

**Estimation of lean meat content in pig carcasses using X-ray Computed Tomography
and PLS regression**

Maria Font i Furnols¹, M.Fabiana Teran, Marina Gispert

IRTA-Food Technology, Finca Camps i Armet, E-17121 Monells (Girona), Spain

¹ Corresponding author: Telf: +34 902 789 449 ext 1412 or 1402; Fax: +34 972 630 373; e-mail: maria.font@irta.eu (Maria Font i Furnols)

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14 **Abstract**

15 Lean meat percentage (LMP) is an important carcass quality parameter. The aim of this work
16 is to obtain a calibration equation for the Computed Tomography (CT) scans with the Partial
17 Least Square Regression (PLS) technique in order to predict the LMP of the carcass and the
18 different cuts and to study and compare two different methodologies of the selection of the
19 variables (Variable Importance for Projection – VIP- and Stepwise) to be included in the
20 prediction equation. The error of prediction with cross-validation (RMSEPCV) of the LMP
21 obtained with PLS and selection based on VIP value was 0.82% and for stepwise selection it
22 was 0.83%. The prediction of the LMP scanning only the ham had a RMSEPCV of 0.97%
23 and if the ham and the loin were scanned the RMSEPCV was 0.90%. Results indicate that for
24 CT data both VIP and stepwise selection are good methods. Moreover the scanning of only
25 the ham allowed us to obtain a good prediction of the LMP of the whole carcass.

26

27 **Keywords**

28 Lean meat percentage, computed tomography, PLS, VIP, stepwise

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30 **1. Introduction**

31

32 The lean meat percentage (LMP) of the carcass is an important carcass quality parameter. The
33 slaughter plants have to estimate this percentage by means of measurements in the carcass
34 taken by different types of equipment. These devices are based on ultrasounds (Autofom and
35 Ultrafom of Carometec A/S, Herlev, Denmark; Ultrameater of CSB-System International,
36 Geilenkirchen, Germany), reflectance (Fat-O-Meat'er of Carometec A/S, Herlev, Denmark;
37 Hennessy Grading Probe of Hennessy Grading System Ltd, Auckland, New Zealand; Capteur
38 Grass-Maigre of Sydel Corporation, Lorient Cedex, France;...), vision (VCS2000 of e+V
39 Technology GmbH, Oranienburg, Germany; Vision of Rovi-Tech S.A., Presles, Belgium) or

lineal measurements in the midline of the carcass (ruler). To calibrate these devices to obtain the best equation to estimate the LMP it is necessary to carry out very difficult and expensive work: The cutting and the dissection using the simplified reference method [1] or the full dissection of at least 120 representative carcasses [2]. The error of prediction of the estimation equations has to be lower than 2.5% [2]. The Magnetic Resonance Image, and especially the Computed Tomography (CT), are very precise techniques that have recently arisen as possible alternatives to the manual dissection to calibrate the classification devices [3][4][5]. For this reason, CT has recently been included in the classification legislation as a reference method [2].

CT is based on the attenuation of X-Ray that depends on the density of the irradiated object. As the lean, fat and bones have different densities, this attenuation allows us to differentiate between these tissues. CT is a very common tool in medicine. This technique has also been used to predict the lean and/or fat composition in live pigs [6][7] and in pig or lamb carcasses [5][8][9][10][11][13].

Data obtained with CT is a three dimensional image of the object scanned. The 3D-image is obtained by stacking a number of slices of a certain thickness. Each slice has a number of voxels (3D unit). Each voxel is associated with a Hounsfield value (HU) obtained as the average attenuation in the corresponding piece of object on a Hounsfield scale. Values vary from -1024 to +3071 HU. Water has an attenuation of 0 HU, air of -1000 HU, fat tissue around -60 HU, meat tissue around +60 HU and bones above 150 HU [12]. Sometimes in one voxel more than one class of tissue can be found and this is known as Partial Volume Effect (PVE). CT data can be treated in different ways: considering the histograms of the Hounsfield value associated with each voxel as a spectrum, or classifying the voxels depending on the tissue they represent [13][14][15][16]. Furthermore, the LMP or the lean meat weight can be obtained using the voxels associated with each Hounsfield value and the densities of the different tissues they represent [11][16][17].

Partial least square regression (PLS) is a very useful statistical technique when there are a lot of highly correlated prediction variables (multicollinearity). PLS regression tries to extract the limited number of latent factors (which are linear combinations of the original prediction variables) that explain as much as possible the covariance between the prediction and response variables. It is a very common technique in the treatment of spectral data [18][19] where the number of prediction variables is greater than the number of observations. Recently it has also been used in CT data (frequency of attenuation values) [5][11][13] with good results. The advantage of this technique is that it is not necessary to classify the voxels into meat or fat, avoiding the problem associated with the PVE [20], because PLS estimates the LMP by spectral analysis of the Hounsfield distribution.

The aim of this work is to obtain a calibration equation for the CT scans with the PLS technique in order to predict the LMP of the carcass, and the different cuts, and to study and compare two different methodologies for the selection of the variables to be included in the prediction equation.

2. Experimental

2.1. Carcass sampling

One-hundred and twenty-three pig carcasses from 70 to 110 kg were selected in one slaughterhouse (Patel S.A.U.) according to their fat thickness following the Spanish national distribution [21]. Fat thickness was measured with Fat-o-Meat'er (SKF-Technology AS, Herlev, Denmark) at 6 cm of the midline between the 3rd and 4th last rib (g34fom). For the selection, three groups of fat were used, the lean carcasses with less than or equal to 12 mm of g34fom, the fat carcasses with more than 17 mm of g34fom and the medium carcasses in between. These levels were obtained according to the Spanish mean of g34fom plus/minus one standard deviation. The number of carcasses in each group of fat can be seen in Table 1.

To be representative of the Spanish pig population carcasses came from more than 20 producers. Moreover all the sexes (castrates, entire males and females) were represented.

