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Robust Cell Detection of Histopathological Brain Tumor Images and Analyzing its Textual Features

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Abstract

Precise and accordant detection and prognosis, CAD (computer aided diagnosis) plays a fair role in predicting the outcome of the treatment and planning of the therapy. Detection and segmentation of the cells are the important steps in a CAD. These steps are difficult due to touching cells, untidy background and variation in the shapes of the cell and changes inside the nuclei. In this paper, we present an analysis based on the textual features of the detected cell after the detection of the cell using adaptive dictionary selection and the sparse reconstruction technique with trivial template. The analysis is done on the basis of the first order and second order statistical features. The proposed method has been tested on a data set with 1000 cells extracted from 20 whole slide scanned images.

Keywords: *Sparse reconstruction, trivial templates, cell detection*

INTRODUCTION

A brain tumor or an intracranial neoplasm affects different parts of the brain and presents with a varied range of symptoms. Diagnosis is usually by medical examination along with computed tomography or magnetic resonance imaging, often confirmed by biopsy. Proper evaluation and study of the histopathology details digitally will aid in a better assessment of the prognosis.

Computer aided diagnosis (CAD) has become one of the major research subjects in medical imaging and diagnostic radiology. CAD is a concept established by taking into account equally the roles of physicians and computers. The performance by computers thereby complements the provisional diagnosis of the physician. Recent studies suggest that CAD is beginning to be applied widely in the detection and differential diagnosis of many different types of abnormalities in medical images obtained in various examinations by use of different imaging modalities. Although early attempts at computerized analysis of medical images were made in the 1960s, serious and systematic investigation on CAD began in the 1980s with a fundamental change in the concept for utilization of the computer output from the automated computer diagnosis to computer aided diagnosis. Commercial CAD systems are available at present for the detection of several cancers.

LITERATURE SURVEY

Distance transform techniques have been used in nuclei detection and segmentation for accurate cell detection [1][4] in histopathological images. It measures the distance of each object point from the nearest boundary and is an important tool in computer vision, image processing and pattern recognition. In the distance transform binary image specifies the distance from each pixel to the nearest non zero pixel. The Euclidean distance is the straight line distance between two pixels and is evaluated using the Euclidean norm. The city block distance, chessboard distance, quasi Euclidean are other metrics that measure the path between the pixels. The disadvantage lies in the fact that it cannot be applied to cells that are clustered in a dense fashion.

Later on the watershed approach [2] was used to exclude the outliers. The watershed transformation is a major tool used in mathematical morphology. Here an image is considered topographically and the catchment basins and the watershed lines are defined by means of a flooding process. This prevents the merging of minima. This is defined on a grayscale image with the brightness of each point representing its height.

In marker based water shed approach the segmentation process involves computing the segmentation function, foreground markers, background markers ,and finally modification of the segmentation function. This ensures that only minima are present at the foreground and background marker

locations. This is followed by computing the watershed transform of the modified segmentation function. This has enabled to arrive at a more confirmatory diagnosis. Nuclear shape is taken into account in H-minima[3] transform. Non homogenously intense nuclei cannot be detected accurately by comparing with the elipse under control. The adjacent local minima are merged with respect to the valley lines between them. However this fails whenever there is intracellular heterogeneity. Laplacian of Gaussian filter can be used to complement the watershed algorithm when there is gross variation in cell size with a lack of well defined cell boundary. Here again nuclei separation is compromised with an increase in heterogeneity. Based on the assumption that the shape of the cell is round radial symmetry transform was clubbed with the marker controlled watershed approach.

Lacks of well defined cellular boundaries, altered shape with overlapping and varied heterogeneity continue to pose hindrance to cell detection for brain tumor data set. The sparse reconstruction handles the shape variations by representing a testing patch as a linear combination of shapes in the learned dictionary. Trivial templates are used to model the touching parts. Robust segmentation of overlapping cells and cells with intracellular heterogeneity is done by clubbing sparse reconstruction and a repulsive level set. .

