COMPARING YEAST CELLS SEGMENTATION THROUGH HIERARCHICAL TREES

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Abstract: Image filtering and segmentation consists of separating an image into regions according to some criteria and to the application finality. Recent publications in the image processing domain make use of a segmentation strategy called *multiscale* or *hierarchical segmentation*. The multiscale segmentation provides a family of partitions of an image, presenting it at several levels of resolution. This work studies a multiscale image representation called *Tree of the Critical Lakes* (TCL), that provides an set of nested partitions of an image. The Tree of the Critical Lakes is defined from the Watershed Transform, the traditional tool of Mathematical Morphology in image segmentation operations. Moreover, we implement a comparison between TCL and another way of image representation, called *Component Tree* (CT). The CT consists of a set of cross-sections images and its connected components, linked thanks to the inclusion relation. We show experiments of image segmentation, based on TCLs and CTs, for a group of yeast cells images.

1 INTRODUCTION

Recent segmentation methods tend to consider the hierarchical structure of images in object oriented analysis, segmentation and coding. A hierarchy allows the utilization of both the superficial and the deep image structure (set of possible regions and contours).

In this work we exploit two graph structures know as *Tree of Critical Lakes* (TCL) and *Component Tree* (CT) in order to implement yeast image segmentation. The Watershed Transform is used to build the TCL which provides a set of nested partitions of the image.

Yeast characterization by image analysis methods (O´Shea and Walsh, 2000)-(Pons et al., 1993) has been developed aiming at segmenting and classifying cells in an automatic or semi-automatic way. The knowledge of yeast features is important to several chemical processes. We exploit geometric and hierarchical properties of all nodes of the Tree of Critical Lakes, such as survival time, ellipse fitting criterion and region attributes, in order to discriminate yeast cells(Carvalho, 2004).

On the other hand, we implemented comparisons with the Component Tree. The CT is a structure builded from the thresholding process of an image, that consists of computing the cross-sections of an image, for each grey level. In the following, the link between connected components at each cross-section is stablished. Several authors have used this representation to implement some morphological operators (Najman and Couprie, 2004), image filtering (Jonnes, 1997) and image matching (Mattes et al., 1999).

The paper is organized as follows. First, we show in Section 2 some graphs concepts and definitions. Section 3 presents how we create a scale-space represented by the Tree of Critical Lakes. Section 4 is devoted to present the Component Tree and the image filtering process. Experimental results of the yeast segmentation by TCL and CT were compared and are shown in Section 5. Finally, the conclusions and future works are presented in 6.

2 GRAPH DEFINITION

Let $G = (V, E)$ be a non-directed graph where V is the set of nodes or vertices and E is the set of edges (i, j), for $i, j \in V$. A weighted graph is a graph where a number (weight) is associated to each edge (i, j), represented by $w\,(i, j)$. A path from i_1 to i_n is a list $(i_1, i_2, \dots i_{n-1}, i_n)$ where $i_k \sim i_{k+1}, k = 1, \dots,$ n-1. Two nodes i and j are connected if there is at least one

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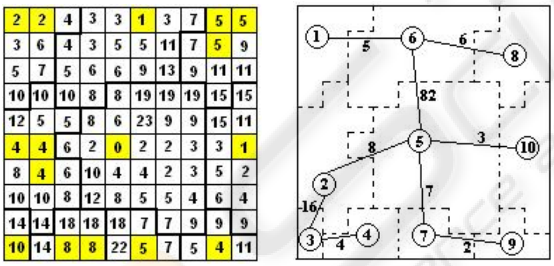
path between i and j. A connected graph G is a graph where all pair of nodes is connected. Let G_1 be a subgraph of G. A connected component CC of G_1 that contains one node i is the union of all paths in G_1 that originate on i. A tree is a connected graph with no cycles. A Minimum Spanning Tree (MST) is a tree that contains all nodes of G and such that the sum of edge weights is minimal.

3 TCL REPRESENTATION

The classical technique in morphological segmentation is the Watershed Transform (WT). We summarize in the following the main concepts of watershed. For a more complete review of watershed variations, we refer the reader to (Beucher and Meyer, 1993).

3.1 Watershed Transform

We consider the gradient image f as a topographic surface. An image is segmented by constructing the catchment basins of its gradient image, as shown in Figure 1. The gradient image is flooded starting from selected sources (regional minima) until the whole image has been flooded. A dam is erected between lakes that meet with others lakes. At the end of flooding process, we obtain one region for each catchment basin of the gradient image.



2	2	4	3	3	1	3	7	5	5
3	6	4	3	5	5	11	7	5	9
5	7	5	6	6	9	13	9	11	11
10	10	10	8	8	19	19	19	15	15
12	5	5	8	6	23	9	9	15	11
4	4	6	2	0	2	2	3	3	1
8	4	6	10	4	4	2	3	5	2
10	10	8	12	8	5	5	4	6	4
14	14	18	18	18	7	7	9	9	9
10	14	8	8	22	5	7	5	4	11

(a) (b)

Figure 1: (a) Original gradient image; the markers are the regional minima, in gray; the dashed lines separate the watershed basins. (b) MST of the image (a); the valuation of the edges corresponds to the volumetric extinction value.