2.2. Carcasses/cuts scanning with CT and image processing

Left half carcasses were transported in refrigerated conditions to IRTA, Monells. Carcasses were prepared according to the European definition 24-48 h *post mortem*: without tongue, bristles, hooves, genital organs, diaphragm, flare fat, kidneys, tail and spinal cord [1]. Moreover, the hind shank, the fore shank and the head were also removed from the half carcasses before the scanning. Due to practical problems in carrying out the scanning, carcasses were divided into two parts, the ham cut at the level of the 1st lumbar vertebrae and the rest of the carcass, which was scanned separately. Moreover in a subsample of carcasses (n=52) (see Table 1) the major cuts (ham, loin, belly and shoulder) obtained following the EU Reference Method [1] were also individually scanned.

Left half carcasses and cuts were scanned 24-48 h *post mortem* with the General Electric HiSpeed Zx/i computed tomography (CT) equipment located at IRTA-CENTA in Monells, Spain. Images were acquired helically every 10 mm, with pitch 1, *id est* without overlapping. The acquisition parameters were 140 kV, 145 mA, Display Field of View (DFOV) 460-500 mm, matrix 512x512, and reconstruction algorithm STD+.

Images were obtained in DICOM format and they were imported into Matlab Version 7.5.0.342 (R2007b) © The MathWorks, Inc.). A program was created to obtain the frequency of pixels associated with each Hounsfield value for each carcass. A piece of polyurethane was placed between the carcass and the table. Polyurethane is radiotransparent and allows the table of the CT to be eliminated from the carcass images. The DFOV was variable, depending on the width of the carcass. Due to this variability pixels were transformed to volume ($X \text{ pixels} \times 10 \text{ mm} \times (\text{DFOV}(\text{mm})/512)^2$) to homogenize the data with which to work. Figure 1 shows the distribution of the volume depending on the attenuation Hounsfield value (from -

120 to +120) for the average of all the carcasses and the different cuts. Moreover, when carcasses were classified in three groups of fat (Table 1) the representation of the volume associated with each Hounsfield value is shown in Figure 2. It can be seen that the amount of muscle, related to the positive Hounsfield values, is higher in the leaner carcasses and that it decreases when the fat level increases. Consequently, related to the fat composition of the tissues, the fat carcasses presented higher volume associated with the negative Hounsfield values.

2.3. Carcass dissection and calculation of the lean meat percentage

After the CT scanning the carcasses were cut in pieces and dissected according to the European Simplified Reference Method [1]. That is to say that the subcutaneous fat+skin, intermuscular fat, bones and lean of the 4 main joints (ham, loin, belly and shoulder) were separated. The lean of these 4 pieces plus the tenderloin was used to determine the dissected lean meat percentage (LMP089) according to the European Regulation definition [2] as follows:

$$LMP089 (\%) = 0.89 \cdot \frac{\sum \text{lean}(\text{ham}, \text{loin}, \text{belly}, \text{shoulder}) + \text{tenderloin}}{\sum \text{weight}(\text{ham}, \text{loin}, \text{belly}, \text{shoulder}, \text{tenderloin})} \cdot 100$$

After the cutting and before the dissection, the four main cuts (ham, loin, belly and shoulder) of a subsample of carcasses (n=52, distributed for fat groups according to Table 1) were also scanned following the same scan parameters used for the carcass.

The LMP of the different cuts was obtained as:

$$LMP \text{ cut } (\%) = \frac{\text{lean of the cut}}{\text{weight of the cut}} \cdot 100$$

2.4. Prediction of the lean meat percentage: variable selection

146 Although the CT produces volume data and the reference method is defined as weight
147 percentage, it was decided to work with the data directly like in [11], without changing
148 volume to weight by means of density as performed in [5]. Moreover [13] performed a
149 previous mean-centering of the histograms before processing and this also was not performed
150 with the present data. This would allow us to know the prediction capacity of the estimation
151 equations, without any previous transformation of the data. All the calculations were
152 performed with the entire data base (n=122) (one of the scanned carcasses of the fattest group
153 was considered outlier and was not used for the calculations).

154 For the prediction of the LMP089 of the carcass the Partial Least Square (PLS) procedure of
155 SAS software (SAS Inst. Inc., Cary, NC) was used. Root Mean Square Error of Prediction
156 (RMSEPCV) was calculated by leave-one-out cross validation by means of a SAS macro
157 [24]. Different PLS regression models were evaluated before choosing the definitive one.
158 First of all 2 different models including 951 variables were used, one including volume
159 associated with Hounsfield values from -100 to +850 HU, and another one from -250 to +700
160 HU in order to include the ranges of the different tissues (conventionally, from -200 to -20 is
161 considered fat, from +20 to +200 HU is considered lean [20][22] and from +134 to +800 HU
162 is considered bones [17]). Variable importance for projection (VIP) statistic represents the
163 value of each predictor in fitting the PLS model for both predictors and responses. Values
164 lower than 0.8 are considered to have small contribution to the prediction [23]. When VIP
165 statistic of these variables was studied (Figure 3) it was seen that the higher VIP values
166 corresponded to the fat and lean area and the bones had lower VIP values. Although below
167 Hounsfield value of -250, some VIP values were higher than 0.8, they were not selected
168 because they were very variable (results not shown). For that reason the other models studied
169 used volumes associated with Hounsfield values that covered the lean and fat area (from -250
170 to 120 HU; from -100 to +120 HU; from -100 to +100 HU) or only the lean area (from 10 to
171 100 HU; from 10 to 120 HU) (see Table 2). The studied model with lower RMSEPCV has 5
172 extracted factors and 221 independent variables (volumes associated with Hounsfield values)

that varied from -100 to +120 HU. This was one of the selected models for the following calculations.

Moreover, as the independent variables were very correlated (see Figure 1 and Figure 2), another kind of selection was evaluated to reduce the number of prediction variables to be included in the model. Data was analysed with the ordinary multiple regression with the REG procedure of SAS (SAS Inst. Inc., Cary, NC) and the stepwise selection was used for the variable selection. Stepwise selection changes the previously identified model repeatedly by adding or removing a predictor variable in accordance with the selection criteria which was the F statistic value. After the selection, PLS was applied to study the different models with different numbers of prediction variables, from 7 to 20. The model with lower RMSEPCV included 20 independent variables (volumes associated to attenuation Hounsfield values) and 5 extracted factors. This was the other selected model for the following calculations.

