



Quantifying growth perturbations over the fattening period in swine via mathematical modelling

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Abstract

Background: Resilience can be defined as the capacity of animals to cope with short-term perturbations in their environment and return rapidly to their pre-challenge status. In a perspective of precision livestock farming, it is key to create informative indicators for general resilience and therefore incorporate this concept in breeding goals. In the modern swine breeding industry, new technologies such as automatic feeding system are increasingly common and can be used to capture useful data to monitor animal phenotypes such as feed efficiency. This automatic and longitudinal data collection integrated with mathematical modelling has a great potential to determine accurate resilience indicators, for example by measuring the deviation from expected production levels over a period of time.

Results: This work aimed at developing a modelling approach for facilitating the quantification of pig resilience during the fattening period, from approximately 34 kg to 105 kg of body weight. A total of 13 093 pigs, belonging to three different genetic lines were monitored (Pietrain, Pietrain NN and Duroc) since 2015, and body weight measures registered (approximately 11.1 million of weightings) with automatic feeding systems. We used the Gompertz model and linear interpolation on body weight data to quantify individual deviations from expected production, thereby creating a resilience index (*ABC*). The estimated heritabilities of *ABC* are low but not zero from 0.03 to 0.04 (± 0.01) depending on the breed.

Conclusions: Our model-based approach can be useful to quantify pig responses to perturbations using exclusively the growth curves and should contribute to the genetic improvement of resilience of fattening pigs by providing a resilience index.

Keywords: modelling, perturbation, resilience, robustness, body weight, big data, pig, precision livestock farming

13 Background

14 Climate change and societal concerns (*e.g.*, animal welfare and use of antibiotics) on livestock
15 production result in important challenges for animal breeding. Alternatives to address these
16 challenges include the implementation of strategies to select animals that can adapt to a
17 changing environment and to promote a healthy environment for facilitating farm
18 management (1). In this context, the last decade has seen an enormous increase in interest in
19 animal robustness to environmental effects. Friggens *et al.* define the robustness as the
20 ability, in the face of environmental constraints, to carry on doing the various things that the
21 animal needs to do to favour its future ability to reproduce (2). Concomitantly, the concept of
22 resilience has emerged in animal sciences encompassing not only the response of the
23 individual to diseases challenge but also the individual's response to other sources of
24 stressors. Colditz and Hine defined resilience as the capacity of the animal to be minimally
25 affected by disturbances or to rapidly return to the state pertained before exposure to a
26 disturbance (3). Several definitions and resilience-associated concepts have been discussed in
27 literature (1), reflecting the interest of this concept in a broad range of scientific disciplines
28 (4).

29 In the era of big data collection on farms, the digitalization process will generate new
30 knowledge in most of the relevant topics in swine production including nutrition, health
31 management, reproduction, genetics, biosecurity, behavior, welfare, and pollutant emissions
32 (5). Sensors (6), such as commercially available automatic feeding systems (AFS), capture
33 longitudinal data (feed intake -FI-, feeding time, daily visits and body weight -BW-). These data
34 can be further exploited using the knowledge of animal requirements and physiology to
35 develop new phenotypes increasing sustainability and efficiency of breeding. Such an
36 exploitation calls for adequate mathematical tools. AFS allow pigs to feed *ad libitum* and
37 recognize individual growing pigs via a radio frequency identification (RFID) transponder. The
38 large number of automatic BW registers measured by AFS could generate knowledge for
39 management decision-making. In particular, the detection of BW deviations from standard
40 trajectories would generate useful insights on the status of animal with minimum effort if
41 automated.

42 Animal breeding is showing an increasing interest for resilience to be included as a trait in
43 breeding goals. However, the incorporation of resilience in swine breeding goals is currently
44 an uncommon practice. One of the main drawbacks that hinder the incorporation of resilience
45 in breeding is the difficulty of providing quantitative resilience indicators (2). Recent
46 technological developments based on longitudinal data give new opportunities to define
47 resilience indicators based on the difference between observed production and an individual's
48 potential production (although the definition of the individual potential is a challenging issue).
49 Several studies have explored continuous recording of pig performance to study the impact
50 of perturbations, including novel phenotypes related to disease resilience using daily FI (7, 8),
51 and modelling approaches to detect potential perturbations as deviations of FI (9). Modelling

52 efforts to characterize the animal response to perturbations in dairy cattle have also been
53 developed (10). Our group has recently developed a modelling approach, for facilitating the
54 quantification of piglet resilience to weaning (11). In our previous work, we proposed a
55 resilience indicator that has the potential to be used in elite breeding populations. Building
56 upon our previous work, the aim of the present study was to develop a modelling
57 methodology for quantifying an individual pig resilience indicator based on longitudinal BW
58 measurements registered routinely by an AFS during the fattening period. Moreover, the
59 genetics underlying this resilience indicator were analyzed in two of the most used
60 commercial breeds to show the potential to improve resilience of swine livestock through
61 inclusion of this indicator in breeding goals.

62

63 **Methods**

64 *Data source*

65 The pigs used in this study belonged to the Piétrain (Pie) and Duroc (Du) pure breeds. Piétrain
66 is an European sire line breed, strongly selected for lean meat content during the last decades
67 (12). The Du breed is also used as a terminal sire when fattening pigs are produced. The Du
68 breed has both an excellent growth rate and high intramuscular fat (13). AXIOM Genetics have
69 two different lines belonging to Piétrain breed namely Piétrain Français NN Axiom line (Pie
70 NN) with pigs free from halothane-sensitivity and Piétrain Français Axiom line with animals
71 positive to this gene.

72 A total of 13 093 boars belonging to three different lines were used in this study: 5 841 and 5
73 032 belonging to Pie and Pie NN line respectively, and 2 220 belonging to Du breed.

