

Computer Vision Algorithms Versus Traditional Methods in Food Technology: The Desired Correlation

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Abstract. Active Contours represent a common Pattern Recognition technique. Classical active contours are based on different methodologies (variational calculus, dynamic programming and greedy algorithm). This paper reviews the most frequently used active contours in a practical application, comparing weights, manually obtained by food technology experts, to volumes, automatically achieved by computer vision results. An experiment has been designed to recognize muscles from Magnetic Resonance (MR) images of Iberian ham at different maturation stages in order to calculate their volume change, using different active contour approaches. The sets of results are compared with the physical data. The main conclusions of the paper are the excellent correlation established between the data obtained with these three non-destructive techniques and the results achieved using the traditional destructive methodologies, as well as the real viability of the active contours to recognize muscles in MR images.

1 Introduction

Active Contours (or snakes) is a low-level processing technique widely used to extract boundaries in many pattern recognition applications [4, 8]. In their formulation, active contours are parameterized curves, defined by an energy function. By minimizing this energy function, the contour converges, and the solution is achieved. An Active Contour is represented by a vector, $v(s)$, which contains all of the n points of the snake. The functional energy of this snake is given by:

$$E = \int [E_{int}(v(s)) + E_{image}(v(s))] ds \quad (1)$$

where E_{int} and E_{image} are the internal and external energy of the contour, respectively.

Energy-minimizing Active Contour models were proposed by Kass *et al.* [11]. They developed a controlled continuity spline which can be operated upon by internal

contour forces, images forces, and external forces which are supplied by an interactive user, or potentially by a higher level process. An algorithmic solution involves derivation of this objective function and optimization of the derived equation for finding an appropriate solution. However, in general, variational approaches do not guarantee global optimality of the solution [1].

On the other hand, Amini *et al.* [1] also proposed a dynamic programming algorithm for minimizing the functional energy. However, the proposed algorithm is slow, having a great complexity. Williams and Shah [15] developed a greedy algorithm which has performance comparable to the dynamic programming and variational calculus approaches.

Active Contours could be used as a pattern recognition technique. A practical application of them could be employed to recognize muscles of Iberian ham images [5, 6]. Particularly, Iberian ham images have been processed in this research. The evolution of the ripening of this meat product has been studied, acquiring images in different stages during the maturation process. The ripening of the Iberian ham is a lengthy procedure (normally 18-24 months). Physical-chemical and sensorial methods are required to evaluate the different parameters in relation with quality, being generally tedious, destructive and expensive [2]. Traditionally, the maturation time is fixed when the weight loss of the ham is approximately 30% [7]. So, other methodologies have long been awaited by the Iberian ham industries.

The use of image processing to analyze Iberian products is quite recent. Processing images from Iberian ham slices taken by a CCD camera is a first approach. However, although Computer Vision is essentially a non-destructing technique, ham pieces must be destroyed to obtain images using these techniques.

On the other hand, MRI (*Magnetic Resonance Imaging*) offers great capabilities to non-invasively look inside the bodies. It is widely used in medical diagnosis and surgery. It provides multiple planes (digital images) of the body or piece. Its application to the Food Technology is still recent and it is confined for researching purposes.

In this work, three algorithm paradigms in active contours have been developed, *variational calculus*, *greedy algorithm* and *dynamic programming*, in order to recognize the two main muscles structures in the Iberian ham (*biceps femoris* and *semimembranosus* muscles). The experiment has been designed having Magnetic Resonance (MR) images from four different stages during the maturation of the ham (*raw*, *post-salting*, *semi-dry* and *dry-cured*). The first goal of this work is to recognize muscles processing MR images, in order to determine the volume of ham, and to study their changes during the ripening process. This objective is an attempt to provide a computer vision alternative to the traditional methods of determining the optimal ripening time. Anyway, the main contribution of the work is the satisfactory relationship (statistical correlation) between the volume and weight of these two muscles. The volume has been obtained by Computer Vision techniques (Active Contours), and the weight has been achieved by manual methods (extracting physically the muscles and weighing them in scales). The fine correlation coefficients obtained in this work verify that Computer Vision methods could be used properly as an alternative to the traditional and destructive customs.

