International Journal of Future Innovative Science and Engineering Research (IJFISER),
Volume-1, Issue-III ISSN (Online): 2454- 1966

Research Manuscript Title

# AUTOMATED ALGORITHM FOR SEGMENTATION OF PAP SMEAR IMAGE FOR CERVICAL CANCER DETECTION

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**Sep – 2015**

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**Kaaviya S, Saranyadevi V, Nirmala M**, "**Automated Algorithm For Segmentation Of Pap Smear Image For Cervical Cancer Detection**", International Journal of Future Innovative Science and Engineering Research (IJFISER), Volume-1, Issue-III, Sep-2015,

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***Abstract***

Cervical cancer is the second most common gynecologic cancer worldwide. Unlike the other cancers it does not show any symptoms in its earlier stage which causes mortality among women. It takes 8 to 10 years to develop from precancerous to severe stage. The important reasons for higher cervical cancer in developing countries are lack of resources, lack of effectual screening programs and inadequately organized health system aimed for detecting precancerous condition before they progress to persistent cancer. So, there is a need of low cost approach for effective cervical cancer screening programs .Cervical cancer is a disease that can be prevented through both primary prevention and early detection. So in developed countries the incidence of cervical cancer has decreased due to screening, early detection and treatment. However in developing countries, 80% of cervical cancers are incurable at the time of detection due to their advanced stage. Several screening modalities are now available for early detection of cervical cancer and its precursor lesions. When cervical cancer occurs, cells in the cervix region cannot function normally and form tumours which destroys the normal cells. It can be easily detected and preventable in its earlier stage with pap smear test. Many screening techniques are introduced for finding the abnormal cells . Pap smear test is also a screening test from which smear is taken from cervix and examined under the microscope. In automatic cervical cancer cell segmentation, a single cell image is segmented into nucleus and non nucleus region. In this paper Fuzzy C-means (FCM) clustering technique is proposed for single cell segmentation.

***Index Terms— Automatic segmentation, Fuzzy C- means, Precancerous, Pap test***

## I. INTRODUCTION

Cervical cancer is the foremost cause of cancer death in females [1]. The analysis for cervical cancer depends on the arena of the cancer .The disease can be cured if diagnosed in the pre-cancerous lesion stage or former. Pap test is a physical examination system widely used to avert cervical cancer. It was expected that, screening test can reduce mortality rates from cervical cancer by 70% or further [2]. The study of automatic cervical cell classification has been done to diminish the inaccuracy of screening result. A number of commercial automated screening systems includes PAPNET, Thin Prep Pap Test, and Thin Prep Imaging System. Automated systems indeed perk up the accuracy of the screening result and reduce the false-negative rate [3–4]. However, cost effectiveness is a major negative aspect of these systems with the cost of PAPNET test far exceeds that of manual screening. Ambiguity in diagnostic capability was also reported [5].It is therefore suggested that the automated system should be used as an aiding tool in combination with the expert's opinion rather than relying on the system as a primary screening and diagnosing tool [6,7]. However, cytology screening is still a default screening method in most countries due to its relatively low cost and its effectiveness in cervical cancer prevention if the screening is regularly performed. The screening process normally starts with gathering cervical cell samples from the uterine cervix and mounting it on a glass slide. The collected sample is visually inspected under a microscope to make out the target cell or grade each cell into categories. The basic characteristics used to classify the

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stage of cells are generally the characteristics of cell nuclei and cytoplasm such as shape, size, texture, ratio of nucleus and cytoplasm. From image processing point of view, the first step in extracting information from cell components is to appropriately identify a region of each component (nucleus, cytoplasm, and non-cell components) by segmentation procedure. There are several research works on nucleus segmentation [8–9]. However, to sort each cervical cell into categories with only nucleus information, it might not yield a superior performance. Hence, segmenting whole cell is more enviable [10–11]. After the segmentation step, each cell is then classified using specific classifiers based on the extracted features from cell components. In the segmentation process, a patch-based fuzzy C-means (FCM) clustering technique is used. A cell image is segmented by using the over segment FCM technique into nucleus, cytoplasm, and background. In the cervix different kinds of cells exist. They are located in separate areas: (a) Squamous area and (b) Columnar area. (a) The squamous areas are located in the underneath of cervix and just outside the vagina . The cells in the cervix are divided into 4 layers: the basal, the parabasal, the intermediate and the superficial layer. The youngest cells in the basal layer, lie on the basal membrane. When the cells adult they shift trough the layers, and finally they get expelled from the surface in the superficial layer. Moving through the layers the cells change shape, color and other uniqueness. Cells in the basal layer are small and round, with a large nucleus and a little cytoplasm. Moving through the layers the cytoplasm becomes larger and the nucleus smaller. (b) The columnar area is located in the upper part - and particularly in the canal of the cervix. Characteristics for these cells are a column-like shape with an small cytoplasm and a large nucleus located at one end. Somewhere in between these two areas, the cells meet in the squamo-columnar junction. This junction may be located either inside or outside the cervix.

