were obtained using the Markov Chain Monte Carlo (MCMC) methods (Gamerman & Lopes, 2006) and more specifically the Metropolis-Hastings algorithm (Chib & Greenberg, 1995). The posterior inferences on parameters and forecasts were based on the MCMC samples generated using the MCMC engine *rjags* (Plummer, Stukalov, & Denwood, 2019). Prior distributions for the parameters are given in the Supplementary Material, together with a justification for their choice for each candidate model. Four independent MCMC parameter chains, each containing 100,000 samples and initialised with different random starting parameter values, were generated, from which the first ten percent samples were discarded as burn-in (Raftery & Lewis, 1996; Plummer, Best, Cowles, & Vines, 2006). Burn-in was applied to stabilise the sampling distribution and maximise the chances of reaching stationarity by reducing the influence of random starting values, which are required to initialise the algorithm. Posterior inference was carried out on the remaining 90,000 samples from each chain; no thinning was applied (Link & Eaton, 2012). Four MCMC chains, rather than one, were used as a way of assessing differences among the sampled parameter distributions and thus, was a first convergence diagnostic (Toft, Innocent, Gettinby, & Reid, 2007). The convergence of each sample chain was also assessed by investigating trace plots (after burn-in) for each model parameter and by calculating the potential scale reduction factor, $\hat{R}$ (Gelman & Rubin, 1992; Brooks & Gelman, 1998). Values of $\hat{R}$ greater than 1.01 were considered to indicate poor convergence (Vehtari, Gelman, Simpson, Carpenter, & Bürkner, 2020). The posterior distribution of sampled parameters used for inference comprised every chain that converged; when the four chains converged, it comprised $N_s$ = 4 x 90,000 = 360,000 sampled parameter values.

## 2.5. Goodness of fit and model comparison

To avoid ambiguity, we refer to a training dataset as past data that was utilised to estimate model parameters, while we refer to a validation dataset as subsequent data that was not utilised to estimate unknown model parameters (Armstrong, 2001). Consequently, fitting refers to the process of estimating unknown model parameters from a training dataset, while forecasting refers to the prediction of data in a validation dataset.

The accuracy of the models quantified in terms of fitting a training dataset (section 2.5.1) or in terms of forecasting tested on a validation dataset (section 2.5.2) are presented for every individual pig in each of the two populations. In addition, for illustration, fitted and forecasted growth responses are presented for four pigs selected from each of the two populations. The four pigs per population were selected such that their observed growth trajectories contained: (a) no perturbation; (b) an early perturbation; (c) a mid perturbation; or (d) a late perturbation during the observation period. A perturbation is defined here as a short-lived, but evident deviation from the previous trend in $CG_t$; these perturbations were identified among the individual pigs by detecting clusters of data points for which $CG_t > CG_{t+1}$ and calculating the magnitude of the downward deviation. Fitted and forecasted growth responses (in terms of the posterior medians and posterior ninety-five percent credible intervals (95% CrIs; the Bayesian equivalent of confidence intervals)) for the remaining pigs in each of the two populations are presented in the Supplementary Material.

### 2.5.1. Fitting evaluation

For each individual pig, we assessed the goodness of fit of the models to a training dataset, through a Bayesian coefficient of determination, $R^2_{Bayes}$ based on the variance of the errors of the fitted model (Gelman, Goodrich, Gabry, & Vehtari, 2019):

$$R^2_{Bayes} = \frac{Var_{i=1}^{N} \hat{Y}_{\tau(i)}}{Var_{i=1}^{N} \hat{Y}_{\tau(i)} + Var_{i=1}^{N} \left( Y_{\tau(i)} - \hat{Y}_{\tau(i)} \right)} \tag{9}$$

where $Y$ are the $N$ observations from the given animal and $\hat{Y}$ are the fitted model values corresponding to a single parameter point in the MCMC sample. The median of $R^2_{Bayes}$ over the $N_s$ parameter points in the MCMC sample was reported as the estimated goodness of fit statistic. For $R^2_{Bayes}$, values closer to one indicate a good fit to the data.

Model comparison was made on the Watanabe Bayesian extension of the usual Akaike Information Criterion ($WAIC$; (Watanabe, 2010, 2013)). $WAIC$ is given by the computed log pointwise posterior predictive density ($lppd$) plus an effective number of parameters ($efp$) to penalise overfitting (Gelman, Hwang, & Vehtari, 2014):

$$WAIC = -2(lppd - efp) \tag{10}$$

where the computed $lppd = \sum_{i=1}^{N} \log(\frac{1}{N_s}\sum_{s=1}^{N_s} \hat{Y}_{\tau(i)})$ and $efp = \sum_{i=1}^{N} Var_{s=1}^{N_s} \log(\hat{Y}_{\tau(i)})$.

