CERVICAL CANCER DETECTION FROM PAPSMEAR IMAGES USING IMAGE PROCESSING TECHNIQUES

T.SIVAPRIYA

11PCA15

A Project Report Submitted to
Avinashilingam Institute for Home Science and Higher Education for Women, Coimbatore-641043

In Partial Fulfillment of the Requirements for the Master's Degree in Computer Applications

March, 2014

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Signature of the External Examiner

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SYNOPSIS

SYNOPSIS

The project entitled "**Cervical Cancer Detection from Papsmear images using Image Processing Techniques**" deals with detection and classification of cervical cancer cells from papsmear images. Many methods currently exist to detect cervical disease, but several factors can increase the risk and very sensitive to identify the cancer cell. So, most effective way of detecting and diagnosing the disease even at an early pre-cancerous stage is cervical screening using papsmear images. Both automated and semi-automated screening procedures involve two main tasks, namely, segmentation and classification. Segmentation mainly focuses on separation of the cells from the background as well as separation of the nuclei from the cytoplasm within the cell regions. Automatic thresholding and morphological operations appear to be the most popular method for the segmentation task. Hence, cells in cancers and pre-cancers are characterized by many morphological and architectural alterations. The classification is to categorize the cervical cells into cancerous and non-cancerous cell based on the features of each single papsmear cell. Features can be extracted from both nucleus and cytoplasm it includes area, nucleus/cytoplasm ratio, brightness, shortest diameter, longest diameter, nucleus position, maxima and minima. Manpower-based smear analysis is a tedious, time-consuming and error-prone job. Therefore, machine-assisted automatic papsmear screening and diagnosing system brings significant benefits to help women prevent cervical cancer.

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INTRODUCTION

1. INTRODUCTION

1.1 PROBLEM DEFINITION

Cervical cancer is a malignant disease that develops in the cells of the cervix or the neck of the uterus. These cells do not suddenly change into cancer. Instead, the normal cells of the cervix first gradually develop precancerous changes which later turn into cancer. In preprocessing stage image noise can be removed using filtering techniques. In segmentation stage nucleus and cytoplasm can be separated using otsu based segmentation and active contour level segmentation. In feature extraction stage image features can be extracted. Cancerous cells show increasing nucleus area when compared to normal cells. This characteristic feature can be used to do a first level of classification of the cervical cells as normal or abnormal. The second of classification of the cervical cell is to ranking the cell based on the features. The normal cell has three levels, namely, Superficial squamous, Intermediate squamous, and Columnar. The abnormal cell has four levels, namely, Mild dysplasia, Moderate dysplasia, Severe dysplasia and Carcinoma in situ. The cells can be identified and detected using different image processing techniques.

1.2 OVERVIEW OF THE PROJECT

The cervical cancer detection from papsmear image is carried out by image processing technique using scientific computing tool MATLAB. The cancer detection and classification process in papsmear images includes the following steps

- Preprocessing
- Segmentation
- Feature Extraction
- Classification

Preprocessing methods use a small neighborhood of a pixel in an input image to get a new brightness value in the output image. A filter is an effect that can be added to an image that affects the overall appearance, or appearance of a selected area, of an image. Using the filtering techniques the noise can be removed.

The threshold segmentation method is applied on the papsmear images to separate the nucleus from a cell. To separate the cytoplasm from a cell using active contour level set segmentation. Then for the feature extraction, segmented papsmear images are taken as input and extract the features from an image such as area, centroid, perimeter, N/C ratio, longest diameter, shortest diameter, roundness, elongation and brightness of both nucleus and cytoplasm. The extracted features are taken as input for the classification method. Classification is posed as a grouping problem by ranking the cells based on their feature characteristics modelling abnormality degrees. The proposed procedure constructs a tree using hierarchical clustering, and then arranges the cells in a linear order using an optimal leaf ordering algorithm that maximizes the similarity of adjacent leaves without any requirement for training examples or parameter adjustment. Finally, the proposed system is designed using GUI. It provides a set of tools for creating graphical user interface to greatly simplify the process of designing. This is done using scientific computing tool MATLAB software.

SYSTEM configuration

2. SYSTEM CONFIGURATION

This section describes the hardware and software specification needed for both development and implementation phases of this project.

2.1 HARDWARE SPECIFICATION

Processor	:	Intel® Core(TM) i3-2370M CPU @ 2.40GHz 2.40 GHz
RAM	:	4.00GB
System type	:	64 –bit Operating System
Keyboard	:	Standard PS/2 key board

2.2 SOFTWARE SPECIFICATION

Software	:	MATLAB 2010b
Operating System	:	Microsoft Windows 7

2.3 ABOUT THE SOFTWARE

MATLAB

MATLAB stands for "MATrix LABoratory" which is an interactive, matrix-based computer program for scientific and engineering numeric computation and visualization. It intended to provide easy access to the matrix libraries developed by Linpack and Eispack projects. These are carefully tested high-quality programming packages for solving linear equations and eigen value problems.

MATLAB will be used extensively in the labs of "Signals and Systems" and "Digital Signal processing" courses. This beginner's guide provides an overview of Matlab, some of its capabilities and the resource of Matlab in the EE department. Matlab is available on a number of computing platforms such as Sun/HP/VAX workstations, 80x86 PCs, Apple Macintosh, and several parallel machines. In the CityU Electronic engineering Department, UNIX version of Matlab 5.0 is available in the Image Processing Lab (P1615) and EDA center. The PC version of Matlab 5.1 is available in Microprocessor Lab (Room 2380). The information of this guide generally applies to all these environments.

The aim of Matlab is to enable us to solve complex numerical problems, without having to write programs in traditional languages like C and FORTRAN. Thus, Matlab interprets commands like Basic does, instead of compiling source code like C and FORTRAN require. By using the relatively simple programming capability of Matlab, it is very easy to create new commands and functions in Matlab. In addition, these developed Matlab programs (or scripts) can run without modification on different computers with Matlab. Today, Matlab has evolved into a very powerful programming environment by providing numerous toolboxes such as signal processing, image processing, and controls, optimization, and statistics computations. The emphasis of this beginner's guide is on the basic Matlab commands with investigation on some aspects of signal processing. It is intend to be used, while sitting at a computer terminal running Matlab.

MATLAB WINDOWS:

Command Window:

The window where user type commands and non-graphic output is displayed. Previous commands can be accessed using the up arrow to save typing and reduce errors.

Typing a few characters restricts this function to commands beginning with those characters.

Command History:

Records commands given that session and recent sessions. It can be used for reference or to copy and paste commands.

Workspace:

It shows the all the variables that user have currently defined and some basic information about each one, including its dimensions, minimum, and maximum values. The icons at the top of the window allow you to perform various basic tasks on variables, creating, saving, deleting, plotting, etc. Double-clicking on a variable opens it in the Variable or Array Editor. All the variables that user defined can be saved from one session to another using File>Save Workspace As (Ctrl-S). The extension for a workspace file is .mat.

GUI-(Graphical User Interface):

A graphical user interface (GUI) is a graphical display in one or more windows containing controls, called components, which enable a user to perform interactive tasks. The user of the GUI does not have to create a script or type commands at the command line to accomplish the tasks. Unlike coding programs to accomplish tasks, the user of a GUI need not understand the details of how the tasks are performed.

GUI components can include menus, toolbars, push buttons, radio buttons, list boxes, and slider. GUIs created using MATLAB tools can also perform any type of computation, read and write data files, communicate with other GUIs, and display data as tables or as plots.

FEATURES:

- High-level language for numerical computation, visualization, and application development.
- Interactive environment for iterative exploration, design, and problem solving.
- Mathematical functions for linear algebra, statistics, Fourier analysis, filtering, optimization, numerical integration, and solving ordinary differential equations.
- Built-in graphics for visualizing data and tools for creating custom plots.
- Development tools for improving code quality and maintainability and maximizing performance.
- Tools for building applications with custom graphical interfaces.

SYSTEM study and ANALYSIS

3. SYSTEM STUDY AND ANALYSIS

3.1 Existing System

There is a high degree of cell overlap in cytological image analysis, the presence of more than one nucleus in a cell and the lack of homogeneity in image intensity. These confront any method to overcome the complexity of conventional cervical cell images and to accomplish a correct segmentation. In addition, the nucleus is a very important structure within the cell and it presents significant changes when the cell is affected by a disease and thus the accurate definition of the nucleus boundary is a crucial task. The identification and quantification of these changes in the nucleus morphology and density contribute in the discrimination of normal and abnormal cells in papsmear images. Manual processes in this field may not always be satisfactory as it may be time consuming to visualize millions of cells and also it is error prone. So an automatic analysis may help pathologist to identify cancer affected cells correctly and with accuracy.

3.2 Proposed System

Pap smear image based identification is the most common method used for early detection of cervical cancer. It is aimed to detect abnormalities in cervix cells before they have been transformed into malignant ones using the image processing techniques. The proposed system uses the ANFIS neural network for image classification. It's give the better result and accuracy compare than other classification techniques. Automated Pap smear analysis system which can help cytotechnician reducing time spent for slide examination in pap screening process. Cervical cancer is identified and classified using the proposed system.

Merits of proposed system:

- The proposed approach could produce accurate segmentation and classification of cervical cells in images having inconsistent staining, poor contrast, and overlapping cells.
- Furthermore, both the segmentation and the classification algorithms are parameter-free and generic.
- So that additional criteria can easily be incorporated to improve the identification of different cell types without any requirement for training examples.

SYSTEM Design

4. SYSTEM DESIGN

4.1 DATASET

In this project the dataset is collected from the Department of Pathology at Herlev University Hospital and the Department of Automation at Technical University of Denmark. It consists of 917 single cell papsmear images. The images were acquired at a magnification of 0.201µm/pixel. Average image size is 156 × 140 pixels. Cyto-technicians and doctors manually classified each cell into one of the 7 classes, namely superficial squamous, intermediate squamous, columnar, mild dysplasia, moderate dysplasia, severe dysplasia, and carcinoma in situ. The first three classes correspond to normal cells and the last four classes correspond to abnormal cells. Each cell also has an associated ground truth of nucleus and cytoplasm regions.

In this project, papsmear images and extracted features are considered as the dataset since the project deals with cancer cell classification and ranking from papsmear image. For automated detection of cervical cell the 100 papsmear images are taken as input. It consists of 50 normal cells and 50 abnormal cells. The dataset is shown in APPENDIX [10.2.1, 10.2.2].

4.2 INPUT DESIGN

The project is concentrated on classifying and ranking the cervical cell. Input form is designed by using scientific computing tool Matlab platform in GUI. The input designs are shown in APPENDIX [10.3.1]. The papsmear images are taken for processing.

For preprocessing, papsmear images are taken as input. These inputs are preprocessed and result images are taken as input for the segmentation. The input screen for the preprocessing is shown in APPENDIX [10.3.2].

For Segmentation, preprocessing result images are taken as input. In this phase, nucleus and cytoplasm can be separated and result images are taken as input for the feature extraction. The input screen for the segmentation is shown in APPENDIX [10.3.3.].

For feature extraction, segmented result images are taken as input. In this phase, geometrical feature, texture feature and statistical feature can be extracted from each image and the results are taken as input for classification. The input screen for the feature extraction is shown in APPENDIX [10.3.4].

For classification, feature extraction values such as area, brightness, n/c ratio, longest diameter, shortest diameter, perimeter, minima and maxima of nucleus and cytoplasm are taken as input. The ANFIS (Adaptive Neuro Fuzzy Inference System) neural network system takes the input of feature extraction values and displays the corresponding classes. The input screen for classification is shown in APPENDIX [10.3.5]. Finally the cervical images are classified and ranked in papsmear image.

4.3 OUTPUT DESIGN

Output design generally refers to the results and information that are generated by the system. The images and dataset are taken as input. In preprocessing phase, the image noise can be removed using different filtering techniques. The filtered papsmear images are generated as an output for pre-processing technique. The results are shown in APPENDIX [10.4.1, 10.4.2].

In segmentation phase, using the pre-processing result image the nuclei and cytoplasm can be separated using the threshold based segmentation and active contour level set segmentation. The results are shown in APPENDIX [10.4.3, 10.4.4].

In feature extraction phase, using the segmented result image feature values can be extracted. It consists of geometrical, texture and statistical features. The results are shown in APPENDIX [9.4.5].

In classification phase, the extracted feature values are trained and tested with the dataset using ANFIS(Adaptive Neuro Fuzzy Inference System) neural network system. The tested and trained datasets are plotted corresponding to their classes. The results are shown in APPENDIX [10.4.6].

SYSTEM DEVELOPMENT

5. SYSTEM DEVELOPMENT

MODULE DESCRIPTION

The project consist of four main modules namely

- Pre-processing
- Segmentation
- Feature Extraction
- Classification and ranking of images

5.1 PREPROCESSING

In cervical cancer detection system, preprocessing stage prepares the image for further processing, analysis and interpretation. In this module the RGB image convert into greyscale image. In this project noise can be removed using five filtering techniques. They are

- Average filter
- Wiener filter
- Median filter
- Gaussian filter
- Minimum filter

5.1.1 Noise Removal

Filtering is one of the common methods which are used to remove the noise from a papsmear images.

Average Filter:

The average filter smooths data by replacing each data point with the average of the neighbouring data points defined within the span. h = fspecial('average', hsize) returns an averaging filter h of size hsize. The argument hsize can be a vector specifying the number of rows and columns in h, or it can be a scalar, in which case h is a square matrix.

The default value for hsize is [3 3].

Median Filter:

The **median filter** is a nonlinear digital filtering technique, often used to remove noise. Such noise reduction is a typical pre-processing step to improve the results of later processing (for example, edge detection on an image). Median filtering is very widely used in digital image processing because, under certain conditions, it preserves edges while removing noise.

Wiener Filter:

The wiener filter is used to produce an estimate of a desired or target random process by filtering another random process through the filter. The wiener filter minimizes the mean square error between the estimated random process and the desired process. The goal of the Wiener filter is to filter out noise that has corrupted a signal.

Gaussian Filter:

The Gaussian Filter block filters the input signal using a Gaussian FIR filter. it filtering is used to blur images and remove noise. It is a non-uniform low pass filter. This filter works by using the 2D distribution as a point-spread function. This is achieved by convolving the 2D Gaussian distribution function with the image. Gaussian filtering is more effective at smoothing images.

Minimum Filter:

The minimum filter is typically applied to an image to remove positive outlier noise. The minimum filter is defined as the minimum of all pixels within a local region of an image. it is a morphological filters that work by considering a neighbourhood around each pixel. From the list of neighbour pixels, the minimum or maximum value is found and stored as the corresponding resulting value. Finally, each pixel in the image is replaced by the resulting value generated for its associated neighbourhood.

In the project, papsmear image is taken as input and apply filtering techniques used to remove the noise from an image. Median filter gave the better result than other filtering techniques. The results are shown in APPENDIX [10.1, 10.2].

PSNR (Peak Signal-to-Noise Ratio)

For papsmear images contaminated with Poisson noise, PSNR value can be calculated by comparing two images one is original image and other resultant image. the PSNR has been

Computed using the formula,

$$PSNR = 10log_{10\left[\frac{R^2}{MSE}\right]}$$

Where, R is the maximum variation in the input image data type.

MSE (Mean Squared Error)

Mean Squared Error (MSE) is one way of measuring this similarity to compute an error signal by subtracting the test signal from the reference, and then to compute the average energy of the error signal

PSNR and MSE value is calculated for papsmear images. The results are shown in APPENDIX [10.3, 10.4].Noise removed image is taken for the segmented process.

5.2 SEGMENTATION

Threshold is one of the widely used methods for image segmentation. Threshold techniques can be categorized into two classes: global threshold and local (adaptive) threshold. Here global threshold method is applied for the segmentation. In the global threshold, a single threshold value is used in the whole papsmear image. The advantage of obtaining first a binary image is that it reduces the complexity of the data and simplifies the process of recognition and classification.

In the project, threshold based segmentation such as otsu based segmentation is applied for separate the nucleus. The results are shown in APPENDIX [10.5, 10.6]. To separate the cytoplasm from a cell using active contour level segmentation. The results are shown in APPENDIX [10.5, 10.6]. The output of segmentation method contains segmented images of nucleus and cytoplasm for normal and abnormal papsmear images. Both image and value are used for the feature extraction process.

5.3 FEATURE EXTRACTION

Feature extraction in image processing is a special form of dimensionality reduction. When the input data to an algorithm is too large to be processed and it is suspected to be notoriously redundant then the input data will be transformed into a reduced representation set of features also named feature vector. Transforming the input data into the set of features is called feature extraction. If the features extracted are carefully chosen it is expected that the features set will extract the relevant information from the input data in order to perform the desired task using this reduced representation instead of the full size input.

Feature extraction involves simplifying the amount of resources required to describe a large set of data accurately. When performing analysis of complex data one of the major problems stems from the number of variables involved. Analysis with a large number of variables generally requires a large amount of memory and computation power or a classification algorithm which over fits the training sample and generalizes poorly to new samples. Feature extraction is a general term for methods of constructing combinations of the variables to get around these problems while still describing the data with sufficient accuracy.

Features extracted from the papsmear images are

1. Nucleus area
2. Cytoplasm area
3. Nucleus/Cytoplasm ratio
4. Nucleus brightness
5. Cytoplasm brightness
6. Nucleus shortest diameter
7. Nucleus longest diameter
8. Nucleus elongation
9. Nucleus roundness
10. Cytoplasm shortest diameter
11. Cytoplasm longest diameter
12. Cytoplasm elongation
13. Cytoplasm roundness
14. Nucleus perimeter

15. Cytoplasm perimeter
16. Nucleus relative position
17. Maxima in nucleus
18. Minima in nucleus
19. Maxima in cytoplasm
20. Minima in cytoplasm

AREA

Area is amount of surface the 2D shapes cover. It’s measured in square unit. A mathematically acceptable definition of area is complex. Area is usually measured or defined on a flat surface, also called a Euclidean plane, or on a spherical surface. The surface area is occasionally determined for irregular objects. In the case of extremely complex or esoteric surfaces, the area might be impossible to define or measure. In this project nucleus and cytoplasm area is calculated by counting the corresponding pixels of the segmented picture

N/C RATIO

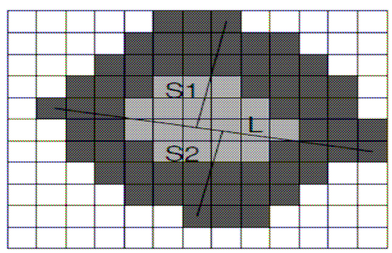
It defines how small the nucleus area is compared to the area of the cytoplasm. It is given by:

$$\mathbf{N/C = \frac{Nucl_{area}}{Nucl_{area} + Cyto_{area}}}$$

BRIGHTNESS

Nucleus and Cytoplasm brightness is calculated as the average perceived brightness that is a function of the colors wavelength. In this project is calculated as Y = 0:299. Red +0:587.Green + 0:114.Blue. Here Red, Green and Blue are the average intensity for each of the colors. They are weighted by the perceived brightness of the human eye.

DIAMETER



A binary cell picture with background (white), cytoplasm (black) and nucleus (gray).For the cytoplasm the longest diameter line (L) and shortest diameter (S1 & S2) are shown.

LONGEST DIAMETER

This is the shortest diameter a circle can have, when circumscribing the whole object. It is measured as the biggest distance between to pixels on the objects border, and forms a line *L* as shown in figure for the cytoplasm.

SHORTEST DIAMETER

This is the biggest diameter a circle can have, when the circle is totally inscribed in the object. This distance is approximated by the sum of the two lines *S* 1 & *S* 2 shown in figure for the cytoplasm. They are perpendicular to the line *L*, and is the longest line to each side inside, fitting in the object.

ELONGATION

The elongation is calculated as the ratio between the shortest diameter and the longest diameter of the object.

$$\mathbf{N_{elong} = N_{short} / N_{long}}$$

$$\mathbf{C_{elong} = C_{short} / C_{long}}$$

ROUNDNESS

The roundness is calculated as the ratio between the actual area and the area inside the circle, given by the longest diameter of the object.

$$\mathbf{N_{roundness} = N_{area} / N_{circle}}$$

$$\mathbf{C_{roundness} = C_{area} / C_{circle}}$$

PERIMETER

Perimeter is the distance around a closed figure and is typically measured in millimetres (mm), centimetres (cm), metres (m) and kilometres (km). In this project perimeter is calculated based on the length around the object.

NUCLEUS POSITION

This is a measure of how well the nucleus is centered in the cytoplasm. It is calculated by finding the distance between the nucleus center and the center of the cytoplasm:

$$N_{pos} = \frac{2a\sqrt{(x_N - x_C)2+(y_N - y_C)2}}{C_{long}}$$

Here the position is given by the center $(x_N; y_N)$ **and** $(x_C; y_C)$ for the nucleus and cytoplasm, respectively.

MAXIMA/MINIMA:

This is a count of how many pixels is a maximum/minimum value inside of a 3 pixel radius.

In feature extraction phase, all the 20 features can be extracted using different image processing techniques for both nucleus and cytoplasm. The results are shown in APPENDIX [10.7]

5.4 CLASSIFICATION AND RANKING OF PAPSMEAR IMAGES:

5.4.1 CLASSIFICATION USING ANFIS (Adaptive Neuro Fuzzy Interference System) NETWORK

In cervical cancer detection system, images can be classified according with their feature extracted values from papsmear images. Classification is needed to classify different target according to their specified classes. In this project, classification can be implemented using ANFIS (Adaptive Neuro Fuzzy Inference System) network system. It is a kind of neural network that is based on Takagi–Sugeno fuzzy inference system. Since it integrates both neural networks and fuzzy logic principles, it has potential to capture the benefits of both in a single framework. Its inference system corresponds to a set of fuzzy IF–THEN rules that have learning capability to approximate nonlinear functions. Hence, ANFIS is considered to be a universal estimator for classification.

In classification the images can be trained and tested. For training purpose the feature extracted values of nucleus area and n/c ratio are taken as input and plotted in the graph. It shows that intermediate and superficial cells have smaller area than columnar and parabasal cells. Also, it is seen that the n/c ratio is smaller for intermediate and superficial cells.

Parabasal cells have medium n/c ratio, columnar cells have medium or large n/c ratio. The results are shown in APPENDIX [10.8.1, 10.8.2, 10.8.3, 10.8.4]. The feature extracted values of nuclei and cytoplasm intensity is taken as input and plotted in the graph. It shows that columnar epithelium have light nuclei, and dark cytoplasm. Intermediate and superficial cells have dark nuclei and light cytoplasm. The results are shown in APPENDIX [10.9.1, 10.9.2, 10.9.3, 10.9.4].

In training phase, nuclei area and n/c area of abnormal cell images feature extracted values are taken as input and plotted in the graph. It shows that normal cell nuclei are smaller than dysplastic cell nuclei and also dysplasia cells have lighter nuclei, severe dysplasia seems have dark nuclei. The results are shown in APPENDIX [10.10.1, 10.10.2, 10.10.3].

The adaptive neuro-fuzzy inference system using a given input/output data set, the toolbox function anfis constructs a fuzzy inference system whose membership function parameters are tuned using either a back propagation algorithm alone or in combination with a least squares type of method. This adjustment allows your fuzzy systems to learn from the data they are modeling.

In this project, extracted feature vectors are taken as the input vector for ANFIS neural network system the images are trained and tested using back propagation method. Finally the output is plotted in the graph corresponding to their classes. The results are shown in APPENDIX [10.4.6]

RMSE (Root Mean Squared Error):

The performance of the network with respect to the test data, is measured using RMSE

$$RMSE = \sqrt{\frac{\sum_{i=1}^{N}(\mathbf{d}_i - \mathbf{z}_i)^2}{n}}$$

Where n=250 is the number of test data and $\mathbf{d_i}$ and $\mathbf{z_i}$ is the desired output and the actual output. Before training the network, the performance is

$$\mathbf{RMSE}_{\mathbf{NoTraining}} = \mathbf{0.9133}$$

The initial membership function for before training the data is shown in APPENDIX [10.11.1]. The network trained using 200 epochs.

The membership function after training is shown in APPENDIX [10.11.2]. The overall performance after training has increased.

$$\mathbf{RMSE}_{\mathbf{200Epochs}} = \mathbf{0.7504}$$

The training error is also calculated for the training data. It decreases through the first 100 epochs and becomes stable at around 200 epochs. The result is shown in APPENDIX

[10.11.3]. The performance of the training and testing dataset is also calculated. The result is shown in APPENDIX [10.11.6].

5.3.2 CLASSIFICATION USING FCM (Fuzzy C Means Clustering)

The fuzzy c-means algorithm finds c cluster centers from a set of n vector x_i, i=1,….,n such that a cost function is minimized. Each data point is assigned a degree of membership between 0 and 1 to each cluster c_i, i = 1,…., c. the c*n membership matrix U holds values between 0 and 1, where u_{ij} represents the degree of membership of each x_i to cluster j and

$$\sum_{i=1}^{c} u_{ij} = 1, \forall j = 1, ..., n.$$

The strategy for using fuzzy c-means to classify cells ,is to let the training data define c cluster centers. Form the training data, a Boolean membership matrix U is created. If the data point belongs to cluster 1, then u_{ij} is set to 1.oterwise, it is set to zero. The boolean membership matrix is then used to calculate the cluster means $c_{i.}$

$$\mathbf{c}_i = \frac{\sum_{k=1}^{n} (u_{ik})^m \mathbf{x}_k}{\sum_{k=1}^{n} (u_{ik})^m}, \text{ for } i = 1, .., c.$$

When the cluster centers are defined, the membership of the test data to each cluster can be found. The membership ui_k of the k_{th} data point in the test data to cluster i is

$$u'_{ik} = \frac{1}{\sum_{j=1}^{c} (D_{ik}/D_{jk})^{2/(m-1)}}$$

Where d_{ik} is the Euclidian distance from the k_{th} data point to cluster center i.

In this project, the normal and abnormal cell can be classified used FCM (Fuzzy C-Means) clustering. The result is shown in APPENDIX [10.11.4, 10.11.5]. The performance of the training and testing dataset is also calculated. The result in shown in APPENDIX [10.11.7]

The dataset used in the project are chosen from papsmear herlev dataset. First, the pre-processed images are taken as an input for the segmentation phase and the segmentation is done using threshold based segmentation technique. Next, the samples were divided into seven classes, class **A** is **Superficial squamous** and class **B** is **Intermediate squamous** and class **C** is **Columnar** and class **D** is **Mild dysplasia** and class **E** is **Moderate dysplasia** and class **F** is **Severe dysplasia** and class **G** is **Carcinoma in situ**. The extracted features are trained with seven classes A, B, C, D, E, F, and G. Finally the output is tested with their feature extracted values of 70 images.

RESULTS AND DISCUSSION

6. RESULTS AND DISCUSSION

In this project, deals with the cervical cancer detection system from papsmear images. The dataset the results are shown in APPENDIX [10.2.1, 10.2.2]. In proprocessing phase noise can be removed using different filtering techniques. Median filter gave the better result than other filtering techniques. The result of preprocessing papsmear images are shown in APPENDIX [10.1, 10.2].PSNR and MSE value is also calculated for the preprocessing image. The results are shown in APPENDIX [10.3, 10.4] Threshold based segmentation method is used for segmentation. As a result of segmentation, nuclei and cytoplasm can be extracted. The results of segmentation are shown in APPENDIX [10.5, 10.6].

Then the segmented images are taken as input images for features extraction. In this project feature vectors are extracted by Statistical features and texture features such as area, perimeter, N/C Ratio, shortest diameter, longest diameter, brightness, roundness, nucleus position, elongation, maxima and minima for both nucleus and cytoplasm. The feature extracted values are shown in APPENDIX [10.7]. The extracted features are taken as input for the classification and recognition method. The classifications of papsmear images are carried out by the ANFIS neural network. The network system used the fuzzy rules for classify the cell as normal and abnormal as well as levels of cervical cell smear image. Then the classifier is tested and the results are plotted in the graph. The results of classification are shown in APPENDIX [10.4.6].

CONCLUSION

7. CONCLUSION

The project "**Cervical Cancer Detection form Papsmear Images using Image Processing Techniques** "is implemented successfully and it is more useful for diagnosis purpose. The objective of cervical cancer detection is to detect and classify the cancer from papsmear images.

