

# Prediction of the sensory quality of bovine meat based on multiscale image analysis approach



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# Introduction



- Bovine meat quality,
- The main criterion of quality for consumers: **Tenderness**,
- Purpose: Evaluation of meat tenderness using image analysis,
- Part of the study: Artificial vision process.



# Outline



- Intramuscular Connective Tissue (IMCT),
- Discrete wavelet transform: «à trous» algorithm,
- Multiscale Vision Model (MVM),
- Detection of significant structures,
- Image analysis and data preparation,
- Prediction of bovine meat tenderness.

# Intramuscular Connective Tissue

## Epimysium

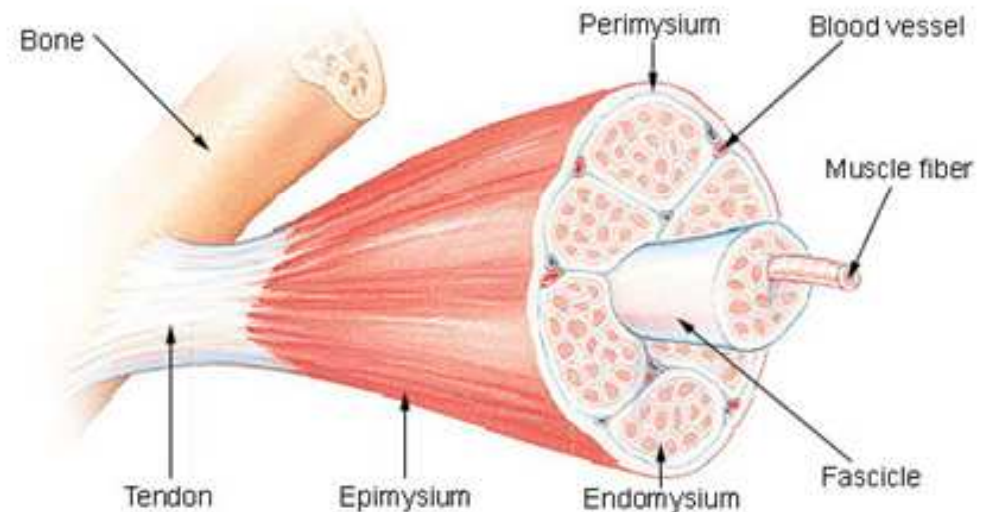
- Trimmed by the butcher,
- Is not consumed,

## Perimysium

- 90% of connective tissue,
- Plays a major role,

## Endomysium

- It doesn't seem involved in the variability of meat texture.



# Discrete wavelet transform



## « A trous » algorithm

■ The discrete approach of the wavelet transform can be done with the special version of the so called « **à trous** » **algorithm**.

■ It allows the computation of **successive approximations** by smoothing:

$$c_{j+1}(k, k') = \sum_{l, m \in \mathbb{Z}} h_{l, m} c_j(k + l2^j, k' + m2^j)$$

■ The approximation  $c_{j+1}$  is obtained from the approximation  $c_j$  with convolution by the filter  $h$  and a step of  $2^j$  between coefficients creating « holes » in the filter hence the name of the algorithm.

# Discrete wavelet transform



## « A trous » algorithm

- Similar recurrence can be obtained for **wavelet planes**:

$$w_{j+1}(k, k') = \sum_{l, m \in \mathbb{Z}} g_{l, m} c_j(k + l2^j, k' + m2^j)$$

- The wavelet plane at scale “j+1” is given by difference between approximations with resolution scales “j” and “j+1”.

$$w_{j+1}(k, k') = c_j(k, k') - c_{j+1}(k, k')$$

# Multiscale Vision Model (MVM)



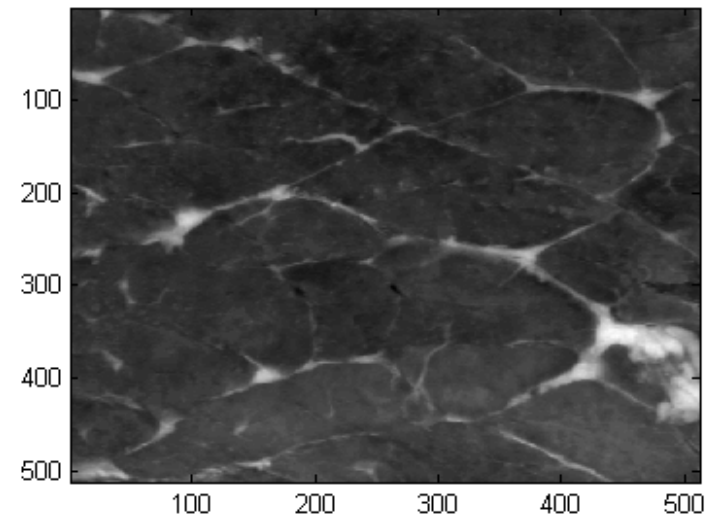
■ For bovine meat image analysis, we chose to implement “à trous” **algorithm**.