To rank the models by the $WAIC$, the following procedure was followed: (1) for each pig, we ordered the $WAIC$ values of the five models (from lowest to highest since lower $WAIC$ indicates a better model); and (2) we counted how many times each model finished 1st, 2nd, …, 5th across all pigs.

### 2.5.2. Forecasting evaluation

Here, we adopt common forecasting terminology from Bergmeir and Benítez (2012). Let the origin ($T0$) be last time point in a training dataset, from which forecasts of future growth responses are generated. Let the forecast horizon ($H$) be the time window, ranging between the first ($T0 + dt$) and the last time point ($T$) in a validation dataset over which forecasts are made. We considered a typical dataset split (Hyndman, 2015) with the validation dataset consisting of the last 30 observations for each individual pig (approximately forty percent of all available data per pig). For most pigs all the lags between observations were one d and the maximum forecast horizon under consideration was $H_m = 30$ d. Model testing was carried out on forecast horizons ranging from one d and $H_m$; in total, thirty different forecast horizons were considered.

To quantify the forecast accuracy of each model in each forecast horizon, we calculated the Bayesian equivalent of the standard absolute percentage error, $MAPE_{Bayes}$, as an average of the model error over the posterior sample and over the data points in the forecast horizon:

$$MAPE_{Bayes} = \frac{1}{\mathrm{H}} \sum_{i\in[1,N]:\, T0<\tau(i)\leq T0+H} \frac{1}{N_S}\sum_{s=1}^{N_S} \left| \frac{Y_{\tau(\mathrm{i})} - \hat{Y}_{\tau(\mathrm{i})}(\boldsymbol{\theta}_S)}{Y_{\tau(\mathrm{i})}} \right| (\%) \tag{11}$$

where the notation is as in equation (9), but $\hat{Y}_{\tau(\mathrm{i})}$ are forecasts rather than fitted values, and the sum over time points $i$ is limited to the forecast horizon $H$ within the validation dataset; $\boldsymbol{\theta}_s$ are the MCMC sample parameters.

To rank the models forecast accuracy by the $MAPE_{Bayes}$ we followed the following procedure: (1) for each pig we ordered the $MAPE_{Bayes}$ values of the five models (from lowest to highest since values closer to zero indicate smaller predictive error) after averaging across the forecast horizons, $H = 1, \dots, 30$ d; and (2) we counted how many times across all pigs each model scored 1st, 2nd, …, 5th.

## 3. Results

### 3.1. Fitting evaluation

The goodness of fit of the models is quantified by the $R^2_{Bayes}$ and $WAIC$ in Figure 1 for every individual pig from the two populations and by the corresponding summary statistics in Table 3. Overall, the $R^2_{Bayes}$ values across individual pigs were high, ranging from 0.970 to 1.00 (Population A) and from 0.980 to 1.00 (Population B). These values suggest that all models fitted the data well. For each pig population, the $WAIC$ values resulted in the same fitting ranking of the models, which was, from the best fitting to the worst fitting (lowest to highest $WAIC$): (1) DES; (2) allometric; (3) rational; (4) monomolecular and (5) linear. Full, tabulated model rankings for each individual pig are given in the Supplementary Material. Note that the summary statistics of the $R^2_{Bayes}$ and $WAIC$ across pigs (Table 3) indicate less variation in the goodness of fit among models within Population B than within Population A.

Figure 2 focuses on how each model fitted growth responses to the four selected pigs per population, whose growth was subject to perturbations. For each population, all models fitted the four individual datasets well, but the following main differences were detected among pigs: (a) the linear model overestimated the growth responses for each of the four pigs per population – this overestimation was particularly apparent during the earlier and the later stages of the measurement period; and (ii) the linear model had considerably wider 95% CrIs than the other models for each of the four pigs per population (section 2.5). These differences were consistent across the two populations.

### 3.2. Forecasting evaluation

The accuracy of forecasts over forecast horizons $H$ ranging from one to thirty d, is quantified by the $MAPE_{Bayes}$ in Figure 3 for every individual pig from the two populations and by the corresponding summary statistics in Table 4. For every model, the overall forecast accuracy decreased with increasing forecast horizon, but this decrease was substantially greater for the linear and DES models (Table 4).

