

# Segmentation Of Medical Images

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**Abstract**—Breast cancer is the most prevailing type of cancer in women and men in and around the world and mostly in India. Breast cancer is growing as one of the most chronic diseases of this age, because of inadequate advancement in medical field pathologists perform qualitative analysis of tissues through visual inspection. This could produce subjective results and is not suitable for large scale processing. The prediction of the accurate percentage of cancer on H and E image is not convincing. H and E -Hematoxylin and Eosin is a conventional, highly seasoned method that allows the localization of an antigen within a cell or a tissue with high resolution. H and E images are used for disease diagnosis, biological researchers and drug development. The methodology used is the neural network (NN) to segment H and E images to acquire the quantitative measurements of the stained nucleus for the determination of over-expressed HER2 protein.

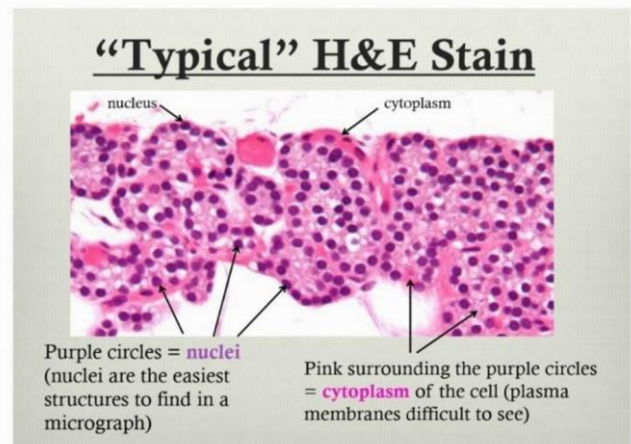


Figure 1: H&E Image

## I. INTRODUCTION

Breast cancer is the most prevailing type of cancer in women and men in and around the world and more in India. Breast cancer is growing as one of the most chronic diseases in this age because of the lack of advancement in the medical field. In the recent trends in image processing, it shows how the medical field can be engineered with the latest technologies. Few problems due to the manual assessment of histology images, such as inter- and intra-observer variability, inability to assess subtle visual features, and the time taken to examine whole slides, can be avoided with the use of computational pathology with the improvements in computer vision techniques and hardware. For the sake of conceptualizing under the microscope, different structures of the tissue are colored with different stains. Then, a detailed study on these stained tissues has been for the detection of lesions or tumors done by a pathologist. Quantitative examination can be used to support pathologists' decision about the closeness or the non-appearance of a disease, besides to help in infection development evaluation. With the use of new advancements in image processing techniques in computer vision several methods have been used for the detection of breast cancer accurately. This project will give the most accepted computer-aided technique for the analysis of breast cancer from a histopathology image.

## II. NEED OF PROJECT

Segmentation of medical image is done so that the accurate percent of protein can be quantified from an H and E image so that it will help in predicting the stage of cancer with accurate measures. At present no such system is developed in pathology field that can quantify the accurate percentage of proteins in a H and E image so in this project we are going to overcome the present system challenges.

Limitation of present visual system are:

- Difficulty in counting positive (or negative) cells
- Overlapped stained nuclei
- Variability of immunostaining presence of other irrelevant objects
- Takes time to manually count these cells
- Wide intra and inter observer results because of subjectivity.

## III. LITERATURE SURVEY

- Breast Cancer in IHC -Nucleus:
  - (a) Di Cataldo, Santa, et al. "Automated segmentation of tissue images for computerized IHC analysis." *Computer methods and programs in biomedicine* 100.1 (2010): 1-15. This paper [1] presents two automated methods for the segmentation of immunohistochemical tissue images that overcome the limitations of the human intervention for assessment and the use of the existing computerized techniques. The first independent method, based on unsupervised color clustering, recognizes the target cancerous areas automatically in the specimen and disregards the stroma; the second method, based on color separation and morphological processing, detects automated segmentation of the nuclear membranes of the cancerous cells. Extensive experimental results on real tissue images demonstrate the accuracy of our techniques compared to manual segmentation; additional experiments show that our

techniques are more performed in immunohistochemical images than the popular approaches based on active contours or supervised learning. The proposed procedure can be exploited for any applications that require tissues and cell exploration and to perform reliable and standardized measures of the activity of specific proteins involved in multi-factorial genetic pathologies.

