

Unsupervised Level Set Parameterization Using Multi-Scale Filtering

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Abstract—This paper presents a novel framework for unsupervised level set parameterization using multi-scale filtering. A standard multi-scale, directional filtering algorithm is used in order to capture the orientation coherence in edge regions. The latter is encoded in entropy-based image ‘heatmaps’, which are able to weight forces guiding level set evolution. Experiments are conducted on two large benchmark databases as well as on real proteomics images. The experimental results demonstrate that the proposed framework is capable of accelerating contour convergence, whereas it obtains a segmentation quality comparable to the one obtained with empirically optimized parameterization.

Keywords—Multi-scale Filtering, Level Sets, Unsupervised Parameterization, Biomedical Applications.

I. INTRODUCTION

Region-based level set approaches have been extensively utilized in image segmentation since they often achieve sufficient segmentation quality without the need of complex data structures. Despite their vital attributes, such as topological adaptability, they are parameter-dependent requiring technical skills by the domain user. The obtained segmentation results are subjective whereas each set of parameters is valid for a specific dataset, or dataset subject.

Unsupervised level set parameterization is still an unsolved issue. An interesting attempt is presented in [1] and [2] where parameters are updated on each iteration of level set evolution. However, because of this dependency, there is a high probability of misconvergence due to errors in the early stages of the evolution. A statistical approach is introduced in [3] which hinges on the posterior probabilities of texture, edge and intensity cues in a locally adaptive manner. Nevertheless, this approach requires extensive technical support. Keuper et al. [4] and Liu et al. [5] dynamically adjust level set parameters for the segmentation of cell nuclei and lips, respectively. It is evident that these approaches are confined on specific image datasets. Two frameworks worth to be mentioned, are proposed in [6] and [7] for optimization of level set parameters according to genetic algorithms. However, they are not computationally efficient since they converge slowly in locally optimal

solutions. In [8] and [9], the trade-off between regularization and data fidelity terms is balanced. Nonetheless, parameter settings are still empirically fixed. A novel framework for unsupervised level set parameterization, based on the gray-level co-occurrence matrix is introduced in [10]. The main limitation of this approach is that it is single-scale, i.e. is incapable of capturing multi-scale localized information. Multiple scales are vital to be considered since they contain salient edges generated by: a) parts, b) cast shadows, and c) projections of target objects.

Multi-scale filtering has been repeatedly applied for retrieving localized edge regions [11]-[13]. The key idea is to compute the scale pyramid by subsampling an image in order to investigate the scale with the largest certainty of containing a target edge. Linear filter-banks and sampling operators are the main tools for such decompositions. In that respect, multi-scale filtering appears as an ideal tool for unsupervised level set parameterization.

In this work a novel framework is presented for unsupervised level set parameterization using multi-scale filtering. A standard multi-scale, directional filtering algorithm [14] is considered for capturing the orientation coherence in edge regions, which is encoded in entropy-based image ‘heatmaps’. The latter are used to intuitively weight region-based forces, which repel the contour from randomly oriented edge regions and guide it towards structured ones.

The remainder of this paper is organized as follows: Section II presents the proposed framework for unsupervised level set parameterization whereas Section III demonstrates the experimental results. Conclusions of this study are summarized in Section IV.

II. PROPOSED FRAMEWORK

The output of multi-scale filtering can be used to calculate entropy measures representing the orientation coherence in target edges, which strongly affect level set convergence. The

derived entropy-based ‘heatmaps’ are used to adjust level set parameters.

To begin with, the image is considered as a grid of $q \times q$ samples. Each sample is fed into the filtering descriptor and is further decomposed to the finest and second finest scales which are partitioned into four directional subbands: 0° , 45° , 90° and 135° . The band-pass directional subbands capture oriented salient edges. For each subband image I_{jk} , entropy measures are calculated according to the following equations:

$$IE_{jk} = - \sum_{n=1}^{N_{jk}} \sum_{m=1}^{M_{jk}} p_{jk}(m,n) \cdot \log p_{jk}(m,n) \quad (2)$$

$$p_{jk}(m,n) = \frac{|I_{jk}(m,n)|^2}{\sqrt{\sum_{n=1}^{N_{jk}} \sum_{m=1}^{M_{jk}} [I_{jk}(m,n)]^2}} \quad (3)$$

where IE_{jk} is the information entropy of the k^{th} direction in the j^{th} level, M_{jk} is the row size and N_{jk} the column size of the subband image.

The entropy measure is utilized contrary to other image features such as energy, since it is able to identify whether a salient edge is a target or non-target edge, by providing a measure of how well ordered is the structure in the neighborhood of an edge element. Provided that an edge neighborhood is unordered, i.e. it consists of edges of multiple orientations, it is associated with noise or background clutter. On the contrary, a target edge is associated with a well ordered neighborhood comprising a single orientation [15]. Among the entropy values calculated for each subband, the maximum entropy of the most informative scale is calculated and assigned to all pixels of each grid. As a result, entropy-based ‘heatmaps’ reflecting local textural information are formulated.