Hierarchical watershed creates a set of nested partitions. A partition P of an image f is a set of disjoint regions R_i, $i = 1, 2 \ldots, n$, where the union of regions is the whole image. Let (P_k) be a sequence of partitions $P_1, P_2, \ldots, P_n$, of an image f. (P_k) is a hierarchy, also called nested sequence of partitions, if a partition at a fine level is obtained by merging regions of the coarse partition.

The watershed problem can be modeled using graphs. The gradient image is represented by a weighted neighborhood graph, where: (i) a node represents a catchment basin of the topographic surface; (ii) an edge links two nodes if their corresponding catchment basins are neighbors (in the sense of a pixel neighborhood); (iii) edge's weights are given by the lowest altitude of pass point separating two catchments basins.

The set of all edges (dams) where merging of different original lakes occur constitutes a minimum spanning tree (MST) of the weighted neighborhood graph(Meyer and Maragos, 1999). Although the regions merging were controlled by the altitude of topographic relief, the evaluation of the levels at which partitions are formed can be performed based on another value, called the *extinction value* (Vachier, 1995). We utilize the volumetric extinction value. Figure 1(b) show the MST of the artificial image presented in Figure 1(a).

3.2 Creation of a Scale-space

The TCL is a morphological representation obtained from Watershed Transform and provides the order of the fusion regions. Due to its hierarchical properties, the TCL has the potential to build a family of nested partitions. The initial partition P_n is the labeled image provided by the Watershed. The other partitions are formed by agglomerating two-by-two regions (Carvalho, 2004).

Frequently, the TCL is build from Minimum Spanning Tree (MST) of the image. Details of the algorithms concerning the MST and the TCL transformation can be found in (Meyer and Maragos, 1999) and (Meyer and Maragos, 1996), respectively.

3.3 Scale-space Analysis

We use some properties of the TCL hierarchical representation, in addition to general attributes, in order to segment yeast cell images. The segmentation algorithm can be summarized by the following 3 steps (Carvalho, 2004): *Scale-space creation*; *Computation of attributes*; and, *Hierarchical analysis* (Start the segmentation analysis by the Survival Time criterion; after, apply the area criterion to eliminate nodes close to the TCL root; Finally, apply the other criteria, as ellipse fitting (Fitzgibbon et al., 1999), region circularity and gray level mean).

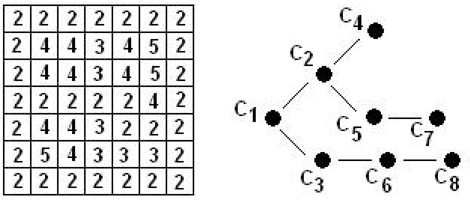
4 CT REPRESENTATION

4.1 Definition

The component tree is a representation of a grayscale image based on the cross-section decomposition between the minimum and maximum grey levels(Najman and Couprie, 2004). There exists links between components at sequential grey levels in the image. A component is defined as:

$$F_k = \{x \in F / F(x) \geq k\} \quad (1)$$

where F is an image and F_k is a section k (level) of F. The Connected Components (CC) of the different cross-sections may be organized in order to form a tree structure. We say that the two CCs C_{k+1} and C_k are linked when C_{k+1} is a subset of C_k (the inclusion relation). The first component C_1 (or C_{min}) in the image corresponds to the whole image domain and its called *root*. Figure 2(b) shows the CT of the grayscale image depicted in Figure 2(a).



2	2	2	2	2	2	2
2	4	4	3	4	5	2
2	4	4	3	4	5	2
2	2	2	2	2	4	2
2	4	4	3	2	2	2
2	5	4	3	3	3	2
2	2	2	2	2	2	2

(a) (b)

Figure 2: (a) The Component Tree of the grayscale image of (b).

We can associate number to the CT nodes, which measure some of the components features, such as: mean graylevel of the component; mininum and maximum greylevel values; area; perimeter; and, the image location of one representative pixel.

4.2 Filtering

Filtering the component tree is a decision-make process which classified nodes into those that are active (preserved) and those that are not (Jonnes, 1997). A grey-level image is decomposed into a stack of binary images, which are processed individually by a filter. When we re-stack these images, we have obtained a grey-level filter and the segmented image is obtained directly from the filtered image. The filtering algorithm can be summarized by the following 3 steps:

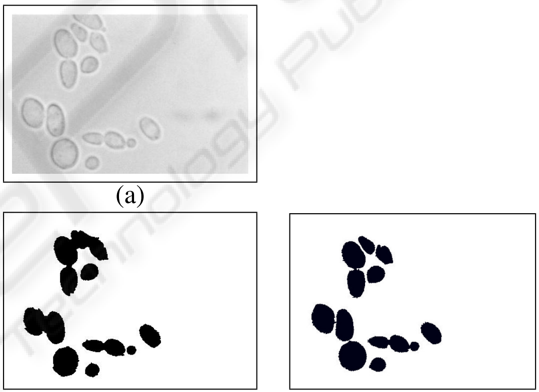
1. *Tree computation* – Compute the corresponding CT for the image.
2. *Computation of attributes* – For all CT cross-sections, compute the attributes area and grey level mean that will be used in the segmentation analysis.
3. *Hierarchical analysis* – Start the segmentation analysis by the grey level criterion. Then, apply the area criterion.