A database consists of 100 images of single cells, classified using image processing techniques, and an effort was made to make these as optimal as possible. The data includes non-keratinizing dysplasia, columnar and squamous epithelliam cells. Each cell is described by 20 nuclear and cytoplasmic features.

An effective method to identify and classify cervical cancer is becoming increasingly needed due to the fact that early detection and a decision of correct therapy may save the patient. Medical images have various limitations such as low quality, presence of noise and human error in interpretation. The proposed papsmear test give the better result compared to conventional non-adaptive *k*-means and fuzzy *c*-means clustering algorithms. The proposed techniques have the capability to segment the papsmear images into nucleus, cytoplasm and background regions. The shape and size of nucleus and cytoplasm of cervical cells were also maintained. It provides a clear segmented papsmear images for easier and better extraction process of morphologies of cervical cells. Automated papsmear detection system, while maintaining and improving the accuracy of the system.

The ANFIS (Adaptive Neuro Fuzzy Interference System) architecture was used for implementing fuzzy rules for classification of the cells in the database. When using its training algorithms, it almost always increases the performance of a system. The effect of training a network depends on the number its adaptive parameters and the number of training data. Choosing a good combination of features/inputs from the database is necessary to get a performance that meets the requirements. The good result can be obtained using ANFIS network system for classify the papsmear cell.

SCOPE FOR FUTURE ENHANCEMENT

8. SCOPE FOR FUTURE ENHANCEMENT

In this project future work will include additional steps for improving the segmentation of nuclei and cytoplasm area within overlapping cell groups. Most of prominent digital image analysis techniques for cervical precancerous screening using papsmear test. It consists of three sets of processing such as cell segmentation, feature extraction and classification. But some images produce the low accuracy of classification, which needs to be improved. The classification between cancer stages is necessary to be done in order to increase the accuracy of the detection system.

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9. BIBILIOGRAPHY

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11. O. Lezoray and H. Cardot, 2002, "Cooperation of color pixel classification schemes and color watershed: A study for microscopic images", IEEE Trans. Image Process., Vol. 11, No. 7, pp. 783–789.
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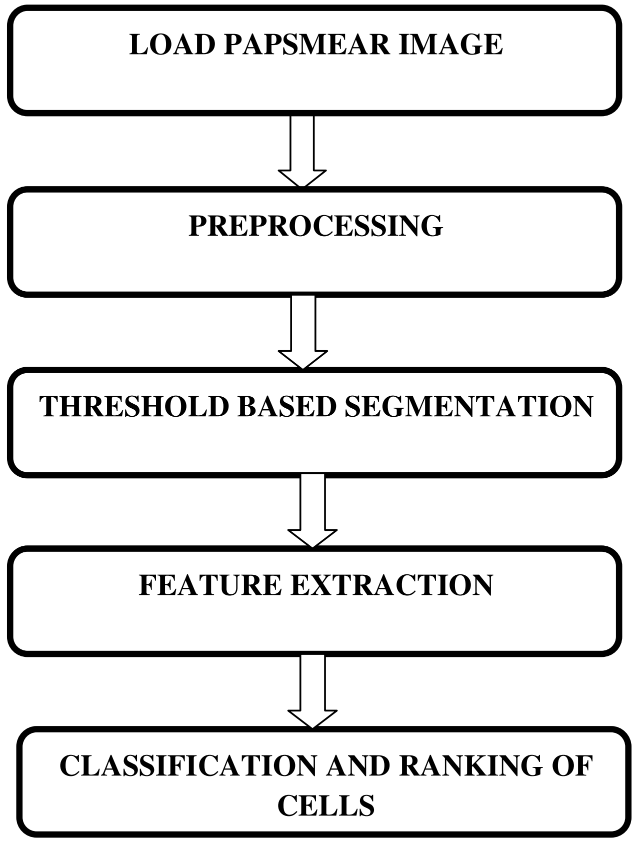
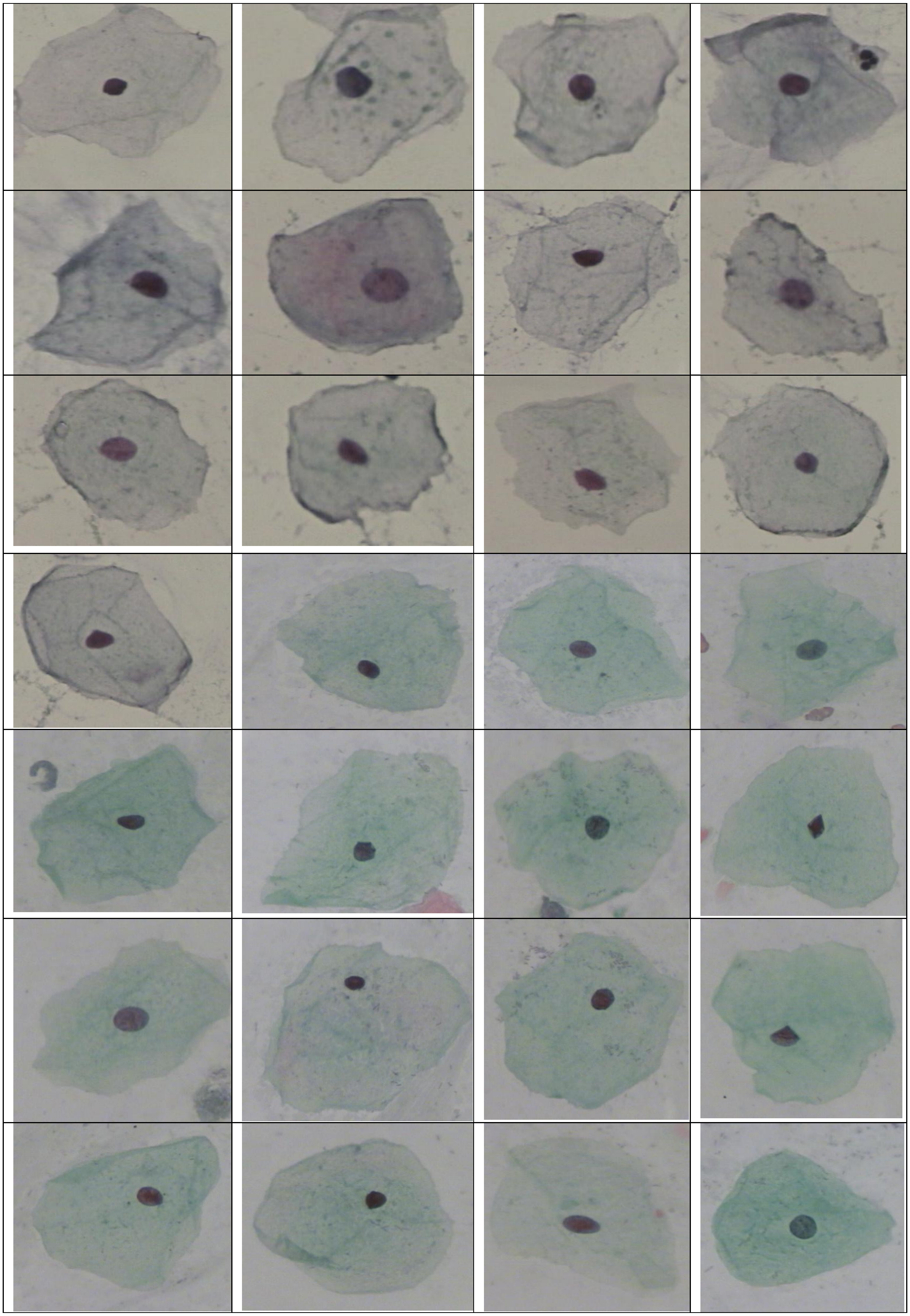
10. APPENDIX

