

1 Highlights

2 **Automatic marbling prediction of sliced dry-cured ham using im-** 3 **age segmentation, texture analysis and regression**

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- 5 • Interested regions for each muscle inside the ham slice are automatically
6 located.
- 7 • Marbling level of ham is predicted using color texture features and
8 regressors.
- 9 • The quality of the automatic prediction is similar to human experts.
- 10 • The system is fast enough to be deployed in quality controls of food
11 industry.

12 Automatic marbling prediction of sliced dry-cured ham
13 using image segmentation, texture analysis and
14 regression

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17 **Abstract**

Dry-cured ham is a traditional Mediterranean meat product consumed throughout the world. This product is very variable in terms of composition and quality. Consumer's acceptability of this product is influenced by different factors, in particular, visual intramuscular fat and its distribution across the slice, also known as marbling. On-line marbling assessment is of great interest for the industry for classification purposes. However, until now this assessment has been traditionally carried out by panels of experts and this methodology cannot be implemented in industry. We propose a complete automatic system to predict marbling degree of dry-cured ham slices, which combines: 1) the color texture features of regions of interest (ROIs) extracted automatically for each muscle; and 2) machine learning models to predict the marbling. For the ROIs extraction algorithm more than the 90% of pixels of the ROI fall into the true muscle. The proposed system achieves a correlation

of 0.92 using the support vector regression and a set of color texture features including statistics of each channel of RGB color image and Haralick’s coefficients of its grey-level version. The mean absolute error was 0.46, which is lower than the standard deviation (0.5) of the marbling scores evaluated by experts. This high accuracy in the marbling prediction for sliced dry-cured ham would allow to deploy its application in the dry-cured ham industry.

18 *Keywords:* Dry-cured ham, intramuscular fat, marbling, support vector
19 regression, texture analysis, image segmentation

20 **1. Introduction**

21 Dry-cured ham is a traditional meat product of many Mediterranean
22 countries that is widely consumed throughout the world, being its flavour
23 and texture characteristics highly appreciated by consumers. There are many
24 factors affecting the final characteristics of dry-cured ham, such as processing
25 conditions and raw material characteristics, i.e. fat content (Coll-Brasas et al.,
26 2021). In sliced dry-cured ham, visual intramuscular fat, subcutaneous fat
27 thickness and color are the parameters most used by the consumers for the
28 product evaluation, therefore affecting consumer’s acceptability and purchase
29 decision (Lorido et al., 2019). Although several non-invasive technologies
30 can be used to categorize entire hams according to its fat content
31 (de Prados et al., 2015), these technologies cannot be used to predict intramuscular
32 fat (IMF) in sliced products because of its variability between the
33 muscles of a ham.

34 Eating quality in meat has been associated to the fat distribution rather
35 than to the total IMF. Distribution of IMF is usually known as marbling,
36 because of its appearance similar to marble (Cernadas et al., 2002). One
37 of the most important challenges for producers is the heterogeneity of the
38 marbling in slices, that can vary significantly among ham pieces and even
39 within the same piece. Classification of slices of dry-cured ham according to
40 the marbling degree is of special interest for the food industry. Producers
41 would be able to segment the market, offering products tailored to consumer's
42 needs and increasing the value of their production.

43 Marbling ranking in different meats and meat products has been per-
44 formed by panels of trained experts or relying on standards consisting of
45 pictures depicting a scale of marbling (from 0.0 to 10.0), as it is the case
46 for the National Pork Producers standards (Moines, 1999). In the case of
47 dry-cured ham, a marbling ranking has been developed but it is not still
48 published. However, marbling evaluations by experts are costly and are not
49 feasible for the ham industry. Computer image analysis might be a solution
50 because it is a fast and non-destructive technology, and it is a replicable and
51 repetitive method that has been successfully applied to the assessment of
52 multiple food characteristics: fish (Dutta et al., 2016), cheese (Dias et al.,
53 2021) or bread (Srivastava et al., 2015). The scientific literature includes
54 several studies that apply computer image analysis to determine IMF and
55 marbling in different meat products. Combining magnetic resonance imag-
56 ing (MRI) and computer vision techniques, the works (Cernadas et al., 2005;

57 Ávila et al., 2019) predicted marbling in the biceps muscle of dry-cured hams
58 and loins, but MRI is a technology that is expensive to install in meat in-
59 dustries.

60 For the segmentation of IMF in meat and meat products, several tech-
61 niques have been applied: K-means clustering in beef Longissimus dorsi
62 muscle (Jackman et al., 2009), automatic thresholding (Liu et al., 2018) and
63 the Otsu method (Uttaro et al., 2021) in pork loin, multi-scale line detec-
64 tion (Cernadas et al., 2002), gradient-based techniques (Santos-Garcés et al.,
65 2014) and convolutional neural networks (Muñoz et al., 2019) for dry cured
66 ham. In general, these segmentation algorithms perform quite well, high
67 correlation values or low classification errors are obtained, depending on
68 the aim of the study. For classification of marbling, the following tech-
69 niques have been applied: chemical pre-treatments and line detection al-
70 gorithms (Faucitano et al., 2004), line detection algorithm (Liu et al., 2012)
71 and (Huang et al., 2013) in pork meat, neural networks (Muñoz et al., 2015)
72 and decision trees in hyperspectral images of dry cured ham (Velásquez et al.,
73 2017). In general, the results of marbling classification are quite satisfactory
74 with low prediction errors and at least 90% of the samples correctly classified.
75 However, the evaluation of IMF and marbling in dry-cured ham slices is still
76 a challenge. A wide range of variation in the color of lean and fat tissues
77 can be observed in slices across hams, which poses a challenge for image seg-
78 mentation and the evaluation of marbling. These differences are explained
79 by the different levels of drying of the hams, and the presence of precipitates

80 such as phosphates of tyrosine crystals, with a white color similar to that of
81 the fat.

82 This paper proposes a prototype to automatically predict marbling of
83 the principal muscles from a ham slice using image segmentation, texture
84 analysis and regression models. Specifically, we define an algorithm that au-
85 tomatically extracts squared regions inside the main muscles. Then, color
86 texture features are computed for each region, which are the inputs to a re-
87 gression model that predicts the marbling score for each muscle. The paper
88 is organised as follows. Section 2 describes the materials used to obtain the
89 ham slice, to develop the sensorial analysis on the ham muscles and to an-
90 notate the contour of ham muscles. Section 3 describes the algorithm used
91 to extract automatically the square ROIs representing each ham muscle, and
92 briefly explains the color texture features extraction techniques and the re-
93 gression models. Section 4 describes the experimental setup and statistical
94 evaluation measures used. Section 5 presents and discusses the results. Fi-
95 nally, section 6 summarises the main conclusions and proposals of future
96 work.

97 **2. Materials**

98 This section describes the material used to obtain the data in this re-
99 search: the system used to capture images of ham slice (subsection 2.1), the
100 traditional procedures to determine the marbling of a ham muscle (subsec-
101 tion 2.2), and the process to draw the outline of each muscle on the ham slice

102 (subsection 2.3).

103 *2.1. Image acquisition*

104 High quality images were acquired with a calibrated digital camera Canon
105 EOS 50D (15.1 megapixels) and an objective Canon EF-S 18–200 mm f/3,5–
106 5,6 IS. The camera was mounted in a black closet ($1.06 \times 1.06 \times 2.50 \text{ m}^3$) with
107 8 equidistant halogen lights Solux Q50MR16 CG/47/36°12 V/50 W/4700 K
108 (Eiko Ltd., Shawnee, Kansas, U.S.A.) to ensure a correct lighting. White
109 balance was carried out with a white card (Lastolite). The camera was
110 connected to a computer to store the images. Slices were placed 30 cm below
111 the camera on a uniform black surface. Photos of both sides of the dry-
112 cured ham slices were taken. All the images were taken during the same
113 session. The white balance of the images was carried out with Capture One
114 PRO 5.0 software (Phase One A/S Inc., Frederiksberg, Denmark) and RGB
115 images of 667×1000 pixels with 16 bits color were obtained, with one pixel
116 corresponding to 0.3968 mm^2 . For the evaluation of marbling, the computer
117 screen was calibrated so that the colors of the images were as close as possible
118 to the colors of the samples (NEC Multisync LCD 2690 WUXI2). Figure 1
119 shows a scheme of the image acquisition system used.

