EFFICIENT SEGMENTATION FRAMEWORK OF CELL IMAGES IN NOISE ENVIRONMENTS

EunSang Bak[1], *Kayvan Najarian*[2], *John P. Brockway*[3]

[1]Electrical and Computer Engineering Department, [2]College of Information
University of North Carolina at Charlotte
9201 University City Blvd, Charlotte, NC 28223, U.S.A.
[3]Memory Testing Corporation
P.O. Box 1621 Davidson, NC 28036, U.S.A.

ABSTRACT

In this paper, we propose an efficient segmentation method that exploits local information for automated cell segmentation. This method introduces a new criterion function based on statistical structure of the objects in cell image. Each pixel is initially assigned to the most probable region and then the pixel assignment process is iteratively updated by a new criterion function until steady state is reached. We apply the proposed method to cervical cell images as well as the corresponding noisy images that are contaminated by Gaussian noise. The performance of the proposed method is evaluated based on the results from both normal and noisy cell images.

Keywords: Cell segmentation, local information, iterative algorithm

1. INTRODUCTION

The capabilities of the computer-aided cell segmentation and classification have been dramatically increasing for the last decade. Such automated systems allow the study of not only individual cell nuclei as local objects but also complex cell structures.

Pap smear test is considered as one of the most routine cytological screenings. Screening is conducted by a trained pathologist based on a standard rule-base often referred to as "The Bethesda System" (TBS) [1]. Although many of the rules and criteria in the TBS have been clearly defined for each cell class and category, the evaluation of these rules may be performed rather differently by each pathologist. This is due to the fact that pathologists make decisions by visual inspection of a large number of cells and evaluating diagnostic features such as the ratio of the size of the nucleus to the size of cytoplasm or the shape of nucleus in each cell. Accurate measurement of such features from all cells is, while critical for reliable clinical determinations, a difficult and tiring process. An automated segmentation and classification system [2, 3] could be an alternative tool to avoid false clinical decisions due to fatigue or other types of human error.

As mentioned above, the key step in any automated cell classification is cell segmentation as a preprocess. There are several methods for cell segmentation that empowers automated cell screening systems. Some of them [4, 5] involve a thresholding algorithm which determines the threshold value either adaptively or recursively. In other methods [6, 7], geometrical shape or configuration is utilized in some manners.

In this paper, we propose an efficient segmentation scheme for cell segmentation and evaluate its performance using Pap smear samples in the presence of heavy additive noise. In the proposed method, in order to improve the segmentation performance, both global and local characteristics of the each object (nucleus, cytoplasm and background) of the cell image are exploited in the segmentation process. A locally adapted likelihood, called local spatial likelihood (LSL), is defined to reflect not only the global but also local characteristics. Combined with local spatial prior probabilities, the LSL forms a new function, called local spatial posterior (LSP), that is treated as a criterion function of the proposed segmentation method. The LSP iteratively updates a segmented image. We illustrate the performance of the local spatial posterior as a criterion function for cell segmentation in the presented experimental results.

The paper is organized as follows: In Section 2, our proposed iterative segmentation process is described. The criterion function, LSP used in the iterative algorithm, is introduced in Section 3. The experimental results are presented in Section 4, and finally conclusions are given in Section 5.

2. ITERATIVE SEGMENTATION

From the segmentation point of view, a cell image has three dominant regions that are occupied by nucleus, cytoplasm, and background. In order to split a sample into three different characteristic regions, we first consider the average intensity of each region. In a cell image, the darker pixels are more likely to belong to the nuclear region and the brighter pixels to the background. The rest of the image, therefore, forms the cytoplasm. As expected, the main feature to separate three different regions is the pixel intensity. Since no distributional forms are known to be successful to describe microscopy images, we assume that the intensity of each region is normally distributed.

2.1. Notations

Considering an image as a rectangular array of pixels **S**, the location of each pixel is indexed by $s \in \mathbf{S}$. Throughout the paper an image is viewed from two different perspectives; one is a set of intensities denoted by $\mathbf{X} = \{\mathbf{X}_s, s \in \mathbf{S}\}$, that are used for extracting statistical information needed for segmentation, and the other representation is a set of labels, denoted by $\mathbf{\Omega} = \{\mathbf{\Omega}_s, s \in \mathbf{S}\}$, that identifies the final segmented image.