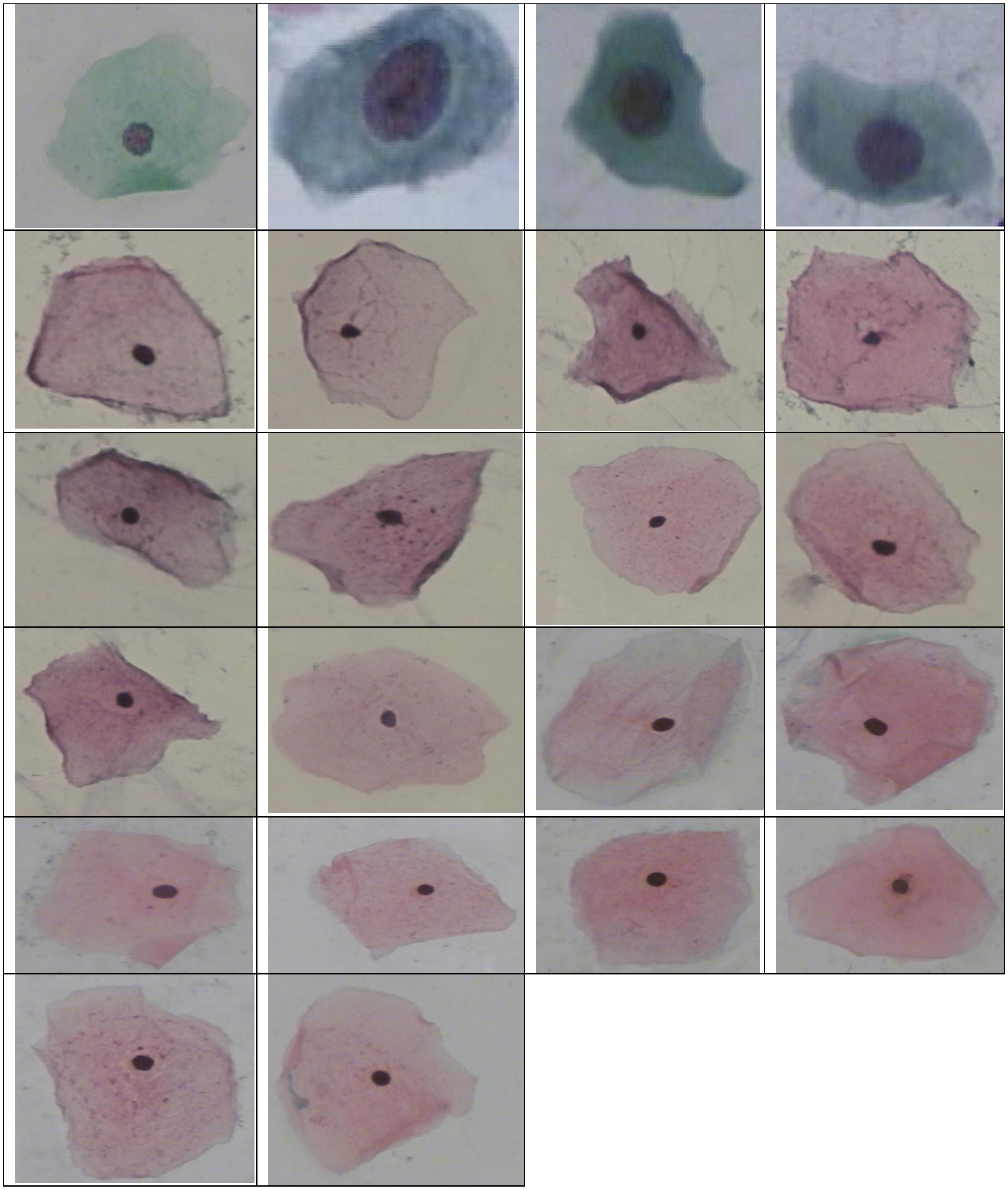
10.1 SYSTEM FLOW DIAGRAM



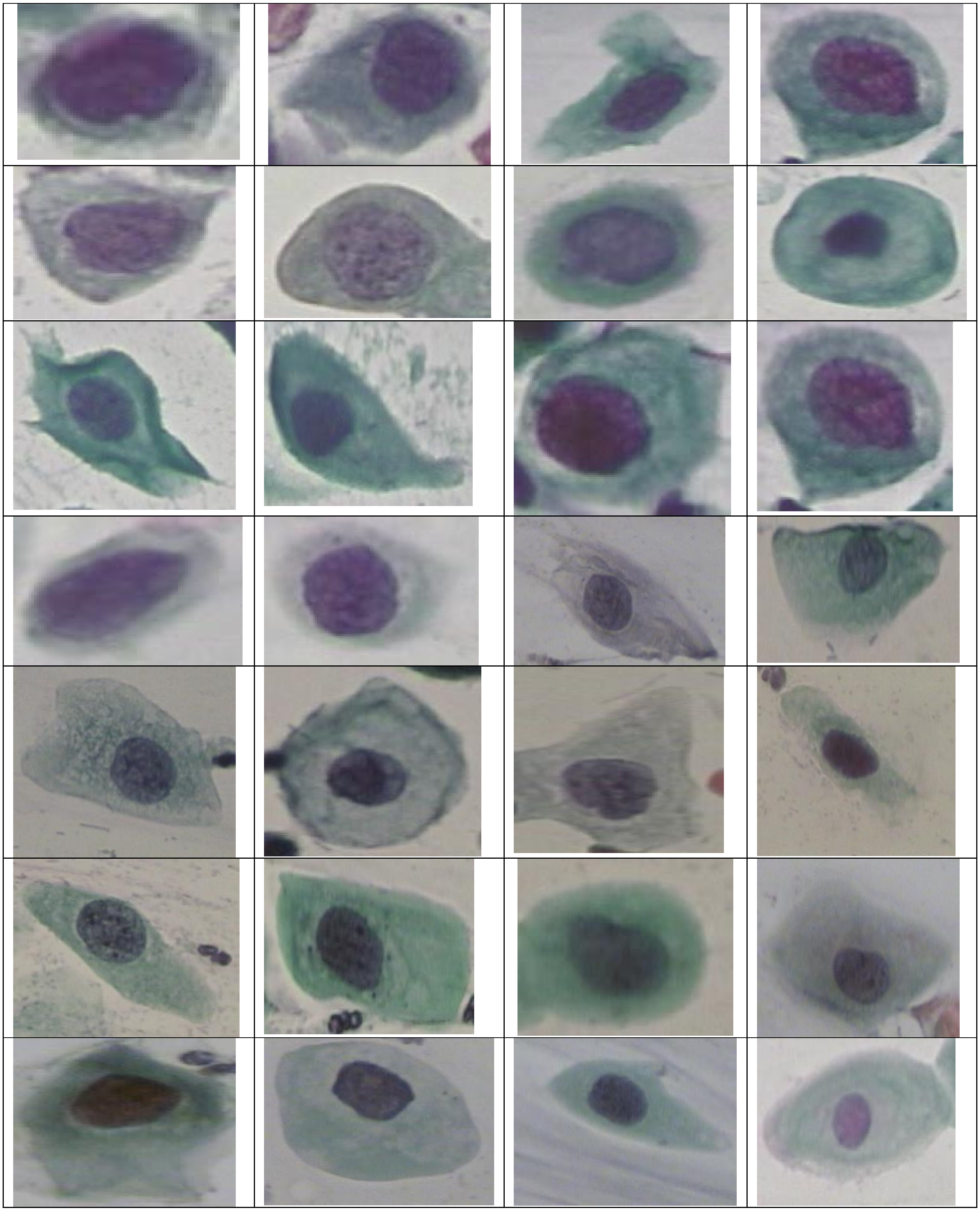
10.2 DATASET USED

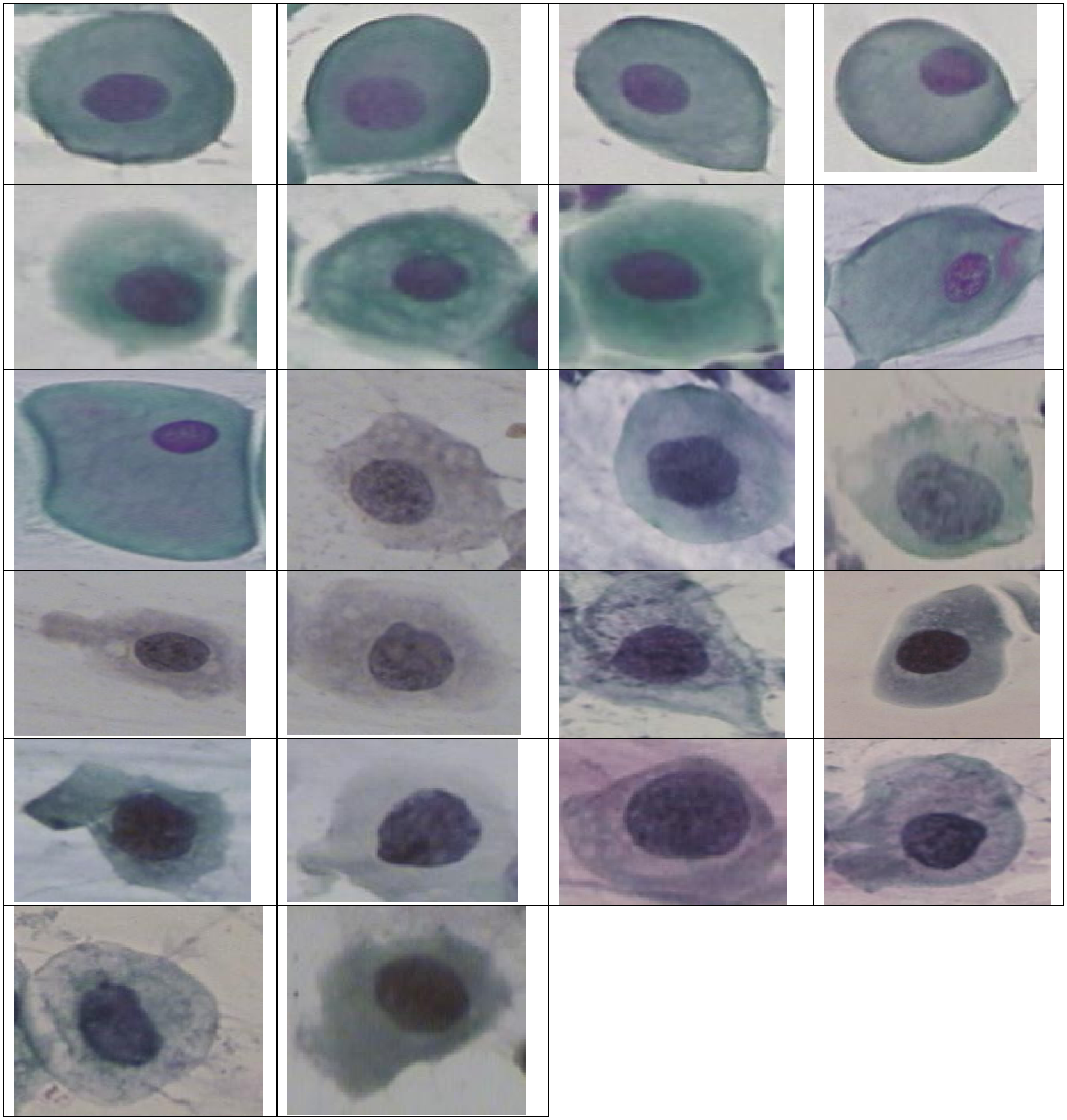
10.2.1 DATASET-NORMAL CELL





10.2.2 DATASET - ABNORMAL CELL





10.3 INPUT SCREENS

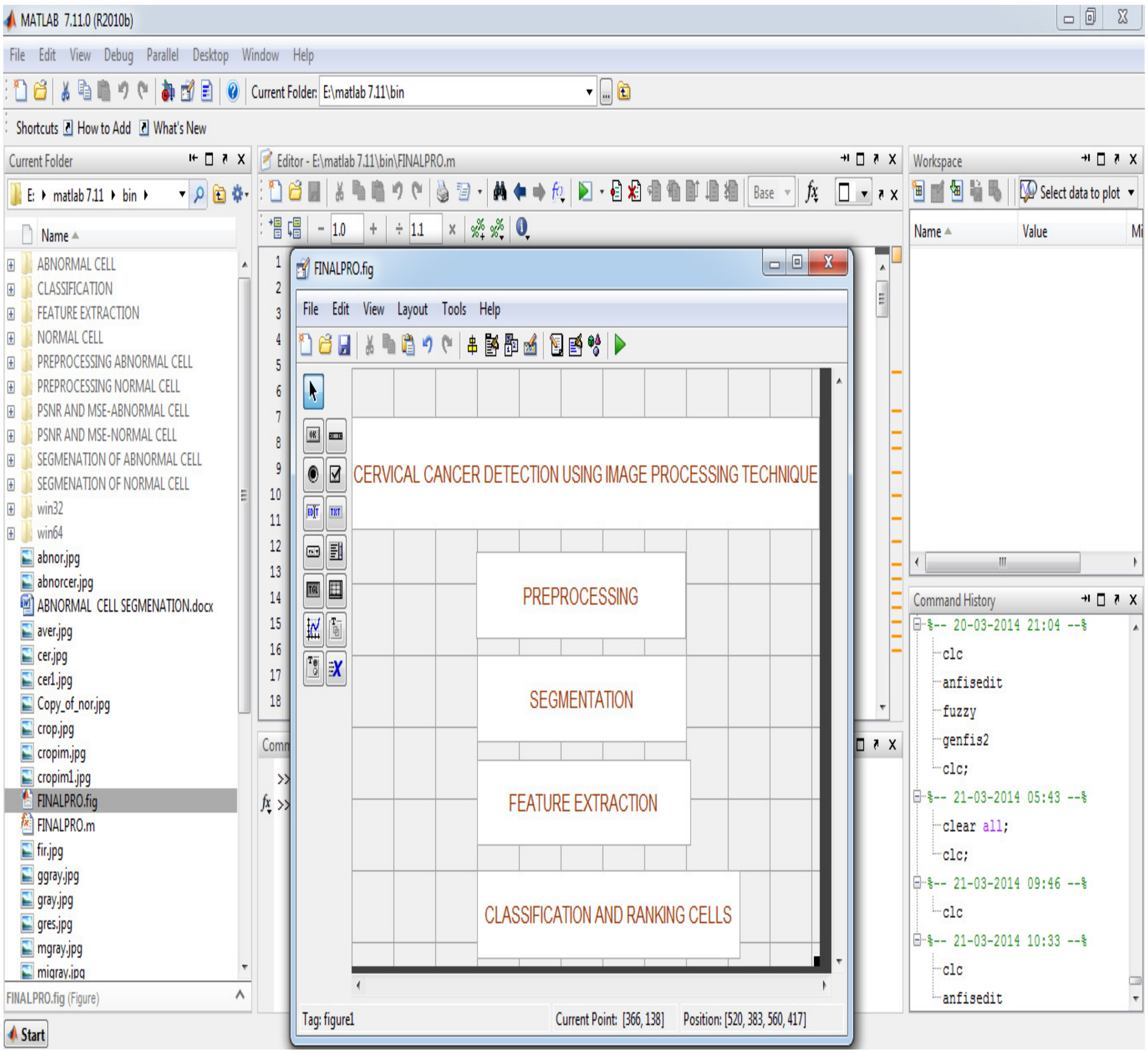


FIG. 10.3.1 MAIN IMAGE

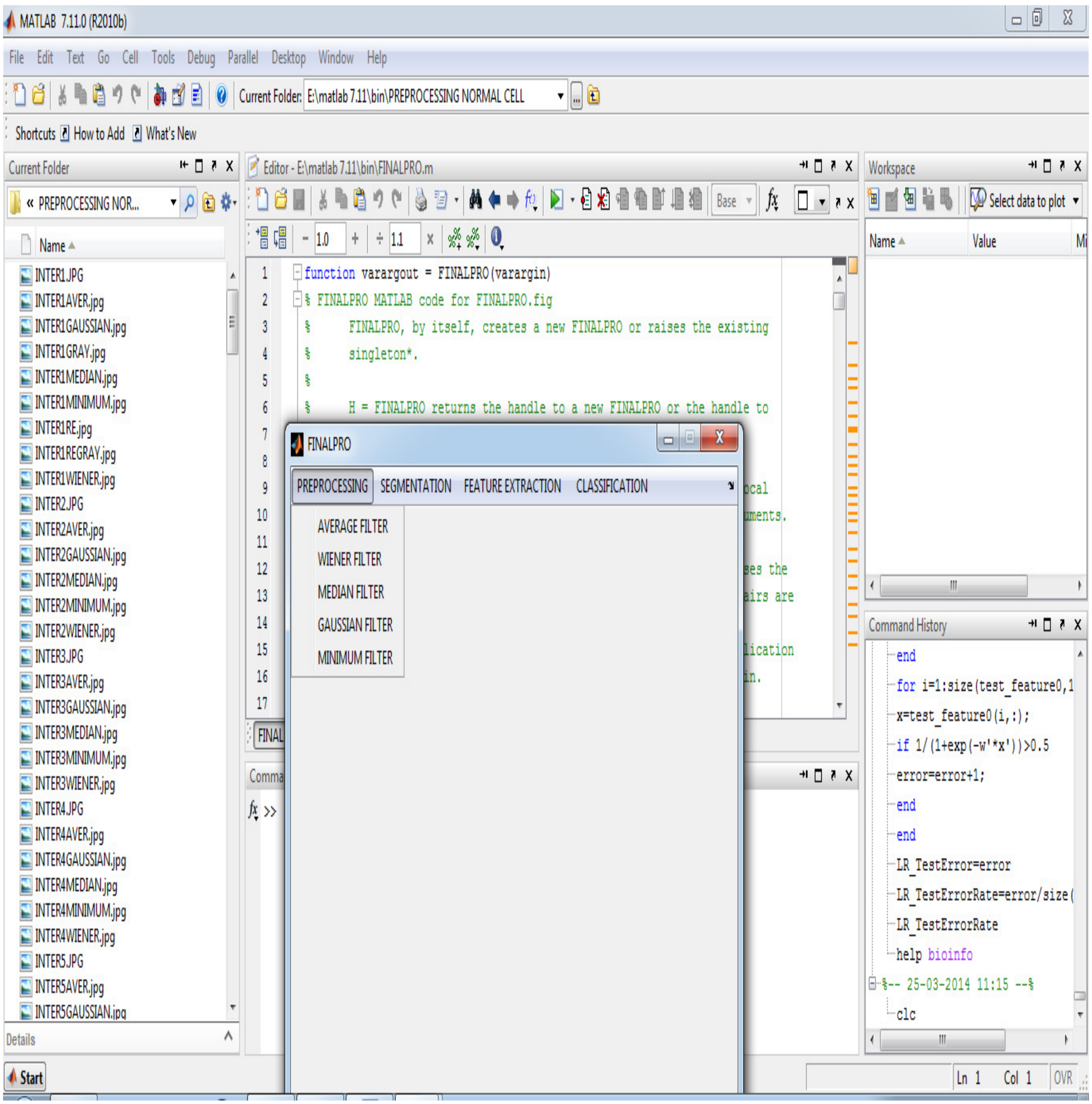


FIG.10.3.2 INPUT SCREEN PREPROCESSING

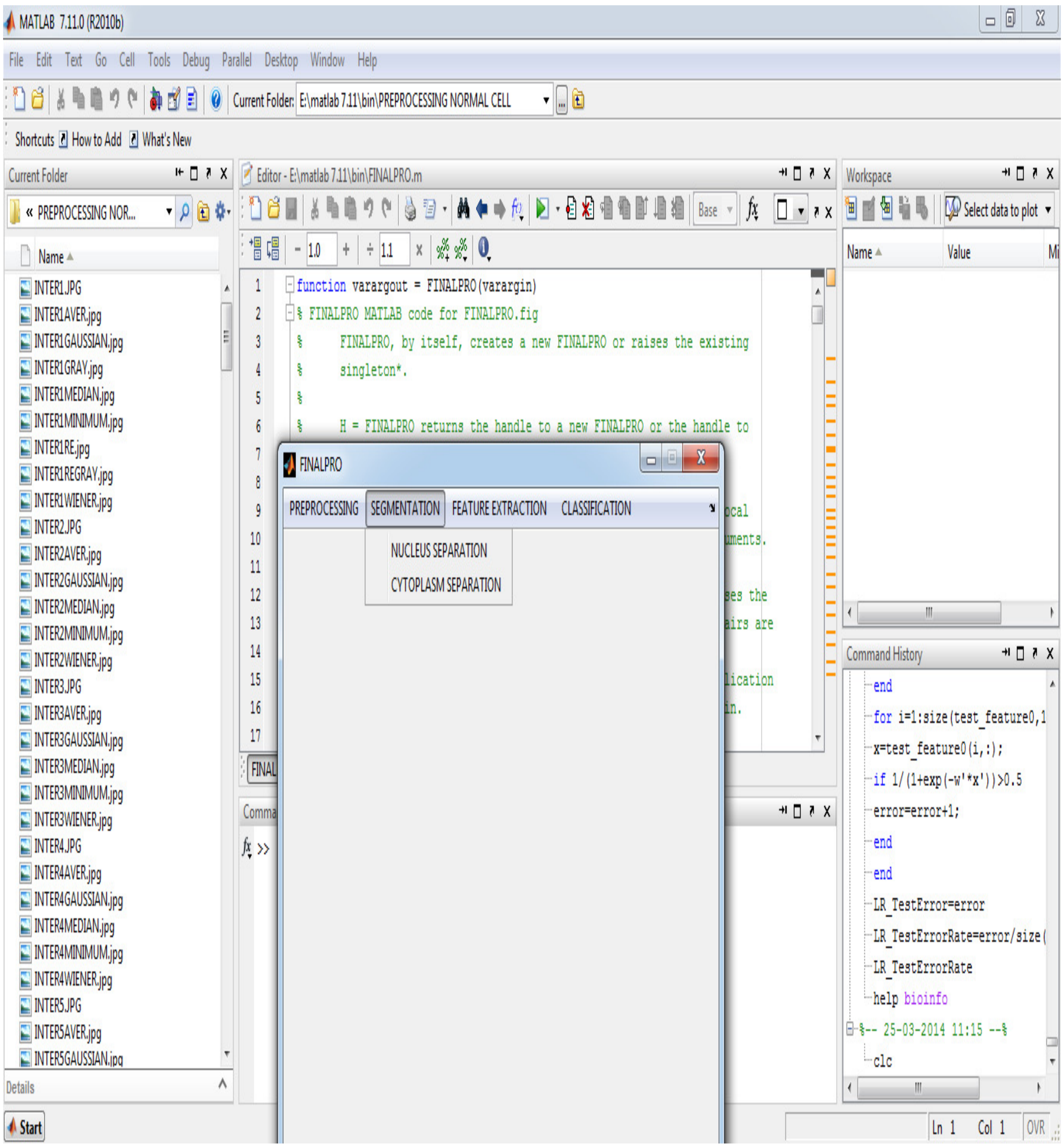


FIG.10.3.3 INPUT SCREEN FOR SEGMENTATION

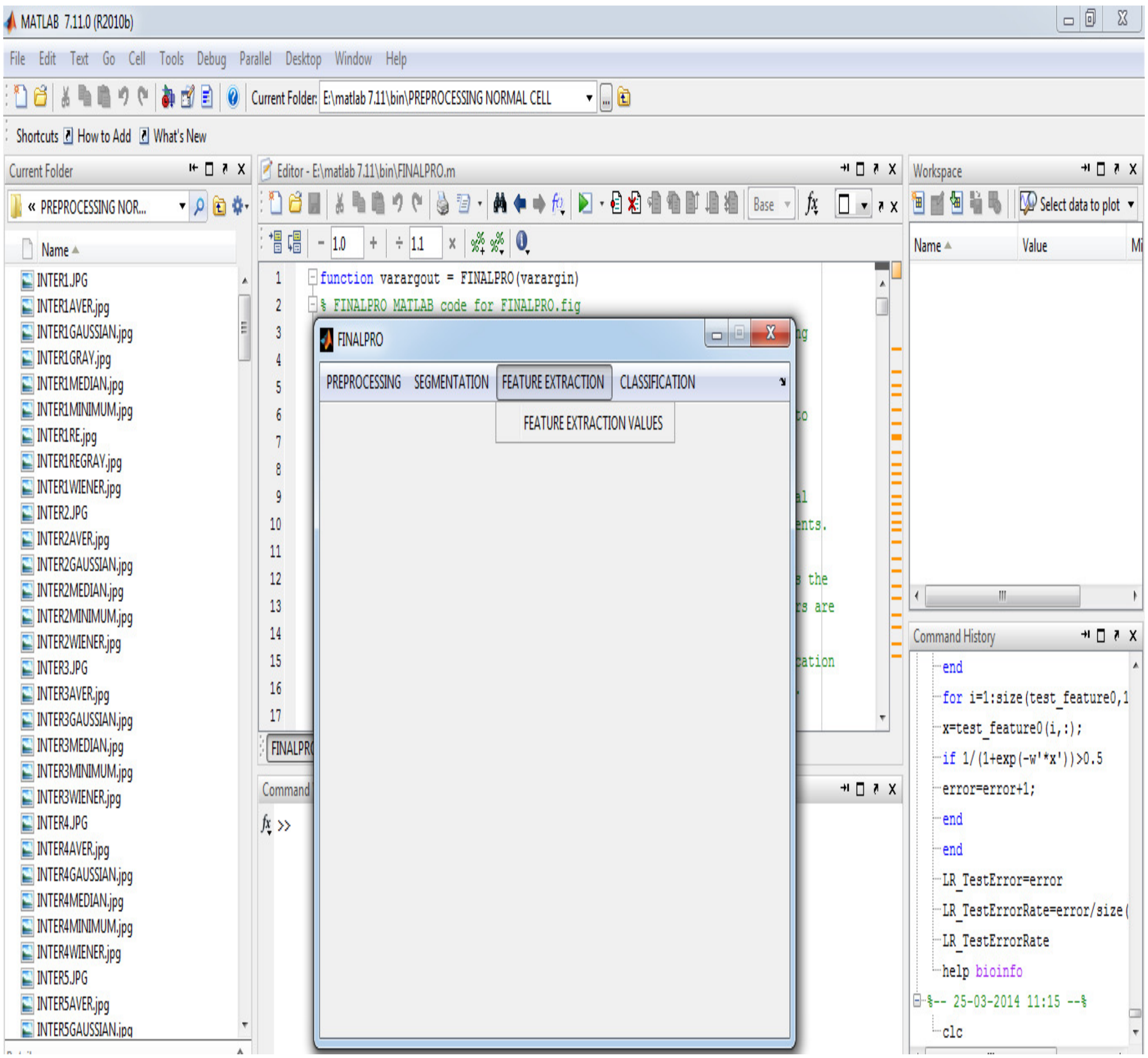


FIG.10.3.4 INPUT SCREEN FOR FEATRE EXTRACTION

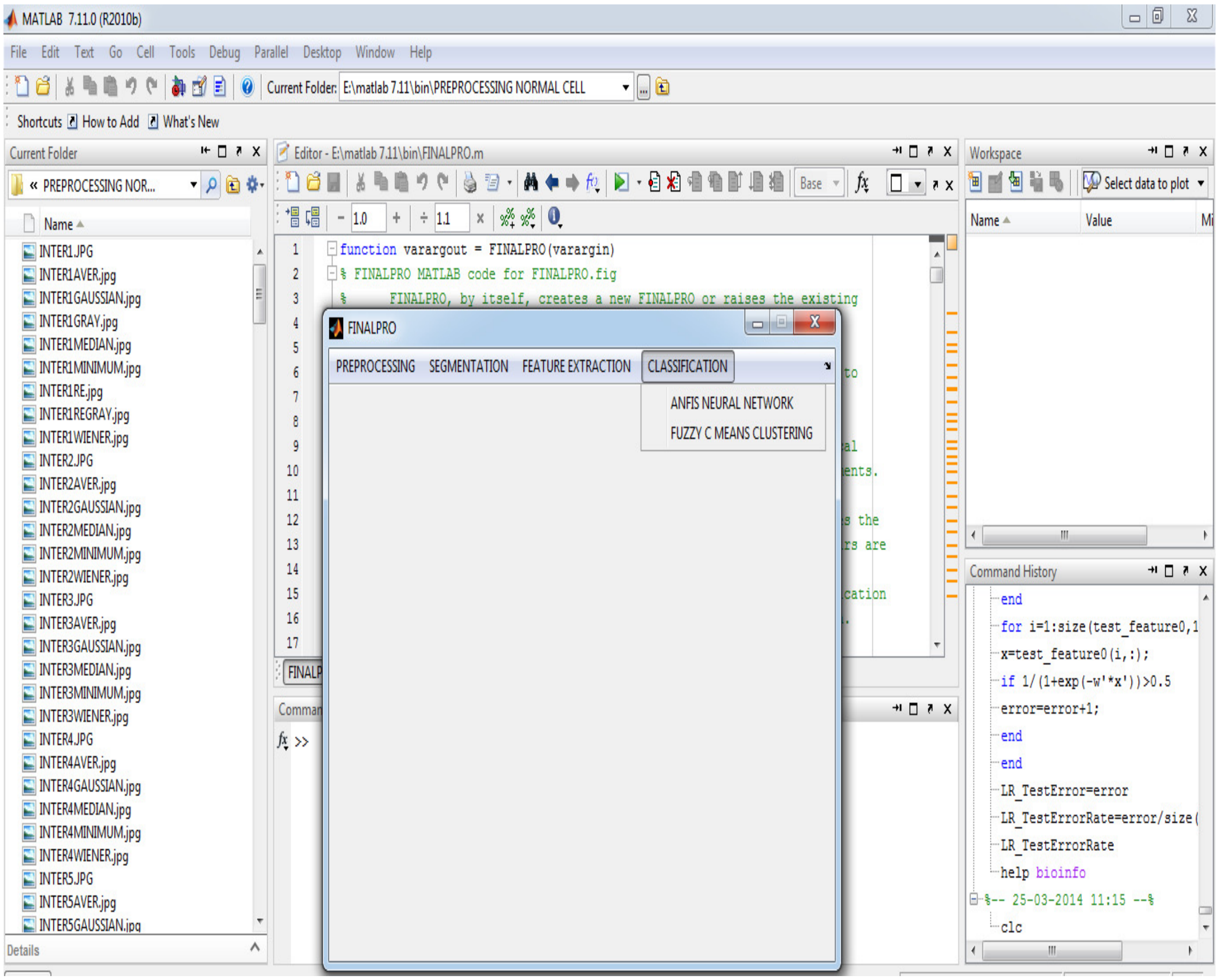
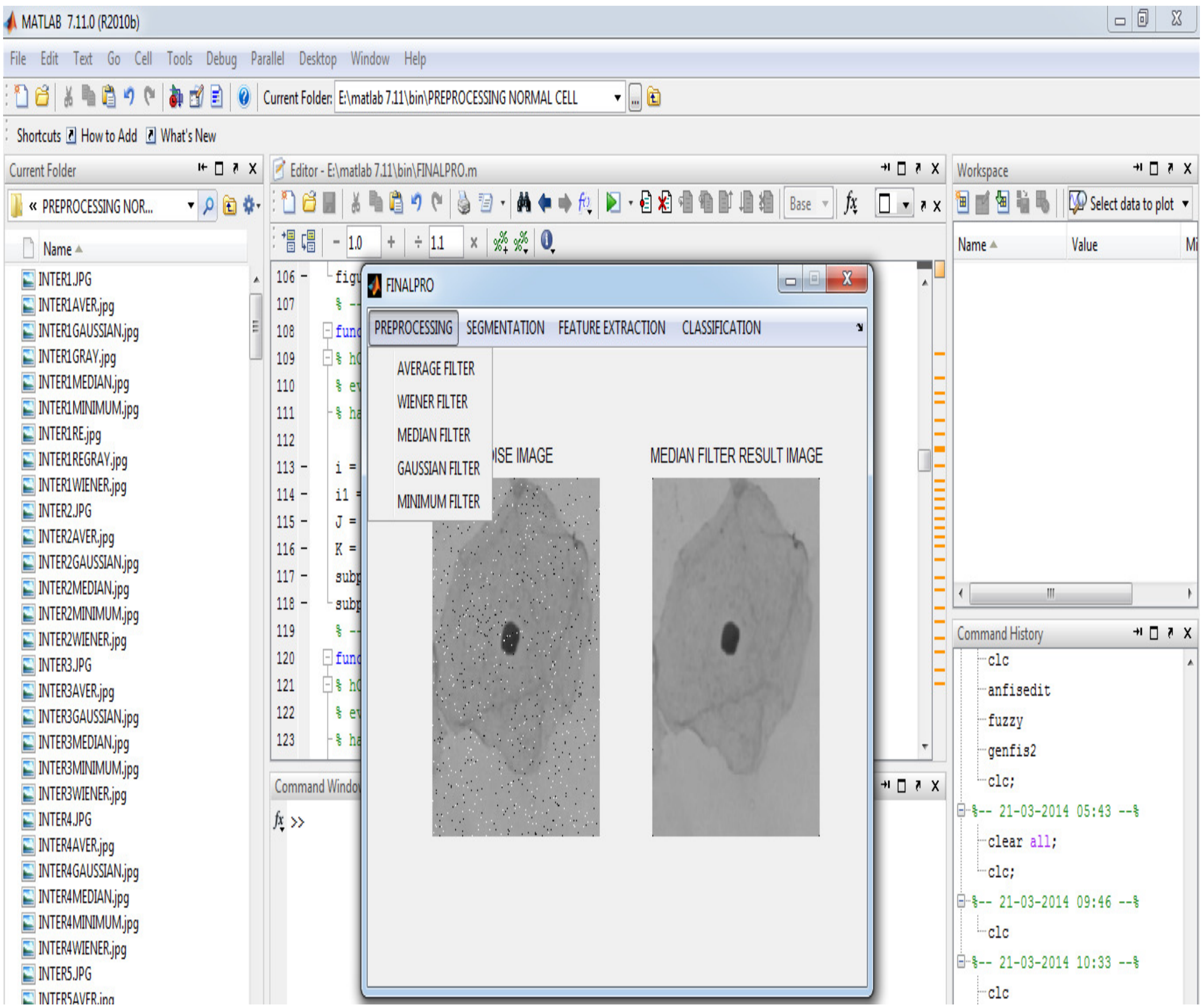