Across the full range of forecast horizons, the allometric model ranked as the most accurate in forecasting the overall growth responses for 28/32 pigs, while the forecasts generated using the monomolecular, rational and linear models ranked as the most accurate for 2/32, 1/32 and 1/32 pigs respectively (Population A: (Figure 3 A). Similar results were also obtained in the context of pigs within Population B (Figure 3 B), but there was more variability. Specifically, the allometric model ranked as the most accurate in forecasting the overall growth responses for 14/30 pigs across the full range of forecast horizons, while the forecasts generated using the monomolecular, rational and linear models ranked first for 9/30, 4/30 and 3/30 pigs respectively. Full, tabulated model rankings for each individual pig based on $MAPE_{Bayes}$ are given in the Supplementary Material.

Figure 4 visualises forecasted growth responses over forecast horizons $H$ ranging from one to thirty d for the selected four pigs per population, whose growth was subject to perturbations (section 2.5). For the pigs within Population A, the following differences in model forecasts across the full range of forecast horizons were identified: (1) no perturbation (Figure 4 A, panel I): the allometric and DES models generated adequate forecasts of the growth trajectory in terms of the median forecast. However, the DES model had considerably wider 95% CrIs, indicating greater uncertainty about the generated forecasts. Forecasts from the monomolecular and rational models were markedly similar and resulted in notable underestimation of the growth response; (2) an early perturbation (Figure 4 A, panel II): forecasts from all five models overestimated the growth response; (3) a mid perturbation (Figure 4 A, panel III): the allometric model generated the most accurate forecasts of the growth response. Forecasts from the linear model considerably overestimated the growth response, while forecasts from the remaining three models (monomolecular, rational and DES) underestimated the trend; (4) a late perturbation (Figure 4 A, panel IV): forecasts of the growth response from the allometric model were the most accurate. Forecasts from the linear and DES models both overestimated the growth trajectory. Contrastingly, forecasts generated using the monomolecular and rational models underestimated the trend.

For the pigs within Population B, the following differences in model forecasts across the full range of forecast horizons were identified: (5) no perturbation (Figure 4, panel V): forecasts using the allometric, monomolecular and rational models were comparable and were more accurate than forecasts from the DES model which underestimated the growth response and forecasts from the linear model which overestimated the growth response; (6) an early perturbation (Figure 4, panel VI): all five models under consideration generated similar forecasts of the growth response, but the DES model again had considerably wider 95% CrIs compared to other models; (7) a mid perturbation (Figure 4, panel VII): forecasts from the linear model considerably overestimated the growth response, while forecasts from the DES model underestimated the growth response. Forecasts from the three nonlinear models (allometric, monomolecular and rational) were more accurate than the linear forecasts; and (8) a late perturbation (Figure 4, panel VIII): nonlinear forecasts from the allometric, monomolecular and rational models were more accurate than forecasts generated using the linear models. Forecasts from the DES model underestimated the growth response, while forecasts from the linear model overestimated the trend.

## 4. Discussion

The main contributions of this study in the context of precision feeding and management of pigs are twofold: (i) to comprehensively evaluate the existing models and the alternative nonlinear models based on straightforward mathematical relationships that approximate the underlying growth trend; and (ii) to implement an alternative, more informative framework for parameter estimation that is expected to generate more robust forecasts for any chosen model. We used two datasets to apply our methodology to address whether similar conclusions could be drawn from pig populations that differed substantially, especially in their growth and feed conversion efficiency characteristics.

### 4.1. Criteria for model selection: ability to fit vs ability to forecast

On the basis of our statistical analysis of individual feed consumption and BW data from growing-finishing pigs, we identified clear differences in the overall classification of models. These differences depended on whether model accuracy was measured in terms of fitting or forecasting. Specifically, our findings suggest that a good fit to a training dataset does not necessarily translate into accurate forecasts of individual growth responses in a validation dataset. Accordingly, while all models under consideration seemed to fit the observed data well, the nonlinear models generated markedly more accurate forecasts of growth responses than the linear models across all forecast horizons. For every model, the overall forecast accuracy decreased with increasing forecast horizon, but this decrease was substantially greater for the linear models.

