Recognition and Classification of the Cancer Cells by Using Image Processing and LabVIEW

Hossein Ghayoumi Zadeh, Siamak Janianpour, and Javad Haddadnia

Abstract—In this work, an image analysis approach for automated detection, segmentation, and classification of particular cells, specially the cancer cells from normal cells is introduced. In this technique we can also count the number of defected cells and find their position with image processing. The results of this analysis are useable in designing a neural network for more accurate analysis. The particular cells segregation is the most important property of this work. Using the LABVIEW Software gave practical usages to this image processing system because it can communicate with other equipments used in this system and controls them in order to have an automatic system. This demonstrates the potential effectiveness of such a system on diagnostic tasks that require the classification of individual cells.

Index Terms—Convolution, fast fourier transforms, gaussian processes, LABVIEW.

I. INTRODUCTION

Object detection, segmentation, and classification are the key building blocks of a computer vision system for image analysis. The goal of detection and segmentation is to locate and extract meaningful objects from the image. In cytological and histological images, this detection and segmentation play important roles in breast cancer classification between malignant and benign [1].

Computing technology has often proven useful in performing tedious or complex tasks quickly, accurately, and consistently. In extensive previous work by this author and others, computational intelligence was used to identify cancerous breast lesions based on radiologist's impressions of various features visible on a mammogram. In other areas of medicine, computational intelligence has been used to separate (or segment) an image (such as an MRI display) into its constituent parts, allowing automated estimations of tissue volumes [2].

Methods based on thresholding and edge detection [3]-[4] only work well if the contrast of the image is excellent. However in most cases, this technique yields broken edges and poor detection in noisy environments. Watershed techniques [5]-[6] have also been applied to the problem of cell segmentation. If the gradients in the image are large enough, then the background can be easily separated from the

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foreground.

The principles that are used in this paper are based on image processing tools such as image enhancements (filter, noise removal and etc.), image segmentation, pattern recognition, vision assistant and LABVIEW software. The most important property of this method is accuracy where preserves its simplicity and promptitude. Also noise removal algorithm that is used in this system for improving the counting ability of the cells is one of the most significant traits of this job.

II. PROCEDURE FOR PAPER SUBMISSION

Now we are going to explain the procedure of this job. First of all the image have to be transferred in to LABVIEW Software by a DAQ (Data AcQuisition) card. After that the image processing stage will be continued by using LABVIEW and MATLAB together. The image enhancement, segmentation and etc. are done with these two software. Whereas LABVIEW has a great ability to communicate with other equipments and can control them, it is used as a processing and controlling unit in this system so by using LABVIEW we can design an automatic system.

The algorithm of this process is shown in Fig. 1.

In Fig. 2 the original cells image that is used for image processing is shown. In this image particular cells are shown besides the normal cells.

If we look at the Fig. 3 carefully, we will see that some of the cells are marked. These are the defected cells and the goal is to mark them between other cells in the image with image processing.

III. GAUSSIAN SMOOTHING

The effect of Gaussian smoothing is to blur an image, in a similar fashion to the mean filter. The degree of smoothing is determined by the standard deviation of the Gaussian. (Larger standard deviation Gaussians, of course, require larger convolution kernels in order to be accurately represented.)

The Gaussian outputs a "weighted average" of each pixel's neighborhood, with the average weighted more towards the value of the central pixels. This is in contrast to the mean filter's uniformly weighted average. Because of this, a Gaussian provides gentler smoothing and preserves edges better than a similarly sized mean filter.

According to Gaussian equation (1) we will have:

$$G(x, y) = \frac{1}{2\pi\sigma^2} e^{-\frac{x^2 + y^2}{2\sigma^2}}$$
(1)

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Fig. 1. Algorithm of this image processing



Fig. 2. The original cells image used in image processing.



Fig. 3. Some of the cells that must be segregated from normal cells are marked.

The mask that is used in Gaussian filter is shown on Fig. 4. Also the output result of this stage in shown in Fig. 5.

IV. CONVOLUTION

Convolution is a neighborhood operation in which each output pixel is the weighted sum of neighboring input pixels. The discrete convolution of I with k, denoted by $I \times K$, is defined to be

1	2	4	2	1
2	4	8	4	2
4	8	16	8	4
2	4	8	4	2
1	2	4	2	1

Fig. 4. Gaussian filter mask that is used for smoothing the image.



Fig. 5. Cells image after applying the Gaussian filter.

$(I \times K)[x, y] = \sum a \sum b I[a, b] \cdot K[x - a, y - b]$ (2)

It is common to embed I and K within larger images to avoid wraparound effects.

The mask that is used in convolution stage is shown in Fig. 6.

The output of this stage is shown in Fig. 7.

V. PRIMARY IMAGE PREPARATION.

In this stage, the threshold diagram of the image is drawn and is changed into metric. (Fig. 8.)

After these stages we do "proper close". The result image of this stage is shown in Fig. 9.

VI. FAST FOURIER TRANSFORMS (FFT)

The FFT spatial frequency resolution is related to the image dimension and to the equivalent pixel dimension, so that it is important to known this parameter in order to compare the results from different images. This can be easily obtained if the same imaging system is used since in that case the resolution only depends on the shooting distance.

In all cases, after the processing required, to extract the parameter to be transformed (i.e. brightness, hue and etc.) the images were windowed by applying a double raised cosine window:

$$W(x, y) = \frac{1}{4} \left[1 + \cos\left(\frac{x\pi}{N}\right) \right] \cdot \left[1 + \cos\left(\frac{y\pi}{N}\right) \right]$$
(3)

where N is the image dimension.

So by changing the truncation frequency percentage value the objected cells are marked. For example the result image with the truncation frequency percentage of 6% and the FFT mode of "LOW PASS" is shown in Fig. 10.

-1	-1	-1
-1	9	-1
-1	-1	-1

Fig. 6. Mask that is used in convolution stage.



Fig. 7. Image after applying convolution filter.



Fig. 8. The image parameters are changed into metric parameters.



Fig. 9. The image resulted from threshold and "proper close" analysis.



Fig. 10. Rresult image after setting the FFT mode.

TABLE I: OUTPUT IMAGE ANALYSIS RESULTS										
Object	Center of Mass X	Center of Mass Y	First Pixel X	First Pixel Y	Bounding Rect Left	Bounding Rect Top	Bounding Rect Right	Bounding Rect Bottom	Max Feret Diameter Start X	
1	278.09	56.52	270	49	263	49	228	66	263	
2	663.06	89.04	660	81	654	81	673	98	673	
3	375.67	126.79	375	115	364	115	388	139	370	
4	558.30	150.91	557	148	556	148	562	155	557	



Fig. 11. The LABVIEW block diagram.

VII. FINAL STAGE

The final stage contains these steps: Filling the Holes, Removing Border Objects and Particle Filtering.

At last the positions of the objected cells are extracted. For example in Fig. 11 the position of a particular cell (cancer cell) is marked. A part of this analysis is available in Table. I.

The considerable point in analyzing the results is that because of the individual difference between the results we can use this analysis to design a neural network for cancer cell recognition in medical images.

The LABVIEW block diagram used in this paper is shown in Fig. 11.

VIII. CONCLUSION

As can be seen the defected cells are extracted and highlighted among the other cells, very well. This technique can be used in large scale cells examination and can improve the accuracy and speed of the examination and counting process of the defected cells. By counting the defected cells we can monitor the effect of medical treatment on the growth of the cancer cells.

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