The energy functional of a region-based level set approach can be described as follows:

$$F = w_{reg} \cdot F_{reg} + w_{df} \cdot F_{df} \quad (4)$$

where F_{reg} and F_{df} are associated with regularization and data fidelity forces, respectively, whereas w_{reg} and w_{df} are weighting parameters. The latter are calculated according to the following equations:

$$w_{reg} \propto (1/w_{df}) \times N \times M, \quad w_{df} = \arg_{I_{jk}} \max(IE_{jk}(I_{jk})) \quad (5)$$

Equation (5) is an interpretation of entropy values adaptive to the direction of data fidelity forces. Once the entropy measures

have obtained high values, the associated neighborhood will correspond to non-target edges, which obstruct correct contour convergence. The key notion is that, by appropriately amplifying data fidelity forces in randomly oriented, high-entropy regions, the contour will be repelled and will be conversely guided towards target edges in the early stages of evolution. Hence, iterations dedicated to erroneous local minima will be avoided, speeding up contour convergence. In addition, the unsupervised parameterization is spatially-varying, in order to reflect local variations over the image. The pipeline of the proposed framework is summarized in the block diagram of Fig. 1.

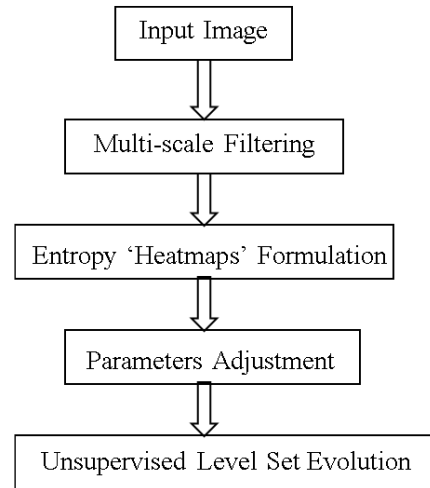


Fig. 1. Block diagram of the pipeline of the proposed framework.

III. RESULTS

The proposed framework has been embedded into the Chan-Vese model [16] and the model of Savelonas et al. [17] and has been experimentally evaluated on 100 images of two large benchmark databases namely the Amsterdam Library of Object Images (ALOI) dataset [18], and the Caltech 101 dataset [19]. Although the background of test images is homogeneous, all target regions consist of varying viewing and illumination angles, resulting in challenging shades. The latter may be associated with local minima of the active contour energy functional. Additional experiments were conducted on a challenging biomedical domain, involving proteomics images provided by the Biomedical Research Foundation of the Academy of Athens in order to evaluate the proposed framework on target regions surrounded by an inhomogeneous background. It should also be noted in the figures to follow that, green and pink contours correspond to the unsupervised and manual version, respectively.

Fig. 2 illustrates segmentation results on images of the ALOI database. Several images of the ALOI database, such as the illustrated ‘candle’, ‘cruesli’, ‘child cup’, ‘tree’ and ‘light pepper’ are not textured, whereas some also contain textured regions, as is the case with ‘sponge’, ‘nut’ and ‘ink fish’. In

addition, various images, such as “chess piece” and “dark pepper”, consist of difficult shades as well as challenging illuminations, as is the case with ‘white lid’. It is evident that the proposed framework aids the level set to converge to the actual object boundaries, resulting in accurate segmentation results.



Fig. 2. Segmentation results on images of the ALOI database.

The proposed framework has also been applied on real proteomics images. In these images, the segmentation task is impeded by the inhomogeneous background intensity as well as the presence of noise, dust particles and cracks on the gel surface. Moreover, the dynamic range of protein concentration results in faint spots which are hardly visible. In addition, the complexity of the protein mixture obstructs protein migration during two-dimensional gel electrophoresis (2D-GE) [20]. This yields to complex regions containing overlapping spots which are difficult to separate. These regions tend to occupy a large portion on the gel surface.

The model of Savelonas et al. described in [17], is the first to successfully exploit the attractive attributes of level sets [21] for the segmentation of proteomics images. It is based on the formation of a spot-targeted level set surface as well as morphologically-derived level set energy terms. It correctly detects boundaries of spot overlap in complex regions and identifies faint spots through histogram adaptation and morphological reconstruction processes. The level set

evolution is guided by region-based energy terms of the proteomics image as well as by information derived from the previous processes. The experimental results demonstrate that it generates more plausible spot boundaries and outperforms various commercial software packages. However, in the original instance of this model, level set parameters are still empirically fixed.

Fig. 3 illustrates segmentation results on samples of proteomics images containing faint and overlapping spots by applying the proposed framework for parameter adjustment of the model of Savelonas et al. It is evident that the proposed framework effectively identifies the boundaries of protein spots and separates overlapping spots despite the inhomogeneous background as well as the presence of noise. In addition, it correctly identifies faint spots. It should be highlighted that the proposed framework is capable of obtaining comparable segmentation quality in an unsupervised fashion, avoiding the laborious and time-consuming process of parameter tuning.