RELATED WORKS

Whole Sliding

The advantage of whole sliding scanners is that it has produced vast quantities to get the ground truth annotations in a form which can be used for development and testing of the image analysis method. It is said so because during the evaluation of pathology reports , we can see that the mitotic activity on that report are analyzed based on the particular region from a single slide, viewed under a microscope and that slide itself has been selected from set of slide prepared from the same sample. By the introduction of WSI scanners into pathology labs, digital slides are accepted for primary diagnosis. 2. Marker Controlled Watershed, Mean Shift and Kalman Filter To understand the effects of drugs on cancer cells, it is important to study and observe the cancer cell cycle progression. So from the large population of cells, time lapse microscopy imaging is used to measure progression of individual cells. Manual analysis is time consuming. Water controlled watershed is based on mathematical morphology and it can segment cells with small over segmentation. It is a process in which, an

object is being segmented from the background and are again themselves segmented into subcomponents.

It creates so many insignificant boundaries. Modified mean shift algorithm is used as a tracking method for those kernels with adaptive shape, scale and direction are designed. This makes the tracking using mean shift more robust. Combining this with kalman filter we can achieve a robust cell nuclei tracking method and can obtain high segmentation.

Automatic Detection and Segmentation Of Cell Nuclei

One of the essential step in image cytometry and histometry is the automatic segmentation of all nuclei. Using a graph cut based binarization an image foreground is extracted. By combining laplacian of gaussian filtering and distance map based adaptive scale selection, nuclear seed points are detected for the initial segmentation these points are used and it can be refined using second graph cut based algorithm ,the method of alpha expansion and graph coloring is incorporated with this to reduce the complexity of computation. Using this automatic segmentation algorithm, we can segment nuclei very fast and accurate, but there will be segmentation errors and it cannot be avoided. To obtain the highest level of accuracy human interaction is to be made.

PROPOSED SYSTEM

Histopathology mainly deals with the microscopic examination of tissues that is processed and fixed onto glass slides to examine and study the manifestations of disease. The aim of our proposed system is to evaluate digitized stained slides of histopathology brain tumor images stained with hemotoxylin and eosin (H E) and statistical features are extracted and classify it as normal and abnormal cell. The purpose of this staining is to show the cellular components, where hemotoxylin stains the nuclei of the cell to blue while Eosin stains the connective tissue and cytoplasm to pink.

