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Keys to Select a Prediction Model for Carcass Composition from Computed Tomography Images

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Abstract

Linear, nonlinear and volume measurements obtained from computed tomography (CT) images of live pigs are good predictors of carcass characteristics. There are different ways to analyse the goodness of a prediction equation, including the decomposition of the predicted error and the biases and coefficient of determination. The present paper compares the goodness of fit of individual prediction equations within three different genotypes and the prediction obtained by a global equation for the different genotypes at the same time. Comparison is performed by means of the error decomposition, the standard deviation of the bias and the coefficient of model determination. The results showed a good mean square prediction error and a high error due to disturbances (random effects) for most of the predictions; however, the prediction of lean obtained by the global equation and applied to the specific genotypes presented a low error due to disturbances and a high error due to central tendency. Different results are obtained when comparing individual and global equations for the estimation of lean without the distinction of the genotype predicted. In general, the comparison shows that both equations are properly developed and useful; however, the utility is not the same for both of them.

Keywords: Error decomposition; Coefficient of model determination; Computed tomography; Pigs, body composition

Introduction

Mathematical prediction models are used to explain the behaviour of natural processes. They are useful for researchers, industries and policy makers to explain knowledge or discoveries acquired in scientific trials and/or to challenge old dogmas [1]. They are commonly used in livestock animals to assist companies in making decisions; thus, model usefulness must be assessed by its sustainability for a particular purpose. This means that adequate statistical analysis is an indispensable step during the development, evaluation, and revision phases of a model the swine and pork industry have used prediction models over the years to assess the growing rate of the animals [2,3], as well as the mortality [4], prolificity [5], behaviour [6], tissue development and deposition [7] and carcass composition [8-10].

When talking about livestock animals, there are different types of prediction models, such as linear regression, allometric, and quadratic [11] , and a model's goodness depends on a mixture of different factors: R^2, coefficient of variation, root mean square error and, mainly, its utility. Moreover, there are a huge variety of predictors for several characteristics of live pigs in swine, for example, predictors can be obtained for live animals on the farm by observing the animals or measuring them with devices, such as vision systems or ultrasounds [12], in the laboratory using samples obtained *in vivo* during growth [13] or, recently, using images obtained with the use of new technologies or devices, such as dual X-ray absorptiometry, magnetic resonance imaging [14,15] and computed tomography (CT) [7,16,17].

The aim of this paper was to compare and discuss the goodness of fit by genotype (GEN) and globally (all GEN together) of two methodologies for predicting the carcass composition of live pigs: (1) individual equations developed for each GEN obtained by Font-i-Furnols et al. [11] and (2) global equations developed for the three GEN together obtained by Carabus et al. [17]. The prediction equations were obtained using the measurements of the pig body obtained from CT image analysis as predictors and the weight of the carcass pieces and tissues obtained by manual dissection as the reference values (observed or "true" values).

Material and Methods

The present paper makes a comparison between the prediction equations obtained by Font-i-Furnols et al. [11] and Carabus et al. [17] using data from the same animals.

Animals and computed tomography scanning

In brief, the study included 90 gilts of 3 different GEN, 30 (Duroc × (Landrace × Large White)) (DU), 30 (Pietrain × (Landrace × Large White)) (PI) and 30 (Landrace × Large White) (LA), with no parental relation within the breeds Landrace and Large White from different companies. The entire bodies of the animals were CT scanned with a General Electric HiSpeed Zx/I tomographer at different target body weights (TBW): 30, 70, 100 and 120 kg. A total of 15 animals (five for each GEN) were scanned at 30, 70 and 100 kg and 45 animals (15 for each gen) were scanned at 120 kg. The instrumental settings of the CT were: 140 kV, 145 mA, matrix dimensions of 512×512, axial, 7 mm thick (30 kg TBW) and 10 mm thick (70, 100 and 120 kg TBW). A custom-built cradle (PVC, Ø 030 m, length of 12 m for the 30 kg pigs and Ø 046 m, length of 18 m for the 70, 100 and 120 kg pigs) was used to hold the pigs during scanning Pigs had free access to water and were fastened for a minimum of 8 hr before weighing and scanning. Pigs were sedated to minimize disturbances in the CT images due to movement.

