A Vision System for Segmentation and Analysis of Colored Cytological Images

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Abstract

In this paper, we present a vision system to segment and analyze colored cytological images. The adopted approach combines, at a time, the principles of region growing and edge detection guided by a fuzzy classification. So the presented cells are presegmented using the fuzzy C-means algorithm, followed by a hybrid segmentation algorithm. Measures of shapes and colors are taken for every cellular object for analysis and interpretation purposes.

Key words: Segmentation - Analysis- cytological images - region-growing – edge detection - fuzzy classification

1. Introduction

The understanding of an image by a vision system can not be made unless one manages to go from a simple structure forming the image to a more abstract structure formed of worked out primitives, ready for analysis and interpretation. This phase of segmentation is the most delicate in the sense that it must allow the interpretation of the image as well as a human observer would make it.

In this paper, we treat the segmentation of cervical colored cytological images obtained from a vaginal_cervico_smear (V.C.S) obtained of the uterus collar (see Fig 1).

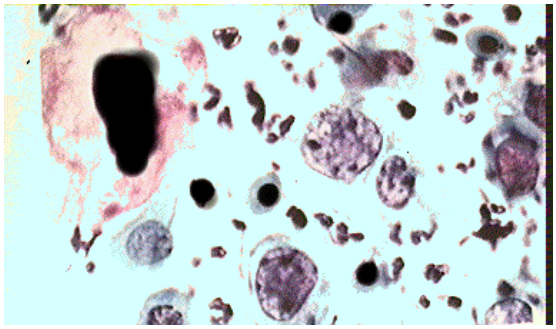


Fig-1- Original image

The V.C.S is a simple exam permitting the study of morphological colorful and fixed organism cells on blades. The uterus collar consists of two parts; namely exocol and endocol. The cells shown in Fig. 1 are of different types[Gom. 82].They are summarized in Fig. 2.

From densitometric side, these regions are not well separated. The cells are poorly contrasted and thus, the border separating the background regions from the cytoplasm regions is weak. On the other hand, the nucleus regions are hidden by the dense granulation due to the presence of chromatin, making segmentation difficult even though their borders are well delimited.

These features brought us to use the properties of homogeneity and the present local discontinuities in the image. Our method can be summarized as follows:

1. Segmentation of contours in order to extract edges nucleus.
2. Detection of cytoplasm regions guided by nucleus edges.

Thus, for every extracted cell, morphometric measures are taken for classification according to the different types of cells that can a V.C.S contains.

The paper is organized as follows: In Section 2 we describe the process of the proposed segmentation. In Section 3, we calculate the morphometric parameters for the recognized cells. The results, conclusion and perspectives of work are given in the section 4.

The cytological image is formed of cellular

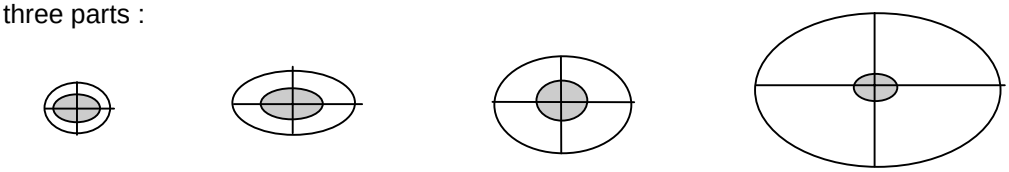
objects surrounded by a more or less homogeneous background. Every object is a nucleus inside a Cytoplasm.

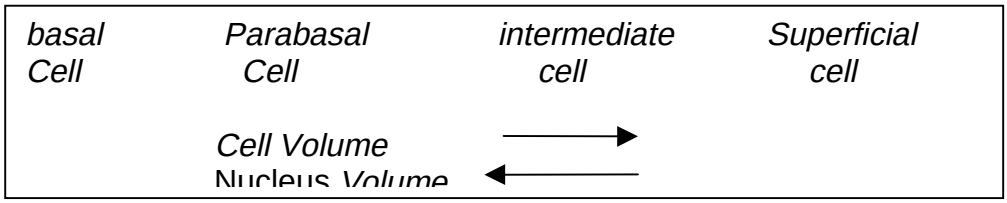
- Visual indicator extraction → down level
- Parameters phase → intermediate level
- Interpretation phase→ high level.

The visual indicator extraction or segmentation

2. Proposed segmentation

Generally, a vision system is constituted of three parts :





Measures / Cells		Cytoplasm			Nucleus		
		Shape	**Size**	**Color**	**Shape**	**Size**	**Chromatin**
Exocol	**Superficial**	Polyhedral	45-50 µm	Éosinophil	Round	5-7 µm	Condensed
	Intermediate	Polygonal	40-50 µm	Green-blue **Color**	Round Or oval	9-11 µm	Finely Granule
	Parabasal	Polyhedral	15-30 µm	Green blue color	Round Or oval	8 - 12 µm	Polychromatic
	Basal	Rare		Very basophil		Big	Polychromatic
Endocol	**Cellule Endocervical**	Rarely or Cylindrical		Clear	Round Or oval		Distribute Finely
Others Cells Elements	**Blood cells**	Round	7-8 µm	Eosinophil	Absent	/	/
	Leukocytes	Round	10-12µm	Weak Grey	Lobed	Average	/