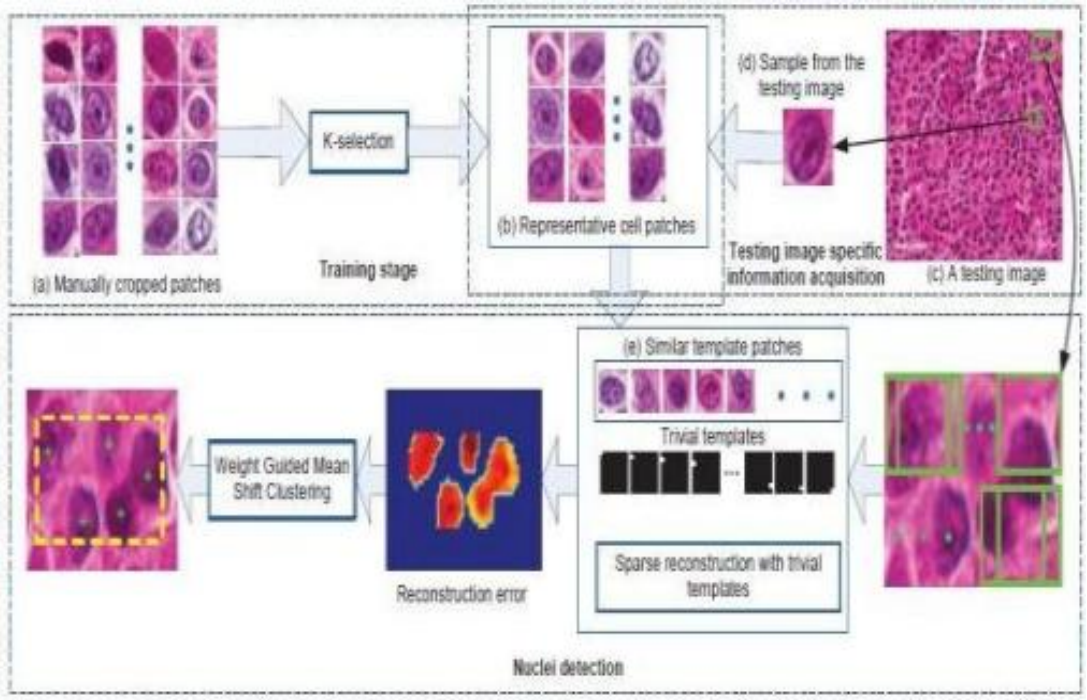

Fig 4.1.System Overview

The stained pathology image is displayed on the computer screen we can morphologically see the cells in blue color. Then comes the feature extraction stage of cropped image cell. Fourteen features were extracted from each cell image. This includes metric features, optical density histogram features and co-occurrence features. After that shape analysis of the cropped image is evaluated, here we took the shape analysis on the basis of circularity for that Form Factor is used. Metric feature includes Area Perimeter, Form factor. Form factor provides a measure of circularity.

circularity = 4∏(area÷perimeter2)

Form factor is a traditional adaptation of perimeter and Area features as described by Round et al. It provides the measure of circularity, a circularity value 1.0 indicates a perfect circle and as the value approaches to 0.0 it indicates an elongated polygon.

Optic density histogram features include :Mean (measure of brightness), Variance(how much gray levels are varying from the mean). Skewness(darker surface has more positively.)Kurtosis(high kurtosis, low noise and resolution Energy.) Entropy (Measure Of randomness) Standard deviation (It is a measure of contrast.)

RESULT AND ANALYSIS

The following section describes the result and statistical analysis. From the statistical

analysis of features that we are taken into consideration for the feature extraction of the cell first order and second order statistical features, we can see that parameters like skewness, variance, standard deviation, contrast, correlation, energy and homogeneity shows a great variation from the normal cell.

Figure 5.1 shows Cropping single cells from the test image to form a dictionary of single cell image patches.