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Dissections

After scanning, animals were slaughtered. The left half carcasses were kept refrigerated at 2°C for 24 to 48 hr until dissected. Each carcass was prepared and cut following the European Union reference method [18]. Thereafter, four primal cuts plus tenderloin were weighed and manually dissected Lean, subcutaneous fat, including the skin, intermuscular fat, and bone of most of the cuts were separated with a knife by trained technicians, and the weights of all of these tissues were recorded to obtain the total amount of different fat, lean and bone in the primal cuts, considering all of the tenderloin weight as lean. Only dissected carcasses were used for the development of prediction equations.

Computed tomography image analysis

The distribution of density volume based on the Hounsfield scale (in Hounsfield units [HU]) was obtained from CT images using the VisualPork software package, which was developed for that purpose by the University of Girona and the IRTA [19,20]. The partial volumes estimated between −149 and −1, between 0 and 140, and between 141 and 1,400 HU were associated with fat, muscle and bone volume, respectively, and were used as independent variables in the regression analysis. Volumes between −1,000 and −150 HU, which belong mainly to the less dense parts of the viscera, were considered only in calculating the total volume.

Moreover, CT phenotypic measurements (thickness, lengths and areas) were manually obtained in a reduced set of images as detailed in Font-i-Furnols et al. [11] and Carabus et al. [17].

Variables of interest to be predicted

Equations, using CT predictors, were derived to predict the total amounts of fat (subcutaneous and intermuscular fat of the four primal cuts) and lean (lean of the four primal cuts + tenderloin), as well as the shoulder weight, the loin and its subcutaneous fat weights, the belly weight and the ham and its fat, lean and bone weights.

Prediction equations

The prediction equations were carried out following two different approaches:

One approach included an individual equation for each GEN and was developed by Font-i-Furnols et al. [11]. Four types of regressions equations for the same parameter estimation were obtained: (1) linear regressions using CT volumes or CT ratios of volumes as predictors, (2) quadratic regressions using the previous CT volumes or CT ratios of volumes and their squared value as predictors, (3) allometric equations ($y = ax^b$ linearized as $\log y = \log a + b \cdot \log x$), in which CT predictors were chosen as for the previous regression models and (4) linear regression using CT volumes, CT ratios of volumes and direct physical measurements recorded on loin and ham images as predictors. Predictors were selected using the stepwise procedure of SAS (selected criteria: P < 015) and subjective criteria maximizing the coefficient of determination (R^2) and minimizing root mean square error (RMSE). The criterion to choose the best prediction equation of this methodology was the lowest CV_p (100 × (RMSE of prediction by cross-validation /mean)). The selected prediction equation was the one used in the present work.

Carabus et al. [17] presented the same equation for the three GEN to apply the equation on animals of different GEN and to a set of animals of different SEX (results not analysed in the present paper). For that, it was necessary to establish a criterion based on the accuracy and the decomposition of the mean square predicted error (MSPE). The accuracy and precision of each equation were evaluated by R^2 and the Root Mean Square Error (RMSE). Moreover, to investigate the lack of fit of the equations for both datasets, without the distinction of GEN or SEX, the MSPE was decomposed and compared. Ideally, most of the error should reside in the random component of MSEP [1]. If the proportion of random error for any of the groups was lower than 070, another regression was performed using different predictors. Furthermore, when necessary to standardize the variance, the dependent and independent variables were transformed into natural logarithms.

Statistical analysis

The criteria selected to compare both models for each parameter predicted were found by decomposing the error into (1) error due to central tendency (ECT), (2) error due to regression (ER) and (3) error due to disturbances or random effects (ED) [1,21]. ECT indicates how the average of the predicted values deviates from the observed values average, ER measures the deviation of the regression coefficient of the slope from one and ED is the unexplained variance due to random effects or disturbances. A good prediction is expected to have a high ED error, considering that ECT and ER errors can be eliminated by linear corrections of the predictions [22]. The decomposition was carried out as follows:

MSE= ECT + ET + ED

$$ECT = \left(\overline{\hat{Y}} - \overline{Y}\right)^2$$

$$ER = \left(S_P - r \times S_O\right)^2$$

$$ED = \left(1 - r^2\right) \times S_O^2$$

where $\overline{\hat{Y}}$ is the mean of the predicted values, $\overline{Y}$ the mean of the observed values, S_p the standard deviation of the predicted values, S_o the standard deviation of the observed values, and r the coefficient of correlation between the predicted and observed values. ECT, ER and ED are expressed in proportion, thus their sum is one.

