A SUPERVISED SEGMENTATION SCHEME FOR CANCEROLOGY COLOR IMAGES

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ABSTRACT

In this paper, we describe a new scheme to color image segmentation which is based on supervised pixel classification methods. Using color pixel classification alone does not extract accurately enough color regions, so we suggest to use a strategy based on four steps : simplification, pixel classification, marker extraction and color watershed growing. We detail on this paper the pixel classification and marker extraction steps. We present a quantitative measure which evaluate the resulting classifications and segmentations with a set of reference images. Our strategy is applicable to the detection of color objects in noisy environment and is particularly efficient on cytological color images.

1. INTRODUCTION

The purpose of the cytological examination is the spreading out of insulated cells. These cells are analyzed under a microscope by a cytopathologist and diagnosed by a medicine doctor. They identify all kinds of anomalies and particularly the cancerous cells. This work remains tiresome, complex and screening errors are possible. That is why, it can be useful to automate the detection of abnormal cells by a semi-automatic system for a quality assurance. In order to provide statistical results of the quality on the normality of a cell, our system must be able to extract correctly the various cellular components i.e. the cytoplasm and the nucleus. A recent survey [1] showed that an unsupervised pixel classification brought satisfactory results but that a supervised pixel classification could improve our segmentation. That is why, our strategy will be based on this last classification. We propose an automatic segmentation scheme based on: a simplification step, a supervised pixel classification in different color spaces, a marker extraction and a color watershed growing. The paper is organized as follows : In section 2, we describe the color segmentation scheme. In section 3, we give experimental results with our evaluation method. Finally we draw a conclusion to the quality of the segmentation.

The authors would like to thank Mr M. Lecluse and the pathological anatomy and cytology department of the Louis Pasteur Hospital Center of Cherbourg for providing the ground truth reference images.

2. THE SEGMENTATION SCHEME

The segmentation scheme (Fig.1) is given in four steps with an evaluation of results :

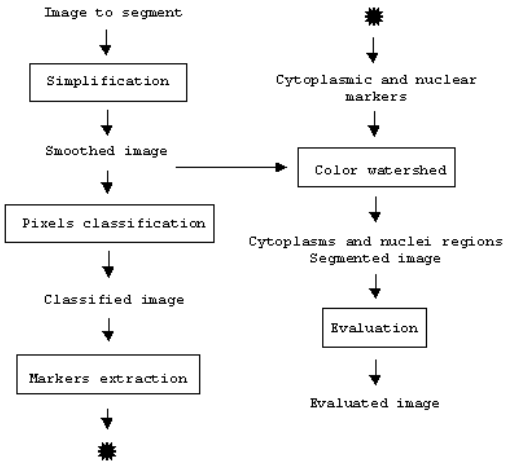


Fig. 1. The segmentation scheme

- Image simplification: The simplification step consists in a pre-treatment phase with the aim of smoothing the initial image to reduce the importance of noise. The produced image is used to calculate the gradient needed in the color watershed step. The growing quality depends greatly on the gradient image. This smoothed image is also used as input to pixel classification step in order to reduce the classifier sensitivity to the presence of noise (see in [2] for more details).
- Pixel classification: The step of classification consists in determining for each pixel of the image, a class among background, cytoplasm or nucleus. To realize this classification, we have tested several decision

functions which have been created by one of the following classifiers: Bayes, kNN, SVM, MLP. Each decision function is determined from four images and their expertise in order to create a training base.

- Marker extraction: With the image produced in the previous step, a pixel subset is recognized as belonging to the cytoplasm or the nucleus, this subset corresponds to true markers. The marker extraction is based on mathematical morphology operations which consists in a variable number of erosions according to the marker type.
- Color watershed: From the markers previously extracted and the smoothed image, the watershed performs a growing using image color information. The obtained regions correspond to the cytoplasm and nucleus (see in [3, 4] for more details.)
- Evaluation: Our evaluation method is based on an improved classification rate and is adapted to our study. This method gives us the classification rate of the object type in relation to a ground truth reference image.

2.1. Pixel classification

2.1.1. Training bases

Our pixel classification belongs to supervised classifiers techniques. For it, we generate a training base from four images containing objects with a wide variability. These images have been manually segmented by an expert in cytopathology. A testing base was also created from four other representative images. With Bayes and MLP classifiers, a training base is generated with all the pixels of the images. With kNN and SVM classifiers, an estimation has showed that the training time on all pixels of the images is too important. An alternative consists in learning on a pixel subset. This subset is built by selecting randomly n pixels from the three classes: background, cytoplasm, nucleus in each images. This method guarantees that every classes is sufficiently represented.

