

Image Segmentation and Classification for Medical Image Processing

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Abstract: Segmentation and labeling remains the weakest step in many medical vision applications. This paper illustrates an approach based on watershed transform which are designed to solve typical problems encountered in various applications, and which are controllable through adaptation of their parameters. Two of these modules are presented: the lung cancer detection, a method for the segmentation of cancer regions from CT images, a watershed algorithm for image segmentation and brain tumor detection from MRI images. Various GLCM features along with some statistical features are used for classification using Neural network and Support Vector Machine (SVM). We describe the principles of the algorithms and illustrate their generic properties by discussing the results of both applications in 2D MRI images of Brain tumor and CT images of lung cancer.

Keywords: Brain tumor detection, Segmentation, Lung cancer, MRI images, CT images, GLCM, Neural network

I INTRODUCTION

Recently, image processing techniques are widely used in several medical areas for image improvement in earlier detection and treatment stages, where the time factor is very important to discover the abnormality issues in target images, especially in various cancer tumours such as lung cancer, breast cancer, etc. Image quality and accuracy is the core factors of this research, image quality assessment as well as improvement are depending on the enhancement stage where low pre-processing techniques is used based on Gabor filter within Gaussian rules. Following the segmentation principles, an enhanced region of the object of interest that is used as a basic foundation of feature extraction is obtained. Relying on general features, a normality comparison is made. In this research, the main detected features for accurate images comparison are pixels statistical features. Medical Image Segmentation is the process of automatic or semi-automatic detection of boundaries within a 2D or 3D image. A major difficulty of medical image segmentation is the high variability in medical images. First and foremost, the human anatomy itself shows major modes of variation. Furthermore many different modalities (X-ray, CT, MRI, microscopy, PET, SPECT, Endoscopy, OCT, and many more) are used to create medical images. The result of the segmentation can then be used to obtain further diagnostic insights. Possible applications

are automatic measurement of organs, cell counting, or simulations based on the extracted boundary information.

This paper deals with two applications of medical image segmentation namely lung cancer detection and brain tumor segmentation. After segmentation various GLCM features and statistical features are extracted from the segmented image. Using neural network, these features are used to classify the image as normal or cancer image.

In this paper an enhanced method of Artificial Neural Network (ANN) and SVM Classifier model is proposed to segment extracted lung regions from human chest Computer Tomography images. The images are acquired using Computer Tomography imaging techniques from normal subjects and others as candidates for lung cancer diagnosis. A combination of various statistical features are used for detection of lung region lobes. Three diagnostic rules are verified as well defined filters of candidate cancerous regions from the status of candidate to false or true positive status.

This study presents a brain tumor segmentation method for MRI which purpose is to easily segment tumor masses in MRI images with reproducible results. Our pipeline is capable of automatically segment tumor masses, which means that there is no need for manual selection of a starting region, unlike semi-automatic segmentation schemes. We use texture analysis techniques for extracting useful information that allow the discrimination between various types of tumor tissues.

II. RELATED WORK

A. Lung Cancer Segmentation

Over the years many different types of computer aided detection (CAD) systems for detecting and localizing lung nodules have been developed and tested in this research field. Since techniques and computing power have improved over the years, so have the CAD systems.