## II . MATERIALS AND METHODS

The patch-based fuzzy C-means (FCM) clustering method is used to segment nuclei and cytoplasm of white blood cells [12]. It was later applied to segment nuclei of cervical cells from the Pap smear images [13]. The FCM is excellent for clustering data with ambiguity. Therefore, FCM method is preferred to cluster the cell image.

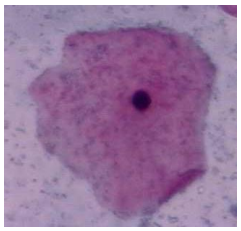

Figure 1. Sinlge cell pap-smear image

In segmentation, a single-cell image is converted to a grayscale image before applying a median filter to even the image and eradicate noise. The processed image is then segmented into 2 or 3 regions, i.e., nucleus and non-nucleus or nucleus, cytoplasm, and background, using the FCM clustering method. Rather than taking into account every pixel value and straightforwardly cluster them into 2 or 3 clusters, then overly cluster the pixels into patches where each patch is represented by its center value. The median filter size and the number of clusters can be selected by experiments because of image variation in different datasets. To merge patches into 2 final clusters (nucleus and non-nucleus), the threshold TN for nucleus is preferred in accordance with the percentages of all patch centers. The patch with the value of centers a lesser amount of(darker) than the nucleus threshold is labeled as nucleus. The nucleus threshold TN is assorted from 60%to 130% (with 10% incremental step) of the mean of patch centers. The threshold that gives the minimum error between automatic segmentation and manual segmentation is elected as the nucleus threshold. If the segmentation upshot in numerous objects, the object in which its centroid is the contiguous to the image center is selected to be the object of interest. On the other hand, to coalesce patched into 3 final clusters (nucleus, cytoplasm, and background), the cytoplasm threshold TC has to also be determined. The nucleus threshold can be found using exactly the same method described in the 2-cluster case. The cytoplasm threshold TC is speckled from 90% to 160% (with10% incremental step) of the mean of

patch centers. The cytoplasm threshold is selected akin to in the nucleus segmentation. Finally, the patch with the value of center lesser amount than the nucleus threshold is labeled as nucleus. The patch with the value of center amid the nucleus threshold and cytoplasm threshold is labeled as cytoplasm. The left behind patches are labeled as background.

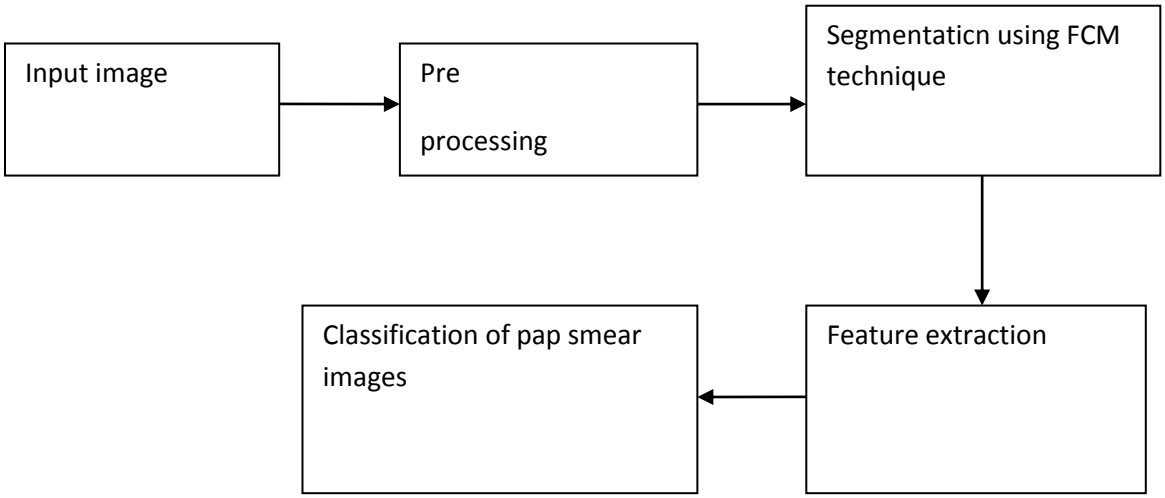


Fig 2. Block diagram

IV PREPROCESSING

The preprocessing steps involves grayscale conversion and filtering. Here median filter is applied to clean up the images . Compared to the other filters its preserves the edges of an image while filtering.