2.1.2. Classification methods

In this section, we present the four classifiers which are used : Bayes, kNN, SVM, MLP.

- Bayes: This classifier is based on the Bayesian decision theory. It is a supervised statistical approach to pattern classification which assumes that the decision problem is expressed in probabilistic terms. Since the algorithm is dealing with color images, a mixture of Gaussian distribution models is used. For each element x, the class that maximizes the probability to contain this element is searched.

$$f(x,i) = -\frac{1}{2}(x-\mu_i)^T \Sigma_i^{-1}(x-\mu_i) - \frac{1}{2}\log|\Sigma_i| - \log p_i + \frac{n}{2}\log 2\pi \quad (1)$$

where n is the number of classes , μ_i the mean attribute vector, Σ_i is the conditional covariance matrix and p_i the prior probability of class i.

- kNN: The k Nearest Neighbors method is well known used for many years in the field of machine learning [5]. Given a training set and a distance defined in the attribute space, the basic kNN rule consists in searching for the k nearest neighbors of an attribute vector. The estimated class probabilities is proportional to the number of C_j class among k nearest neighbors (with $1 \leq j \leq n$ and n is the number of classes), then the chosen j corresponds to the class which has the maximum probability. The value of k must be chosen to minimize the expectation of test error.
- SVM: The Support Vector Machine method has received a considerable attention in the recent years and many successful applications of SVM have been described in the literature [6, 7]. The objective of SVM is to maximize the margin of separation between the classes. Larger margin ensures smaller Vapnik and Chervonenkis (VC) dimension, which yields a good generalization performance. The maximum margin hyperplane found with SVM can be represented as a linear combination of training points called support vectors. Many specific algorithms can solve the convex quadratic problem of SVM, the most competitive being Sequential Minimal Optimization [8]. It remains two hyper-parameters (C and σ) that must be chosen to minimize the expectation of test error. The training algorithm produce a decision function where each support vectors has a α_i value characterizing his weight on the hyperplane position.

$$k(x_i, x_j) = \exp\left(\frac{-\parallel x_i - x_j \parallel^2}{2\sigma^2}\right) \quad (2)$$

$$\varphi(x) = \sum_{i \in SV} \alpha_i y_i k(x_i, x) + b \quad (3)$$

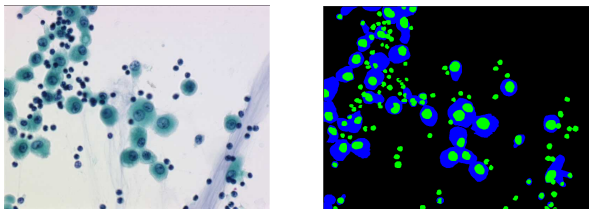
where $0 \leq \alpha_i \leq C$ and (x_i, y_i) is an example of the training base.

- Neural Networks : The Neural Networks that we use are Multi Layer Perceptron (MLP) with back propagation of gradient error. They are used for many years

in the field of classification. The mean idea is to group formal neurons by layer and to connect each layer at another adjacent layers. The training step modifies the weight between formal neurons, by the back propagation algorithm, in order to the output class matchs to the class of the objet presented in input [9].

2.1.3. Marker extraction

This step keeps a pixel subset as belonging to the nucleus or the cytoplasm. The removed pixels correspond either to : small regions belonging to anomalies (fragments can have been on the leaf during the preparation step), missclassified pixels (nuclear membrane, and transparent chromatine) due to the noise in the image. All these treatments are done from an operation of mathematical morphology named erosion. The size of the different objects not being identical, it is necessary to find the good number of erosions in order to optimize the number of valid markers. For it, we fix experimentally to one erosion for the nucleus and four erosions for the cytoplasm.



(a) Initial image (b) Reference segmentation

(c) Bayesian segmentation (d) kNN segmentation

(e) SVM segmentation (d) MLP segmentation

Fig. 2. The segmented images

3. EXPERIMENTAL RESULTS

Our study on the abnormal cells detection should allow to improve the quality of the diagnosis. The resulting evaluation step is then very important. We compare results at the output of the pixel classification step (classified image) and at the end of treatment (segmented image, Fig. 2) in order to choose the best classifier and evaluate the color watershed importance. For that, we use our method which is based on a classification rate and is adapted to our study.

