TIP-SEEKING ACTIVE CONTOURS FOR BIOIMAGE SEGMENTATION

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ABSTRACT

In the present paper, we address the problem of segmenting biological objects featuring corners. The main ingredients of our approach are automated feature-detection methods and mechanisms for introducing kinks in parametric spline snakes. We formulate a novel corner potential that enables the accurate segmentation of objects exhibiting sharp tips or acute angles. The optimization of active contours using the proposed keypoint-based energy yields robust segmentation results and requires fewer parameters than traditional spline-snap approaches for the same task. The performance of our method is illustrated on microscopic images of two families of Rhabditidse roundworms.

Index Terms—Segmentation, bioimage analysis, active contours, keypoints, feature detection, roundworms.

1. INTRODUCTION

The ultimate goal of segmentation is the quantification or tracking of objects of interest, making it an essential step in bioimage analysis [1, 2]. Active contours, usually referred to as snakes [3], are tools of choice for this task. Active-contour algorithms are traditionally composed of two key elements: the snake model and the snake energy. Many different active-contour models can be found in the literature [4]. We focus in this work on the family of spline snakes [5]. While the model defines the actual snake curve, the energy is a functional to be minimized for the snake to properly segment the objects of interest. Most snake energies are constructed using image-based information (external energy) or snake-curve properties (internal energy). While many approaches to detect features (or keypoints) exist in the computer-vision community [6], landmark-based segmentation approaches relying on the automated detection of interest points can hardly be found in bioimage informatics where most methods rely instead on points that are defined manually [7].

Our goal in this paper is to make the link between automatic feature detection and active-contour methods in a bioimaging context. To do so, we propose a novel corner potential in combination with the control of tangents offered by Hermite bases [8]. These functions can indeed be used to construct a snake model that provides a direct control over the tangent field of the curve. Unlike active contours that generate curves that are smooth by construction, this model has the ability to also represent sharp angles. Hence, it is well-suited to outline biological structures with pointy tips such as worms or protists. Classical spline snakes are smooth by design and require a large number of control points to approximate discontinuous curves. By contrast, the tangent-based snake model is able to perfectly reproduce such features with one control point only. To the best of our knowledge, this is the first time an energy relying on this property is proposed. The corner potential, which unifies automated feature-detection methods and active contours, can be seen as an extension of landmark-based energies. It not only relies on keypoints to attract the snake at corner locations, but also constrains the snake curve to create a sharp angle. Combined with other energy terms, it promotes the robustness of the active contour.

The paper structure is as follows: First, we introduce the tools we rely on to define the corner potential. We then formulate and describe its expression. We illustrate and discuss its capabilities on synthetic images. Finally, we apply our new feature-based energy in two bioimage segmentation problems.

2. ACTIVE CONTOURS WITH TANGENTIAL CONTROL

The choice of our snake model is driven by two main considerations. First, we aim at segmenting bioimages, which often feature partially elliptic objects. Relying on a contour model that spans the space of ellipses therefore opens the possibility to generalize the method to various kinds of bio-data. Second, our goal is to capture sharp features, a task that smooth parametric curves can hardly perform.

The active contour with tangential control proposed in [8] meets both requirements as it benefits from ellipse-reproducing capabilities and is able to generate sharp transitions. This snake model is schematically represented in Figure 1. Formally, it is defined by an $M$-periodic sequence of anchor points $\{r[k]\}_{k \in \mathbb{Z}}$ and tangent vectors $\{r'[k]\}_{k \in \mathbb{Z}}$, where $r[k] = r[k+M] = r(t)\vert_{t=k}$ and $r'[k] = r'[k+M] = r'(t)\vert_{t=k}$. The continuous-domain
Fig. 1: Spline-snake model with tangential control. The continuous curve $r(t)$ is defined by a collection of anchor points $r[k]$ and their associated tangent controls $r'[k]$. The parameterization of the contour is then expressed as

$$r(t) = \sum_{k=0}^{M-1} (r[k] \phi_{1,M,\text{per}}(t - k) + r'[k] \phi_{2,M,\text{per}}(t - k))$$

with $t \in \mathbb{R}$. As the active contour curve is closed, it relies on the $M$-periodized versions of the basis functions

$$\phi_{1,M,\text{per}}(t) = \sum_{n=-\infty}^{\infty} \phi_{1,M}(t - M n),$$

$$\phi_{2,M,\text{per}}(t) = \sum_{n=-\infty}^{\infty} \phi_{2,M}(t - M n).$$

The expression of the two exponential Hermite B-splines $\phi_{1,M}$ and $\phi_{2,M}$ is given in [8]. The positive integer $M$ encodes the complexity of the snake shape: while small values of $M$ yield simpler curves, large ones grant more flexibility and generate a richer variety of contours. Increasing the value of $M$ therefore allows one to approximate closed curves of arbitrary complexity at the expense of a larger number of parameters.