FIG.10.3.5 INPUT SCREEN FOR CLASSIFICATION

10.4 OUTPUT SCREENS

FIG.10.4.1 OUTPUT SCREEN FOR PREPROCESSING-NORMAL CELL



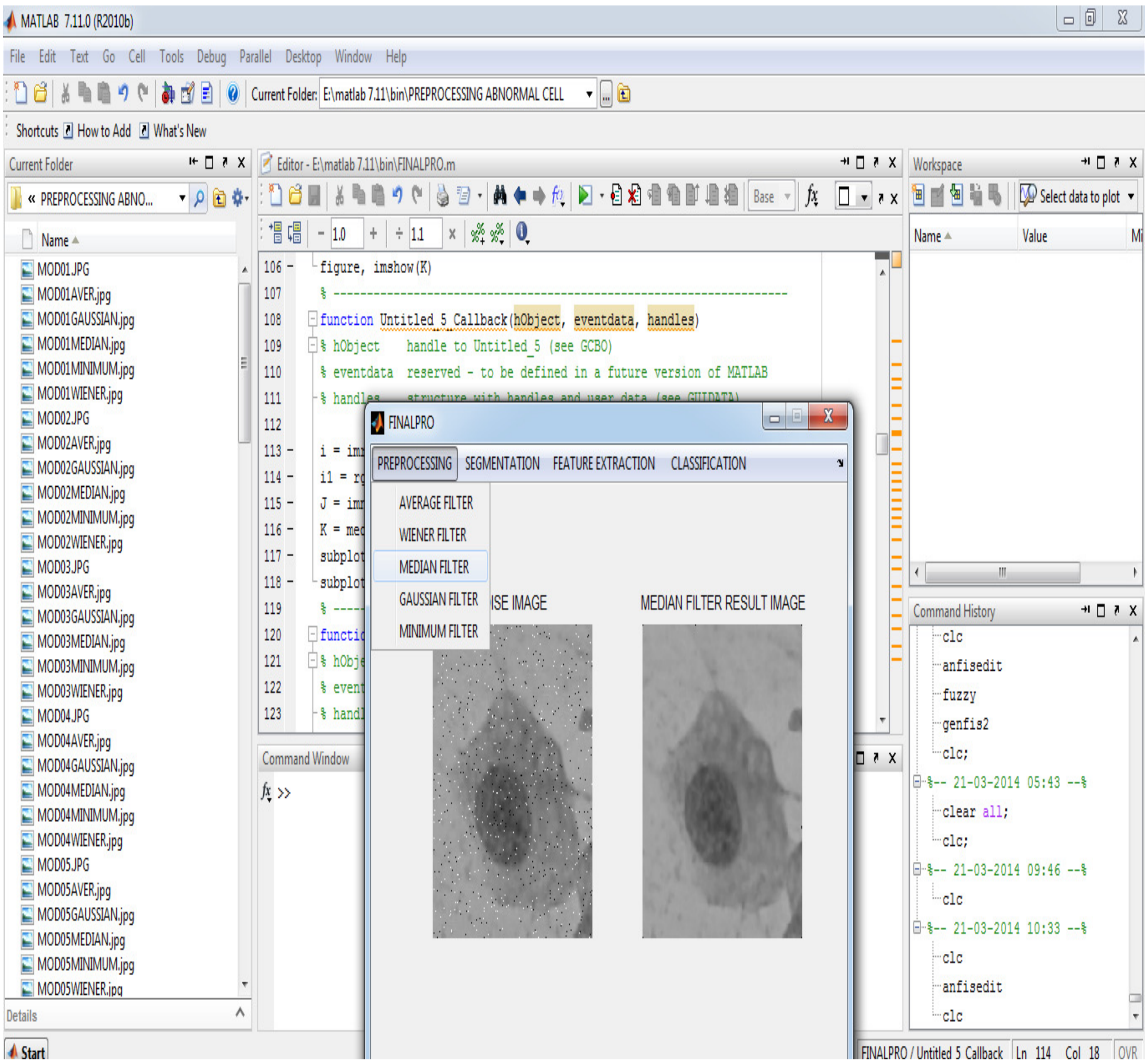


FIG.10.4.2 OUTPUT SCREENS PREPROCESSING-ABNORMAL CELL

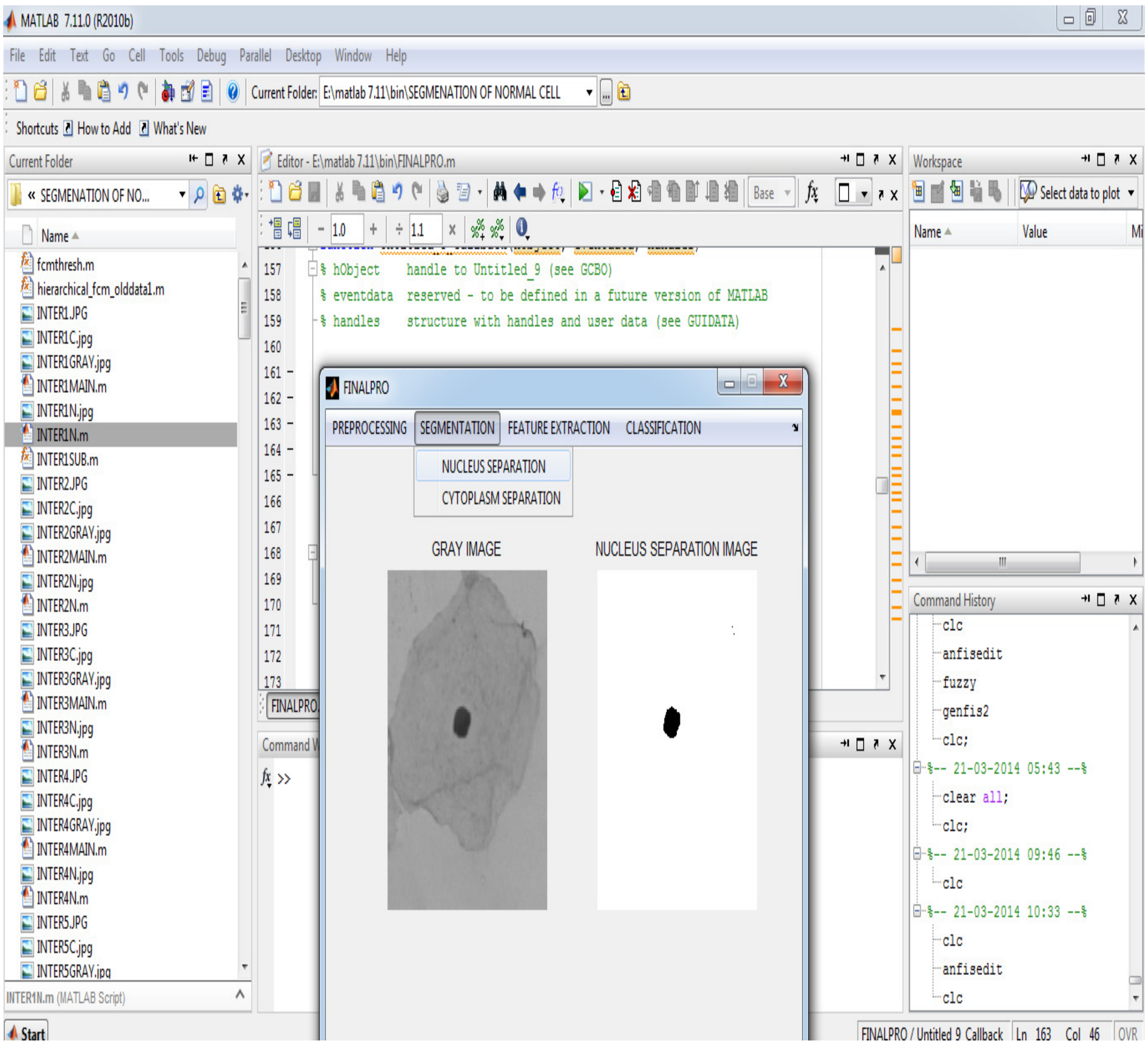


FIG.10.4.3 OUTPUT SCREEN FOR SEGMENTATION-NORMAL CELL

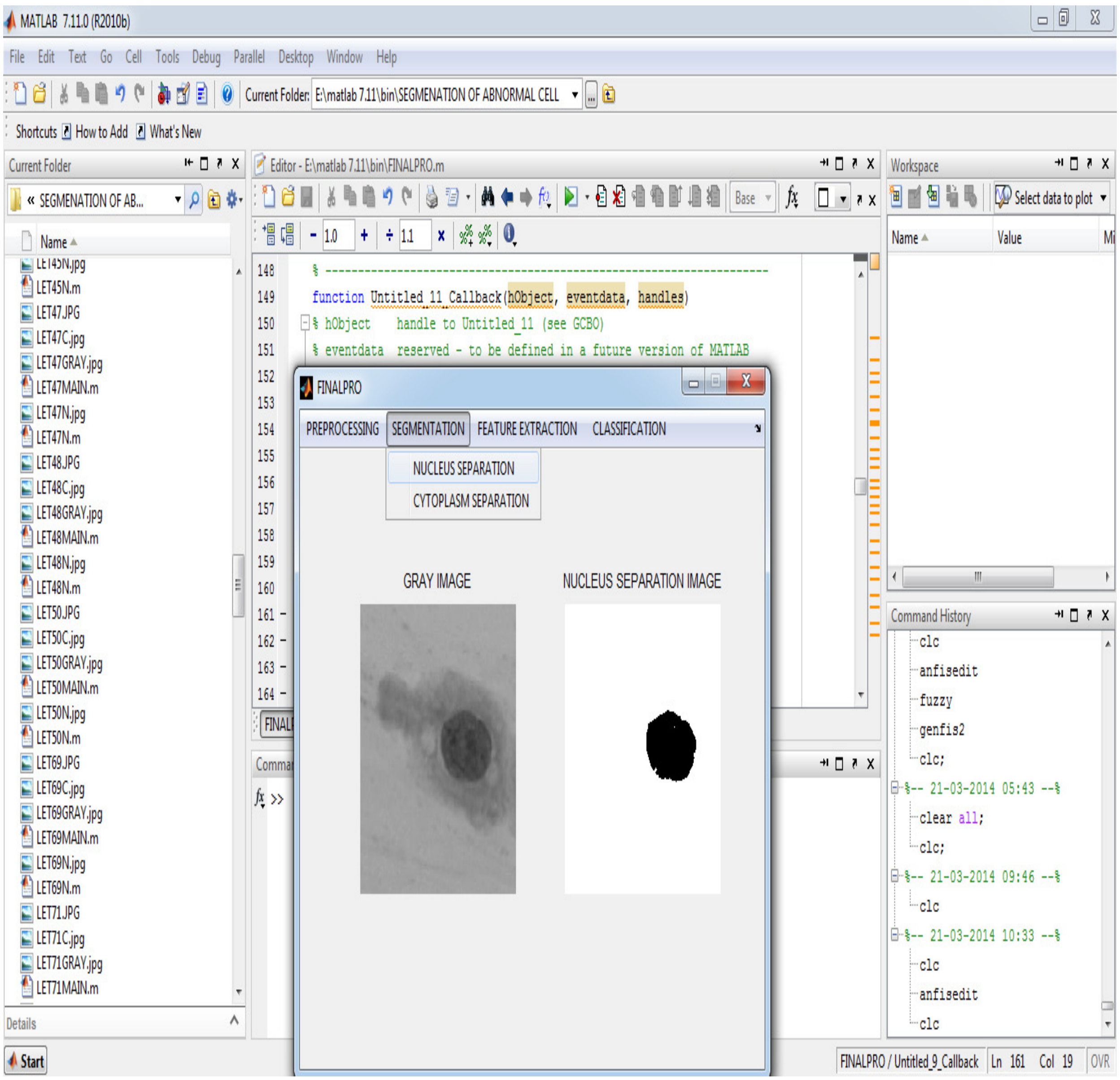


FIG.10.4.4 OUTPUT SCRREN FOR SEGMENTATION-ABNORMAL CELL

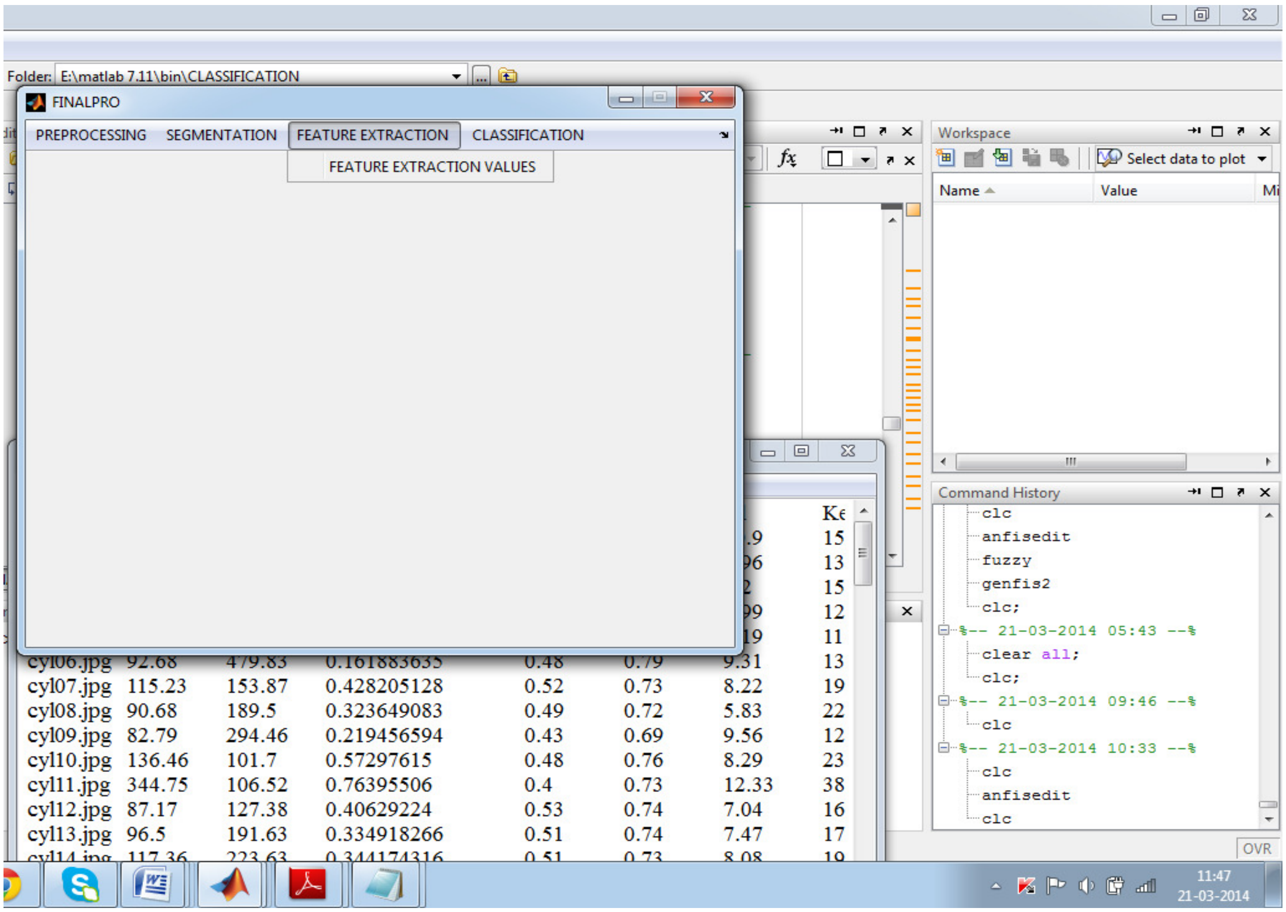


FIG.10.4.5 OUTPUT SCREEN FOR CLASSIFICATION

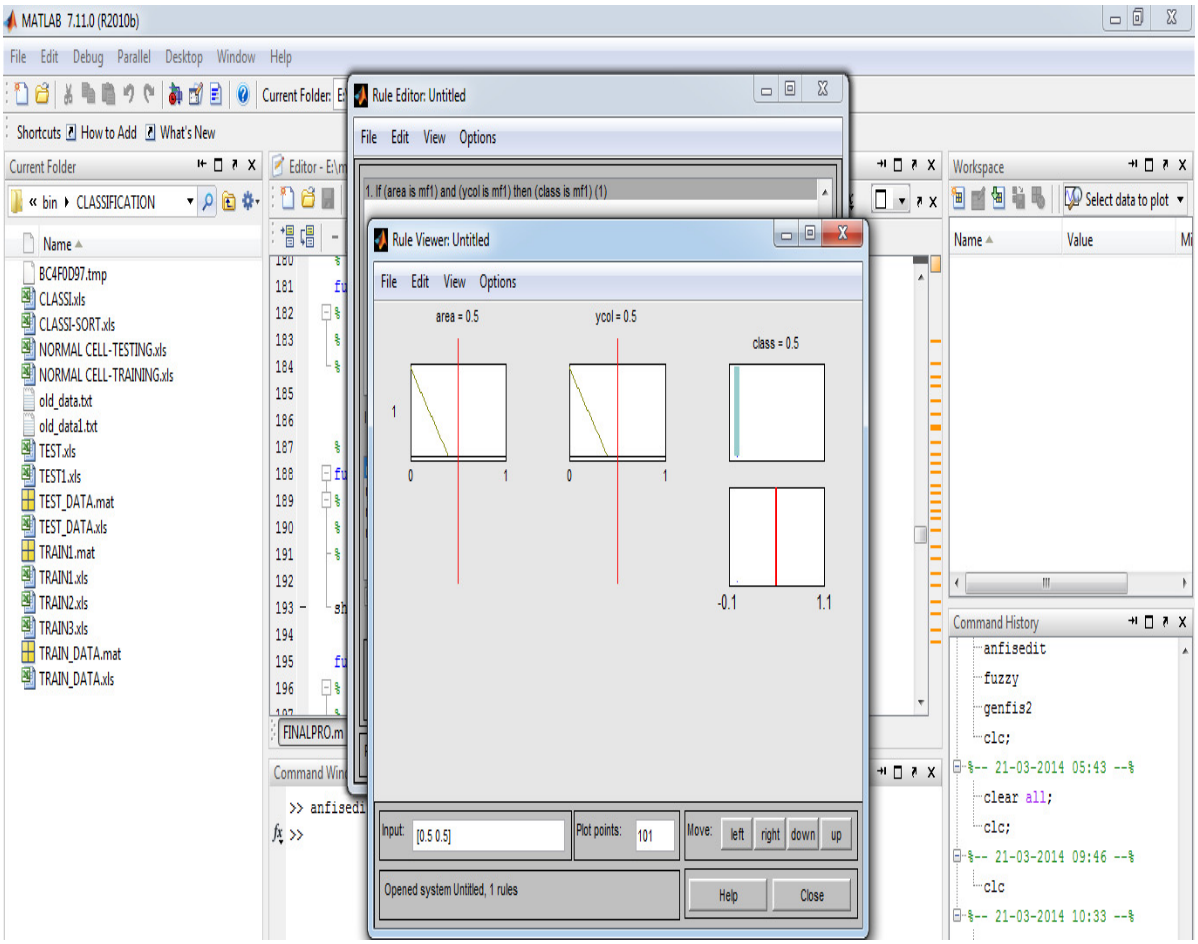
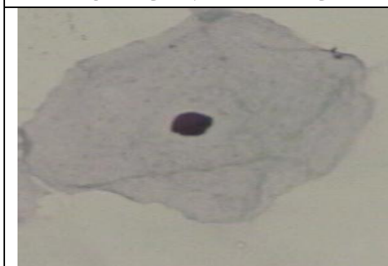
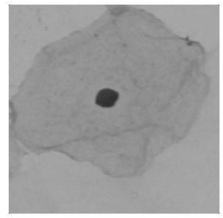
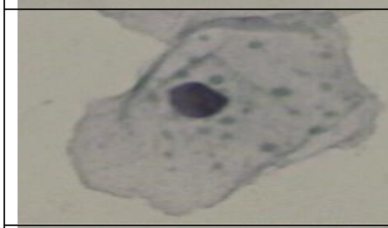
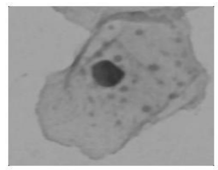
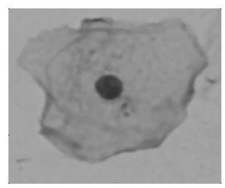
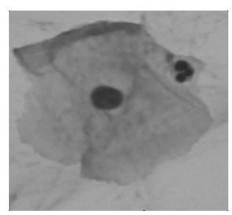
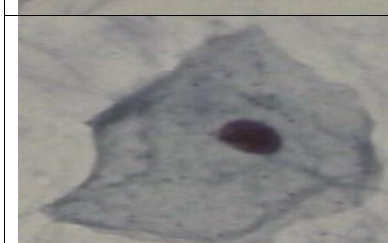
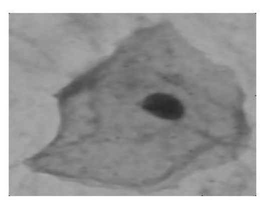
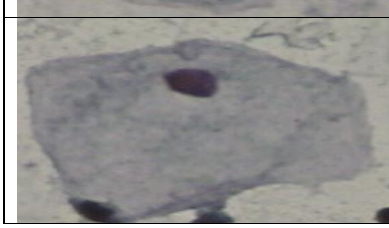
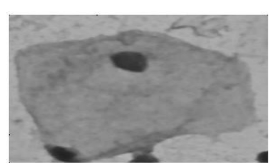
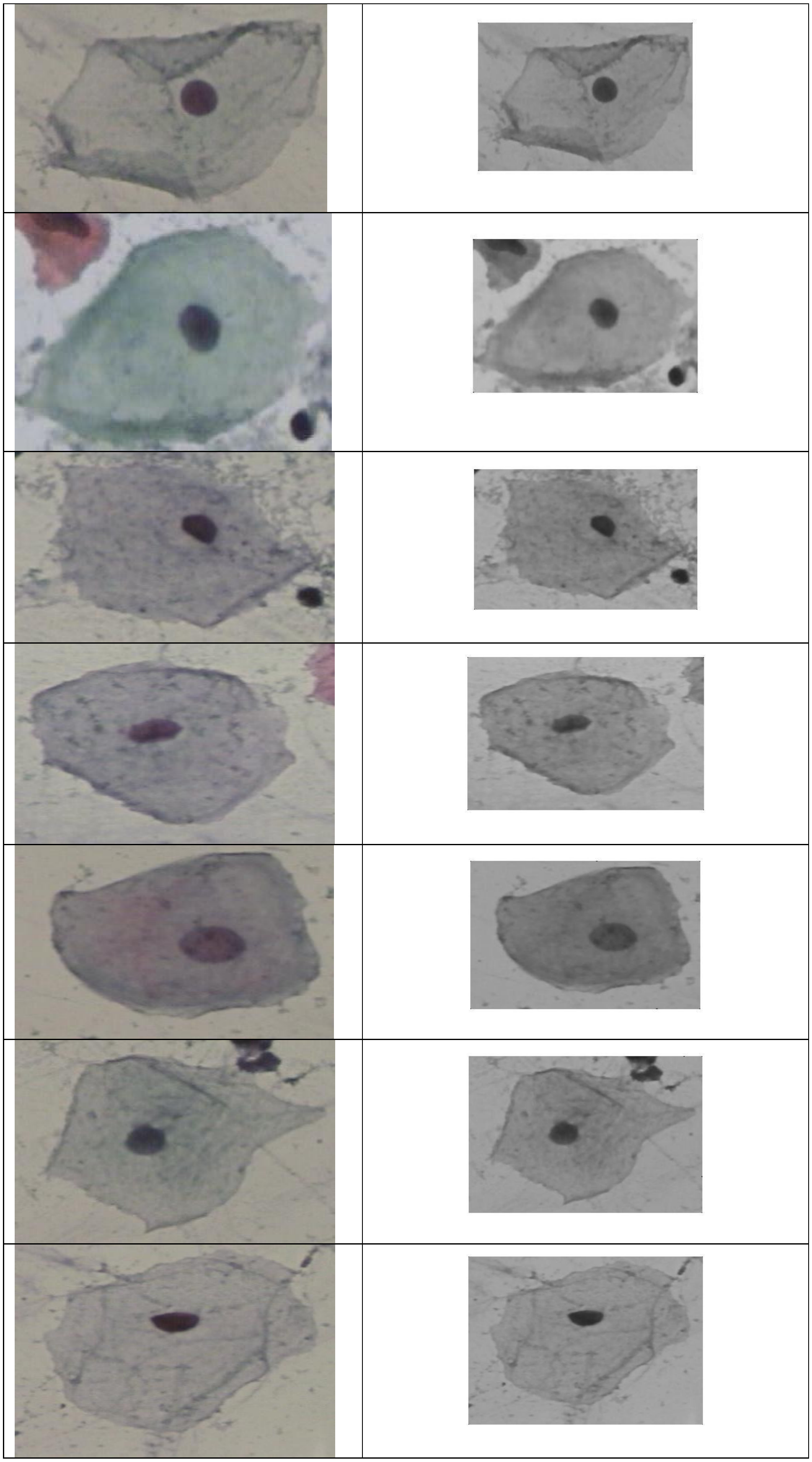


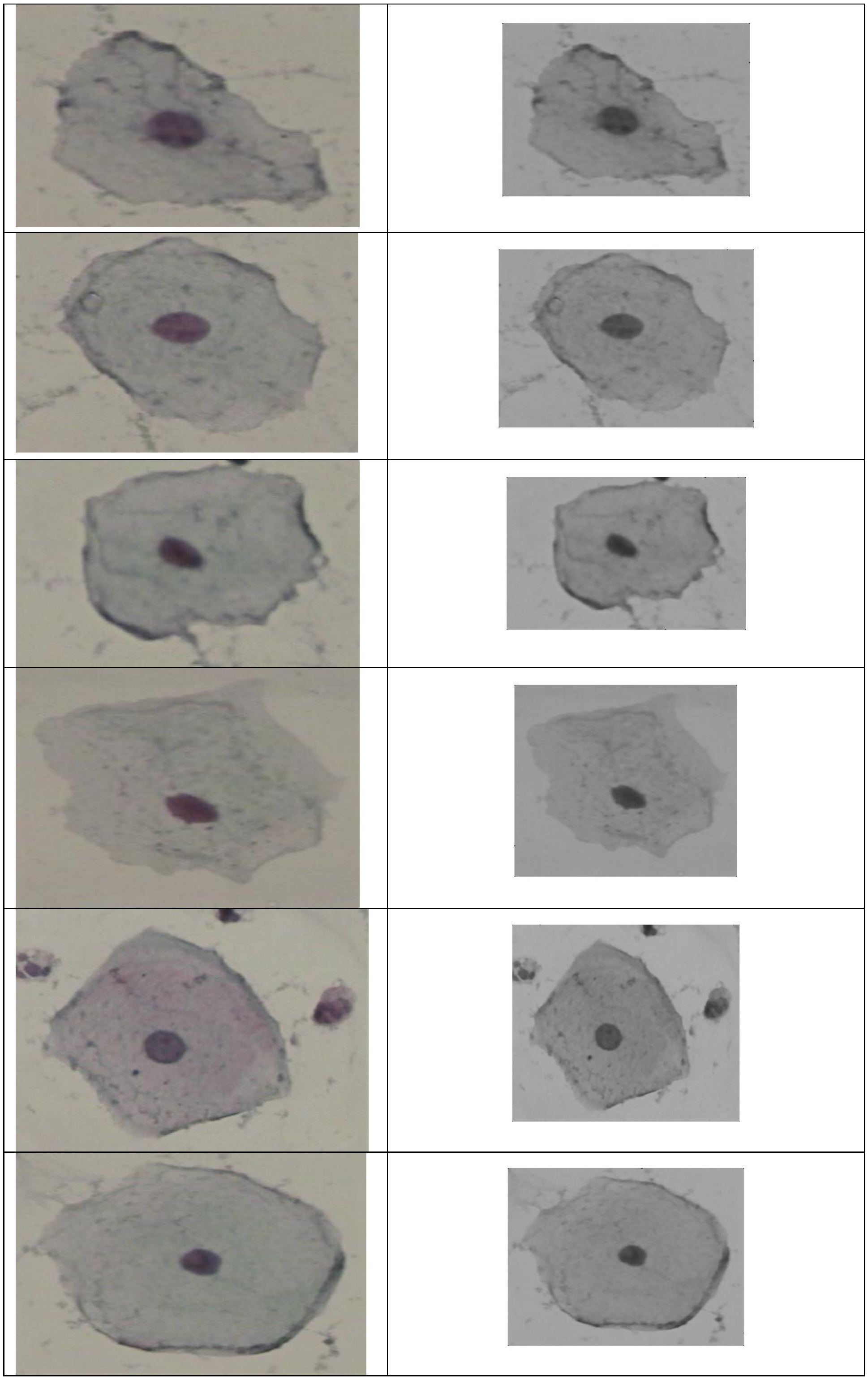
FIG.10.4.6 OUTPUT SCREEN FOR CLASSIFICATION

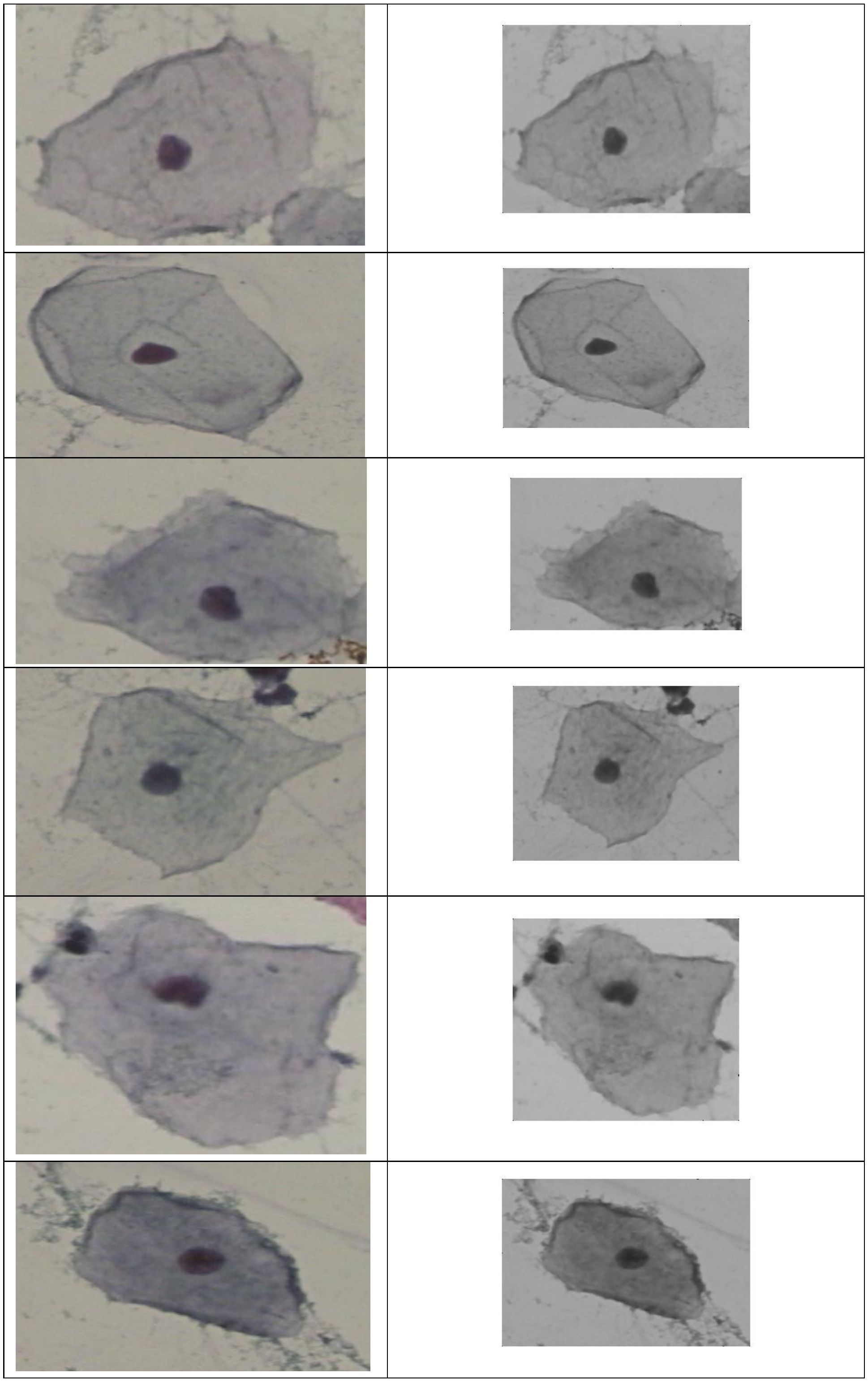
10. RESULTS

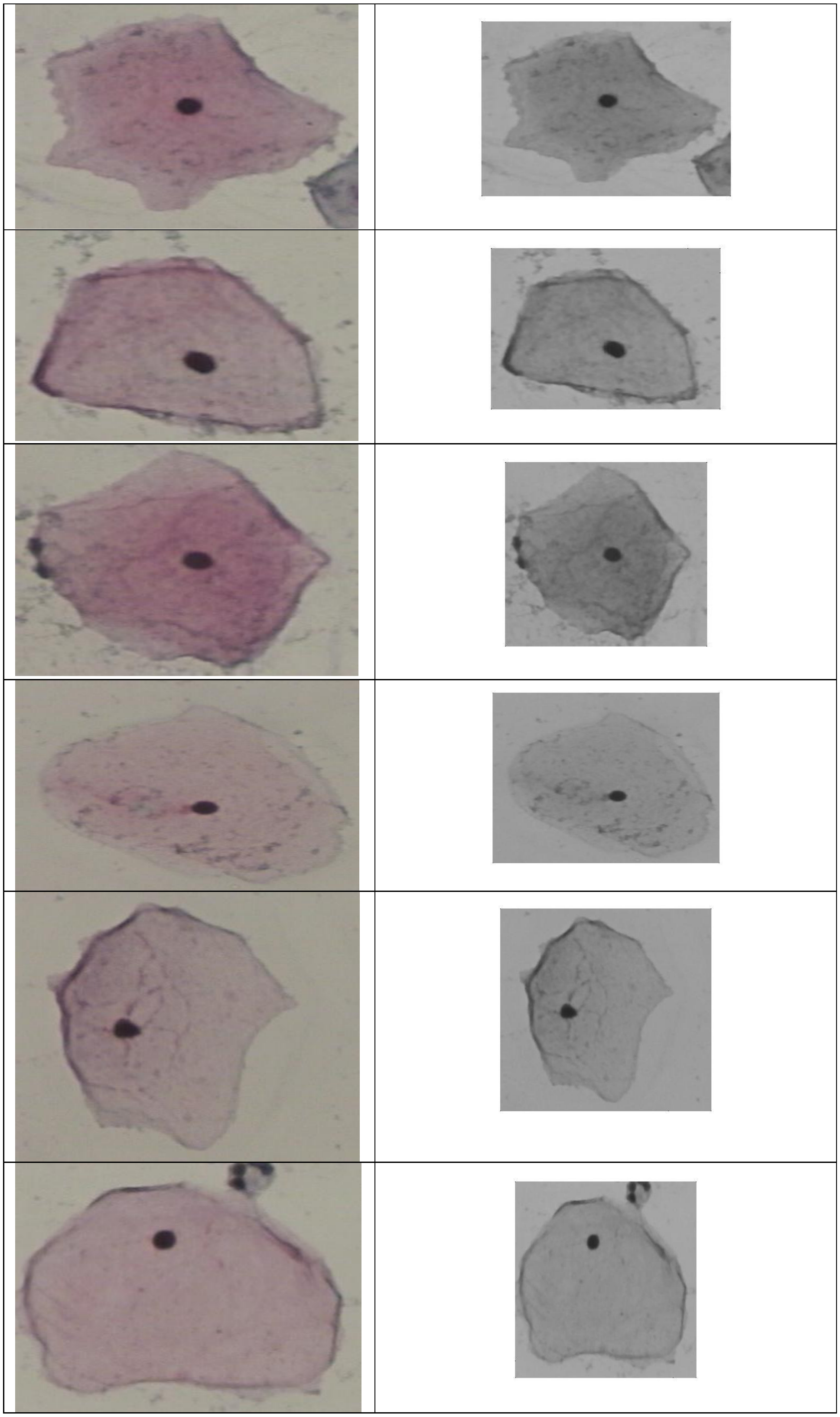
TABLE 10. 1 RESULTS FROM PREPROCESSING-NORMAL CELL

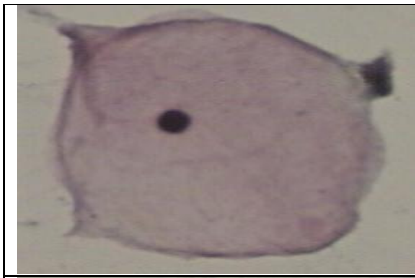
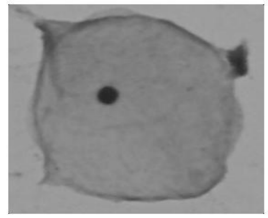
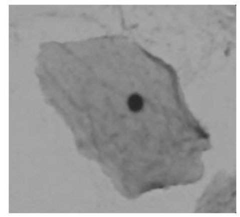
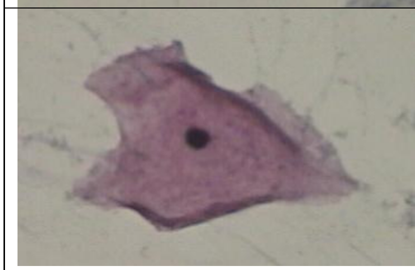
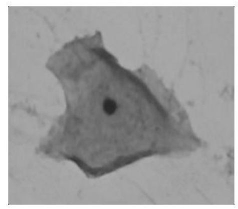
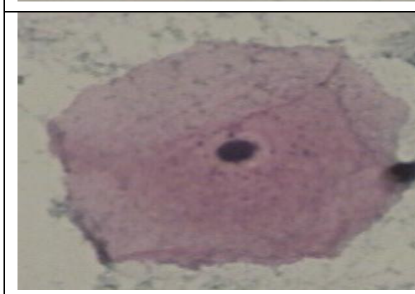
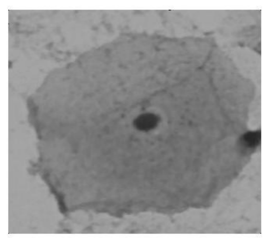
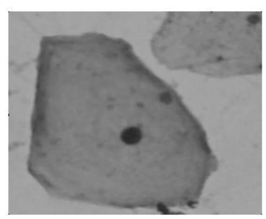
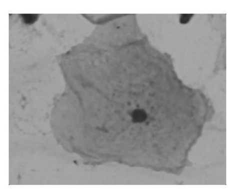
ORIGINAL IMAGE	RESULT IMAGE
	
	
	
	
	
	

