THICKNESS PROFILE MEASUREMENT BETWEEN CLOSED CURVES

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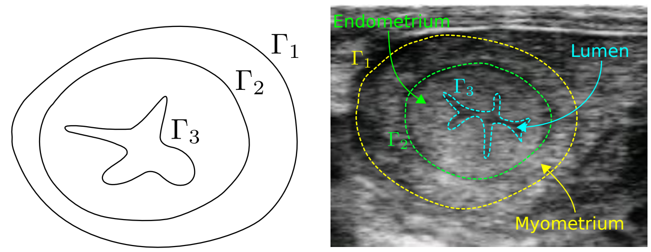
ABSTRACT

In this paper the problem of defining and measuring a thickness profile between closed curves is presented. Based on the normal evolution of curves, we developed an algorithm which find the correspondence between points of different curves and measures the thickness profile. Ensuring in each step a good sampling of all curves by mechanisms of creating and deleting points, the algorithm splits the evolution in two parts, evolving from the convex hull of the interior curve to each one of the others. Synthetic and real results are shown and a particular application of classification using descriptors extracted from the thickness profile is presented. Finally we present the conclusions and future work.

***Index Terms*—** Curves evolution, thickness, width, distance

1. INTRODUCTION

This work addresses the problem of finding an entire width profile between two closed curves. The particular application considered is to detect a common uterine disease in dairy cattle using ultrasonographic images. An expert in ultrasonographic diagnosis affirms (Giovanni Gnemmi, personal communication, May 18th, 2013) that the relation between some muscles thickness can be a relevant characteristic to diagnostic this disease. In this work we explore this possibility developing a system to measure this feature. Figure 1a shows a typical setting of the closed curves involved in the problem: Γ_1, Γ_2, Γ_3. Curves are always in this order and there is no intersection between them, since they are the limits of muscles and tissues in cattle uterus. Γ_1 and Γ_2 are not assumed to be convex but presents a smooth curvature variation, while Γ_3 is non convex, with high curvature variation and even not differentiable in some points. The main goal is to define and measure the thickness profile of the muscles, which means to find the thickness of the region between Γ_1 and Γ_2, and between Γ_2 and Γ_3. In the literature there are some measures of distance between two curves, such as Housedorff [1] or Sobolev [2] distance that provides a numeric value for the distance or dissimilarity between curves, but we are interested, as said, in the entire thickness profile. Several methods, like the one presented in [3], finds the correspondence between



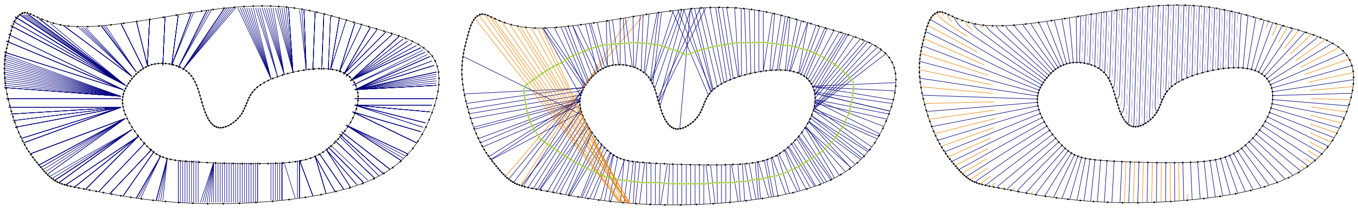
(a) Curves definition. (b) Application definition.

Fig. 1. Definitions.

two morphologically different objects by the minimization of a similarity criterion function. Other methods resolve the correspondence by circle mapping [4]: the vertices of the source and target curves are projected on circles of the same radius, and then merged. The merged set of vertices are projected back onto each curve, obtaining curves with the same number of vertices, and in a pairwise correspondence.

To compute the region width, the first question to ask is how to conceptually define the width between two curves. It is clear that is a local characteristic that depends of at least two points. The distance function for each point of a curve to the other curve leads to a non-intuitive definition of width, see Figure 2. In this work we propose an algorithm based on the normal evolution of one curve and considering the other curve as target. In the evolution are included some mechanisms of creating and deleting points to ensure a correct sampling of the curves at all steps. The width is measured as the length of the path in the evolution from one curve to the other. This algorithm finds an intuitive correspondence between points of the different curves and leads to an appropriate width definition.