3. KEYPOINT-BASED SNAKE ENERGY

Algorithms for parametric snakes usually consist of two steps: a rough initialization of the contour followed by an automated optimization to precisely segment its target. The optimal segmentation is found as the minimizer of a cost functional called the snake energy [9]. We now describe our main contribution, a novel feature-based energy that relies on automatically detected corner points.

3.1. Formulation

Energies attracting parametric snakes towards a set of user-defined points can be found in the literature [7], as well as methods to drive contour extremities to automatically detected landmarks [10]. We aim at extending this idea by not only imposing automatically detected landmarks to attract the contour, but also to benefit from the direct control on the tangents granted by our snake construction to constrain the local behavior of the curve. In particular, our goal is to derive a corner potential—an energy functional that enables the generation of controlled discontinuities at precise locations on the curve. We propose the feature-based energy

$$E = \sum_{i=1}^{N_f} ||r[k_i^*] - f_i||^2 + M^2 \frac{||r'[k_i^*]||^2}{||r[r[k_i^*]] - f_i||^2},$$

where

$$k_i^* = \arg\min_{0 \leq k < M} ||r[k] - f_i||^2.$$
4. APPLICATION TO BIOIMAGES

4.1. Segmentation of *Caenorhabditis Elegans*

We segmented images from the *C. elegans* infection live/dead image set Version 1 provided by F. Ausubel (BBBC10) and available from the Broad Bioimage Benchmark Collection (BBBC, [11]). The living *C. elegans* worms appear on these images as elongated with pointy extremities and exhibit a variety of curved shapes. The difficulty in segmenting these data stems from the need to have a method that is flexible enough to accommodate the sinuous shapes of the worms while retaining the capability to capture sharp features. Sample results are shown in Figure 3.

In Table 1, we report a quantitative comparison of our results against the manually annotated ground truth provided on the BBBC website\(^1\). A multiscale optimization scheme was used to boost robustness in such potentially crowded environment. Contours are first optimized using the feature-based energy (2) to approach the extremities of the worms, and an edge-based energy is then used to fit the rest of the contour. Our segmentation results are robust to initial conditions provided that the initial snakes do not significantly overlap nearby worms.

### Table 1: Jaccard index—Keypoint-driven active contours versus ground truth.

<table>
<thead>
<tr>
<th>Worm #</th>
<th>B07</th>
<th>C03</th>
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<tbody>
<tr>
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<td></td>
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<tr>
<td>14</td>
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</tbody>
</table>

4.2. Segmentation of *Heligmosomoides Polygyrus Bakeri*

We also tried our approach on images of unstained *Heligmosomoides Polygyrus Bakeri* (*H. bakeri*) worms\(^2\). This organism, which is a natural parasite of mice and is a purely enteric nematode, appears as translucent and is more difficult to segment than *C. elegans*. Moreover, as these worms are moving very fast, their extremities appear blurred in most images, although being very pointy in reality. Typical results are shown in Figure 4. We had to initialize snakes closer to the actual contour to get a satisfactory result because of the difficulty of the task.

5. CONCLUSION

Our contribution in this paper is the formulation of a corner potential for the optimization of parametric active contours relying on automatically detected features. The proposed energy, inspired from the difficulties encountered in segmenting bioimages, has two main advantages. First, it reduces the sensitivity of snake-based methods to initial conditions or unfavorable imaging settings. Second, it allows the segmentation of objects with sharp corners using a global and flexible model with few parameters. An interesting aspect of the method is that its robustness to noise boils down to the robustness of the feature detector. Similarly, the invariance properties of the detector are inherited by the feature-based energy.

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1. In Table 1, the nomenclature corresponds to the ground truth provided at http://www.broadinstitute.org/bbbc/BBBC010/.
2. Images courtesy of J. Esser, Laboratory of Intestinal Immunology, École polytechnique fédérale de Lausanne (EPFL), Switzerland.
We first demonstrated the added value of our approach with respect to existing techniques on synthetic data and then illustrated its usefulness for different segmentation tasks on real bioimages. An added benefit of our approach is that the detected objects have a parameterization with landmarks matching the extremities, which facilitates further shape analysis and feature extraction.

6. REFERENCES