2.5. Prediction of the lean meat percentage: modelling

The two selected equations, one with 221 variables and the other one with 20 variables, were used to predict the lean meat percentage (LMP) of all the carcasses. Furthermore, a regression was carried out between the predicted and the dissected LMP with the REG procedure of SAS (SAS Inst. Inc., Cary, NC).

The LMP of the whole carcass was also predicted with the data obtained from scanning the four different cuts separately, using the PLS procedure (SAS Inst. Inc., Cary, NC). The RMSEPCV was calculated by means of an SAS macro [24]. Prediction variables included in the models were volumes associated with attenuation Hounsfield values from -100 to +120 HU. Furthermore, the LMP of the four main joints was predicted, also with the same PLS procedure described before, with the volumes associated with the Hounsfield values obtained by scanning the half carcass and also with those obtained by scanning each joint separately. RMSEPCV was also calculated as explained before.

3. Results and discussion

3.1. Selection and characteristics of the variables for the prediction

The prediction of the carcass LMP depending on the variables included in the model and the selection method is presented in Table 2. All the models would be correct from the legal point of view, because the legislation allows a prediction error lower than 2.5% [2]. Nowadays CT cannot be an on-line device but it can be used as a reference method instead of the dissection according to the legislation [2]. In that case it is important to see that the error obtained with CT is lower than those obtained with dissection which is 1.96% (maximum difference between butchers [25]) or 0.98% (average error between butchers [26]). It can be seen that the selection based on VIP statistic values includes much more variables in the model than those based on the stepwise selection method. Moreover, the number of extracted factors and the RMSEPCV is very changeable depending on the variables included in the model. In PLS it is very important to have a low number of extracted factors, to avoid over-fitting. Also, it is important, for the prediction, to have a low RMSEPCV. For that reason, when the selection method based on VIP values was used, the model that includes 221 variables, those volumes associated with attenuation Hounsfield values from -100 to +120, was selected as the working model. Figure 4 shows the coefficient value of each of the 221 variables and it also includes the histogram line of an “average” carcass. This enabled us to see that the higher the volume associated with each Hounsfield, the lower the coefficient value. Moreover the product between the coefficient value and the volume associated with each Hounsfield unit (for the average carcass) gave us an idea of the importance of each variable in the prediction of the LMP. This product varies from -0.29 to +1.26 and it is represented in Figure 5. The variables placed at the lean area are the most important positive variables in the prediction of the LMP. The most important negative variables in the prediction of the LMP are placed mainly in 3

different areas, at the fat (negative Hounsfield values), around the water area (close to Hounsfield value 0) and around Hounsfield value 100.

When the stepwise selection was used, the number of variables decreases considerably. Moreover, it is possible to choose different numbers of variables. To have a similar error to those obtained with the selection based on VIP values, 20 variables with 5 extracted factors were selected as the working model. Figure 6 shows the regression coefficients of the 20 variables included in the model. The variables are placed in 3 areas; in the fat area, in the water area and in the lean area. Moreover, as in the previous model, the higher the volume associated with each selected variable, the lower the regression coefficient, indicating that all the variables were important for the prediction. Furthermore, when the product of the volume associated with each selected Hounsfield value by the regression coefficient is represented (Figure 7) it can be seen that, like in the previous model, the positive variables for the prediction of the LMP are placed in the lean area.

Although the two models studied are different, some similarities between them can be seen. Obviously the importance of each of the selected variables in the prediction of the LMP is higher in the model with fewer variables. However, the pattern of importance of the variables for the prediction of the LMP is very similar in both models.

3.2. Prediction of the carcass lean meat percentage

The root mean square error (RMSE) and the determination coefficient of the regression between carcass LMP predicted with CT with both equations and those obtained by manual dissection of the carcass is presented in Table 3. Moreover these parameters are presented by all the carcasses and by the carcasses grouped by fat thickness (see part 2.1.). It can be seen that, in both equations, the fat carcasses presented a higher RMSE. This is probably due to the fact that the fatter carcasses are more difficult to dissect due to the greater amount of fat and

the response error is probably higher. As the LMP obtained by dissection (LMP089) is used as a dependent variable the prediction is worse, probably due to the fact that LMP089 is less precise. Moreover, the maximum error of prediction of the dissection of carcasses with different fat thicknesses is 1.96% according to [25], although in that paper they did not present the prediction error depending on the fatness of the dissected carcasses. Furthermore, in the present work, the cutting was only performed by one butcher, in order to reduce the error of cutting. However, the error for the fatter carcasses (1.00% or 0.94%) is very low compared to the error obtained with classification equipment like Fat-o-Meat'er, VCS2000, Autofom which varied from 1.75 to 2.45 [27][28][29]. These types of equipment can be used on line in a slaughter plant, while, for the moment, it is not possible to use CT on line. Furthermore, the prediction equation was calculated for the Fat-O-Meat'er using carcasses which were almost the same scanned with CT. The prediction equation, which includes only one fat thickness (g34fom) and one muscle depth (m34fom) ($LMP = 66.91 - 0.895 * g34fom + 0.144 * m34fom$) had a RMSEPCV of 1.84% and a RMSE of 1.82%. This allows us to see that with only two measurements on the carcass we can obtain a good prediction error, which can be reduced when all the carcass is scanned. Moreover, with the scanning of all the carcass additional information can be obtained (other fat and muscle thicknesses, areas, volumes,...).

The RMSEPCV, with both studied equations (see Table 2), was very similar and it was lower than those obtained by [11] and higher than the SEC obtained by [5] which was 0.56. However, although the CT scanning parameters were similar, the equipment was not the same and this could be part of the cause of this difference. Another difference was that [5], before doing PLS, performed a transformation of the volumetric data to weight data applying different densities depending on the Hounsfield value. Moreover in our paper the dissection was the simplified EU Reference, which means that only four joints (the major cuts) were dissected to predict the LMP of the whole carcass, while the whole half carcass was scanned.

