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Detection of Cervical Cancer from Dark Cervical Cell Based Pap Smear Image

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Abstract

Now a days, worldwide most of the women are affected by cervical cancer disease, since, day by day death rate of this disease become increased. So many researchers have focused keen interest in the field of detecting this disease and found some solutions also for that. But they proved more good results only in advanced high expensive techniques such as liquid based cytology, colposcopy not in very basic test of Pap Test. So the rich people they may able to do the high cost test and they will prevent from the disease. But poor people can't do the same. Hence the reason basic test of pap test image based detection of cervical cancer techniques is proposed in this paper. The results of this technique proved a better solution than the advanced techniques. In this paper, we proposed automatic fast and effective bi-level Thresholding segmentation algorithm applied for segmenting dark portion of cervical cell nucleus from the original image and followed by effective pixel based feature extraction and classification is used for detecting cervical cancer. The final result would be more precise and useful to the histopathologists.

1.Introduction

Cancer is incurable disease all around the world [1-3]. So many researchers, pathologists have found many number of methodologies to cure the cells which can be affected by cancer. In earlier days so many methodologies are available to detect the symptoms of cancer [4-6]. All around the world women were affected by two types of cancer viz., breast and cervical cancer [7,8]. Un controlled growth of cells in the part of breast is breast cancer [9].

The cells in part of the Cancer that forms in tissues of the cervix is cervical cancer [10]. Cervical Cancer cells originates from pre-cancerous, benign lesions in the uncontrolled cells which are present inside the cervix. The results interpreted by World Health Organization (WHO), the initial stage for the development of cervical cancer is mild dysplasia, thereafter its moderate dysplasia, severe dysplasia, finally leads to carcinoma in situ (CIS) as well as invasive Cervical cancer.[11,12].

Pap Smear is the most popular screening method to detect cervical cancer from cervicted portion (leisons). To detect the portion which is affected by cervical cancer, it requires an recognized laboratory, trained cytologist and their repeatable visited reports used for evaluate the results[13]. In order to detect cervical cancer automatically with the help of screening tests. Among them one of the most important method is the segmentation of cell nuclei from the stained specimens [14]. However,



isolated nuclei of the cells in high-quality acquisitions provide difficult tricks in the segmentation is more number of nuclei with various characteristics under occurring different acquisition conditions in good-resolution scans of the complete microscope slide[15]. Thresholding is the most important method for segmentation process[16] and also it is an easiest method to convert gray scale image into binary image based on the global or local threshold value[17,[18]. Bilevel thresholding is a method which must be classifies the pixels into two groups. First one represents in which the pixels with gray levels are lie above a certain threshold value, whereas the other in which the pixels are lie below a certain threshold value [19,20].

Binary classification is one of the method which classifies the elements of a given cell into two groups based on the classification rule. Binary classification is one of the characteristic method used to determine if the patient which has been affected by the cancer[21]. Principally classification process focussed the detection of cancer with the help of pap smear screening test results. But, it is difficult to detect the critical stage of the cancer from the pap smear screening test images[22].

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In this present work, we have generated a type of algorithm from the process of segmentation. The results obtained from the algorithm we have split up the pixels into two levels (i.e.binary level). As a results produced from algorithm we have determine whether the cell is affected by cancer.

2. Proposed Methodology

A Framework for Proposed Methodology is shown in Figure 1. The Working Methodology contains the following processes used in the detection of cancer affected cell with the help of Pap Smear Images obtained from microscopic results.

- 1. Segmentation Process.
- 2. Feature Extraction Process.
- 3. Classification Process.





2.1. SEGMENTATION PROCESS.

Initially the process for detecting cancer affected cells, first we have obtained the images in terms of Red, Green and Blue plane from its corresponding images known as Pap Smear Images [23,24].

Essentially, the cancer is identified by the anomalous growth of nucleus in the cell. Cervical cancer is the abnormal growth of nucleus inside the cervical cell. To detect the cervical cells which must be affected by cancer it is necessary to isolate the nucleus from its surrounded cytoplasm is



known as segmentation process. To carry out this process, we have utilize a fast and automatic bi level thresholding algorithm. This algorithm is purely effective for finding the dark portion of the cervical nucleus, which was present in the original image. The above mentioned algorithm is individually applied for Red, Green and Blue plane of the original Image. It uses to calculate the threshold value iteratively. Based on the iterative threshold value, we have segment the nucleus from pap smear image. The threshold value (Red Initial TH, Green Initial TH and Blue Initial TH) value is calculated iteratively. Based on the threshold value which must be produced finally we have classified nucleus pixels as well as background pixels. The threshold value is iteratively updated by the following steps which must be indicated in the below mentioned algorithm.