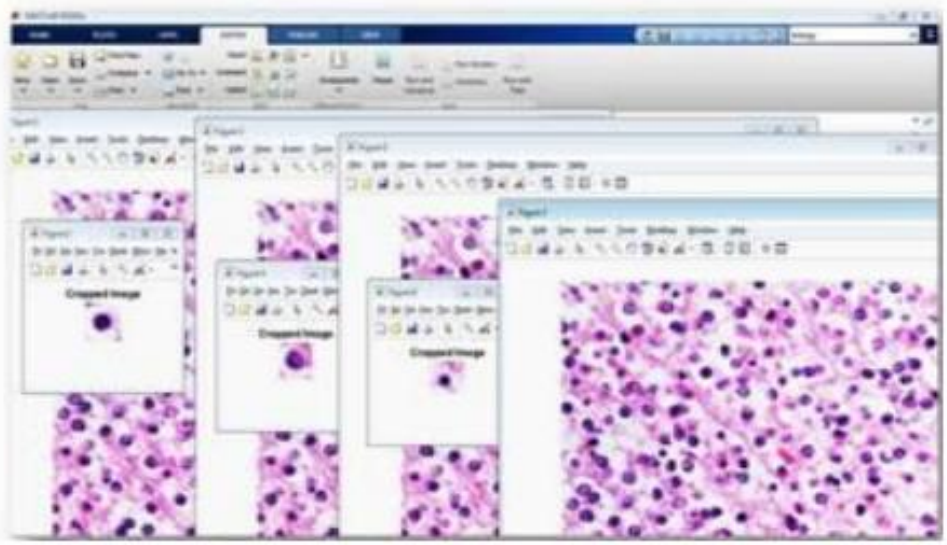

Fig. 5.1 single cell image patches

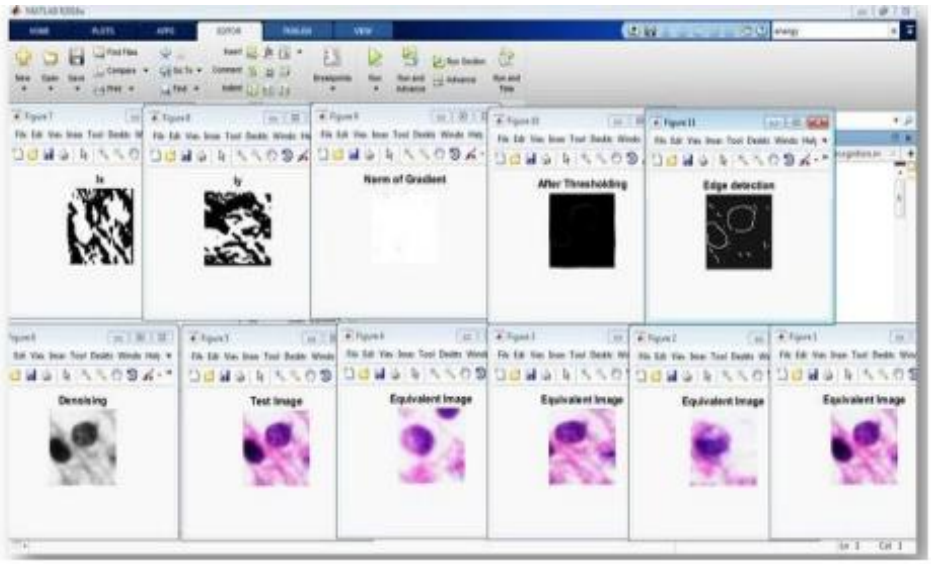

Fig.5.2.representative cell patches selected using pca

Figure 5.2 shows Principal component analysis. In principle component analysis similar image patch corresponding to the test image is being selected from the

manually cropped patches using minimum euclidean distance Figure 5.3 shows sparse reconstruction with trivial template. Reconstruction of test image patch using similar template patches selected from the manually cropped patches along with trivial template is used here for sparse reconstruction.