■ Fourth-order binomial filter was chosen:

$$h(0) = 3/8, h(\pm 1) = 1/4, h(\pm 2) = 1/16, h(n) = 0 \text{ if } |n| > 2$$

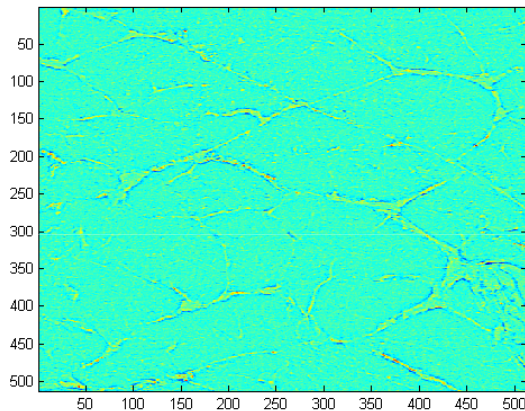
■ **Example** of an analysed meat image:

Acquired under **visible polarized lighting**

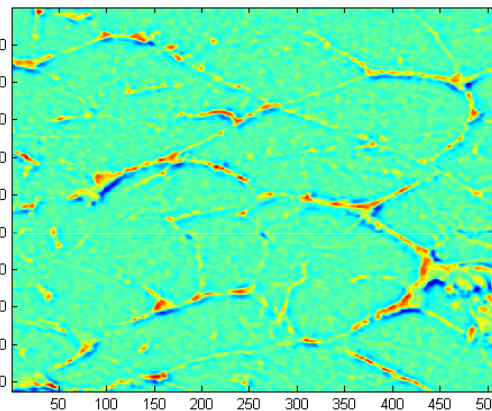


# Multiscale Vision Model (MVM)

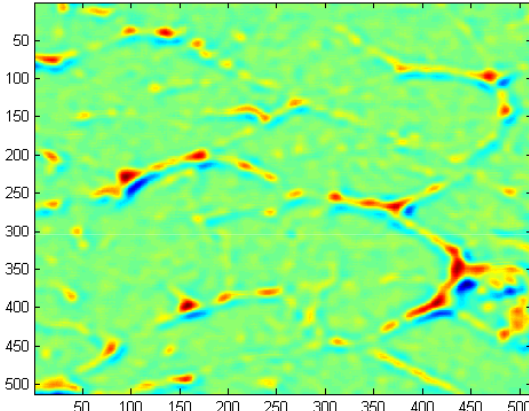
## « A trous » algorithm results



(a)



(b)



(c)

The first three wavelet planes obtained by « **à trous** » algorithm, using fourth-order binomial filter **h**.