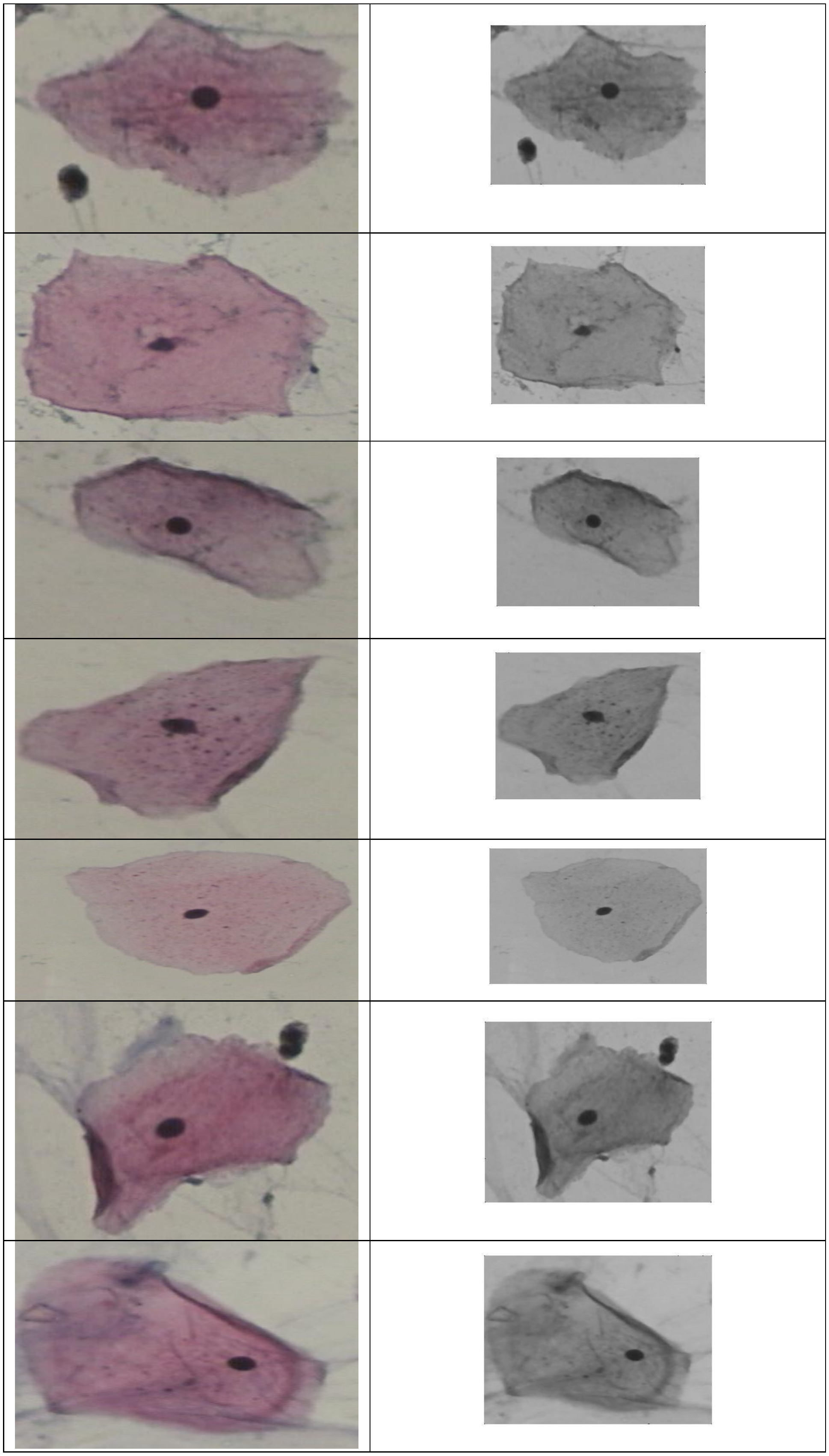










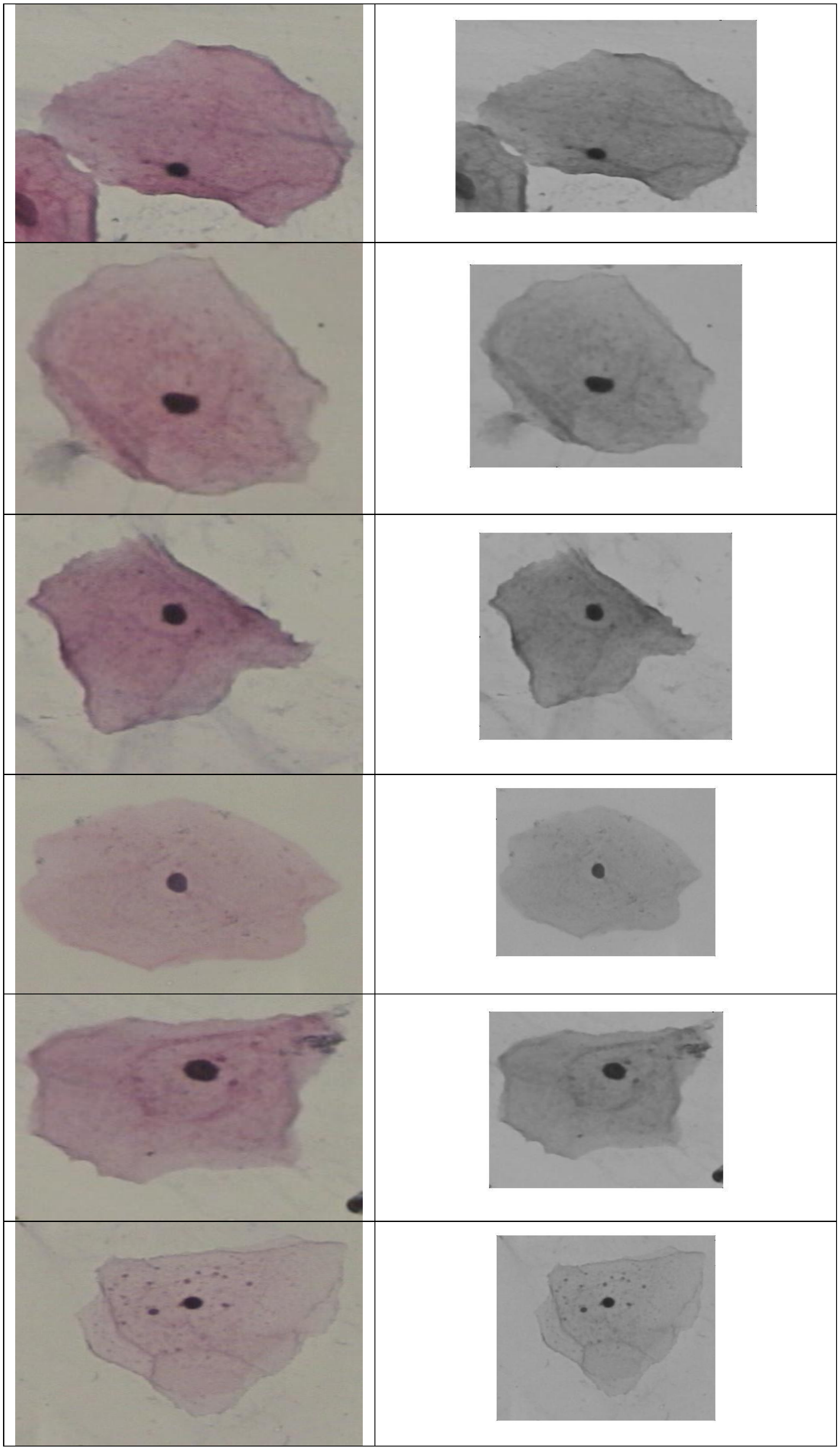
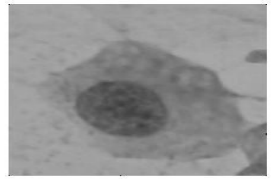
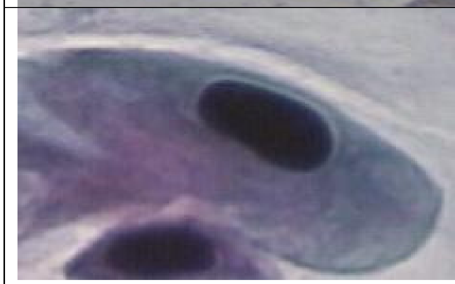
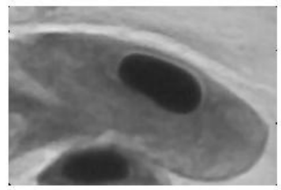
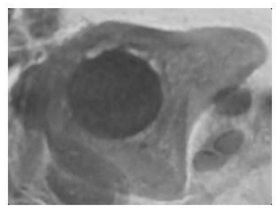
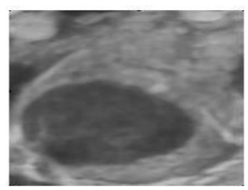
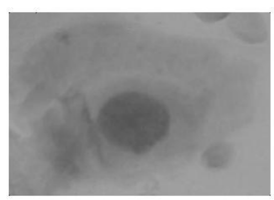
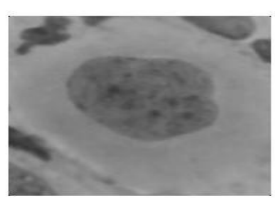
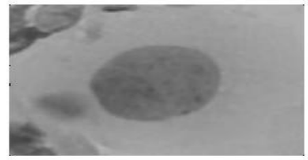
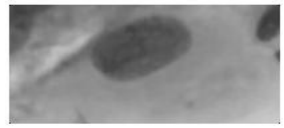
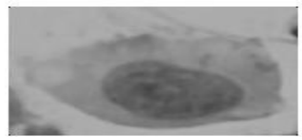
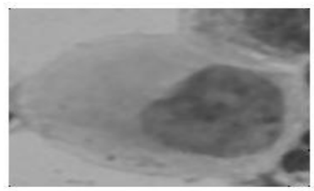
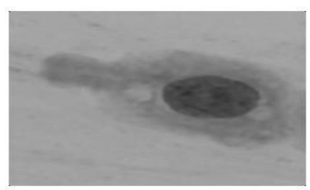
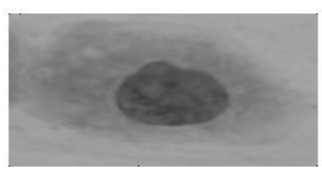
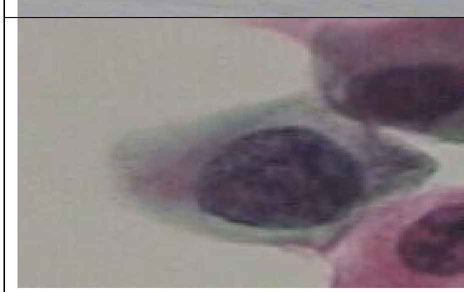
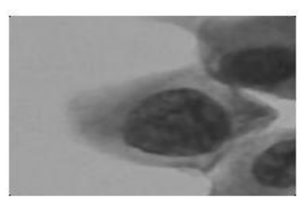
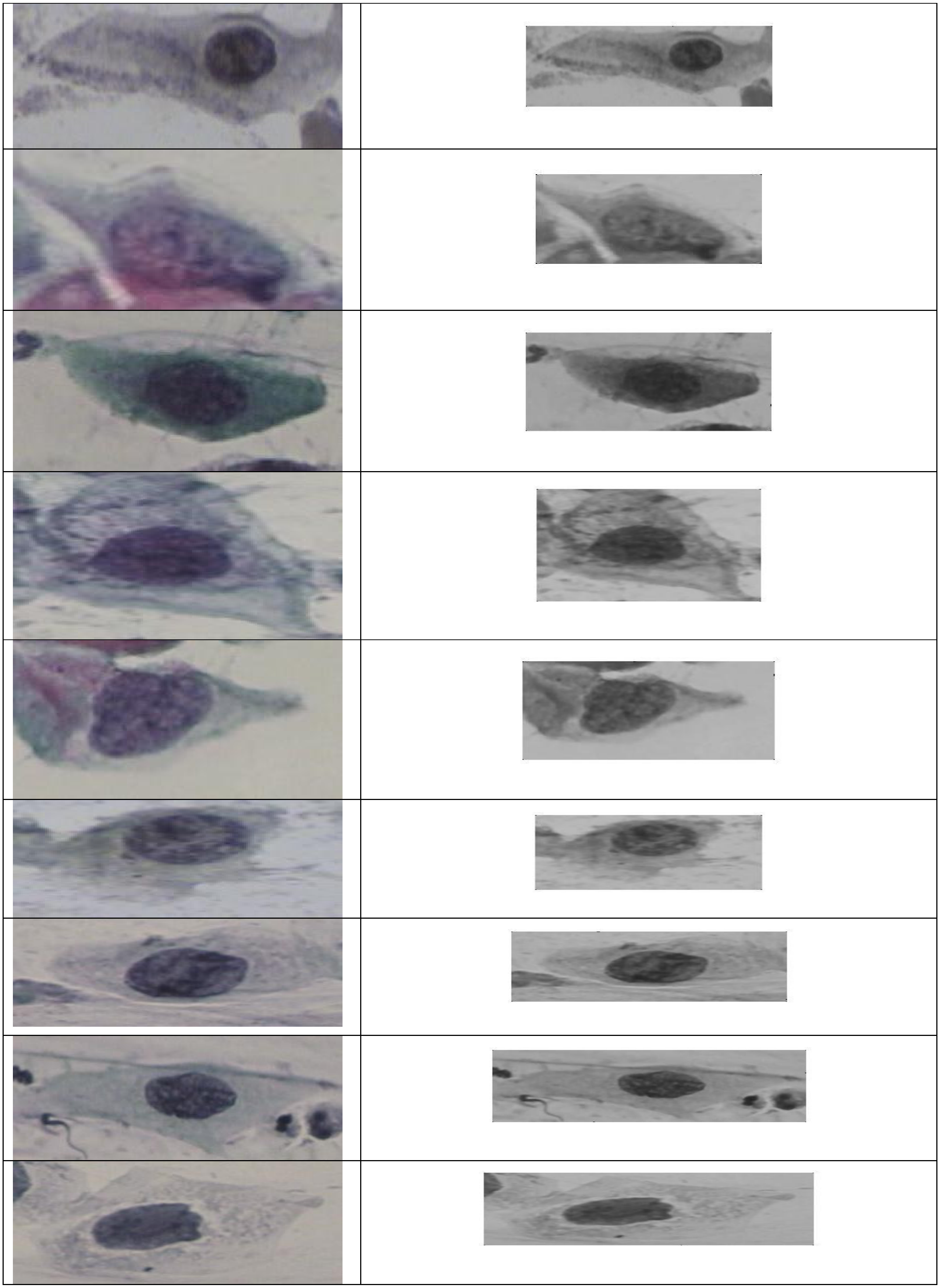
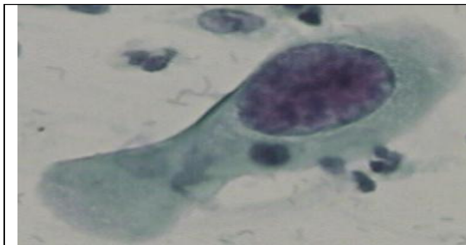
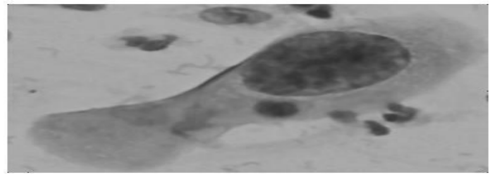
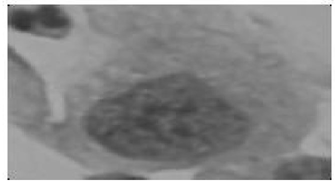
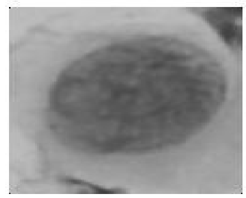
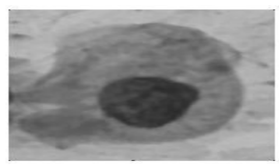
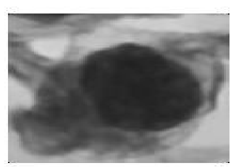
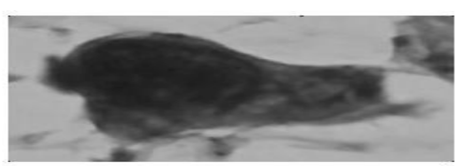


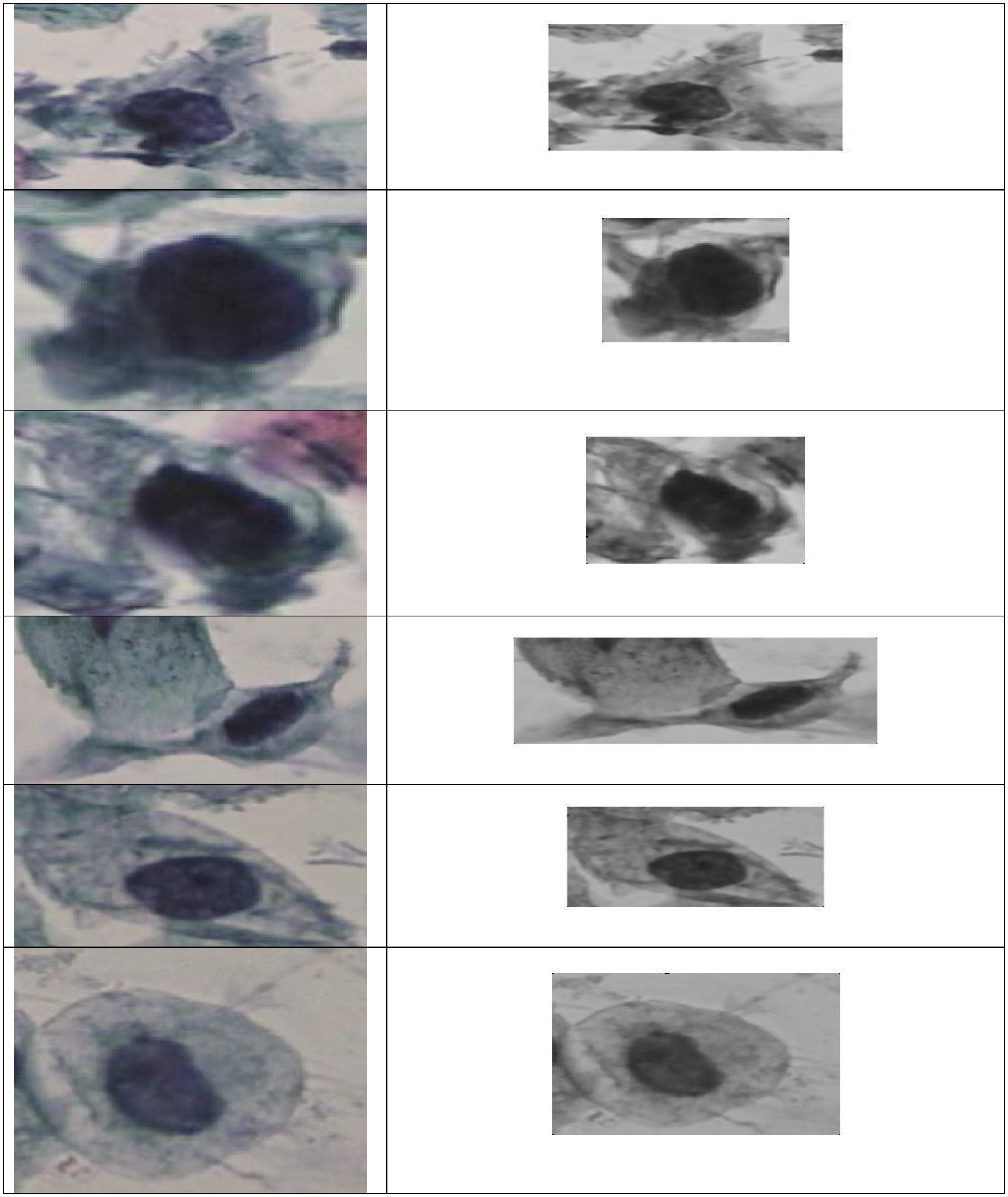
TABLE 10.2 RESULTS FROM PREPROCESSING-ABNORMAL CELL

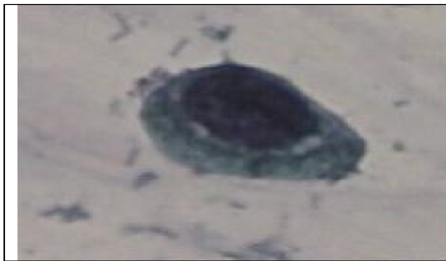
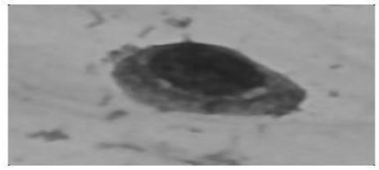
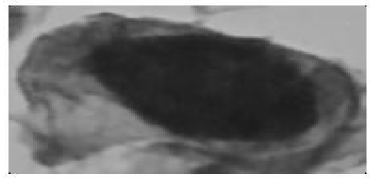
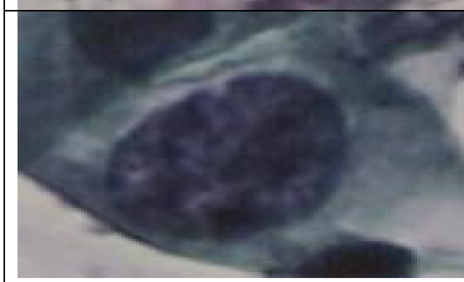
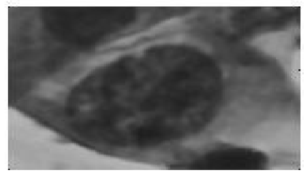
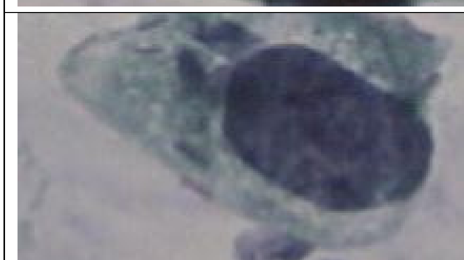
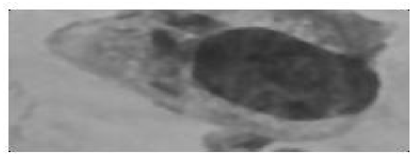
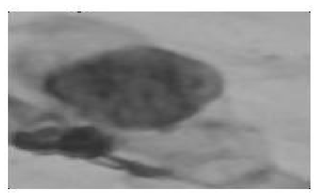
ORIGINAL IMAGE	RESULT IMAGE
	
	
	
	
	
	





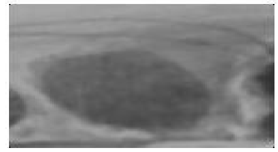
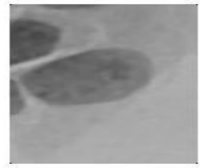
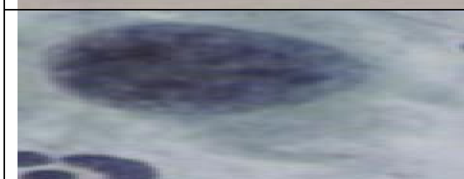
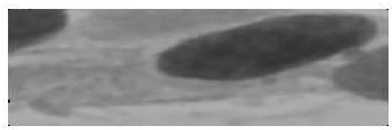
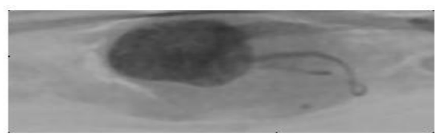
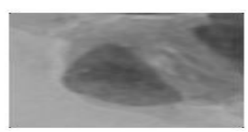
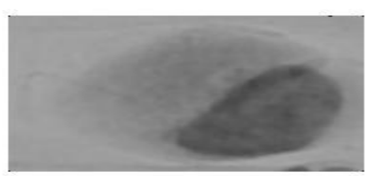
	
	
	
	
	
	
	
	

TABLE 10.3 PSNR AND MSE-NORMAL CELL

NAME	AVERAGE		WIENER		MEDIAN		GAUSSIAN		MINIMUM	
	PSNR	MSE	PSNR	MSE	PSNR	MSE	PSNR	MSE	PSNR	MSE
INTER1	37.1470	12.5424	36.2008	15.5954	51.6033	0.4495	34.0950	25.3270	25.1330	199.4264
INTER2	36.8258	13.5051	36.7774	13.6564	50.6375	0.5615	33.5751	28.5476	24.6019	225.3654
INTER3	36.5879	14.2657	36.6182	14.1664	50.2174	0.6185	33.3885	29.8007	24.3827	237.0343
INTER4	36.9953	12.9882	36.3349	15.1214	50.0290	0.6459	33.8281	26.9320	24.7677	216.9269
INTER5	36.9844	13.0209	36.5069	14.5341	49.8389	0.6748	33.8613	26.7267	24.8623	212.2532
INTER6	36.9038	13.2649	36.3792	14.9678	48.9503	0.8280	33.7432	27.4636	24.7219	219.2271
INTER7	37.0126	12.9366	36.1599	15.7430	50.9400	0.5237	33.9807	26.0023	25.0093	205.1873
INTER8	36.1541	15.7642	36.8826	13.3298	49.0328	0.8125	32.7711	34.3533	23.8322	269.0647
INTER9	36.7570	13.7209	36.0765	16.0483	49.9894	0.6518	33.4859	29.1398	24.6452	223.1321
INTER10	37.0186	12.9187	36.1312	15.8475	50.7264	0.5501	33.9436	26.2254	24.8474	212.9783
INTER11	37.0336	12.8742	36.2260	15.5052	49.8214	0.6776	34.0904	25.3537	25.0581	202.8953
INTER12	38.0571	10.1711	36.0895	16.0006	50.0982	0.6357	34.5154	22.9903	25.4496	185.4034
INTER13	37.5701	11.3781	35.6421	17.7368	51.6001	0.4499	34.4375	23.4063	25.4391	185.8538
INTER14	37.0643	12.7834	36.2962	15.2568	50.8246	0.5378	34.0239	25.7447	24.9942	205.9016
INTER15	37.3669	11.9230	36.1357	15.8310	49.8281	0.6765	34.2657	24.3505	25.2525	194.0132
INTER16	37.1137	12.6390	36.0379	16.1917	49.5335	0.7240	33.9596	26.1289	24.8812	211.3308
INTER17	37.4671	11.6513	36.1765	15.6831	51.2482	0.4878	34.6020	22.5361	25.5360	181.7528
INTER18	37.3667	11.9238	35.7421	17.3327	50.5224	0.5766	34.2308	24.5474	25.1554	198.3985
INTER19	37.0586	12.8004	35.9412	16.5564	50.2583	0.6127	33.9897	25.9485	24.9276	209.0830
INTER20	36.9437	13.1435	36.2274	15.5002	50.2491	0.6140	33.8613	26.7272	24.7906	215.7843
INTER21	37.3028	12.1005	35.9003	16.7129	50.0693	0.6400	34.2179	24.6203	25.1697	197.7480
INTER22	36.8284	13.4970	36.4297	14.7949	50.3091	0.6056	33.6221	28.2404	24.7359	218.5188
INTER23	37.4130	11.7972	35.9377	16.5694	51.1794	0.4956	34.2578	24.3952	25.2632	193.5365
INTER24	36.3160	15.1871	36.4450	14.7427	48.4849	0.9217	32.9346	33.0840	23.9180	263.8023
INTER25	37.0516	12.8209	35.9359	16.5766	48.7762	0.8619	33.7553	27.3873	24.8206	214.2971

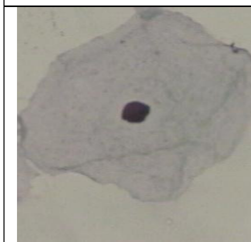
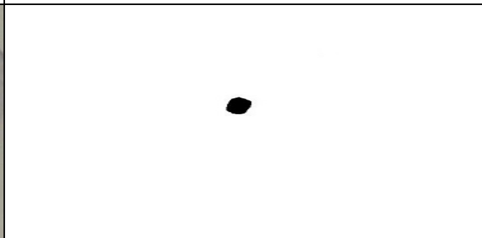
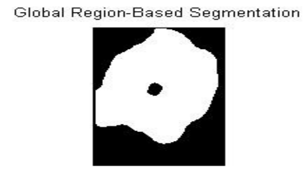
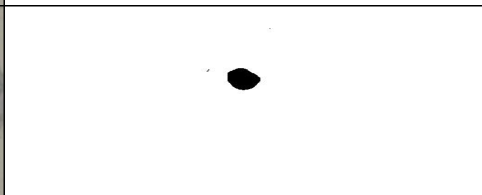
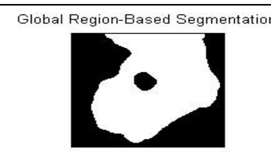
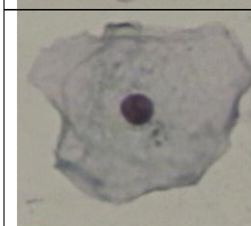
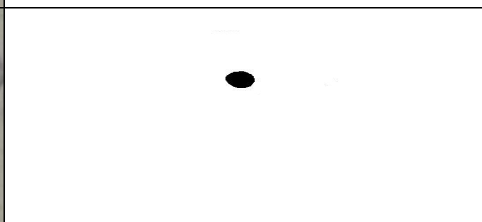
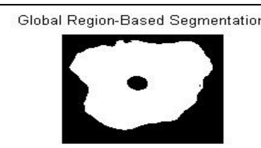
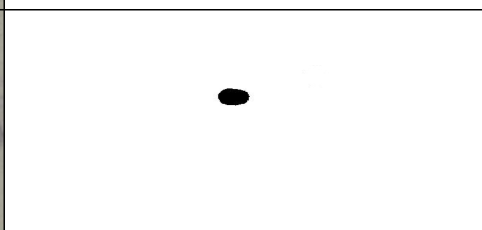
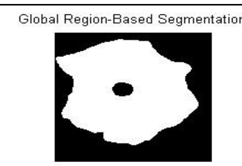
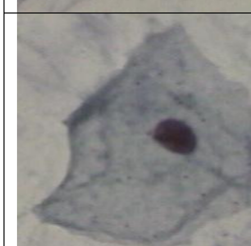
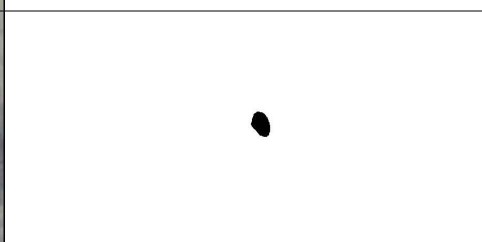
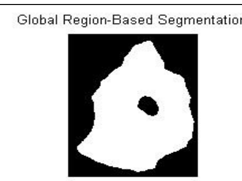
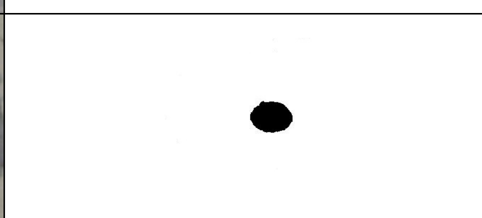
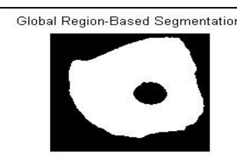
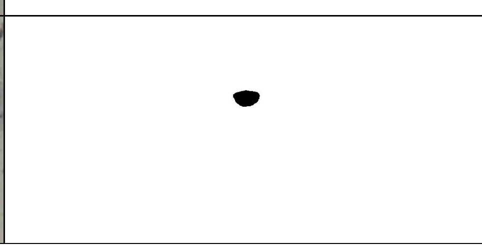
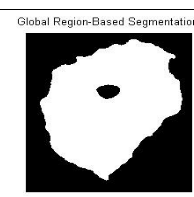
SUPER01	37.1430	12.5538	36.1954	15.6150	50.8014	0.5407	34.0934	25.3359	24.9662	207.2318
SUPER02	36.7532	13.7329	36.4143	14.8474	49.1258	0.7952	33.3882	29.8033	24.3985	236.1720
SUPER03	37.0846	12.7239	36.3377	15.1118	50.5907	0.5676	33.8822	26.5988	24.9476	208.1243
SUPER04	37.5808	11.3500	35.8870	16.7642	52.5977	0.3575	34.8542	21.2647	25.8009	170.9958
SUPER05	37.5444	11.4457	35.8778	16.7996	51.9856	0.4116	34.6302	22.3903	25.5154	182.6175
SUPER06	37.1395	12.5642	36.0874	16.0082	50.5737	0.5698	33.9683	26.0766	24.9354	208.7070
SUPER07	37.0899	12.7085	36.2348	15.4739	51.1827	0.4952	33.9248	26.3392	24.9712	206.9946
SUPER08	37.8307	10.7155	36.5054	14.5392	52.7685	0.3437	34.4224	23.4878	25.2080	196.0123
SUPER09	36.7921	13.6104	36.1056	15.9412	50.8367	0.5363	33.6213	28.2453	24.5400	228.6025
SUPER10	37.1960	12.4016	35.9586	16.4899	49.3080	0.7626	34.2198	24.6094	25.2602	193.6707
SUPER11	37.1313	12.5879	36.2651	15.3663	49.4110	0.7447	33.8950	26.5203	24.9125	209.8106
SUPER12	37.4370	11.7322	35.8346	16.9675	50.9529	0.5221	34.1688	24.8998	25.1961	196.5497
SUPER13	36.7633	13.7008	36.2695	15.3508	49.1148	0.7973	33.4872	29.1310	24.4803	231.7669
SUPER14	37.1176	12.6277	35.8033	17.0905	50.7121	0.5519	34.0026	25.8715	24.9097	209.9483
SUPER15	37.1474	12.5411	36.2961	15.2571	50.9257	0.5254	34.1389	25.0718	25.0715	202.2715
SUPER16	36.9952	12.9884	36.2898	15.2792	50.5705	0.5702	33.8650	26.7042	24.8813	211.3263
SUPER17	37.5493	11.4328	35.7973	17.1141	52.0098	0.4094	34.5454	22.8316	25.4734	184.3901
SUPER18	36.7491	13.7458	36.2807	15.3111	50.0022	0.6499	33.4724	29.2305	24.4141	235.3287
SUPER19	36.8401	13.4608	36.2898	15.2791	49.3054	0.7630	33.6807	27.8619	24.6192	224.4708
SUPER20	37.5149	11.5236	35.8394	16.9490	49.8119	0.6790	34.4562	23.3056	25.4943	183.5047
SUPER21	37.0655	12.7799	36.2209	15.5236	51.1596	0.4979	34.1118	25.2288	25.0510	203.2285
SUPER22	37.2717	12.1874	36.0499	16.1470	50.2080	0.6198	34.2693	24.3302	25.1553	198.4058
SUPER23	37.7810	10.8389	35.7443	17.3242	52.0655	0.4041	34.9060	21.0125	25.7425	173.3133
SUPER24	37.1159	12.6326	36.4257	14.8084	50.4798	0.5822	34.0028	25.8701	24.9749	206.8199
SUPER25	37.7106	11.0159	35.6657	17.6407	51.5025	0.4601	34.7952	21.5554	25.7104	174.5992

