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Automatic Segmentation of Cell Nuclei in Breast Histopathology Images and Classification Using Feed Forward Neural Network

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Abstract
Automatic image analysis of breast histopathology images helps in efficient detection of breast cancer. Breast cancer is one of the most frequently diagnosed cancers in women. Breast cancer is one of the most common cancers among woman of the developing countries in the world, and it has also become a major cause of death.For cancer diagnosis and grading ,it is essential to examine the tissue specimens of histopathological images. This examination depends on visual interpretation of pathologists .To overcome this problem, it is important to develop computational quantative tool in which segmentation plays a vital role. This paper proposes an efficient segmentation of cell nuclei in breast histopathology images and its classification using neural network. The segmentation of cell nuclei is an important step in automatic analysis of digitized microscopic images, hence Graph cut algorithm is used for segmentation .After segmentation of cell nuclei features are extracted and are given as input to the Feed Forward Neural Network for classification of cell nuclei as benign or malignant.

Keywords— Histopathology image analysis, Graph cut segmentation, Feed Forward Neural Network (FFNN).

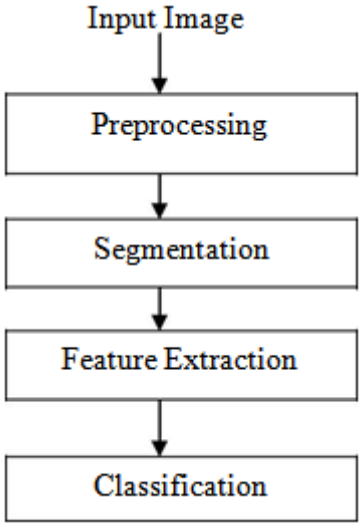
I. INTRODUCTION

Histopathological examination includes examining a biopsy tissue under a microscope for the identification of tissue changes associated with certain disease. Nucleus segmentation is an important task since many of the characteristics of diseases, especially cancer, are expressed in the cell nuclei. The knowledge of microscopic structures and their functions at the cellular, tissue is veryimportant for the study of disease proliferation and prognosis of disease. Also to study and analyze histopathology image under microscope, pathologists identify the morphological characteristics of tissue which indicates the presence of disease like cancer. The biopsy sample is processed and its sections are placed onto glass slides to observe them under microscope for analysis. Pathologist examine the tissue slides under a microscope and observe it at various magnification levels to view cells, nucleus, glands, and detects the resemblance of these structures with normal versus Malignant (diseased)tissue. If the disease detects the grading process is performed which deals with spreading of infected cells all over the tissue. Then for each patient the prognosis and further treatment is planned by considering grade of disease. This diagnosis by pathologist is subjective and prone to inter, intra observer variations. Therefore a quantitative assessment of these images is very essential for objective diagnosis.. Thus, computer assisted disease diagnosis (CAD) plays a very important role and has become a major research subject in histopathological imaging and diagnostic where different image processing techniques can be used to analyze these images fordisease diagnosis and prognosis. Therefore, histology provides a scientific foundation for clinical research, education, and practice.

The aim of this paper is to investigate robust and accurate image analysis algorithms for computer-assisted interpretation of histopathology images. Different image processing techniques will be applied for image texture classification, gland & nuclei segmentation, cell counting, cell type identification or classification to deriving quantitative measurements of disease features from Histological images and automatically determine whether a disease is present within analyzed samples or not. Also this research will help to decide the different grades or severity of disease if the disease is present in the sample. Computer aided histopathological study has been conducted for various cancer detection and grading applications. Using different segmentation, feature extraction and classification techniques the researchers analyzed histopathology images. The paper is organized to discuss the need for, and analyze

the procedure for computer aided histopathology image segmentation and classification. After acquiring digital histology image through biopsy sample, the manual examination of images leads to variability in diagnosis. To overcome this problem, computer assisted systems are employed which gives objective analysis of diseases. The basic steps required for implementing computer assisted analysis system consists of digital image processing techniques such as image segmentation, feature extraction, classification etc.

II. METHODOLOGY



A. Pre processing

The aim of pre-processing is an improvement of the image data that suppresses unwanted distortion or enhances some image features important for further processing. Image pre-processing is the technique of enhancing data images prior to computational processing. The goal of image pre-processing is to increase the accuracy of the data during the image processing.

1) Conversion of colour image into Gray scale image

The image should be converted to grayscale because the results are good, processing of the image is easy and the intensity of the image.

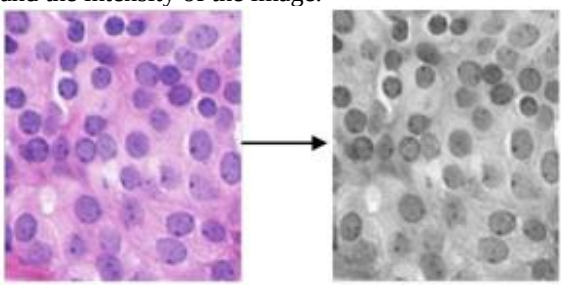


Fig. 1 Gray Scale Image Conversion

2) Reducing noise using Filter

Filtering in image processing is a process that cleans up appearances and allows for selective highlighting of specific information. Histopathology images are corrupted with different kinds of noise while image acquisition.The noise in the image is reduced by using Median fliter.