There are two key implications associated with the aforementioned findings. Firstly, testing the extrapolative ability of models based solely on their goodness of fit could be misleading. While this lack of connection between quality of the fitting and quality of the forecasting is not unusual and has been documented in the wider forecasting literature, particularly in economics (Meese & Rogoff, 1983; Inoue & Kilian, 2005; Silvey, 2007; Rossi, 2013), it has not been previously raised in animal science. Overconfidence in fitting is typically associated with overfitting short-term dynamics and does not guarantee capturing of the underlying mechanisms generating the data (Clark, 2004), which is essential in forecasting a trend. Secondly, care should be taken when models are compared within- and across- studies based on differing evaluation criteria, as different metrics could often lead to conflicting inferences and conclusions.

### 4.2. Forecasting ability of the considered models

Our data-based results indicated that there were considerable disparities between models in their ability to forecast individual growth responses, with the nonlinear models generating more accurate forecasts compared to the linear approaches for all forecast horizons ranging from one to thirty d (Figure 3). The lower level of forecast accuracy of the linear models compared to the nonlinear models was more pronounced for longer-term forecast horizons, with modest variation among pigs. Our study demonstrates that it may be quantitatively acceptable to use these linear response models in the context of (very) short forecast horizons, such as one or two d, which are more frequently utilised in precision feeding because the magnitude of the error is constrained. However, our study also demonstrates that alternative models are also available without invaliding the former approaches for short-term forecasting but allowing for more accuracy and greater reliability for short-term, as well as long-term forecasting. These findings highlight the necessity to implement nonlinear forecasting approaches, particularly in the context of precision management strategies, which could include scheduling processes associated with the purchase of raw feed ingredients, pen allocation and transportation or slaughter of animals through end-BW prediction. The more sustained accuracy of the nonlinear models offers potential multipurpose capacity for both precision feeding and management purposes, and could also improve their application, as it would reduce the need for different models in an eventual decision support tool where different forecast horizons are considered.

While the linear model relating cumulative feed intake to cumulative BW gain model overestimated growth trends of most pigs, the other linear approach, DES, which predicts growth responses solely as a weighted moving average over time (Holt, 1957; Brown, 1959) displayed a less systematic inaccuracy, with notable trend deviations in both directions (up or down). Furthermore, when longer forecast horizons, such as ones exceeding one week were considered, the DES model typically generated forecasts with very large uncertainty intervals (Figure 4), which were low in information, and in biological plausibility (predicting either excessively large gains or excessively large losses). The concurrence of an excellent fitting and a comparatively poor forecast accuracy indicates that this model can overfit the data by extracting excessive amounts of noise, at the cost of reducing its ability to forecast the future trend. This inherent construction of DES that trades-off short-term flexibility for long-term unreliability could potentially limit its usefulness in the context of precision feeding and management. Thus, while DES have been reported to produce satisfactory accuracy for one d forecasts in experimental assessments of the proposed precision feeding strategies (Andretta et al., 2014; Andretta et al., 2016), caution should be exercised when using this model in scenarios where forecast horizons exceed one d.

To express cumulative BW gains as a function of cumulative feed intake, rather than time (Whittemore & Green, 2001; Black, 2009), as it is the case in the DES model, and to overcome limitations of the linear model, we developed alternative nonlinear models relating these two traits. The accuracy of forecasts of the monomolecular and rational models was often very similar and almost indistinguishable for many individual animals from the two populations. Both models typically underestimated growth responses for most pigs. While the use of the monomolecular model to relate feed intake to BW is relatively common in monogastric livestock research (Spillman, 1924; France et al., 1996; Schulin-Zeuthen et al., 2008; Kuhi et al., 2010), the use of the rational model is less so (Powell et al., 2017). However, these two models are mathematically similar being bounded by an asymptote, which is the BW at maturity. As commercial growing-finishing pigs do not approach their mature size, which have been reported to be up to three-four times larger than the typical size at slaughter (Strathe, Danfær, Sørensen, & Kebreab, 2010), the asymptotic feature of these two models may not be necessary (van Milgen et al., 2008; Filipe, Leinonen, et al., 2018). Particular concerns relate to considerable technical challenges and uncertainty in the estimation of the asymptote from the usually available data and a general ambivalence on whether these models can adequately approximate growth responses prior to the point of fastest growth (Filipe et al., 2019). Thus, forecasts of growth responses obtained using these models may not be optimal, although they were more accurate than those obtained using the two aforementioned linear models.