74

75 *Station conditions*

76 The boar testing station of the breeding company AXIOM Genetics (Azay-sur-Indre, France),
77 built in 2015, located in the Centre region in France housed the animals used in this study. A
78 group of 336 piglets were introduced to the station every 3 weeks. AXIOM's requirements for
79 biosafety are applied: forward march, showers and change of clothes, cleaning and
80 disinfection program, blood monitoring. The boars arrived, after weaning, from 7 different
81 birth farms (5 farms for Pie, 1 farm for Pie NN and 1 farm for Du) to the herd when they were
82 between 25 and 35 days of age (8 ± 3 kg BW). Birth farms are integrated into the AXIOM
83 breeding scheme, comply with AXIOM's biosafety and health requirements (monitoring,
84 vaccination plan) and are negative for major diseases. For each batch, all pigs arrived within 1
85 successive week and were kept in the same pen of 14 animals. Each pen is made up of 14 male
86 piglets from the same breed and from the same birth farm. The composition of the pens is
87 never modified, **with** no reallocation. They were kept in air-filtered quarantine rooms
88 (nursery) for 5 weeks, the time needed for seroconversion control and to validate there are

89 not positive to major disease, such as porcine reproductive and respiratory syndrome (PRRS),
90 brucellosis, swine influenza, etc. They were then raised in post-weaning rooms for 2 weeks.
91 The three lines are present in each group in the station and meet the same breeding
92 conditions. Then they were transferred in fattening rooms when they were approximately
93 between 70 and 80 days of age (34.4 kg). They were kept in fattening rooms for 65 to 77 days
94 until the individual testing (weighing, ultrasonic backfat and muscle measurements) around
95 150 days of age (104 kg BW). Animals were kept in the same pen from arrival until slaughter.
96 The station consisted in 2 nursery rooms, 2 post-weaning rooms and 10 fattening rooms with
97 12 identical pens each, housing a maximum of 14 pigs per pen, leading to a total capacity of 2
98 638 pig places. Only fattening rooms are equipped with AFS. Each pen had one water nipple
99 available for the animals. One group, from the same week of introduction in the station, is
100 divided in two fattening rooms (24 pens with 14 pigs).

101

102 *Automatic individual body weight data collection*

103 An AFS pig performance testing feeding station (Nedap N.V.; Groenlo, the Netherlands) was
104 located in the front of each of the pen. The feeder was 0.7 m wide, and the total length was
105 1.69 m. The feeder included a feed trough and had no gates. The feeder only allows the
106 entrance of one animal. The pig entering the feeder was individually identified via an
107 electronic RFID transponder located in the ear. All animals were maintained under standard
108 intensive rearing conditions and were fed individually *ad libitum* from the feeder with a
109 standard diet non limiting in amino-acids. Briefly, the growing diet provided 9.75 MJ/kg of net
110 energy with 15% of crude protein and 0.9% of lysine. The boars were not castrated.

111 Data collection started when animals were transferred in fattening pens and finished 1 week
112 after individual testing. Animals were individually weighted the day of transfer (IW: initial
113 weight) and the day of individual testing (WT).

114 The data analyzed in this study used information registered at each visit in the AFS on
115 individual pigs relating to identification number, date, location, duration of the visit, FI and
116 BW. The dataset included boars raised at the station from September 2015 to July 2019.
117 During that period, 65 batches arrived at the station (13 093 pigs in total).

118

119 *Data pre-treatment*

120 Datasets were processed separately for the three lines. Each dataset from the AFS was
121 thoroughly assessed in order to validate the data, and identify important data gaps and quality
122 issues using SAS (14). The different datasets were analyzed independently but using the same
123 procedure.

124 In the raw data file, one record corresponded to one animal visit to an AFS. A first processing
125 step consisted of eliminating the records without an RFID tag detected, and without a valid
126 association between animal ID and RFID tag.

127 As a second step of quality control for each visit, the weight was considered as null for records
128 without BW record, with a duration of the feeder visit <5s (scale stabilization) and for weights
129 measured during the 6 first days of the fattening period that were out of a range between
130 $0.7*IW$ and $1.3*IW$. Indeed, during the first 6 days, the pigs are in the adaptation phase and
131 the AFS stalls remain open. It is possible that two pigs try to enter in the AFS stall at the same
132 time or that a pig puts a leg in the feeder causing an incorrect weight measurement.

133 For the third control step, a quadratic regression of weight on age + age² for each animal was
134 applied to eliminate aberrant weights. The ratio between the residual value and the fitted
135 value was calculated for each visit of each animal. If the ratio was > 0.15, the measured weight
136 was considered to be null. The ratio of 0.15 was selected by using a trial-and-error approach
137 to find a compromise between the data cleaning and the number of data points to be kept for
138 further analysis. This step was repeated a second time excluding the initially identified
139 aberrant weights. Following this step, the visits of an animal during a day were aggregated in
140 a single record. The weight of the day was estimated from the median of the non-null weights
141 (WM) measured during the day's visits. If the number of non-null weights for the day was <3,
142 the median of daily weights was considered to be null.

143 The fourth control step consisted in analyzing all of data from each AFS within fattening group
144 (AFS*Group) in order to detect inconsistencies linked to the AFS machine. A linear regression
145 of WM on days (number of days since the beginning of measurements) was applied. The
146 standard deviation of the residual value is calculated for each day for each AFS*Group. If more
147 than 10% of the weights measured on AFS*Group were > 3 * standard deviation, then
148 AFS*Group records have been removed from the data set. The objective is to rule out animals
149 from AFS with a mechanical problem. Animals with less than 15 AFS measurements in total or
150 more than 10 consecutive days without measurements were removed from the analysis. We
151 accepted that animals had missing weights during the fattening period.

152 The total FI (TFI) during control period was calculated as the sum of FI for all visits during the
153 control period. When a control day is missing (*i.e.*, due to a mechanic problem of AFS or loss
154 of a RFID tag), the missing daily FI is estimated by using local regression, "*proc loess*"
155 implement in SAS (14).

156 Finally, for visualization purpose a kernel density estimation was performed to produce a
157 smoothed color representation of a scatterplot by using the "*smoothScatter*" function
158 implement in R (15). Multivariate kernel smoothing is described by Wand and Jones (16).

159

160 *Two-step mathematical model approach*

161 Our modelling approach comprises two steps. The first step looks at determining a theoretical
162 (potential) growth curve of each animal. The second step looks at constructing the actual
163 perturbed growth curve. The resulting two curves are the ingredients for further
164 determination of an individual resilience indicator.