Gurcan et al. [1] proposed a multistage CAD system that segments the lung regions of interest using k-means clustering and detect lung nodules using rule-based classifiers and linear discriminant analysis (LDA). They report a sensitivity of 84% and an average of 1.74 false positives per slice. McCulloch [2] also proposed a multistage CAD system in which every stage captures different anatomic information and lung structures. Their system produces 8.3 false positives per scan. Ge et al. [3] extracted three-dimensional (3D) features from volumes of interest to detect nodules. Within these features they obtain a sensitivity of 80% with around 0.77 false positives per section. Localizing a nodule on an image or scan means getting the exact x, y- and z-coordinates. With that in mind, Lee et al. [4] proposed a sliding window method, in which moving windows across the image are classified. They report a sensitivity of 100% and 1.4 false positives per slice, tested on 20 selected slices. With the breakthrough of deep convolutional neural networks (CNN) in image classification with the AlexNet [5], developed by Alex Krizhevsky, many computer vision tasks are being done by CNN's. Ever since, the technique is often referred to as "deep learning". They also have found great success in medical imaging applications as Kayalıbay proved in his research [6]. Therefore, more recent CAD systems for detecting lung nodules use CNN architectures. Since CNN's often need many examples to generalize well, Yang et al. [7] investigated whether data augmentation improved performance on a 2D CNN. Their main conclusion is that data augmentation does improve performance on their CNN. In the recent research of Hamidian et al. [8] a 3D CNN is investigated, which reaches a sensitivity of 80% and 22.4 false positives per scan. CT scans are 3D volumes and are usually anisotropic. Deep convolutional networks have also been shown to perform well in 3D segmentation as shown by Milletari et al. [9]. They also have been successfully adapted from 2D to 3D by Cicek et al. [10]

B. Brain Tumor Segmentation

Authors show that segmentation of brain tumor can be achieved by watershed segmentation by grouping pixels of an image based on their intensity values but, suffers from over segmentation problem due, to presence of noise or variation of intensity [11]. In case of the region growing based segmentation user has to select the seed. Hence it needs more interaction of user in selection of seed. Seed is center point of the tumor cells. Region growing method may cause intensity in

homogeneity problem. And it lacks to give accurate results for all the images[12]. Edge detection will give exact and clear boundaries or edges. But its disadvantage is that if the intensity difference between normal and tumor cells is less, it will not be detected. But it will give exact size of tumor when detected. The edge detection technique work well on high contrast images and it lacks to detect the edges in low contrast noisy images due to the weak gradient magnitude [13]. Fuzzy c means is also another approach used used segmentation and detection of abnormal tissues in slice of MRI image [14]. This method involves many mathematical operations and formulas, hence has a high computation complexity like mean shift algorithm, FCM is suitable when the number of clusters is unknown a priori [15]. In marker controlled watershed segmentation the internal and external markers required for segmentation purpose are computed based on connected components of pixels. Internal markers are the connected components of pixels associated with objects of interest. The external markers are the connected components of pixels associated with the background of the objects. These markers are used for segmentation purpose to extract the tumor portion. In marker based segmentation algorithm selecting markers manually is very crucial hence automatic selection of marker is required [16].

III. WATERSHED TRANSFORM FOR IMAGE SEGMENTATION

Segmentation is used to divide an image into different small regions or objects. It has many applications in the medical field for the segmentation of the 2D medical images. It is an important process for most image analysis following techniques. There are various methods available for image segmentation. In this paper, thresholding and marker controlled watershed segmentation methods are used. Thresholding is the most effective tool for the image segmentation purpose. It is used to converts a gray scale image into a binary image. These two levels are assigned to pixels, below or above the particular threshold value. The image obtained from thresholding segmentation has smaller storage space, and fast processing speed.

Watershed transformation also called, as watershed method is a powerful mathematical morphological tool for the image segmentation. It is more popular in the fields like biomedical and medical image processing, and computer vision [17]. In geography, watershed means the ridge that divides areas drained by different river systems. If image is viewed as geological landscape, the watershed lines determines boundaries which separates image regions. The watershed transform computes catchment basins and ridgelines (also known as watershed lines), where catchment basins corresponding to image regions and ridgelines relating to region boundaries [18]. Segmentation by watershed embodies many of the concepts of the three techniques such as threshold

based, edge based and region based segmentation. Watershed algorithms based on watershed transformation have mainly two classes. The first class contains the flooding based watershed algorithms and it is a traditional approach where as the second class contains rainfalling based watershed algorithms. Many algorithms have been proposed in both classes but connected components based watershed algorithm shows very good performance compared to all others. It comes under the rainfalling based watershed algorithm approach. It gives very good segmentation results, and meets the criteria of less computational complexity for hardware implementation.