Furthermore, on the basis of our statistical analyses, the allometric cumulative feed intake-cumulative BW gain model generated the most accurate forecasts of the growth responses for most pigs in the two populations. While the exact knowledge of the data-generating process could be questioned (Brooks, Gelman, Jones, & Meng, 2011), the allometric model seemed to reliably approximate the underlying trend of the available data, which is consistent with the hypothesis and demonstration of the allometric relationship across multiple species in Filipe et al. (2019). Thus, this model seems to offer a relatively straightforward and reliable way of forecasting individual growth responses both in the short-term and long-term.

### 4.3. Forecasting ability under growth perturbations

Our findings demonstrated that the timing of a perceived short-lived growth perturbation, caused e.g. by infrequent, temporary physiological and/or environmental disturbances (Kyriazakis, 1997; Kyriazakis & Tolkamp, 2011) could impact the ability to reliably forecast individual growth responses in different ways. Based solely on a subset of illustrative animals, whose growth trajectories were examined because they were perturbed, we found the following: when a single, short-lived growth perturbation occurred early in the training dataset (and away from the time point of the last known value, from which the forecasts were performed), all considered models were largely able to cope with this unexpected deviation from the trend. Contrastingly, when a perceived single, short-lived growth perturbation occurred late in the training dataset (and near the time point of the last known value, from which the forecasts were performed), the forecast accuracy of all models was reduced, but to different extents. Specifically, the DES model generated the least reliable forecasts leading to a marked underestimation of growth responses, probably related to the fact that this approach mainly relies on the most recent past observations to inform the trend forecasts, which can be unduly influenced by perturbations. While it is possible to give more weight to older observations in the DES model (Young, 2012) to negate, at least partly, the possible adverse effects of short-term perturbations on the estimation (Hauschild et al., 2012), this typically requires manual adjustment of the unknown tuning parameters.. Thus, the DES model and other extensions of the exponential smoothing methods (Hyndman et al., 2002), as well as models from a closely related family of autoregressions and moving averages, commonly referred as ARIMAs (Shumway & Stoffer, 2017), should be used with caution for precision feeding and management since they can be unduly influenced by single, short-lived growth disturbances occurring near the forecast horizon.

The examined approaches were shown to cope with relatively short-lived (or with constant level, diet driven) growth perturbations, but as they stand, are not specifically designed to forecast under considerable growth retardation and subsequent compensation, which could be observed in pigs kept in suboptimal conditions facing multiple physiological, infectious or environmental challenges (Sandberg, Emmans, & Kyriazakis, 2006; Kyriazakis & Houdijk, 2007). Recently, an approach to quantify individual feed intake responses of growing pigs to such perturbations was developed by Nguyen-Ba, van Milgen, and Taghipoor (2019), but this research area still warrants further attention.

### 4.4. Bayesian methodology in the context of precision feeding and management

To our knowledge, precision feeding and management strategies in pigs have not yet fully utilised Bayesian estimation methods for fitting and forecasting. Traditionally, the estimation of parameters from data in this area is carried out using maximum likelihood (Myung, 2003). However, an estimation framework constructed on Bayesian principles may offer important advantages, including: (i) Bayesian point estimates based on the median values of posterior distributions are generally more robust than modal point estimates, such as those generated by maximum likelihood (Beerli, 2005; Filipe & Kyriazakis, 2019); (ii) Bayesian probabilistic outputs translate into robust uncertainty statistics that inform on the reliability of the predictions for decision making; this uncertainty is due to the data and potential adequacy of the model in capturing the underlying processes (Bijak, 2010; Bijak & Bryant, 2016); (iii) Bayesian methodology, through the usage of the MCMC algorithms (Dunson, 2001) is particularly suitable for data which is sparse or incomplete, which may be relevant in cases where there are minor malfunctions of the data collection devices or where there are issues obtaining regular measurements from some animals. These aforementioned aspects of

Bayesian estimation methods make them particularly suitable for precision feeding and management purposes, as they could provide more accurate forecasts of growth responses and could lead to a more robust estimation of the expected nutrient requirements, while also informing on their reliability through uncertainty statistics. Thus, an implementation of these Bayesian principles could further optimise precision feeding and management strategies.

## 5. Implications and future research

We provided an in-depth comparison of alternative approaches to forecasting individual growth or intake responses that could be utilised in the context of precision feeding and management of growing-finishing pigs. It is likely that our approach may be of relevance to other livestock species where precision feeding and management could be applied (González, Kyriazakis, & Tedeschi, 2018). Specifically, the methods described in this paper could be particularly relevant in the context of optimising feed efficiency and could contribute towards increasing profitability of commercial farming operations. These methods could also be useful for preventing obesity in companion and captive animals. It is also likely that the developed approaches could be useful in the context of genetic selection (Knol, Nielsen, & Knap, 2016). For example, Filipe et al. (2019) suggested that the variation in the parameters of the allometric model is likely to be (at least partially) of genetic origin  and could potentially be heritable.