The description of the particular problem considered and the proposal is presented in Section 2. In Section 3 are presented synthetic and real results and a final application to diagnostic an uterine disease using descriptors extracted from the thickness profile. Finally, in Section 4 we present some conclusions and future work.



(a) Distance function (b) Normal to middle curve (c) Proposed method

Fig. 2. Comparison between different proposals.

2. PROBLEM DESCRIPTION AND PROPOSAL

2.1. Problem description

In order to understand the particular application considered it is important to define some concepts. In the Figure 1b a transverse cut of cattle uterus is shown. We can imagine uterus as a tube with two coatings: Endometrium and Myometrium. The Myometrium is the region delimited by Γ_1 and Γ_2 and the Endometrium is the region delimited by Γ_2 and Γ_3. The problem is to measure the thickness of those two regions, using a manual segmentation of the regions made by the expert. While searching for a definition of the distance between two curves, euclidean distance comes to head. In this case, for each point of curve Γ_i the nearest point of Γ_j is found and the euclidean distance between this two points is used as thickness. As can be seen in Figure 2a, this thickness definition cannot capture the curves structure, deriving in a wrong profile. Another idea is to measure width in the normal direction of each point of the curve. Considering the normal to curve Γ_2, we cannot ensure that this direction will intersect Γ_3. With the purpose of obtaining a more regular curve and define the thickness in the normal direction of this new curve, we consider the skeleton of the region defined by Γ_2 and Γ_3, defined as the curve Γ_{23} equidistant to both curves. The results of measuring the thickness in the normal direction of each point of Γ_{23} are not as expected and in some directions the normals do not intersect curve Γ_3 (See Figure 2b). Finally, in Figure 2c is presented our proposed algorithm. In this case, the structure of the curves is effectively captured, obtaining a distance between curves that can be interpreted as thickness.

Another possibility is to create synthetic images form the given curves in order to use other methods like GAC [5] o Chan-Vese [6], that uses image data to perform the evolution. However, this methods introduce other terms representing for example the curve regularity or area measures that are not linked to the original problem and may hinder the real problem of measuring a region thickness.

2.2. Proposal

Our proposal is based on the simplest curves evolution: the normal evolution. Letting η be the evolution step and $\vec{n}^t_{p_i}$ the normal to the curve at the point p_i at time t, the evolution is governed by the equation:

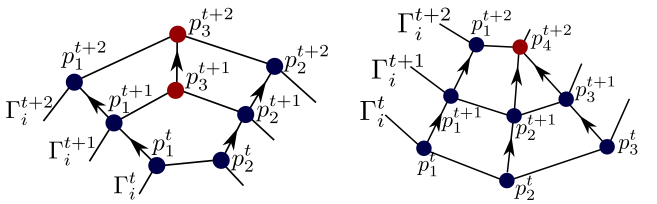
$$p_i^{t+1} = p_i^t + \eta\, \vec{n}^t_{p_i}. \tag{1}$$

Due to the nature of the curves described in Section 1, we propose to perform three separated evolutions, which in the final step are joined to obtain a single result. Apart from curves $\Gamma_i, \quad i = 1\ldots3$, an auxiliary curve is considered: the convex hull of curve Γ_3 (Γ_3^{CH}), [4]. The three separated evolutions are:

1. Evolution from Γ_3^{CH} to Γ_3
2. Evolution from Γ_3^{CH} to Γ_2
3. Evolution from Γ_2 to Γ_1

The final width, or distance between curves, is calculated as the distance of the path traveled by each point of the curve. The original curves are created with a cubic interpolation of a few points indicated by the expert and then re-sampled according to curvature, using more points in regions with higher curvature. The sampling of Γ_3^{CH} is done by two different ways according to each point nature: points $p_i \in \Gamma_3$ that also belongs to Γ_3^{CH} are directly used, and in regions where Γ_3 do not match Γ_3^{CH}, an uniform sampling is performed such that both curves have the same number of points.