2 Materials

The presented research is based on MRI sequences of Iberian ham images. A technique to recognize the main muscle form (*biceps femoris* and *semimembranosus*) is employed. Six Iberian hams have been scanned, in four stages during their ripening time. The images have been acquired using an MRI scan facilitated by the "Infanta Cristina" Hospital in Badajoz (Spain). The MRI volume data set is obtained from sequences of T1 images with a FOV (*field-of view*) of 120x85 mm and a slice thickness of 2 mm, i.e. a voxel resolution of 0.23x0.20x2 mm. As a result, a great image database is obtained. The total number of images used in this work is 600 for the *biceps femoris*, and 504 for the *semimembranosus* muscle. So, the total amount of images is 1104.

3 Methods

Three different algorithm paradigms in active contours (*variational calculus*, *greedy algorithm* and *dynamic programming*) have been proven in order to obtain results using several methodologies (section 3.1). Afterwards, the practical application of these three methodologies over MR Iberian ham images from different maturation stages will be shown in 3.2.

3.1 Classical Active Contour Approaches

An Active Contour is represented by a vector, v , of points [4]. The complete energy functional in all the developed methods is given by:

$$E = \sum \{ \alpha E_{cont} + \beta E_{curv} + \gamma E_{image} \} \quad (2)$$

The internal energy of the contour consists of continuity energy (E_{cont}) plus curvature energy (E_{curv}). E_{image} represents the proper energy of the image [12, 16]. All the energy terms are normalized to produce similar effects to the solution. α , β and γ are values chosen to control the influence of the three energy terms [13, 14].

Although most of the active contour algorithm and practical approaches consider a fixed number of n points for the snake, the three different active contour approaches developed in this work maintain a variable number, n , of points of the snake. This is the best way to ensure the finest muscle recognition. To achieve that, two distances have been consider, d_{max} and d_{min} . When two consecutive points of the snake exceed the maximum distance between points d_{max} , a new point appears between the two original points. In such a way, when two consecutive points go beyond the minimal distance d_{min} , one of them disappears. As a result, the total number of points of the snake varies, adjusting perfectly the final snake to the pattern.

The variational calculus approach is based on the finite difference method proposed by Kass et al. [11]. The equation (1) is solved iteratively by matrix inversion, using the *lower and upper triangular decomposition*, a well-known technique in linear algebra. A detailed description of the principle behind this numerical method is

described in [10, 16]. The initial group of results has been achieved using this method.

On the other hand, the developed dynamic programming approach is based on the method proposed by Amini [1]. Although it is natural to view energy minimization as a static problem, to compute the local minima of a functional such as equation (1) a dynamical system can be constructed, governed by the function and allowing the system to evolve to equilibrium. Following these ideas, a dynamic programming active contour has been designed and used to reach a set of results.

Finally, the implemented greedy algorithm approach is based on the Williams and Shah's proposals [15]. This technique achieves the final solution by steps, trying to take always an optimal decision for each stage. The algorithm considers a square neighborhood for each point of the snake. The energy function is computed for the current location of v_i and each of its neighbors. The location having the smallest value is chosen as the new position of v_i . Using this methodology, the last active contour approach has been developed obtaining the last set of results.

3.2 Practical Application: Active Contours on Iberian Ham MRI

An experiment was designed using the three considered methods above to study the ripening process of the hams. Four stages were selected: *raw*, *post-salting*, *semi-dry* and *dry-cured*, acquiring MR images of the hams in each of the stages. These images have been processed using non-destructive computer vision techniques, as the three Active Contour approaches presented in 3.1. The initial analysis began with 15 hams in the raw stage. Moreover, three of these hams were destroyed being extracted the muscles by an expert in each stage, to make the chemical analysis on *biceps femoris* and *semimembranosus* muscles. These two muscles were weighed too, for each of the three analysed hams. The chemical analysis implies the destruction of the considered ham, so, there only were 12 hams in the post-salting stage, 9 in the semi-dry stage, and finally 6 hams in the dry-cured stage. Therefore, there only are MR images for the six considered Iberian hams in all the four stages.

As a previous step, a pre-processing stage is introduced, in order to obtain the values used as image energy. In addition, the initial snakes for all the images have been previously calculated too.

Once the complete database of images and the initial values of the snakes for these images are obtained, the application of Active Contours to compute the area of the muscle is needed. Every of the three active contours methods exposed above (variational calculus, greedy algorithm and dynamic programming) have been developed, obtaining three different sets of results.