Step1: The input is scaled image RedImage, GreenImage, BlueImage. The initial threshold value (Red Initial TH, Green Initial TH, Blue Initial TH) is selected by calculating the average of the maximum and minimum pixel value of the image.

Red Initial TH = (MinR + MaxR)/2

Green Initial TH = (MinG + MaxG)/2

Blue Initial TH = (MinB + MaxB)/2

MaxR = maximum pixel value of IRed

MinR = minimum pixel value of IRed

MaxG = maximum pixel value of IGreen

MinG= minimum pixel value of IGreen

MaxB = maximum pixel value of IBlue

MinB= minimum pixel value of IBlue

Step 2 to 7 for Red Plane Image

Step2: For all Pixels in an Red Plane Image both the row and column size does not greater than the corresponding Image size. Do begin

Step3: Initialize SumabR, SumblR, CountabR, CountblR to zero where SumabR, SumblR are sum of pixel values above the threshold and below the

threshold value respectively. CountabR, CountblR are the count of pixels above and below the threshold respectively.

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Step4: If (RedImage(i,j)> Red Initial TH)then update SumabR and CountabR as

SumabR = SumabR + RedImage(i,j)

CountabR=CuntabR+1

Else, update SumblR and CountblR as

SumblR = SumblR + RedImage(i,j)

CountabR=CountblR+1

Step5: Calculate

T0R=SumabR/CountabR

T1R=SumblR/CountblR

Red New TH = (T0R+T1R)/2

Step6:

If (Red New TH \neq Red Initial TH) then

Else, Update initial threshold value Tinitial as

Red Initial TH = Red New TH

Step7: Perform segmentation using the new threshold value

If RedImage(i,j) < Red New TH, make the pixel values to 1 else 0.

Step 2 to 7 for Green Plane Image

Step2: For all Pixels in an Green Plane Image both the row and column size does not greater than the corresponding Image size. Do begin

Step3: Initialize SumabG, SumblG, CountabG, CountblG to zero where SumabG, SumblG are sum of pixel values above the threshold and below the threshold value respectively. CountabG, CountblG are the count of pixels above and below the threshold respectively.

Step4: If (GreenImage(i,j)> Green Initial TH)then update SumabG and CountabG as

Journal of Coastal Life Medicine

SumabG = SumabG + GreenImage(i,j)

CountabG=CuntabG+1

Else, update SumblG and CountblG as

SumblG = SumblG + GreenImage(i,j)

CountabG=CountblG+1

Step5: Calculate

T0G=SumabG/CountabG

T1G=SumblG/CountblG

Green New TH = (T0G+T1G)/2

Step6:

If (Green New TH \neq Green Initial TH) then

Update initial threshold value Green initial TH as

Green Initial TH = Green New TH

Step7: Perform segmentation using the new threshold value

If GreenImage(i,j) < Green New TH, make the pixel values to 1 else 0.

Step 2 to 7 for Blue Plane Image

Step2: For all Pixels in an Blue Plane Image both the row and column size does not greater than the corresponding Image size. Do begin

Step3: Initialize SumabB, SumblB, CountabB, CountblB to zero where SumabB, SumblB are sum of pixel values above the threshold and below the threshold value respectively. CountabB, CountblB are the count of pixels above and below the threshold respectively.

Step4: If (BlueImage(i,j)> Blue Initial TH) then update SumabB and CountabB as

SumabB = SumabB + BlueImage(i,j)

CountabB=CuntabB+1

Else, update SumblB and CountblB as

SumblB = SumblB + BlueImage(i,j)

CountabR=CountblR+1

Step5: Calculate

T0B=SumabB/CountabB

T1B=SumblB/CountblB

Blue New TH = (T0B+T1B)/2

Step6:

If (Blue New $TH \neq Blue$ Initial TH) then

Update initial threshold value Tinitial as

Blue Initial TH = Blue New TH

Step7: Perform segmentation using the new threshold value

If BlueImage(i,j) < Blue New TH, make the pixel values to 1 else 0.

