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# 1 **Bayesian comparison of models for precision feeding and management in** 2 **growing-finishing pigs**

3

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12

13

## 14 **Abstract**

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

33 strategies and inform management decisions, including pen allocation or end-weight  
34 prediction.

35

36 Keywords: Precision feeding; Forecasting; Bayesian modelling

37 **1. Introduction**

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

45

46 The implementation of precision feeding and management strategies typically require  
47 mathematical models to forecast performance of individual animals from past data. Successful  
48 forecasting of individual growth or feed intake responses in the context of precision feeding  
49 and management is conditional on: (1) how well the mathematical model approximates the  
50 underlying biological process; (2) how accurately the parameter values of the model can be  
51 estimated from the information on past performance of the animals; and (3) whether the  
52 estimates are accompanied by a quantification of uncertainty to inform the extent to which they  
53 can be relied upon. While previous precision feeding and management studies in pigs  
54 (Hauschild, Lovatto, Pomar, & Pomar, 2012; Brossard, Taoussi, Van Milgen, & Dourmad,  
55 2017; Quiniou, Brossard, & Marcon, 2017; Peña Fernández et al., 2019) often provide  
56 assessments of different forecasting approaches, the aforementioned three conditions are rarely  
57 taken into full consideration, which may limit the conclusions about the applicability of these  
58 approaches. Here, we compare the most frequently utilised approaches in the literature with  
59 alternatives aimed at addressing some of the identified main limitations.

60

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

71 Van Buggenhout, Aerts, Vranken, & Berckmans, 2004; Schulin-Zeuthen et al., 2008; Demmers  
72 et al., 2018). Most responses can be approximated by a linear relationship within a short-term  
73 window and this is the implicit basis on which linear models are then applied. The length of  
74 this window is often unknown in advance but is necessarily limited because the responses  
75 change nonlinearly during the course of growth, as growth slows down and eventually stops  
76 (Fitzhugh & Taylor, 1971; Blaxter, Fowler, & Gill, 1982; Filipe, Leinonen, & Kyriazakis,  
77 2018). Thus, in forecasting growth, the confidence in a linear relationship is expected to  
78 decrease, as the forecast horizon increases, from e.g., one day to three or to seven days, and so  
79 on. Consequently, the key question concerns which nonlinear relationship should be used for  
80 longer forecasts. Currently, the answer to this question is unknown and is the main reason why  
81 we test several nonlinear deterministic relationships between the two traits of interest (i.e., feed  
82 consumption and BW), which are associated with the conversion of feed into biomass.

83

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

95

96 Considering the above limitations of the current approaches to the problem of forecasting  
97 individual pig growth and intake responses based on past performance, the objectives of this  
98 paper were to develop and evaluate quantitatively alternative approaches to this problem. We  
99 hypothesised that non-linear approaches would perform better than the current approaches,  
100 which assume linearity. These alternative approaches were selected with the following criteria  
101 in mind: (a) models should describe the relationship between feed consumption and consequent  
102 BW gain rather than the relationships of these traits to time; (b) fewer and interpretable model  
103 parameters are preferred; (c) estimation methods should give sufficient information on  
104 uncertainty and correlations in estimated variables. The results of this study were expected to

105 enhance the understanding of how underlying biological growth responses of growing-  
106 finishing pigs could be approximated using straightforward mathematical relationships and  
107 could be used to deliver more optimised precision feeding and management strategies.

108

## 109 **2. Materials and methods**

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

112

### 113 **2.1. Data**

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

130

### 131 **2.2. Model structure and candidate functions**

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

138 
$$CFI_t = \sum_{i=1}^{n(t)} DFI_{\tau(i)} \text{ (kg)} \quad (1)$$

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

140 
$$CG_t = \sum_{i=1}^{n(t)} (BW_{\tau(i)} - BW_{\tau(i-1)}) = BW_t - BW_{t_0} \text{ (kg)}, \quad (2)$$

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

145

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

153

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

155 
$$CG_t = f(CFI_t, \boldsymbol{\theta}) + \epsilon_t, \quad (3)$$

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

161 
$$CG_t = g_1(t, \boldsymbol{\theta}_{1,t}) + \epsilon_{1,t} \text{ and } CFI_t = g_2(t, \boldsymbol{\theta}_{2,t}) + \epsilon_{2,t} \quad (4)$$

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

165 
$$\epsilon_t \sim N(0, \sigma^2), \quad (5)$$

166 with zero mean and constant variance,  $\sigma^2$ , with  $\sigma^2$  estimated from the data. This simplified

167 error term could be modified if there was *a priori* belief or evidence supporting alternative  
168 assumptions.