IV. PROPOSED METHODOLOGY

The method that we proposing in this paper consist of four following major steps

- 1) Preprocessing the CT Image or MRI image using median filtering for noise removal;
- 2) Segmentation of lung cancer nodes or brain tumor from lung CT images or brain MRI images using watershed transform;
- 3) Feature extraction from the segmented lung cancer nodes or brain tumor using various GLCM and statistical features.
- 4) Neural network and SVM classification for classifying the lung cancer image or brain tumor image.

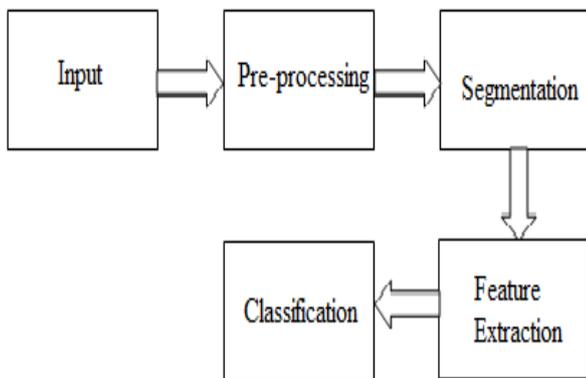


Figure 1. Proposed Block Diagram for Image Processing

A. Input images

The CT scan images which are used for processing are collected from the hospitals. This image dataset contains lung CT scan images with tumour and without tumour. The figure 2 shows some of the lung CT scan images with tumour and without tumour.

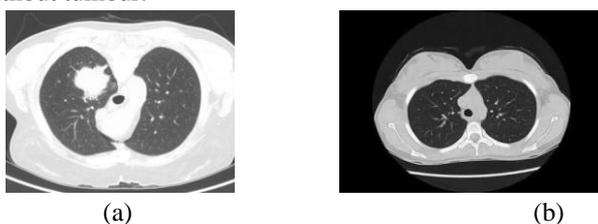


Figure 2. CT scan image (a) Lung without tumor (b) Lung with tumor

This brain tumor dataset containing 3064 T1-weighted contrast-enhanced images from 233 patients with three kinds of brain tumor: meningioma (708 slices), glioma (1426 slices), and pituitary tumor (930 slices) Figure 3 shows brain tumor images from the dataset.

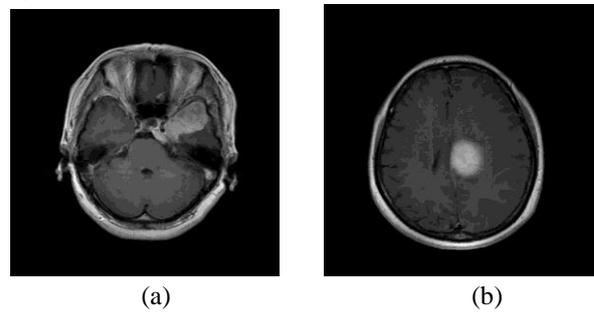


Figure 3. MRI Scan Image with Brain Tumor

B. Preprocessing

The median filter is a nonlinear digital filtering technique, often used to remove noise from an image or signal. Such noise reduction is a typical pre-processing step to improve the results of later processing (for example, edge detection on an image). Median filtering is very widely used in digital image processing because, under certain conditions, it preserves edges while removing noise (but see discussion below), also having applications in signal processing. The main idea of the median filter is to run through the signal entry by entry, replacing each entry with the median of neighboring entries. The pattern of neighbors is called the "window", which slides, entry by entry, over the entire signal. For 1D signals, the most obvious window is just the first few preceding and following entries, whereas for 2D (or higher-dimensional) signals such as images, more complex window patterns are possible (such as "box" or "cross" patterns). Note that if the window has an odd number of entries, then the median is simple to define: it is just the middle value after all the entries in the window are sorted numerically. For an even number of entries, there is more than one possible median

Matlab function $B = \text{medfilt2}(A)$ performs median filtering of the image A in two dimensions. Each output pixel contains the median value in a 3-by-3 neighborhood around the corresponding pixel in the input image. medfilt2 pads the image with 0s on the edges, so the median values for points within one-half the width of the neighborhood ($[m\ n]/2$) of the edges might appear distorted.