(b) Azimi, Vahid, Young Hwan Chang, Guillaume Thibault, Jaclyn Smith, Takahiro Tsujikawa, Benjamin Kukull, Bradden Jensen, Christopher Corless, Adam Margolin, and Joe W. Gray. "Breast cancer histopathology image analysis pipeline for tumor purity estimation." In *2017 IEEE 14th International Symposium on Biomedical Imaging (ISBI 2017)*, pp. 1137-1140. IEEE, 2017. In this paper[7] we develop a quantitative image analysis pipeline which includes annotation, classification, and segmentation. The method was introduced to provide a systematic comparison between pathologists' TP and image-based TP estimations. We envision that this framework will allow us to do a better understanding of TP estimation based on quantitative image analysis.

- Breast Cancer In IHC Membrane

(a) Kumar, Neeraj, Ruchika Verma, Sanuj Sharma, Surabhi Bhargava, Abhishek Vahadane, and Amit Sethi. "A dataset and a technique for generalized nuclear segmentation for computational pathology." *IEEE transactions on medical imaging* 36, no. 7 (2017): 1550-1560. In this paper[8] Nuclear segmentation in digital microscopic tissue images can enable the extraction of high-quality features for nuclear morphometrics and other analysis in computational pathology. Conventional image processing techniques such as watershed segmentation and Otsu thresholding do not work effectively on challenging cases, such as crowded nuclei and chromatin sparse. In contrast, segmentation using machine learning can generalize across various nuclear appearances. However, training algorithms of machine learning require datasets of images in which a huge number of nuclei have been annotated. Publicly accessible and annotated datasets, along with widely agreed upon metrics to compare techniques, have catalyzed tremendous innovation and progress on other image classification problems, specifically in object recognition. Inspired by their success, we introduce a huge dataset of HE stained tissue images that can be accessed publicly with more than 21,000 pink stained annotated nuclear boundaries, whose quality was validated by a medical doctor. Our dataset is taken from multiple hospitals that include various nuclear appearances from several patients, organs and disease states, techniques trained on it are likely to generalize well and work right on other HE stained images. We also propose a new metric to evaluate thesegmentation of nucleus results that penalizes object and pixel level errors in a uniform manner. Unlike previous metrics where only one type of error is penalized. We also propose a deep learning based on segmentation technique that lays special emphasis on identifying the nuclear boundaries, including those between the touching or overlapping nuclei, and works well on a diverse set of test images.

(b) Pezoa, Raquel, Rodrigo Rojas, Luis Salinas, Luis Pizarro, J. Reyes, and R. Gonzales. "Segmentation of IHC stained Breast Tissues Images using SVM." Center of Technological Innovation in HPC (CTIHPC) Universidad Tecnica Federico. 2015. The present study[3] is focused on the processing of breast cancer images, specifically immunohistochemistry (IHC) stained images. IHC is a technique which allows the detection of specific proteins in

tissue sections. This technique is fundamental for patient treatment and the prognosis of certain cancers. The present study is focused on a specific IHC technique, that allows the detection of HER2 protein over-expression and is displayed by membrane staining known as HercepTest. As a rule, pathologists perform qualitative analysis of tissues through visual inspection, this produces subjective results and which is not suitable for large scale processing. This paper describes the use of Support Vector Machine (SVM) to segment IHC images in order to obtain quantitative measurements of the stained membranes for the determination of over-expressed HER2 protein.

(c) Pezoa, R., Maureira-Fredes, C., Arce, P., Hartel, S., Salinas, L. and Torres. Segmentation of HER2 protein overexpression in immunohistochemically stained breast cancer images using Support Vector Machines." In *J. Phys. Conf. Ser. Vol. 762*, p. 012050, 2016. Breast cancer is one of the most common cancers in women worldwide. Patient therapy is done after the analysis of immunohistochemically (IHC) stained tissue sections of the patient. The analysis of HER2 overexpression by immunohistochemistry helps to determine when patients are suitable for HER2-targeted treatment. Computational HER2 overexpression analysis is still a challenging task and an open problem principally because of the subjectivity of the specialists to assess the samples and variability of immunohistochemistry tissue samples. In addition, the immunohistochemistry process can produce diverse artifacts that makes it difficult for the HER2 overexpression assessment. In this paper[5] we study the segmentation of HER2 overexpression in IHC stained breast cancer tissue images using a support vector machine (SVM) classifier. We assess the SVM performance using diverse color and texture pixel-level features including the RGB, CMYK, HSV, CIE L\*a\*b\* color spaces, color deconvolution filter; and Haralick features. We measure classification performance for three datasets containing a total of 1750 H and E images that were previously labelled by a pathologist.