However in [5] and [11] the entire carcass was dissected (full dissection) and the lean dissected was closer to the lean measured with CT.

The dissected *vs* the predicted LMP for both equations is plotted in Figure 8 and it can be seen that both equations present a similar pattern and results, because the regression lines were overlapped.

In a subsample of 52 carcasses the four main cuts were scanned separately. The error of prediction of the LMP of the carcass using the frequency of attenuation values (in volume) from the scanning of each cut is presented in Table 4. Considering the joints separately, the scanning of the ham produces the lowest error of prediction in the estimation of the LMP of the whole carcass (0.97%). Furthermore the RMSEPCV is 1.37% when the loin is scanned and 1.73% and 1.75% for the belly and the shoulder, respectively. The higher error of prediction for the belly and the shoulder is probably due to errors in the cutting and dissection of these cuts, because for the butchers the shoulder is the most difficult joint to cut and the belly is difficult to dissect [25]. When the ham and the loin were considered together the error was somewhat lower than that obtained with only the ham (0.90% *vs.* 0.97%). These results indicate that the scanning of only the ham allows us to have a good prediction of the lean of all the carcass and it also allows us to reduce the cost of the scanning, because the number of images is much lower (average of 41 for the hams and 144 for the carcasses). This result makes sense because the ham is the cut which is easier to perform and with less error due to the fact that the cutting points are better defined than for the rest of the cuts [25]. Moreover, the LMP of the ham, as well as the loin, are very representative of the LMP of the carcasses [30]. One can see that a lower RMSEPCV is obtained when the four main cuts are used together. This makes sense due to the fact that the LMP of the whole carcass was obtained by means of the dissection of those four main cuts (simplified dissection) and not from the dissection of all the half carcasses (full dissection). However, the amount of images obtained with the scanning of the four main cuts is somewhat higher than those obtained with the

scanning of the whole carcass (average of 154 vs 144, respectively), and for that reason, it is not good from a practical and economical point of view.

3.3. Prediction of the lean meat percentage of the cuts

The RMSEPCV of the prediction of the LMP of the different cuts using images from the cut or images from the whole half carcass is presented in Table 5. It can be seen that for the ham and the belly the error is higher when only the images of the cut are used for the prediction, while for the loin and the shoulder the error is higher when the images of the half carcass are used for the prediction. The error is always higher than those obtained for the prediction of the carcass LMP. The best prediction errors using the images of each cut were for the loin (1.57%), followed by the shoulder (1.61%) and the ham (1.66%). The worst was for the belly (2.15%), probably because it is the most difficult joint to dissect [25] due to the fact that it consists of multiple thin tissue layers [19]. When the scan of all the carcass is used to predict the different cuts, the lowest error was for the ham (1.53%), followed by the shoulder (1.85%) and the belly (1.99%). The worst one was for the loin (2.30%).

4. Conclusions

It can be concluded that with the CT data the selection of the variables included in the prediction equation of the carcass lean meat percentage can be done either with the ‘variable importance for projection-VIP’ statistic criteria and with the stepwise selection criteria and that the results are good with the two techniques.

Prediction of carcass LMP with the CT is very good and, if it is necessary to reduce the costs of the scanning, it is possible to have a good prediction of the carcass LMP by scanning only the ham.

The prediction of the LMP of the different cuts, although good, is worse than the prediction of the carcass LMP.