C. Image Segmentation

Segmentation using the watershed technique works well if the foreground objects and background regions are identified or marked. It is a simple, perceptive method and it is fast. Watershed Division Method extracts seeds, which indicate the nearness of items or foundation at particular areas. There Marker areas are then set to be the local minima inside the topological surface and the watershed calculation is connected.

The advantage of watershed division is that it creates an extraordinary answer for a specific picture input. After getting watershed image, the cancers are spotted out in input image. Figure 4 shows the cancer spotted image.



Figure 4. Cancer Spotted Image

For definitely visible cancer spot, Red mark color is used, so as to highlight the total no. of cancer present in given binary or input picture. Figure 5 shows the cancer cells outlined with red border.

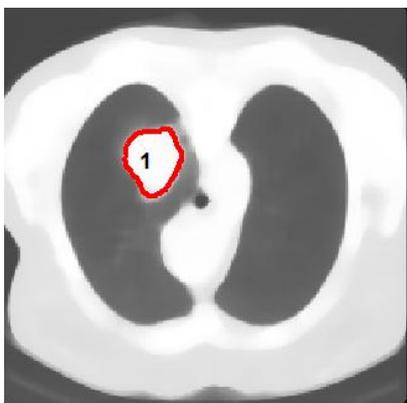


Figure 5. Cancer Outlined By Red Color In Input Image

Similarly watershed algorithm is used for brain tumor segmentation. Figure 6 shows the brain tumor segmentation using watershed transform.

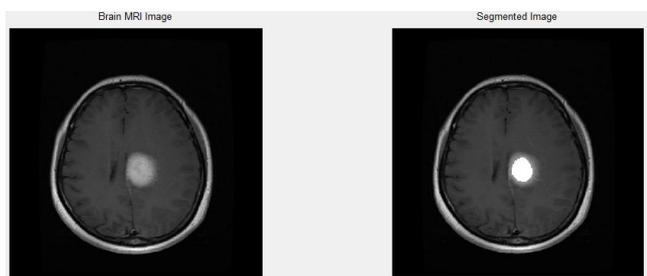


Figure 6. Brain Tumor Segmentation

D. Feature Extraction

After the segmentation is performed on lung region, the segmented nodules are used for feature extraction. Feature extraction is one of the most important steps in this system. A feature is a significant piece of information extracted from an image which provides more detailed understanding of the

image. A feature is defined as a function of one or more measurements, the values of some quantifiable property of an object, computed so that it quantifies some significant characteristics of the object.

a. GLCM Features

A gray level co-occurrence matrix is a second order statistical measure. GLCM is the gray-level co-occurrence matrix (GLCM), also known as the gray level spatial dependence matrix. The Gray-Level Co-occurrence Matrix (GLCM) is based on the extraction of a gray-scale image. The GLCM functions characterize the texture of an image by calculating how often pairs of pixel with specific values and in a specified spatial relationship occur in an image, creating a GLCM, and then extracting statistical measures from this matrix. Statistical parameters calculated from GLCM values are as follows:

The matlab function `GLCM = graycomatrix(I)` creates a gray-level co-occurrence matrix (GLCM) from image I. `graycomatrix` creates the GLCM by calculating how often a pixel with gray-level (grayscale intensity) value i occurs horizontally adjacent to a pixel with the value j. (You can specify other pixel spatial relationships using the 'Offsets' parameter -- see Parameters.) Each element (i,j) in GLCM specifies the number of times that the pixel with value i occurred horizontally adjacent to a pixel with value j.

The matlab function `graycomatrix` calculates the GLCM from a scaled version of the image. By default, if I is a binary image, `graycomatrix` scales the image to two gray-levels. If I is an intensity image, `graycomatrix` scales the image to eight gray-levels.

`stats = graycoprops(GLCM, properties)` calculates the statistics specified in properties from the gray-level co-occurrence matrix GLCM. GLCM is an m-by-n-by-p array of valid gray-level co-occurrence matrices. If GLCM is an array of GLCMs, stats is an array of statistics for each GLCM. `graycoprops` normalizes the gray-level co-occurrence matrix (GLCM) so that the sum of its elements is equal to 1.