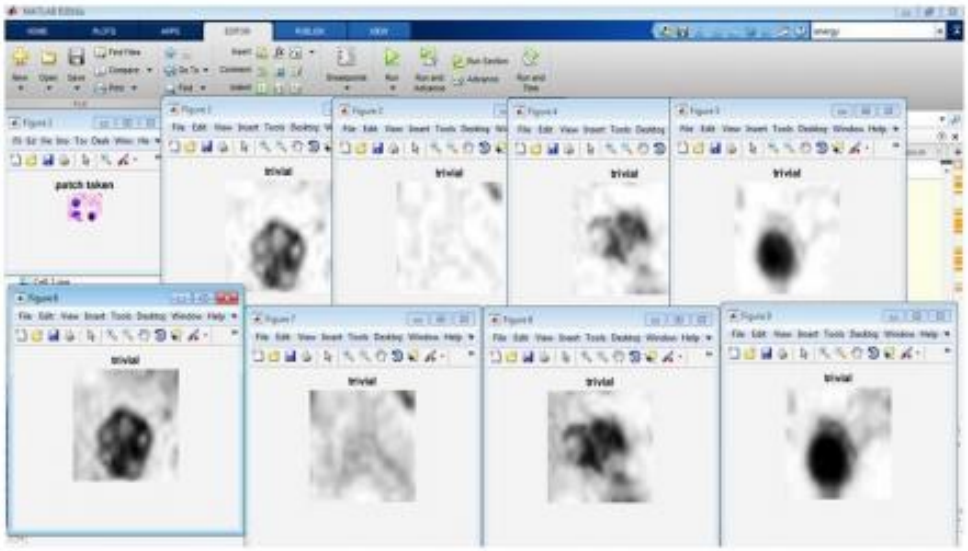

Fig. 5.3 formation of trivial template

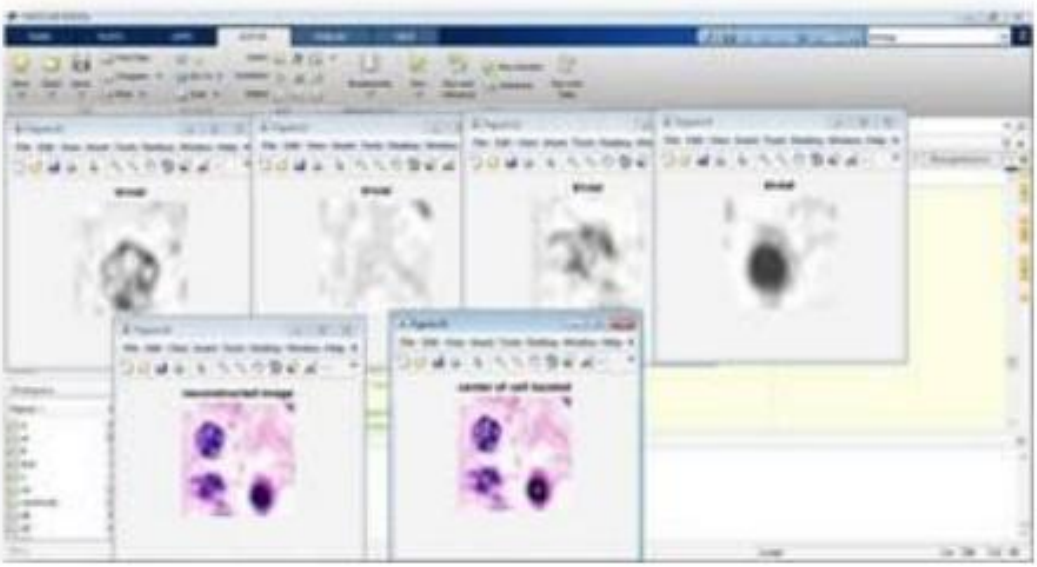

Fig. 5.4 reconstructed image

Figure 5.4 shows Single cell cropped from the reconstructed image. It is evaluated based on the three statistical features ie metric features, optic density histogram features and co occurance features

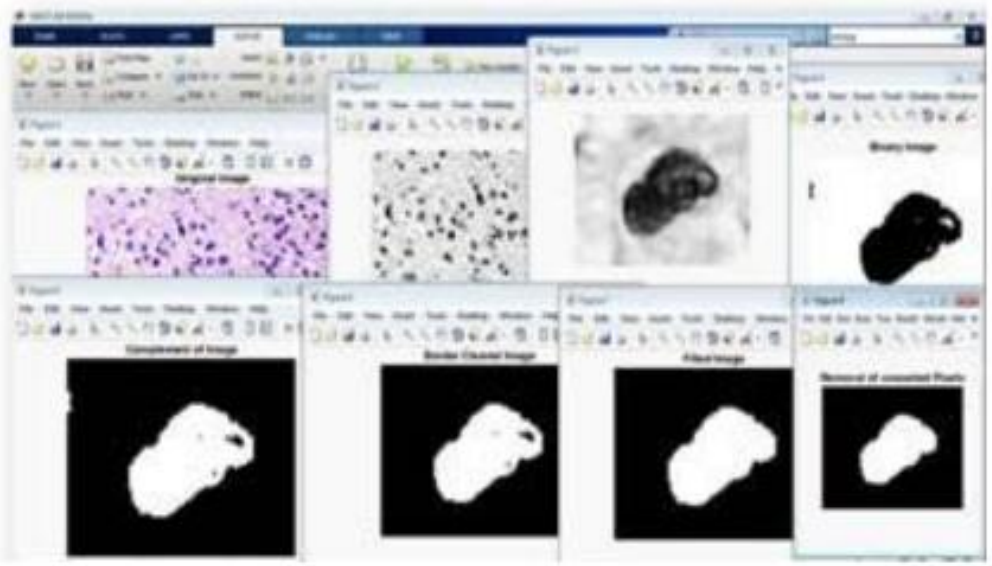

Fig. 5.5 textual feature analysis

Figure 5.5 shows textual feature analysis which depends on the reconstructed image.