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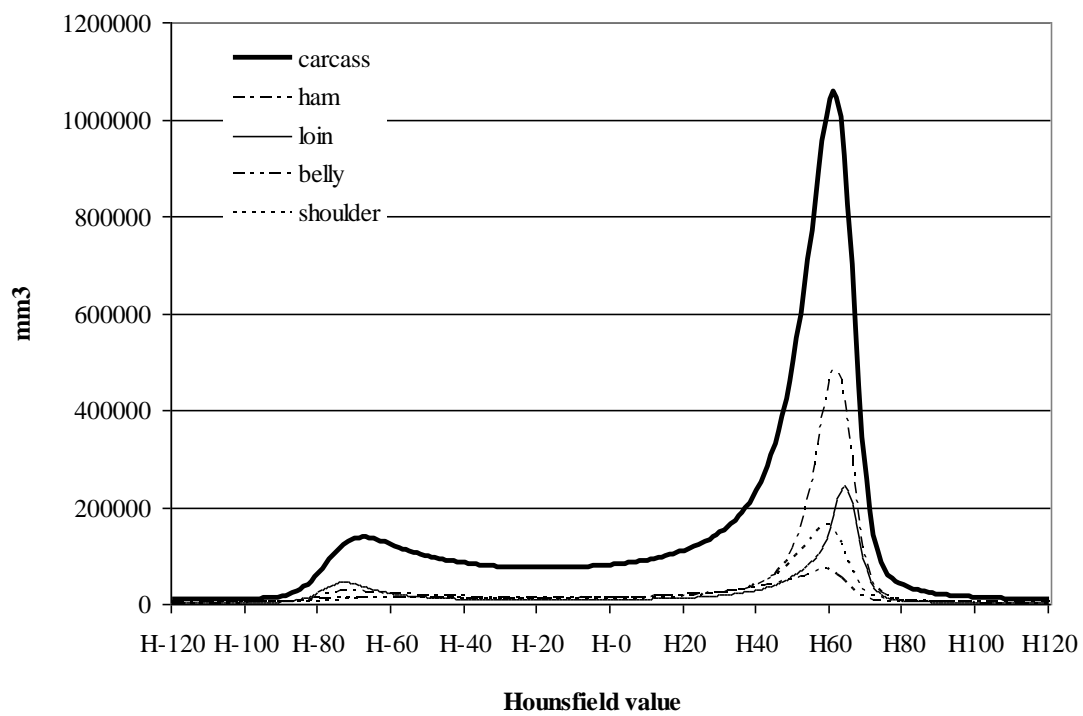
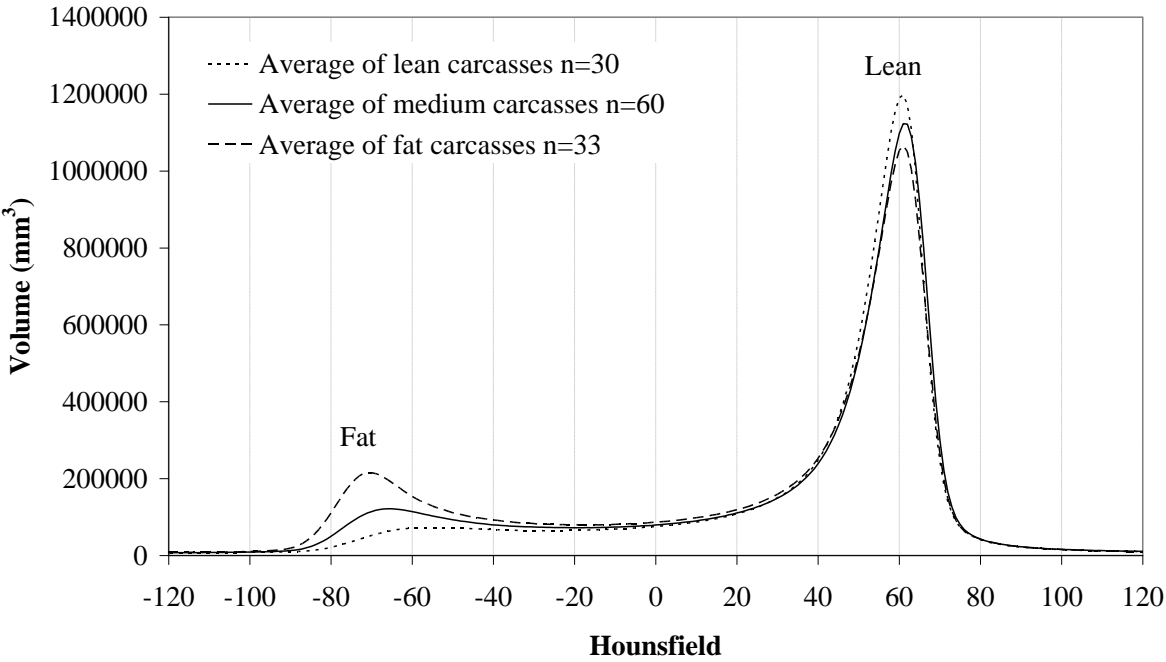


Figure 1: Mean volume associated with each attenuation Hounsfield value for the average carcasses and cuts scanned.

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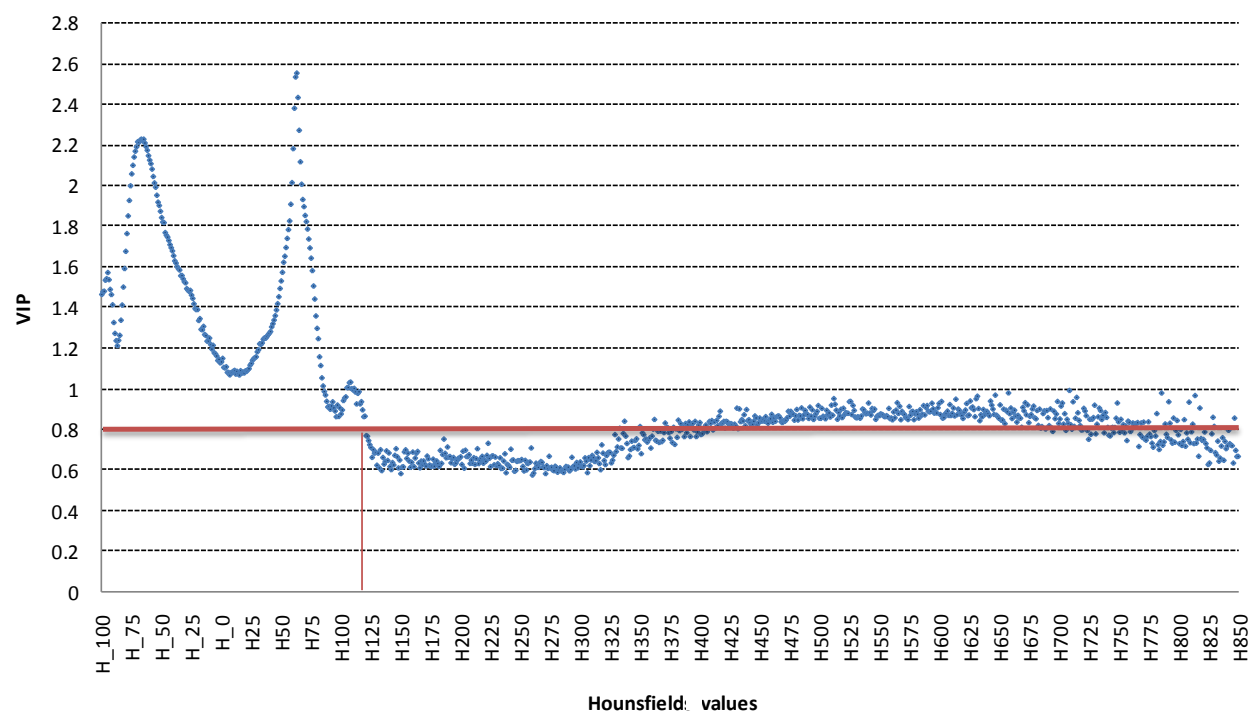


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420 Figure 2: Mean volume associated with each attenuation Hounsfield value for the average of
421 lean, medium and fat carcasses scanned.