120 *2.2. Marbling evaluation*

121 Sensory analysis (marbling evaluation) of the samples was carried out by
122 six trained panelists (ISO 8586-2: 2012) and consisted of a visual assess-
123 ment of the marbling of the most representative muscles: *Biceps femoris*

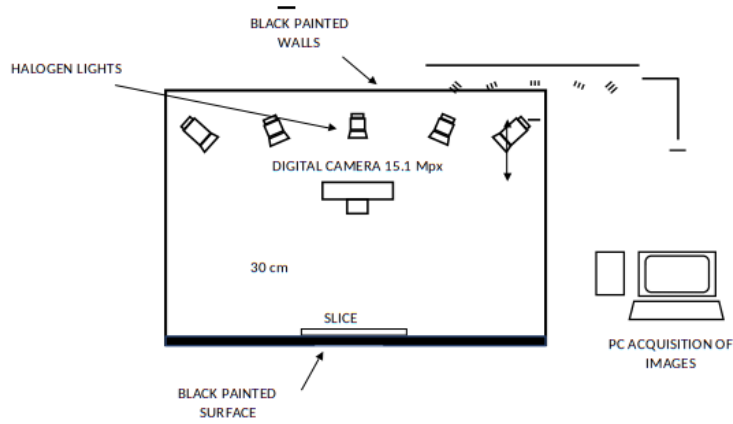


Figure 1: Scheme of the image acquisition system.

124 (BF), *Semimembranosus* (SM) and *Semitendinosus* (ST) of a dry-cured ham
 125 (Bermúdez et al., 2014). Marbling was scored by consensus (in our case
 126 three panelists) by means of scoring scale from 0.5 (minimum marbling) to
 127 10 (maximum marbling) at intervals of 0.5. When scoring marbling, the
 128 panelists considered the total amount and the distribution of the fat streaks.
 129 Marbling evaluation was done in triplicate by the panelists. The standard
 130 deviation of the panelists among trials was determined at 0.5 points.

Muscle	#images	Min.	Max.	Avg.	Dev.
Biceps femoris	337	1	7	3.1	1.0
Semimembranosus	322	0.5	6	2.0	1.0
Semitendinosus	55	4	9	6.2	1.2

Table 1: Number of images, minimum, maximum, average and standard deviation of the marbling values for the different ham muscles used in this experimentation.

131 A collection of commercial dry-cured hams were obtained from different
 132 ham producers with crosses from different pig breeds (Large White, Lan-

drace, Duroc and Iberian) and having a wide range of marbling. A 2 cm thick slice containing muscles BF, SM and ST was obtained at 10 cm from the aitch bone in the distal direction (at the widest part of the ham) and packed into plastic bags of polyamide/polyethylene (oxygen permeability of 50 cm³/m²/24 h at 23°C and water permeability of 2.6 g/m²/24 h at 23°C and 85% RH, Sacoliva[©] S.L., Spain). The image dataset is composed of 714 images obtained in the following way: photos were obtained from 180 commercial dry-cured hams, 2 slices/ham (at different points in the ham, obtaining slices quite different one from another) and 2 muscles for each slice, giving a total of 180 hams $\times$ 2 slices $\times$ 2 muscles = 720 photos. Six of these photos were not included in the evaluation due to defects on the surface such as cuts and phosphate crystals. For each image, it was only provided the measure of marbling for one muscle with values between 0.5 and 9 with the distribution shown in table 1. Figure 2 shows examples of different marbling scores for biceps muscle.

2.3. Muscle annotation

To develop the first experiment, the experts delineated the contour of the muscle for which the marbling was estimated by sensorial analysis. To draw the contours for all images, they used a home-made software, as it can be seen in figure 3.

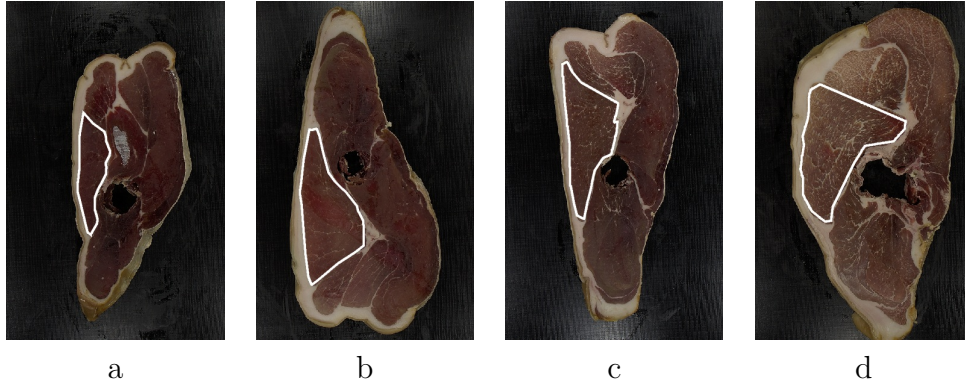


Figure 2: Examples of marbling scores for biceps muscle: a) slice 8372 with score 1; b) slice 8485 with score 1; c) slice 8274 with score 3; and d) slice 8424 with score 6.5.

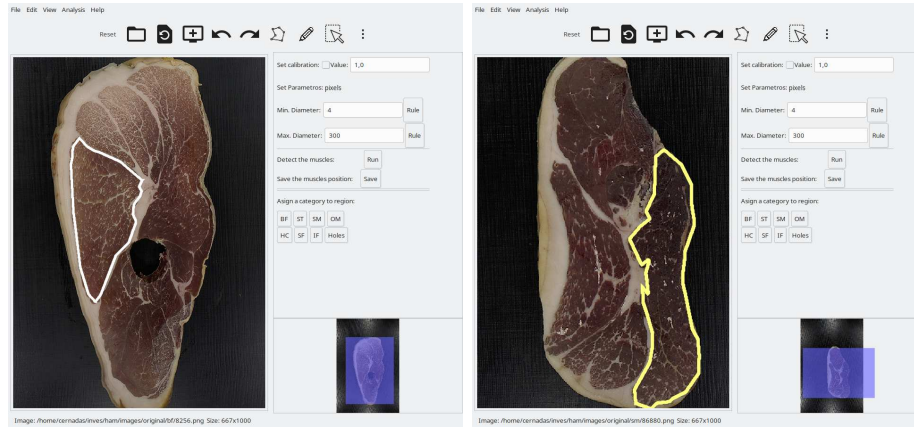


Figure 3: Examples of the contours of biceps (left panel) and semimembranosus (right panel) muscles overlapped to images of ham slice.

153 3. Methods

154 The system proposed to predict the marbling from dry-cured ham slices,
 155 shown in figure 4, encloses the following stages: 1) the image acquisition
 156 system already described in section 2.1; 2) the automatic extraction of the
 157 ROIs in the ham slice; 3) the computation of features from the ROI extracted;

158 and 4) the regression model to predict the marbling score of each muscle in
 159 the ham slice. The subsections 3.1, 3.2 and 3.3 describe the stages 2, 3 and
 160 4, respectively.

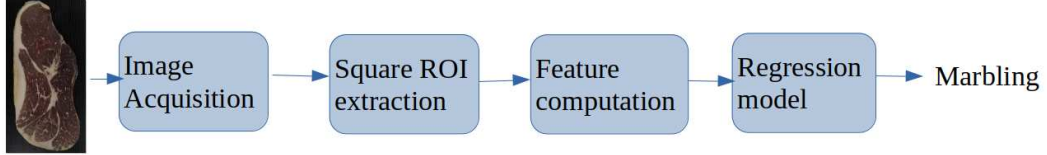


Figure 4: Stages of the method to predict the marbling from dry-cured ham slices.

