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An Automatic Recognition, Identification and Classification of Mitotic Cells for the Diagnosis of Breast Cancer Stages

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Abstract: The identification of breast cancer stages plays a vital role for understanding the aggressiveness of cancer disease and the patient survival as an outcome. The main parameter of breast cancer staging is counting the mitotic cells in biopsy samples of breast cancer tissues. In the present scenario the manually counting of the mitotic cells in histopathology image slides of the tissue examined by the expert under clinical microscope is 10X, 20X ,40X ,100X,400X magnification of the sample. The manual process is laborious, inaccurate, erroneous and tedious, hence the traditional method demands the computerized approach to recognize and identify the cancer stages for the expert to come up with robust decision. In this work we proposed a novel approach for automatic recognition and identification through computer aided diagnosis systems (CAD). In this CAD proposed model the work is divided into five stages. In the first stage histopathological image are preprocessed to enhance the contrast of the mitotic cells and non mitotic cells using image adjustment technique. In second stage the foreground and background is segmented using Otsu segmentation algorithm. In the third stage the Bit plane slicing is applied to separate the mitotic and non mitotic cells. In the fourth stage the number of mitotic cells is counted in the samples. In the fifth stage of the work, based on the number of mitotic cells the cancer stages are determined. In this work, ICPR 2012 database images are adopted for the experimentation. The diagnosis of the stage of the cancer will help the oncologist to take proper decision and also reduces the burden of the work.

Index Terms: Histopathology, mitotic cell, Otsu segmentation, CAD, ICPR 2012 database, Bit Plane slicing

1. Introduction

According to Bloom Richardson [1] grading (BRG), the most generally used technique for detection of disease called breast cancer using histopathological image**.** This strategy includes three components 1) Counting mitotic cells 2) Nuclear pleormorphism and 3) Tubule formation. The first component indicates the number of dividing cancer cells (i.e. mitoses), an excellent predictor of breast cancer stage. The Hematoxylin and Eosin (H & E) [5,6] are used as standard for histopathological detection of mitotic cells. In medical screening the cancer specialist consider mitotic cell count as the number of mitotic cell identified visually in a fixed number of High Power Fields (HPF)[4]. Hence the manual detection of mitotic cell often suffers inter-interpreter agreement due to the highly variable texture and morphology between mitoses.

In addition to that, manual counting is very laborious and time consuming and inaccurate process through multiple high power field on microscopic instruments. Hence a fully computerized technique for mitotic cells detection will lead to higher accuracy and consistency. And also equally minimizes the detection time and cost for breast cancer diagnosis. The counting of mitotic cell in (H & E) shaped histopathology image is very cumbersome.

There are two major issues associated with mitosis cell. The first mitosis is a complex biological process during which the transformation of stages (prophase, metaphase, anaphase, telophase) that leads to highly variation in size and shapes throughout the mitotic cells within the same histopathology image. The second major issue is rare event detection that complicates classification. And the mitotic cells are remarkably less prevalent than the non mitotic cells and difficult to identify.

The mitotic cells are the result of the accumulation of genetic material in the cell nuclei. The division of nuclei will lead to the formation of new cells. The mitotic cells are very difficult to differentiate from the non mitotic cells. Even with a high power field most of the oncologists are not capable of identifying the mitotic cells from the other cells. In this work a CAD approach [4] is used for fully automatic mitotic cells identification is to be done by image analysis technique to overcome the limitations of the biopsy method. The progress of the cell in different phases of mitosis and identification of the cell using bit plane slicing method is concentrated in the work to address the above mentioned challenges. Fig.1 (a) to (d) describes histopathological sample of normal, stage-I, stage-II, and stage-III mitotic cells respectively.

The organization of the work is as follows. In section 2 we have described about previous work. The section 3 presents materials and methods. The section 4 demonstrates experimental results, discussion and justification. The section 5 presents the concluding remark of the proposed work followed by the references.