# Detection of significant structures

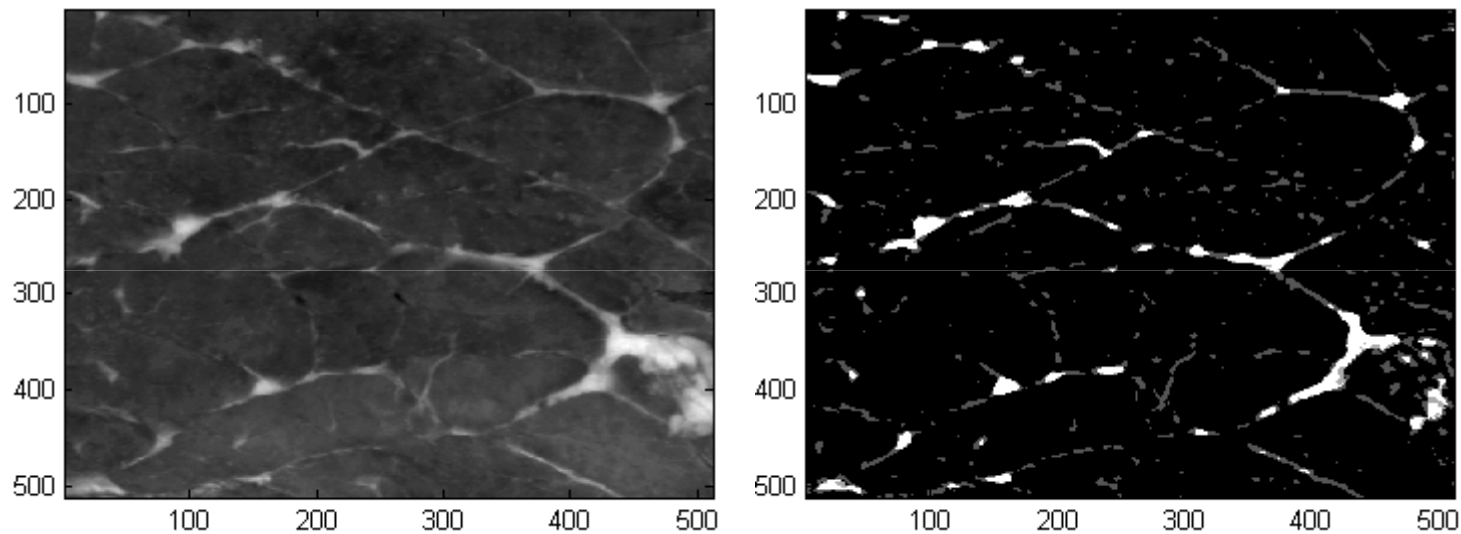


- It consists to threshold the wavelet planes with a threshold  $S$  properly determined by the noise model.
- For each wavelet plane  $\mathbf{w}_j$  only the values greater than  $S$  were retained.
- Universal threshold (Donoho et al., 1995) was applied:  $S = \sigma \sqrt{2 \log(n)}$
- The standard deviation of the noise is estimated from the first wavelet plane  $\mathbf{w}_1$ :

$$\hat{\sigma} = \frac{MED(|w_1|)}{0.6745}$$

# Detection of significant structures

## Segmentation result

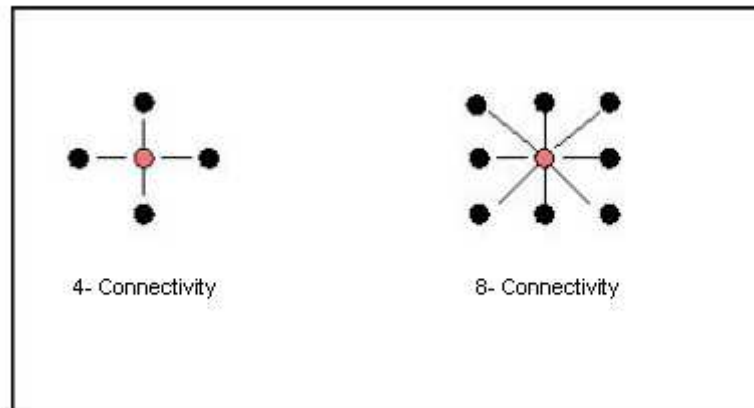


**Example** of a segmented meat image acquired by a visible polarized lighting system.

# Image analysis and data preparation

## Data extraction

- Segmented images were then binarized,
- Whole set of data represents object surfaces in pixel,
- Calculated using a quantification algorithm based on neighborhood-pixels (**8-connectivity**).



# Image analysis and data preparation

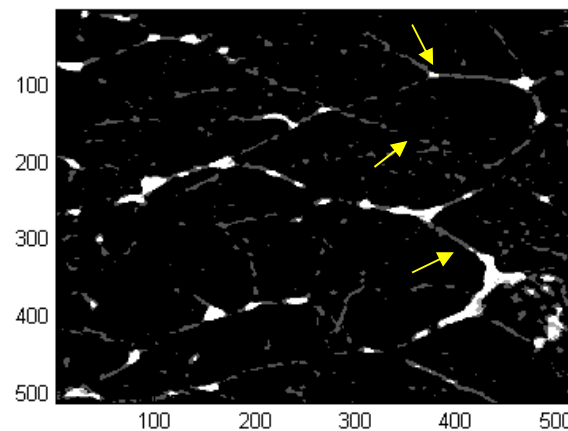
## Data preparation

- T transformation data:  $Y = T(X_{ik})$  with  $T = \text{Log}$ ,

$X_{ik}$  is the surface of kth object in the image i,  $1 \leq k \leq n_i$

$n_i$  is the number objects in the image i,

- Information retained: distribution of object surfaces belonging to the **perimysium**



# Image analysis and data preparation

## Data discertisation

- **Number of classes:**  $n_c = 1 + \log_2(N)$  (Sturges formula)
- **Class limits:** classification according to the arithmetic progression, with ratio **r**,