The decomposition of the prediction errors obtained using the equations developed by Font-i-Furnols et al. [11] and Carabus et al. [17] were analysed by first considering the prediction and observed values of all of the GEN at the same time globally and then considering them by each GEN individually. The bias between the dissection and the predictions of Font-i-Furnols et al. [11] and Carabus et al. [17] was analysed, and the standard deviation was obtained as a measure of imprecision, also considering both all three GEN together and each GEN separately. Moreover, the coefficient of model determination (CD), which is the ratio of the total variance of the observed data to the square of the difference between the predicted and the mean of the observed data, was calculated for both predictions using the data of the three GEN together and for each GEN separately. It is calculated as follows [1]:

$$CD = \frac{\sum_{i=1}^{n}\left(Y_i - \overline{Y}\right)^2}{\sum_{i=1}^{n}\left(\hat{Y}_i - \overline{Y}\right)^2}$$

where $\hat{}$ is the observed i^{th} value, $\overline{Y}$ is the mean of the observed values and $\hat{Y}_i$ is the predicted i^{th} value. The CD statistic represents the proportion of the total variance of the observed values explained by the predicted values [23].

Results and discussion

The decomposition of the error in both methodologies, when predictions of all of the animals (three GEN) were considered together, is presented in Table 1. Both methodologies showed high ED (>95% in all of the cases), indicating that the prediction is correct. All of the estimated parameters presented a similar MSPE between both equations and also a high proportion of random error; however, the global equations developed by Carabus et al. [17] did present better results for the ED, exhibiting values higher than >0.99 in 10 of the 11 predicted parameters. Only the estimation of the weight of the four main cuts was lower.

This high ED is most likely because this was the criterion for selecting the prediction equation in that paper. This means that these equations are useful for the entire population of DU, LA and PI studied in Carabus et al. [17] and Font-i-Furnols et al. [11]. Moreover, the genotypes used are the typical ones used for commercial conditions in Spain, thus these equations could also be useful for a large number of animals. The coefficient of model determination and the standard deviation of the bias for both approaches when all of the GEN were considered together are presented in Table 2. The highest imprecision (standard deviation of the bias) was for the weight of the four main cuts in both approaches. The CD values close to one indicate a good prediction, while CD values lower than 1 indicate over prediction of the model and CD values higher than 1 indicate under prediction of the model.

The individual equation approach [11] presents almost all of the CD values as close to 1. Only the ham lean and bone were slightly under predicted (5%), and, for the rest of the parameters, the over- or under prediction was less than 5%. Regarding the global equation approach [17], it generally yields CD values close to one and always with a variation lower than 5%. This can be related with the fact that this approach was carried out considering all of the GEN together

The comparison of the errors using individual equations within GEN is presented in Table 3. In general, both methodologies presented high ED, which means that the prediction is correct, and, as expected, equations from Font-i-Furnols et al.[11] developed individually for each specific GEN showed higher levels of accuracy when comparing both predictions within GEN. Table 3 shows the estimated parameters and the distribution of the predicted errors by each approach within GEN. The individual equations approach of Font-i-Furnols et al. [11], which developed one individual equation for each GEN, generally showed better results (lower MSPE and higher ED) than the global equation approach of Carabus et al. [17], which developed a global equation for all of the GEN together and for pigs of a different genotype and different sexes. This makes sense because different equations for each GEN would allow a better adjustment within genotype than