Each element (r,c) in the normalized GLCM is the joint probability occurrence of pixel pairs with a defined spatial relationship having gray level values r and c in the image. `graycoprops` uses the normalized GLCM to calculate properties.

Property	Description	Formula
'Contrast'	Returns a measure of the intensity contrast between a pixel and its neighbor over the whole image. Range = [0 (size(GLCM,1)-1)^2]	$\sum_{i,j} i - j ^2 p(i, j)$

Property	Description	Formula
	Contrast is 0 for a constant image.	
'Correlation'	Returns a measure of how correlated a pixel is to its neighbor over the whole image. Range = [-1 1] Correlation is 1 or -1 for a perfectly positively or negatively correlated image. Correlation is NaN for a constant image.	$\sum_{i,j} \frac{(i - \mu_i)(j - \mu_j)p(i, j)}{\sigma_i \sigma_j}$
'Energy'	Returns the sum of squared elements in the GLCM. Range = [0 1] Energy is 1 for a constant image.	$\sum_{i,j} p(i, j)^2$
'Homogeneity'	Returns a value that measures the closeness of the distribution of elements in the GLCM to the GLCM diagonal. Range = [0 1] Homogeneity is 1 for a diagonal GLCM.	$\sum_{i,j} \frac{p(i, j)}{1 + i - j }$

Table 1: GLCM properties

Along with GLCM following features are extracted

b. Mean

M = mean(A) returns the mean values of the elements along different dimensions of an array. If A is a vector, mean(A) returns the mean value of A. If A is a matrix, mean(A) treats the columns of A as vectors, returning a row vector of mean values.

c. Standard Deviation

s = std(X), where X is a vector, returns the standard deviation using (1) above. The result s is the square root of an unbiased estimator of the variance of the population from which X is

drawn, as long as X consists of independent, identically distributed samples.

If X is a matrix, std(X) returns a row vector containing the standard deviation of the elements of each column of X. If X is a multidimensional array, std(X) is the standard deviation of the elements along the first nonsingleton dimension of X.

d. Entropy

E = entropy(I) returns E, a scalar value representing the entropy of grayscale image I. Entropy is a statistical measure of randomness that can be used to characterize the texture of the input image. Entropy is defined as

$$-\text{sum}(p.*\log_2(p))$$

where p contains the histogram counts returned from imhist. By default, entropy uses two bins for logical arrays and 256 bins for uint8, uint16, or double arrays.

I can be a multidimensional image. If I has more than two dimensions, the entropy function treats it as a multidimensional grayscale image and not as an RGB image.

d. RMS

The RMS block computes the true root mean square (RMS) value of the input signal. The true RMS value of the input signal is calculated over a running average window of one cycle of the specified fundamental frequency

e. Variance

V = var(X) returns the variance of X for vectors. For matrices, var(X) is a row vector containing the variance of each column of X. For N-dimensional arrays, var operates along the first nonsingleton dimension of X. The result V is an unbiased estimator of the variance of the population from which X is drawn, as long as X consists of independent, identically distributed samples. var normalizes V by N - 1 if N > 1, where N is the sample size. This is an unbiased estimator of the variance of the population from which X is drawn, as long as X consists of independent, identically distributed samples. For N = 1, V is normalized by 1.

f. Kurtosis

k = kurtosis(X) returns the sample kurtosis of X. For vectors, kurtosis(x) is the kurtosis of the elements in the vector x. For matrices kurtosis(X) returns the sample kurtosis for each column of X. For N-dimensional arrays, kurtosis operates along the first nonsingleton dimension of X.

g. Skewness

y = skewness(X) returns the sample skewness of X. For vectors, skewness(x) is the skewness of the elements of x. For matrices, skewness(X) is a row vector containing the sample skewness of each column. For N-dimensional arrays, skewness operates along the first nonsingleton dimension of X.

