

Automation of Liver Hypertrophy by Extracting Nucleus Count

¹Ravindranath K, ²SUSHMA G

¹Asst Professor, Dept of ECE, DBIT , Bangalore, India,
e-mail:ravindranath321@gmail.com

²Asst Professor Dept of ECE, Alliance university, Bangalore, India

Abstract— Liver Hypertrophy is the case where the excessive enlargement of the organ takes place if the condition is not treated at the early stage it later leads to necrosis and cirrhosis to identify the condition proper diagnosis has to be done, to support the diagnosis I have come up with an paper where the enlargement is identified by reduction in the number of cells in the cytoplasm of the standard size image (which is obtained from the electron microscope) the nucleus is been extracted from the tissue and the number is used to conclude the case.

Keywords—Hyper trophy , cell, Nucleus,Tissue.

I. INTRODUCTION

The advancement in the medical field is scaled to a greater heights but still there is a serious threat to human life due to negligence of diseases at initial stages, indicating symptoms of the major damage at advanced stages, sometimes it may cause death too one such case is hypertrophy (derived from Greek word hyper means excessive and trophy means enlargement) - condition in which the liver cells size is enlarged. The cell count of standard image size 317X295 for normal person is 11 and abnormal person is 6. At the advanced stages, it leads to necrosis and cirrhosis/fibrosis (the cell size is enlarged such that the overlapping takes place with the adjacent cells).

The development of my module ensures the early detection of the Hypertrophy disease at the cell level with greater accuracy and at lower cost despite of availability ratio of the physicians compared to the patients and available equipments are less so we can save precious life of the patients.

The methodology I have proposed to detect the hypertrophy disease at the cell level is based on the nucleus count algorithm.

II. APPROACH TO DETECT THE HYPERTROPHY CONDITION

Block diagram implementation

Samples can be collected from patient through different biopsy techniques example

Grenze ID: 02.ICCTEST.2017.1.153

© Grenze Scientific Society, 2017

- Needle biopsy
- Surgical biopsy
- Stereotactic biopsy
- Ultrasound

The collection of sample depends on the amount of sample required

Segmentation

Segmentation is the process of partitioning an image into a set of non-overlapping regions whose union is the entire image. It is also defined as the process of classifying the pixels as foreground or background. The pixel intensities which are determined to be foreground will be used for the analysis of cell detection. The pixel intensities which are determined to be background are considered as noise which will be eliminated. In our project, the part which is the particular segment of interest is separated from the background segment.

Since the segmentation involves only simple subtraction and no multiplication or addition, this method reduces the power, area and increases speed during the implementation.

Different methods have been used to choose the best method of segmentation which reduces the computation time and complexity while maintaining the accuracy

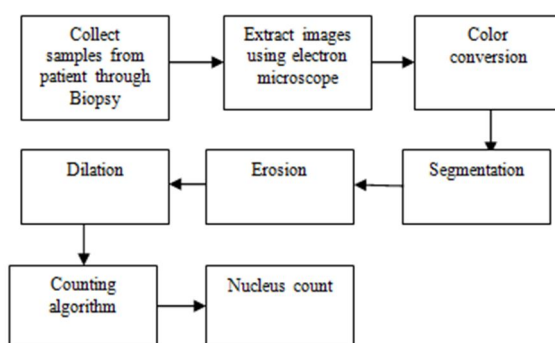


Figure 2.1: system module

Method- I

The cell count is obtained based on stain, as the cytoplasm stain's red in color and nucleus stain black in color so nucleus can be detected based on the different colors through vision large number of colors present was red and magenta. So these components are held and other components are removed to extract the nuclei count from the tissue as shown in Fig 2.2 the darker parts were nuclei and lighter parts (red) represent cytoplasm

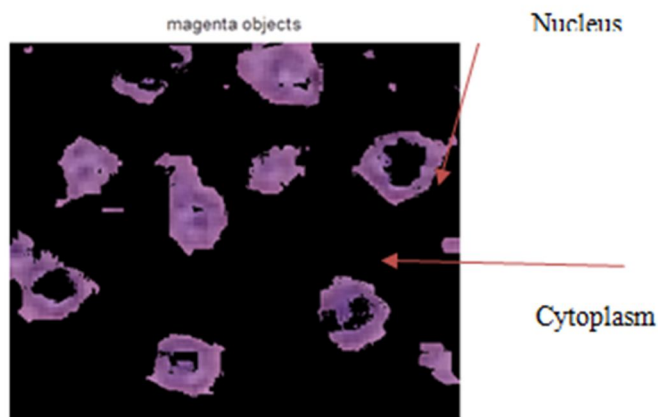


Figure 2.2: Image showing the presence of Magenta objects as nucleus

This procedure is repeated for different colors to check its presence if the particular color is present then it is retained and other Colors are removed to extract the region of interest.