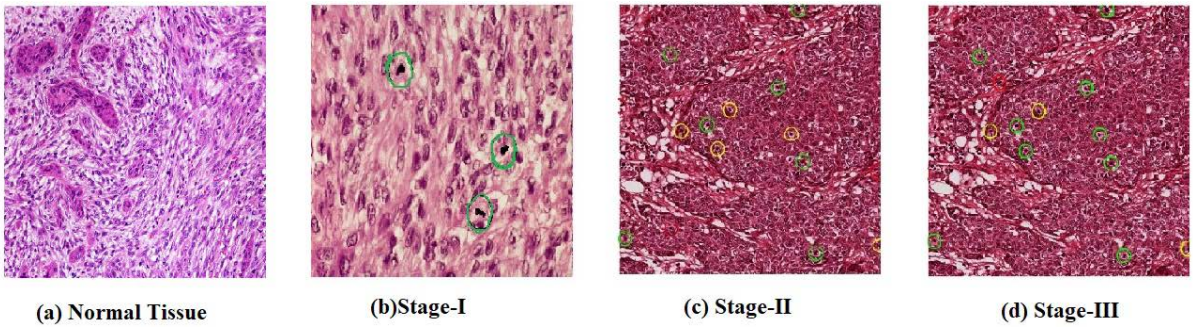

Fig. 1. The mitotic cells in various stages

2. Literature Review

This section presents the various author works so far on the breast cancer detection and its limitations. Haibo wang et.al. [1] have presented work on automatic detection and classification of breast cancer different stages .The breast cancer stages such as stage1 to stage 3 are nominated based on mitotic cell present in biopsy cell. biopsy cell consists of 3-4 mitotic count and nuclei diameter(0.4 mm) is named stage-1 cancer, the mitotic cell counts are in the range of 6-8 is called stage-2 cancer and finally mitotic count cell are above 9 are called as stage-3 cancer. In this work automatic detection and classification. Convolution Neural Network(CNN) had been used with an accuracy of 73.45%. The author combined first hand crafted feature and convolution neural network in a cascaded way and the result achieved in Fscore is 73.45%. This experimental outcome presents that it is still unsatisfactory with respect to accuracy in current medical world science.

Abdukadir Albayrak & Gokhan Bilgin [2] presented work on histopathological images from the cellular structures in “mitosis detection using convolution neural network based features” .The cellular structures are found using cluster based segmentation and BLOB analysis. The patches are cropped and given as input for CNN for feature discrimination.Myung Iae Lim et.al.[3] presented a work on deep convolution Neural networks for medical image analysis. The CNN algorithm VGG16 and inceptionV3 were used. The author worked on histopathological image dataset classifying the malignant and benign of Breakhis inception v3 achieved an accuracy of 80%. The deep learning approach was adopted to analyze mitotic cell for automatic identification and classification of breast cancer stages. Ashkem Tashk et. al. [4] demonstrated a work on CAD system for automatic diagnosis of breast cancer stages. In this work three features were extracted such as Complete Least Binary Feature (CLBF) namely texture feature, stiffness matrix and statistical moment entropy. This feature set is given as input to the convolution neural network for the classification of the grades of the breast cancer.

R.Geetha & M.Sivajothi [5] had shown mitotic cells and other patches which present on the biopsy samples almost similar ,hence counting the mitotic cells manually is tedious and inaccurate process, hence author has adopted CNN technique for identification & classification but couldn’t achieved a satisfying accuracy.Cheng Lu[6] presented work on “Towards automatic mitotic cells detection and segmentation in multispectral images”. The author presents a new approach on efficient method identification and segmentation of the mitotic cells in high resolution multi spectral image. This method includes three stages: 1) discriminative image generation 2) region of mitotic cell detection and extraction and 3) mitotic cell patches classification. In the first stage a discriminative image is generated by linear discriminant analysis through 10 different spectral band images. The Mitotic Region was extracted using local threshold technique and Bayesian modeling. The imbalanced classification framework had been adopted to classify real mitotic cells

Tan Xiao Jian et.al.[7] describes the Nottingham grading procedure and mitotic count is an indication for the speed up the breast cancer stage growth, Hence identification of mitotic count plays an important role for the identification of stages of cancer. The overall accuracy of the work is 91.85%. The various methods like critical exponent method for microscopic images, sonographic features to understand malignancy grade, fractal features are

referred for the understanding the detection of cancer stage[8][9][10][15].The overall summary of the previous work had been tabulated in the table 1 and as follows,

Table 1. The summary of the previous work

Sl.No.	Name of author	Title of the Paper	Method	Features	Advantages	Disadvantages
1.	Jian, Tan Xiao[6]	Segmentation Based Classification for Mitotic Cells Detection on Breast Histopathological Images (2018)	Otsu	Minimizes mitotic candidates	The efficiencies had been achieved with 91.85%	i) The author had worked only on five histopathological images that are not sufficient. ii) The author had not described proper feature of the mitotic candidate such as circular, ellipse, hollow.
2.	Lu, Cheng, and Mrinal Manda[5]	Toward automatic mitotic cell detection and segmentation in multispectral histopathological images (2013)	Local Segmentation	Nearly 226 features like eccentricity, solidity, major and minor axis length and many more	An accuracy of 81.5% and 33.91%	The achieved accuracy is not sufficient.
3	R. Geetha et. al [4]	Automated Mitotic Cell detection and classification for Breast Cancer Histopathological Images, December 2018.	1.LACM & ABC segmentation 2.Random Forest	1.Intensity based 2. Shape based 3. Texture feature	1.Accuracy = 89.6% 2.Sensitivity = 86.3% 3.Specitivity = 84.2 % 4.Fscore = 85.29 % 5. Time=21.3	1.Time consumption is more 2. memory consumption is more 3. Features are not described for mitotic and non mitotic cells
4	Wang, Haibo, et al [1]	Mitosis detection in breast cancer pathology images by combining handcrafted and convolutional neural network features (2014)	Cascaded by combining the Hand crafted and CNN	No features	Accuracy of 73.45%	The accuracy is not sufficient.

