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Fish fillet authentication by image analysis

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ABSTRACT

The work aims at developing an image analysis procedure able to distinguish high value fillets of Atlantic cod (*Gadus morhua*) from those of haddock (*Melanogrammus aeglefinus*). The images of fresh *G. morhua* (n = 90) and *M. aeglefinus* (n = 91) fillets were collected by a flatbed scanner and processed at different levels. Both untreated and edge-based segmented (Canny algorithm) regions of interest were submitted to surface texture evaluation by Grey Level Co-occurrence Matrix analysis. Twelve surface texture variables selected by Principal Component Analysis or by SELECT algorithm were then used to develop Linear Discriminant Analysis models. An average correct classification rate ranging from 86.05 to 92.31% was obtained in prediction, irrespective the use of raw or segmented images. These findings pave the way for a simple machine vision system to be implemented along fish market chain, in order to provide stakeholders with a simple, rapid and cost-effective system useful in fighting commercial frauds.

1. Introduction

A large number of computer vision systems have been investigated and applied in the agri-food system answering the need of simple, rapid, and non-destructive but reliable evaluation tools for the assessment of food quality and safety during production and processing (Ma et al., 2016). The computer vision bases go back to '60s (Baxes, 1994), though its implementation in the food industry grew mainly in the last two decades. Even if food products are extremely different, computer vision is a cross-approach aiming at the estimation of color, morphological features and surface texture characteristics directly linked to food quality and safety.

Few vision systems have been applied in the fishery industry, as reported in the reviews by Mathiassen et al. (2011), Dowlati et al. (2012), and Zion (2012). Main applications are devoted to fish counting, definition of several physical parameters (e.g. length, width, thickness, volume, weight, perimeter, area, compactness and roundness) (Balaban and Ayvaz, 2016), gender identification, chemical, biochemical and sensory quality assessment, as well as species and stock identification (Mathiassen et al., 2011). They have been implemented both in aquaculture or fish farm and in industrial conveyor belts during processing operations.

Promising results have been achieved in species identification. Zion et al. (1999) were able to correctly classify grey mullet images acquired under different lighting conditions. Storbeck and Daan (2001) described a system to recognize fish species by computer vision and a neural network, reaching more than 95% of correctly classified fish. White et al. (2006) implemented a computer vision machine to identify and measure different species with an accuracy ranging from 95.8 to 98.8%. Alsmadi et al. (2011) extracted several features, based on ventral part of fish images, for the differentiation between fish families, especially between poison and non-poison families. All these systems are more or less complex and implemented at different levels of the fish market chain, but they all deal with intact whole fishes. To the best of our knowledge, no systems have been thought for species identification in fish fillets. However, the actual food market, driven by consumers' needs for healthy but ready-to-cook products, highly demands for fillets more than whole fishes. Thus, rapid and easy tools for authenticity assessment of these products are needed to face economic frauds (e.g. the substitution of valuable species with cheaper ones) along the whole fish supply chain.

Even if there are a number of recognized techniques for food authentication, such as molecular, chromatographic, and isotopic techniques, genomics, proteomics, vibrational and fluorescence spectroscopy, NMR and non-chromatographic mass spectrometry (Danezis et al., 2016), portable technologies for rapid and non-destructive testing would be advantageous (Stadler et al., 2016). In particular, vision systems could respond to the need of fast, reliable, non-destructive, and *in situ* analyses for fish authentication.

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A fundamental role in computer vision is played by image analysis, which is composed by three main steps: low-level processing (i.e. image acquisition and pre-processing), intermediate-level processing (i.e. segmentation and object measurement), and advanced image processing. All these steps should be optimized in order to meet the defined purpose of the developed computer vision system, while reducing potential errors and ensuring result accuracy (Brosnan and Sun, 2004). Thus, the aim of this work was the development of an image analysis procedure to be implemented in a vision system in order to distinguish high value fillets of Atlantic cod (*Gadus morhua*) from those of haddock (*Melanogrammus aeglefinus*).

2. Materials and methods

2.1. Samples

Fresh *Gadus morhua* (Gm, n = 90) and *Melanogrammus aeglefinus* (Ma, n = 91) were provided by a trusted supplier (Copromar S.r.l., Milan, Italy) in thirteen different batches from March to June 2016. The left fillets were portioned from the whole fishes by qualified personnel and carried to the university laboratories ensuring the cold chain. Samples were stored at 4 ± 1 °C prior to analyses that were performed within the sampling day.