2.2. Iterative segmentation procedure

In the first step, an image is partitioned into non-overlapping windows and the sample mean and variance are estimated from these windows. Estimated values provide sample vectors that constitute the feature vector space. Since we are dealing with ternary images, the vector space needs to be clustered into three classes. As a result, the center point of each cluster gives representative parameters of the distribution of the corresponding region in the image. We use the K-means algorithm for initial clustering of the feature vectors.

The image resulted from the clustering of the feature vector space becomes an initial coarsely segmented image on which our first parameter estimation process is performed. Since we assume a normal distribution, a parameter set of mean and variance is estimated from each region. After parameter estimation, every pixel is assigned to the region in which the criterion function of the pixel is larger. The criterion function is a measure of the probability of the pixel being included in the given region. This function is built on the assumption of normal distributions and will be derived and described in more detail in Section 3.

Given the noisy image **X**, and the provisional labeled image $\mathbf{\Omega}^{(i)}$ in the i^{th} iteration, the updated label assignment of a pixel is made based on the value of the criterion function. After the labels of all pixels in the image $\mathbf{\Omega}^{(i)}$ have been updated, the parameter set of each updated region is estimated in turn for the next iteration. The overall process is described in the Fig. 1.

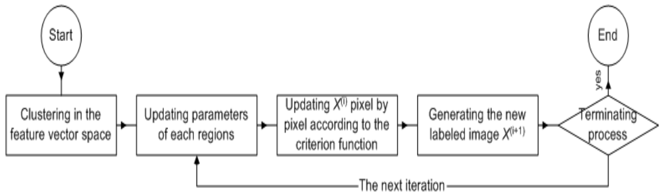

Fig. 1. Iterative segmentation procedure.

3. CRITERION FUNCTION

The most important part of the iterative segmentation process is the criterion function by which the pixel is assigned to the most probable region. In this section, we develop the local spatial posterior as a novel criterion function.

3.1. Assumptions

In general, the state space of $\mathbf{\Omega}_s$ is much smaller than that of $\mathbf{X}_s$ and we shall take advantage of this to develop our idea. Making a statistical relation between **X** and **Ω**, we make the following two assumptions. We assume that the random variables, $\mathbf{X}_1, \mathbf{X}_2, \ldots, \mathbf{X}_n$, are conditionally independent, and each $\mathbf{X}_i$ has the same known class conditional density function. We also assume that $\mathbf{X}_i$ depends only on $\mathbf{\Omega}_i$. With these assumptions, the joint conditional probability density function over the specific neighborhood area can be described as (1), where N_s is a set of indices of neighboring pixels centered at site *s*, and $\tilde{N}_s$ is a set that includes N_s as well as the index of the center pixel.

$$\begin{aligned} & p\left(\mathbf{X}_{\tilde{N}_s} = x_{\tilde{N}_s} | \mathbf{\Omega}_{\tilde{N}_s} = \omega_{\tilde{N}_s}\right) \\ & = \prod_{s \in \tilde{N}_s} p\left(\mathbf{X}_s = x_s | \mathbf{\Omega}_s = \omega_s\right) = \prod_{s \in \tilde{N}_s} p\left(x_s | \omega_s\right) \end{aligned} \quad (1)$$

3.2. Local spatial likelihood

The class conditional probability density function of $\mathbf{X}_s$ given $\mathbf{\Omega}_s$ is called the likelihood of $\mathbf{\Omega}_s$ and is defined as:

$$l\left(\omega_s; x_s\right) = p\left(x_s | \omega_s\right), \quad (2)$$

where ω_s is the variable of the function. This function is normally distributed based on the assumptions we made. If prior information is available, the likelihood function can be replaced by the posterior function (3) using Bayes' theorem.

$$P\left(\omega_s | x_s\right) = \frac{l\left(\omega_s; x_s\right) P\left(\omega_s\right)}{\sum_{\omega_s} l\left(\omega_s; x_s\right) P\left(\omega_s\right)} \quad (3)$$