The above limitations motivated to take up the research work. The limitations had lead to selection of materials and methods, design of objectives like simple computational approach to enumerate mitotic cells with high accuracy. The next section describes the materials and methods for the detection of mitotic cells.

3. Materials and Methods

This section describes the materials and methods used to conduct the experiments. The details of the materials and methods had been described in the following subsections, 3.1 Mitotic cell process and 3.2. Data flow diagram

3.1. Mitotic cell process

A mitotic object is a cell that will divide and generate two new cells. This system is referred as mitosis. The oncologist can view mitotic objects in the tissue under microscopy instruments. Mitotic objects are simple to view because the genetic material within the nucleus get changes in shape and color before the cell divide into two new cells. There are four different stages of mitosis [6] such as (1) Prophase (2) Metaphase (3) Anaphase and (4) Telo-phase. In the Prophase two new cells are yielded because of the doubling in the number of genetic material. In the metaphase the genetic material will start getting line up in the centre of the cell. In the anaphase the cell get start to divide into two new cells and the genetic material (GM) is split into half each. In the telo-phase two new cells are generated with it genetic material within the nucleus. This complete process has been shown in figure 2, in 2(a). Division of cell and 2(b) the development of different phases of the mitotic cell. Fig.2(c) shows the appearance of the mitotic cells under the microscopic slide.Fig.2.(d) represents five mitotic cells in stage –II cancer biopsy samples.

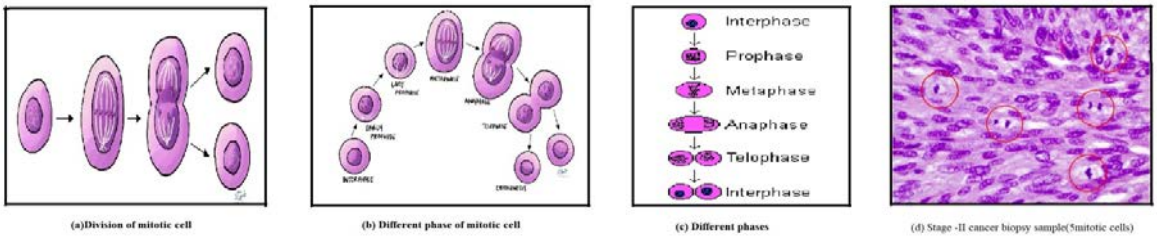

Fig. 2 Stages of mitoses

3.2. Data flow diagram

This section describes the data flow diagram of the work carried out to conduct the experiment. The data flow diagram is divided into four phases namely phase-I, phase-II, phase-III and phase-IV. The phase-I is database of mitotic cell samples taken from ICPR-2012 dataset. In phase-II the enhancement and segmentation of the image sample had been performed by image adjustment and Otsu segmentation respectively. In phase-III the extraction of the mitotic cells from the segmented samples using bit plane slicing. The phase-IV mitotic cells are counted and the stages of cancer is determined based on the number of mitotic cells. The four phases are depicted in fig.3 and details of each phase is elaborated in the following subsections.