169

170 For the trend functions, we considered (Table 2) the linear model (Cangar, Aerts, Vranken, &  
171 Berckmans, 2006) and three candidate nonlinear models, namely: allometric (Filipe et al.,  
172 2019), monomolecular (Spillman, 1924; France, Dijkstra, & Dhanoa, 1996; Schulin-Zeuthen  
173 et al., 2008) and rational (Powell et al., 2017). These models were chosen to capture the  
174 concavity of the empirical growth response to feed intake within the observed data range. The  
175 following sets of functions were rejected and not considered further: (i) polynomials of  
176 degree greater than one, since their parameters would not be biologically meaningful (Yin,  
177 Goudriaan, Lantinga, Vos, & Spiertz, 2003); (ii) piecewise functions due to complexities  
178 associated with identification and interpretation of switch points (Bolker, 2008); (iii) S-  
179 shaped functions, since the relationship between cumulative BW gain and cumulative feed  
180 intake does not appear to follow a sigmoidal pattern during growth (Schulin-Zeuthen et al.,  
181 2008; Kuhi et al., 2010); (iv) functions that are not monotonically increasing, since under  
182 normal conditions feed consumption should lead to an overall increase in body size during  
183 the growth period.

184

### 185 **2.3. Benchmark model: double exponential smoothing**

186 Double exponential smoothing is typically expressed as an iterative process involving the  
187 observed variable and latent (unobserved) states (Hyndman, Koehler, Snyder, & Grose,  
188 2002), which for  $CG_t$  is:

$$189 \quad CG_t = l_{t-1} + b_{t-1} + \epsilon_t \quad (6)$$

$$190 \quad l_t = l_{t-1} + b_{t-1} + \phi_1 \epsilon_t \quad (7)$$

$$191 \quad b_t = b_{t-1} + \phi_2 \epsilon_t, \quad (8)$$

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

196

197 A similar process with its own specific parameters is assumed for  $CFI_t$ . Traditionally,  $\epsilon_t$  is  
198 assumed to have the same distributional form as in equation (3). Note that the models in



199 equations (4, 6-8) are specified with time as independent variable, as opposed to the generic  
200 model from equation (3) which is specified in relation to  $CFI_t$ .

201

#### 202 **2.4. Fitting models to the data**

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

207

208 To account for the uncertainty and correlations between the parameter estimates for each  
209 candidate model, we utilised a Bayesian inference approach, which outputs estimated  
210 distributions rather than point estimates of the parameters (Gelman et al., 2013). Sample  
211 parameter distributions were obtained using the Markov Chain Monte Carlo (MCMC) methods  
212 (Gamerman & Lopes, 2006) and more specifically the Metropolis-Hastings algorithm (Chib &  
213 Greenberg, 1995). The posterior inferences on parameters and forecasts were based on the  
214 MCMC samples generated using the MCMC engine *rjags* (Plummer, Stukalov, & Denwood,  
215 2019). Prior distributions for the parameters are given in the Supplementary Material, together  
216 with a justification for their choice for each candidate model. Four independent MCMC  
217 parameter chains, each containing 100,000 samples and initialised with different random  
218 starting parameter values, were generated, from which the first ten percent samples were  
219 discarded as burn-in (Raftery & Lewis, 1996; Plummer, Best, Cowles, & Vines, 2006). Burn-  
220 in was applied to stabilise the sampling distribution and maximise the chances of reaching  
221 stationarity by reducing the influence of random starting values, which are required to initialise  
222 the algorithm. Posterior inference was carried out on the remaining 90,000 samples from each  
223 chain; no thinning was applied (Link & Eaton, 2012). Four MCMC chains, rather than one,  
224 were used as a way of assessing differences among the sampled parameter distributions and  
225 thus, was a first convergence diagnostic (Toft, Innocent, Gettinby, & Reid, 2007). The  
226 convergence of each sample chain was also assessed by investigating trace plots (after burn-  
227 in) for each model parameter and by calculating the potential scale reduction factor,  $\hat{R}$  (Gelman  
228 & Rubin, 1992; Brooks & Gelman, 1998). Values of  $\hat{R}$  greater than 1.01 were considered to  
229 indicate poor convergence (Vehtari, Gelman, Simpson, Carpenter, & Bürkner, 2020). The  
230 posterior distribution of sampled parameters used for inference comprised every chain that

231 converged; when the four chains converged, it comprised  $N_s = 4 \times 90,000 = 360,000$  sampled  
232 parameter values.