Fig. 2 Cells types

is a preliminary step permitting the description of the different objects of the image. Generally,

we can say that it is not simple to extract some visual indicators without ambiguousness and mistakes which makes this task crucial in all systems of vision .
In the case of the images under consideration, a good segmentation would give a good

extraction of cells from the background such that to every cell correspond a nucleus and a cytoplasm.
The densitometric characteristics presented by cytological images under study lead us to make the following observations:

- Edges segmentation permits the extraction of edges of dense nucleus. But it doesn't permit the extraction of limits of the cytoplasm because of the overlap of colors between the background and the cell.
- Regions segmentation leads to over-segmentation of the heterogeneous nucleus because of the presence of the chromatin, without detects the background from the cytoplasm.

To alleviate to shortcomings to each method, we decided to use both of them together. The idea is to find cytoplasm regions by an image of points with contours precalculated from an image segmented by the fuzzy C-means algorithm. Several works showed the importance of such integration edge-region. Pavlidis and liow [Pav and lio.90] developed a method for segmentation cooperating the growth of regions and the detection of edges. A split and merge segmentation is first done which is improved using a criteria of contrast and regularity of border.
O. Monga [Mon.87] used a method of edge-region segmentation based on an algorithm of initial region growth. He constructed the corresponding adjacency graph to regions obtained to apply a strategy of grouping at the end. The luminance regions for which the gradient to the border is weak are merged.
J. Benois and D.Barba [Ben and Bar.92] have proposed to combine the edge detection and the region segmentation process. The idea is to use the edge detection procedure to obtain a chain of contours on which are placed the central points. The image is then split into a representation quadtree in simple homogeneous blocs and others containing central points. An initial partition of the image is then obtained by grouping simple blocs around the blocs containing central points. Finally, the similar adjacent regions, and not separated by contour points are merged. Gambotto [Gam.93] described an algorithm of growing region controlled by the border and the model of regions.

P. Bertolino and A. Montanvert in [Ber et Mon.96] used the irregular pyramidal region segmentation with the contours approach. The idea was to determine the edges map by an edge detector and to transmit this information from the base of the pyramidal to all its levels by weighting the adjacency graph and updating the similarity graph.

The method of segmentation proposed is described by the Fig. 3 :

1. Presegmentation of cytological images by the FCM algorithm putting in evidence the dense nucleus regions .

2.Thus, the segmented image is presented to the process of edge detection. Edges are extracted by the infinite size symmetric exponential filter ISEF, followed by an hysterisis threshold [Cas and al. 90]. Edge points are then chained and closed [Oua.97].

3. Nucleus edges are distinguished of the other closed edges by their average gradients. This is the phase of nucleus validation.

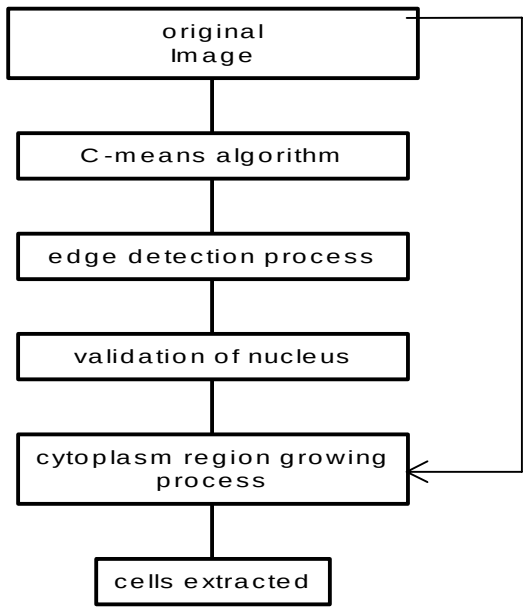


Fig. 3

4. Computation of the luminance histogram to detect the right peak in order to set the background threshold. So pixels with luminance value lower than the threshold are considered background pixels and they don't participate during the extraction of region cytoplasm.

5. Pixels aggregation to a cytoplasm region is based on an iterative method using as uniformity criterion, a color distance which was proposed in [Gar and al.80]. Two pixels

p1(l1,s1,h1) and p2(l2,s2,h2) belong to a same region if the difference of their color in terms of hue, saturation and luminance is lower than a threshold.

$\Delta d = \Delta l^2 + \Delta s^2 + ((s1+s2)/2)^2 \Delta h^2$

Indeed, Garbay [Gar and al.85] proposed an iterative segmentation method of convex cellular objects poorly contrasted and surrounded by a relatively homogeneous background. The proposed technique of segmentation is based on a local criterion: the color and another global criterion related to the convex shape of the object to segment.

The process of segmentation in its phase of region growing is based on the idea developed in [Gar and al.85] and then, making more general in the sense that [Oua.97]:

- The growth of every cytoplasm region is guided by edge points of its nucleus making the algorithm more exact and therefore faster.
- No hypothesis is made on the shape and the number of cells to be treated.