165 Animal growth models aim at describing the pattern of growth over the animal's lifetime,
166 defining an upper limit to growth. In our study, we assumed that, under ideal conditions,
167 animal growth follows the theoretical (potential) growth of the animal not experiencing any
168 perturbation. The potential growth of each pig was modelled using the Gompertz equation (i)
169 (17), using the formulation described on Schulin-Zeuthen *et al.* (18).

$$W = W_0 \exp \left[\frac{\mu_0}{D} (1 - e^{-D*(t-t_0)}) \right] \quad (i)$$

171
172 where W_0 is the value of live weight W (kg) at the initial time of the recordings (t_0), μ_0 (d^{-1}) is
173 the initial value of the specific growth rate at t_0 , the constant D (d^{-1}) is a growth rate
174 coefficient that controls the slope of the growth rate (μ) curve and t (days) is time since birth.
175 All parameters are positive. In the remaining text, we will call the trajectories that resulted
176 from this calibration as the unperturbed curve. The unperturbed growth model resulted in
177 two parameters to be estimated, μ_0 and D . As explained below in the model calibration
178 section, we constructed the unperturbed curve such that the perturbed data cannot be above
179 the unperturbed curve by a margin of 5%. The value of 5% was set in accordance with the
180 accuracy provided by AFS.

181 For our second modelling step, since the Gompertz equation is a monotonic function that does
182 not account for possible decrease of BW due to perturbations, we construct a perturbed
183 growth curve using the daily BW measurements registered routinely by the AFS. For missing
184 records, values were estimated using the linear interpolation method implemented in the
185 “*interp1*” function in Scilab (19). It should be noted that if high frequency data are available,
186 the linear interpolation step is not needed.

187 We further calculated the difference of the area under the curve between the perturbed curve
188 and the unperturbed growth. The area under the curve was calculated using the trapezoidal
189 rule implemented in the “*inttrap*” Scilab function. The resulting value was called Area Between
190 Curves (ABC) index, and was considered as a proxy of resilience (the lower ABC the higher the
191 resilience or an animal faced to low perturbation). **For those non-normal distributed values,**
192 **the ABC** parameter results were normalised applying the \log_2 transformation. Visualization of
193 the quartiles distribution of this parameter was performed with the ‘*ggridges*’ R package (15).

194 Finally, correlation analyses were performed to explore the relationships between growth
195 model parameters to be estimated (μ_0, D) and ABC. Pearson correlations were analyzed in R
196 using the ‘*cor*’ function in the base package.

197

198 *Model calibration*

199 The parameters μ_0, D of the Gompertz model for each animal were estimated by minimizing
200 the normalized least square error with a penalized function (ii):

201

$$J_E = \omega \cdot \sum_{i=1}^{n_t} \left[\frac{W_i - W_{d,i}}{W_{d,i}} \right]^2 \quad (\text{ii})$$

202
 203 where W_d is the weight data (kg), W the weight predicted by the model, and n_t the total
 204 number of measurements. The parameter ω is a penalization factor that we constructed to
 205 constrain the unperturbed curve to envelope all experimental data. The penalization factor is
 206 defined as follows (iii):

$$\omega = 10^{\frac{n_r}{n_t-1}} \quad (\text{iii})$$

208
 209 Where n_t is the number of measurements for each animal and n_r is the number of records
 210 where the ratio between the residual (real BW – predicted weight) and the real BW was higher
 211 than 5%.

212

213 *Phenotypic swine production traits*

214 When the average weight of the group was approximately 100 kg, the individual testing was
 215 performed. Measurements made during the test were: weight (WT), average ultrasonic
 216 backfat thickness (BF: mean of 3 measurements) and ultrasonic *longissimus dorsi* thickness
 217 (LD: 1 measurement). BF and LD were adjusted to 100 kg live weight (BF100 and LD100
 218 respectively) by applying linear coefficients. These equations are based on those established
 219 by Jourdain *et al.* (20).

220 The average daily gain (ADG) was calculated as the ratio between the BW gain (WG),
 221 difference between WT and IW, and number of days of control period, expressed in g/day.
 222 The feed conversion ratio (FCR) was calculated as the ratio between TFI during the fattening
 223 period and WG, expressed in kg/kg.

224 The selection traits estimated in the 3 lines are BF100, LD100, ADG and FCR.

225

226 *Statistical analyses*

227 For each breed, each trait was first analyzed separately with a linear mixed model (LMM). The
 228 global statistical model was defined as (iv):

229

$$y = X\beta + Z\mu + e \quad (\text{iv})$$

230

231

232 where y is the vector of phenotype measures for a trait, β is the vector of fixed effects
 233 depending on the trait considered (Table S1). X is the known matrix for fixed effects. μ is the
 234 vector of animal genetic random effects with $\sim N(0, A \sigma_u^2)$ where A is the pedigree-based
 235 relationship matrix. Z is the known design matrices for animal genetic effect. e is a vector of
 236 residual random effects with $e \sim N(0, I \sigma_e^2)$ where I is the identity matrix of appropriate size.

237 Variance components (variance and covariance) were estimated using the REML method with
238 ASReml 3.0 (21) separately for each line.

239 Heritability was calculated as the ratio of animal genetic variance to the phenotypic variance.
240 Due to convergence issues, correlations between *ABC* and selection traits were estimated
241 using two-trait analyses for lines Pie and Pie NN. Genetic correlations have not been estimated
242 for Duroc due to insufficient data.

243

244 For Pie, 24 generations of pedigree information comprising 57 459 animals from 1991 to 2019
245 were included in the analysis. For Pie NN, 24 generations of pedigree information comprising
246 16 137 animals from 1993 to 2019 were included in the analysis. For Du, 22 generations of
247 pedigree information comprising 20 632 animals from 1995 to 2019 were included in the
248 analysis.

249

250 **Results**

251 *Data pre-treatment procedure*

252 From a total of 13 093 animals, more than 11.1 million measurements (1 measurement = 1
253 visit including BW and FI recording) were registered using the AFS. These numbers correspond
254 to the raw dataset. We implemented a data pre-treatment procedure to provide high quality
255 data for the modelling approach. This dataset was analyzed separately in three different data
256 subsets belonging to Pie, Pie NN and Du breed lines, and the same procedure was applied in
257 each dataset. The comparison between the number of animals in the filtered data and the raw
258 dataset showed a ratio of 0.93, 0.91 and 0.87, for Pie, Pie NN and Du lines, respectively.
259 Regarding the number of AFS measurements, the ratios between the-filtered and the raw
260 dataset were 0.76 for Pie, 0.69 for Pie NN, and 0.77 for Du. Complete descriptive statistics for
261 the dataset used in this study are shown in Table 1.