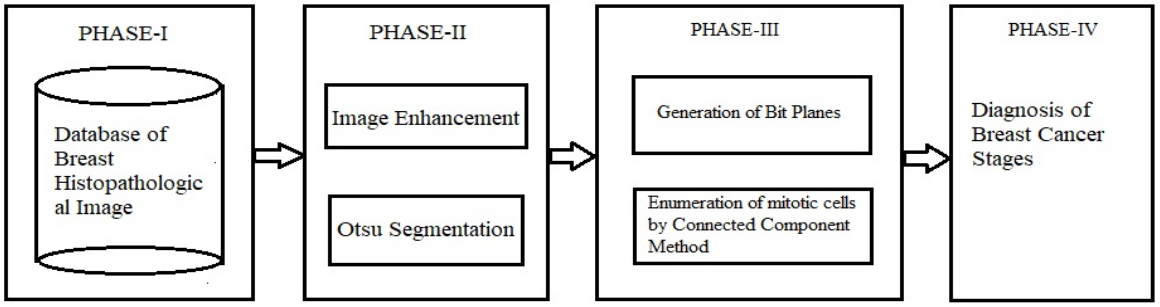

Fig.3. Data flow diagram

3.2.1 Databases: Phase-I

There are several databases available such as BreakHis, Breast Image Reasoning and Data System (BIRADS) and ICPR-2012 &2014 etc [9]. Among all these ICPR-2012 was selected for the sample dataset. The mitosis cell database had been designed using state of art technique collecting samples from ICPR-2012 dataset [2,17]. This database has 50 slide High Power Field (HPF) H & E samples. The different number of mitotic cell is found in the samples. The samples are categorized into the different ranges like 3-5, 6-8, 9-11 and above 11. The presence of mitotic cell in the range 3-5 is categorized into stage-I, and the range of mitotic cells 6-8, 9-11and above 11 are categorized into stage-II, stage-III and stage-IV samples respectively. The database has four datasets for the four stages of breast cancer. The samples in the dataset are named for the patients Pgrade1.001(P indicates Patient) to Pgrade1.009. The stage-II samples of the patients are named as Pgrade2.001 to Pgrade2.009. The stage-III samples of the patients are named Pgrade3.001 to Pgrade3.009. The stage-IV samples of the patients are named Pgrade4.001 to Pgrade4.009.The details of the equipment and description of the database had been tabulated in the table 2.

Table 2. Details of equipments, image resolution and dimensions

Equipment	Resolution	Dimension of HPF to cover an area of 512 × 512 μm^2
Scanner A	0.2456 μm per pixel	2084 × 2084 pixels
Scanner H	0.2273 μm horizontal and 0.22753 μm vertical per pixel	2252 × 2250 pixels
Microscope M	0.185 μm per pixel	2767 × 2767 pixel

3.2.2 Enhancement & Segmentation: Phase-II

The enhancement of histopathological image samples is adopted by various linear filtering and non-linear filtering techniques such as ESIHE, MMSICHE, R-ESIHE,AGCWD,CLAHE,BPDHE [16], Homomorphic filters and Guided filters etc. Among all these filters image adjust filters had given better contrast among other filter. This filter plays an important role for the segmentation and Bit plane slicing. In this stage cancerous biopsy samples are extracted by using

Otsu algorithm for segmentation. The suitable threshold had been computed for all four stages of cancerous sample. Based on histogram technique the normalized histograms, goodness graph are plotted. In the experiment around 150 threshold values was obtained for the separation of background and cell nucleus.

The filters enhance the quality of the image. The cells in the sample will be of the different size and shapes. The more elongated shaped cells are mitotic cells. These cells will be more intense in color compared to non mitotic cells. The enhancement of the image will be able to provide the differentiation of the cells with respect to intensity in color and shapes. The segmented image shows mitotic and non mitotic cells clearly. The KNN segmentation is also one of the technique for segmentation on mammograms and had been well dealt in the research article [14]. The pseudo code of the Otsu segmentation is as follows,

Algorithm: Otsu segmentation

Algorithm: Otsu Sgmentation	
Input	Histopathological Image
Output	Segmented Image
1	inputimage←read_image()
2	If(inputimage=3D) Img←Convert RGB to Gray Then Img ← Img
3	Consider the initial threshold value T and compute global threshold
4	Segment the image into two regions R1 and R2 of pixel using threshold T, where one region of pixel is greater than threshold value T and another one with less than global threshold value T.
5	Estimate the average pixel intensity values m1 and m2 for the pixel in segmented R1 and R2
6	Estimate new global threshold values using equation $T = \frac{1}{2}(m1 + m2)$
7	Repeat step 5 and step 6 until the difference in global threshold T in consecutive steps is smaller than initial defined value ΔT
8	Segment the regions of the mitotic cells and non mitotic cells from the back ground

The result of Segmentation will be given as input for the Bit Plane Slicing Method .Using the bit plane slicing the mitotic cells are identified and detailed bit plane slicing is explained in the phase –III in the next section.

3.2.3 Bit Plane slicing: Phase-III

Bit plane slicing is a method where the image is sliced into several planes .In this method image objects are formed on all 8 bit grey scale image. The bit plane 8,7,6 contain almost non mitotic and mitotic cells where as bit plane contain only mitotic cells. The brief description of the Bit plane slicing is as follows. It ranges from plane -1 to plane-N, from Least Significant Bit (LSB) for plane-1 and most significant bit (MSB) for plane -N. The total number of planes is defined based on the bit depth used to represent the image[11]. It means how many bits are required to represent 1-pixel intensity. For example RGB image have 24–planes because bit depth is 24-bit where as grey scale image have 8-plane then the depth is 8-bit and it will be divided into 8 –planes. The first bit in the binary number is the LSB that is not so effective and its value is very small and usually not effect on the pixel intensity. While the MSB that is effective and contains the important information of the pixel value.