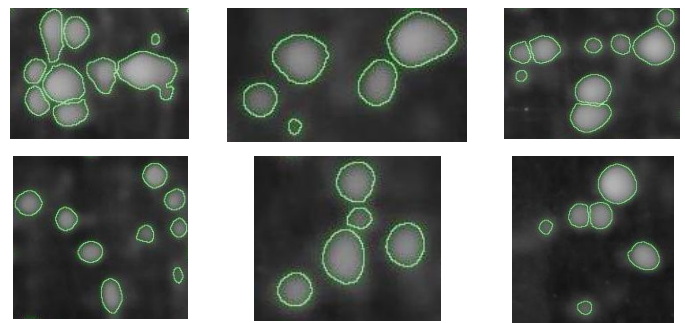


Fig. 3. Segmentation results on real proteomics images.

Fig. 4 illustrates segmentation results on images of the Caltech 101 database. The proposed framework has been embedded into the Chan-Vese model [16]. It is clear that, it accurately segments the objects of interest despite the challenging shades, which yield to false local intensity minima.

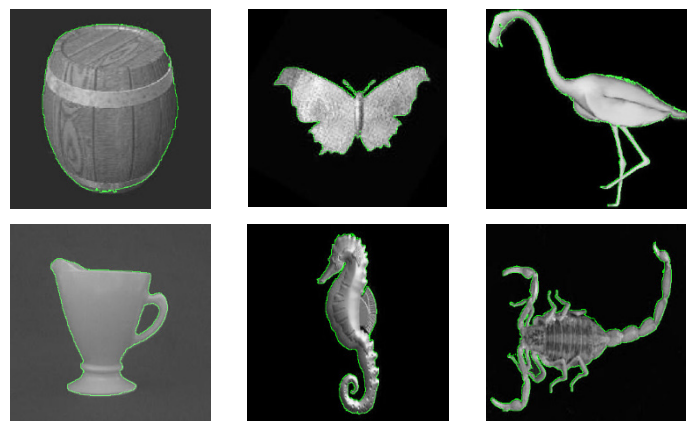


Fig. 4. Segmentation results on images of the Caltech 101 database.

Aiming at evaluating the unsupervised level set evolution of the proposed framework, comparisons with the manual case were conducted. All manual parameters were set to their optimal values according to the original paper [16] and the measure utilized is known as the Tanimoto Coefficient (TC) [22]:

$$TC = \frac{N(A \cap B)}{N(A \cup B)} \quad (6)$$

where A is the region delineated by the segmentation method under evaluation, B is the ground truth region and $N()$ indicates the number of pixels of the enclosed region.

First column of Fig. 5 depicts ground truth images of ALOI and Caltech 101 databases. Second column illustrates segmentation evolution of the manual case in the iteration that the proposed framework has converged whereas third column depicts segmentation results of the proposed framework. It is evident that in the manual case, the level set convergence is delayed. In the unsupervised case of the proposed framework, forces guiding level set evolution are appropriately amplified in non-target, high-entropy regions, accelerating convergence.

TC is calculated once the level set has converged, so as to quantify the difference between the regions embedded by the level set of the unsupervised and manual versions, in this specific iteration. The unsupervised version achieves an average TC value of $96.9 \pm 1.6\%$, which is comparable to the TC obtained by the manual version. Nonetheless, the unsupervised version converges in 10-20 times less iterations. The manual version, in the specific iteration that the unsupervised version has converged, achieves a TC value of $58.4 \pm 14.3\%$ with regards to all images tested.

IV. CONCLUSIONS

This work introduces a novel framework for unsupervised level set parameterization using multi-scale filtering. The proposed framework uses a standard multi-scale, directional filtering algorithm so as to capture the orientation coherence in edge regions. The latter is fed into entropy-based image ‘heatmaps’ which are capable of guiding level set evolution. Segmentation results are no longer subjective, as is the case with manual parameterization, whereas technical skills are not required by the domain user.

The proposed framework has been experimentally evaluated on two large benchmark databases as well as on a challenging biomedical dataset, involving real proteomics images. The automatically parameterized level set is compared to the manually parameterized version. The experimental results demonstrate that the former is capable of accelerating contour convergence, whereas it obtains a segmentation quality comparable to the one obtained with manual parameterization. Future work involves investigation of the proposed framework on various biomedical applications. Furthermore, unsupervised

level set parameterization by means of multi-scale filtering may be used in conjunction with well-established methods addressing level-set efficiency, such as the work of Adalsteinsson and Sethian [23], to further speed-up convergence.



Fig. 5. First column: ground truth images of ALOI and Caltech 101 databases. Second column: segmentation evolution of the manual case in the iteration that the proposed framework has converged. Third column: segmentation results of the proposed framework.

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