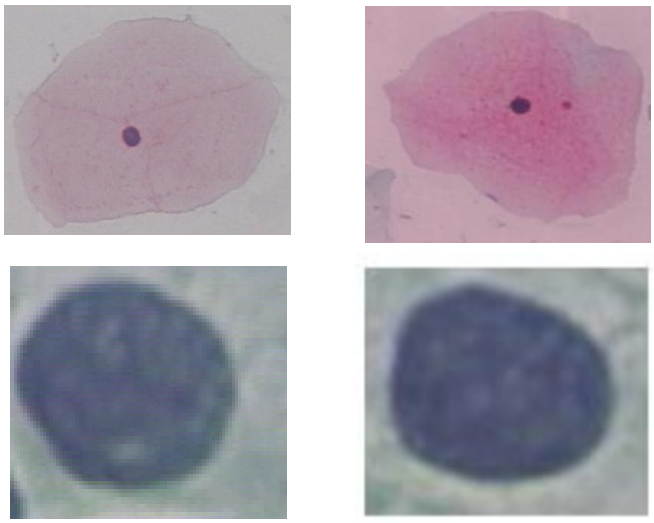

Fig 3. Original pap smear images

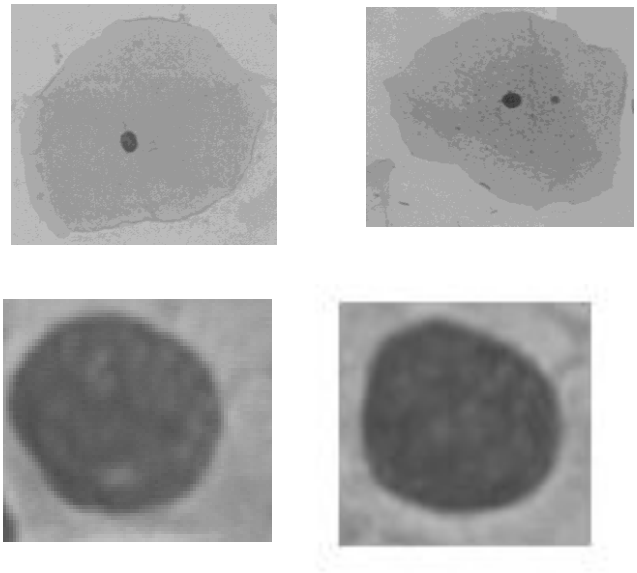

Fig 4. Grayscaled images

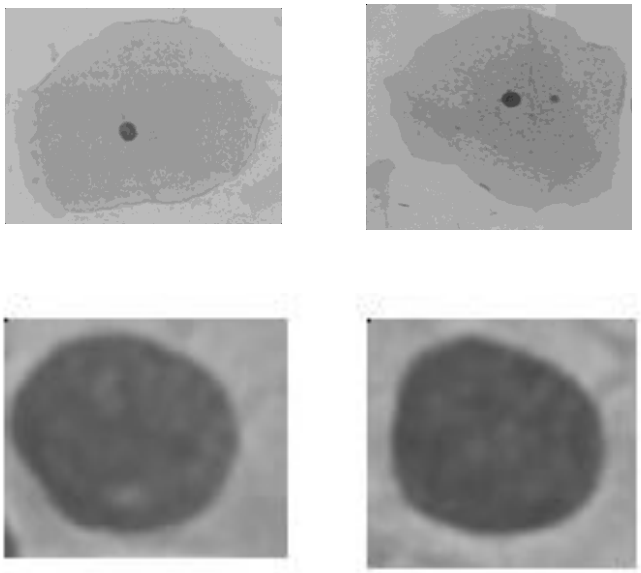

Fig 5. Median filtered images

## V MORPHOLOGICAL OPERATIONS

Morphological operations are non-linear, translation invariant transformations [30]. In this paper, morphological dilation and erosion are applied to clean up the segmented images. Dilation grows or thickens the objects in the image and erosion shrinks or thins the objects in the image.