#### IV. METHODOLOGY

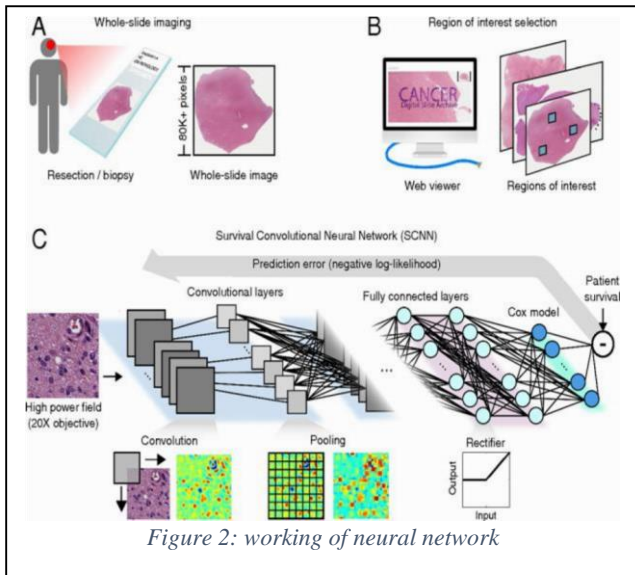


Figure 2: working of neural network

1. In this paper neural networks technique is used initialization is the first step we do in neural networks this is done because before we use weights we have to initialize them, because we don't have values for the weights yet, we use random values between 0 and 1. In python we use random. Seed to generate random numbers.
2. The second step is to define and format network input and target data.
3. The third step is to divide the data into three sets training data, test data and validation.
4. The fourth step is to create feed forward, back propagation three network layers and this is done to train our data in a better way so that it gives us a better accuracy
5. The fifth step is to train the network and for training neural network has to undergo many epochs or iteration and this is done in order to reach the optimal weights and biases that will give us the desired output and accurate prediction for the given input.
6. The sixth step is to make the total error zero if the total error is less than the final target error we can simulate the network and end the training and if the total error is not zero we need to do the process gain and make it zero or less than the final target error.
7. Last and final step is to simulate the network after all the above steps are satisfied and end the

process.