The parameters of the likelihood function are often estimated from the entire image, and as a result, the estimation process inevitably ignores the local information in the area where $\mathbf{\Omega}_s$ exists. This causes inherent segmentation errors in the probability distribution-based approaches. To circumvent such errors, we derive a modified likelihood in which local information is efficiently considered and incorporated in the criterion function. More specifically, while likelihood function considers only $\mathbf{X}_s$ given $\mathbf{\Omega}_s$, the modified likelihood takes into account the neighborhood of $\mathbf{X}_s$, $\mathbf{X}_{\tilde{N}_s}$ given $\mathbf{\Omega}_s$. We call this function local spatial likelihood (LSL) and is defined as:

$$l\left(\omega_s; x_{\tilde{N}_s}\right) = \sum_{x_{\tilde{N}_s}} p\left(x_{\tilde{N}_s} | \omega_{\tilde{N}_s}, \omega_s\right) P\left(\omega_{\tilde{N}_s} | \omega_s\right) \tag{4}$$

Eq. (4) can be rearranged as (5) by applying the assumptions in Section 3.1. It can be seen that the new likelihood function (5) is composed of a common likelihood *l* and a weight factor w. The weight factor is the average value of the joint conditional probability density in the neighborhood.

$$\begin{aligned} l\left(\omega_s; x_{\tilde{N}_s}\right) &= \sum_{\omega_{\tilde{N}_s}} P\left(\omega_{\tilde{N}_s} | \omega_s\right) \prod_{i \in \tilde{N}_s} p\left(x_i | \omega_i\right) \\ &= \sum_{\omega_{\tilde{N}_s}} P\left(\omega_{\tilde{N}_s} | x_s\right) \prod_{i \in N_s} p\left(x_i | \omega_i\right) p\left(x_s | \omega_s\right) \\ &= w\left(\omega_s\right) l\left(\omega_s; x_s\right) \\ \text{where} \quad w\left(\omega_s\right) &= \sum_{\omega_{N_s}} P\left(\omega_{N_s} | \omega_s\right) \prod_{i \in N_s} p\left(x_i | \omega_i\right) \end{aligned} \tag{5}$$

Although Eq. (5) is a meaningful candidate for a criterion function, we improve this function further for the reason described here. As the iterative segmentation process proceeds, the current label field $\mathbf{\Omega}_{N_s}$ gets closer to the most probable neighborhood map to estimate the LSL at site *s*. Hence, there is no need for averaging in the weight factor w. Instead of averaging in w, LSL consider only the exact label map $\mathbf{\Omega}_{N_s}$ of the neighborhood. This changes the form of LSL as follows.

$$\begin{aligned} l\left(\omega_s; x_{\tilde{N}_s}\right) &= p\left(x_{\tilde{N}_s} | \omega_s\right) \\ &\approx P\left(\omega_{\tilde{N}_s} | \omega_s\right) p\left(x_s | \omega_s\right) \prod_{i \in N_s} p\left(x_i | \omega_i\right) \end{aligned} \tag{6}$$

Consequently, the local spatial likelihood (6) indicates the likelihood of $\mathbf{\Omega}_s$ being ω_s when not only its intensity is x_s, but also its intensity field of the neighborhood is $\mathbf{X}_{\tilde{N}_s}$ while considering the label field $\mathbf{\Omega}_{\tilde{N}_s}$. The choice of using this LSL creates significant improvements throughout the process.

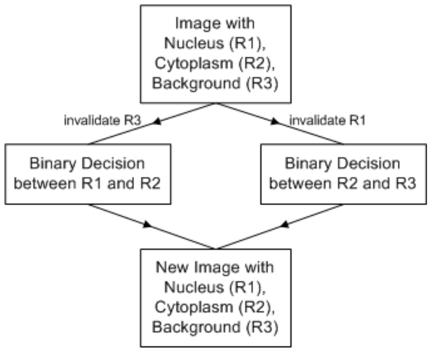

Fig. 2. Decision process.

3.3. Local spatial posterior

Just as the likelihood is replaced by the posterior providing prior probabilities, LSL can also be converted into the corresponding local spatial posterior (LSP). Since LSL takes into account local information, in order to have consistency it is important that the prior also contain the local characteristics. We define the local spatial prior as a probability distribution of $\mathbf{X}_s$ over certain size of the local area. The Eq. (7) shows the result of the derivation of the proposed LSP.

$$\begin{aligned} P\left(\omega_s | x_{\tilde{N}_s}\right) &= \frac{l\left(\omega_s; x_{\tilde{N}_s}\right) P\left(\omega_s, s \in \hat{N}_s\right)}{\sum_{\omega_s} l\left(\omega_s; x_{\tilde{N}_s}\right) P\left(\omega_s, s \in \hat{N}_s\right)} \\ &\propto w\left(\omega_s\right) l\left(\omega_s; x_s\right) P\left(\omega_s, s \in \hat{N}_s\right) \end{aligned} \tag{7}$$

where $\hat{N}_s$ is a set of indices of local area in which the local spatial priors are estimated.