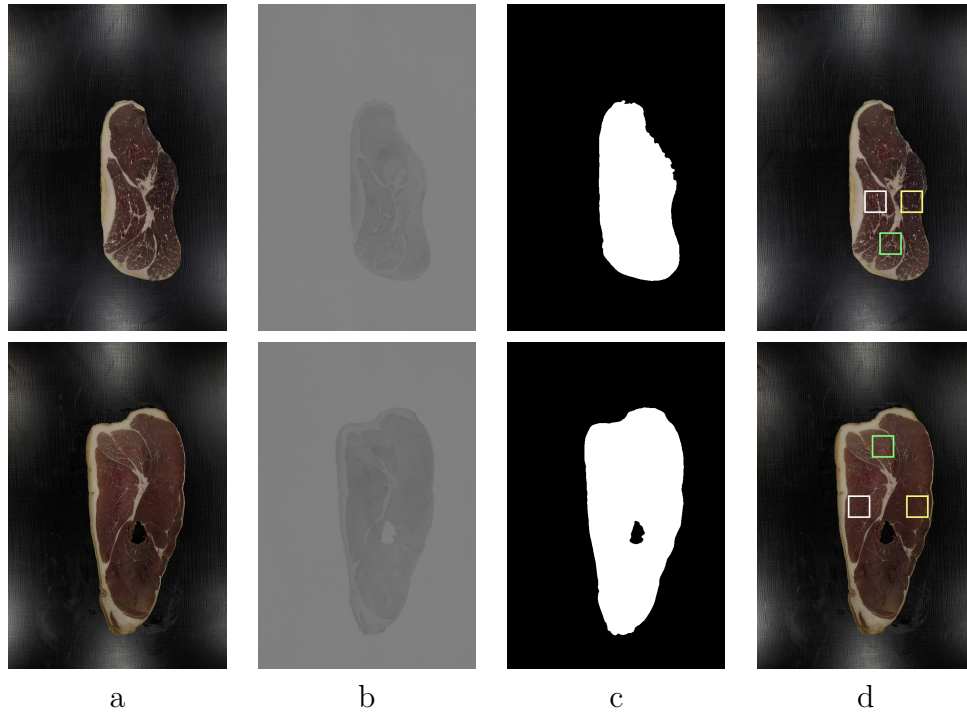


Figure 5: Examples of the extraction of square ROIs from the ham slice for all muscles: a) original images; b) channel b of Lab color space after smoothing; c) binary mask with the ham slice and bone hole and d) the extracted ROIs for each muscle, white for biceps, yellow for semimembranosus and green for semitendinosus.

161 3.1. Automatic extraction of ROIs

162 The ham slice images are processed to automatically extract square ROIs
163 from the biceps femoris, semimembranosus and semitendinosus muscles. These
164 extracted ROIs will be used in the third experiment. In this process, we take
165 into account the anatomical information about the distribution of the mus-
166 cles and subcutaneal/intermuscular fat within the ham. As it can be seen in
167 figure 3, some slices present a hole in the slice (left panel), due to the slice
168 is cut by the ham bone, and others not (right panel). As well, the biceps
169 muscle can be in the right or left side of the image. The algorithm to extract
170 the square ROIs encloses the following steps: 1) extract the ham slice from
171 the image; 2) check if the slice has the bone hole; 3) if there is not a hole
172 in the slice, find the biggest intermuscular fat region in the slice; 4) in both
173 previous cases (step 2 or 3), a reference position is calculated to know the
174 slice orientation, which allows to know if the muscles are upper/bottom or if
175 the BF muscle is on left/right side of the slice; and 5) extract a square region
176 for each muscle. In our case, we use a ROI with length $s = 64$ pixels.

177 To extract the ham slice, the original RGB image $I(x, y)$, with $x =$
178 $1, \dots, N$, and $y = 1, \dots, M$, of dimensions $N \times M$, is transformed to the
179 Lab color space, because it is more robust to illuminance variance than the
180 RGB space (Cernadas et al., 2017). Let $I_b(x, y)$ be the b channel of the ham
181 slice after smoothing with a mask (we use a mask of 5 pixels) in order to
182 attenuate the small fat features and noise (column b in figure 5). Let h_b be
183 the histogram of image $I_b(x, y)$. The maximum value H_b of h_b is chosen to

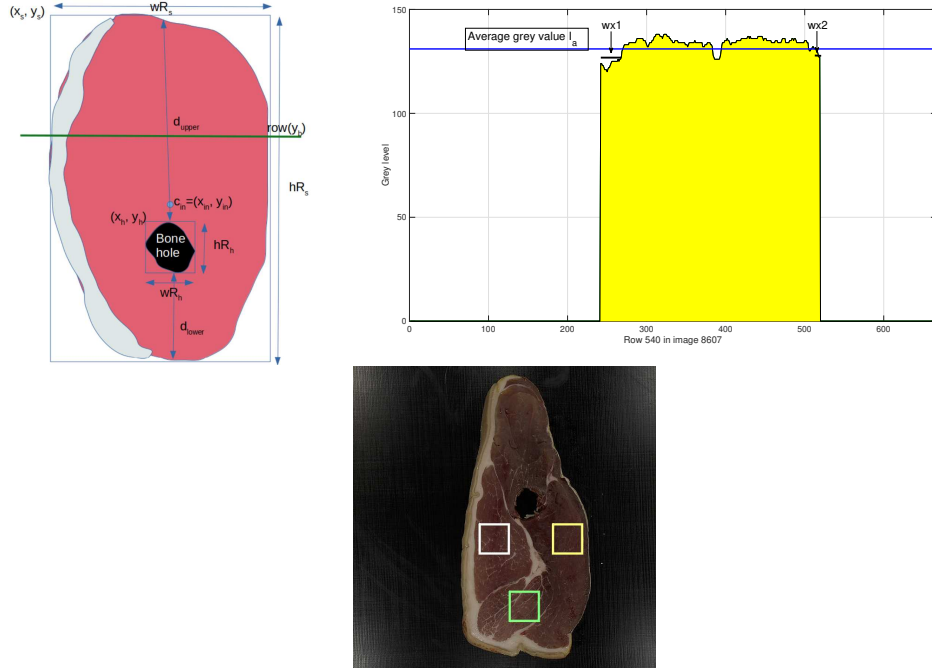


Figure 6: Extraction of the square ROIs of each muscle. Upper left panel: scheme of a ham slice. Upper right panel: row 540 of the transformed version I_a of the ham slice no. 8607. Lower panel: the ham slice with the extrated ROIs overlapped: *biceps* (white), *semimembranosus* (yellow) and *semitendinosus* (green).

184 calculate the area of ham slice. The $I_b(x, y)$ image is thresholded to calculate
 185 the binary image $B(x, y)$ using the following expresion:

$$B(x, y) = \begin{cases} 0 & |I_b(x, y) - H_b| \leq 5 \\ 255 & \text{otherwise} \end{cases} \quad (1)$$

186 After thresholding, we apply morphological operators to the binary image
 187 B in order to fill small holes. First, the biggest region of B is extracted and it

Algorithm 1: Automatic extraction of square ROI images for each muscle from a ham slice.

```

1 Algorithm:  $[I_{BF}, I_{SM}, I_{ST}] = \text{ExtractSquaredROI}(I, s)$ 

   Data:  $I$ : original RGB image of ham slice;  $s$ : size of ROI
   Result:  $I_{BF}, I_{SM}, I_{ST}$ : square ROI images for biceps,
             semimembranosus and semitendinosus muscles

2  $I_b \leftarrow b$  channel of Lab image smoothed by box filter
3  $h_b \leftarrow$  histogram of  $I_b$ 
4  $H_b \leftarrow$  maximum of  $h_b$ 
5  $B \leftarrow$  binary image using eq. 1 and morphological processing
6  $B_m \leftarrow$  image mask with ham slice outline and hole if exist
7  $R_s \leftarrow (x_s, y_s, wR_s, hR_s)$  rectangle enclosing ham slice
8  $I_a \leftarrow a$  channel of Lab image smoothed and masked by  $B_m$ 
9  $\mu_a \leftarrow$  average value of  $I_a$  inside  $B_m$ ; offset $\leftarrow 10$ 
10 if existsHole( $I_b$ ) then
11    $R_h \leftarrow (x_h, y_h, wR_h, hR_h)$  rectangle enclosing hole
12    $d_{upper} \leftarrow y_s - y_h$ ;  $d_{lower} \leftarrow y_s + hR_s - (y_h + hR_h)$ 
13   if  $d_{upper} > d_{lower}$  then
14      $y_c \leftarrow y_s - (y_s - y_h)/4$ 
15      $y_e \leftarrow y_h - s/2 - \text{offset}$ 
16   else
17      $y_c \leftarrow y_s + hR_s - s - (y_s + hR_s - y_h - hR_h)/4$ 
18      $y_e \leftarrow y_h + hR_h + s/2 + \text{offset}$ 
19   end
20    $x_c \leftarrow \text{middlePointX}(\text{row}(y_c + s/2))$ 
21    $I_{ST} \leftarrow \text{extST}(x_c - s/2, y_c, s)$ 
22    $[I_{BF}, I_{SM}] \leftarrow \text{extBSM}(y_e)$ 
23 else
24    $T_2 \leftarrow$  second Otsu's threshold of  $I_a$ 
25    $(x_{in}, y_{in}) \leftarrow$  centroid of the largest inner region inside  $I_a$  after
     thresholding using  $T_2$ 
26    $I_{ST} \leftarrow \text{extSTC}(x_{in}, y_{in}, s)$ 
27    $[I_{BF}, I_{SM}] \leftarrow \text{extBSM}(y_{in})$ 
28 end