E. Classification using Neural Networks and SVM

Neural networks are composed of simple elements operating in parallel. These elements are inspired by biological nervous systems. As in nature, the connections between elements largely determine the network function. You can train a Neural network and SVM to perform a particular function by adjusting the values of the connections (weights) between elements. Typically, neural networks are adjusted, or trained, so that a particular input leads to a specific target output. The next figure illustrates such a situation. There, the network is adjusted, based on a comparison of the output and the target, until the network output matches the target. Typically, many such input/target pairs are needed to train a network. Figure 7 shows the typical neural network architecture.

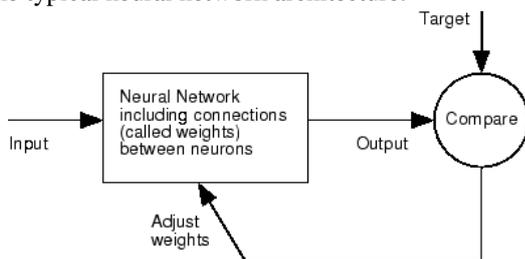


Figure 7. Neural Network Architecture

a. Artificial Neural Network (ANN)

Artificial neural network (ANN) is one of the classification methods commonly used in image processing techniques. ANN is collections of mathematical models that emulate the real neural structure of the brain. ANN has three layers. They are input layer, hidden layer and output layer. Architecture of a general ANN is shown in Figure 8.

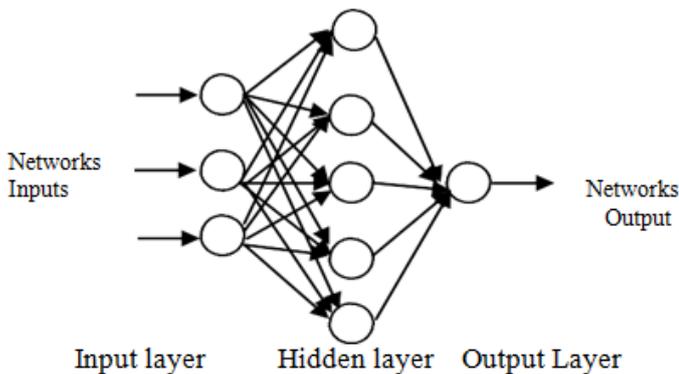


Figure 8. Architecture of a General ANN

b. Support Vector Machine (SVM)

To analyze data and recognize patterns for classification purpose, supervised learning models with associated learning algorithms are used in this paper also known as support vector machine. It initializes by taking a set of input data and predicts for each given input the specified class among the two choices available, which makes it a non-probabilistic binary linear classifier. For mapping the given data into a different space SVM uses kernel function such as polynomial, BF, quadratic,

Multi-Layer Perceptron (MLP). The separations can be made even with very complex boundaries.

Neural networks and SVM have been trained to classify the given lung cancer CT image as normal image or cancer image. Also for brain tumor segmentation, neural networks and SVM are used for classification of the brain tumor as meningioma, glioma, and pituitary tumor.

V. EXPERIMENT AND RESULTS

The experiment was carried out in two scenarios namely, Lung cancer detection from CT scan images and brain tumor segmentation from MRI images.

a. Lung Cancer Segmentation and Classification

The experiments are conducted on the lung cancer detection system where the inputs are CT images of lung. CT image is successfully processed at each step in lung cancer detection system and the desired result is obtained. CT image of lung is given to various image enhancement techniques and the resultant output is obtained. Various image enhancement techniques used are- median filtering and thresholding. The Output obtained from image enhancement technique is used as an input to the image segmentation module. In this work output from median filter is used as input. For the purpose of image segmentation marker-controlled watershed segmentation is used. Resultant output from the segmentation method are generated and evaluated. Obtained results are shown in Figure 9.