4. EXPERIMENTAL RESULT

The criterion function in the proposed iterative segmentation procedure conceptually determines the most probable region for a pixel between nucleus and cytoplasm or cytoplasm and background (since nuclei are mostly surrounded by cytoplasm and cytoplasm is surrounded by background). Such a characteristic in cell images enables us to apply a binary decision rule to the ternary case. Fig. 2 briefly shows the decision process.

The cell images used in our experiments are cervical cell images. We evaluate our method with two groups of cell images in Fig. 3,4. One is a group of normal images which are obtained from relatively good environment for data acquisition, and the other is a group of degraded images from the environment which could be exposed to noisy factors, which, in this paper, is represented as Gaussian noise.

The degraded images are contaminated with Gaussian noise, $N(0, 0.05^2)$. The main reason to test degraded images for obtaining segmentation performance is to see how robust the proposed segmentation framework is regardless of the quality of images. Depending on the data acquisition process, different kinds of images can be obtained with different qualities. Thus, the segmentation procedure should be resistant to the quality of input images. Even though we choose the case that are exposed to Gaussian noise environments, the proposed method is not restricted to a particular noise environment. Any parametric or nonparametric distributional forms for noise environments can be merged into the proposed segmentation framework. This is a significant advantage of the proposed method.

Since we are using real images, we have no information about the corresponding true segmented image except for visual inspection. Therefore, we compare the results from normal cell images with those from degraded cell images to evaluate the robustness of the proposed method and the performance of segmentation process itself.

As can be seen in Fig. 3,4, the boundaries resulted from the proposed method clearly separate each class of the image regardless of the heavy noise. Even though the boundaries of the results from the degraded images are partially fuzzy, they are still in good shape compared to the ones from normal cell images. Therefore the proposed segmentation method provides robust segmented images for extracting features that are needed for the next classification step in automated cell classification system.

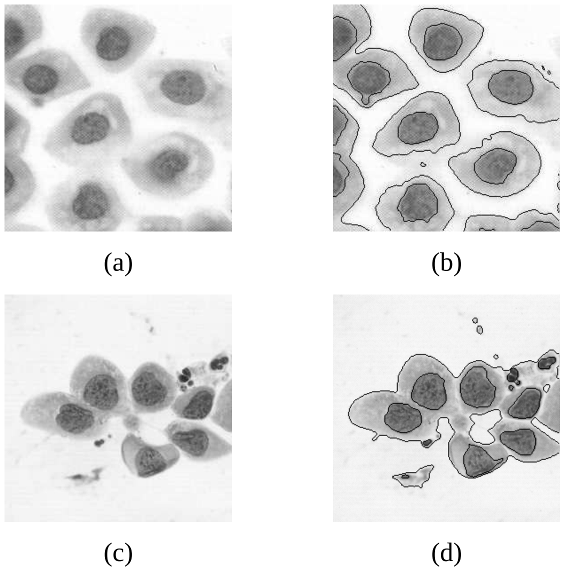

Fig. 3. Segmentation results from normal cell image groups.

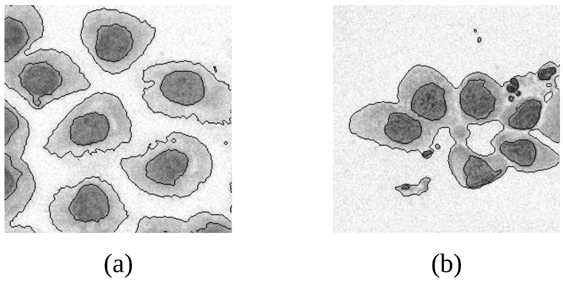

Fig. 4. Segmentation results from degraded cell image groups.

5. CONCLUSION

A new segmentation framework based on statistical properties of objects in cell image is introduced. This method is proved to be resistant to the heavy noise and is not restricted to a particular noise environment represented by specific noise distribution form. Such a flexibility indicates various possibilities for the proposed method to be extended to different applications.

6. REFERENCES

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