The disadvantage of the method is the identification of colors and the computational steps.

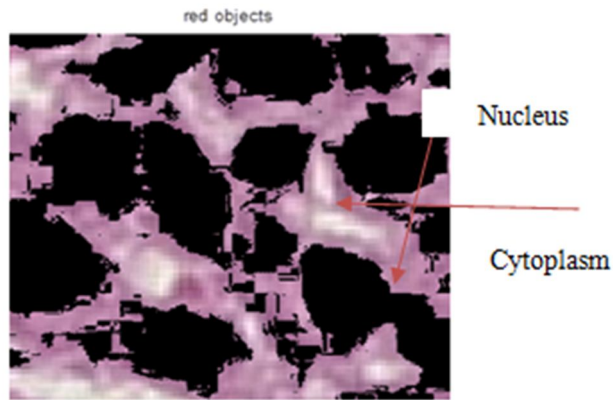


Figure 2.3: Image showing the presence of Red objects as cytoplasm

Method-ii

The color image is made up of the three color components red, green and blue. Nucleus count is extracted based on the presence of the red, blue and green components. Here particular color is eliminated and the other two colors are retained and the procedure is repeated for other colors as shown in the Fig's 2.5, 2.6 and 2.7.

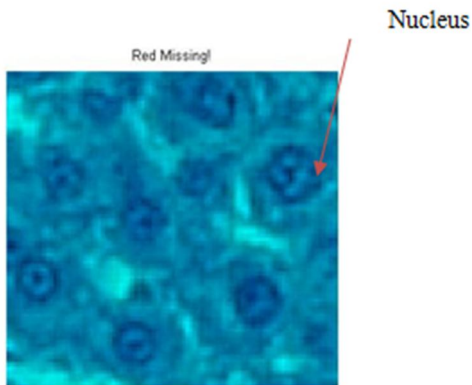


Figure 2.5: Image showing the missing of red components

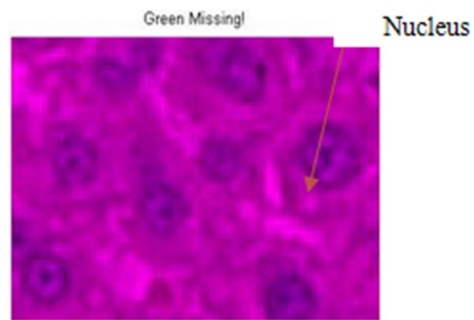


Figure 2.6: Image showing the missing of green components

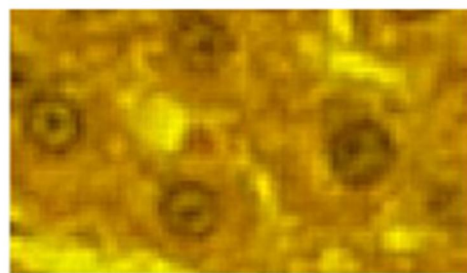


Figure 2.7: Image showing the missing of blue components

In spite of the method providing the exact nucleus count the disadvantage is the need for checking three different colors with high computational steps.

Method -iii

The next method of segmentation employed is edge detection in which the algorithm checks for sharp edges and sudden change in intensity levels.

Different edge detection algorithms are used to segment the nucleus from cytoplasm of cell some of the techniques are as follows.

1. Sobel edge detection
2. Canny edge detection
3. Prewitt edge detection
4. Compass edge detection
5. Robert edge detection