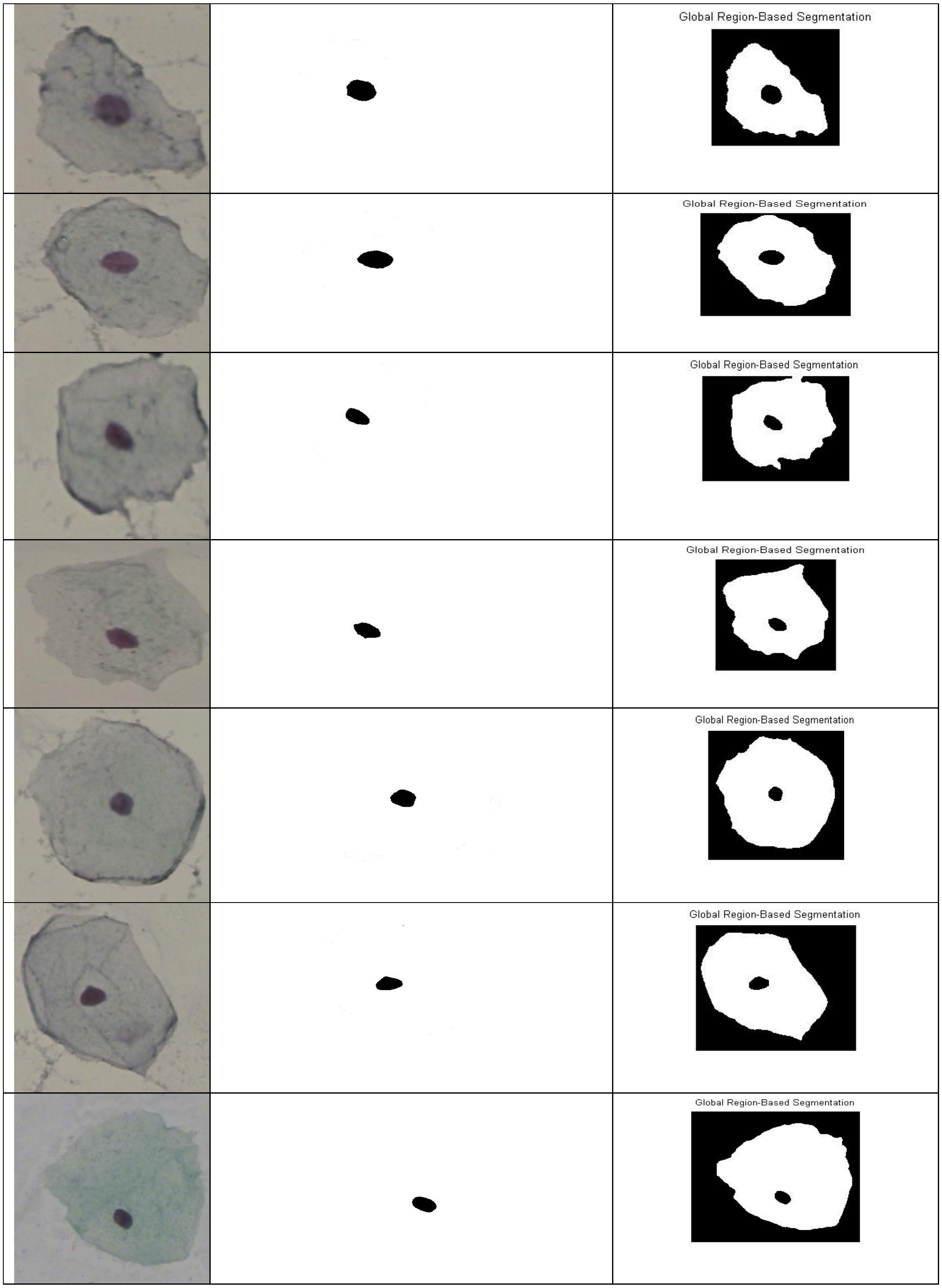
TABLE 10.4 PSNR AND MSE-ABNORMAL CELL

NAME	AVERAGE		WIENER		MEDIAN		GAUSSIAN		MINIMUM	
	PSNR	MSE	PSNR	MSE	PSNR	MSE	PSNR	MSE	PSNR	MSE
MOD01	37.0601	12.7959	36.6991	13.9051	**49.4855**	**0.7320**	34.0126	25.8116	24.9396	208.5087
MOD02	36.2164	15.5397	36.8889	13.3103	**45.6384**	**1.7752**	32.5756	35.9353	23.7621	273.4421
MOD03	36.2844	15.2984	36.5232	14.4796	**49.4363**	**0.7404**	32.7298	34.6814	23.9038	264.6697
MOD04	37.7054	11.0292	37.4573	11.6776	**47.2905**	**1.2135**	34.1233	25.1625	25.6056	178.8621
MOD05	37.3406	11.9955	36.3880	14.9375	**51.2073**	**0.4924**	34.2923	24.2021	25.2628	193.5529
MOD07	37.6071	11.2817	37.1240	12.6089	**49.6404**	**0.7064**	34.3022	24.1468	25.4448	185.6100
MOD08	36.6805	13.9645	37.0220	12.9085	**47.8739**	**1.0609**	33.4281	29.5305	24.6630	222.2185
MOD09	36.6908	13.9316	37.7584	10.8953	**49.6898**	**0.6984**	33.1675	31.3566	24.3574	238.4189
MOD10	36.2947	15.2621	37.8653	10.6303	**48.8634**	**0.8448**	32.9636	32.8637	23.9098	264.3020
MOD11	37.2338	12.2943	37.3997	11.8335	**48.4542**	**0.9282**	34.0556	25.5576	25.0112	205.0960
MOD12	36.7091	13.8730	36.8163	13.5346	**50.5693**	**0.5704**	33.6919	27.7902	24.6673	221.9967
MOD13	36.6613	14.0266	37.2542	12.2367	**49.1653**	**0.7880**	33.5014	29.0365	24.4837	231.5845
MOD14	37.3007	12.1064	37.3494	11.9712	**49.8237**	**0.6772**	34.2989	24.1653	25.2796	192.8042
MOD15	35.9819	16.4018	37.0683	12.7716	**49.3716**	**0.7515**	32.7055	34.8760	23.6576	280.1059
MOD16	36.6425	14.0873	38.0524	10.1823	**48.7361**	**0.8699**	33.4310	29.5107	24.4790	231.8351
MOD17	36.5772	14.3007	37.1134	12.6399	**47.5639**	**1.1394**	33.4135	29.6302	24.3348	239.6609
MOD18	36.3148	15.1913	37.2264	12.3150	**48.0476**	**1.0193**	32.7810	34.2754	23.9633	261.0686
MOD19	36.0841	16.0203	37.2700	12.1923	**47.6414**	**1.1193**	32.6550	35.2845	23.7402	274.8289
MOD20	35.6961	17.5174	37.4752	11.6294	**48.4007**	**0.9398**	32.4052	37.3731	23.4029	297.0198
MOD21	35.6566	17.6773	37.4212	11.7751	**47.8621**	**1.0638**	32.3526	37.8282	23.4707	292.4238
MOD23	36.4226	14.8189	36.9307	13.1830	**47.3644**	**1.1930**	33.0565	32.1684	24.1144	252.1392
MOD24	36.1920	15.6271	36.3734	14.9878	**48.5318**	**0.9118**	32.7837	34.2537	23.8677	266.8749
MOD25	36.2885	15.2839	36.6277	14.1355	**49.0974**	**0.8005**	32.9635	32.8650	24.0760	254.3763
MOD26	36.9329	13.1763	36.0907	15.9959	**50.1534**	**0.6277**	33.5434	28.7566	24.5551	227.8090
MOD27	37.1350	12.5772	37.4450	11.7107	**49.5290**	**0.7247**	33.9484	26.1961	25.1305	199.5424

SVAR01	36.0447	16.1663	37.8900	10.5701	**48.8194**	**0.8534**	32.9849	32.7029	24.0109	258.2189
SVAR02	36.2186	15.5319	37.2096	12.3630	**47.7125**	**1.1011**	32.7719	34.3472	23.8739	266.4981
SVAR03	36.1139	15.9107	37.2148	12.3480	**49.1023**	**0.7996**	32.5688	35.9919	23.7573	273.7496
SVAR04	36.1853	15.6513	38.2363	9.7601	**47.7335**	**1.0958**	32.2574	38.6671	23.7200	276.1073
SVAR05	36.1779	15.6779	36.7640	13.6987	**48.5037**	**0.9177**	32.6584	35.2564	23.5344	288.1634
SVAR06	36.0456	16.1629	36.8188	13.5268	**48.1896**	**0.9866**	32.2888	38.3882	23.5009	290.3968
SVAR07	36.3777	14.9731	37.9133	10.5135	**48.3447**	**0.9519**	32.5034	36.5378	23.8011	271.0029
SVAR08	36.0998	15.9626	37.3690	11.9174	**46.9211**	**1.3212**	32.2798	38.4685	23.8844	265.8494
SVAR09	36.1164	15.9015	36.6969	13.9120	**48.9656**	**0.8251**	32.4253	37.2009	23.6851	278.3386
SVAR10	37.1593	12.5069	37.2870	12.1445	**48.0311**	**1.0232**	33.3797	29.8612	24.8566	212.5307
SVAR11	36.8056	13.5681	37.0988	12.6823	**48.2725**	**0.9679**	33.3802	29.8583	24.4976	230.8431
SVAR12	36.5944	14.2443	36.9719	13.0583	**49.6452**	**0.7056**	33.3450	30.1012	24.3341	239.7009
SVAR13	36.2765	15.3261	37.0521	12.8196	**48.1101**	**1.0048**	32.7547	34.4832	23.9993	258.9112
SVAR14	38.2155	9.8070	37.9478	10.4303	**48.3837**	**0.9434**	34.2058	24.6887	25.9058	166.9164
SVAR15	36.2738	15.3355	37.0141	12.9321	**48.3611**	**0.9484**	32.8348	33.8533	24.1626	249.3586
SVAR16	36.4177	14.8357	37.4121	11.7996	**47.9570**	**1.0408**	33.1057	31.8063	24.2711	243.2055
SVAR17	36.4823	14.6168	37.8563	10.6524	**48.5086**	**0.9167**	33.0425	32.2727	24.3795	237.2112
SVAR18	37.3127	12.0728	38.2206	9.7953	**48.8420**	**0.8490**	34.3456	23.9068	25.4406	185.7878
SVAR19	36.8748	13.3536	38.3084	9.5993	**48.9401**	**0.8300**	33.4079	29.6684	24.6077	225.0645
SVAR20	36.0969	15.9731	37.9492	10.4270	**47.5226**	**1.1503**	32.6737	35.1323	23.8595	267.3795
SVAR21	36.7845	13.6342	37.7492	10.9183	**47.4420**	**1.1719**	33.1687	31.3479	24.5072	230.3338
SVAR22	36.5374	14.4326	36.9793	13.0362	**48.2583**	**0.9711**	33.2339	30.8807	24.4988	230.7799
SVAR23	36.1694	15.7088	37.4672	11.6508	**48.1747**	**0.9899**	33.1169	31.7244	24.2264	245.7184
SVAR24	37.3247	12.0397	38.1926	9.8586	**49.2555**	**0.7719**	34.1329	25.1069	25.1113	200.4251
SVAR25	36.5080	14.5304	37.3779	11.8931	**49.2544**	**0.7720**	33.7106	27.6705	24.6570	222.5270

TABLE 10.5 RESULTS FROM SEGMENTATION-NORMAL CELL

IMAGE	NUCLEUS	CYTOPLASM
		
		
		
		
		
		
		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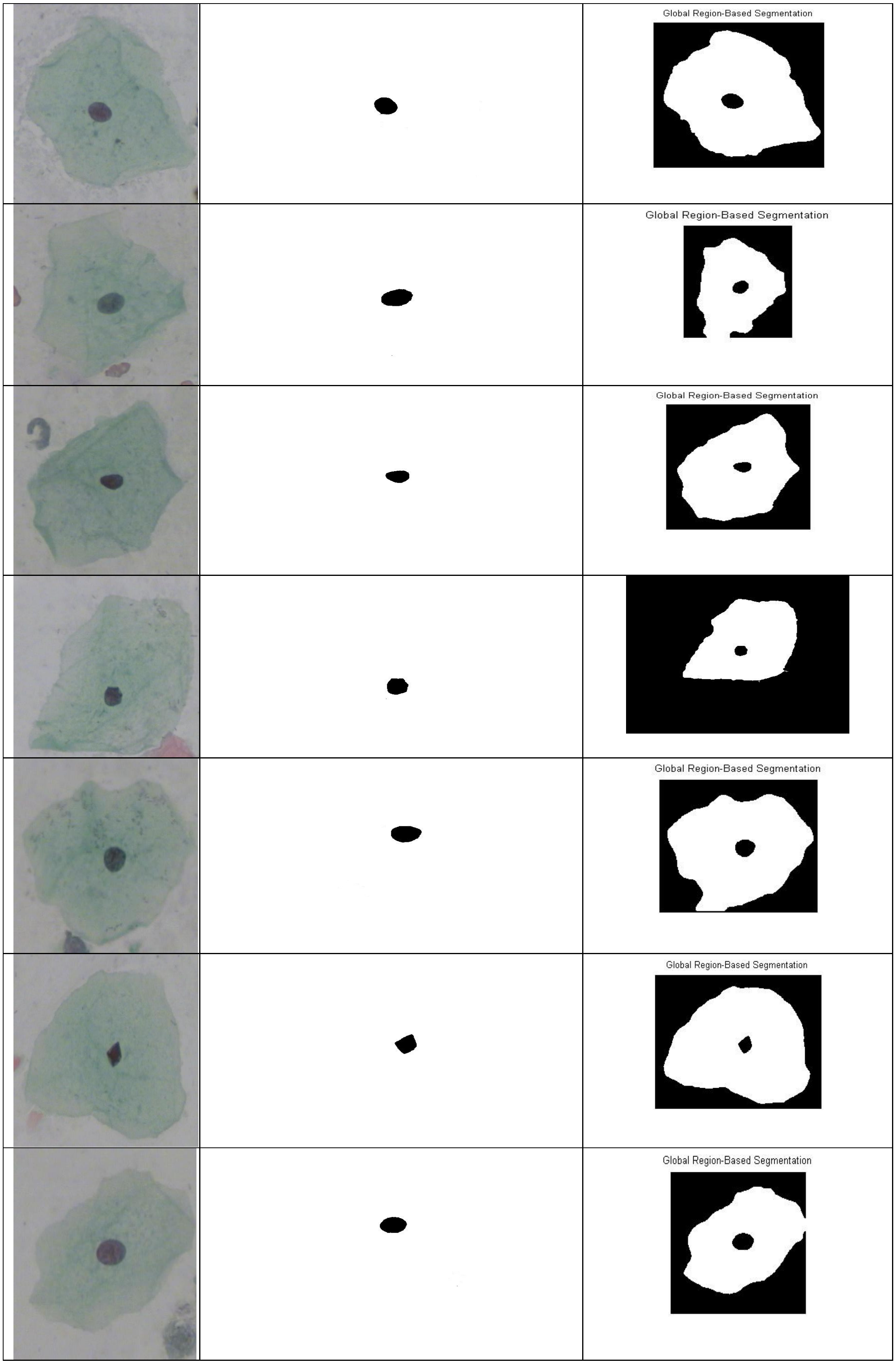
Global Region-Based Segmentation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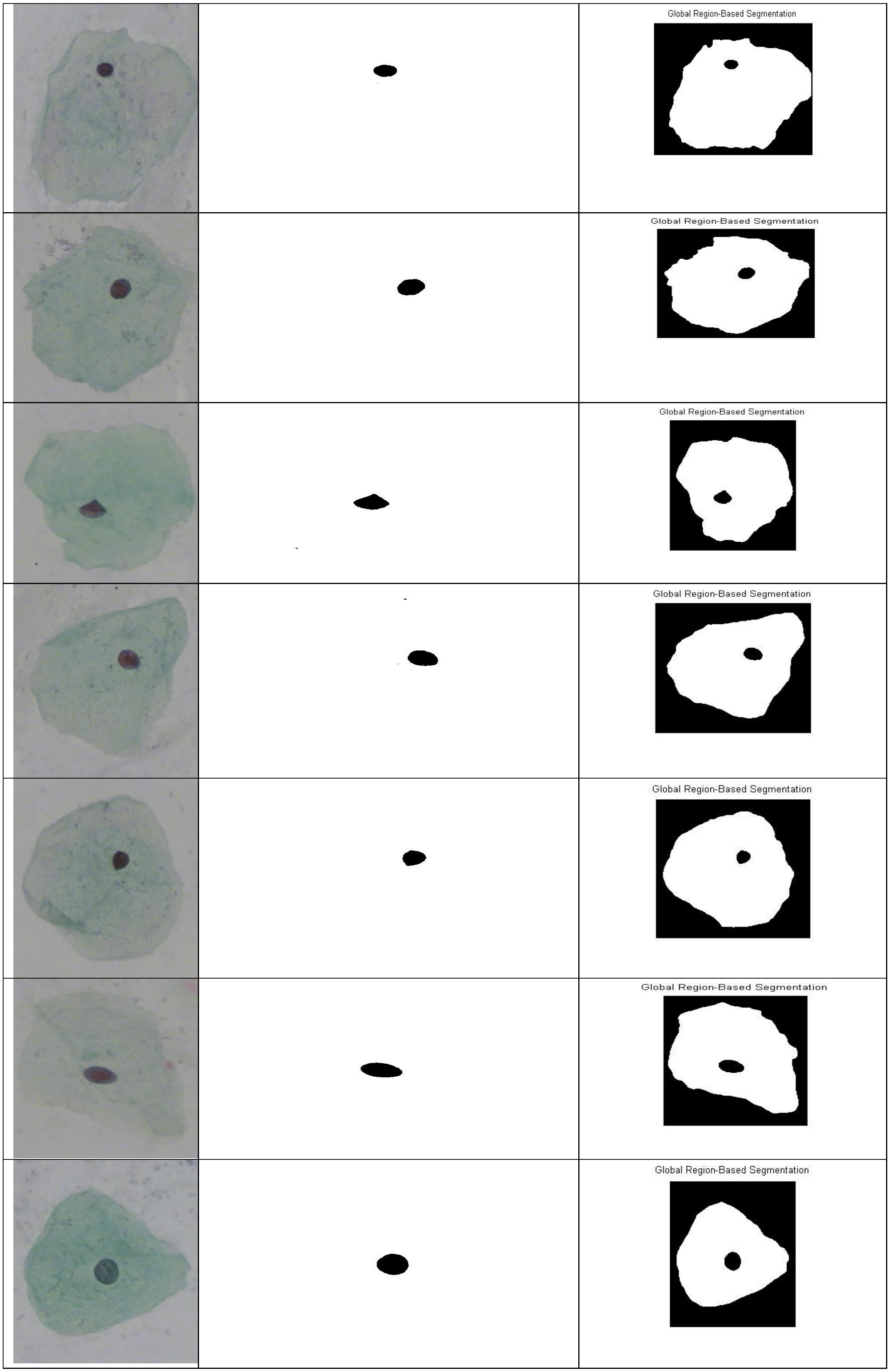
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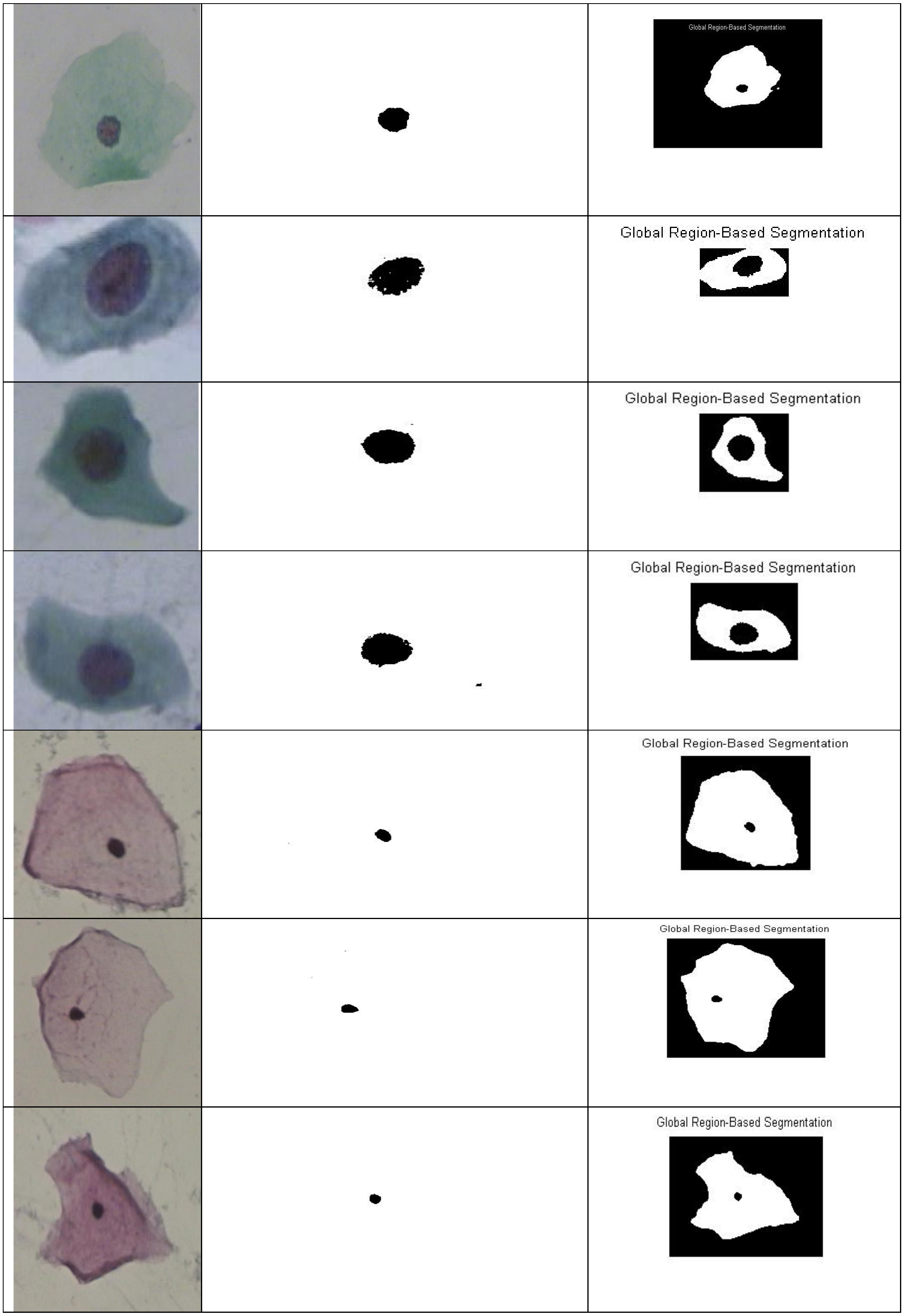
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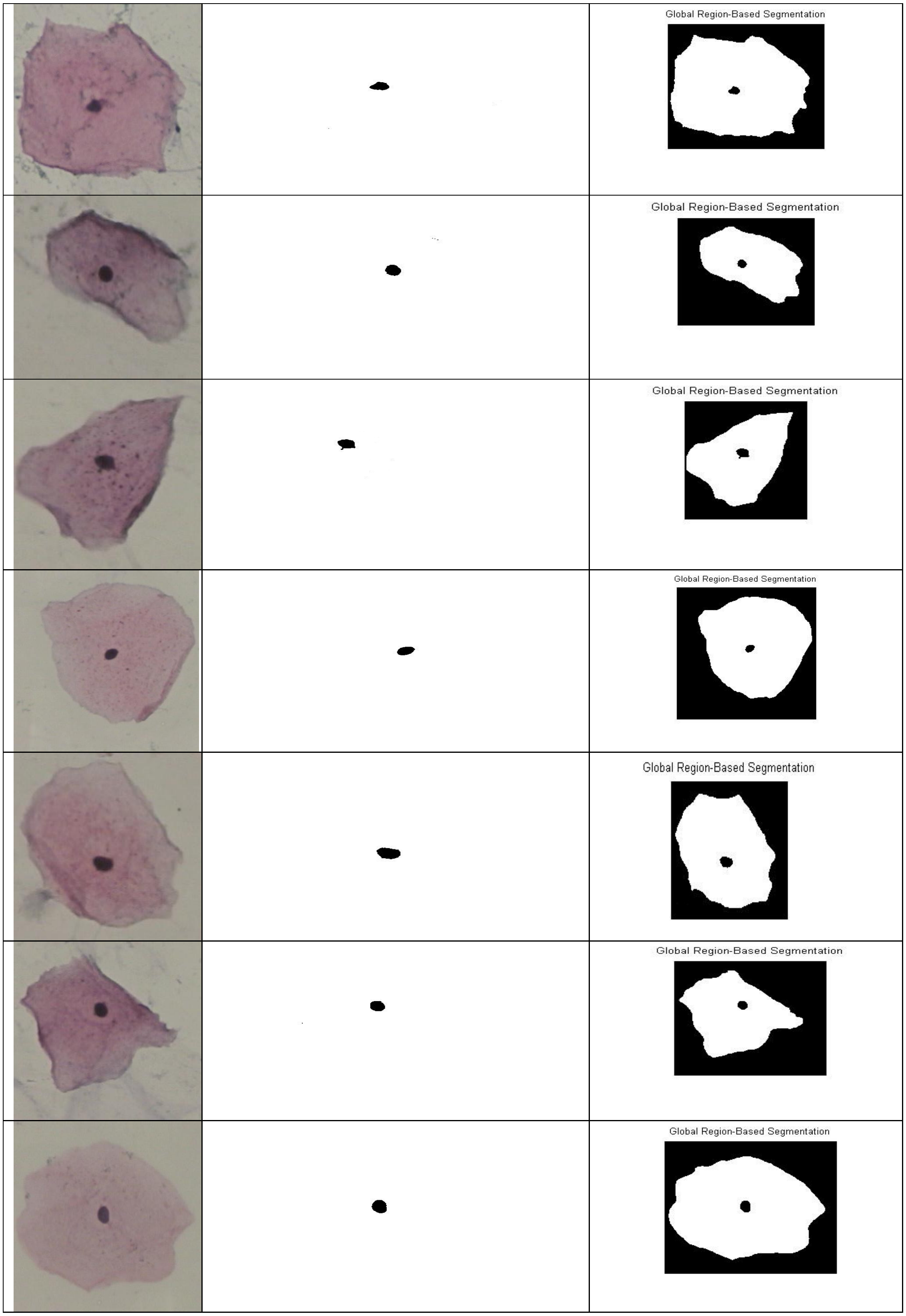