Estimated parameter (kg)	Individual equations approach				Global equation approach			
	Font-i-Furnols et al. [11]				Carabus et al. [17]			
	MSPE	ECT	ER	ED	MSPE	ECT	ER	ED
Lean[a]	0.382	0.000	0.001	0.999	0.410	0.000	0.001	0.999
Fat[b]	0.148	0.002	0.017	0.981	0.156	0.000	0.001	0.999
Four cuts[c]	1.077	0.000	0.001	0.999	1.204	0.024	0.018	0.958
Ham	0.138	0.000	0.003	0.997	0.147	0.000	0.000	1.000
Ham fat	0.027	0.007	0.029	0.964	0.024	0.000	0.000	1.000
Ham lean	0.095	0.018	0.013	0.969	0.110	0.000	0.000	1.000
Ham bone	0.001	0.007	0.012	0.981	0.005	0.0004	0.005	0.999
Loin	0.083	0.000	0.002	0.998	0.089	0.000	0.000	1.000
Loin fat	0.031	0.012	0.011	0.978	0.028	0.000	0.001	0.999
Shoulder	0.043	0.000	0.001	0.999	0.046	0.000	0.000	1.000
Belly	0.032	0.001	0.012	0.987	0.034	0.000	0.003	0.997

[a]Lean of the ham, loin, belly, shoulder and tenderloin; [b] Fat of the ham, loin, belly and shoulder; [c]Ham, loin, belly and shoulder.

Table 1: Decomposition of the mean square prediction error (MSPE) considering all of the genotypes together in error due to central tendency (ECT), error due to regression (ER) and error due to disturbances (ED) depending on the prediction approach.

Estimated parameter (kg)	Individual equations approach		Global equation approach	
	Font-i-Furnols et al. [11]		Carabus et al. [17]	
	CD	SDBias	CD	SDBias
Lean[a]	1.00	0.37	1.01	0.48
Fat[b]	0.99	0.25	1.01	0.29
Four cuts[c]	1.01	0.66	0.98	0.62
Ham	1.00	0.37	1.01	0.38
Ham fat	0.97	0.15	1.02	0.16
Ham lean	1.05	0.31	1.02	0.33
Ham bone	1.05	0.03	1.01	0.02
Loin	1.02	0.27	1.01	0.25
Loin fat	0.99	0.19	1.03	0.20
Shoulder	1.02	0.27	1.01	0.19
Belly	1.04	0.26	1.02	0.26

[a]Lean of the ham, loin, belly, shoulder and tenderloin; [b]Fat of the ham, loin, belly and shoulder; [c]Ham, loin, belly and shoulder.

Table 2: Coefficient of model determination (CD) and standard deviation of the bias (SDBias) of the prediction approaches considering all of the genotypes together.

Estimated parameter (kg)	GEN	Individual equations approach				Global equation approach			
		Font-i-Furnols et al. [11]				Carabus et al. [17]			
		MSPE	ECT	ER	ED	MSPE	ECT	ER	ED
Lean[a]	DU	0.125	0.018	0.001	0.981	0.173	0.296	0.132	0.572
	LA	0.181	0.020	0.009	0.971	0.224	0.087	0.002	0.911
	PI	0.132	0.002	0.004	0.994	0.313	0.428	0.034	0.538
Fat[b]	DU	0.078	0.024	0.028	0.948	0.089	0.026	0.048	0.926
	LA	0.051	0.004	0.012	0.984	0.082	0.008	0.027	0.966
	PI	0.071	0.010	0.046	0.945	0.087	0.064	0.011	0.925
Four cuts[c]	DU	0.122	0.005	0.003	0.992	0.052	0.009	0.020	0.972
	LA	0.886	0.002	0.004	0.993	0.111	0.004	0.009	0.987
	PI	0.366	0.013	0.011	0.975	1.099	0.237	0.094	0.669
Ham	DU	0.064	0.018	0.002	0.979	0.180	0.402	0.195	0.403
	LA	0.061	0.009	0.012	0.979	0.114	0.000	0.140	0.859
	PI	0.075	0.048	0.036	0.916	0.174	0.423	0.016	0.561
Ham fat	DU	0.014	0.000	0.001	0.999	0.021	0.053	0.029	0.918
	LA	0.011	0.0003	0.005	0.995	0.027	0.037	0.078	0.884
	PI	0.042	0.046	0.159	0.795	0.028	0.0001	0.038	0.962
Ham lean	DU	0.046	0.007	0.010	0.983	0.060	0.014	0.187	0.799
	LA	0.069	0.006	0.0003	0.994	0.088	0.125	0.011	0.864
	PI	0.180	0.041	0.022	0.937	0.190	0.094	0.006	0.900
Ham bone	DU	0.000	0.006	0.003	0.991	0.0004	0.058	0.003	0.940
	LA	0.001	0.016	0.036	0.948	0.001	0.006	0.046	0.948
	PI	0.001	0.003	0.006	0.991	0.001	0.103	0.023	0.874
Loin	DU	0.101	0.0002	0.001	0.999	0.088	0.011	0.064	0.925
	LA	0.077	0.00002	0.0065	0.993	0.063	0.102	0.003	0.895
	PI	0.056	0.001	0.001	0.998	0.045	0.056	0.086	0.858
Loin fat	DU	0.025	0.002	0.0002	0.998	0.056	0.002	0.055	0.943
	LA	0.023	0.000	0.012	0.988	0.020	0.029	0.022	0.949
	PI	0.069	0.037	0.133	0.830	0.054	0.023	0.140	0.837
Shoulder	DU	0.035	0.004	0.0002	0.996	0.024	0.065	0.004	0.931
	LA	0.152	0.000	0.000	1.000	0.045	0.054	0.0002	0.946
	PI	0.044	0.0003	0.0002	0.999	0.048	0.002	0.003	0.995
Belly	DU	0.041	0.0002	0.0001	1.000	0.044	3.10^{-5}	0.003	0.997
	LA	0.097	0.003	0.006	0.991	0.078	0.011	0.0001	0.989
	PI	0.076	0.000	0.000	1.000	0.088	0.009	0.001	0.990