The output these edge detection algorithms are shown in Fig 2.7



Figure 2.7a: Original image

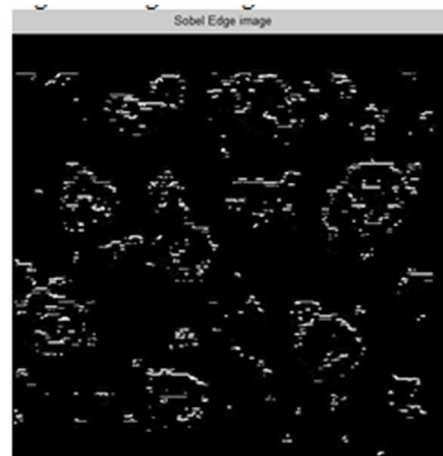


Figure 2.7b: Sobel edge detection

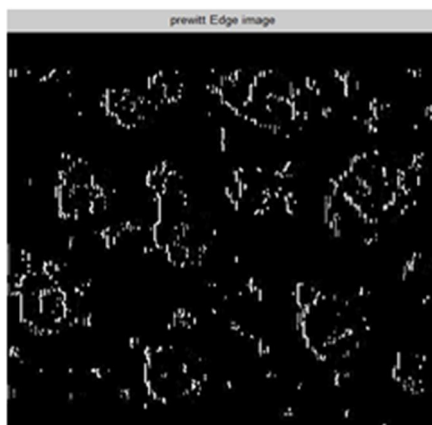


Figure 2.7c: Prewitt edge detection

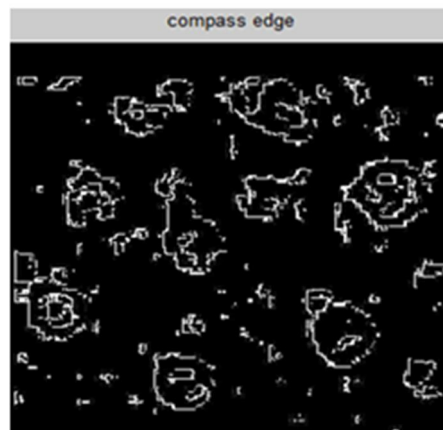


Figure 2.7d: Compass edge detection

Comparison of edge detection algorithms:

Compass method has shown the better results compared to other detection algorithms with the edges shaped well the disadvantage of edge detection is the computation steps.

Method- IV

Next method used to extract the nuclei count from the tissue with less complexity and computation steps is based on threshold value here used is 0.45 in the gray image the components with less than threshold are made to black (0) and greater than threshold are made white (255) given by equation 2.1 which gives the image as shown in fig 2.8 with some additional noise components which can be removed through dilation, erosion and other morphological operations

$$f_{bw}(x,y) = \begin{cases} 0 & \text{if } p(x,y) < \text{Threshold limit} \\ 255 & \text{if } p(x,y) > \text{Threshold limit} \end{cases}$$

f_{bw} represents the final binary image, $p(x,y)$ = pixel value of a particular image

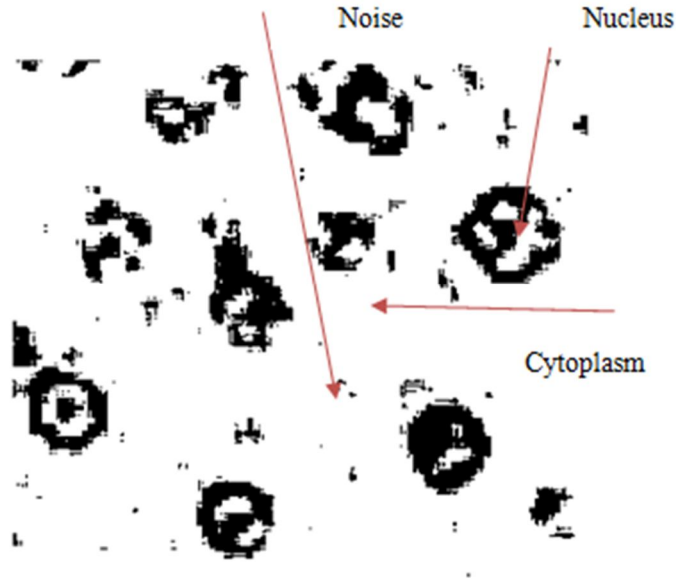


Figure 2.8: Image representing the binary image

Comparison of different segmentation techniques

TABLE II(1): COMPARISON TABLE OF SEGMENTATION

| Methodologies (segmentation) | Performance | Complexity | Computation steps |
|------------------------------|-------------|------------|-------------------|
| Color | Good | High | More |
| Color intensity | Better | High | More |
| Edge detection | Good | High | Less |
| Intensity | Best | Low | Less |

III. MORPHOLOGICAL OPERATIONS

The threshold binary image obtained after segmentation process will have noise component present in the image. This can be filtered by the application of the morphological operations such as Erosion allows objects to be expanded from its original borders. Dilation shrinks the objects by etching away its boundaries. The Block diagram of the Morphology module is shown in the Fig.3.1dilation performed followed by erosion on the input image.

