ORIGINAL RESEARCH PAPER

Computer Science

PIXEL CLASSIFICATION METHODS FOR M-FISH IN CHROMOSOMES IMAGE ANALYSIS

KEY WORDS:

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INTRODUCTION

Themaximum-likelihood classifier is one kind, which estimates the class parametersfrom the training data and an unknown sample is classified to aclass that yields the maximum likelihood of the sample belonging to the class.When the number of samples representing classes is large, the estimation ofthe parameters will become close to the true parameters. On the contrary,when the number of training samples is small (e.g. the face recognition problemwhere only a few images are available for each class), the estimation ofthe class parameters will be inaccurate or even impossible. For such cases, thenearest neighbor classifier or k-nearest neighbor classifier is a suitablechoice, which assigns samples to the class of the nearest training sample.If the labels are not available, the class parameters can be estimatedusing an unsupervised method.The samples can be grouped into a numberof classes without estimating the parameters, and this is called an unsupervisednonparametric method.

Foreground-background Segmentation

In order to compute reliable boundaries between objects and background,we combined multiple methods that utilize not only spectral informationbut also edge information.Laplacian of Gaussian (LoG) edge detectionperformed on the DAPI channel provides nice closed boundaries of chromosomes that correspond well to human perception. However, it also picks upunwanted artifacts from the background. In general, chromosome intensities are brighter than the neighboring background, although the background surface is not globally uniform. When object intensity is brighter than the neighboring pixels, adaptive thresholding is an effective segmentation method. This method effectively separates chromosomes from background. Due to its simplicity and effectiveness, adaptive thresholding is widely used for chromosome image segmentation.

However, when a number of pixels in the foreground are darker than neighboring foreground pixels, adaptive thresholding creates holes inside the chromosome or disconnects the chromosome into pieces. To utilize the spectral information, 6-feature 2-class K-means clustering method is used. This clustering method is preferable to the maximum-likelihood method because it does not require training. It groups six dimensional data into two classes while iteratively regrouping the data points until the class means converge. Its classification results are similar to those of the maximum-likelihood classifier since they both utilize the same information. Adaptive thresholding, LoG edge detection, K-means clustering, and global thresholding methods are combined together to achieve a final segmentation result. A composite binary image is obtained after voting among those 4 methods. For example, a pixel becomes foreground when a majority (3 out of 4) is foreground. Prior to the segmentation, a non-uniform background was corrected by fitting a cubic surface to the estimated background pixels and subtracting it from each channel.
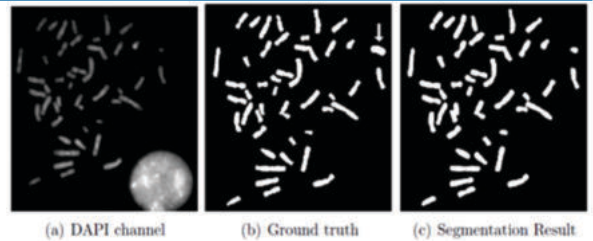

(a) DAPI channel (b) Ground truth (c) Segmentation Result

Figure 1.1: Segmentation Result

Detailed Procedure For Cell Removal

The cell identification procedure is as follows.

1. All six channels are summed together and scaled to fit 8bit grayscales since the cells do not always appear in the DAPI channel.

2. This composite image is thresholded using the iterative global thresholding method having the prior of 0.4 for the lower gray scales.

3. The holes inside cells are filled.

4. A morphological open operation with a 5×5 circular structuring elementis applied to smooth the boundary. Let's call the resulting imageT1.

5. A morphological erode operation with a 51×51 circular structuring elementis applied to T1 to remove objects smaller than 25 pixels in width.The structuring element is chosen to ensure that most of the chromosomesare removed and only cells are left.Let's call the resulting imageT2.

6. Each blob (found by 8-connectivity) on T2 are examined for the circularity.Let's call a blob T3.

7. T3 is further smoothed by the open operation using a 7×7 circular structuringelement, creating T4.

8. The circularity of T4 is measured using $S = 4\pi A/P^2$, where A = areaof T4 and P = length of perimeter. The length P is measured usingFreeman's chaincode by tracking the boundary, and $P = \square \times Ne + \square \times No + \square \times Nc$, where $\square$, $\square$, and $\square$ are 0.980, 1.406, -0.091 respectivelyand Ne = number of even chaincode, No = number of odd chaincode,and Nc = number of corners where the chaincode changes. Let's call thecircularity of T4 S1.

9. If S1 is larger than 0.65, the corresponding blob on T1 is examined for itscircularity. If its circularity is larger than 0.75 then the blob is identifiedas a cell.

EXPERIMENTAL RESULTS

Table 2.1: PSNR

Existing 1	Existing 2	proposed
27	44	55
55	67	67
67	87	89
145	176	107
167	189	178

Table 2.1 represents PSNR values in this table. Proposed values are compared with Existing 1 and Existing 2 values.

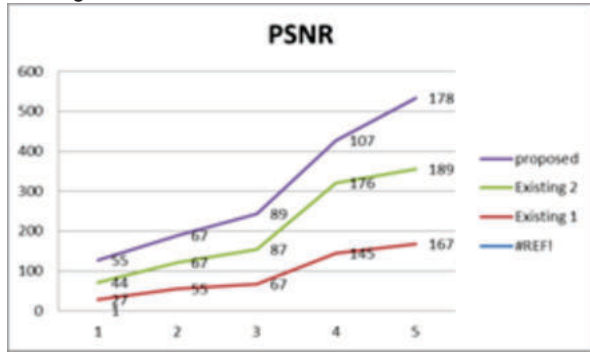Their proposed values are higher than compare with other existing values.

Figure 2.1: PSNR

Figure 2.1 represents PSNR values are compare with them. All values are only positive. The proposed values are higher than in this diagram. Existing 1 is a lower than compare with existing 2 and proposed values.

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