```

188 is associated with the contour of ham slice. Next, the algorithm searches for
 189 a large black region inside this contour. If this region is found, it is associated
 190 to the bone hole. The contours of ham slice and bone hole are used to create
 191 a binary mask image $B_m(x, y)=0$ (black color in column c of figure 5) when
 192 (x, y) is inside the contour and outside the bone, and $B_m(x, y)=1$ (white
 193 color) when (x, y) is outside the contour or inside the bone. This process
 194 is shown in the columns a, b and c of the figure 5. The process to extract
 195 the ROI for each muscle, denoted as I_{BF} , I_{SM} and I_{ST} for *biceps femoris*,
 196 *semimembranosus* and *semitendinosus*, respectively, is drawn in figure 6 and
 197 summarized by algorithm 1. Let R_s be the rectangle enclosing the ham slice,
 198 which is defined by the top left vertex (x_s, y_s) and by its width (wR_s) and
 199 height (hR_s). Let I_a be the a channel of Lab image of the ham slice masked
 200 (multiplied) by B_m . Two cases can be considered:

- 201 a) When the ham slice has visible bone hole, the algorithm uses as refe-
 202 rence its enclosing rectangle R_h , with initial coordinates (x_h, y_h) and
 203 width and height wR_h and hR_h , respectively.
- 204 b) When the ham slice has not a visible bone hole, the algorithm searches
 205 for the largest intermuscular fat region and calculates its centroid. In
 206 order to discard the background from the image I_a , we selected a thresh-
 207 old applying the Otsu's method (Otsu, 1979) with three thresholds
 208 $\{T_i\}_{i=1}^3$, that correspond to different types of materials in the image
 209 (background, subcutaneal fat and muscle). Experimentally, we checked

210 that threshold T_2 ensures an accurate segmentation of background from
 211 the remaining materials. In the binary image generated by threshold-
 212 ing I_a with T_2 , the inner biggest region is selected as representing the
 213 intermuscular fat region, whose centroid is (x_{in}, y_{in}) .

214 These reference points (bone hole or centroid of intermuscular fat) allow
 215 to select the height where the different muscles should be extracted. In order
 216 to extract the BF and SM muscles, the algorithm finds out whether the biceps
 217 is on the left or right side of the ham slice. The position in the horizontal
 218 axis for extracting the BF and SM muscles is determined analysing a specific
 219 row in the image I_a . This row is smoothed in order to attenuate the random
 220 noise and it is denoted as $\mathbf{row}(y_b) = I_a(x, y_b)$, $x = 1, \dots, M$ (see upper left
 221 panel of figure 6). In order to locate the BF muscle, we estimate the pixels
 222 representing the subcutaneal fat (close to the *biceps* muscle) along the $\mathbf{row}(y_b)$
 223 counting the number of values. Specifically, the procedure is as follows:

- 224 1. Let k_1 be the first value of x where $I_a(x, y_b) > 0$ coming from left to
 225 right (see the upper right panel of figure 6). Let $wx1$ be the number of
 226 values of x where $I_a(x, y_b) < \mu_a$, for $x = k_1, k_1 + 1, \dots, M$ (i.e. going
 227 from left to right side), where μ_a is the average value of I_a inside B_m .
- 228 2. Let k_2 be the first value of x where $I_a(x, y_b) > 0$ coming from right
 229 to left, and $wx2$ the number of values that $I_a(x, y_b) < \mu_a$, for $x =$
 230 $k_2, k_2 - 1, \dots, 2, 1$ (i.e. going from right to left side).

231 If $w x_1 > w x_2$ the BF muscle is on the left side of ham slice. Otherwise, it
 232 is on the right side. This process is performed by the `extBSM(y)` function in
 233 the algorithm 1, where y represents the row to be analysed in the image. So
 234 the square ROIs for muscles BF and SM, of size s , are extracted at positions
 235 $(k_1 + w x_1 + s/2 + \text{offset}, y)$ and $(k_2 - w x_2 - s/2 - \text{offset}, y)$ (we use an offset of
 236 10 pixels in order to avoid defects in the contour of ham slice). The regions
 237 extracted for each muscle are shown overlapped to the ham slice in the column
 238 d of the figure 5. When there is bone hole, the y coordinate for extracting
 239 muscles are determined calculating the distances $d_{upper} = y_s - y_h$ and $d_{lower} =$
 240 $y_s + h R_s - (y_h + h R_h)$. If $d_{upper} > d_{lower}$, the muscles are above the bone
 241 hole, otherwise the muscles are below the bone hole. The `middlePointX(y)`
 242 function returns the middle point of the ham slice for the image row y . The
 243 `extST(x,y,s)` function extracts a square ROI of size s for the ST muscle
 244 from the original RGB image in the point (x, y) for ham slices with visible
 245 hole. The `extSTC(x,y,s)` function extracts a square ROI of the ST muscle
 246 for ham slices without visible hole. Let $x_{c1} = \text{middlePointX}(\text{row}(y_{in} + s/2))$
 247 and $x_{c2} = \text{middlePointX}(\text{row}(y_{in} - s/2))$ be two middle points in the ham
 248 slice in the horizontal axis near the centroid of intermuscular fat. Let r_1
 249 and r_2 be two ROIs of size s , extracted from the image I_a in the points
 250 $(x_{c1} - s/2, y_s - (y_s - y_{in})/6)$ and $(x_{c2} - s/2, y_s + w R_s - s - (y_s + w R_s - y_{in})/3)$
 251 respectively. To select which ROI corresponds to the ST muscle, the mean
 252 value of both ROIs, μ_{r1} and μ_{r2} , are calculated and the ST muscle is the ROI
 253 with the highest mean value, which corresponds with the ROI containing

254 more fat.

255 3.2. Color texture features

256 Texture analysis has been employed in previous works to predict different
257 qualities or attributes of meat products from MRI images (Cernadas et al.,
258 2005; Ávila et al., 2019), which are grey level images. Nevertheless, it is
259 known that the color is also a very important characteristic in other computer
260 vision applications (González-Rufino et al., 2013; Cernadas et al., 2017). Color
261 texture analysis can be tackled from different paradigms: simple color fea-
262 tures, grey level texture features and integrative color texture analysis. A
263 recent work (Cernadas et al., 2017) concluded that parallel approaches, that
264 concatenate the two former, are superior than analysing directly the color
265 texture with integrative approaches.

266 There are many methods to extract only the color in a strict sense (Cernadas et al.,
267 2017). In this work we use two color spaces, RGB and Lab, where the chro-
268 matic channels are a and b . We use first-order features of three types, each
269 with 2 feature vectors:

- 270 1. Only mean value for each chromatic channel, denoted as CM, that
271 stands for “color mean”: 1) **CMRGB**, 3 features: mean color of the
272 channels R, G, and B of the muscle; 2) **CMab**, 2 features: mean color
273 of the channels a and b of the Lab image. In both cases, the mean
274 values are only calculated inside the muscle regions.
- 275 2. Mean and variance for each chromatic channel, CMV, or color mean

276 and variance: 1) **CMVRGB**, 6 features: mean and variance of the
277 channels R, G and B of the RGB image. 2) **CMVab**, 4 features: mean
278 and variance of the channels a and b of the Lab image.

279 3. First order statistics, denoted as FOS, for each chromatic channel, that
280 include mean, variance, skewness, kurtosis and entropy: 1) **FOSRGB**,
281 15 features: 5 features $\times$ 3 color channels of the RGB image. 2)
282 **FOSab**, 10 features: 5 features $\times$ 2 color channels of the Lab image.

283 The most popular grey level texture features belong to the families of
284 statistical, such as second-order features and local binary patterns (LBP),
285 and frequencial, including wavelet and Gabor features. The grey level version
286 of the original image is obtained following two alternative approaches: 1)
287 converting a RGB image to grey level image; and 2) using the L channel of
288 a Lab image.