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Figure 3: Variable importance for projection (VIP) of each prediction variable (attenuation

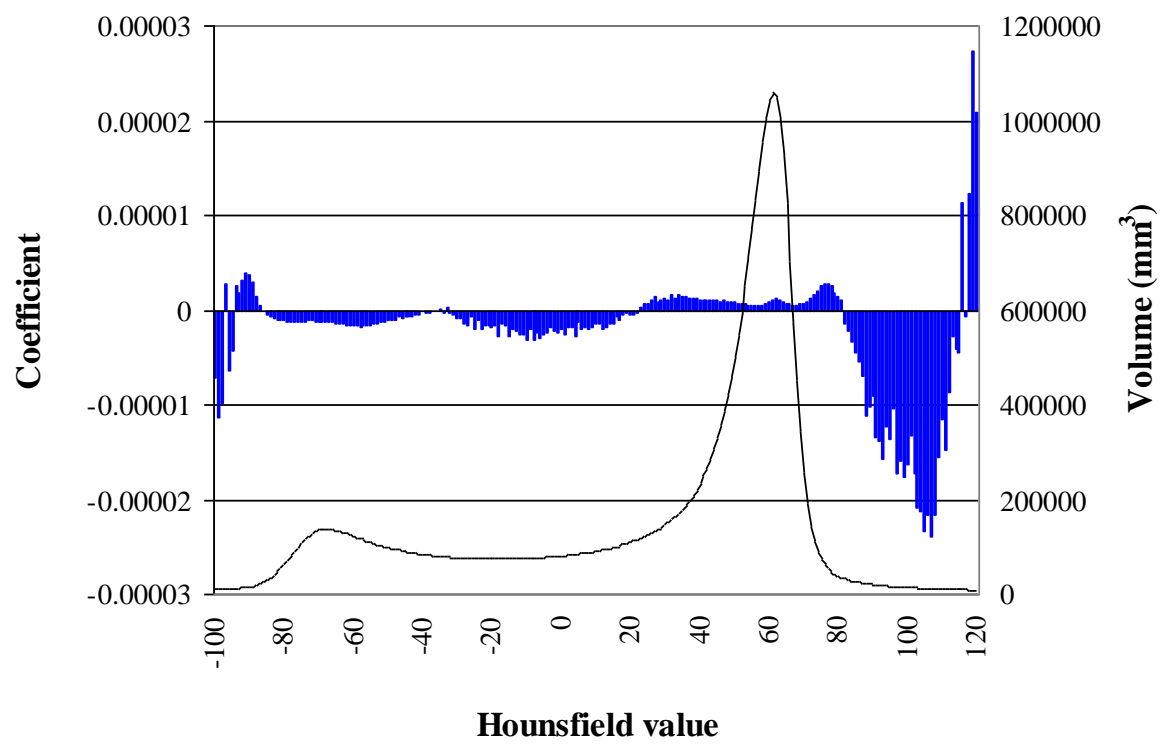
426

Hounsfield values).

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432 Figure 4: Coefficients of the regression equation when 221 variables were considered in the
433 equation (intercept=61.34). The line is the volume associated with each attenuation
434 Hounsfield value for the average carcasses scanned.

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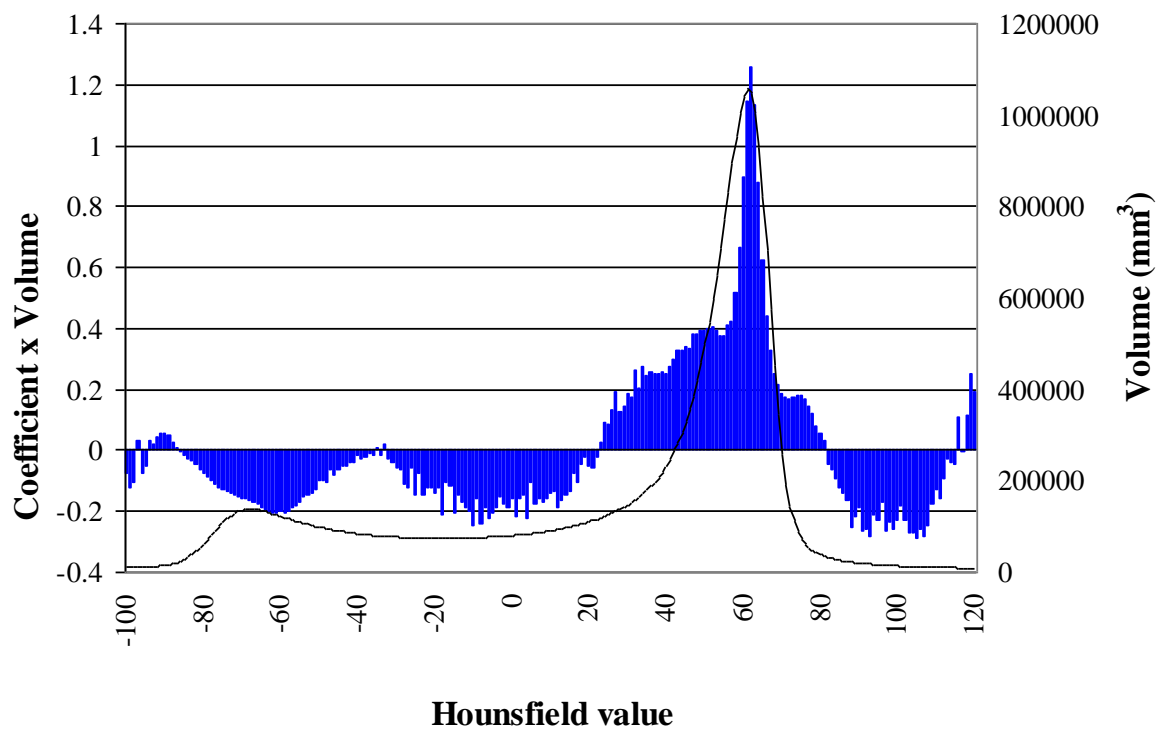
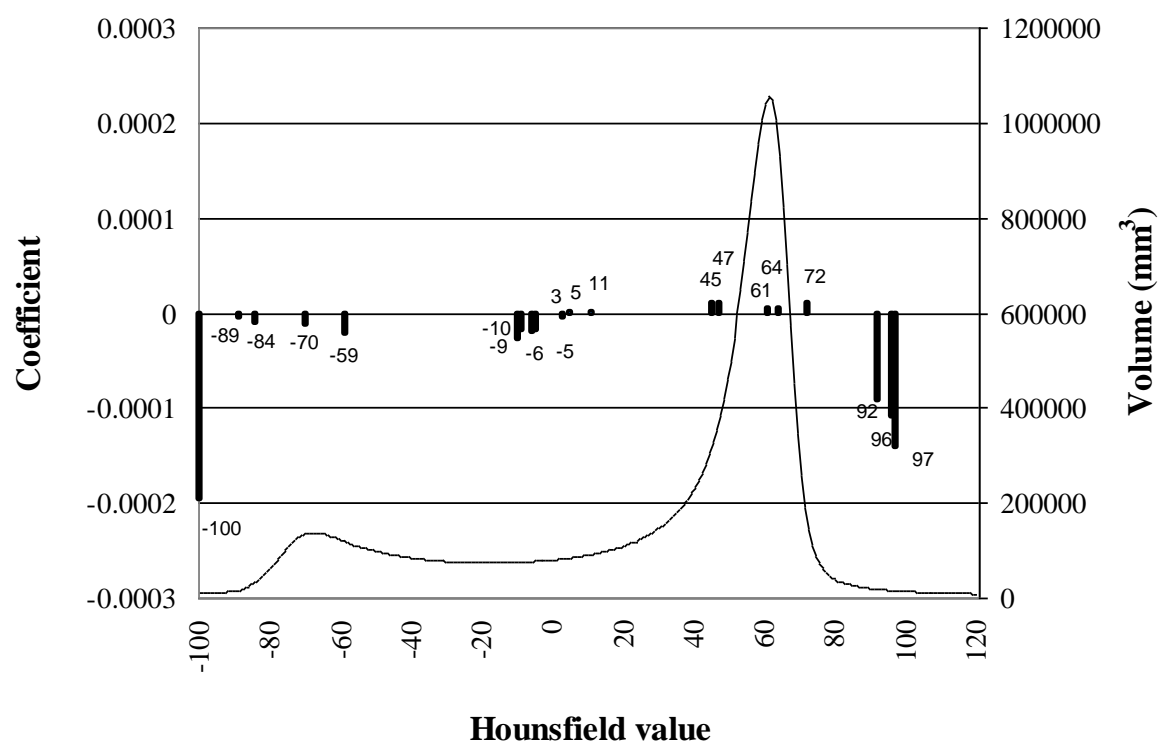