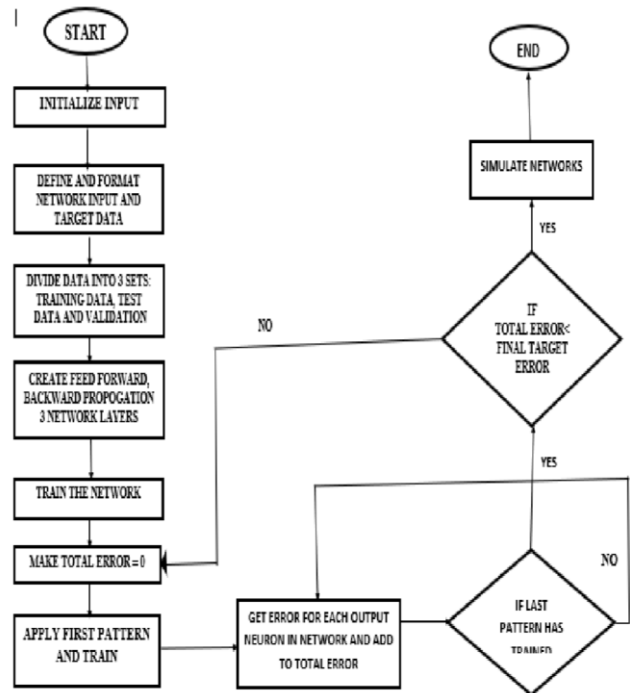


Figure 3:Flow Chart Of Program

V. RESULTS & DISCUSSION

Accuracy Percentage:

```

Console 1/A
Train on 1728 samples, validate on 192 samples
Epoch 1/10
1728/1728 [=====] - 2s 1ms/step - loss: 3.5788 - accuracy: 0.7865 -
val_loss: 0.3944 - val_accuracy: 0.8802
Epoch 2/10
1728/1728 [=====] - 2s 931us/step - loss: 0.5525 - accuracy: 0.8432 -
val_loss: 0.6085 - val_accuracy: 0.8594
Epoch 3/10
1728/1728 [=====] - 2s 910us/step - loss: 0.2661 - accuracy: 0.8756 -
val_loss: 0.5104 - val_accuracy: 0.8594
Epoch 4/10
1728/1728 [=====] - 2s 935us/step - loss: 0.1899 - accuracy: 0.8877 -
val_loss: 0.5235 - val_accuracy: 0.8594
Epoch 5/10
1728/1728 [=====] - 2s 1ms/step - loss: 0.1912 - accuracy: 0.8883 -
val_loss: 0.5313 - val_accuracy: 0.8594
Epoch 6/10
1728/1728 [=====] - 2s 959us/step - loss: 0.1940 - accuracy: 0.8889 -
val_loss: 0.5398 - val_accuracy: 0.8594
Epoch 7/10
1728/1728 [=====] - 2s 943us/step - loss: 0.1866 - accuracy: 0.8895 -
val_loss: 0.5529 - val_accuracy: 0.8690
Epoch 8/10
1728/1728 [=====] - 2s 971us/step - loss: 0.1933 - accuracy: 0.8779 -
val_loss: 0.5627 - val_accuracy: 0.8750
Epoch 9/10
1728/1728 [=====] - 2s 969us/step - loss: 0.1861 - accuracy: 0.8947 -
val_loss: 0.5377 - val_accuracy: 0.8594
Epoch 10/10
1728/1728 [=====] - 2s 943us/step - loss: 0.1872 - accuracy: 0.8918 -
val_loss: 0.5747 - val_accuracy: 0.8750
Accuracy: 88.0787458986511%
In [3]:
    
```

Figure 4: Results

The algorithm used to train the model is neural networks and the model will detect the malignant and benign H and E stain tissues images of breast cancer and these images are of [50,50] which is the resized form of the original image and [50,50] are given as an input for better computation and result of the model, 1200 breast cancer tissue images are used as dataset on which the neural network will work. The model uses two activation functions, first is 'relu'(y = max(0, x)) and the second is 'softmax' ((σ): g(z) = 1 / (1 + e<sup>-z</sup>)) to increase the accuracy and the model is trained with 30 epochs and three layers of networks to retain a better accuracy. With the use of these activation function it gave a very good percentage of accuracy of 80.07 percentage.

**Activation Functions used here are:****i. SOFTMAX:**

- The softmax function squashes the outputs of each unit to be between 0 and 1, just like a sigmoid function. But it also divides each output such that the total sum of the outputs is equal to 1 (check it on the figure above).
- The output of the softmax function is equivalent to a categorical probability distribution, it tells you the probability that any of the classes are true.
- Mathematically the softmax function is shown below, where  $z$  is a vector of the inputs to the output layer (if you have 10 output units, then there are 10 elements in  $z$ ). And again,  $j$  indexes the output units, so  $j = 1, 2, \dots, K$ .

$$(\sigma): g(z) = 1 / (1 + e^{-z_j})$$

**ii.****RELU:**

A rectified linear unit has output 0 if the input is less than 0, and raw output otherwise. That is, if the input is greater than 0, the output is equal to the input. ReLUs' machinery is more like a real neuron in your body. ( $y = \max(0, x)$ )

ReLU activations are the simplest non-linear activation function you can use, obviously. When you get the input is positive, the derivative is just 1, so there isn't the squeezing effect you meet on back propagated errors from the sigmoid function. ReLUs result in much faster training for large networks. Most frameworks like Tensor Flow and TFLearn make it simple to use ReLUs on the the hidden layers, so you won't need to implement them yourself.

**ACKNOWLEDGMENT**

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**FUTURE SCOPE**

Currently, it is possible to detect the cancer cells in a given picture in future it can be used for finding other skin diseases by providing images to the system.

**CONCLUSION:**

Thus with respect to the above lying scope decided for the project, we have successfully implemented 'segmentation of medical images' which is a prototype which can be used in

hospital and pathology to detect whether the H and E stained breast cancer tissue is malignant or benign and this is achieved by using neural networks algorithm .

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