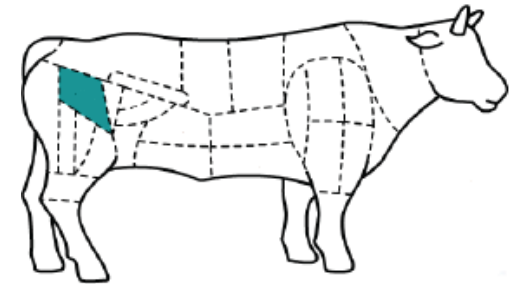
$$r = \frac{\max - \min}{1 + 2 + 3 + \dots + i + \dots + n_c}$$
$$\begin{aligned} & [\min, \min + r] \\ & ] \min + r, (\min + r) + 2r ] \\ & \dots \end{aligned}$$

- For each muscle  $i$ , we calculate the **proportion of objects** belonging to each class.

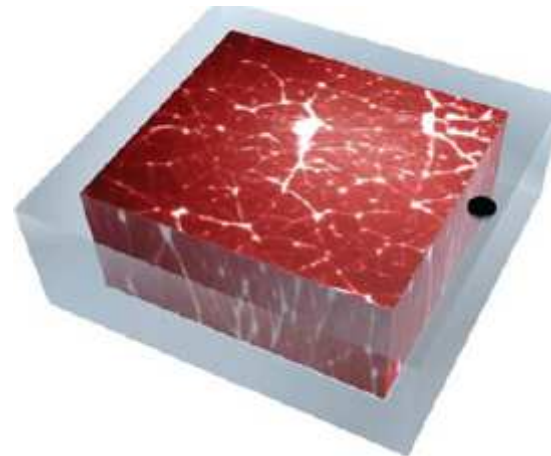
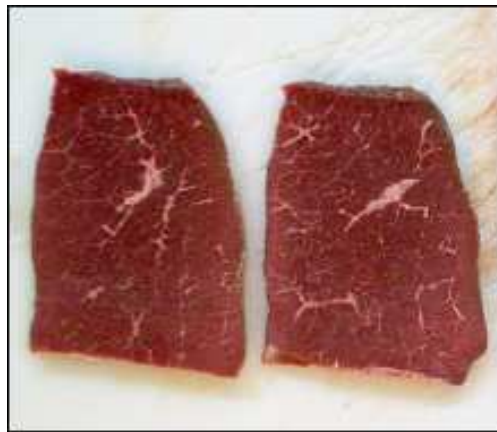
# Prediction of bovine meat tenderness



- The analysis were performed on *Semimenbranosus* (**SM**) muscle samples from two cattle breeds: Holstein (n=11) and Salers (n=9).



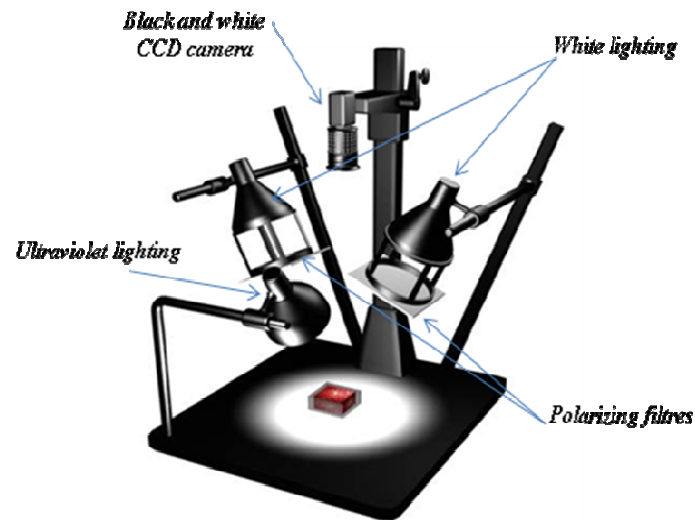
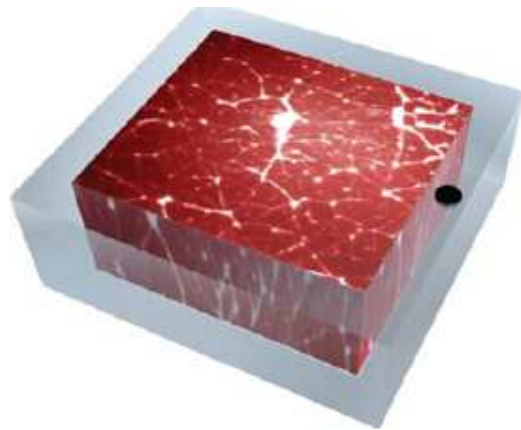
- Muscle samples (n=20) were cut into  $5 \times 4.5 \times 2 \text{ cm}^3$  cube with largest face.