Figure 5: Coefficients of the regression equation multiplied by the volume associated with each variable (attenuation Hounsfield value) when 221 variables were considered in the equation (intercept=61.34). The line is the volume associated with each Hounsfield value for the average carcasses scanned.



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Figure 6: Coefficients of the regression equation when 20 variables were considered in the equation (intercept 61.56) and volume associated with each attenuation Hounsfield value for an average carcass. The line is the volume associated with each Hounsfield value for the average carcasses scanned.

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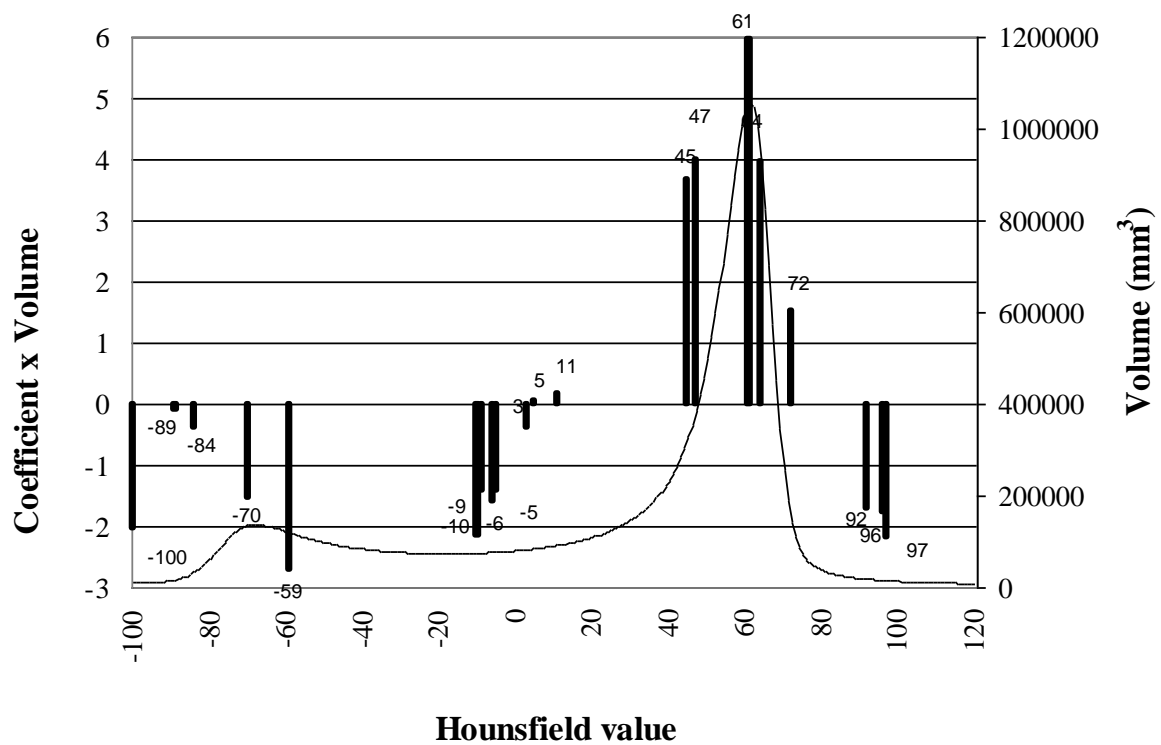


Figure 7: Coefficients of the regression equation multiplied by the volume associated with each variable (attenuation Hounsfield value) when 20 variables were considered in the equation (intercept=61.56). The line is the volume associated with each Hounsfield value for the average carcasses scanned.