So, a first phase permits to aggregate the neighboring edge pixels of nucleus which are close terms of color.

A second phase permits the addition of new neighboring pixels in terms of connexity to cytoplasm pixels aggregated in the first pass. This treatment is iterative. The cytoplasm region in progress of construction grows until to stumble on lines of contrast representing the border of the cell, either until no pixel is added.

3. Parameters phase

This phase consists of associating to every extracted cellular object its nucleus and cytoplasm morphometric measures. These measures will permit to identify the present cells on the image. Shapes and color Parameters calculated are:

Perimeter: $\sum$ Pi pixels on the contour of the object

Area: $\sum$ pi pixels inside the object

Circularity : $p*(D_{max}/2)^2$ / area

Ellipsis : $p*(D_{max}/2)*(D_{min}/2)$ /area

Triangular : $(D_{max} * D_{min})$ /2 / area

Elongation: D_{max}/D_{min}

The Hue: it's the hue value obtained from HLS space.

4. Results and conclusion

The vision system has been applied on some cells Fig.5. First the cell images were presegmented by the c-means algorithm which put in evidence the nucleus regions. Then a hybrid segmentation algorithm was applied. The vision system recovers the cells quantitative measures of the image. Discriminate densitometric and colorimetric parameters represent every cellular type. The results are summarized in Fig.5. These measures permit the construction of reference models for each cell type. The obtained results are satisfactory.

The work in progress permits to use our vision system to help the diagnosis of uterus collar cancer. The idea is to use models of reference in relation of the shape, size and color of the observed cells for identification of cellular types. Cells not identified are considered anomalous. Then, a degree of this anomaly is measured.

5. Bibliography

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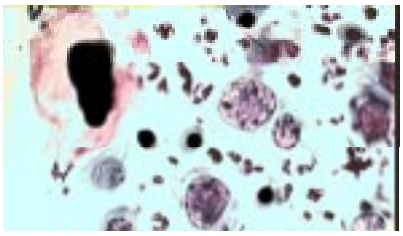
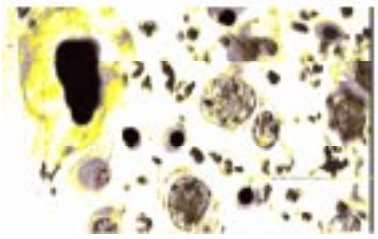
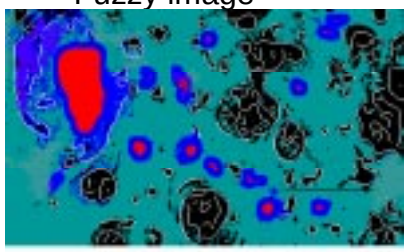


cytologic image source



Fuzzy image

edges image



cells extracted

Cells	**Cell1**		**Cell2**		**Cell3**		**Cell4**	
Measures	Nuclei	Cyto	Nuclei	Cyto	Nuclei	Cyto	Nuclei	Cyto
Dmin	17	22	15	24	11	24	86	185
Dmax	8	19	10	20	11	18	47	139
Perimeter	38	75	37	76	32	74	208	225
Area	88	1013	97	1009	92	889	2964	12067
Circularity	2.43	0.37	1.68	0.45	0.92	0.51	1.96	2.21
Ellipsis	1.14	0.32	1.13	0.37	0.92	0.38	1.07	1.66
Cyto/nuclei	0.087		0.096		0.103		0.246	
Cells	**Cell5**		**Cell6**		**Cell7**		**Cell8**	
Measures	nuclei	cyto	nuclei	cyto	nuclei	cyto	nuclei	Cyto
Dmin	31	45	17	24	12	16	19	23
Dmax	13	21	11	18	11	15	17	23
Perimeter	66	132	41	79	32	62	50	90
Area	177	1815	103	1097	93	861	242	1456
Circularity	4.19	0.85	2.07	0.41	1.21	0.23	1.10	0.27
Ellipsis	1.72	0.40	1.34	0.31	1.11	0.22	0.98	0.27
Cyto/nuclei	0.098		0.094		0.108		0.166	
Cells	Cell9		Cell10		Cell11		Cell12	
Measures	Nuclei	Cyto	Nuclei	Cyto	Nuclei	Cyto	Nuclei	Cyto
Dmin	16	36	21	25	18	29	16	33
Dmax	15	28	15	23	14	18	15	32
Perimeter	44	143	61	102	50	99	47	143
Area	181	1439	62	1532	87	1311	191	1482
Circularity	1.11	0.70	5.32	0.31	2.92	0.48	1.05	0.560
Ellipsis	1.04	0.55	3.80	0.28	2.27	0.30	0.98	0.543
Cyto/nuclei	0.126		0.040		0.066		0.129	

Cells	Cell13	
Measures	Nuclei	Cyto
Dmin	12	18
Dmax	11	16
Perimeter	35	68
Area	97	958
Circularity	1.166	0.266
Ellipsis	1.069	0.236
Cyto/nuclei	0.101	

Fig. 5