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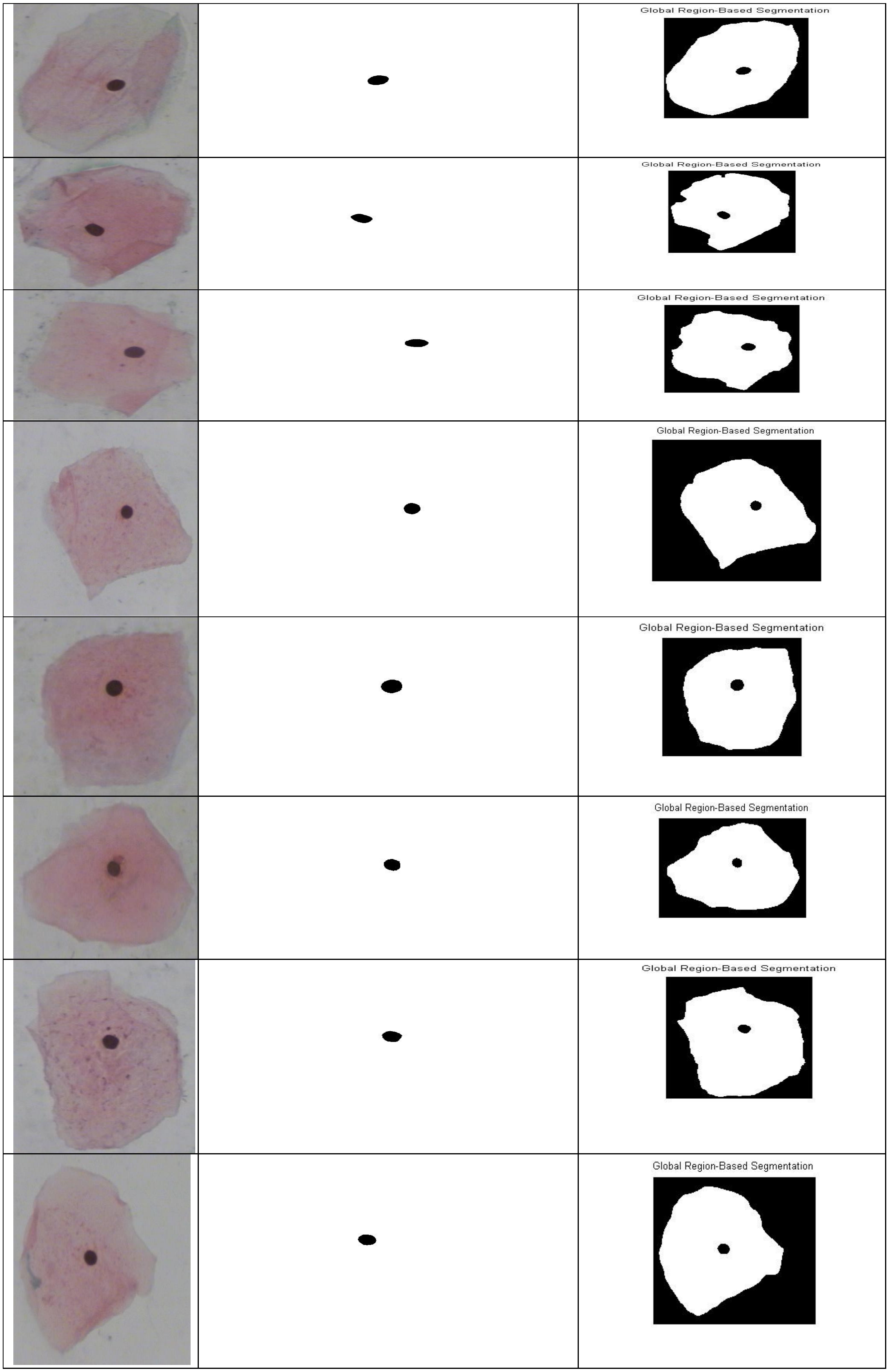
Global Region-Based Segmentation
Global Region-Based Segmentation


Global Region-Based Segmentation
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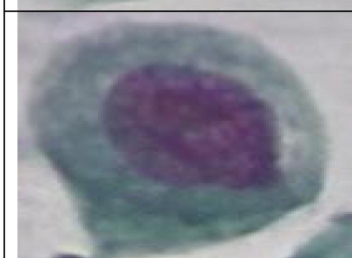
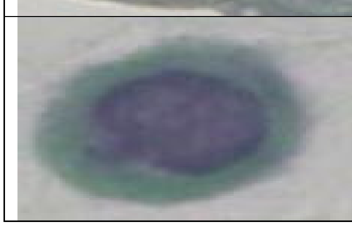
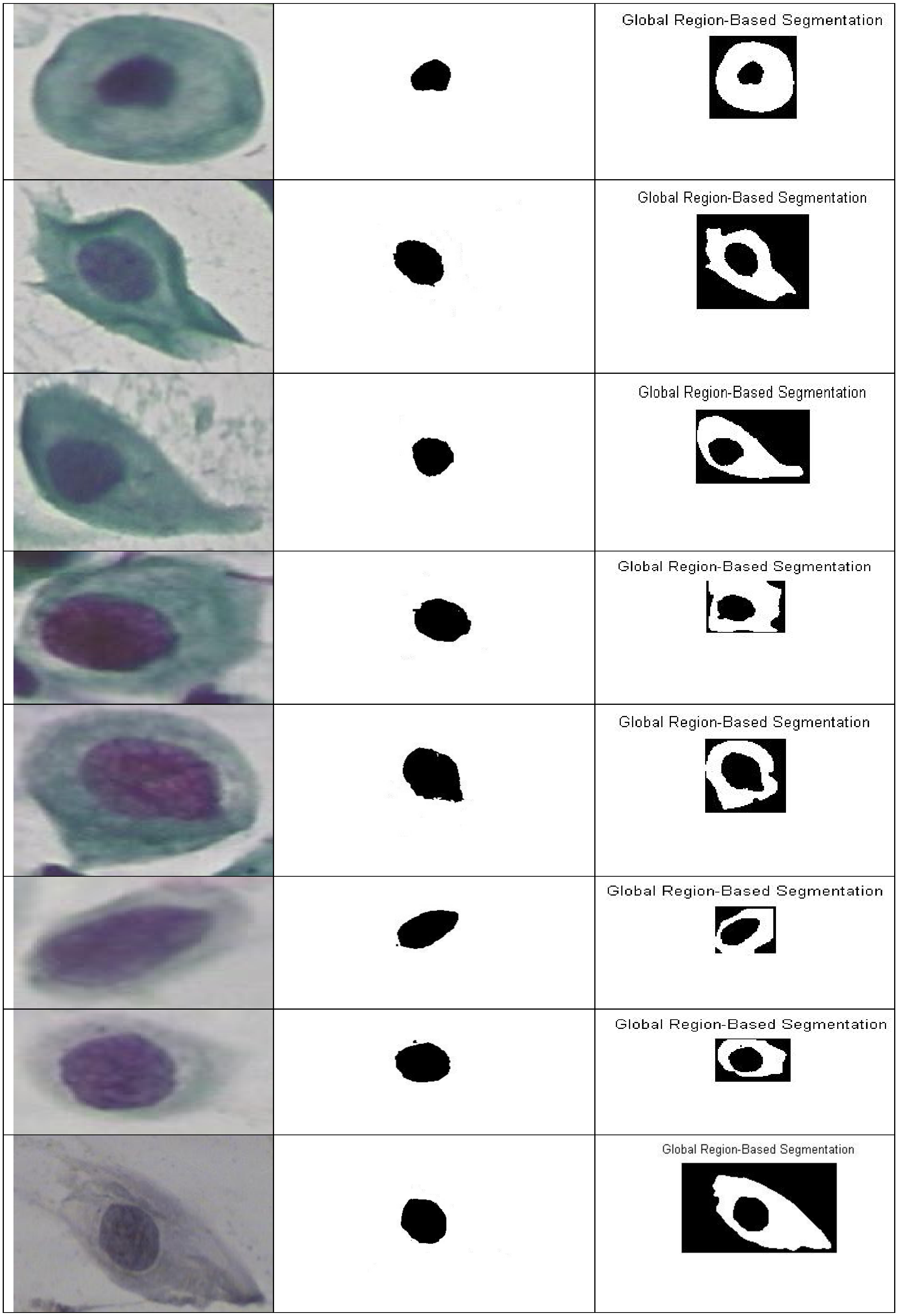
Global Region-Based Segmentation
Global Region-Based Segmentation
Global Region-Based Segmentation
Global Region-Based Segmentation
Global Region-Based Segmentation

TABLE 10.6 RESULTS FROM SEGMENTATION-ABNORMAL CELL

IMAGE	NUCLEUS	CYTOPLASM
		
		
		
		
		
		
		


Global Region-Based Segmentation
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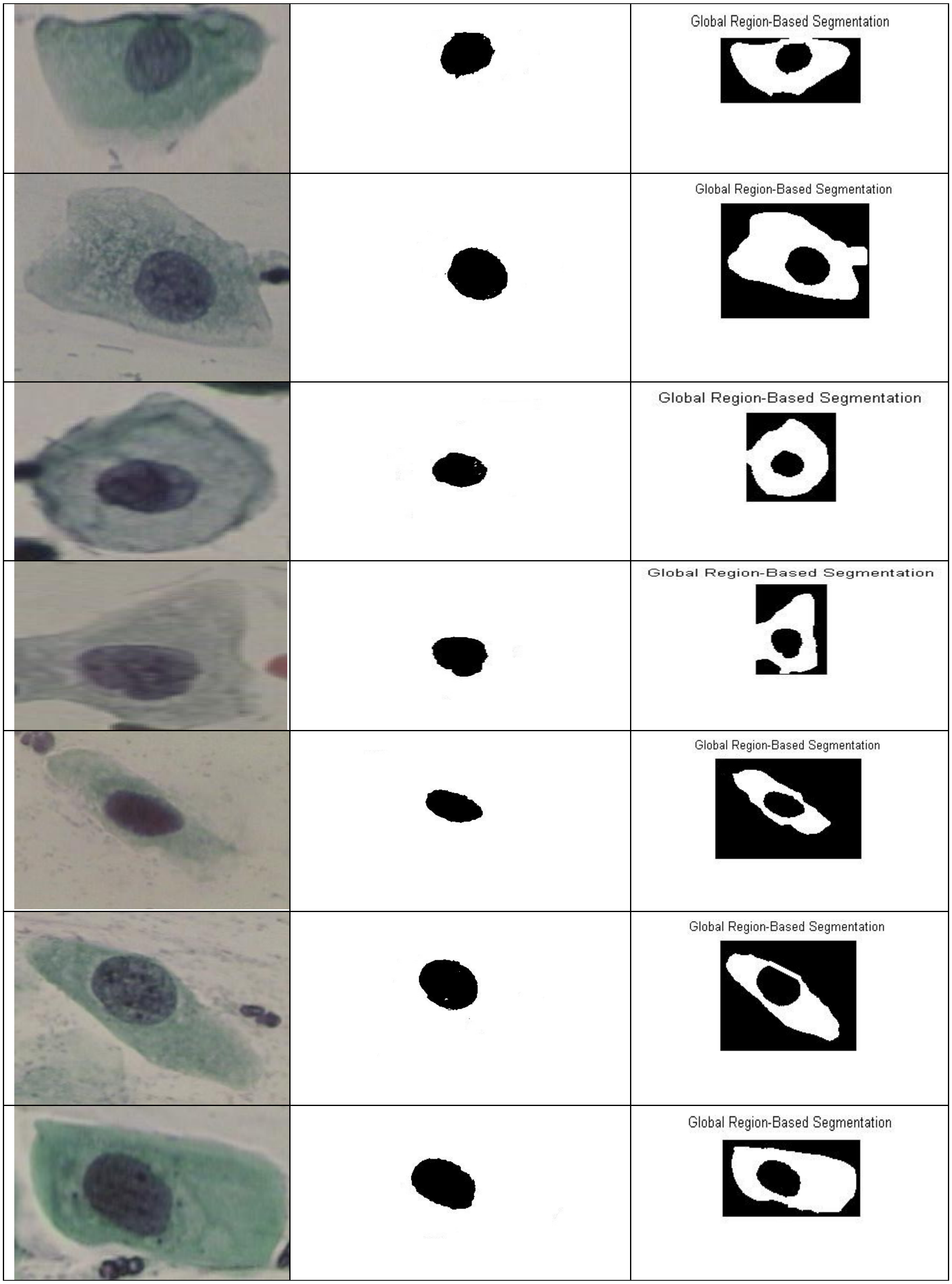
Global Region-Based Segmentation
Global Region-Based Segmentation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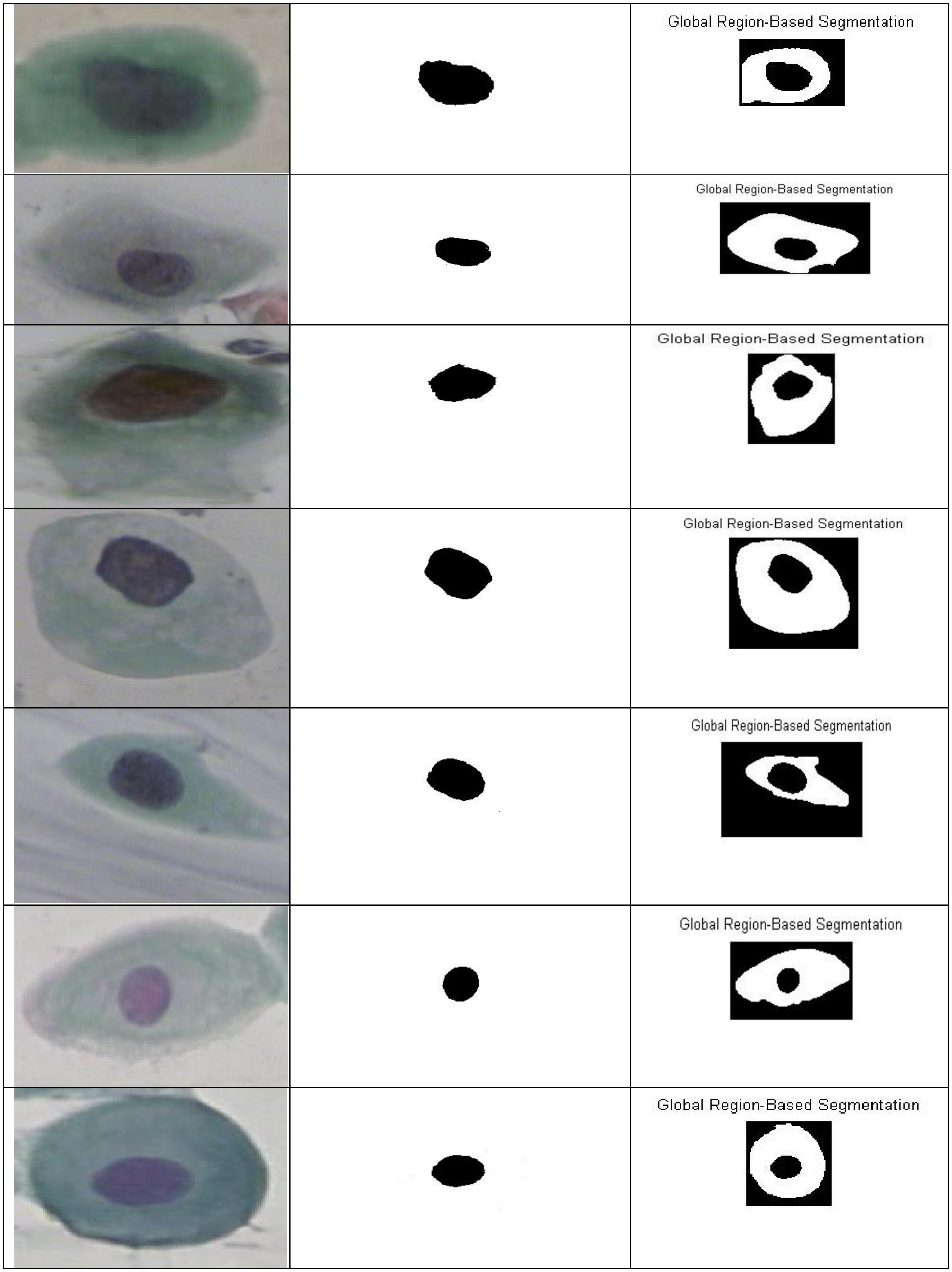
Global Region-Based Segmentation
Global Region-Based Segmentation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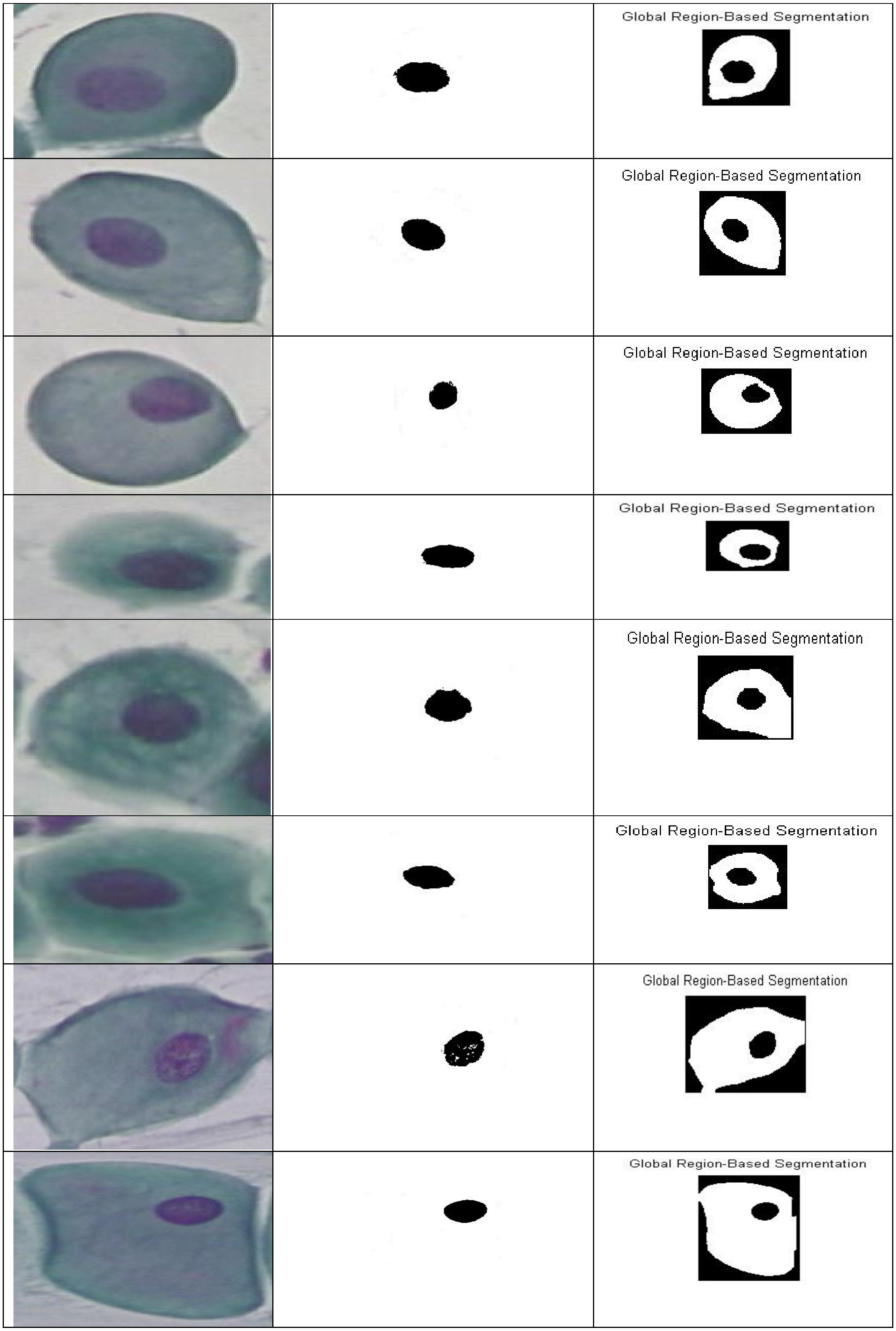
Global Region-Based Segmentation
Global Region-Based Segmentation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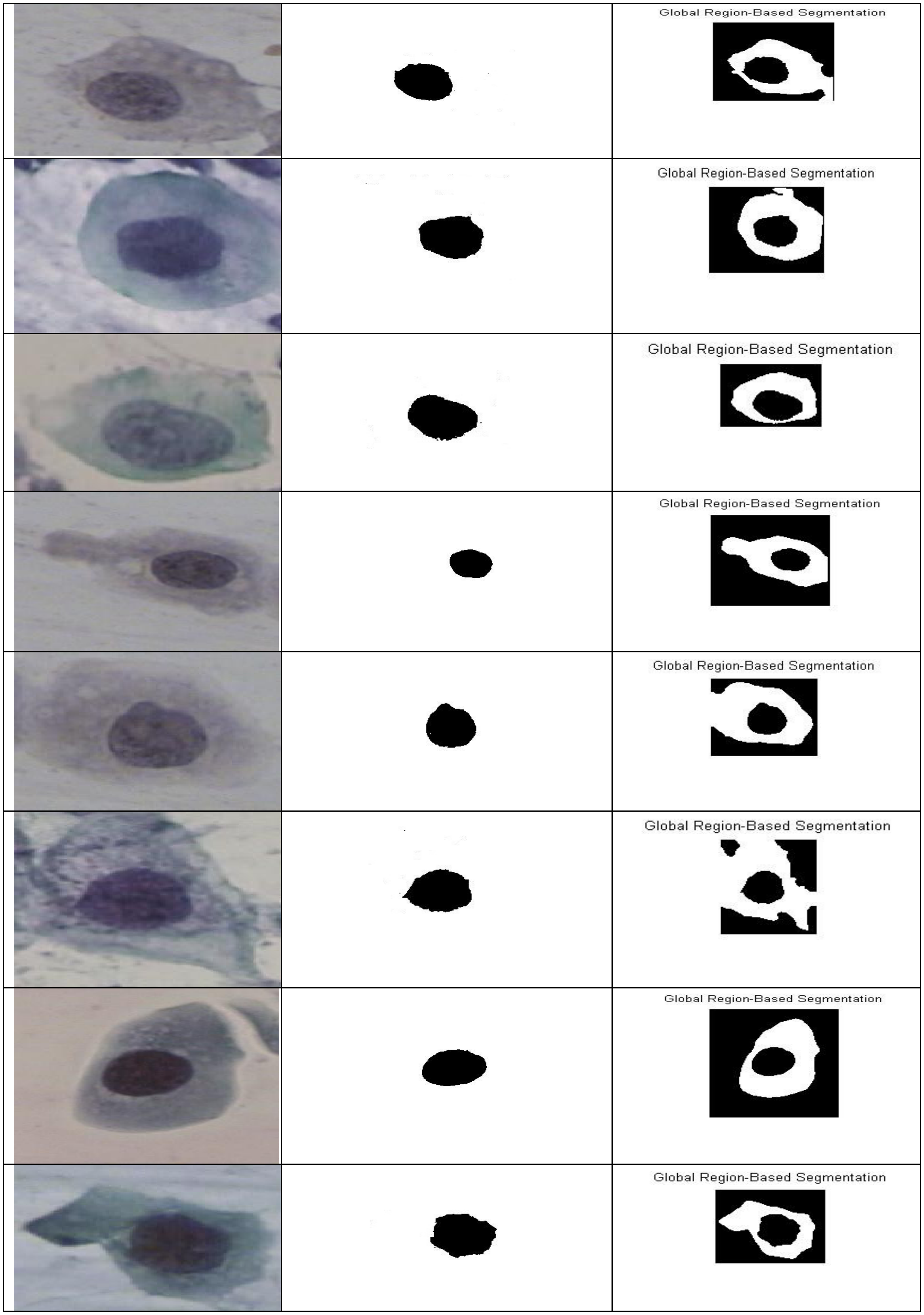
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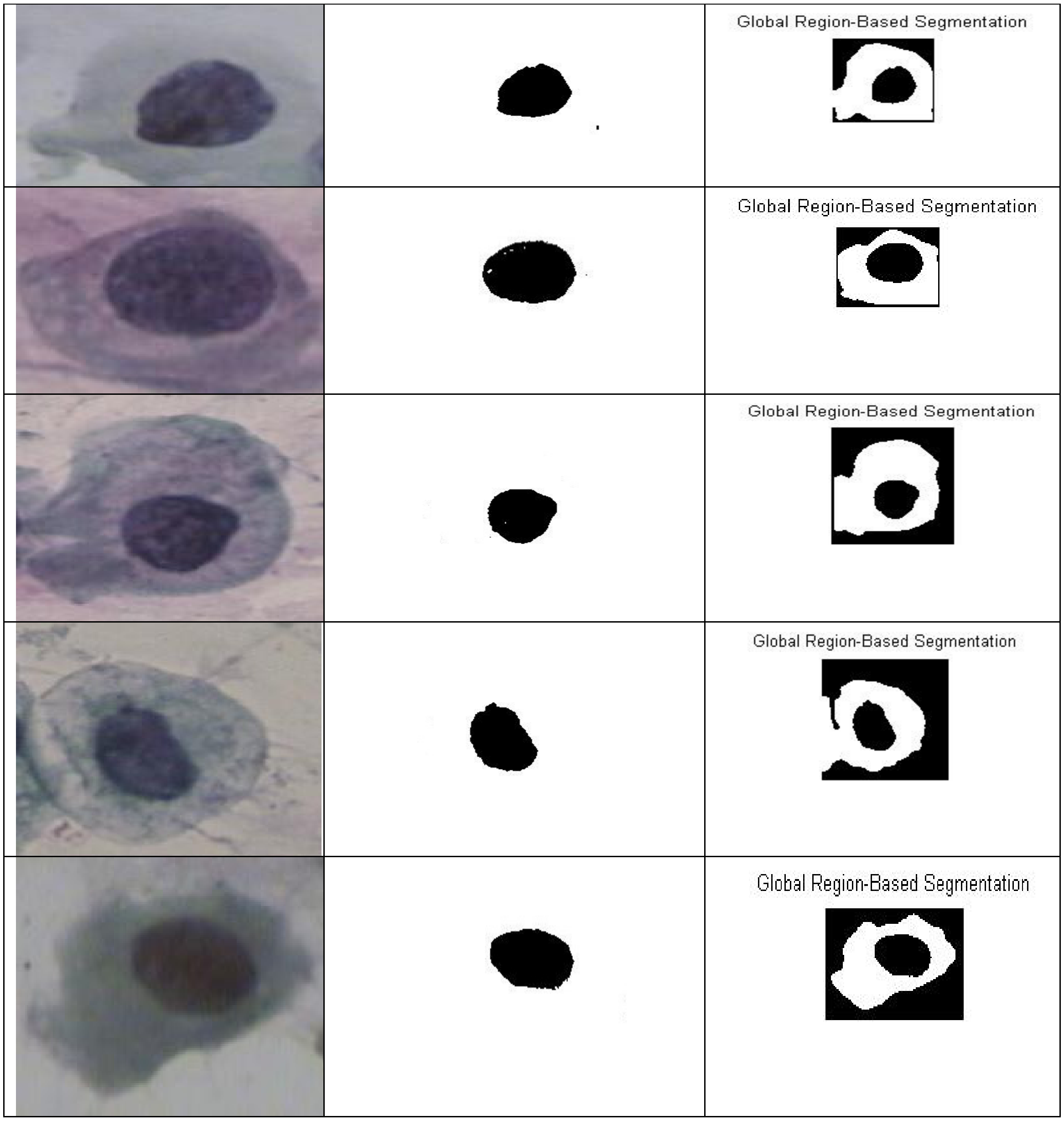
Global Region-Based Segmentation