Each of the obtained final snakes determines the surface of the muscle over the image. The final step computes surfaces and volumes for the extracted muscles. Calculating the surface of the final snake obtained for each image is possible to determine the volume for the muscle.

Eventually, in average, the error made has been estimated at less than 10%, considering the manual expert delineation of the muscles compared with the final area of the snake-segmented muscle.

Figure 1 contains MR images with the final snake for both *biceps femoris* (a) and *semimembranosus* (b) muscles.

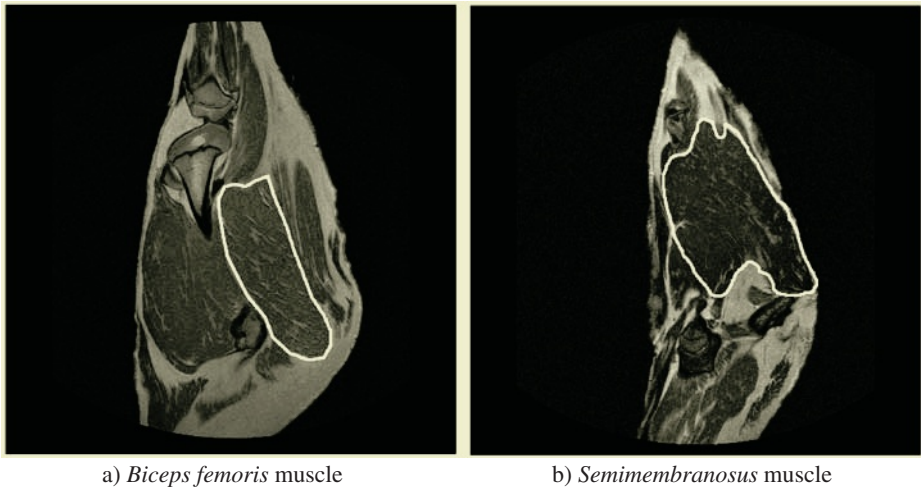


Fig. 1. Illustration of Iberian ham MR images, which include the detection of the muscles

4 Results and Discussion

The practical application of the three active contour approaches computes the volume of the Iberian ham *biceps femoris* and *semimembranosus* muscles during their ripening stages. These three sets of results have been obtained by means of Computer Vision techniques. Considering the results reached by the three different Active Contour techniques, it is particularly interesting to emphasize that they are certainly similar, independently of what method is used. They have been compared with the physical data, which have been obtained manually weighing the two muscles for all the three hams.

Table 1. Correlation coefficient (Correlation) and Pearson's correlation coefficient (Pearson) for the *Biceps Femoris* and *Semimembranosus* muscles

Method	<i>Biceps Femoris</i> muscle		<i>Semimembranosus</i> muscle	
	Correlation	Pearson	Correlation	Pearson
Variational	0.963	0.928	0.823	0.678
Dynamic	0.971	0.932	0.825	0.681
Greedy	0.965	0.944	0.821	0.674

So, different ways to obtain the data have been considered: manual and destructive techniques to weigh the hams, and automatic and non-destructive methods to compute volumes. The relationship between volumes and weights is shown in Table 1. This table shows the correlation coefficient [3] and the Pearson's correlation coefficient [3] achieved by the three methods. Both correlation coefficients, which mathe-

matically vary from -1 to 1, are greater than 0.67 in all being the obtained results. That implies a good / excellent correlation between the data sets under consideration, according to the Colton's classification for statistical correlation coefficients [9].

Table 2 and 3 show the correlation coefficient in all the four maturation stages (raw, post-salting, semi-dry and dry-cured) for the *Biceps Femoris* and *Semimembranosus* muscles, respectively. Again, the obtained results could be considered as remarkable.

Table 2. Correlation coefficient (Corr.) and Pearson's correlation coefficient (Pearson) for the *Biceps Femoris* muscle

Method	Raw		Post-salting		Semi-dry		Dry-cured	
	Corr.	Pearson	Corr.	Pearson	Corr.	Pearson	Corr.	Pearson
Variational	0.841	0.708	0.900	0.811	0.870	0.758	0.915	0.838
Greedy	0.851	0.724	0.905	0.819	0.873	0.762	0.906	0.822
Dynamic	0.865	0.748	0.927	0.860	0.857	0.735	0.902	0.814

Table 3. Correlation coefficient (Corr.) and Pearson's correlation coefficient (Pearson) for the *Semimembranosus* muscle