Sampling conditions are considered at each step to ensure a correct representation of the curve. For that purpose we developed a simple mechanism of creating and deleting points while evolving the curve. At the beginning of the evolution, the mean distance, δ, between adjacent points is computed. The procedure of creating new points consists on evaluating at each evolution step t if the distance between two adjacent points p_i^t and p_{i+1}^t is grater than 2δ. In this case, a new point, p_k^t, is created. p_k^t is initialized with the mean of the distance traveled by points p_i^t and p_{i+1}^t. See Figure 3a. The procedure to delete points is based on the evaluation of a proximity condition. If $\eta\frac{\vec{n}_{p_i}}{||\vec{n}_{p_i}||}$ and $\eta\frac{\vec{n}_{p_i+1}}{||\vec{n}_{p_i+1}||}$ are intersected, points p_i and p_{i+1} will be joined into a new one. See Figure 3b. If the curvature of curve Γ_2 is very high, the procedure should change a little, considering the convex hull of Γ_2 and perfoming the same procedure as the described for Γ_3.



(a) Creating new points (b) Deleting redundant points

Fig. 3. Synthetic results.

3. RESULTS

3.1. Synthetic

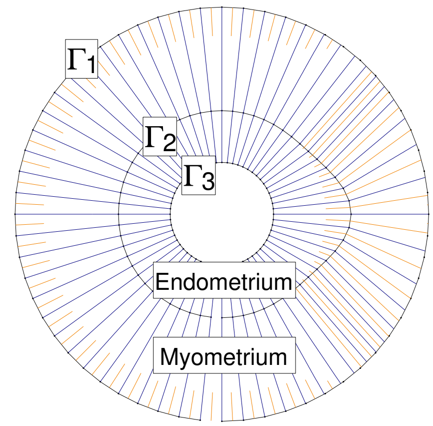
In order to evaluate the algorithm performance, a synthetic example is presented. This example was designed considering Γ_i, $i = 1 \ldots 3$ as three concentric circles and adding a perturbation in Γ_2. This perturbation is introduced by adding in the normal direction of each point of the curve a Gaussian distribution $X \sim \mathcal{N}(0, 1)$ centered in points with null phase. In the point where X is maximal (null phase), the width of the region delimited by Γ_1 and Γ_2 is equal to the width of the region delimited by Γ_2 and Γ_3. The results are shown in Figure 4. In Figure 4.a is shown the trajectory of the points while evolving. The trajectory of the original points is represented in blue color, while the trajectory of points created during evolution is represented in orange color. In figure 4.b is shown the thickness profile obtained. As can be seen, the results are as expected. Region between Γ_1 and Γ_2 presents a decay in width while the region between Γ_2 and Γ_3 shows an increase. For the points with null phase the widths are equal.

3.2. Real

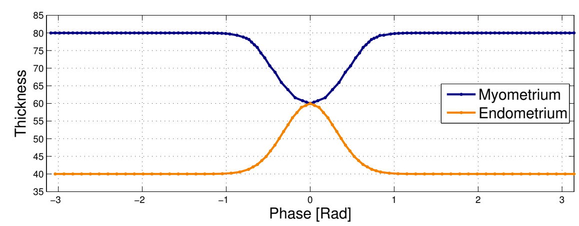
Postpartum uterine diseases, such as endometrium damage and ovarian cyclic activity disruption, has become one of the most important causes of reproductive inefficiency in dairy cattle and are associated with infertility [7, 8]. Endometritis is an uterine disease defined as inflammation limited to the endometrium occurring at least 21 days after calving and not associated with systemic illness [9]. This disease do not always presents clinical symptoms, so sub-clinical Endometritis detection using ultrasonography images is used [10, 11]. The sub-clinical endometritis diagnostic is very difficult, even for an expert, so image processing techniques to aid veterinaries in diagnostics get special relevance.

In this section we present results obtained in real ultrasonography images. The curves were manually segmented by the expert and our algorithm applied to obtain the thickness profile. Results are shown in Figure 5 for three real examples.

The algorithm was applied to a database tagged by the expert, knowing which cows has sub-clinical endometritis. In a



(a) Evolution



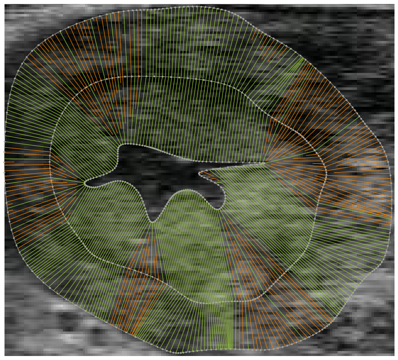
(b) Widths

Fig. 4. Synthetic results.