## VI FEATURE EXTRACTION

After applying the automatic segmentation based on FCM clustering, a set of features are extracted from nucleus and cytoplasm in each image. The features are elected based on the nucleus and complete cell morphology during the cell

division process. In the usual condition, chromosomes are not observable under the examination by a light microscope. But during the cell division process, chromatin condenses and becomes noticeable [14–15]. For the abnormal cells, the cell division occurs with hysterical and high rate. The abnormal cell division action can be seen from the nucleus characteristics [16]. Chromatin patterns in tainted slide are well visible. When inspected under the light microscope, one of the features used for grading the level of abnormality in cervical cell is the texture of nucleus [17]. The roughness of nucleus texture represents the allocation of chromatin. It increases according to the level of severity [18]. In the normal grade, granular of nucleus appears to be smooth and superior. Therefore, six nucleus-based features are chosen.

Feature 1: Area of nucleus

$A_{nu}$ = Total number of pixels in the nucleus region.

Feature 2: Compactness of nucleus

$$C_{nu} = \frac{P_{nu}^2}{A_{nu}},$$

where $P_{nu}$ is the perimeter of the nucleus.

Feature 3: Major axis of nucleus

$L_{nu}$ = the length of the major axis of an ellipse that completely encloses the nucleus region.

Feature 4: Minor axis of nucleus

$D_{nu}$ = the length of the minor axis of an ellipse that completely encloses the nucleus region.

Feature 5: Aspect ratio of nucleus

$$R_{nu} = \frac{W_{nu}}{H_{nu}},$$

where $W_{nu}$ is the width of the nucleus and $H_{nu}$ is the height of the nucleus region.

Feature6: Homogeneity of nucleus

$$H_{nu} = \sum_{i=1}^{K} \sum_{j=1}^{K} \frac{P(i,j)}{1+|i-j|},$$

where P(i, j) is the probability of occurrence of a pair of pixel values (i, j) in the nucleus region computed from gray-level co-occurrence matrix. K is the number of gray levels in the image . The other three features based on the entire cell are as follows:

Feature 7: Nucleus-to-cytoplasm (N/C) ratio

$$NC = \frac{A_{nu}}{A_{cy}},$$

where $A_{nu}$ is the nucleus area and $A_{cy}$ is the cytoplasm area.

Feature 8: Compactness of the entire cell

$$C_{en} = \frac{P_{en}^2}{A_{en}},$$

where Pen is the perimeter of the entire cell and

Aen is the entire cell area.

Feature 9: Area of entire cell

$A_{en}$ = Total number of pixels in the entire cell region.

VI EXPERIMENTAL RESULTS

The pap smear image collected and segmented into nucleus and cytoplasm for easy identification of normal and abnormal cells. In this paper Fuzzy C- means clustering technique is used for the segmentation of pap smear image.

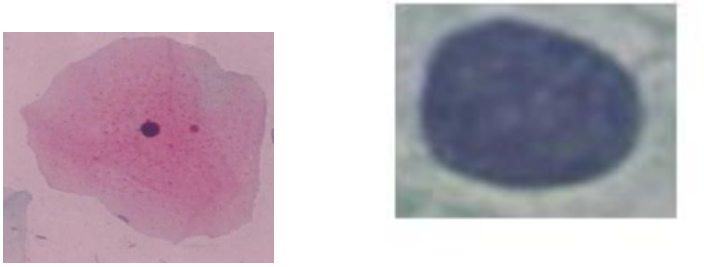

Fig 6.Input images

ig 7. Nucleus extracted from the original image .

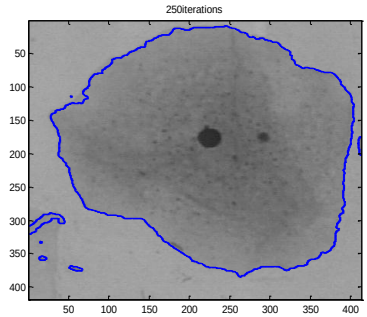


Fig 8. Cytoplasm extracted from the original input image.

## VII CONCLUSIONS

This paper proposes a method of automatic cervical cell image segmentation. .Fuzzy C-means clustering technique is used to segment every cell into 2 or 3 regions. The results show that our segmentation method provides a superior set of features for the classifiers. Not only accuracy, sensitivity is extremely important because it is the indication of the fatal false negatives. From the results, the features extracted from our segmentation method also provide better sensitivity. Future work is based on the classification of normal and abnormal cells.

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