Method	Raw		Post-salting		Semi-dry		Dry-cured	
	Corr.	Pearson	Corr.	Pearson	Corr.	Pearson	Corr.	Pearson
Variational	0.682	0.465	0.848	0.720	0.798	0.638	0.889	0.791
Greedy	0.681	0.464	0.859	0.739	0.806	0.650	0.886	0.785
Dynamic	0.683	0.466	0.915	0.837	0.817	0.668	0.896	0.803

Figure 2 shows the statistical correlation coefficients obtained between the three different Active Contour methods (variational calculus, greedy algorithm and dynamic programming) and the physical data, for the *biceps femoris* muscle. Both physical and computer vision results are certainly comparable. Moreover, a tendency line has been added in Figure 2, in order to show the predisposition of the data.

Similarly, figure 3 shows the same results corresponded to semimembranosus muscle. The physical extraction of this last muscle by Food Technology experts is a complex procedure. For this reason, these results are not as good as the data obtained for the biceps femoris muscle. However, there is a high correlation too.

The results in figures 2 and 3 show the good correlation between the Computer Vision results and the physical data, from the initial phase (raw) to the last stage (dry-cured), 21 months after the initial stage. Therefore, a significant relationship has been established and corroborated in this work: weight (manually obtained) and volume (automatically obtained) of the Iberian ham are correlated.

5 Conclusions

The real viability of the three classical active contour approaches for muscle recognition in MRI has been proved in this paper. An excellent correlation between the data

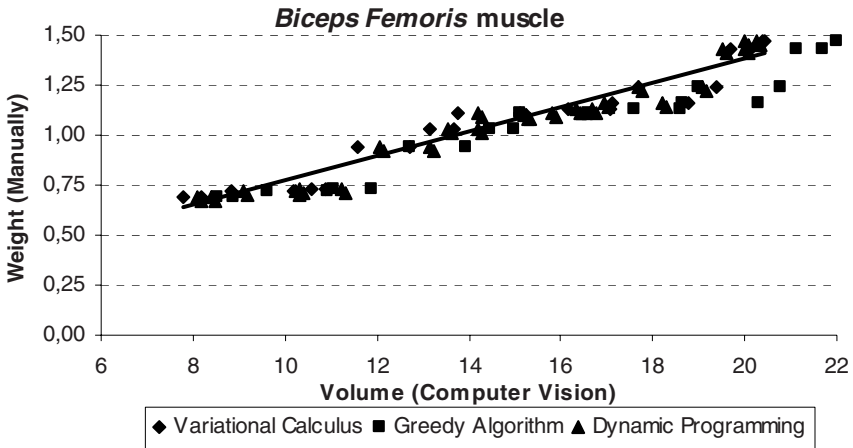


Fig. 2. Correlation coefficient for the *biceps femoris* muscle, in all the ripening stages

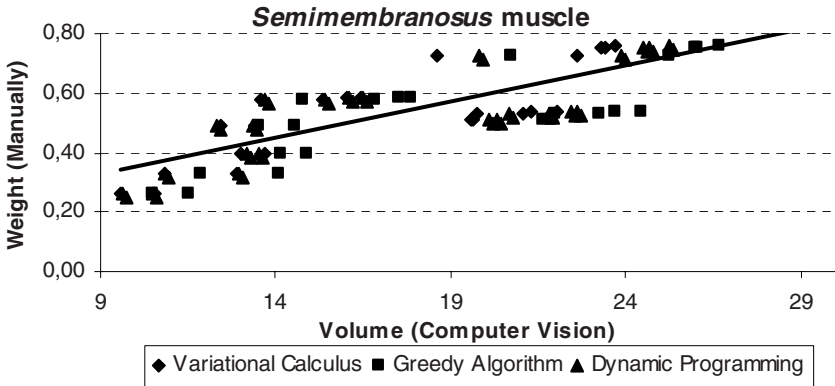


Fig. 3. Correlation coefficient for the *semimembranosus* muscle, in all the ripening stages

obtained with these three non-destructive techniques and the results achieved using the traditional methodologies have been reached. These significant correlations demonstrate the robustness of the employed methodology. Additionally, the practical feasibility of applying Computer Vision techniques to automate the ripening process of the Iberian ham constitutes a key finding in this research. Such computer vision techniques will introduce new and alternative methods for future work, which have long been awaited for the meat industries.

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