233

## 234 **2.5. Goodness of fit and model comparison**

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

240

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

254

### 255 **2.5.1. Fitting evaluation**

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

$$259 \quad R_{Bayes}^2 = \frac{Var_{i=1}^N \hat{Y}_{\tau(i)}}{Var_{i=1}^N \hat{Y}_{\tau(i)} + Var_{i=1}^N (Y_{\tau(i)} - \hat{Y}_{\tau(i)})} \quad (9)$$

260 where  $Y$  are the  $N$  observations from the given animal and  $\hat{Y}$  are the fitted model values  
261 corresponding to a single parameter point in the MCMC sample. The median of  $R_{Bayes}^2$  over

262 the  $N_s$  parameter points in the MCMC sample was reported as the estimated goodness of fit  
 263 statistic. For  $R_{Bayes}^2$ , values closer to one indicate a good fit to the data.

264

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

$$269 \quad WAIC = -2(lppd - efp) \quad (10)$$

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

271

272 To rank the models by the *WAIC*, the following procedure was followed: (1) for each pig, we  
 273 ordered the *WAIC* values of the five models (from lowest to highest since lower *WAIC*  
 274 indicates a better model); and (2) we counted how many times each model finished 1<sup>st</sup>, 2<sup>nd</sup>, ...,  
 275 5<sup>th</sup> across all pigs.

276

### 277 **2.5.2. Forecasting evaluation**

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

288

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

$$292 \quad MAPE_{Bayes} = \frac{1}{H} \sum_{i \in [1, N]: T0 < \tau(i) \leq T0 + H} \frac{1}{N_s} \sum_{s=1}^{N_s} \left| \frac{Y_{\tau(i)} - \hat{Y}_{\tau(i)}(\theta_s)}{Y_{\tau(i)}} \right| (\%) \quad (11)$$

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

296

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

302

### 303 **3. Results**

#### 304 **3.1. Fitting evaluation**

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

315

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

324

#### 325 **3.2. Forecasting evaluation**

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

331

332 Across the full range of forecast horizons, the allometric model ranked as the most accurate  
333 in forecasting the overall growth responses for 28/32 pigs, while the forecasts generated using  
334 the monomolecular, rational and linear models ranked as the most accurate for 2/32, 1/32 and  
335 1/32 pigs respectively (Population A: (Figure 3 A). Similar results were also obtained in the  
336 context of pigs within Population B (Figure 3 B), but there was more variability. Specifically,  
337 the allometric model ranked as the most accurate in forecasting the overall growth responses  
338 for 14/30 pigs across the full range of forecast horizons, while the forecasts generated using  
339 the monomolecular, rational and linear models ranked first for 9/30, 4/30 and 3/30 pigs  
340 respectively. Full, tabulated model rankings for each individual pig based on  $MAPE_{Bayes}$  are  
341 given in the Supplementary Material.

342

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

358 and DES models both overestimated the growth trajectory. Contrastingly, forecasts generated  
359 using the monomolecular and rational models underestimated the trend.

360

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

376

#### 377 **4. Discussion**

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

386

#### 387 **4.1. Criteria for model selection: ability to fit vs ability to forecast**

388 On the basis of our statistical analysis of individual feed consumption and BW data from  
389 growing-finishing pigs, we identified clear differences in the overall classification of models.  
390 These differences depended on whether model accuracy was measured in terms of fitting or  
391 forecasting. Specifically, our findings suggest that a good fit to a training dataset does not

392 necessarily translate into accurate forecasts of individual growth responses in a validation  
393 dataset. Accordingly, while all models under consideration seemed to fit the observed data  
394 well, the nonlinear models generated markedly more accurate forecasts of growth responses  
395 than the linear models across all forecast horizons. For every model, the overall forecast  
396 accuracy decreased with increasing forecast horizon, but this decrease was substantially  
397 greater for the linear models.