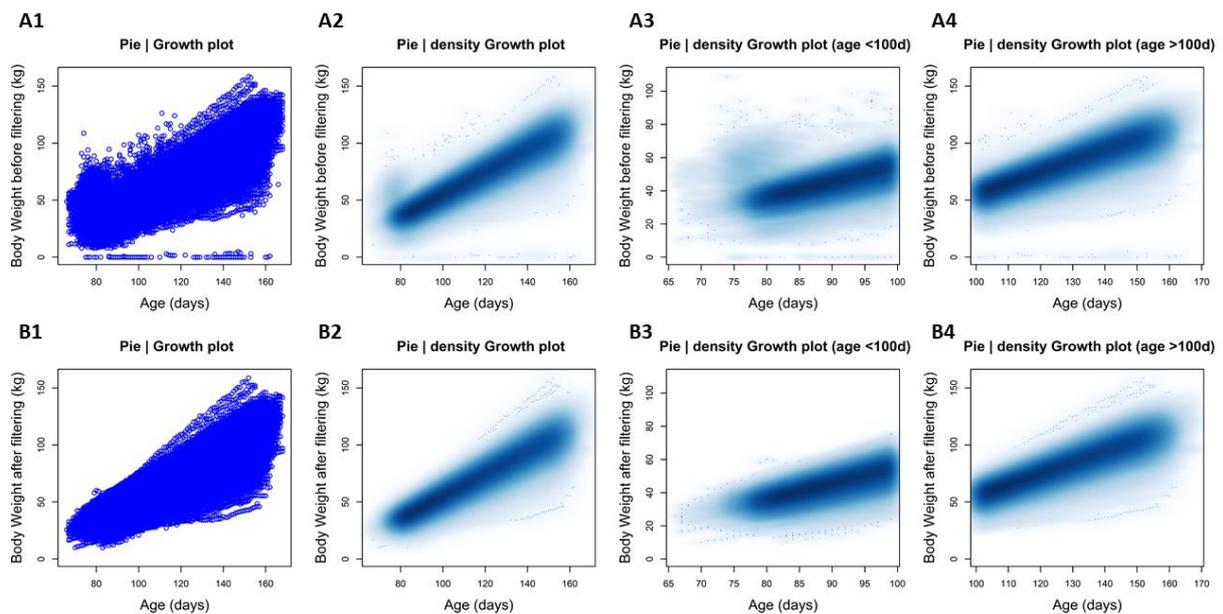
262 **Table 1. Descriptive statistics for the datasets used in this study**

Breed		Piétrain	Piétrain NN	Duroc
No. of pigs		5 841	5 032	2 220
No. of Batch		63	65	62
No. of pigs per batch		92.7 ± 39.5	77.4 ± 18.5	35.8 ± 12.3
Initial average weight at fattening period (kg)		34.3 ± 5.9	34.5 ± 5.4	34.3 ± 5.5
Initial average age at fattening period (days)		78.4 ± 3.3	77.6 ± 2.5	78.4 ± 3.0
Average weight at the individual testing (kg)		105.8 ± 11	102.4 ± 10.2	105.6 ± 10.4
Average age at the individual testing (days)		150.4 ± 4.1	147.2 ± 2.7	147.8 ± 3.0
Raw data	No. of AFS measurements	4 870 323	4 438 121	1 833 941
	No. of animals	5 841	5 032	2 220
After cleaning procedure	No. of AFS measurements	3 704 692	3 061 330	1 420 317
	Daily AFS visits	7.7 ± 3.6	8.4 ± 4	8.5 ± 5.4
	No. of animals	5 430	4 602	1 938

263

264 The data analyzed in this study included information from a total of 11 970 boars, belonging
 265 to three of the most common lines used in swine industry. The final data set consisted of daily
 266 median BW records from 409 770, 337 964, and 140 170 Pie, Pie NN and Du measurements,
 267 respectively.

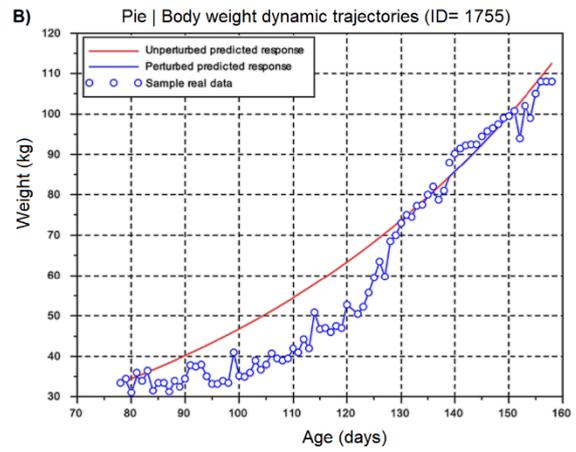
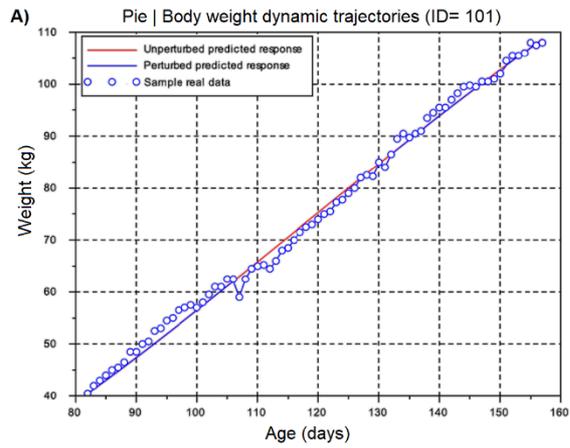
268 A visual comparison of the AFS measurements dataset of Pie line before and after the data
 269 cleaning procedure is shown in Figure 1. Moreover, a graphic representation of Pie NN and Du
 270 lines filtering procedure is shown in Figure S1 and S2, respectively. The figure illustrates the
 271 proportion of measurement points discarded from the analysis before filtering (Figure 1: A1-
 272 A4; Figure S1: A1-A4 and Figure S2: A1-A4 - Raw data) and after filtering (Figure 1: B1-B4;
 273 Figure S1: B1-B4 and Figure S2: B1-B4 - Filtered data), especially weights with a value close to
 274 zero.
 275



276
 277 **Figure 1. Comparison of body weight density plots before (A) and after (B) applying data cleaning procedure in Pie line.** In A1 and B1 plots
 278 each point represent the median of the individual daily body weight registered by the AFS during the pig fattening period. A2 and B2 are
 279 smoothed color density representations of a scatterplot. Shaded areas are constructed to illustrate the density of points falling into each
 280 part of the plot allowing for an intuitive visualization of very large datasets. A zoom in the density scatter plot before (A3-B3) and after (A4-
 281 B4) 100 days of individual age is illustrated.