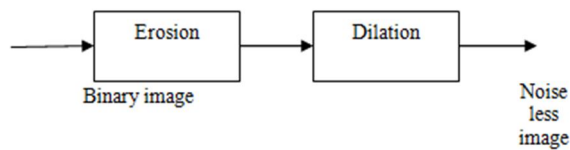


Figure 3.1: Morphological operation

Erosion

It is a type of morphological operator which increases the cell size in the image by adding pixels to its boundaries. It also removes the noise in the image which has size less than the structuring element. The number of pixels removed from the object in the image depends on the size and shape of the structuring element used to process the image. It takes in the binary image and a 3*3 structuring element as the inputs. The structuring element moves over the input image by “OR” ing all the surrounding structuring elements except the middle one. The resultant value is applied to the input image as shown in Fig 3.2.

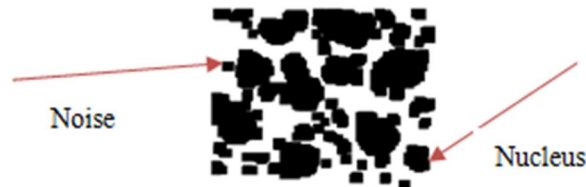


Figure 3.2: Output of erosion

Dilation

It is a type of morphological operator which increases the cell size in the image by adding pixels to its boundaries. By enlarging the image of the cell. It opens up the cell region in an image which was partially eroded during the erosion operation. The number of pixels removed from the objects in an image depends on the size and shape of the structuring element used to process the image. It also uses a 3*3 structuring element similar to erosion.

It takes the eroded image and a 3*3 structuring element as the inputs. The structuring element moves over the input image by “AND” ing all the surrounding structuring elements except the middle one. The resultant value is applied to the input image as shown in Fig 3.3.

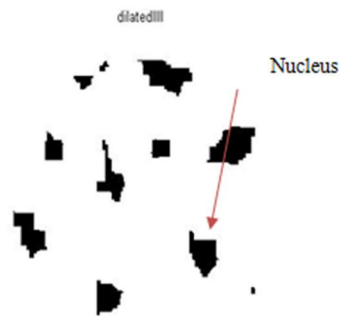


Fig 3.3: Output of dilation



Fig 3.4: output of edge detection

Edge detection

The purpose of detecting sharp changes in image brightness is to capture important events and changes in properties of the world. It can be shown that under rather general assumptions for an image formation model, discontinuities in image brightness are likely to correspond to:

- discontinuities in depth,
- discontinuities in surface orientation, In the ideal case, the result of applying an edge detector to an image may lead to a set of connected curves that indicate the boundaries of objects and surface markings as well as curves that correspond to discontinuities in surface orientation. Thus, applying an edge detection algorithm to an image may significantly reduce the amount of data to be processed and may therefore filter out information that may be regarded as less relevant, while preserving the important structural properties of an image. If the edge detection step is successful, then the subsequent task of interpreting the information contents in the original image may therefore be substantially simplified as shown in Fig 3.4

IV. NUCLEUS COUNT ALGORITHM

Steps involved in the nucleus count algorithm is as follows:

- invert the edge detected image so as to get the black outline
- scan the rows and columns of the image
- initialize the count value equal to 5
- start row wise search for the black pixel
- if it is a hit make pixel value equal to count else continue step 4 until row is checked
- Add 5 to previous count continue steps 4 and 5
- Continue until entire image is completed
- Finally divide the count by 5, the now count value is the exact count.

V. RESULTS

The edge detected image is inverted so as to get the nucleus boundaries with black color as shown in fig 4.1, so the exact nucleus count is obtained with less chances of error.