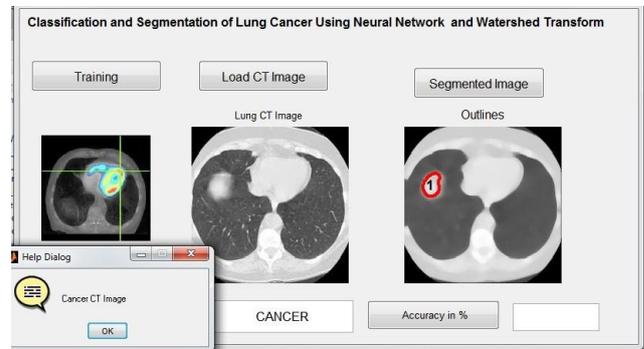


Figure 9. Lung Cancer Detection

From the segmented image various features are extracted. Neural networks are trained using these features. The lung cancer image is classified as cancer CT image or Normal image. Using Neural networks we get the accuracy of 100% for lung cancer detection and classification.

b. Brain Tumor Segmentation and Classification

The experiments are conducted on the brain tumor detection system where the inputs are MRI images of brain. MRI image is successfully processed at each step in brain tumor detection system and the desired result is obtained. MRI image of brain is given to various image enhancement techniques and the resultant output is obtained. Various image enhancement techniques used are- median filtering and thresholding. The

Output obtained from image enhancement technique is used as an input to the image segmentation module. In this work output from median filter is used as input. For the purpose of image segmentation marker- controlled watershed segmentation is used. Resultant output from the segmentation method are generated and evaluated. Obtained results are shown in Figure 10.

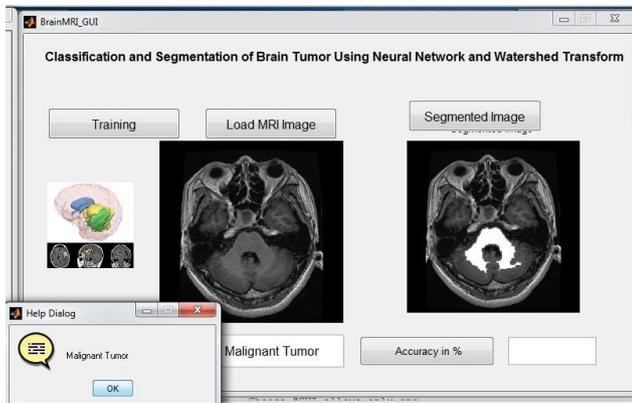


Figure 10. Brain Tumor Segmentation and Classification

From the segmented image various features are extracted. Neural networks are trained using these features. The brain tumor image is classified as meningioma, glioma, and pituitary tumor. Using Neural networks we get the accuracy of 100 % for brain tumor detection and classification

Figure 11 shows the comparison of Neural network and SVM for classification of brain tumor and lung cancer images.

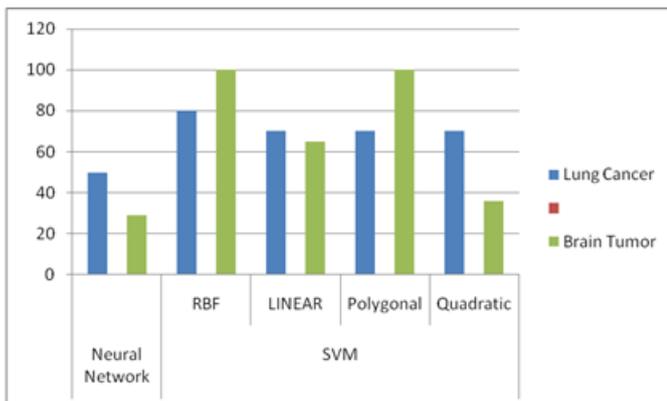


Figure 11 Performance Evaluation of SVM and Neural Network

VI. CONCLUSION

The goal of this research was to develop a system that is able to detect and localize lung nodules in CT scans of humans and to detect brain tumors from MRI image of the brain. The system proposed in this paper is able to do so with the stated accuracy. Many Nodule detection and brain tumor detection algorithms were surveyed and discussed in this paper. After analyzing the different methods, we proposed the optimum method for detecting the nodules in lungs and detecting brain tumor from brain MRI images which comprise of 3 steps say

preprocessing, segmentation and classification based nodule detection respectively. It has been proposed to use median filter for noise removal, watershed transform for brain tumor or lung cancer nodules segmentation and Neural network and SVM classification using various statistical features. With an accuracy of 100% we can conclude that SVM improve performance..

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