5 EXPERIMENTS

We present some results of yeast segmentation by analysis of its hierarchy. Other results and analysis are found in (Carvalho, 2004). The images were obtained from *School of Food Engineering* (FEA - Faculdade de Engenharia de Alimentos) at UNICAMP.

In all results we eliminate the objects that touch the image frame. No markers are used in this approach. Also, we use ST (survival time), area, ellipse fitting and gray level mean criteria in TCL analysis. The yeast segmentation based on CT filtering has accomplished by the utilization of grey-level mean and area parameters of each component connected of the image. All experiments are implemented in MATLAB.

Figure 3 show an example of the yeast segmentation obtained from CT and TCL analysis. A detailed observation of these images show that there are small differences at border and connectivity between cells.

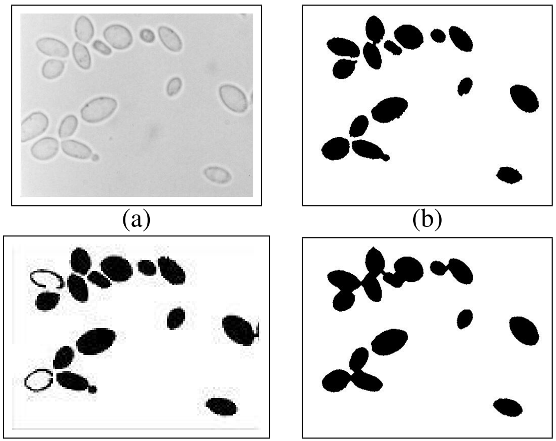


(a)
(b) (c)

Figure 3: (a) original image; (b) yeast segmentation by TCL analysis; (c) yeast segmentation by CT analysis.

Figure 4 illustrates the comparison between three different approachs in order to segment yeast cells. Figure 4(d) show the segmented image of Figure 4(a), obtained from O´Shea analysis (O´Shea and Walsh, 2000). In this case, it was necessary some morphological operations (dilation, closing hole and erosion) in order to remove some noises (regions not associated to yeast cells) in the processed image. As we can see, there are great differences between resulting images. The main problems are the contour preservation, the cells holes and the connectivity between cells. The TCL approach, based on Watershed Transform, preserve the cells contours; also, there is no holes.

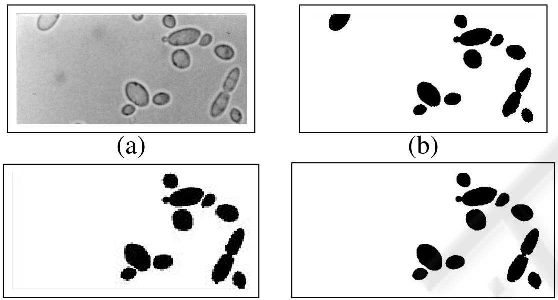
Figure 5 show an last example of the yeast segmentation obtained from TCL, CT and O´Shea analysis. Comparison shows that the method based on TCL representation preserves the yeast contours and provides cells area 10%, approximately, lower than CT and O´Shea methods.



(a) (b)

(c) (d)

Figure 4: (a) original image; (b) yeast segmentation by TCL analysis; (c) yeast segmentation by CT analysis; (d)yeast segmentation by O´Shea (O´Shea and Walsh, 2000) after morphological operations.



(a) (b)

(c) (d)

Figure 5: (a) original image; (b) yeast segmentation by TCL analysis; (c) yeast segmentation by CT analysis; (d)yeast segmentation by O´Shea (O´Shea and Walsh, 2000) after morphological operations.

6 CONCLUSION

In this paper we presented an analysis based on tree representation in order to segment yeast cells. We implemented two approachs based on image representation by Tree of Critical Lakes and Component Tree.

The results of the multiscale analysis for a group of yeast images were satisfactory and demonstrated the robustness of the method, even using few criteria. Usually, the classical Watershed is not able to segment correctly this type of images, due to the lack of markers and also to the supersegmentation problem. Scale-space analysis is usually a costly computational task. In the future, we will try to start from coarser image partitions in order to reduce the range of the computational analysis. Also, experiments was done to segment yeast cells based on Component Tree filtering. The filter parameters used in this work were area and grey level mean.

The investigations into the complexity of CT or TCL computation algorithms are necessary in order to enhance the efficacy of the performance. Finally, experiments will be done to classify yeast cells according to the taxonomy presented by O´Shea (O´Shea and Walsh, 2000).

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