Let's take an example to illustrate the above concept the decimal number that can be represented as a binary number. In the example, the decimal number can be represented as a binary number. For example the decimal number 225 can be shown in the following binary form with decimal weight for each bit and shown in table 3,

Table 3. Decimal weight for binary digits

	128	64	32	16	8	4	2	1	
MSB→	1	1	1	0	0	0	0	1	←LSB

With respect to the example shown above the intensity value of each pixel can be represented by 8-bit binary vector Bit -k (Bit-8,Bit-7,Bit-6,Bit-5,Bit-4,Bit-3,Bit-2,Bit-1). Bit k, where k is from 1 to 8 and each bit k is either 0 or 1. The formation of bit plane is given by the below equation

$$BitPlane_k = \mathrm{Re}\,mainder\left\{\frac{1}{2}\left[\frac{1}{2^{k-1}}\,\mathrm{Im}\,g\right]\right\} \quad (1)$$

(a)

97	32	15
18	47	54
33	72	85

(b)

01100001	00100000	00001111
00010010	00101111	00110110
00100001	01001000	01010101

(c)

Bit Plane-8			Bit Plane-7			Bit Plane-6			Bit Plane -5		
0	0	0	1	0	0	1	1	0	0	0	0
0	0	0	0	0	0	0	1	1	1	0	1
0	0	0	0	1	1	1	0	0	0	0	1

Bit Plane -4			Bit Plane			Bit Plane -2			Bit Plane-1		
0	0	1	0	0	1	0	0	1	1	0	1
0	1	0	0	1	1	1	1	1	0	1	0
0	1	0	0	0	1	0	0	0	1	0	1

(d)

Fig.4 Example of Bit plane slicing(a) Grayscale value (b) Binary data of the grayscale (c) Bit plane MSB values

In the grey scale of the biopsy sample, the fig.4(a) depicts the region cropped [8] out of mitotic sample. The fig.4(b) represents the pixel value of the grey scale image of the cropped region from the mitotic cell sample. The fig.4(c) provides 8-bit binary representation of each cell pixel value of fig.4(b).The fig.4(d) describes the Bit plane 8 to Bit Plane 1 of the selected cropped region of the mitotic sample. The Most Significant Bit (MSB) of the fig.4(c) all three bytes each of first row, second row and third row are all zeros. Hence the Bit Plane-8 matrix (3X3) all elements are zero. Similarly the 7-Bit Plane first row elements are 1,0,0 second row elements are 0,0,0 and third row are 0,1,1.Hence the bit plane -7 is 3X3 matrix as shown in fig.4(d). Similarly the remaining Bit Planes-6 to Bit Plane-1 are represented in fig.4(d).

Algo. Bit Plane Slicing

The following pseudo code illustrates the algorithm for the Bit Plane Slicing for the separation of the mitotic cells from the non mitotic cells.

Algorithm: Bit Plane Slicing

Input: Image
Output: Bit Planes Slices

1. Begin
2. Input the segmented image
3. Divide the sample into 8 bit plane i.e bit plane-1 to bit plane-8
4. All planes are separated for the biopsy sample
5. Select the planes that contain only mitotic cell (Plane5)
6. Count the number of mitotic cells using connected component method in the bit plane
7. Diagnose with different stages of cancer progress.
8. Stop

Among all various shaped detected cells the elongated large shape cell is considered as mitotic cell. These conditions are to be checked if the cell is mitotic with specified size. If all the cells are with specified one, then treated as the mitotic cell and each cell is to be counted using connected components and result will be announced that is the stages of the breast cancer disease. The result is obtained for the biopsy samples and presented in the section 4. Result and discussion,

3.2.4 Diagnosis of the breast cancer stages-Phase-IV

The fifth plane of the bit plane slicing of the images will enable us to identify the mitotic cells from the rest of the cells and the mitotic cells are counted. The count of mitotic cells in the range 3-5 leads to the given sample will be of stage-I cancer, the count of mitotic cells in the range 6-8 will decide the sample as of stage-II cancer. The mitotic count

of 9-11 in the sample will decide the sample as of stage-III cancer. More than 11 counts of mitotic cells will decide the sample as of stage-IV cancer. The detailed description of the result and discussion had been elaborated in the next section.