282
 283 *Growth curve modelling over pig fattening period*

284 To quantify the deviation of the unperturbed curve from the perturbed curve, we constructed
 285 the parameter *ABC* as a resilience indicator. Figure 2 displays the BW dynamic trajectories of
 286 two animals belonging to Pie line exhibiting different patterns. For an animal with a growth
 287 performance close to the unperturbed model (Figure 2A), *ABC* was 37 657. For an animal with
 288 high degree of perturbation (Figure 2B), *ABC* was 493 007. The parameter *ABC* is a useful
 289 indicator of the degree of perturbation of an animal and allows comparison within a
 290 population. Table 2 summarizes the complete descriptive statistics of the model parameters.
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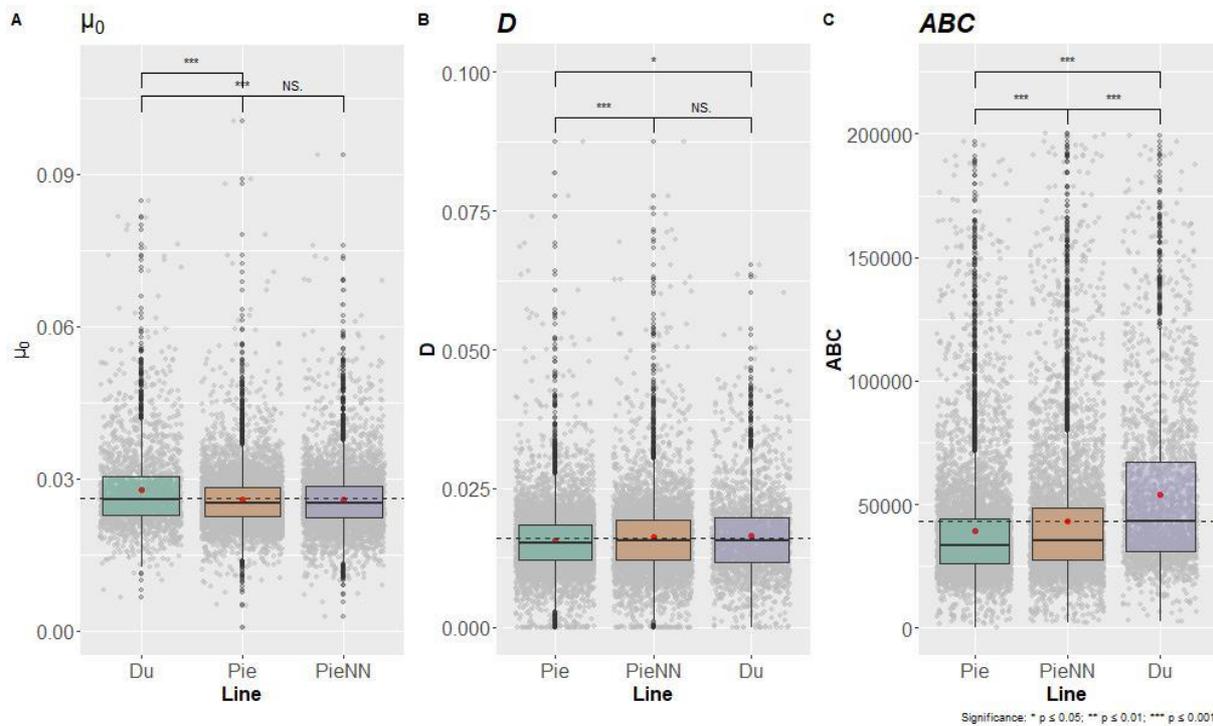
Figure 2. Comparison of the perturbed (blue line) and the unperturbed (red line) predicted response based on the body weight dynamic trajectories recorded during the whole fattening period. Circles represent the median daily body weight measures of the individual pig. Two different animals belonging to Pie line are represented.

297 **Table 2. Descriptive statistics of the parameters for the growth curve modelling in the three pig lines analyzed**

Breed		Piétrain	Piétrain NN	Duroc
μ_0	Range	$7.13 \times 10^{-04} - 1.00 \times 10^{-01}$	$2.79 \times 10^{-03} - 9.34 \times 10^{-02}$	$6.58 \times 10^{-03} - 8.46 \times 10^{-02}$
	Mean	2.62×10^{-02}	2.59×10^{-02}	2.78×10^{-02}
	SD	1.95×10^{-02}	6.19×10^{-03}	8.40×10^{-03}
D	Range	$1.18 \times 10^{-16} - 7.19 \times 10^{-01}$	$1.00 \times 10^{-09} - 2.66 \times 10^{-01}$	$1.03 \times 10^{-15} - 6.52 \times 10^{-02}$
	Mean	1.16×10^{-02}	1.64×10^{-02}	1.65×10^{-02}
	SD	2.22×10^{-02}	8.83×10^{-03}	7.85×10^{-03}
ABC parameter	Min.	239	2 253	2 788
	1 st quartile	26 244	27 489	31 518
	Median	33 564	35 804	44 069
	Mean	41 556	46 474	58 441
	3 rd quartile	44 524	49 257	69 738
	Max	703 283	595 914	407 425

298 μ_0 : individual growth rate (d^{-1}); D : extent of the exponential decay of the growth (d^{-1}); ABC : area between the perturbed and the unperturbed growth curves; SD: standard deviation.

299 Furthermore, Figure 3 represents a visual comparison of the model parameters for the three
 300 analyzed lines. Parameter μ_0 (Figure 3A) showed no significant differences when Pie and Pie
 301 NN lines were analyzed, nevertheless both of them were significantly different (p -value \leq
 302 0.001) compared with Du line. In the case of parameter D (Figure 3B) significant differences
 303 were found between Pie and Pie NN (p -value \leq 0.001), and Pie and Du lines (p -value \leq 0.05).