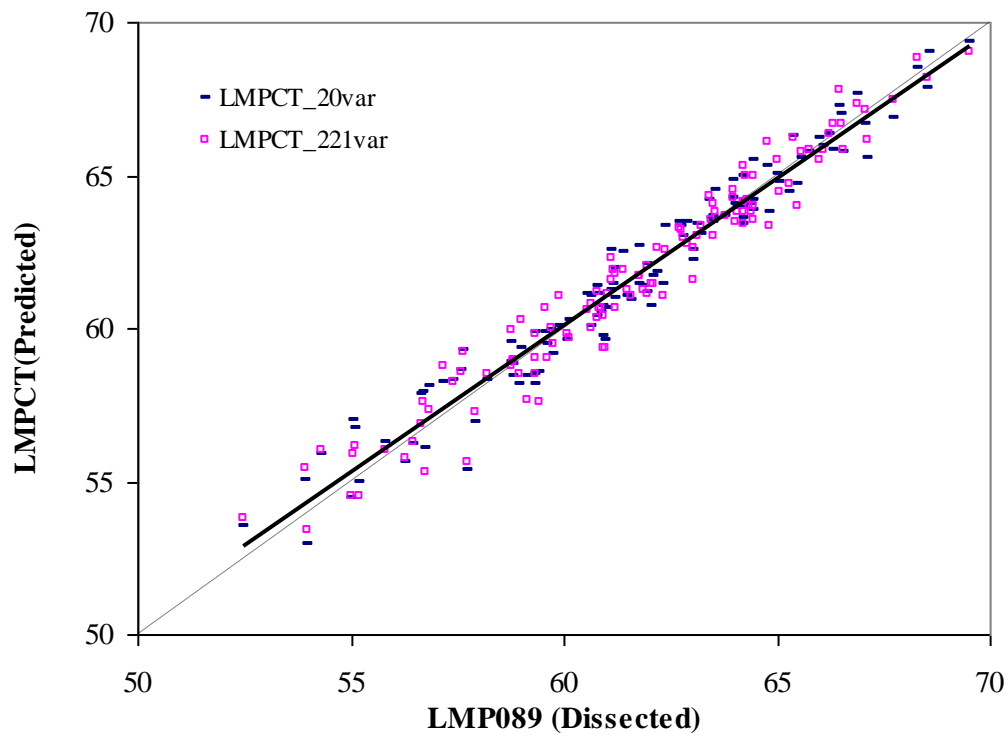


Figure 8: Dissected *versus* predicted lean meat percentage using the equation with 221 or 20 variables and regression line for each set of data (overlapping).

472

473 Table 1: Scanned carcasses and joints depending on the fat thickness.

474

	Fat thickness*			Total
	Lean	Medium	Fat	
Carcasses	30	60	33**	123
Cuts	16	18	18	52

* Measured with Fat-O-Meat'er at 6 cm of the midline and between the 3rd and 4th last ribs. Lean ≤ 12 mm, $12\text{mm} < \text{Medium} \leq 17$ mm, Fat > 17 mm

** One of the carcass of this group was considered outlier and was removed from all the calculations

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479 Table 2: Error of prediction of the carcass lean meat percentage depending on the variables
 480 included in the model and the selection method (n=122).

481

Selection method	Variable number (range)	PLS extracted factors	RMSEPCV(%)
No selection	951 (H-100 to H850)	5	1.05
No selection	951 (H-250 to H700)	5	1.01
VIP	371 (H-250 to H120)	7	0.92
VIP*	221 (H-100 to H120)	5	0.82
VIP	201 (H-100 to H100)	5	0.91
VIP (lean area)	90 (H10 to H100)	3	1.07
VIP (lean area)	110 (H10 to H120)	4	0.96
Stepwise	7	3	1.05
Stepwise	10	4	0.90
Stepwise	14	4	0.87
Stepwise*	20	5	0.83

*Selected variables for the following calculations

RMSEPCV: Root Mean Square Error of Prediction by Cross-Validation leave-one-out

VIP: Variable importance for projection statistic

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485

486 Table 3: Parameters of the regression between carcass lean meat percentage predicted with
 487 CT (with equations with 20 and 221 variables) and those obtained by manual dissection for
 488 all the carcasses and for the different groups of carcasses selected depending on their fat
 489 thickness.

490

	n	R ²	RMSE (%)
Equation with 20 variables			
All the carcasses	122	0.955	0.77
Fat carcasses	32	0.816	1.00
Medium carcasses	60	0.907	0.65
Lean carcasses	30	0.857	0.65
Equation with 221 variables			
All the carcasses	122	0.958	0.79
Fat carcasses	32	0.841	0.94
Medium carcasses	60	0.900	0.68
Lean carcasses	30	0.835	0.70

R²: Coefficient of determination

RMSE: Root Mean Square Error

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495 Table 4: Prediction of the lean meat percentage of the carcass by means of the CT scanning of
496 the main joints (prediction variables from -100 to +120 Hounsfield) (n=52).

497

Joint	Extracted factors	RMSEPCV (%)
Ham	5	0.97
Loin	4	1.37
Belly	2	1.73
Shoulder	2	1.75
Ham+Loin	6	0.90
Ham+Loin+Belly+Shoulder	6	0.71

RMSEPCV: Root Mean Square Error of Prediction by Cross-Validation leave-one-out

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501 Table 5: Prediction of the lean meat percentage (LMP) of the different cuts from the CT
502 images of the whole carcass and of each cut.

503

LMP of:	Images of:	N	Extracted factors	RMSEPCV (%)
Ham	Ham	52	4	1.66
Ham	Carcass	122	4	1.53
Loin	Loin	52	4	1.57
Loin	Carcass	122	4	2.30
Belly	Belly	52	2	2.15
Belly	Carcass	122	4	1.99
Shoulder	Shoulder	52	3	1.61
Shoulder	Carcass	122	3	1.85

RMSEPCV: Root Mean Square Error of Prediction by Cross-Validation leave-one-out

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