Overall, the utilisation of Bayesian methods for estimation, particularly in the context of nonlinear forecasting of individual pig performances has the potential to overcome some of the limitations of the current approaches implementing linear forecasting functions. However, further extensions to our Bayesian approach developed in this study are possible and could be the subject of the future research. First, the final estimated population-level distribution of individual traits was not fully Bayesian, as it was based on point (median) estimates from the individual posterior distributions. As such, these estimates did not contain uncertainty about the median, but are expected to be more accurate than point estimates based on maximum likelihood (Filipe and Kyriazakis 2019). This approach was used for simplicity, but a full Bayesian approach would account fully for uncertainty in the pig phenotypes. In the context of our paper this was appropriate given the relative uniformity of the pig populations. Second, instead of relying on forecasts generated from a single model, Bayesian model averaging (Eklund & Karlsson, 2007) to obtain forecast combinations of multiple models (Winkler & Makridakis, 1983) could be applied. Such forecast combinations have been reported to outperform other types of forecasts from single models (Barrow & Kourentzes, 2016; Makridakis, Spiliotis, & Assimakopoulos, 2018).

An alternative framework for forecasting individual growth responses to nutrient supplies could be based on machine learning algorithms, such as neural networks (Kotsiantis, Zaharakis, & Pintelas, 2006; Dey, 2016). Such methods have been previously utilised in the context of growth control and prediction of groups of broiler chickens (Demmers et al., 2018; Johansen, Bendtsen, Jensen, & Mogensen, 2019), but their application in precision feeding systems of individual pigs has been so far limited (Brossard et al., 2017).

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| Sample size | Breed | Sex | Initial average BW (kg) | Final average BW (kg) | Trial length (d) | ADFI (kg/d) | ADG (kg/d) |
|---|---|---|---|---|---|---|---|
| **Population A** | | | | | | | |
| 32 | (LW x L) x P | Barrows and gilts | 35.2 (4.70) | 118 (9.87) | 81 (-) | 2.80 (0.275) | 1.03 (0.0911) |
| **Population B** | | | | | | | |
| 30 | Non-commercial | Boars | 32.9 (0.574) | 109 (4.49) | 74 (9) | 1.91 (0.239) | 1.04 (0.0967) |

**Table 1**. Descriptive statistics (mean (SD)) of experimental data collected on growing-finishing pigs from two distinct populations. Dataset A corresponds to a trial by the INRAE at the UE3P unit (Pig Physiology and Phenotyping Experimental Facility, https://doi.org/10.15454/1.5573932732039927E12), Saint Gilles, France. Dataset B corresponds to a trial by Topigs Norsvin at their commercial facilities.

Abbreviations: LW, Large White; L, Landrace; P, Pietrain; BW, bodyweight; ADFI, average daily feed intake; ADG, average daily gain; d, days

| Function name | Equation | Parameter description |
|---|---|---|
| Allometric | $CG_t = \theta_1 CFI_t^{\theta_2} + \theta_3$ | $\theta_1 -$ proportionality parameter associated with feed conversion (Filipe et al., 2019)<br>$\theta_2 -$ exponent varying shape of the curve (Filipe et al., 2019)<br>$\theta_3 -$ vertical shift operator (*y*-axis intercept) accounting for the cumulative measurement bias |
| Linear | $CG_t = \theta_1 CFI_t + \theta_3$ | $\theta_1 -$ proportionality parameter associated with feed conversion ratio (slope of the line) (Cangar et al., 2006)<br>$\theta_3 -$ vertical shift operator (*y*-axis intercept) accounting for the cumulative measurement bias |
| Monomolecular | $CG_t = \theta_2 \left(1 - e^{\frac{CFI_t}{\theta_1}}\right) + \theta_3$ | $\theta_1 -$ rate of approach to the asymptote (Spillman, 1924; France et al., 1996; Schulin-Zeuthen et al., 2008)<br>$\theta_2 -$ the upper asymptote corresponding to the size at maturity (Spillman, 1924; France et al., 1996; Schulin-Zeuthen et al., 2008)<br>$\theta_3 -$ vertical shift operator (*y*-axis intercept) accounting for the cumulative measurement bias |
| Rational | $CG_t = \dfrac{\theta_2 CFI_t}{1 + \dfrac{CFI_t}{\theta_1}} + \theta_3$ | $\theta_1 -$ *x*-axis scaling<br>$\theta_2 -$ *y*-axis scaling<br>$\theta_1\theta_2 -$ product of parameters corresponding to the size at maturity<br>$\theta_3 -$ vertical shift operator (*y*-axis intercept) accounting for the cumulative measurement bias |