3.1. Our evaluation method

Our method is an extension method based on a classification rate. This method uses a reference segmentation and provides a classification rate on the cytoplasm (TxCyt) and on the nucleus (TxNuc). The image that we analyze presents a variable number of cells. To compute these rates, we calculate the number of pixels belonging to every classes in the image. The common rate (ComCyt or ComNuc) shows the number of pixels which are correctly identified in the reference image. Whereas the difference rate (DifCyt ou DifNuc) globalizes for a C class (cytoplasm or nucleus), the two following errors: a pixel of the C class in the reference image is not recognized as the same class in the segmented image, and a pixel not being of the C class in the segmented image is recognized as the C class in the reference image.

$$Tx_{\varphi} = \frac{Com_{\varphi} + (1 - Dif_{\varphi})}{2} \tag{4}$$

$$Com_{\varphi} = \frac{\left|E^R_{\{\varphi\}} \cap E^A_{\{\varphi\}}\right|}{\left|E^R_{\{\varphi\}}\right|}$$

$$DifCyt = \frac{\left|(E^R_{\{C\}} \cap E^A_{\{B\}}) \cup (E^R_{\{B\}} \cap E^A_{\{C\}})\right|}{\left|E^R_{\{C\}} \cup E^A_{\{C\}}\right|}$$

$$DifNuc = \frac{\left|(E^R_{\{N\}} \cap E^A_{\{B,C\}}) \cup (E^R_{\{B,C\}} \cap E^A_{\{N\}})\right|}{\left|E^R_{\{N\}} \cup E^A_{\{N\}}\right|}$$

$$E^{\beta}_{\alpha} = \{(x, y) \in I : I_{\beta}(x, y) \in \alpha\}$$

with B : background, C : cytoplasm, N : nucleus, R : reference image, A : automatic image, φ : Cyt or Nuc

3.2. Evaluation of the proposed scheme

The images come from microscopic cytology images of bronchial tumours. We present the classification and segmentation results obtained on four cytologycal color images 24 bits of 574*752 pixels, each one containing about one hundred cells. We present the segmentation results of nucleus for each classifier in several color spaces (Fig. 3) and the classification and segmentation results for each classifier in the best color space (Table 1).

We note that the classification rate to the cytoplasm or the nucleus is very variable following the color space and the classifier used. We verify for the nuclei, that the watershed growing improves the segmentation results in comparison with the pixel classification results. The segmentation of the nucleus bringing more information to the experts, we privilege this rate in relation to the cytoplasm rate. That is why the weak reduce of the cytoplasm rate with the segmentation step is not a drawback. Moreover this watershed growing reduce the noise and the oversegmentation produced by the pixel classification step.

We note that the best color space to the pixel classification step is the same to the segmentation step for each classifier. The Bayes classifier gives better results for the nucleus segmentation in YUV, YC_bC_r, YCh_1Ch_2 color space and his computational time is faster (with a PC 2Ghz - 512Mo RAM: Bayes= 2s, kNN= 420s, SVM= 120s, MLP= 20s). The SVM and MLP classifiers also give good results.

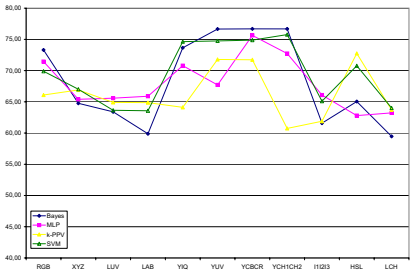


Fig. 3. Segmentation rate of nucleus (TxNuc) with our evaluation in different color spaces

4. CONCLUSION

We proposed a segmentation color scheme to cytologycal images and a new evaluation method. We show the importance of each steps (simplification, pixel classification, marker extraction, color watershed growing). The study shows the importance of the choice of supervised classifiers and of the color spaces. Our method is adapted to the segmentation of color objects in a noisy environment (under some restrictions) and particularly to the segmentation of cellular objects. We obtained very good results on the segmentation of nuclei in accordance with our waitings ($>$ 76 %) as well as the segmentation of cytoplasms ($>$ 73 %).

In order to improve the cytoplasm segmentation, we will consider a marker adaptive extraction step depending on the quality of the pixel classification. Another improvement will consist for SVM classifier in selecting a smaller subset of the training base which would improve the pixel classification and the computational time.

	Bayes	SVM	kNN	MLP
Space	YCh_1Ch_2	YCh_1Ch_2	HSL	YC_bC_r
Pixel classification				
TxCyt	72.4 %	77.4 %	80 %	56.9 %
TxNuc	74.6 %	74.2 %	70 %	73 %
Segmentation				
TxCyt	71.2 %	73.2 %	72.4 %	57.0 %
TxNuc	76.7 %	75.8 %	72.8 %	75.6 %

Table 1. The best pixel classifications and segmentations with different classifiers

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