4. Result & Discussion

The section presents the result obtained by the experiment conducted on MATLab 2020 using ICPR-2012 dataset. In the ICPR-2012 dataset, 50 samples corresponding to 50 high power field in 5 various biopsy slide stained with H & E. Each field represents 512X512 μm^2 area and obtained with three different set up H & E- two slide scanners i.e. A & H and a multispectral microscope. The author considered the samples obtained from the widely used device called Aperio Scanner. This scanner has a resolution of 0.2456 µm/pixel and the resolution of image for one of the scanner (A) is 2084 X 2084 color image samples for each fields. These images are experimented for the research. The obtained results of detection of stages of breast cancer are depicted in fig.5 (result of stage-I cancer) and the consolidated result number of mitotic cells in stages-II and stage-III is presented in fig.6.

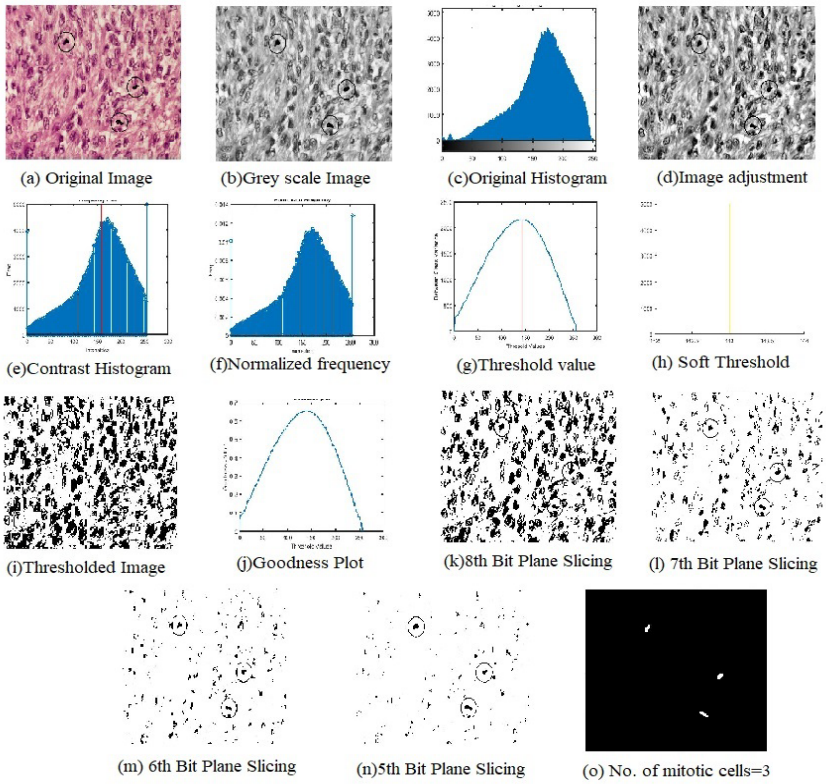

Fig.5. Result of Stage-1Breast Cancer

The detailed description of the results obtained for stage-I cancer is given in fig.5 and as follows.Fig.5(a) to 5(o) describe a complete process of result obtained for grade-1 mitotic sample.Fig.5.(a) is an original color sample of size 512X512 µm that is converted into grey image scale image to process on 8 bit data shown in fig.5(b). In Fig.5(c) the contrast of the image is enhanced using image adjust filter technique for the better segmentation. Fig.5.(d) shows the contrast image using image adjust function. We can observe mitotic cells have higher spike over the non mitotic cell. Fig.5(e) shows contrast histogram of 5(d) and 5(f) shows normalized histogram of obtained contrast image.The fig.5(g) shows the result obtained for threshold value for the segmentation, here we can observe 148 is automatically selected as threshold to segment the mitotic sample. Fig.5(h) shows the normalized histogram for the image to be segmented. Fig.5(i) reveals the segmented image with threshold value 148. Fig.5(j) shows the goodness plot of the segmented image. Fig.5.(k) to fig.5.(n) describes the result of bit plane slicing from 8^{th} bit plane to 5^{th} , Along with the mitotic cells other cells also present in the plane, so to remove such cell objects ,are individually accessed and estimated size where size of the mitotic cell should be above 1.248 µm (0.001248mm).These are extracted and counted using connected component method. We can see three mitotic cell in the fig.5(o).Hence it is stage-I cancer. Similarly The final results for cancer stage-II and Stage-III are obtained and are depicted in the fig.6.