2.2. FEATURE EXTRACTION PROCESS

Feature Extraction second one process depends upon the binary image results of automatic bi level thresholding algorithm. The results obtained from bi level thresholding algorithm such as Red, Green and Blue Plane of the Binary Image, we have seen the portion of the nucleus very clearly, since it has represented in white pixel, whereas the remaining fragment are appeared as Black Pixels and it has been indicated as Background Pixels. Hence, to find out the caner from the binary image we count the total no of white pixels are occupied as nucleus pixels from each and everyone of Red, Green, Blue Plane of the segmented resulting image. Then we have identify the area of nucleus in an image. The Formula for finding the area of nucleus in Red, Green and Blue Image in equations (2.1 - 2.3):

Red Image Nucleus Area =

Total no of Nucleus Pixels in Red Image \rightarrow (2.1)

Green Image Nucleus Area =

Total no of Nucleus Pixels in Green Image \rightarrow (2.2)

Blue Image Nucleus Area =



Total no of Nucleus Pixels in Blue Image \rightarrow (2.3)

2.3. CLASSIFICATION PROCESS.

The last process is the classification process. This process is principally based on the results of feature extraction process. From the final result of feature extraction process, total no of nucleus pixel value is calculated by using equations (21-2.3),Further we have find out which one is the maximum total no of nucleus pixel value to identify the cancer affected area with the help of the equations (2.4, 2.5).

Cancered Nucleus Area : Maximum pixel value of the nucleus from Red or Green or Blue Image x Area of one pixel (um^2) \rightarrow (2.4)

Cancered Nucleus Area : Maximum pixel value of the nucleus from Red or Green or Blue Image x 0.201 um²

→(2.5)

The Value used for area of one pixel (0.201 um^2) is taken out from the cyto technician Microscopic Resolution Per Pixel and this value is referred by Pap-smear Benchmark Data for Pattern Classification[25]. After find out the area of nucleus portion we have classified the cell image based on the Decision Tree Classification Rule.

2.3.1 Decision Tree Classification Rule:

The rule of the Decision Tree Classification which was shown as given.

If (the nucleus area <= 50 um^) then

print, "The Given cell represents Normal and the Image was Classified as Normal Image"

else

print, "The Given cell represents Abnormal and the Image was Classified as Cancer Image"

3. Experimental Results

3.1. PAP SMEAR SCREENING TEST IMAGES:

Pap Smear Screening Test Images is the first process and the aim of the process is to convert the pap smear slides into pap smear images. This process has been carried out in well-equipped pathological laboratory. In our case I have used standard Harlev database. To carry out this investigation I have collected around 97 samples of pap smear images (This Images has been taken out from Olympus Ch20i Microscope under 100x Magnification). Cervical cyto pap smear image result obtained from Olympus Ch20i Microscope under 100x Magnification is shown in Figure 2.

Figure.2: Cervical Cyto Pap Smear Image.





3.2. SEGMENTATION PROCESS.

The input image of our sample taken out from coloured image which is obtained from pathological laboratory. The aim to find out the cancer from the coloured image first we have obtained the image in terms of red, green and blue plane of the corresponding original image which is shown in Figure.3.

Figure 3: Red, Green and Blue Plane of the Original Image.



Then the Segmentation (Bi level thresholding algorithm) process applied the corresponding original red,green and blue plane results (binary images with the initial and final threshold values) obtained in Table 1.

Table.1: Segmentation Results of Red, Green and Blue Plane of the Corresponding Original Image.

Red	Green Initial	Blue Initial TH:
Initial TH: 6	TH: 7	3
Red New TH:	Green New TH:	Blue New TH:
107	92	97

3.3. FEATURE EXTRACTION PROCESS:

To find out the cancer from the results produced by bi level thresholding algorithm, we have to calculate total number of white pixels occupied inside the nucleus for each red, green and blue plane based resulted binary images which is given in Table 2.

Table.2: Result of the Feature Extraction Process.

Total no of Red Nucleus Pixel	Total no of Green Nucleus Pixel	Total no of Blue Nucleus Pixel
5207 Pixel	5228 Pixel	4878 Pixel

Journal of Coastal Life Medicine

3.4. CLASSIFICATION PROCESS:

According to the results obtained from feature extraction process we have got different value of nucleus pixels for red, green and blue plane of the original image which are indicated in Table 2.Further we have find out which one occupies maximum pixel value inside the nucleus and also to cancer affected area of the nucleus with the help of the equations (3.1 & 3.2).

Maximum Pixel Value from Red, Green & Blue Plane of an Image: 5228 Pixels ->3.1

Nucleus Area: 5228 x 0.201um² = 1050.828 um² - > 3.2

The area of the nucleus is calculated with the help of equation 3.2, we know that the cell is classified as abnormal and came to a conclusion if the patient is affected by cancer.

4. Conclusion

In the present work we were successfully generated a automatic bi level thresholding algorithm effectively segmented the dark cervical nucleus and it determine whether the cervical cell was affected by cancer as well as normal. Based on the results obtained from the classification process. we were calculated the cancer affected area of the nucleus. The results obtained from the present work which must be given most précised results for finding cancer.

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