398

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

410

#### 411 **4.2. Forecasting ability of the considered models**

412 Our data-based results indicated that there were considerable disparities between models in  
413 their ability to forecast individual growth responses, with the nonlinear models generating  
414 more accurate forecasts compared to the linear approaches for all forecast horizons ranging  
415 from one to thirty d (Figure 3). The lower level of forecast accuracy of the linear models  
416 compared to the nonlinear models was more pronounced for longer-term forecast horizons,  
417 with modest variation among pigs. Our study demonstrates that it may be quantitatively  
418 acceptable to use these linear response models in the context of (very) short forecast  
419 horizons, such as one or two d, which are more frequently utilised in precision feeding  
420 because the magnitude of the error is constrained. However, our study also demonstrates that  
421 alternative models are also available without invalidating the former approaches for short-term  
422 forecasting but allowing for more accuracy and greater reliability for short-term, as well as  
423 long-term forecasting. These findings highlight the necessity to implement nonlinear  
424 forecasting approaches, particularly in the context of precision management strategies, which  
425 could include scheduling processes associated with the purchase of raw feed ingredients, pen

426 allocation and transportation or slaughter of animals through end-BW prediction. The more  
427 sustained accuracy of the nonlinear models offers potential multipurpose capacity for both  
428 precision feeding and management purposes, and could also improve their application, as it  
429 would reduce the need for different models in an eventual decision support tool where  
430 different forecast horizons are considered.

431

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

448

449 To express cumulative BW gains as a function of cumulative feed intake, rather than time  
450 (Whittemore & Green, 2001; Black, 2009), as it is the case in the DES model, and to  
451 overcome limitations of the linear model, we developed alternative nonlinear models relating  
452 these two traits. The accuracy of forecasts of the monomolecular and rational models was  
453 often very similar and almost indistinguishable for many individual animals from the two  
454 populations. Both models typically underestimated growth responses for most pigs. While the  
455 use of the monomolecular model to relate feed intake to BW is relatively common in  
456 monogastric livestock research (Spillman, 1924; France et al., 1996; Schulin-Zeuthen et al.,  
457 2008; Kuhl et al., 2010), the use of the rational model is less so (Powell et al., 2017).  
458 However, these two models are mathematically similar being bounded by an asymptote,  
459 which is the BW at maturity. As commercial growing-finishing pigs do not approach their



460 mature size, which have been reported to be up to three-four times larger than the typical size  
461 at slaughter (Strathe, Danfær, Sørensen, & Kebreab, 2010), the asymptotic feature of these  
462 two models may not be necessary (van Milgen et al., 2008; Filipe, Leinonen, et al., 2018).  
463 Particular concerns relate to considerable technical challenges and uncertainty in the  
464 estimation of the asymptote from the usually available data and a general ambivalence on  
465 whether these models can adequately approximate growth responses prior to the point of  
466 fastest growth (Filipe et al., 2019). Thus, forecasts of growth responses obtained using these  
467 models may not be optimal, although they were more accurate than those obtained using the  
468 two aforementioned linear models.

469

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

478

### 479 **4.3. Forecasting ability under growth perturbations**

480 Our findings demonstrated that the timing of a perceived short-lived growth perturbation,  
481 caused e.g. by infrequent, temporary physiological and/or environmental disturbances  
482 (Kyriazakis, 1997; Kyriazakis & Tolcamp, 2011) could impact the ability to reliably forecast  
483 individual growth responses in different ways. Based solely on a subset of illustrative  
484 animals, whose growth trajectories were examined because they were perturbed, we found  
485 the following: when a single, short-lived growth perturbation occurred early in the training  
486 dataset (and away from the time point of the last known value, from which the forecasts were  
487 performed), all considered models were largely able to cope with this unexpected deviation  
488 from the trend. Contrastingly, when a perceived single, short-lived growth perturbation  
489 occurred late in the training dataset (and near the time point of the last known value, from  
490 which the forecasts were performed), the forecast accuracy of all models was reduced, but to  
491 different extents. Specifically, the DES model generated the least reliable forecasts leading to  
492 a marked underestimation of growth responses, probably related to the fact that this approach  
493 mainly relies on the most recent past observations to inform the trend forecasts, which can be

494 unduly influenced by perturbations. While it is possible to give more weight to older  
495 observations in the DES model (Young, 2012) to negate, at least partly, the possible adverse  
496 effects of short-term perturbations on the estimation (Hauschild et al., 2012), this typically  
497 requires manual adjustment of the unknown tuning parameters.. Thus, the DES model and  
498 other extensions of the exponential smoothing methods (Hyndman et al., 2002), as well as  
499 models from a closely related family of autoregressions and moving averages, commonly  
500 referred as ARIMAs (Shumway & Stoffer, 2017), should be used with caution for precision  
501 feeding and management since they can be unduly influenced by single, short-lived growth  
502 disturbances occurring near the forecast horizon.