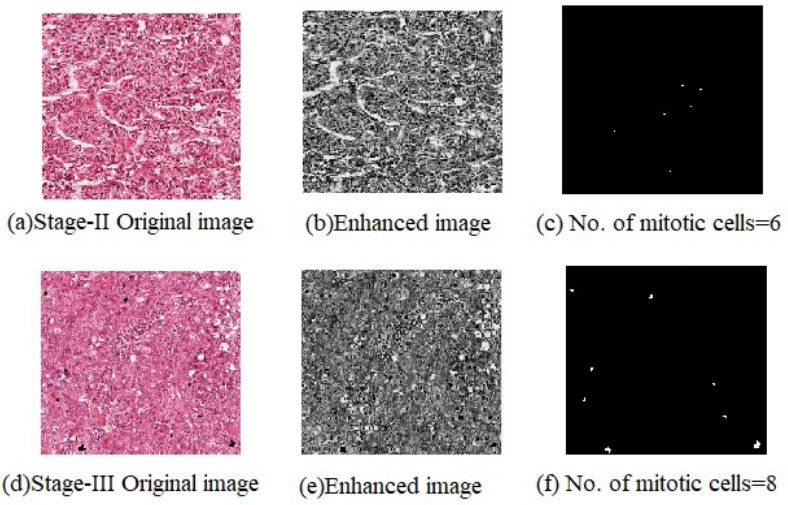

Fig.6. Result of Stage -II and Stage-III Breast Cancer

Performance Measures

The performance of the work is measured using metrics like recall, precision, f-score[7] etc. The recall and precision are defined over the attributes [3] such as true positive (TP), false positive (FP), and false negative. With respect to the research, the true positive (TP) is defined as the mitotic cells detected in the input image. The false positive defined as non mitotic cells detected as mitotic cells and false negative is defined as mitotic cell detected as non mitotic cells. We estimate the performance of the experimental result by the following equations,

$$\mathrm{Re}\,call = \frac{TP}{TP + FN} \tag{2}$$

$$\mathrm{Pr}\,ecision = \frac{TP}{TP + FP} \tag{3}$$

$$F - ScoreMeasure = \frac{2 * \mathrm{Pr}\,ecission * \mathrm{Re}\,call}{\mathrm{Pr}\,ecission + \mathrm{Re}\,call} \tag{4}$$

The result of proposed approach is compared with the different approaches as reported in [7]. The mitosis cell identification and detection of various methods such as HC, CNN, IDSIAS, IPAL, SUTECH, NEC for the ICPR-2012 dataset are shown in the Table 4.Our novel method produced a higher F-score measure (0.858) than all other approaches. The table 4 describes the result obtained by HC+CNN (Hand Crafted + Convolution Neural Network) technique [1] and proposed method. In HC+CNN method different threshold values had been selected for the detection of mitotic cell. In HC+ CNN method optimal result arrived with a binary threshold value 0.58 as tabulated in Table 4. In the proposed technique optimal result is achieved with respect to precision, recall and F-score at Bit Plane 5 is 0.89, 0.83 and 0.86 respectively as shown in table 4. This shows that proposed method is better in comparison with HC+CNN and others, is as shown below.

Table 4.Mitosis cell detection result of proposed method and comparative technique of the ICPR -2012 dataset

Dataset	Approach	TP	FP	FN	Precision	Recall	F-Score
Scanner Aperio	Proposed Technique	33	4	7	0.890	0.830	0.858
	HC+CNN	64	12	35	0.840	0.650	0.730
	HC	64	22	36	0.740	0.640	0.680
	CNN	53	32	47	0.630	0.530	0.570
	IDSIA	70	9	30	0.890	0.700	0.780
	IPAL	74	32	26	0.700	0.740	0.720
	SUTECH	72	31	28	0.700	0.720	0.700
	NEC	59	20	41	0.750	0.590	0.650

The most difficult parameter of the proposed technique is classification of the mitotic cells from the non mitotic cells. The application of bit plane slicing was a good decision for the separation of mitotic cells. In the experiment result, the 5th bit plane was identified as best mitotic extractor in process of bit plane slicing. Usually a higher bit plane will lead to lesser TPs, FPs and FNs and vice-versa. The fig.7 describes the accuracy of the proposed method that is resilient to the accuracy of the other methods such as HC+CNN and others [1,10] for the classification. In the graph precision v/s recall, the precision and recall is 0.89 and 0.83 is depicted in green color, the accuracy is 0.86 and the results of other methods in red color. The precision and recall of the HC+CNN for different threshold is shown in the blue color line.