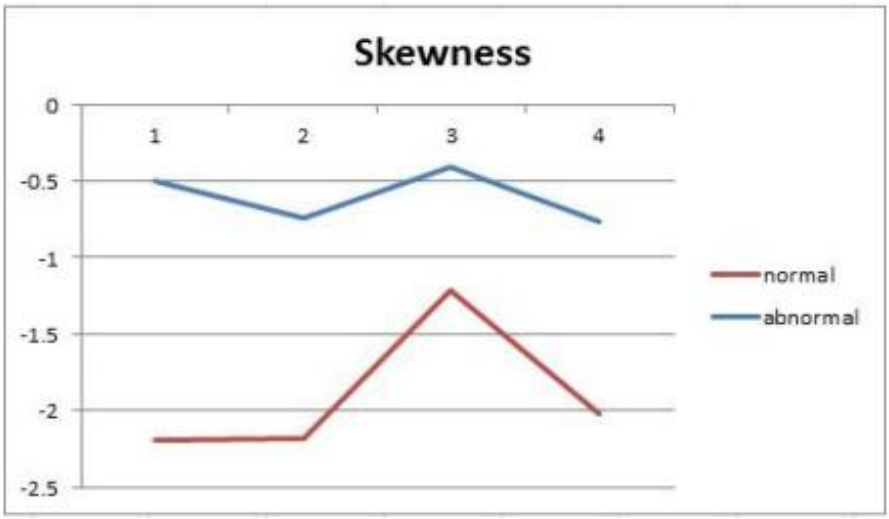

Fig: 5.6Skewness

Figure 5.6 shows Skewness. It is the darker surface which is more positively skewed. X-axis represents skewness, Y-axis represents circularity

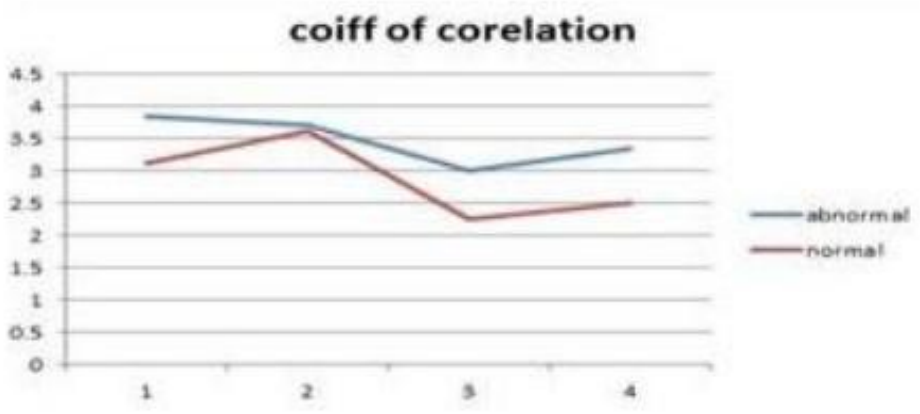

Fig: 5.11coefficient of correlation

Figure 5.11 shows the correlation coefficient. Correlation is the gray level linear dependency of image. X- axis represents correlation coefficient, Y-axis represents circularity.