2.2. Fillet morphological characterization

The method proposed by Malandra and Baldisserotto (2014) was applied to characterize the collected fillets according to their morphology. It is focused on some characteristics of the external side of the fillets, fundamental to distinguish *G. morhua* and *M. aeglefinus*. In particular, the analysis of myomeres and myosepta organization and orientation in the cranial region of the external side permitted to discriminate the considered species. Indeed the myosepta are angled against the line of the body with the innermost edge nearer the front of the body and the outermost edge nearer the tail, thus shaping like a "W". The characteristic "W" defines three main angles, one for each change of direction, called dorsal posterior (DP), central anterior (CA) and ventral posterior (VP). In the cranial region of *G. morhua* fillets, the W-shaped myomeres have small angle amplitude, symmetry in DP and VP angles and DP angle touching the dorsal side by an imaginary line perpendicular to the lateral line (Fig. 1a). In the cranial region of *M. aeglefinus* fillets (Fig. 1b), the W-shaped segments have angles broader than those in *G. morhua* and the imaginary line touches both the PD angle, but in the front side, and the VP angle close to the lateral line.

2.3. Image analysis

2.3.1. Image low-level processing

The acquisition of the images of each fillet was performed with a flatbed scanner (HP Scanjet 8300, HP Inc., Palo Alto, CA, USA), covering samples with a black box to prevent light losses. Images were acquired at a resolution of 600 dpi, with a color depth of 48 bit and saved in uncompressed TIFF format. Image analysis was carried out on a selected region of interest (ROI; 800 × 1200 pixels) cropped in the cranial area of each fillet and converted in grayscale (8 bit).

2.3.2. Image intermediate-level processing

Each image ROI was edge-based segmented through Canny multi-stage algorithm. The application of this algorithm aimed at significantly reducing the amount of data by filtering useless information out while preserving the important structural properties in the image, represented in this case by the muscular tissue pattern. In details, Canny edge algorithm consists of: noise reduction by Gaussian filter; image intensity gradient identification with four filters to detect horizontal, vertical and diagonal edges in the blurred image; non-maximum suppression to define a set of edge points known as "thin edges"; edges' tracing through a double thresholding; suppression of all the edges that are weak and not connected to strong edges by hysteresis (Nosrati et al., 2013).

2.3.3. Image high-level processing

Both untreated and edge-based segmented ROI matrices were submitted to high level processing, through surface texture evaluation by Grey Level Co-occurrence Matrix (GLCM) analysis and multivariate analysis.

GLCM, a classical second-order statistical method, was applied to create a symmetric matrix reporting the frequency of the different combinations of grey levels co-occurring in the selected ROIs. Indeed, it calculates how often two pixels with intensity values i and j ($p_{i,j}$) at a particular distance (δ) along a given direction (expressed in angles, θ) occur in an image. Since the calculation is strongly affected by pixel pitch and direction, a single GLCM might not be enough to describe textural features of the input image. For this reason, 40 GLCMs for a single input image were calculated considering ten distances (δ from 1 to 10 pixels) and all the four directions (θ of 0°, 45°, 90°, 135°). Then, four main texture features were calculated for each matrix. Texture feature calculation uses the GLCM to give a measure of the intensity variation among the pixels of interest (Haralick et al., 1973). In this work, the following features were calculated:

- Contrast: it measures the intensity contrast between a pixel and its neighbor over the whole image, evaluating the local variation

$$Contrast = \sum_i \sum_j (i-j)^2 p_{ij} \quad (1)$$

It ranges from 0 (for a constant image) to the root mean square of the size of GLCM-1.

- Correlation: it measures how a pixel is correlated to its neighbor over the whole image, evaluating the joint probability occurrence of specified pixel pairs

$$Correlation = \sum_i \sum_j \frac{(i-\mu i)(j-\mu j)}{\sqrt{(\sigma i^2)(\sigma j^2)}} p_{ij} \quad (2)$$

where μ and σ are mean and standard deviation values, respectively. It ranges between −1 and 1, which stand for a perfectly negatively or positively correlated image.

- Energy, also known as uniformity or angular second moment: it returns the sum of squared elements in the GLCM

$$Energy = \sum_i \sum_j {p_{ij}}^2 \quad (3)$$

It ranges from 0 to 1, being 1 the value for a constant image.

- Homogeneity, or Inverse Difference Moment: it measures the closeness of the distribution of elements in the GLCM to the GLCM diagonal

$$Homogeneity = \sum_i \sum_j \frac{1}{1+(i-j)^2} p_{ij} \quad (4)$$

It ranges from 0 to 1. Homogeneity is 1 for a diagonal GLCM.

Considering these four texture features, two matrices composed of 181 samples and 160 variables were obtained for the untreated