Table 5. The values of Precision and Recall for CNN+HC and Proposed Method

HC+CNN					Proposed Method				
Sl.No	Threshold	Precision	Recall	F-Score	Sl.No	Bit Plane	Precision	Recall	F-Score
1.	0.70	0.41	0.76	0.53	1.	8	0.40	0.77	0.53
2.	0.68	0.48	0.77	0.32	2.	7	0.46	0.78	0.58
3.	0.65	0.51	0.78	0.61	3.	6	0.54	0.70	0.61
4.	0.58	0.65	0.84	0.73	4.	5	0.90	0.82	0.86
5.	0.55	0.77	0.71	0.74	5.	4	0.79	0.74	0.76
6.	0.48	0.84	0.67	0.75	6.	3	0.83	0.63	0.72
7.	0.45	0.88	0.62	0.73	7.	2	0.89	0.50	0.64

The fig.7 precision –recall curve of the proposed method, the performance of the other methods is also drawn for the analysis. The F-score infers that the performance of the proposed method is dominating the performance of other existing methods. Hence the performance of proposed is resilient for the choice of the classification of stages of breast cancer. The work comprises different samples and for different stages. The reliability test could not be conducted for the single experiment of detecting the mitotic cells in all the samples. But the accuracy had been computed and achieved 0.858, considering the parameters like precision, recall and F-Score.

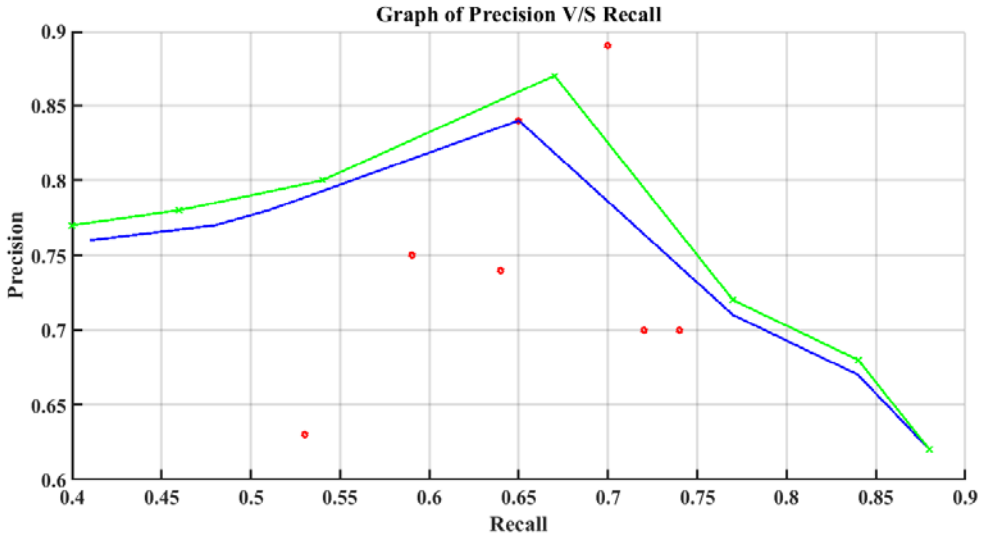

Fig.7 Precision and Recall graph for proposed method, HC+CNN and other existing methods

5. Conclusion

In this novel approach the recognition and identification of breast cancer stages is carried out by counting mitotic cells in histopathological image. The input images are enhanced using imadjust filter, the foreground and background are segmented using Otsu segmentation and mitotic cells are separated using bit plane slicing. The separated mitotic cells are counted using connected component method. The stages of breast cancer are diagnosed as follows. If the mitotic cells count are in the range of 3 to 5 then it is stage-1 breast cancer, mitotic cells in the range of 6-8 is stage-2 cancer and mitotic cell count 9-11 is the stage-3 breast cancer. The approach has yielded high true positive rate (TP) and lower false positive rate. The accuracy is measured in terms of precision, recall and F-Score. The estimated area under

Receptor Operator Curve (ROC) gave an outstanding performance as compared to HC+CNN and other methods. The computational cost and accuracy of the novel approaches for the diagnose of breast cancer stages is ideal.

The method had been compared with HC+CNN, HC, CNN, IDISA, IPAL, SUTECH and NEC in the detection of mitotic cell. Mitotic cell identification is one of the novel approache for the classification of the breast cancer stages. The conventional approach tried to identify the mitotic cells either CNN learned features or stacked Handcraft features. Thus the problem with stacked handcraft method was poor accuracy and CNN based method suffering from high computational complexity. The Fscore of CNN is 0.57 and HC is 0.68. If we cascade HC and CNN the accuracy achieved is not so promising in the medical field and it is having an Fscore 0.75. In our approach, we have cascaded image adjustment filter, Otsu segmentation, Bit plane slicing to detect the mitotic cells in the histopathological image is simple in computational cost and higher accuracy (0.86) compared to conventional methods. In future, the accuracy of the method and computational cost can be enhanced by working on GPU platform.

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