**Table 2**. Selected models relating cumulative feed intake (kg) to cumulative bodyweight gain (kg)

Abbreviations: $CG_t$, cumulative bodyweight gain (kg); $CFI_t$, cumulative feed intake (kg)

|  | **Population A** |  | **Population B** |  |
|---|---|---|---|---|
| **Model** | $R^2_{Bayes}$ | $WAIC$ | $R^2_{Bayes}$ | $WAIC$ |
| Allometric | 0.998<br>(0.00112) | 166<br>(64.6) | 0.998<br>(0.00110) | 143<br>(49.3) |
| Monomolecular | 0.998<br>(0.00108) | 191<br>(39.2) | 0.998<br>(0.000600) | 143<br>(39.7) |
| Rational | 0.998<br>(0.00107) | 189<br>(40.9) | 0.998<br>(0.000600) | 143<br>(37.8) |
| Linear | 0.990<br>(0.0072) | 323<br>(68.8) | 0.995<br>(0.00250) | 218<br>(36.9) |
| DES | 1.00<br>(0.0002) | 103<br>(52.7) | 1.00<br>(0.000275) | 89.6<br>(26.6) |

**Table 3**. Fitting evaluation of candidate models relating cumulative feed intake (kg) or time (d) to cumulative bodyweight gain (kg): median (IQR) of the calculated $R^2_{Bayes}$ and $WAIC$ for each model. Each model was fitted separately to each training dataset of each individual pig (Population A: $n = 32$ pigs; Population B: $n = 30$ pigs). For $R^2_{Bayes}$, values closer to one indicate that the model provides good fit to the data. For $WAIC$, lower $WAIC$ indicates a model that fits better and is more parsimonious. For description of the dataset see Table 1. Abbreviations: $R^2_{Bayes}$, Bayesian coefficient of determination; $WAIC$, Watanabe extension of the Akaike Information Criterion; DES, double exponential smoothing; d, days

| | $MAPE_{Bayes}$ (%) | | | | |
|---|---|---|---|---|---|
| **Model** | **H = 1** | **H = 5** | **H = 10** | **H = 20** | **H = 30** |
| **Population A** | | | | | |
| Allometric | 1.01 (0.526) | 1.28 (0.855) | 1.82 (1.75) | 1.89 (1.79) | 2.07 (3.25) |
| Monomolecular | 1.16 (0.631) | 1.51 (1.36) | 3.72 (2.49) | 5.09 (3.69) | 7.87 (4.17) |
| Rational | 1.22 (1.07) | 1.61 (1.55) | 3.83 (2.25) | 4.66 (4.43) | 6.64 (4.14) |
| Linear | 3.83 (1.52) | 4.51 (2.34) | 4.86 (3.25) | 8.35 (3.96) | 11.0 (5.81) |
| DES | 1.47 (1.04) | 4.69 (1.64) | 9.29 (3.00) | 20.2 (5.59) | 31.3 (9.39) |
| **Population B** | | | | | |
| Allometric | 1.30 (0.853) | 1.84 (1.22) | 1.77 (1.49) | 2.38 (2.83) | 2.98 (3.72) |
| Monomolecular | 1.33 (1.16) | 1.95 (1.77) | 1.77 (2.72) | 2.86 (3.79) | 4.66 (5.51) |
| Rational | 1.38 (0.898) | 2.07 (2.02) | 1.93 (2.34) | 3.56 (3.55) | 4.77 (5.86) |
| Linear | 1.69 (1.13) | 2.13 (2.62) | 3.04 (2.18) | 5.35 (2.81) | 6.87 (4.53) |
| DES | 1.90 (1.42) | 6.44 (2.94) | 12.4 (5.83) | 24.9 (10.1) | 36.4 (15.0) |

**Table 4.** Forecasting evaluation of candidate models relating cumulative feed intake (kg) or time (d) to cumulative bodyweight gain (kg): median (IQR) of the calculated $MAPE_{Bayes}$ (%) for each model. Each model was fitted separately to each training dataset of each individual pig (Population A: $n = 32$ pigs; Population B: $n = 30$ pigs), followed by trend forecasts tested on each validation dataset of each individual pig. Forecasts were generated over forecast horizons $H$ ranging from 1 to 30 d. For $MAPE_{Bayes}$, percentage values closer to zero indicate smaller predictive error.