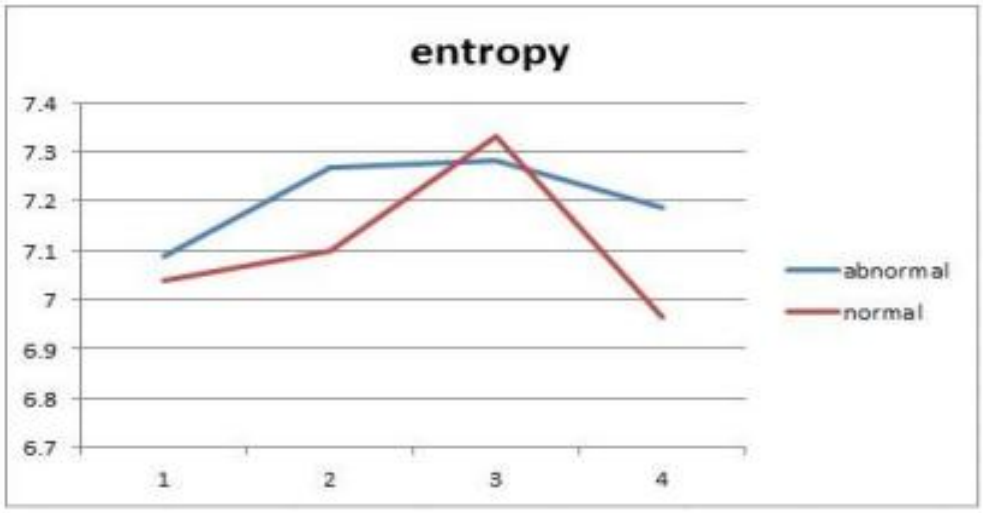

Fig 5.13: Contrast

Fig 5.13 shows the Contrast. It defines how sharp the structural variation in the image is. X-axis represents contrast, Y-axis represents circularity

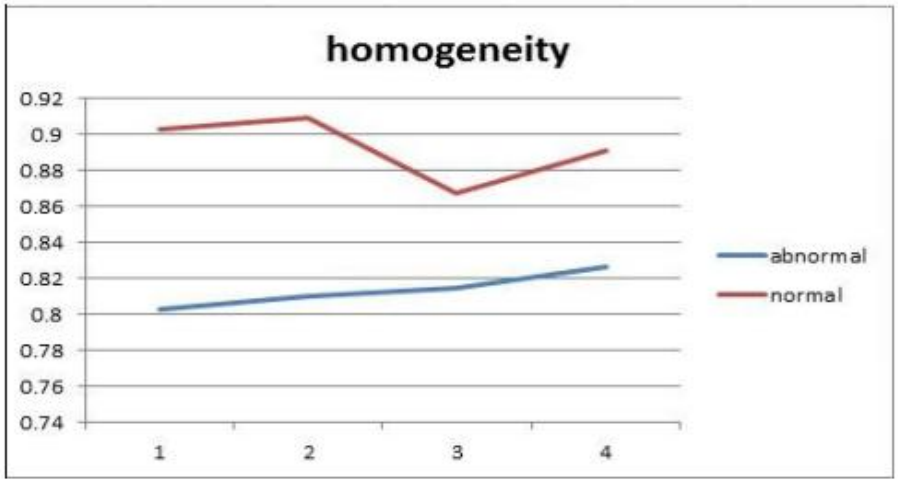

Fig: 5.14homogeneity

Fig 5.14 shows Homogeneity. It is the measure that increases with less contrast. Xaxis represents Homogeneity, Y-axis represents circularity

CONCLUSION

In this paper, the occluded tumor cells are detected and segmented in a more proper way. The variations inside the nuclei can be detected. To handle the variations appear in the cell and to split touching cells, a sparse reconstruction method and an adaptive dictionary selection is used. The cells formed after the reconstruction using trivial template are then subjected to statistical analysis. It includes first order and second order statistical analysis and also shape analysis. By using these feature extraction methods and also considering the circularity of the cells, we can classify it into normal or abnormal cells. Along with that, we can understand the changes, that are reflected on the statistical features taken under consideration for the feature extraction of cells.

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