304 **Figure 3. Comparison of μ_0 , D and ABC statistics in the three pig lines analyzed.** Parameter μ_0 (A - initial growth rate value), parameter D
 305 (B – exponential rate of decay of growth rate), and parameter ABC (C – area between the perturbed and unperturbed growth curves) are
 306 represented. Red points show the average value of the model parameters for each line. The dotted line represents the global average of the
 307 parameter. Significant differences between groups are indicated as * p -value \leq 0.05, ** p -value \leq 0.01, and *** p -value \leq 0.001.
 308

309
 310 For the parameter ABC (Figure 3C) significant differences were identified in all the
 311 comparisons performed (p -value \leq 0.001). Despite the observed significant differences for the
 312 parameter ABC , their distribution between Pie and Pie NN lines were similar (Figure 4A and
 313 4B), compared with the distribution observed for Du line (Figure 4C). This result is logical due
 314 to the close genetic origin of both lines.

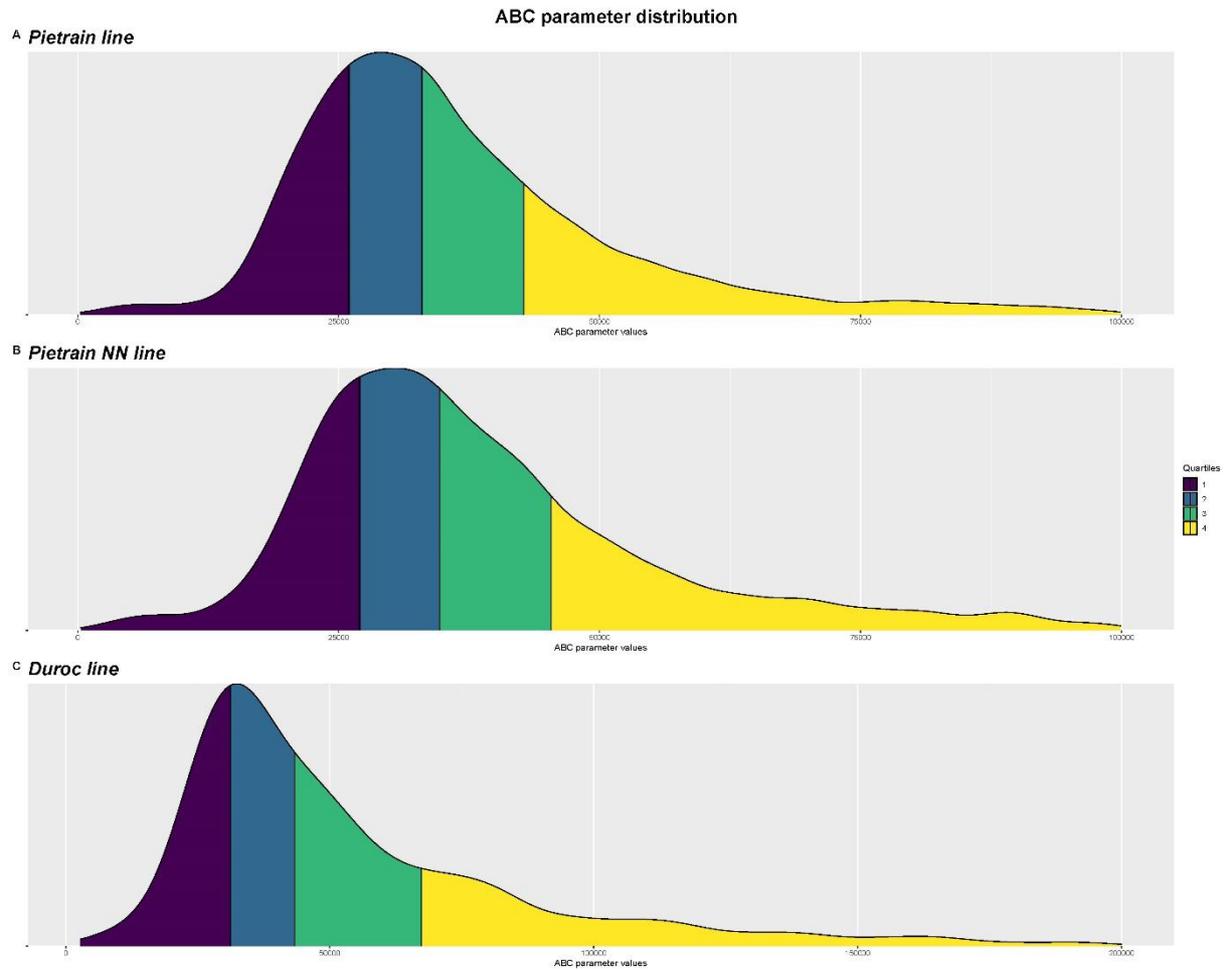


Figure 4. ABC parameter distribution in the three pig lines analyzed. ABC: area between the perturbed and the unperturbed growth curves. Colors represent quartiles information.

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319 Moreover, correlations between the model parameters of the three lines were analyzed
320 (Table 3). The parameter μ_0 showed positive significant correlations with parameter D in the
321 three analyzed lines, 0.88 for Pie, 0.81 for Du, and 0.62 for Pie NN. In the case of parameter
322 μ_0 and parameter ABC significant correlations were only identified in Du (0.37) and Pie NN
323 lines (0.20). A similar pattern was also identified between parameter D and parameter ABC ,
324 being Du (0.30) and Pie NN (0.19) lines those that showed significant correlations.

325

326 **Table 3. Pearson's correlation coefficients among the growth curve model parameters in the**
327 **three pig lines analyzed**

Breed	Piétrain	Piétrain NN	Duroc
R_{μ_0-D}	0.88*	0.62*	0.81*
R_{μ_0-ABC}	-0.01	0.20*	0.37*
R_{D-ABC}	-0.01	0.19*	0.30*

328 * P-value less than 0.05 were considered as significant. μ_0 : initial growth rate value, D : exponential rate of decay of growth rate, ABC : area
329 between the perturbed and unperturbed growth curves.

330
331

332 *Estimating trait heritability and genetic correlations*

333 The heritability of the *ABC* parameter was analyzed (Table 4), ranging between 0.03 and 0.04.
334 Both pig breeds had similar heritability. Phenotypic and genetic correlations were also
335 performed between the *ABC* parameter and important swine production traits such as BF100,
336 LD100, ADG and FCR (Table 5). Phenotypic correlations between *ABC* and production traits
337 are close to 0 for both breeds, ranging from -0.09 to 0.10. Genetic correlations between *ABC*
338 and production traits are low to moderate. In both breeds, the highest genetic correlation is
339 between the resilience index and ADG, with values of 0.59 for Pie and 0.39 for Pie NN.