Abbreviations: $MAPE_{Bayes}$, Bayesian equivalent of the percentage error, characterised in terms of its median value; H, time window for which forecasts are made (for most pigs all lags between observations were 1 d, therefore H corresponds to number of d ahead for which forecasts are made); DES, double exponential smoothing; d, days

**Figure 1.** Fitting evaluation of candidate models relating cumulative feed intake (kg) or time (d) to cumulative bodyweight gain (kg): goodness of fit and comparison of models in terms of the (I) individual $R^2_{Bayes}$ values for the Population A pigs; (II) individual $R^2_{Bayes}$ values for the Population B pigs; (III) individual $WAIC$ values for the Population A pigs; (IV) individual $WAIC$ values for the Population B pigs. Each model was fitted separately to each training dataset of each individual pig (Population A: $n = 32$ pigs; Population B: $n = 30$ pigs). For $R^2_{Bayes}$, values closer to one indicate that the model provides good fit to the data. For $WAIC$, lower $WAIC$ indicates a model that fits better and is more parsimonious. Abbreviations: $R^2_{Bayes}$, Bayesian coefficient of determination; $WAIC$, Watanabe extension of the Akaike Information Criterion; d, days

**Figure 2.** Fitting evaluation of candidate models relating cumulative feed intake (kg) or time (d) to cumulative bodyweight gain (kg): fitted growth responses, in terms of cumulative bodyweight gain (kg) of the selected pigs, whose growth trajectories were assessed to contain: (A) for Population A (I) no-perturbation, (II) an early-perturbation, (III) a mid-perturbation, (IV) a late-perturbation, and (B) for Population B (V) no-perturbation, (VI) an early-perturbation, (VII) a mid-perturbation, (VIII) a late-perturbation. Perturbations were identified among the individual pigs by detecting clusters of data points for which $CG_t > CG_{t+1}$ and calculating the magnitude of the downward deviation. Each model was fitted separately to each training dataset of each individual pig. Posterior model fit is summarised by median $\pm$ 95% CrIs.

Abbreviations: $CG_t$, cumulative bodyweight gain at time $t$; 95% CrIs, 95% credible intervals; Monom, monomolecular; DES, double exponential smoothing; d, days

**Figure 3.** Forecasting evaluation of candidate models relating cumulative feed intake (kg) or time (d) to cumulative bodyweight gain (kg): the accuracy of cumulative bodyweight gain forecasts over forecast horizons $H$ ranging from 1 to 30 d, presented as $100 - MAPE_{Bayes}$ (%). Each model was fitted separately to each training dataset of each individual pig (Population A: $n = 32$ pigs; Population B: $n = 30$ pigs), followed by trend forecasts tested on each validation dataset of each individual pig. Large $100 - MAPE_{Bayes}$ values indicate better forecast accuracy relative to smaller values.

Abbreviations: $MAPE_{Bayes}$, Bayesian equivalent of the percentage error, characterised in terms of its median value; d, days

**Figure 4.** Forecasting evaluation of candidate models relating cumulative feed intake (kg) or time (d) to cumulative bodyweight gain (kg): fitted and forecasted growth responses, in terms of cumulative bodyweight gain (kg), of the selected pigs, whose growth trajectories were assessed to contain: (A) for Population A (I) no-perturbation, (II) an early-perturbation, (III) a mid-perturbation, (IV) la ate-perturbation, and (B) for Population B (V) no-perturbation, (VI) an early-perturbation, (VII) a mid-perturbation, (VIII) a late-perturbation. Perturbations were identified among the individual pigs by detecting clusters of data points for which $CG_t > CG_{t+1}$ and calculating the magnitude of the downward deviation. Each model was fitted separately to each training dataset of each individual pig, followed by trend forecasts tested on each validation dataset of each individual pig. Forecasts were generated over forecast horizons ranging from 1 to 30 d. Vertical dotted lines mark the forecast origin. Posterior model fit is given in terms of median $\pm$ 95% CrIs.

Abbreviations: $CG_t$, cumulative bodyweight gain at time $t$; 95% CrIs, 95% credible intervals; Monom, monomolecular; DES, double exponential smoothing; d, days

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