503

504 The examined approaches were shown to cope with relatively short-lived (or with constant  
505 level, diet driven) growth perturbations, but as they stand, are not specifically designed to  
506 forecast under considerable growth retardation and subsequent compensation, which could be  
507 observed in pigs kept in suboptimal conditions facing multiple physiological, infectious or  
508 environmental challenges (Sandberg, Emmans, & Kyriazakis, 2006; Kyriazakis & Houdijk,  
509 2007). Recently, an approach to quantify individual feed intake responses of growing pigs to  
510 such perturbations was developed by Nguyen-Ba, van Milgen, and Taghipoor (2019), but this  
511 research area still warrants further attention.

512

#### 513 **4.4. Bayesian methodology in the context of precision feeding and management**

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

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

533

## 534 **5. Implications and future research**

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

547

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

562 outperform other types of forecasts from single models (Barrow & Kourentzes, 2016;  
563 Makridakis, Spiliotis, & Assimakopoulos, 2018).

564

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

571

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583

Sample size	Breed	Sex	Initial average BW (kg)	Final average BW (kg)	Trial length (d)	ADFI (kg/d)	ADG (kg/d)
<b>Population A</b>							
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)
<b>Population B</b>							
30	Non-commercial	Boars	32.9 (0.574)	109 (4.49)	74 (9)	1.91 (0.239)	1.04 (0.0967)

584 **Table 1.** Descriptive statistics (mean (SD)) of experimental data collected on growing-  
585 finishing pigs from two distinct populations. Dataset A corresponds to a trial by the INRAE  
586 at the UE3P unit (Pig Physiology and Phenotyping Experimental Facility,  
587 <https://doi.org/10.15454/1.5573932732039927E12>), Saint Gilles, France. Dataset B  
588 corresponds to a trial by Topigs Norsvin at their commercial facilities.  
589 Abbreviations: LW, Large White; L, Landrace; P, Pietrain; BW, bodyweight; ADFI, average  
590 daily feed intake; ADG, average daily gain; d, days

591

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

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

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

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

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

603  
604

Model	$MAPE_{Bayes}$ (%)				
	H = 1	H = 5	H = 10	H = 20	H = 30
<b>Population A</b>					
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)
<b>Population B</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)

605 **Table 4.** Forecasting evaluation of candidate models relating cumulative feed intake (kg) or  
606 time (d) to cumulative bodyweight gain (kg): median (IQR) of the calculated  $MAPE_{Bayes}$  (%)  
607 for each model. Each model was fitted separately to each training dataset of each individual  
608 pig (Population A:  $n = 32$  pigs; Population B:  $n = 30$  pigs), followed by trend forecasts  
609 tested on each validation dataset of each individual pig. Forecasts were generated over  
610 forecast horizons  $H$  ranging from 1 to 30 d. For  $MAPE_{Bayes}$ , percentage values closer to zero  
611 indicate smaller predictive error.  
612 Abbreviations:  $MAPE_{Bayes}$ , Bayesian equivalent of the percentage error, characterised in  
613 terms of its median value; H, time window for which forecasts are made (for most pigs all  
614 lags between observations were 1 d, therefore H corresponds to number of d ahead for which  
615 forecasts are made); DES, double exponential smoothing; d, days



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

626

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

639 **Figure 3.** Forecasting evaluation of candidate models relating cumulative feed intake (kg) or  
640 time (d) to cumulative bodyweight gain (kg): the accuracy of cumulative bodyweight gain  
641 forecasts over forecast horizons  $H$  ranging from 1 to 30 d, presented as  $100 - MAPE_{Bayes}$   
642 (%). Each model was fitted separately to each training dataset of each individual pig  
643 (Population A:  $n = 32$  pigs; Population B:  $n = 30$  pigs), followed by trend forecasts tested  
644 on each validation dataset of each individual pig. Large  $100 - MAPE_{Bayes}$  values indicate  
645 better forecast accuracy relative to smaller values.  
646 Abbreviations:  $MAPE_{Bayes}$ , Bayesian equivalent of the percentage error, characterised in  
647 terms of its median value; d, days

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

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