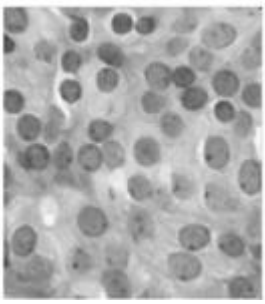


Fig. 2 Filter Image

3) Image Enhancement

It is the process of adjusting digital image so that the results are more suitable for display or future image analysis, such as sharpen or brighten an image, making it easier to identify key features.In this paper fuzzy enhancement technique is used.

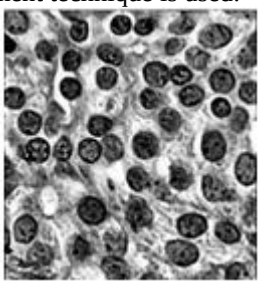


Fig. 3 Fuzzy enhancement Image

B.Graph cut segmentation

Graph cut segmentation is an image segmentation method based on combinatorial optimization techniques. The method is applicable to images of any dimension and gives a binary partitioning of the image into background and object. In graph cut segmentation the image is interpreted as a graph, where image elements correspond to nodes and paths between adjacent elements correspond to graph edges. Each graph edge is assigned a nonnegative cost. Two special nodes are added to the graph, the source node and the sink node. Image elements that are a priori known to belong to the object are connected to the source node with zero cost edges. Similarly, elements that are known to belong to the background are connected to the sink node. A cut on the a graph is a set of edges that, if removed from the graph, separate the source from the sink. A cut thus associates each node with either the source or the sink. The cost of a cut is the sum of the cost of all edges in the cut, and a minimal cut is a cut such that no other cut has a lower cost. A computationally efficient

algorithm for computing minimal graph cuts was described in (Boykov and Kolmogorov, 2004). The fundamental idea of graph cut segmentation is that a minimal cut on the graph of an image corresponds to an optimal partitioning of the image into background and object, subject to the constraints given by the edge weights and the geometry of the graph. An illustration of this concept is shown in Fig.4. The graph cut method produces a binary segmentation, where the boundary between the object and the background is located at strong edges in the image.

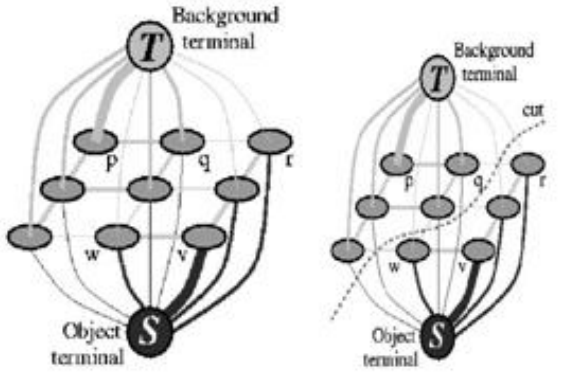


Fig.4 Principle of graph cut segmentation. Left: Initial state of the graph. Right: A cut on the graph.

Segmentation of an object from the background can be formulated as a binary labeling problem. Given a set of labels *L* and a set of sites *S*, the labelling problem is to assign a label $fp \in L$ to each of the sites $p \in S$. The graph cuts framework proposed by Boykov and Jolly [9] addresses the segmentation of a monochrome image, which solves a labeling problem with two labels. The label set is $L = \{0,1\}$,where 0 corresponds to the background and 1 corresponds to the object.

Let $f = \{f_p | f_p \in L\}$ stand for a labeling, i.e. label assignments to all pixels.

An energy function is formulated as:

$$E(f) = \sum_{p \in S} Dp(fp) + \lambda \sum_{\{p,q\} \in N} \omega pq.T(fp \neq fq)$$

On the right hand side of above equation, the first term is called data term, which consists of constraints from the observed data and measures how sites like the labels that *f* assigns to them. where *Dp* measures how well label *fp* fits site *p*. A common approach, and the one we use in our work, is to build the foreground and background histograms models from the user input seeds, respectively. Then the *Dp*(*fp*) are defined as the negative log likelihoods of the constructed forground/background models.

The second term is called the smoothness term and measures the extent to which *f* is not piecewise smooth. where *N* is a neighborhood system, such as a 4-connected neighborhood system or an 8-connected neighborhood system. The smoothness term typically used for image segmentation. Here

$T(fp \neq fq)$ is 0 if $fp = fq$ and 1 otherwise. This model is a piecewise constant model because it encourages labelings consisting of several regions where sites in the same region have the same labels.

