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Malignant Melanoma detection using Digital Image Processing

A Rupali[1], Akhilesh Kumar[2]

[1,2]Department of Computer Science and Engineering,
IMS Engineering College, Ghaziabad, NH-24, Ghaziabad, Uttar Pradesh, India

ABSTRACT

In recent years, due to increase in global warming the risks of several hazardous diseases has also increased. Skin cancer is one of them. There are three types of skin cancer: Basal Cell Carcinoma, Squamous Cell Carcinoma and Malignant Melanoma. Malignant Melanoma is most dangerous and most unpredictable type of skin cancer. Early stage diagnosis of Malignant Melanoma makes it easy to cure. The accuracy of diagnosis of such type of cancer depends upon the training of dermatologists. Dermatologists use ABCD(A: Asymmetrical shape, B: Border irregularity, C: Color Difference, D: Diameter of the mole)[1] rule to detect Malignant Melanoma. Therefore, manual diagnosis is a time consuming process. Hence, there is a need for an automatic system to help the dermatologists for fast and accurate diagnosis. In this paper, we have proposed a method to extract the necessary features of skin tissues which are required to detect Malignant Melanoma. This system takes Histological images of the skin tissues as input. These images are preprocessed and necessary features are extracted. These features are: Nuclei to cytoplasm ratio, Nuclei number, Nuclei size and variance. According to the predefined conditions of the features, the system predicts the presence of cancerous cells in the skin tissues. This system can be used to examine the degree of seriousness of the skin cancer diagnosed patient.

Keywords: *Malignant Melanoma Detection, Histological images, ABCD rule, Nuclei to cytoplasm ratio, Nuclei number, Nuclei size and variance*

1. INTRODUCTION

Malignant melanoma, is a type of cancer that develops from the pigment-containing cells. Melanomas typically occur in the skin, but may rarely occur in the mouth, intestines, or eye. In women, they most commonly infected areas are legs, while in men most commonly occurring area is on the back. Sometimes they develop from a mole with changes such as an increase in size, irregular edges, change in color, itchiness, or skin breakdown. Malignant Melanoma is considered as most unpredictable kind of skin cancer as it becomes difficult to differentiate between a normally occurring mole and a cancerous mole. Malignant Melanoma is a deadly form of skin cancer. Although it accounts for only 4% of all skin cancers, but it is observed that 75% of skin cancer deaths are due to this form of skin cancer. It is also observed that if it is diagnosed in an early stage then it can be easily cured but a slight delay in diagnosis can cause severe damage in skin cells and the cancer can spread to other parts of the body. Melanoma is caused due to presence of melanocytes in the cells of our body. Excessive exposure of skin to ultraviolet radiations is the main cause of Malignant Melanoma.[2] A study says that globally, in 2012, it newly occurred in 232,000 people. In 2015 there were 3.1 million with active disease which resulted in 59,800 deaths. Australia and New Zealand have the highest rates of melanoma in the world. There are also high rates in Northern Europe and North America, while it is less common in Asia, Africa, and Latin America. Melanoma is more common in men than women. Melanoma has become more common since the 1960s in areas which are mostly populated with white people.

The diagnosis of melanoma from melanocytic nevi cannot be performed straight forwardly, especially in the early stage. The Accuracy of prediction of Malignant Melanoma by a dermatologist is based on training which he/she has undergone. Even when the expert dermatologists uses the dermoscopy for diagnosis, the accuracy of melanoma diagnosis is estimated to be about 75-84%[3]. Therefore, for better prediction of early

stage malignant melanoma, a dermatologist needs an automated system which could help him/her. A computer-based system will help in fast result production with much better accuracy. Though a computer is not more intelligent than a human, but can better help feature extraction, parameter calculations and classification. This system is not a substitute for dermatologists instead it will help them to save time of diagnosis, so that the dermatologists can utilize their valuable time in further treatment.

The system will be using a sample dataset containing histological images of both normal skin as well as cancerous skin for training. The relevant features i.e., Nuclei to cytoplasm ratio, Nuclei number, Nuclei size and variance, are extracted. According to some necessary conditions of these extracted features, the normal and cancerous skin images are classified. Now the system uses the previously classified data to predict skin cancer for new images.

2. LITERATURE REVIEW

In previously proposed works for Malignant melanoma detection, the researchers have used basic ABCD rule for detecting Malignant Melanoma[1]. Features to perform skin lesion segmentation that are presented in various researches are: Color, texture, shape and luminance diameter, evolution of moles etc[2]. Many border detection methods are presented in literature[5,6]. Some of the border detection methods include histogram thresholding[7], global thresholding on optimized color channels followed by morphological operations[8], hybrid thresholding[8]. There are many digitital image processing methods which are used for feature extraction, see for example[5,10,11]. In [10], the authors have used the technique of dividing the input image into various clinically significant regions using the Euclidean distance transform for the extraction of color and texture features. In Some techniques, the symmetry feature is calculated based on geometrical measurements on the whole lesion, e.g. symmetric distance and circularity[9] Other studies, propose the circularity index, as a measure of irregularity of borders in dermoscopy images[12,13]. The paper [11] gives the overview of the most important implementations in the literature and compares the performance of several classifiers on the specific skin lesion diagnostic problem.