[a]Lean of the ham, loin, belly, shoulder and tenderloin; [b]Fat of the ham, loin, belly and shoulder; [c]Ham, loin, belly and shoulder.

Table 3: Decomposition of the mean square prediction error (MSPE) considering the genotypes (DU = Duroc x (Landrace × Large White); LA = Landrace × Large White; PI = PI × (Landrace × Large White)) separately and together in error due to central tendency (ECT), error due to regression (ER) and error due to disturbances (ED) depending on the prediction approach.

more general equations. However, as in the prediction of the fat, good results are obtained from both predictions. It is important to notice that the number and type of animals used to obtain these predictions were not the same in both cases. Individual equations within GEN were obtained from a reduced number of animals, which were the animals of each GEN that were CT scanned, slaughtered and dissected, while global equations had more than three times as many reference samples because there were the animals from the three GEN together plus some additional animals from another GEN and different sexes. Nevertheless, although the global approach [17] yielded predictions more useful for a larger population than the individual ones [11], sometimes they are also less accurate.

One of the worst results from the global equation approach was found in the prediction of the total lean. When decomposing the error of the estimated lean for the individual equations approach within GEN, it can be observed that the MSPE is lower than 0.200 kg and that the ED is higher than 95%, but the same decomposition of the error by GEN for the global equation approach within GEN does show different results. The error for DU and PI presented a low ED and a high ECT. Figures 1 and 2 present the visual decomposition of the error for the individual and global equations within GEN, respectively. Figure 1 shows no difference between the lines and no tendency in the biases Figure 2 shows the higher ECT in the DU and PI lines. In this case, for PI pigs, there is an underestimation at all levels of the ham's lean, although it is higher at higher levels.

In DU pigs, there is an overestimation at higher lean content, also indicating the high ER. In the case of LA, the decomposition shows high ED and a slightly high ECT, which can be seen in the plot, because the regression line is slightly superior to the zero line (slight overestimation). A similar situation occurred with the weight of the ham. It presented a very low MSPE for the individual equations approach and a good distribution of the errors (Table 3, Figure 3) However, the decomposition of the errors for the global equation approach was worse, mainly for the DU and PI lines (Table 3, Figure 4) They presented low values for ED (<0.60), high values for ECT (>0.40) and DU and medium values for ER (>0.19) LA also presented an ER of 0.14 Thus, in this case, for PI pigs, there is an underestimation at all levels of the ham's lean (high ECT). In DU pigs, there is an overestimation only at higher lean content, indicating the high ECT and also the high ER. The high ER obtained for LA pigs can also be seen