289 Among the second-order statistics we selected the Haralick coefficients
290 (Haralick et al., 1973), derived from the grey level cooccurrence matrix (GLCM).
291 These coefficients describe the probability of finding two pixels with the same
292 value at different scales, or distances, and orientations, or angles. The pa-
293 rameters used normally are: 1) the orientations 0° , 45° , 90° and 135° ; and 2)
294 three scales, with pixel distances of 1, 2, and 3. For each scale, the GLCM
295 matrix is averaged over all orientations, and the contrast, homogeneity, cor-
296 relation and energy of the matrix is computed. Two feature vectors were
297 considered: 1) **HarRGB**, that includes the four previous features for scales

298 $\{1, 2, 3\}$ calculated on the grey version of the RGB image, with $4 \times 3 = 12$ fea-
 299 tures; and 2) **HarLab**, which is similar to **HarRGB** but calculated on the
 300 L channel of Lab image. When the input is an irregular region, the features
 301 are computed only on pixels included in the region (González-Rufino et al.,
 302 2013). The Haralick’s coefficients were computed using the `graycomatrix()`
 303 function of the Matlab Image Processing Toolbox¹.

304 The LBP operator is a state-of-art texture analysis approach proposed by
 305 Ojala et al. (2002), which describes each pixel comparing its value with the
 306 neighboring pixels. For each neighboring pixel, the result will be set to one
 307 if its value is higher than the value of central pixel, otherwise the result will
 308 be set to zero, developing a binary code for each pixel. We use the uniform
 309 LBP, which considers the binary patterns with only two transitions (from
 310 0 to 1 and vice versa). In a circularly symmetric neighbor set of P pixels
 311 can occur $P + 1$ uniform binary patterns. The number of “1’s” in the binary
 312 pattern is the label of the pattern, while the nonuniform patterns are labelled
 313 by $P + 1$. This process can be applied to different scales, as in the case of
 314 cooccurrence image. The histogram of the pattern labels accumulated over
 315 the intensity image is employed as texture feature vector. The most common
 316 values for these parameters are $\{(P, R) \in (8, 1), (12, 2), (16, 3)\}$, where P is
 317 the number of neighbors and R is the distance between the central pixel
 318 and the neighbors. We construct the texture feature vectors **LBPRGB** and

¹<https://www.mathworks.com>

319 **LBPLab** to be applied on the grey version on RGB image and on the L
320 channel of the Lab image, respectively. Both vectors have $42 = (8 + 2) +$
321 $(12 + 2) + (16 + 2)$ features, because the uniform LBP are $P + 2$ features. We
322 use the LBPMatlab² implementation provided by the LBP creators.

323 Discrete wavelet transform (DWT) representation is a theory for multi-
324 dimensional signal decomposition (Walker, 2008; Laine and Fan, 1993) which
325 recursively apply filters to decompose the image into low-pass and high-
326 pass frequency bands. A compact representation for texture analysis can
327 be computed taking the mean and variance of the energy distribution for
328 the transformed coefficients in each sub-band and decomposition level. We
329 compute texture feature vectors calculating the mean and variance of the
330 energy over 3 levels of decomposition and create the feature vectors $\mathbf{WT}_{ijk}$,
331 where: 1) $i = \{Haar, Daub\}$ is the type of filters to use, namely Haar (2
332 coefficients) or Daubechies filtering with four coefficients; 2) $j = \{RGB, Lab\}$
333 is the grey level version of the RGB image or the L channel of the Lab image;
334 and 3) $k = \{LL, All\}$ represents if only the low-low decomposition sub-bands
335 are considered ($6 = 2 \times 3$ features) or all the sub-bands ($24 = 2 \times 3 \times 4$
336 features). We used the functions `wfilters()` and `dwt2()` of the Matlab
337 Wavelet Toolbox.

338 Gabor filters are sinusoidal waves modulated by a Gaussian envelope
339 that can be used for texture classification (Randen and Husoy, 1999). The

²<http://www.cse.oulu.fi/CMV/Downloads/LBPMatlab>

340 filters are applied to the images varying their frequency and orientation.
 341 Bianconi and Fernández (2007) analysed the influence of these parameters
 342 for texture classification. After applying a set of digital Gabor filters $G_{ij}(x, y)$
 343 with $i \in \{1, \dots, n_F\}$ and $j \in \{1, \dots, n_O\}$, where n_F and n_O are respectively
 344 the number of frequency and orientations, some statistical features are com-
 345 puted over each filtered image. We used the `gabor()` and `imgaborfilt()`
 346 functions of the Matlab Image Processing Toolbox considering the wave-
 347 lengths $[3, 6, 9, 12]$ and orientations $[0, 30, 60, 90, 120, 150]$, recommended by
 348 (Bianconi and Fernández, 2007). We compute the feature vectors **Gabor-**
 349 **RGB** and **GaborLab**, both with 48 features, that include the mean and
 350 standard desviation for each filter ($n_F \times n_O = 6 \times 4 = 24$ filters) applied on
 351 the grey level version of the RBG image or the L channel of the Lab image,
 352 respectively.

353 3.3. Regression models

354 We selected for this experimentation several state-of-art regression models
 355 of different families that provided good performances in the comparative
 356 analysis (Fernández-Delgado et al., 2019). One of them is implemented in
 357 the Octave³ scientific programming language, and the remaining ones in the
 358 R⁴ statistical computing language. Most regressors in our collection have
 359 tunable hyper-parameters, i.e., parameters whose values must be specified

³<http://www.octave.org>

⁴<http://www.r-project.org>

previously to training, that often have a strong influence on the regressor performance. In these cases, it is a good practice to try several values for each hyper-parameter in a trial-and-error procedure, and to select the value that provides the best performance on a separate data collection. This method is called “grid search” tuning. The following is a list of these regressors, with its tunable hyper-parameters and the list of values tried for each one in the grid search. For the regressors programmed in R, these values were provided by the `getModelInfo()` function of the `caret` R package (Kuhn, 2016).

1. **lm** is the linear regression provided by the `stats` R package, which performs multivariate linear regression and has no tunable hyper-parameter (Bates and Chambers, 1992).
2. **svr**: epsilon-support vector regression with radial basis function kernel, using the `LibSVM` library (Chang and Lin, 2011) through its Octave interface. The regularization hyper-parameter C and $\gamma = 1/2\sigma^2$, where σ is the kernel spread, are tuned with values $\{2^i\}_{-5}^{15}$ and $\{2^i\}_{-10}^{10}$, respectively.
3. **M5**: regression tree (Quinlan, 1992) implemented by the Weka Data Mining Software⁵ and accessed from a R program through the `RWeka` package. It has no tunable hyper-parameter.
4. **cubist**: M5 rule-based regressor with corrections based on nearest

⁵<http://www.cs.waikato.ac.nz/ml/weka>

380 neighbors in the training set (Quinlan, 1993), implemented by the
381 **Cubist** R package. Its tunable hyper-parameters are the number of
382 neighbors $[0,5,9]$ and the number of committees $[1,10,20]$.

383 5. **gbm**: generalized boosting regression model (**gbm** R package) with
384 Gaussian distribution. The tunable hyper-parameters are the maxi-
385 mum depth of input interactions, with values $[1,2,3,4,5]$ and the number
386 of trees for prediction, with values from 50 to 250 step 50.

387 6. **rf**: random forest (Breiman, 2001) ensemble of averaged random regres-
388 sion trees (**randomForest** R package). The number of inputs selected
389 at each tree (**mtry**) is tuned with 10 values between 2 and the number
390 of features.

391 4. Experimental setup

392 In order to achieve a fully automatic system, which can operate on-line
393 in the meat industries, we will develop three experiments to compare the
394 computer predictions with the sensorial procedures:

395 1. **Experiment 1**: prediction of the marbling from irregular regions of the
396 ham muscles that are delineated and annotated by the food technology
397 experts. In this case, the prediction is done using the same information
398 (irregular region) as the experts.

399 2. **Experiment 2**: prediction of the marbling using square regions ex-
400 tracted from the irregular regions of the experiment 1. This experiment

401 tests the reduction of performance when a region of the slice smaller
402 than the whole irregular region is used to do the prediction.

403 **3. Experiment 3:** fully automatic extraction of square regions of interest
404 (ROI) for each ham muscle, and prediction of the marbling using these
405 ROIs. This experiment will test the performance loss when the ROI
406 extraction may be suboptimal, but the method is fully automatic and
407 does not require any food technology expert.

408 In order to test the performance of the ROI extraction algorithm, we
409 define the overlapping percentage (OP) as:

$$OP_m = 100 \frac{NO_m}{R_t} \quad (2)$$

410 where m may be biceps, semimembranosus or semitendinosus, R_t is the num-
411 ber of pixels of the ROI (in our case $s^2=64 \times 64=4,096$ pixels) and NO_m is
412 the number of pixels overlapped to the true region annotated by the expert
413 for the muscle m .