# Prediction of bovine meat tenderness



- Images of SM slices were acquired under visible lighting,
- Photographic measurement bench equipped with a black and white camera model (MACC7, Sony ),
- Two white light lamps with polarized filters were used.

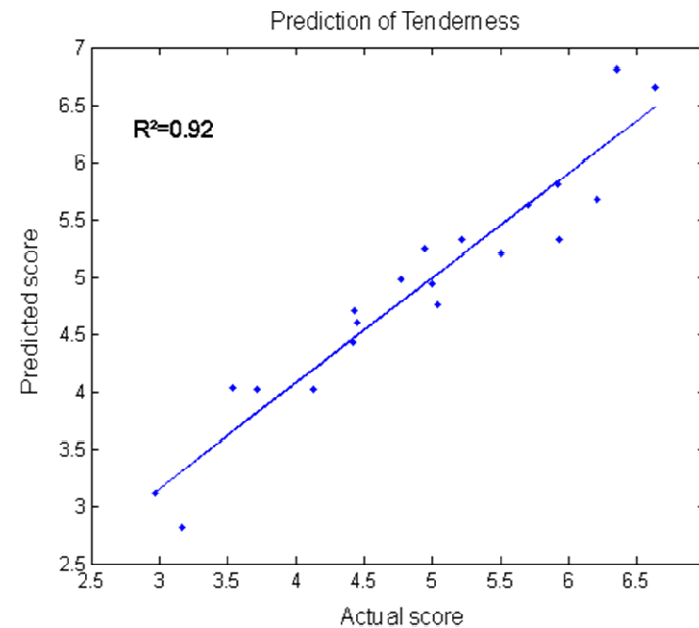
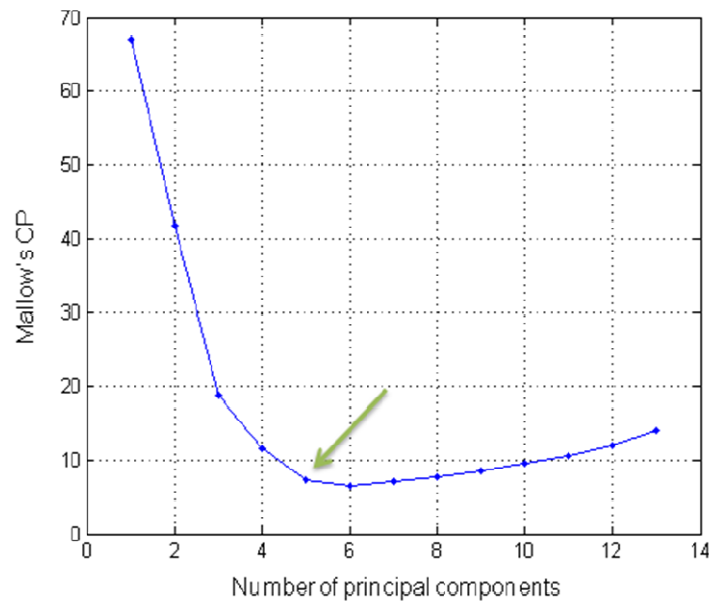


- The tenderness was evaluated by a trained panel using the recommended method of (Dransfield et al., 2003)

# Prediction of bovine meat tenderness



- Principal Component Regression (PCR) analysis was applied to data issued from image processing steps.
- Five variables were selected from thirteen.
- Their linear combination has good prediction of meat tenderness ( $R^2 = 0.92$ ).





# Conclusion



- The analysis was performed on bovine **raw meat** images,
- The tenderness was assessed by a trained taste panel on **cooked meat**,
- Simple imaging equipment was used : **Polarized white lighting** system,
- Image analysis approach was developped, based on a **multiscal image analysis**, allowing a good estimation of IMCT,
- The information extracted from the images represent the **distribution** of Intramuscular Connective Tissue (IMCT) , which contributes significantly to the intrinsic hardness of meat,

# Conclusion



- The data analysis was carried out using the *Sturgers* technique (number of classes) and the **arithmetic progression** method (length of classes),
- Principal Component Regression was applied (PCR). Five principal components were selected for the final model allowing to predict **92%** of tenderness variability,
- This model depends on both image segmentation and object sizes classification,
- It would be interesting to test large data set with this method, including other animal biological factors as breed, sex and age.