340

341 **Table 4. Estimated heritabilities (h^2) and corresponding standard errors (SE) of ABC parameter in Pie and Pie NN**

Breed	Piétrain	Piétrain NN
h^2 (SE)	0.04 ± 0.01	0.03 ± 0.016

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343

344 **Table 5. Estimates of heritabilities (diagonal) and of genetic (above diagonal) and phenotypic (below diagonal) correlations among ABC and**
 345 **four commercial selection traits in Pie and Pie NN**

Breed	Piétrain					Piétrain NN				
	ABC	BF100	LD100	ADG	FCR	ABC	BF100	LD100	ADG	FCR
ABC	0.04 (0.01)	0.19 (0.16)	-0.02 (0.16)	0.59 (0.17)	0.30 (0.17)	0.03 (0.016)	-0.31 (0.21)	-0.24 (0.23)	0.39 (0.23)	0.37 (0.20)
BF100	0.01 (0.02)	0.57 (0.04)	-	-	-	-0.03 (0.02)	0.42 (0.04)	-	-	-
LD100	-0.04 (0.02)	-	0.46 (0.04)	-	-	-0.03 (0.02)	-	0.23 (0.03)	-	-
ADG	-0.09 (0.02)	-	-	0.45 (0.04)	-	-0.06 (0.01)	-	-	0.33 (0.04)	-
FCR	0.10 (0.02)	-	-	-	0.32 (0.04)	0.06 (0.02)	-	-	-	0.26 (0.04)

346

347

ABC: area between the perturbed and unperturbed growth curves; BF100: backfat thickness at 100kg; LD100: *longissimus dorsi* thickness at 100kg; ADG: average daily gain during control; FCR: feed conversion ratio.
 * Standard errors of correlations are given in parentheses.

348 Discussion

349 Although the performance of on-farm fattening pigs has improved over the last decades,
350 phenotypic expression of certain traits remains below their genetic potential. In this context,
351 obtaining reliable estimates of growth potential (unperturbed) and resilience over the
352 fattening period in large populations is a challenge in actual swine breeding conditions. In a
353 perspective of quantifying swine resilience and as an attempt to identify indicator traits for
354 this complex trait, here we described a modelling approach based on pig BW registered
355 routinely by AFS in station conditions: *ad-libitum* feeding, high sanitary level, controlled
356 temperature. Even if conditions are optimal, animals have to face to macro (heat stress,
357 disease outbreak) and micro (social hierarchy, AFS mechanic problem) environmental
358 perturbations that modify expression of growth potential. The modelling approach was tested
359 on different swine breeds and their genetic contribution was analyzed in each one of them.
360 Our modelling approach can further facilitate a real implementation at large scale in pig
361 breeding systems.

362

363 *Pretreatment and validation of data registered by AFS*

364 A prerequisite for the linkage of animal data to precision livestock farming systems is through
365 animal identification systems, such as RFID, that are automated and affordable both for the
366 farmer and breeder (22). The development of AFS not only increases the convenience and
367 control of the feeding process, it also allows a precision phenotyping. This development was
368 made possible by the amount of data registered by these devices. These devices routinely
369 record the individual identification, date, age, daily frequency of feeder visits, timing and
370 duration of the visits, FI, and BW (23). However, unlocking the potential of new technology
371 for precision livestock farming requires a deep understanding of how to manage the huge
372 amount of data. Within this framework, data pre-treatment procedures to guarantee high
373 quality data are essential as a first step to exploit the available information. Understanding
374 the data and identifying the main data quality issues require deep data exploration (Figure 1),
375 because modelling approaches are strongly dependent on data quality.

376

377 *Quantifying animals' response to perturbations*

378 Developing models that are able to capture perturbations during the fattening period is a
379 challenge in swine breeding industry. In recent years, the development of more frequent data
380 acquisition and more sophisticated statistical methods have allowed modelling approaches to
381 focus explicitly on perturbations. Revilla *et al.* (11) focused on piglets BW change induced by
382 the weaning event to propose an index to quantify animal robustness during this critical
383 phase. Such a study is based on the modeling of growth, by using with the Gompertz–
384 Makeham function, following an identified disturbance: the weaning. This was shown to
385 correlate with a number of health-related parameters. Nguyen-Ba *et al.* (9) developed a data

386 analysis procedure to detect the impact of perturbations on FI in growing pigs. These two
387 studies aim to analyze and quantify the consequences of an identified disturbance. In the
388 context of our study, pigs can be subjected to different perturbations at different scales
389 depending on the groups: temperature, social hierarchy, health situation. **Our model
390 approach does not include an explicit representation of the perturbations and thus differ from
391 other approaches in which the number of perturbations and its duration are either fixed and
392 know (11, 24) or are to be estimated (9, 10).** In this study, we described a combined model
393 approach to extract, in a two-step mathematical model approach, perturbed and unperturbed
394 individual growth curves over the pig-fattening period. The Gompertz function (17) was
395 chosen as it is suitable to describe the potential growth of pigs in non-limiting conditions (18,
396 25). It needs only two parameters, with biological meaning, that can be estimated simply from
397 data (25). The assumption was that the resulting model is an approximation of the theoretical
398 growth rate of the animals not experiencing any perturbation (unperturbed model). The
399 second step characterizes the perturbed growth curve that reflects the production permitted
400 by the farm environment and captures different types of perturbations. With this two-step
401 mathematical model and by comparing the unperturbed and perturbed model a very
402 informative parameter was created, the *ABC* parameter, which gives an estimate of the
403 degree of resilience (11) over the pig-fattening period. Animals can be ranked according to
404 the values of this parameter, with this ranking being an indication on the magnitude of the
405 perturbation and animal resilience. In this case, an *ABC* value parameter closer to zero, means
406 good animal resilience properties. With respect to interpretation, an *ABC* parameter of zero
407 could mean either that the animal is perfectly resilient or that it did not experience any kind
408 of environmental perturbation. In this study, an important hypothesis has been made, we
409 consider that, on average, all animals are subjected to the same perturbations, and so the *ABC*
410 parameter really indicates the resilience response. With this resilience indicator, animals can
411 be ranked based not only on the measured production level, but also on their capacity to cope
412 with perturbations. This kind of approach opens the perspective to use this information for
413 breeding selection. Our hypothesis has however the limitation that we cannot guarantee that
414 all animals are subjected equally to the perturbations. A key challenge is to extend the model
415 to account for the specific perturbations that the individual animals face. Integration of
416 observational data and precision livestock farming technologies are alternatives to explore in
417 future work. For our case study, the interest of genetic analysis is to make it possible to
418 estimate the individual resilience potential by estimating the impact of the environment in
419 which the animal was fattened.