414 To test the performance of regression models in the prediction of marbling,
415 we used the classical K-fold cross-validation methodology, which uses training
416 and test sets. The most popular performance measures are the Pearson's
417 correlation coefficient (R) between the true and predicted marbling, the mean
418 absolute error (average absolute difference between the predicted and true
419 marbling, MAE) and the root mean square error (square root of the mean

420 squared difference between them, RMSE):

$$R = \frac{\sum_{i=1}^N (y_i - \bar{y})(o_i - \bar{o})}{\sqrt{\left(\sum_{i=1}^N (y_i - \bar{y})^2\right) \left(\sum_{i=1}^N (o_i - \bar{o})^2\right)}} \quad (3)$$

$$MAE = \frac{1}{N} \sum_{i=1}^N |y_i - o_i| \quad (4)$$

$$RMSE = \sqrt{\frac{1}{N} \sum_{i=1}^N (y_i - o_i)^2} \quad (5)$$

421 where y_i and o_i are the predicted and true values of marbling respectively for
 422 ham slice i , $\bar{y}$ and $\bar{o}$ are the mean values of $\{y_i\}_{i=1}^N$ and $\{o_i\}_{i=1}^N$, respectively,
 423 and N is the number of ham slices. The $|R|$ values can be interpreted ac-
 424 cording to Colton (1974) as: true and predicted values are not correlated at
 425 all (0-0.25), bad to moderate correlation (0.25-0.5), moderate to good (0.5-
 426 0.75), very good to excellent (0.75-1). In our study, we use $K = 4$ folds or
 427 trials, devoting $K - 2 = 2$ folds for training, one for validation and one for
 428 test. Since all the folds have the same size, 50%, 25% and 25% of the data
 429 are devoted to training, validation and test sets, respectively. In our case,
 430 each data corresponds to the image of a ham slice, and it is composed by the
 431 texture feature vector extracted from the image (input) and the marbling
 432 value (output) corresponding to that slice image. In order to guarantee that
 433 training, validation and test sets contain output values distributed across the

whole range of marbling values, the data are sorted by increasing marbling. After sorting, data 1, 2, 3 and 4 are included in folds 1, 2, 3 and 4, respectively. Data 5, 6, 7 and 8 are added to folds 1, 2, 3 and 4, respectively, and so on. Let $\{T_k, V_k, S_k\}_{k=1}^K$ be the training, validation and test folds on k -th trial. Trial 1 uses folds 1 and 2 for training, fold 3 for validation and fold 4 for test (see table 2). Trial 2 uses folds 2 and 3 for training, fold 4 for validation and fold 1 for test, and analogously for trials 3 and 4. Therefore, training, validation and test sets in all the trials include data with marbling values in the whole range of values, composing training sets of higher quality that are expected to allow regressors learn better.

$K=4$	Trial 1	Trial 2	Trial 3	Trial 4
Train	$T_1=\{1,2\}$	$T_1=\{2,3\}$	$T_1=\{3,4\}$	$T_1=\{4,1\}$
Validation	$V_1=\{3\}$	$V_1=\{4\}$	$V_1=\{1\}$	$V_1=\{2\}$
Test	$S_1=\{4\}$	$S_1=\{1\}$	$S_1=\{2\}$	$S_1=\{3\}$

Table 2: Distributions of folds in training, validation and test for each trial.

Table 2 reports the experimental methodology. For each combination C_i of hyper-parameter values of the model, with $i = 1, \dots, N$, and for each trial k , with $k = 1, \dots, K$, the set T_k is used to train the model using the combination C_i of hyper-parameter values, while the set V_k is used as validation set to evaluate the performance P_{ik} of the trained model using C_i on V_k . The average P_i of $\{P_{ik}\}_{k=1}^K$ is thus the performance associated to the combination C_i of hyper-parameter values. The process is repeated for all the combinations $\{C_i\}_{i=1}^N$, and the combination C_I with the highest performance $I = \operatorname{argmax}\{P_i\}_{i=1}^N$ is selected. Then, for $k = 1, \dots, K$ the model with this

best combination C_I is trained on the set $\{T_k, V_k\}$, that includes $K - 1$ folds,
 and tested on the set S_k (1 fold), achieving a performance P_k . The average
 of $\{P_k\}_{k=1}^K$ is the final test performance P of the model.

Algorithm 2: Experimental methodology, combining K -fold cross-validation and hyper-parameter tuning.

```

1 for  $i = 1 : N$  do
2   for  $k = 1 : K$  do
3     Train the model with  $C_i$  on dataset  $T_k$ 
4     Validate the model with  $C_i$  on dataset  $V_k$ 
5      $P_{ik}$ =performance with  $C_i$  on  $V_k$ 
6    $P_i$ =average of  $\{P_{ik}\}_{k=1}^K$ 
7  $I = \operatorname{argmax}\{P_i\}_{i=1}^N$ 
8 for  $k = 1 : K$  do
9   Train the model with  $C_I$  on  $\{T_k, V_k\}$ 
10  Test the model with  $C_I$  on  $S_k$ 
11   $P_k$ =performance with  $C_I$  on  $S_k$ 
12  $P$ =average of  $\{P_k\}_{k=1}^K$ 

```

5. Results and discussion

We present the results obtained from the different points of view: the automatic extraction of ROIs to represent each muscle (subsection 5.1), the performance of marbling prediction model (subsection 5.2), comparison among the performance of different prediction models (subsection 5.3), the method stability with the muscles (subsection 5.4) and the computational time of the different stages of the procedure (subsection 5.5).

463 5.1. Extraction of ROIs

464 We tested the performance of the automatic algorithm to extract square
465 ROIs, of size 64×64 pixels, for each muscle described in section 3.1, by
466 using the measures described in eq. 2 of section 4 between the true muscle
467 and the extracted ROI for each muscle m . We compared the results with
468 the extraction done for experiment 2, in which the ROI is extracted from
469 the centroid of the irregular region (muscle) annotated by the expert (see
470 section 2.3). This extraction is normally satisfactory: in experiment 2, an
471 overlapping of 100% is achieved for the 47% of images, and the overlapping
472 is below 80% for only the 8% of the images. In experiment 3, the extraction
473 is perfect for the 52% of images and the overlapping is lower than 80% for
474 only the 12% of the images. Figure 7 shows some examples of suboptimal
475 ROI extraction: for the ROI extraction using centroid (experiment 2), the
476 causes of suboptimal extraction are muscles smaller than the ROI size (figure
477 7a) and muscles not rounded (figure 7c). For the automatic ROI extraction
478 (experiment 3), the causes of failure are: i) suboptimal extraction (figure 7d)
479 and ii) exchange SM and ST muscles due to artefacts in the ham slice (figure
480 7b). Table 3 shows the OP_m achieved by the ROI extraction algorithm for
481 each muscle m in both experiments.

482 5.2. Marbling prediction

483 The texture features described in section 3.2 are computed for all the ham
484 slices. In the experiment 1, the texture features are computed on the irregular

Muscle (m)	#images	OP_m	
		Experiment 3	Experiment 2
Biceps femoris	351	93.79	98.54
Semimembranosus	335	89.92	89.20
Semitendinosus	55	94.76	99.84

Table 3: Average percentage of overlapping pixels of the automatic extracted ROI (column **Experiment 3**) and the extraction from the centroid (column **Experiment 2**) with the true muscle annotated by the experts used in the experiment 1 for every muscle.

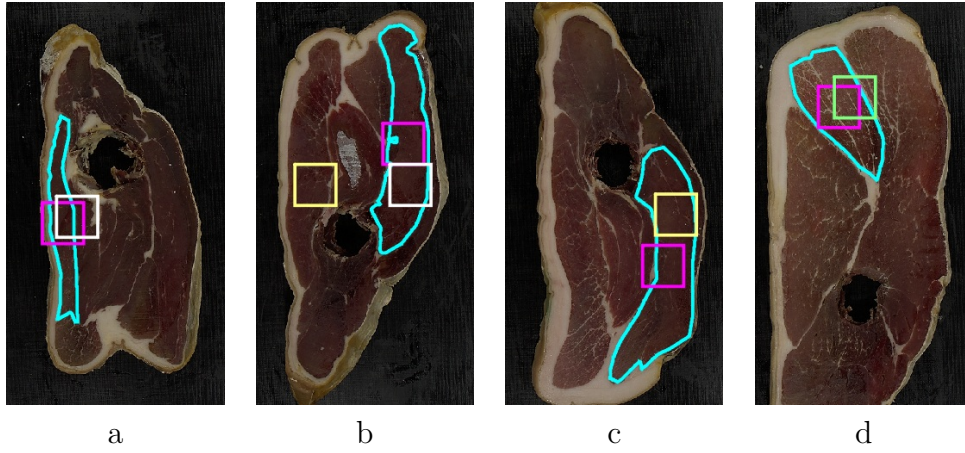


Figure 7: Examples of square ROI extraction, in cyan the muscle contour, in pink the square ROI extracted in the centroid, in white, yellow and green the square ROI automatically extracted for BF, SM and ST muscles respectively: a) ROI bigger than the BF muscle; b) the automatic ROI extractor fails in SM muscle; c) and d) suboptimal ROIs for SM and ST, respectively.