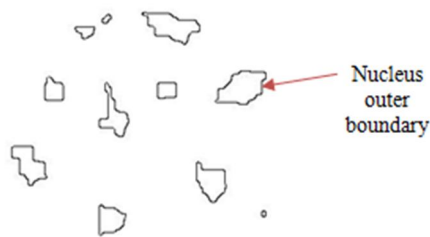


Figure 4.1: image showing the nucleus boundary

The MATLAB showing the nucleus count displayed as shown in the Fig 4.2

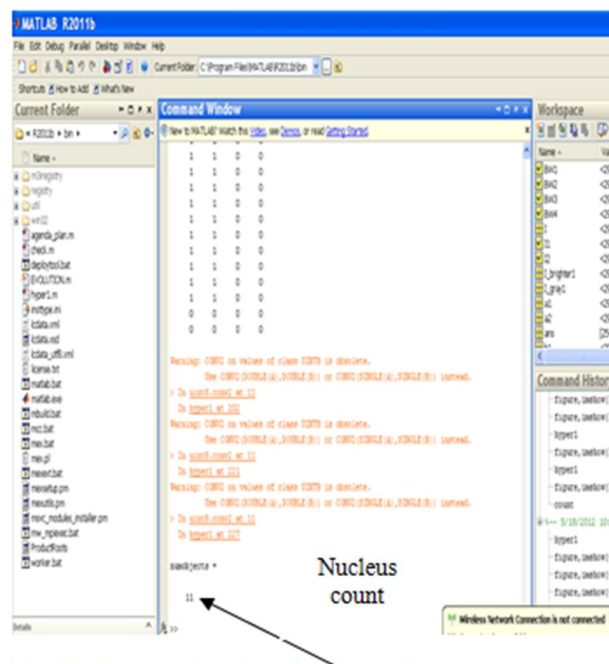


Figure 4.2: Number of nucleus found were 11

From Fig 4.3 and 4.3 we can observe that the nucleus count has been reduced drastically indicating the condition of hypertrophy.

The same procedure can be applied for any image where size is not constraint.

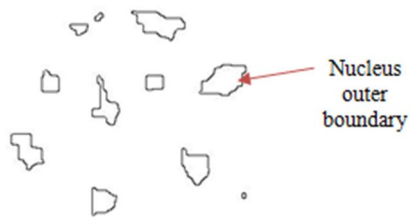


Figure 4.3: Number of nucleus found were 11 for healthy person image

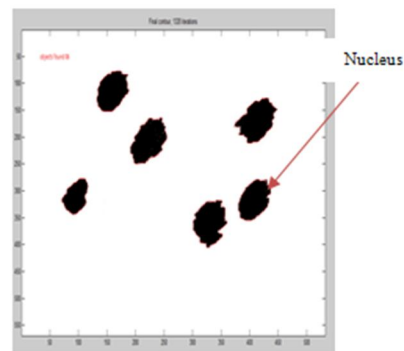


Figure 4.4: Number of nucleus found were 6 for person detected with hypertrophy

VI. CONCLUSION:

The paper deals with the early stage detection of hypertrophy disease by counting the number of nucleus present in the image. Thereby it ensures that the liver cells are not further affected or else it might lead to necrosis and further to cirrhosis.

REFERENCES

- [1] C. Li, R. Huang, Z. Ding, C. Gatenby, D. Metaxas, and J. Gore, "A variational level set approach to segmentation and bias correction of images with intensity inhomogeneity," *Int Conf Med Image Comput Comput Assist Interv*, vol. 11, no. Pt 2, pp.1083–91, 2008.
- [2] A Ruiz, M Ujaldon, J.A Andrades, J. Becerra, Kun Huang, T. Pan, and J. Saltz, "The gpu on biomedical image processing for color and phenotype analysis," *Proceedings of IEEE BIBE*, pp. 1124–1128, 2007.
- [3] A.E. Carpenter, T.R. Jones, M.R. Lamprecht, C. Clarke, I.H.Kang, O. Friman, D.A. Guertin, J.H. Chang, R.A. Lindquist, J.Moffat, P. Golland, and D.M. Sabatini, "Cellprofiler: image analysis software for identifying and quantifying cell phenotypes," *Genome Biol.*, vol. 7, no. 10, 2006.
- [4] W.Wang, J.A. Ozolek, and G.K. Rohde, "Detection and classification of thyroid follicular lesions based on nuclear structure from histopathology images," *Cytometry A*, 2010, In Press.
- [5] S. Haker, L. Zhu, A. Tennennaum, and S. Angenent, "Optimal mass transport for registration and warping," *Intern. J. Comp. Vis.*, vol. 60, no. 3, pp. 225–240, 2004.
- [6] Y. Rubner, C. Tomassi, and L. J. Guibas, "The earth mover's distance as a metric for image retrieval," *Intern. J. Comp. Vis.*, vol. 40, no. 2, pp. 99–121, 2000.
- [7] Y. Boykov and G. Funka-Lea, "Graph cuts and efficient n-d image segmentation," *Intern. J. Comp. Vis.*, vol. 70, no. 2, pp. 109–131, 2006.
- [8] T. Peng, W. Wang, G.K. Rohde, and R.F. Murphy, "Instancebased generative biological shape modeling," *Proceedings of the 2009 IEEE International Symposium on Biomedical Imaging*, pp. 690–693, 2009
- [9] Ohata M, Koyama Y, Suzuki T, et al. Effects of tea constituents on cell cycle progression of human leukemia U937 cells. *Biomed Res* 2005;26(1):1-7