420 Here Pie and Pie NN lines presented a lower average mean score of parameter *ABC*, -28.89%
421 and -20.48% respectively, compared with Du line (Table 2, Figure 3C). The objective of this
422 comparison is not to conclude that one breed copes better than as other but to illustrate the
423 potential to include a resilience indicator in the selection index. In this scenario, the Du line
424 has a higher level of improvement in terms of selection response to resilience.

425
426

427 Resilience trait in the breeding objective

428 The response to societal concerns (*e.g.*, antibiotics use, viability, *etc*) and the need to identify
429 pigs that adapt to diverse and changing environmental conditions make essential that
430 resilience traits, or their indexes, are included in the breeding objective (26). Two pre-
431 requisites to the success of this approach are: a practical and accurate quantitative definition
432 of this resilience trait, and a positive selection response measured with the heritability
433 estimation. The inclusion of heritabilities of functional traits and their feasibility in the
434 breeding objective has been reported (27). In this context, the genetic improvement of
435 resilience traits, maximizing the bottom line instead of performance in a single trait, could be
436 beneficial for the total system profitability (28). Undoubtedly, directly including resilience
437 traits in future selection criteria will depend on having quantifiable traits that can be recorded
438 cost-effectively and reliably on the large number of animals that are necessary for a breeding
439 program. The estimated heritabilities found in this study are low, ranging from 0.03 to 0.04,
440 suggest that selection for this trait would result in a limited positive selection response.
441 However, the favorable genetic correlations observed between resilience index (*ABC*), and
442 ADG or FCR indicate that gains in both traits can be achieved at the same time, if resilience
443 traits are properly included in the selection criteria. It means that an increase of the resilience
444 index (= a decrease of *ABC*) is globally positively correlated to a genetic improvement of feed
445 efficiency and FCR. Conversely, *ABC* is genetically correlated with growth (ADG), which could
446 be interpreted as that an increase in the genetic potential for ADG increases the risk of a
447 greater deviation of this potential in case of perturbation/stress, that is to say a loss of
448 resilience. Although accuracies of estimates are low, the trends in these correlations must be
449 taken into account in the choice of the weighting applied on each trait of the global index. One
450 difficulty is to define what weighting to give to this resilience index in order to propose a
451 breeding objective balanced with the production traits. Berghof *et al* (2) proposed a first
452 approach of estimating an economic value of resilience index based on the reduction of time
453 to manage alerts and observations. Beyond the economic value, this approach answers to
454 environmental and societal concerns, that are difficult to quantify.

455 Conclusions

456 This study describes a method to quantify individual resilience during the pig-fattening period,
457 by modelling routine BW measures registered by AFS. In addition, we have identified low to
458 moderate genetic relationship between a resilience indicator and important phenotypic traits
459 in swine production. The heritabilities found for the proposed resilience indicator are low but
460 gives opportunity to be considered as a selection criterion and thus improve resilience. This
461 first approach to building a resilience index, based on an analysis of the growth pattern could
462 be enriched by the inclusion of observations of the environment (health observations, room
463 temperature) and the concomitant analysis of feeding behavior (FI or feeding duration).
464

465 **List of abbreviations**

466 **ABC:** Area between curves; **ADG:** average daily gain; **AFS:** automatic feeding system; **BF:**
467 backfat thickness; **BF100:** backfat thickness at 100kg; **BW:** body weight; **Du:** Duroc; **FCR:** feed
468 conversion ratio; **FI:** feed intake; **IW:** initial weight; **LMM:** linear mixed model; **LD:** *longissimus*
469 *dorsi*; **LD100:** *longissimus dorsi* thickness at 100kg; **Pie:** Piétrain ; **Pie NN:** Piétrain Français NN
470 Axiom line; **PRRS:** porcine reproductive and respiratory syndrome; **RFID:** radio frequency
471 identification; **TFI:** total feed intake; **WG:** weight gain; **WM:** non-null weights; **WT:** individual
472 testing.

473

474 **Declarations**

475 *Ethics approval and consent to participate*

476 All animal procedures were performed in accordance with French Animal Welfare legislation.
477 All procedures regarding animal handling and treatment were approved by AXIOM Genetics.

478

479 *Consent for publication*

480 Not applicable.

481

482 *Availability of data and materials*

483 Data and the Scilab source codes of the procedure described in this article are available under
484 request for academic purposes on the Zenodo data repository (doi:
485 [/10.5281/zenodo.4109395](https://doi.org/10.5281/zenodo.4109395)).

486

487 *Competing interests*

488 The authors declare that they have no competing interests.

489

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494

495 *Author's contributions*

496 NCF, RMT, LFG, GL, and MR conceived and designed the study. LFG and GL managed the
497 phenotype recording at the farm. MR and RMT analyzed the data. MR wrote the first draft
498 with input from NCF, RMT and GL. All authors read and approved the final manuscript.

499

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579

580 **Additional files**

Additional File 1 Table S1.

Format: .xlsx

Title: Fixed effects in linear mixed models.

Additional File 2 Figure S1.

Format: .tiff

Title: Comparison of body weight density plots before (A) and after (B) applying data cleaning procedure in Pie NN line.

Description: In A1 and B1 plots each point represent the median of the individual daily body weight registered by the AFS during the pig fattening period. A2 and B2 are smoothed color density representations of a scatterplot. Shaded areas are constructed to illustrate the density of points falling into each part of the plot allowing for an intuitive visualization of very large datasets. A zoom in the density scatter plot before (A3-B3) and after (A4-B4) 100 days of individual age is illustrated.

Additional File 3 Figure S2.

Format: .tiff

Title: Comparison of body weight density plots before (A) and after (B) applying data cleaning procedure in Du line.

Description: In A1 and B1 plots each point represent the median of the individual daily body weight registered by the AFS during the pig fattening period. A2 and B2 are smoothed color density representations of a scatterplot. Shaded areas are constructed to illustrate the density of points falling into each part of the plot allowing for an intuitive visualization of very large datasets. A zoom in the density scatter plot before (A3-B3) and after (A4-B4) 100 days of individual age is illustrated.

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