485 region, R_i , defined by each muscle and annotated by the food technology
486 experts. So, Gabor and wavelet features were not computed because they
487 must be applied on a square image. In experiment 2, squared regions RS_i of
488 size 64×64 pixels are extracted from the centroid of R_i and all the texture
489 features were computed. In experiment 3, the texture features were computed
490 on the square regions automatically extracted from the ham slice using the

491 algorithm described in the section 3.1.

	Experiment 1		Experiment 2		Experiment 3	
Feature vector	R	MAE	R	MAE	R	MAE
Pure color features						
CMRGB	0.85	0.62	0.79	0.70	0.72	0.79
CMab	0.69	0.82	0.63	0.86	0.58	0.93
CMVRGB	0.90	0.50	0.86	0.57	0.81	0.67
CMVab	0.74	0.75	0.66	0.83	0.68	0.86
FOSRGB	0.91	0.47	0.87	0.54	0.84	0.63
FOSab	0.81	0.68	0.74	0.76	0.71	0.78
Grey-level texture features						
HarRGB	0.91	0.49	0.88	0.56	0.80	0.72
HarLab	0.90	0.50	0.85	0.61	0.77	0.76
mlbpRGB	0.93	0.43	0.83	0.62	0.73	0.79
mlbpLab	0.92	0.45	0.81	0.66	0.71	0.80
WTrgbHaarLL	—	—	0.85	0.57	0.80	0.67
WTrgbHaarAll	—	—	0.88	0.54	0.80	0.66
WTLabHaarLL	—	—	0.85	0.57	0.80	0.67
WTLabHaarAll	—	—	0.88	0.54	0.82	0.65
WTrgbDb4LL	—	—	0.86	0.58	0.79	0.70
WTrgbDb4All	—	—	0.88	0.53	0.79	0.70
WTLabDb4LL	—	—	0.87	0.57	0.80	0.70
WTLabDb4All	—	—	0.89	0.53	0.79	0.70
GaborRGB	—	—	0.89	0.54	0.80	0.70
GaborLab	—	—	0.88	0.55	0.80	0.71
Color texture features						
CMVHarRGB	0.95	0.38	0.91	0.47	0.84	0.64
FOSHarRGB	0.95	0.39	0.92	0.46	0.83	0.63
CMVmlbpRGB	0.93	0.41	0.89	0.51	0.79	0.68
FOSmlbpRGB	0.94	0.40	0.90	0.48	0.80	0.67
CMVWTLabHaarAll	—	—	0.89	0.53	0.82	0.65
FOSWTLabHaarAll	—	—	0.89	0.51	0.83	0.62
CMVGaborRGB	—	—	0.91	0.48	0.82	0.65
FOSGaborRGB	—	—	0.91	0.48	0.82	0.64

Table 4: Correlation (column R) and mean absolute error (column MAE) for the marbling prediction using pure color features (upper part of the table), grey level texture features (middle part of the table) and color texture features (lower part of the table) using the support vector regression (svr) for the three experiments.

492 Table 4 shows the correlation (R) and the mean absolute error (MAE) for
493 marbling prediction using the support vector regression (svr) for the three

494 experiments. The feature vector FOSRGB achieved the highest R and lowest
 495 MAE among all pure color features (upper part of the table), with $R=0.91$,
 496 0.87 and 0.84 in experiments 1, 2 and 3, respectively. As expected, when the
 497 performance of the automatic detection degrades, the regression accuracy
 498 decreases. But, it is still quite high for the third experiment, very good to
 499 excellent following the Colton's criteria. In relation with grey-level texture
 500 features (middle part of table), the use of irregular regions of the muscle
 501 (experiment 1) achieves the highest performance ($R=0.93$ and $MAE=0.43$
 502 using the texture vector mlbpRGB). In general, the performance achieved in
 503 experiment 2 is higher than the experiment 3 for all the features vectors used,
 504 noting the loss of information in the automatic selection of the ROIs. Com-
 505 paring the different families of grey-level texture features for square ROIs, the
 506 wavelet features achieve the highest performance for experiment 3 ($R=0.82$
 507 and $MAE=0.65$) followed very close by the Haralick's coefficients and Ga-
 508 bor features ($R=0.80$), which means that the model is also from good to
 509 excellent. From the color space point of view, although the best results with
 510 wavelet features are achieved using the Lab color space, the difference with
 511 the use of RGB color space is not significant and the highest performance
 512 with the remaining feature vectors is better using RGB color space.

513 We developed experiments combining the best pure color features (vectors
 514 FOSRGB and CMVRGB) with the best grey-level texture features of each
 515 texture features families. Specifically, we chose the grey-level texture vectors
 516 HarRGB for Haralick's coefficients, mlbpRGB for local binary patterns, WT-

517 LabHaarAll for wavelet features and GaborRGB for Gabor features. The
 518 results are shown in the lower part of table 4. The performance increases 0.2
 519 for the first experiment (from $R=0.93$ for mlbpRGB to $R=0.95$ for CMVHar-
 520 RGB) and 0.3 for the experiment 2 (from $R=0.89$ for GaborRGB to $R=0.92$
 521 for FosHarRGB), but R does not increase in experiment 3. In all the cases,
 522 the best results were achieved combining the color information (CMVRGB
 523 or FOSRGB vectors) and the grey-level texture information provided by the
 524 Haralick's or LBP coefficients (vector HarRGB and mlbpRGB). The MAE
 525 is a performance measure easier to interpret than R from the point of view
 526 of food technology experts. Figure 8 shows the reliability of the prediction
 527 using the **svr** regressor for experiments 1 (left panel) and **rf** regressor for
 528 experiment 3 (right panel) for the best feature vectors. The blue line rep-
 529 resents the true marbling for each ham slice provided by the experts. The
 530 red points represent the predicted marbling by **svr** or **rf** for each ham slice.
 531 The average difference between the blue and red values for each ham slice
 532 is the MAE (0.38 and 0.60 in the left and right panels, respectively). This
 533 means that the prediction of the computer is the true value $\pm$ MAE in aver-
 534 age. Taking in mind that the expert's tolerance in the sensorial analysis to
 535 establish the marbling is 0.5, the prediction of the computer is comparable
 536 with the precision of the experts.

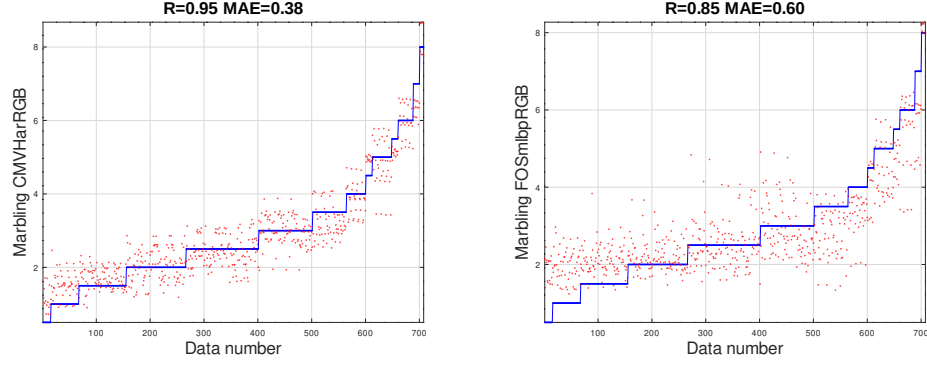


Figure 8: Graphical representation of the true (blue line) and predicted (red points) ham marbling (vertical axis) for all ham slices (horizontal axis) using the svr regressor: (left panel) using the CMVHarRGB vector in the experiment 1 and (right panel) using the FOSRGB plus LBPRGB vector in the experiment 3.