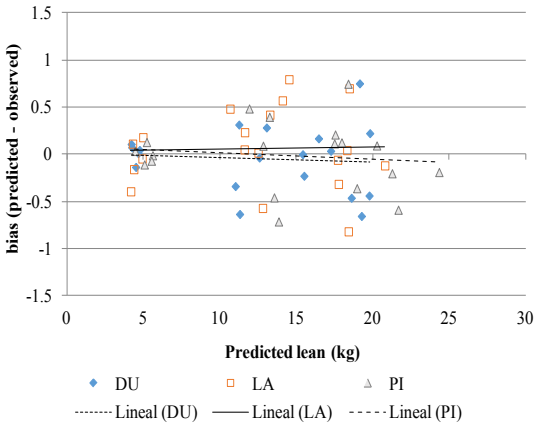

Figure 1: Residuals of the estimation of the lean obtained by (a) the individual equations approach [11].

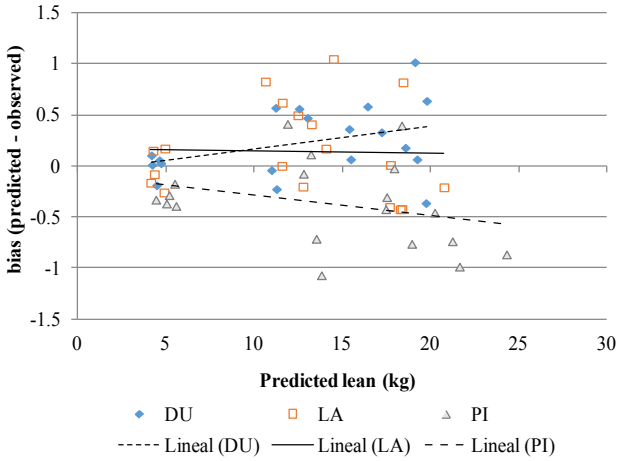

Figure 2: Residuals of the estimation of the lean obtained by the global equation approach [17].

in the plot because there is an overestimation at lower lean content and an underestimation at higher lean content. In this case, the ECT is low because the positive and negative biases are compensated.

The coefficient of model determination and the standard deviation of the bias for both approaches when the GEN were considered separately are presented in Table 4. Although the lean of the four main cuts' estimation had lower ED values in the global equation approach than the individual equations approach, no differences in CD and in the standard deviation of the bias can be seen between the two approaches, with CD being lower than 5% for all of the GEN. Ham fat in the individual equations approaches a CD value of 089 for PI GEN, indicating an over prediction, while, in the global equation approach, the CD value of LA was 111, indicating an under prediction. In both cases, the error of disturbances was lower than in the other GEN. Loin fat estimation also presented some different CD values, from 1: 089 for PI in the individual equations approach and 114 and 090 for DU and PI, respectively, in the global equation approach. For PI in both approaches, the ED was lower than 85%.

Thus, except for certain parameters and GEN mentioned above, the CD generally reflects a small shift in the predicted and observed values, indicating the good model predictions.

Conclusion

Linear, nonlinear and volume measurements obtained from CT images at specific anatomical positions in live pigs are good predictors of carcass characteristics. There are different methodologies to obtain a prediction equation depending on the purpose, including prediction models that are useful only for a specific type of animal (eg, the same genotype) or generalized for several types of animals (eg, different genotypes and sexes). The comparison performed in the present work shows that both approaches for predicting carcass and cut compositions from CT images of growing live pigs are properly developed and useful. Errors are similar for the majority of the parameters, although the predictions are slightly better for some parameters if individual specific equations were used. However, the global equation permits generalization of the predictions to a larger number of animals; thus, it is preferable to use it when the population is mixed or when the parameter estimated does not need a high level of accuracy for a specific line. When this is needed, such as in the case of breeding companies, it is preferable to use individual equations specifically developed for that GEN. Nevertheless, when choosing individual equations, it is important to increase the size of the sample to have greater confidence in the results.