Global Region-Based Segmentation
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Global Region-Based Segmentation

10.8 RESULTS FOR TRAINING DATA-CLASSIFICATION-NORMAL CELL

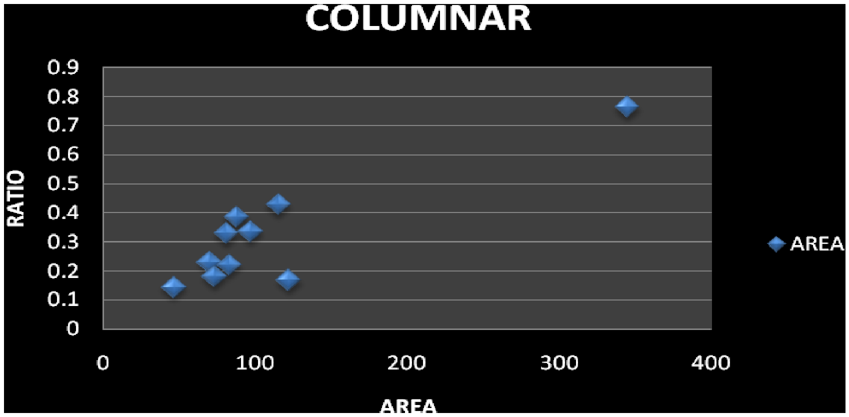


FIG.10.8.1 COLUMNAR

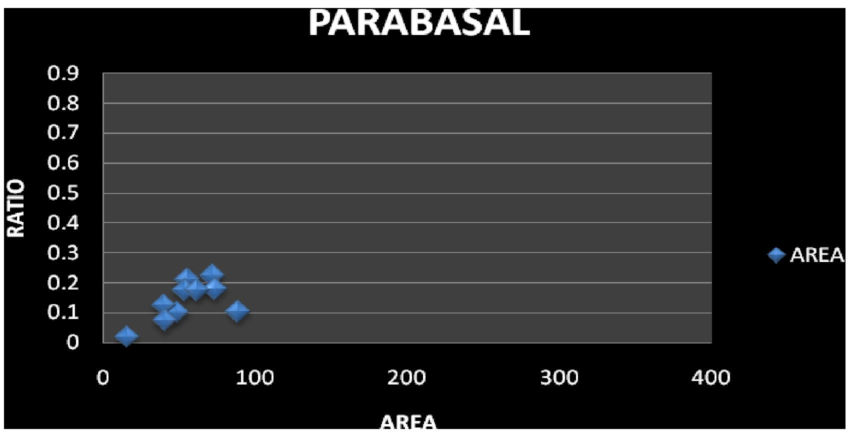


FIG.10.8.2 PARABASAL

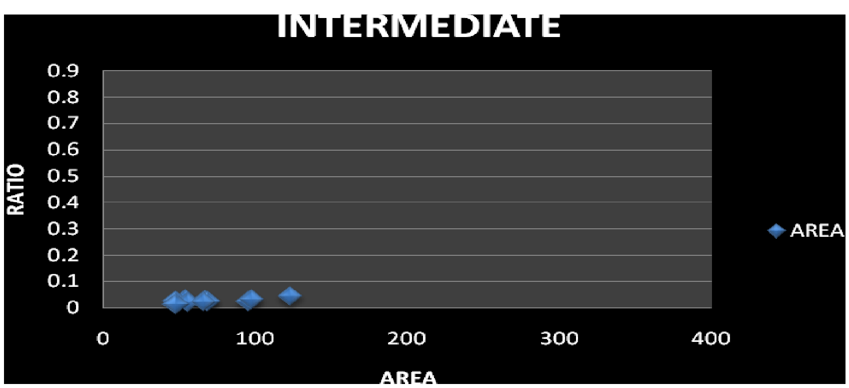


FIG.10.8.3 INTERMEDIATE

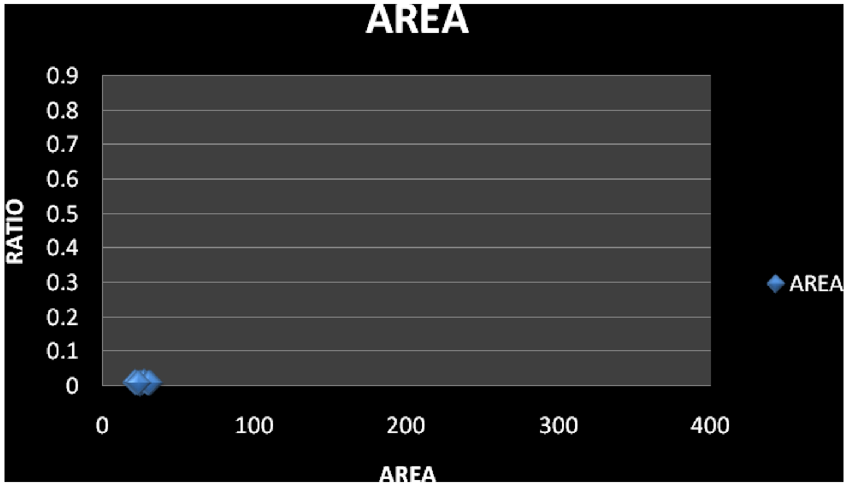


FIG.10.8.4 SUPERFICIAL

10.9 RESULTS FOR TRAINING DATA-CLASSIFICATION-NORMAL CELL

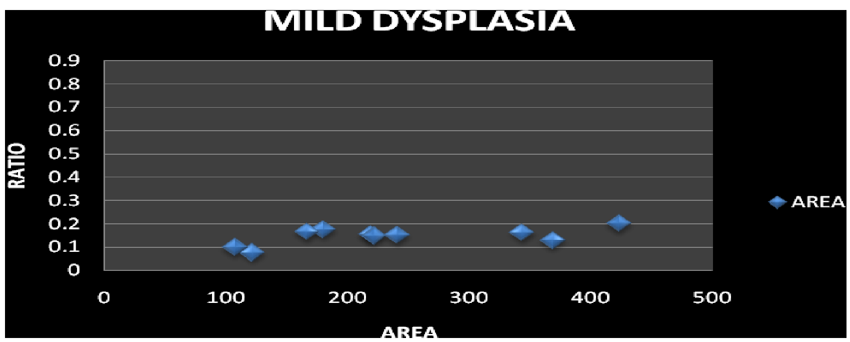


FIG.10.9.1 MILD DYSPLASIA

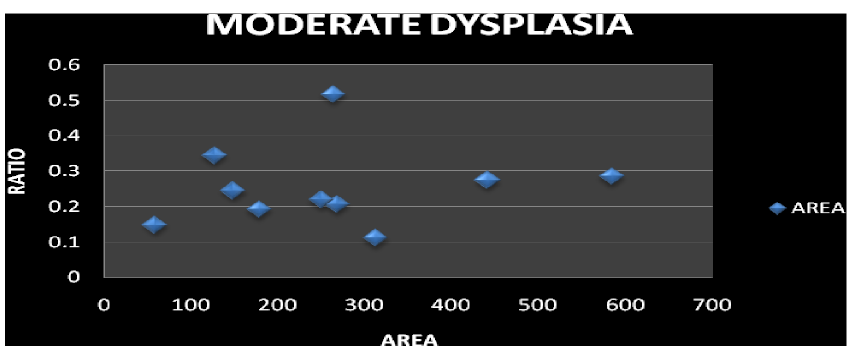


FIG.10.9.2 MODERATE DYSPLAIA

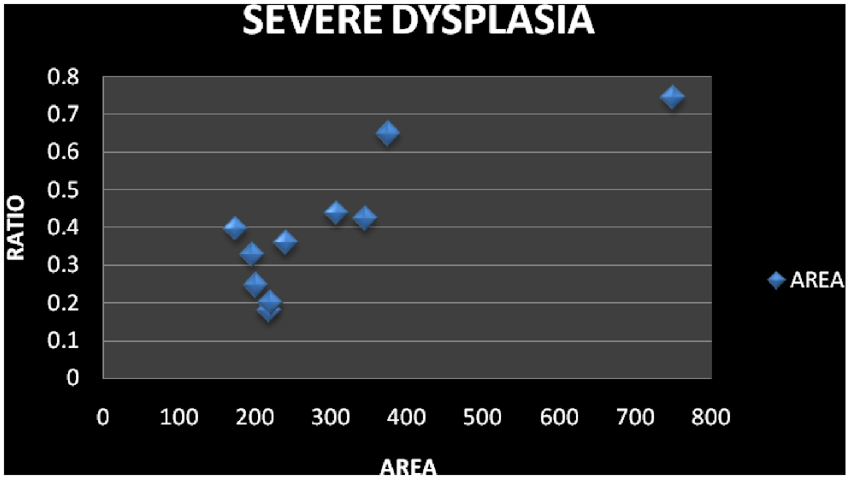


FIG.10.9.3 SEVERE DYSPLASIA

10.10 NCOL VS CCOL-NORMAL CELL

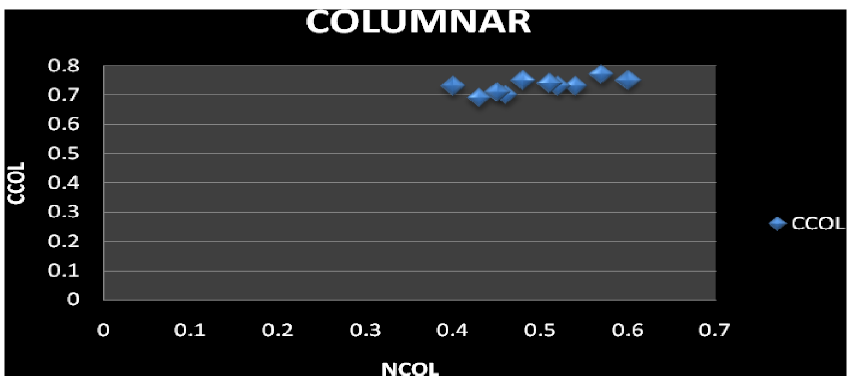


FIG.10.10.1 COLUMANR

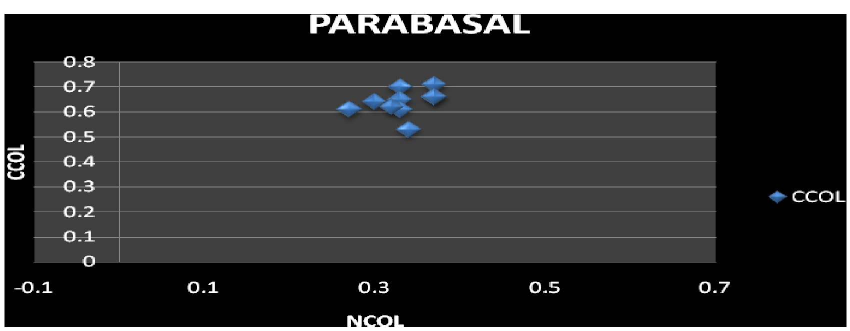


FIG.10.10.2 PARABASAL

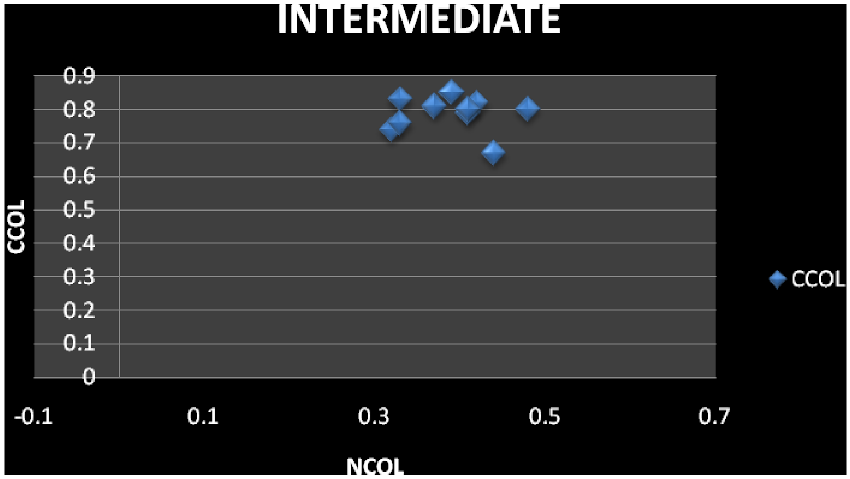


FIG.10.10.3 INTERMEDIATE

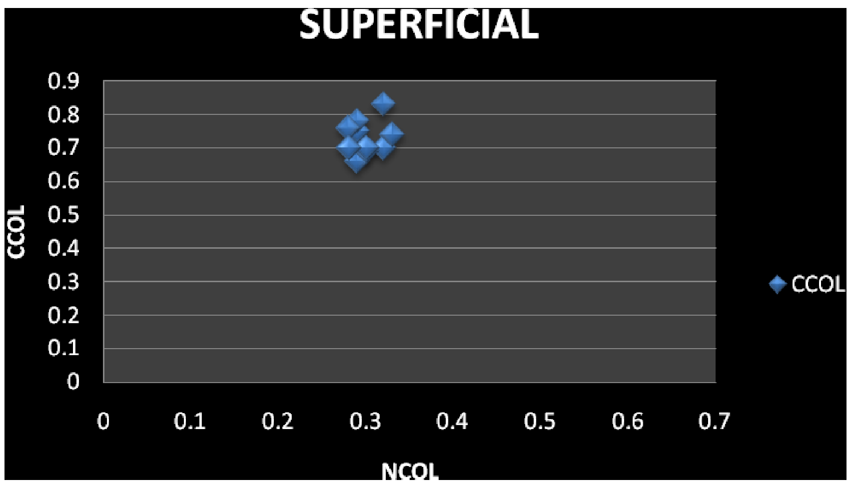


FIG.10.10.4 SUPERFICIAL

10.11 ANFIS RESULTS

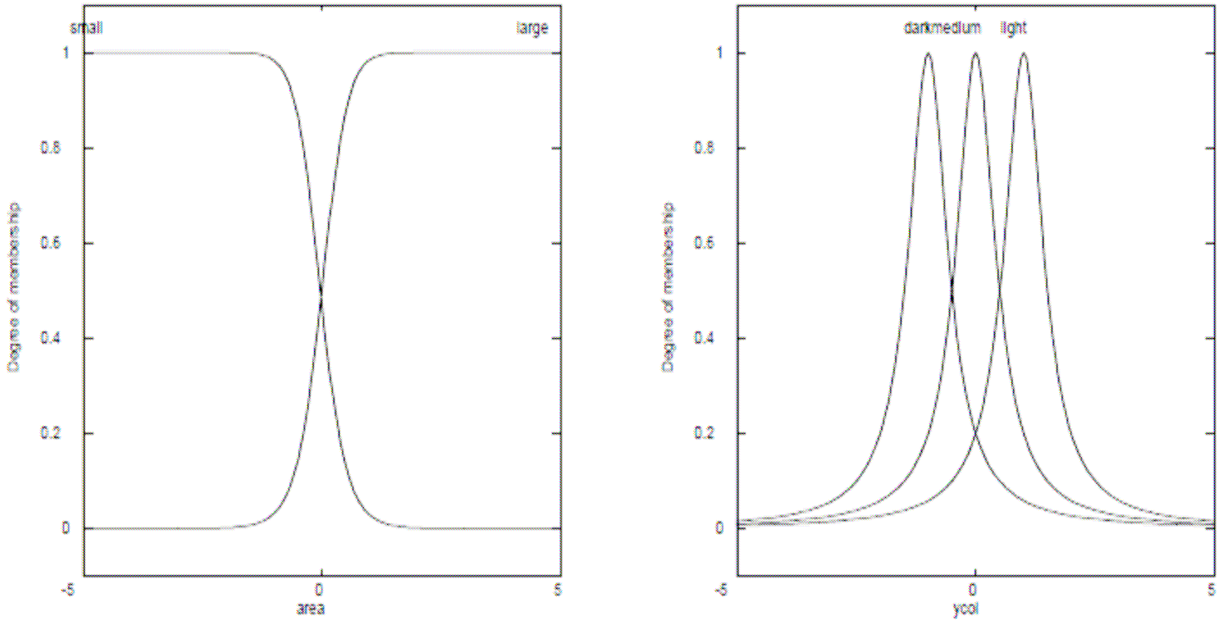


FIG. 10.11.1 MEMBERSHIP FUNCTION FOR BEFORE TRAINING

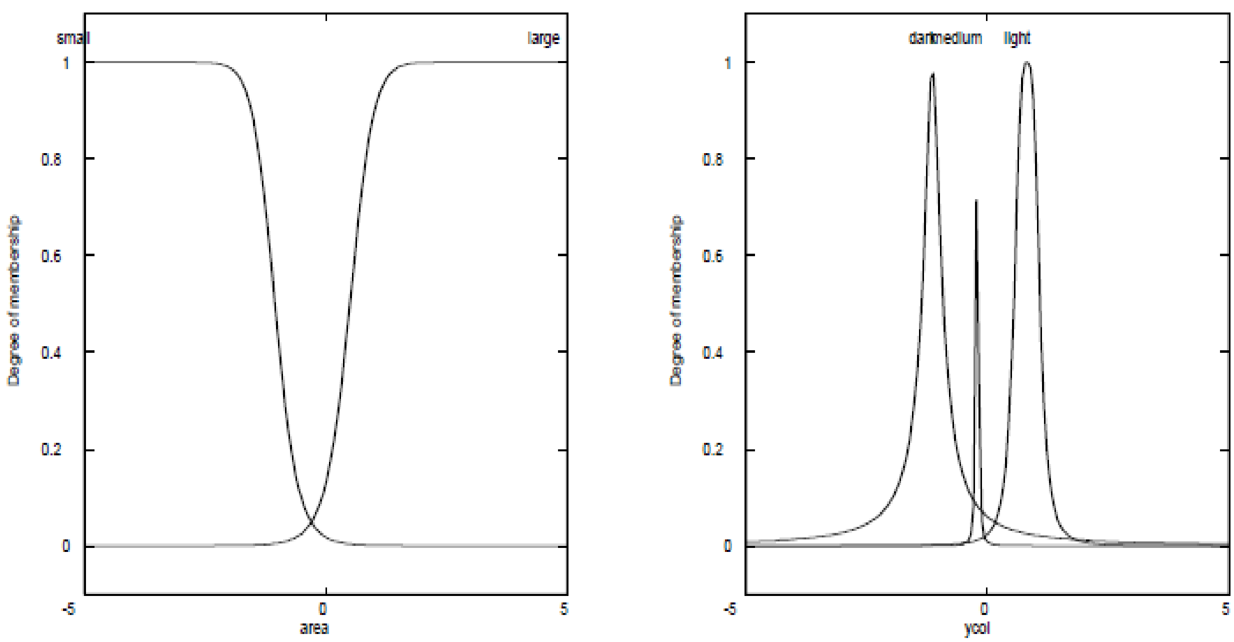


FIG.10.11.2 MEMBERSHIP FUNCTION FOR AFTER TRAINING 200 EPOCHS

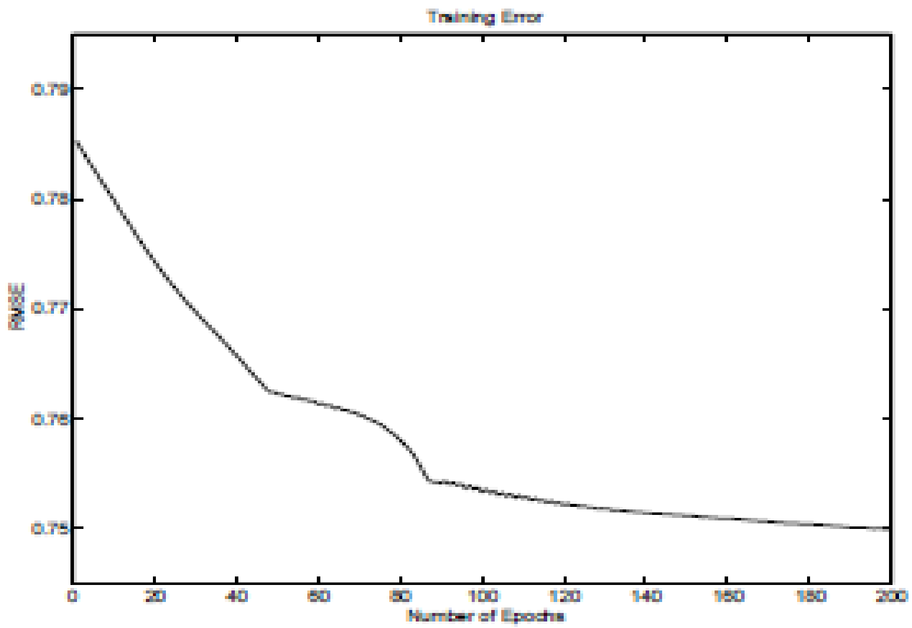


FIG. 10.11.3 ANFIS TRAINING ERROR

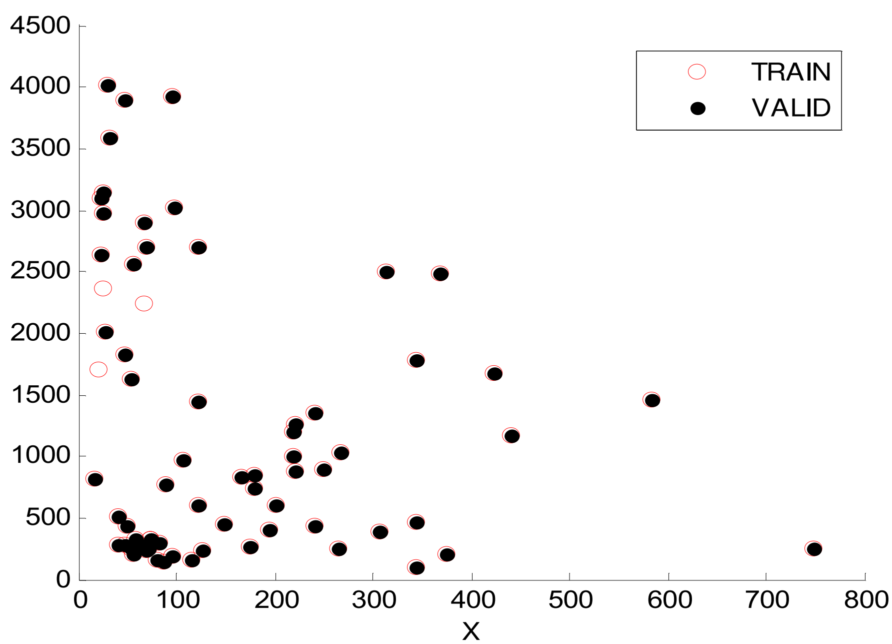


FIG. 10.11.4 RESULT FROM FCM CLUSTERING

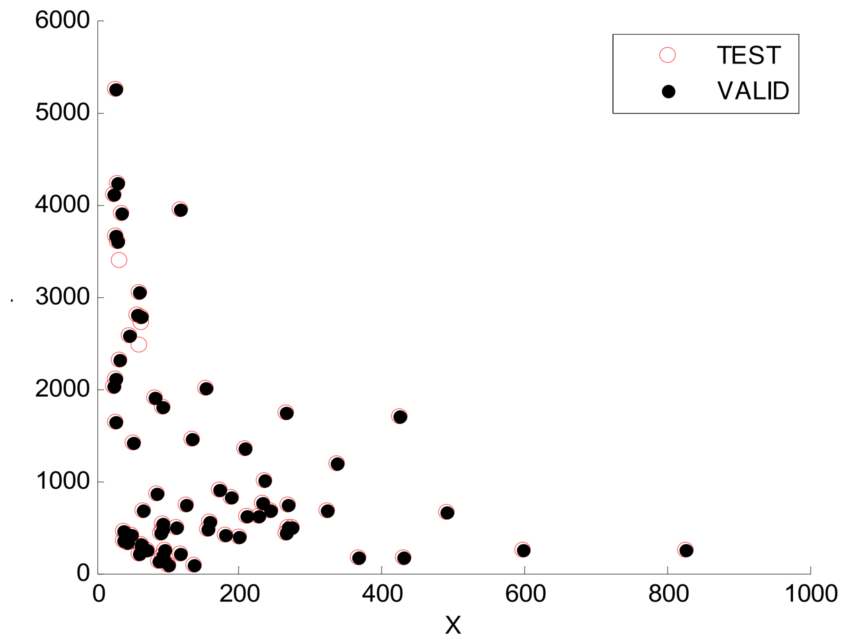


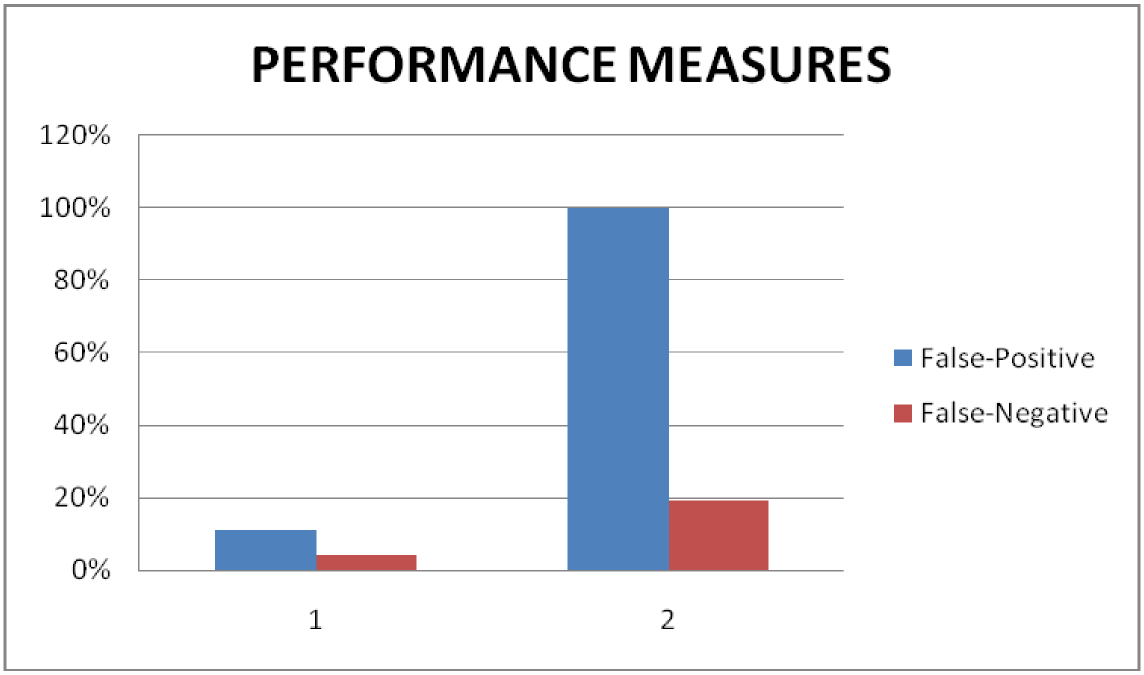
FIG. 10.11.5 RESULT FROM FCM CLUSTERING

TABLE 10.11.6 PERFORMACE MEASURES

	BEFORE TRAINING	**AFTER TRAINING**
RMSE	0.39	0.64
FN (%)	2%	11%
FP (%)	38%	100%

TABLE 10.11.7 PERFORMANCE MEASURE OF FEM CLUSTERING

	AFTER TRAINING
RMSE	0.32
FN (%)	4%
FP (%)	19%



1-ANFIS 2-FCM

FIG.10.11.8 COMPARING TWO CLUSTERING