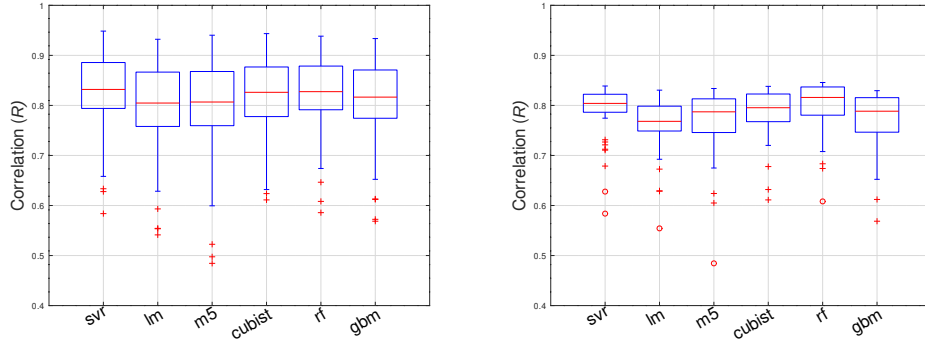


Figure 9: Box plots showing the correlation R for the different regressors (horizontal axis) considering all the experiments together (left panel) and only the experiment 3 (right panel).

537 5.3. Comparing different regressors for marbling prediction

538 In order to find the best prediction of marbling score, we applied the
 539 regressors described in section 3.3 to the color texture features described in
 540 section 3.2 for the three experiments. Figure 9 shows the box plots com-

541 paring the correlation for all regressors considering all feature vectors in the
 542 experiments 1, 2 and 3 (left panel) and only in experiment 3 (right panel).
 543 The upper and lower edges of each box indicate the 25th and 75th percentiles,
 544 respectively, the upper and lower blue segments enclose the remaining data
 545 and the red crosses are the data considered outliers. The red line inside the
 546 box is the median of the data. In both panels, there are not large difference
 547 among regressors. Considering the tree experiments (left panel), svr, rf and
 548 cubist have the highest medians, and svr has the smaller box, similar to rf
 549 but with higher median. In experiment 3 (right panel), the rf box shows the
 550 best median, followed by svr with a shorter box. Table 5 shows the color
 551 texture vector that achieved the highest correlation R , with the standard
 552 deviation over the K folds in the cross validation, for each regressor on the
 553 first (irregular regions for each muscle) and third experiments (square regions
 554 for each muscle). In experiment 3, the highest values of R are achieved by
 555 the rf regressor using the feature vector FOSmlbpRGB ($R = 0.846 \pm 0.008$).
 556 Considering that the MAE values (0.38 and 0.60) reflect the dispersion of the
 557 computer marbling prediction from the true marbling values, the computer
 558 predictions fall near the experts' tolerance, which is 0.5. Hence, for the first
 559 experiment, the computer predicts correctly the 90.4% (67.8% for the third
 560 experiment) of samples within a tolerance of ± 0.5 (the expert's tolerance)
 561 and within a tolerance of ± 1 , the 99.3% (88.8% for the third experiment).

Regressor	Experiment 1		Experiment 3	
	Feature	R	Feature	R
lm	CMVmlbpRGB	0.932 ± 0.003	FOSHarRGB	0.831 ± 0.014
svr	CMVHarRGB	0.948 ± 0.004	CMVHarRGB	0.839 ± 0.005
m5	FOSmlbpRGB	0.940 ± 0.003	FOSHarRGB	0.834 ± 0.017
cubist	FOSmlbpRGB	0.943 ± 0.007	FOSHarRGB	0.838 ± 0.012
gbm	FOSmlbpRGB	0.934 ± 0.001	FOSRGB	0.829 ± 0.013
rf	FOSmlbpRGB	0.938 ± 0.004	FOSmlbpRGB	0.846 ± 0.008

Table 5: Correlation (R) for the marbling prediction using all the regressors and the best feature vector (column Feature) for the first and third experiments.

5.4. Comparing performance for different muscles

In order to test if the regressor behaviour is stable over the different muscles, we create two datasets with images belonging to the third experiment: 1) BFData for images of *Biceps femoris* (BF) muscle; and 2) SMDData for images of *Semimembranosus* (SM) muscle. *Semitendinosus* muscle is not analysed because there are few images. For BF muscle, the best performance is achieved by the feature vector FOSGaborRGB using the **cubist** regressor ($R=0.80$ and $MAE=0.50$). For the SM muscle, the best performance is achieved by the feature vector FOSmlbpRGB using also the **cubist** regressor ($R=0.74$ and $MAE=0.55$). Although the correlation loss is 0.12 ($0.92-0.80$) and 0.18 ($0.92-0.74$) for the BF and SM muscles respectively, the loss in MAE is only 0.04 ($0.50-0.46$) and 0.09 ($0.55-0.46$) respectively. Thus, the computer predictions with a tolerance of ± 1 are correct for the 93.5% of BF and 94.1% of SM muscles. This facts lead to conclude that our system is stable with the different muscles.

577 5.5. Computation time

578 In order to design a computer system to predict the marbling from a
579 ham slice, which should operate in real time in the meat industry, it is very
580 important the computational time needed by the different stages of the pro-
581 cess. The experiments were performed on a desktop computer with Intel®
582 CoreTM i7-9700 processor at 3.6GHz and 64GB RAM memory under Ubuntu
583 20.04. The algorithm for the extraction of a square ROIs for the different
584 muscles was done in the C++ programming language using the computer vi-
585 sion library OpenCV⁶ and the remaining processing was done using Matlab
586 2021a⁷. The average computational time to extract the ROIs was 18.7, 18.4
587 and 19.9 milliseconds for *biceps*, *semimembranosus* and *semitendinosus* mus-
588 cles, respectively. The time required to compute the color texture features
589 depends on the method used and the type of experiment (irregular regions
590 in experiment 1 and square regions in experiments 2 and 3). For square
591 regions of 64×64 pixels, the average computational time for each family of
592 features was: 1) for pure color features the time ranges from 0.48 ms. for
593 CMRGB to 2.21 ms. for FOSLab; 2) for Haralick's features: 7.59 and 9.20
594 ms. for HarRGB and HarLab, respectively; 3) for LBP texture features,
595 the time is 170.03 ms. for mlbpRGB and 172.20 ms. for mlbpLab; 4) for
596 wavelet features (vectors WT_{ijk} , where $i = \{Haar, Daub\}$, $j = \{RGB, Lab\}$
597 and $k = \{LL, All\}$) the time ranges from 1.17 ms. for WTrgbHaarLL to 2.73

⁶<https://opencv.org>

⁷<https://mathworks.com>

ms for WTLabDb4All; and 5) for Gabor texture features: 19.17 and 20.99
ms. for GaborRGB and GaborLab, respectively. The time spent by the
svr regressor to predict the marbling using the texture feature vector is less
than 1 milisecond per image. Overall, the computational time required by
the whole process depicted in figure 4, discarding the acquisition of the ham
slice image, can be estimated as 19 ms. for the automatic ROI extraction,
plus less than 10 ms. for color texture feature computation, plus 1 ms. for
regression model, summarized approximately 30 ms.

6. Conclusions and future work

This paper proposes a system to predict the marbling of dry-cured ham
from a ham slice image. After the acquisition of ham image, a square ROI of
the *semimembranosus* (SM), *semitendinosus* (ST) and *biceps femoris* (BF)
muscles is automatically extracted using the procedure described by algo-
rithm 1. The overlapping of the ROIs extracted by this method with the
true muscle area is, in average, higher than 90% for all the muscles. The
prediction of ham marbling using the support vector regression is: 1) a cor-
relation R of 0.95 using the true ham muscles areas annotated by experts
(experiment 1) and the feature vector CMVHarRGB, composed by the mean
and variance of each channel of RGB color image combined with the Har-
alick's coefficients of the grey-level image; and 2) $R=0.85$ for square ROIs
automatically extracted, in the experiment 3, using the feature vector FOS-
mlpbRGB (statistics of each channel of RGB color image combined with the

620 MLBP texture features of the grey-level image). The MAE achieved is 0.38
621 in the first case and 0.60 in the second one. These values are comparable to
622 0.5, which is the estimated standard deviation of the panelists. This leads
623 to think that the computer system can perform the prediction similarly to
624 a human expert. The computational time to do the prediction (without the
625 image acquisition time) is approximately 30 milliseconds to extract the square
626 ROI, compute the color texture features and predict the marbling in a general
627 purpose personal computer.

628 The good results and high speed of the marbling prediction for sliced dry-
629 cured ham suggest that this application could be deployed in the dry-cured
630 ham industry. Future work will be the development of a software to predict
631 the marbling and other dry-cured sensorial measures.

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