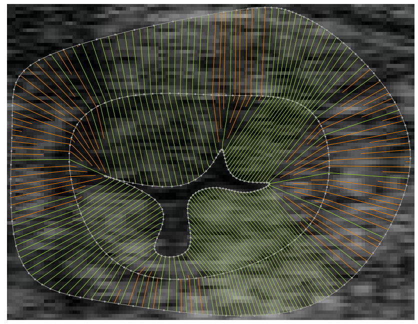
preliminary study of the problem the thickness obtained for each image was used to obtain some descriptors in order to perform an automatic supervised classification of cattle with or without endometritis. Although the results are preliminary, seems to be very promissory. With the descriptors used, we were able to detect 88% of infected cows. habria que explicar mejor todo esto?. This results are showing that descriptors obtained from the thickness profile, which could not be extracted using other measures such as euclidean distance, can play an important role in detecting sub-clinical endometritis.

4. CONCLUSION

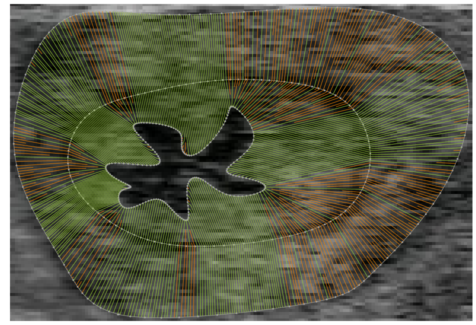
In this work we present a proposal to measure the thickness of a region delimited by two closed curves, without any regularity assumptions on the curves. The curves are sampled according to curvature and the algorithm is based on the normal evolution with constant velocity of the points of the curve to evolve. Mechanisms of creating and deleting points during evolution were designed and implemented, ensuring a good representation of the curve in each step. To deal with the "irregularity", meaning the high variation of curvature of a curve, the convex hull is considered as an auxiliary curve and the evolution is performed in two steps: evolving from the convex hull to the start curve and evolving from the convex hull to the target curve. This algorithm leads to an intuitive thickness definition, and an entire thickness profile is



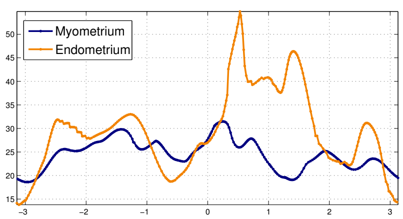
(a) Evolution



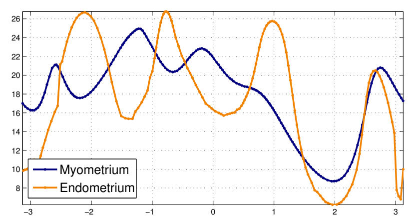
(c) Evolution



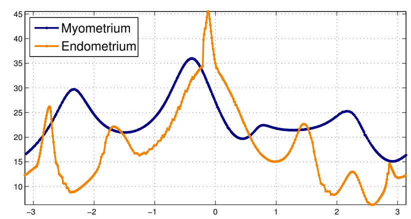
(e) Evolution



(b) Evolution



(d) Evolution



(f) Evolution

Fig. 5. Real results.

obtained. When defining the thickness, the correspondence between the curves is not clear. This algorithm finds a reasonable correspondence, resolving an entire mapping between curves. Also, it is important to mention that the algorithm is fast and efficient.

The algorithm was applied to a particular situation, where the goal is to measure the thickness of a muscle of cattle uterus in order. This thickness appears to be very relevant to help the detection of a sub-clinical uterine disease: endometritis. Some descriptors were extracted from the thickness profile, and a classification system was implemented in order to classify sick cows. The results were very promissory, giving good prospects for automatic detection.

4.1. Future work

As future work we plan to explore in extracting better descriptors from the thickness profile and obtain other descriptors such as texture or shape descriptors in order to obtain a more accurate classification. Also we plan to enlarge the database.

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