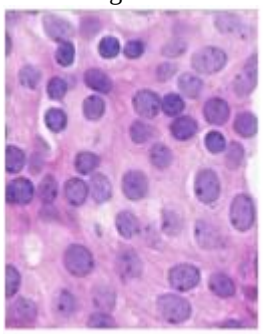


Fig.5 Histopathology Image

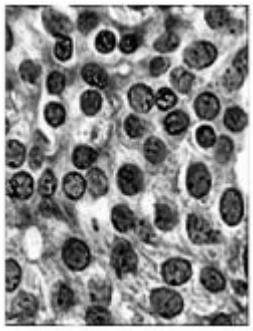


Fig.6 Fuzzy enhancement Image

Fig.7 Initial Binarization

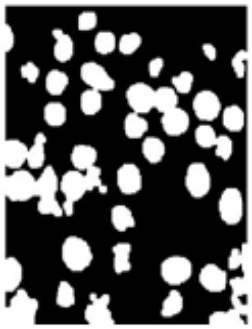


Fig.8 Graph cut algorithm

C.Feature Extraction

Automated cancer diagnosis relies on capturing (i) the deviations in the cell structures , and (ii) the changes in the cell distribution across the tissue . The features are extracted to quantify these changes ina given sample. To measure the deviations at the cellular-level, morphological, textural, fractal, and/or intensity-based features can be used. The extraction and use of relevant image features for automated analysis of cancer imagery is a topic of great interest. The vast majority of these features are nuclear features. After segmentation, features are extracted either at the cellular or at the tissue-level to measure morphological

characteristics of image for abnormality or to classify the image for different grades of disease. The cellular-level features focuses on quantifying the properties of individual cells without considering spatial dependency between them. For a single cell, the morphological, textural, fractal, and/or intensity-based features can be extracted. The aim of the diagnosis step is (i) to distinguish benignity and malignancy or (ii) to classify different malignancy levels by making use of extracted features.. These can be used for analysis of histology image as 1) normal or abnormal image, 2) for identifying grades of cancer.Gray Scale, Texture,Symmetrical and morphological features are extracted. These extracted features are given as input to feed forward neural network for classification of cell nuclei as benign or malignant.

D.Classification by Neural Network

Neural network is an information-processing unit that is much inspired by the way the human brain works. The human brain consists of an intricate web of billions of interconnected cells called neurons. The study of neural networks aims to understand how such a large collection of connected elements can produce useful computations, such as pattern recognition. In Neural Network the information is processed in parallel all neurons work simultaneously.A neural network learns and does not need to be reprogrammed.

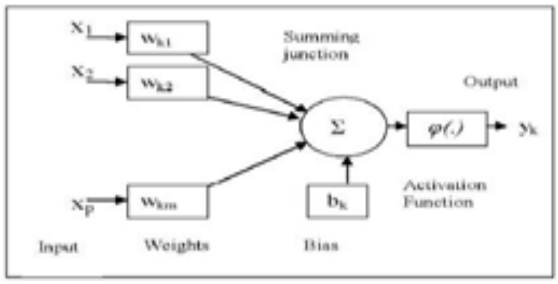


Fig.9 Neural Network

1) Feed Forward Neural Network (FFNN)

FFNN is an ANN based model where connection between units do not form directed cycle. The neurons in this model are grouped into the layers, which are connected to the direction of passing signal. There are no lateral connections within each layer and no feed-backward connections within the network. In FFNN information moves in only forward direction. The information is distributed and processing is parallel. FFNN are trained with a back-propagation learning algorithm, which are the most popular neural networks. The Feed Forward neural network consists of neurons,that are arranged into the layers. The first layer is the input layer, the last layer is called the output layer, and the layers between input layer and output layers are hidden layers. This networks information flows only in one direction that is forward, from input towards the output. The training of such a network with hidden layer is complicated. That's why when there exists an output error; it is hard to know how much error comes from the input nodes, other nodes and how to adjust the weights according to their contributions. The problem can only be solved by finding the effect of all the weights in the network. This is solved by the back-propagation algorithm. In FFNN the output values are compared with the correct answer to compute the value of some predefined error-function. By various techniques, the error then is fed back through the network. By using this information, algorithm adjusts the weights of each connection in order to reduce the value of the error function. The input to this Feed Forward neural network is the features extracted from the cell nuclei of the Histopathology image.The Back propagation algorithm is used to train this Feed forward neural network.

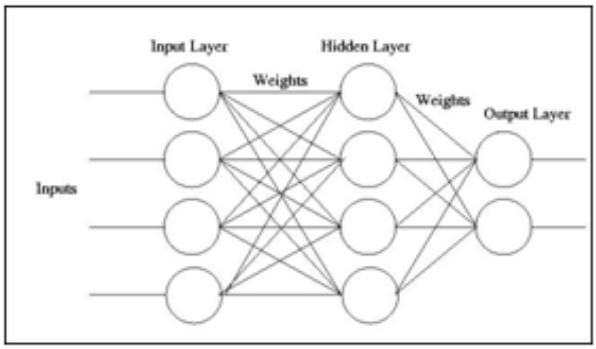


Fig. 10 Feed Forward Neural Network (FFNN)

III. CONCLUSIONS

This paper depicts, efficient segmentation of cell nuclei in breast histopathology image with the help of Graph cut algorithm with reduced segmentation error. After segmentation, texture features, gray scale features are extracted from the cells and these features are given as input to the feed forward neural network which gives correct classification of cell nuclei whether it is benign or malignant.

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