3. METHODOLOGY

This system performs skin cancer detection according to the flow diagram(shown below this section). The system then using principle component analysis(PCA) for dimensionality reduction and feature extraction. Features such as Nuclei to cytoplasm ratio(NCR), Nuclei count, Nuclei size and Nuclei size variance(Pleomorphism) are extracted. The nucleus to cytoplasm ratio is a parameter defined by the size of a cell's nucleus compared to its cytoplasm. Because of the uncontrolled growth of cancer cells, the NCR is increased. To compute it, we have simply counted the number of 1s present in the binary image (which represent the nuclei) and divided them by the total image size.

To calculate the numbers of nuclei in the histology sample the algorithm counts the number of connected components in an 8-pixel neighborhood.

Pleomorphism describes the variability of size, shape and staining of cells. The additional content of DNA in cancerous cells changes its form and size. Since we already knew the number of nuclei (i.e. the number of connected components in an 8-pixel neighborhood), we counted how many pixels where in each of these and then computed the variance.

Then a graph is plotted between size variance and NCR which plots all cancerous cells in red dots and normal cells in blue dots.

By using this study, now the system is capable of identifying a new image as cancerous or normal.

4. FLOW DIAGRAM

Figure 1. *Flow diagram*

5. METHODS USED

5.1 Image pre-processing

Before analyzing the histological images for features to differentiate cancerous cells from normal cells it is necessary to do some image processing. We have cropped the images to get rid of margins and converted them into grayscale. Now we have extracted the nuclei using a simple thresholding algorithm. In order to isolate it from other small low intensity components, all connected components of the image that had less than 30 pixels are removed. Then, to improve the automatic segmentation and fill the holes in the segmented nuclei binary dilation followed by binary erosion is performed so that size of the nuclei remained unchanged.

5.2 Feature Extraction

Feature extraction is about building new abstract features from the physically meaningful ones. One of the most used methods of feature extraction is Principal Component Analysis (PCA), which can help reduce the dimensionality of our problem by computing features which are orthogonal and thus independent among them. The principal components built by PCA are ordered so that the first component is the one which englobes the maximum variability of the data, the second component is the second direction in which data varies the most, etc. Therefore, we have applied PCA to the extracted feature vectors.

Greatest Diameter (GD): The length of the line passing through lesion centroid and connecting the two farthest boundary points.

$$(x, y) = \sum_{i=0}^{n} \frac{x(i)}{n}, \sum_{i=0}^{n} \frac{y(i)}{n}$$

This formula is also used to calculate the diameter of the mole. If the diameter exceeds the size of 6mm, then it is said to be cancerous mole.

5.3 Data Analytics: Machine Learning

Data analytics is the science of examining raw data with the purpose of drawing conclusions about that information. Machine learning is one of the disciplines of data analytics which uses data and produces a program to perform a task. In our case, the data provided are the features obtained from the histological samples after performing PCA; the program will be a classifier that will perform the task of deciding whether a new sample is cancerous or not.
We studied many classification algorithms from machine learning toolbox from MATLAB and we used Complex Tree, Coarse Gaussian SVM, Linear Discriminant and Subspace Discriminant.

6. RESULTS

In first step the system is successfully able to convert the histological image into grayscale images as shown below.

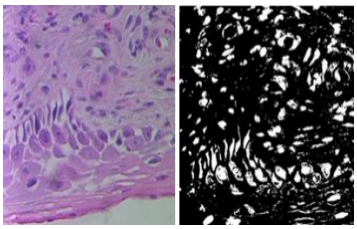

Figure 2. *Histological image(left) converted into Grayscale image*

In second step, the converted grayscale images are processed to extract the relevant features and then are plotted in feature space as shown below.

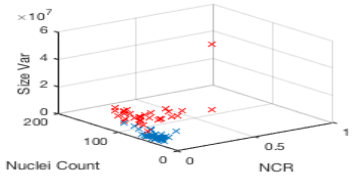

Figure 2. *Plotting of graph of extracted features(red cross are cancer images and blue cross are normal images)*

7. CONCLUSION

In this paper it is clearly observed that the system is detecting the Malignant Melanoma infected skin tissue images accurately and the outputs are correctly plotted in the feature space. It is also observed that the accuracy of the system is around 95%. We can conclude that the proposed method will accurately detect Malignant Melanoma infected skin tissues images. This system can be useful for dermatologists for fast and accurate diagnosis. Using this system, dermatologists can check the degree of seriousness of the patients by looking at the values of nuclei to cytoplasm ratio, Nuclei number and Nuclei size variance so that appropriate and timely treatment can be provided to the patient.

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