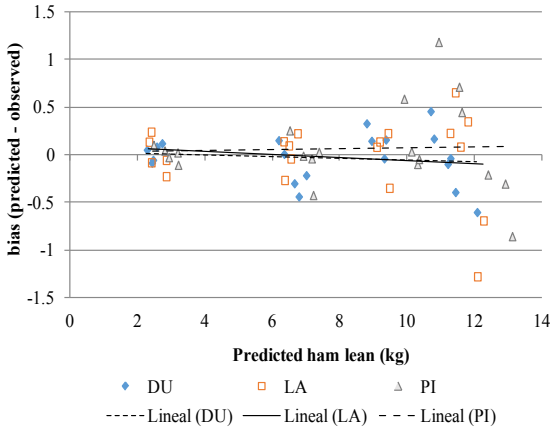

Figure 3: Residuals of the estimation of the lean of the ham obtained by the individual equations approach [11].

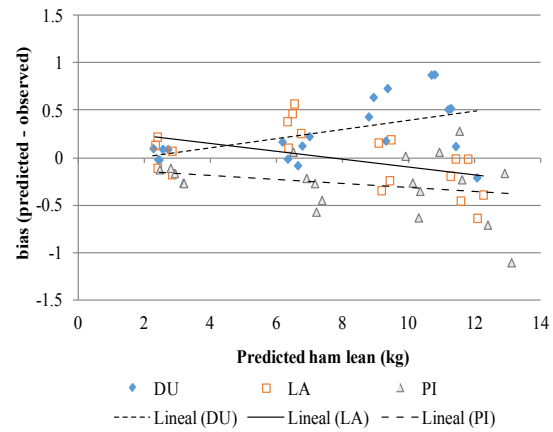

Figure 4: Residuals of the estimation of the lean of the ham obtained by the global equation approach [17].

Estimated parameter (kg)	GEN	Individual equations approach		Global equation approach	
		Font-i-Furnols et al[11]		Carabus et al. [17]	
		CD	SDBias	CD	SDBias
Lean[a]	DU	1.00	0.35	0.97	0.35
	LA	1.00	0.42	1.00	0.45
	PI	1.01	0.36	1.04	0.42
Fat[b]	DU	0.98	0.28	0.97	0.29
	LA	0.99	0.23	1.03	0.28
	PI	0.98	0.26	1.02	0.29
Four cuts[c]	DU	1.00	0.35	0.99	0.23
	LA	1.02	0.94	1.01	0.33
	PI	0.99	0.60	0.95	0.91
Ham	DU	1.01	0.26	0.91	0.32
	LA	1.02	0.41	1.08	0.32
	PI	0.97	0.43	1.05	0.31
Ham fat	DU	1.02	0.12	0.97	0.14
	LA	1.00	0.11	1.11	0.16
	PI	0.89	0.20	0.96	0.17
Ham lean	DU	1.03	0.21	0.92	0.24
	LA	1.01	0.26	1.06	0.28
	PI	1.09	0.42	1.07	0.42
Ham bone	DU	1.02	0.02	1.01	0.02
	LA	1.07	0.03	1.05	0.02
	PI	1.05	0.04	0.98	0.02
Loin	DU	1.02	0.32	1.06	0.29
	LA	1.03	0.28	1.00	0.24
	PI	1.01	0.24	0.96	0.21
Loin fat	DU	1.02	0.16	1.14	0.24
	LA	1.04	0.15	1.05	0.14
	PI	0.89	0.26	0.90	0.23
Shoulder	DU	1.01	0.19	1.00	0.15
	LA	1.04	0.39	1.01	0.21
	PI	1.01	0.21	1.02	0.22
Belly	DU	1.02	0.20	1.03	0.21
	LA	1.06	0.31	1.02	0.28
	PI	1.03	0.28	1.02	0.30

[a]Lean of the ham, loin, belly, shoulder and tenderloin; [b]Fat of the ham, loin, belly and shoulder; [c]Ham, loin, belly and shoulder.

Table 4: Coefficient of model determination (CD) and standard deviation of the bias (SDBias) of the prediction approaches considering the genotypes (DU = Duroc × (Landrace × Large White); LA = Landrace × Large White; PI = Pietrain × (Landrace × Large White)) individually.

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