

# LUNG TUMOR SEGMENTATION IN MEDICAL IMAGE SEQUENCES

S.Irinsherly<sup>1</sup>, D.Kavitha<sup>2</sup>, D.Sneha<sup>3</sup>, V.Jyothsana<sup>4</sup>

<sup>1</sup> Assistant Professor, Department of Information Technology, Panimalar Institute of Technology

<sup>2,3,4</sup> Student, Department of Information Technology, Panimalar Institute of Technology

**Abstract**— Cancer is a disease in which cells in the body grow out of control .Lung cancer is the leading cause of cancer death and the second most diagnosed cancer in both men and women in the United States. Cigarette smoking is the number one cause of lung cancer. Lung cancer also can be caused by using other types of tobacco, breathing secondhand smoke, being exposed to substances such as asbestos or radon at home or work, and having a family history of lung cancer It is one of the cancers which have the highest mortality rate in the world. Each year, the morbidity and mortality of lung cancer increase steadily. Computed tomography (CT) is the widely used imaging method for screening, diagnosing, staging, and even prognosis assessment of lung cancer. The Proposed system focus on interactive tumor segmentation of medical image sequences using deep neural network. The proposed work utilizes pattern based classification using neural network function. Fuzzy c means clustering is designed in the proposed area. The feature selection is performed which includes Gray Level Co-Occurrence Matrix (GLCM).The feature selection aims at selecting the most relevant feature subset based on certain evaluation criteria. Finally the deep neural network is used to check whether the input image is normal or abnormal.

**Keywords**— Lung Tumor, Deep Neural Network, Fussy c means clustering, Segmentation, Back propagation Technique.

## I. INTRODUCTION

Lung cancer is the deadliest of all cancers in the United States and the world. It kills more Americans than the next four most common cancers combined .Lung cancer is largely preventable; inroads in reducing cigarette smoking are having a positive influence, though other environmental exposures also put people at risk. Advances in understanding this disease are leading to new means of diagnosis and treatment. Lung cancer symptoms typically include persistent cough, difficulty breathing, coughing up blood, and chest discomfort, though many patients are asymptomatic. Patients with advanced disease often have weight loss, fatigue, or pain outside the chest. This patient's evaluation included diagnostic studies generally performed in a lung cancer evaluation, the purpose of which is to determine the cancer stage. Lung cancer classification strives to correlate tumor cell morphology with tumor biological characteristics, thus facilitating therapeutic decision-making and effective prognostic outcome prediction in the era of personalized medicine. In small biopsy specimens or cytology specimens, major types of lung cancers are established by morphologic evaluation, that is, adenocarcinoma and squamous cell carcinoma. When poorly differentiated carcinomas are encountered, judicious application of immunohistochemical stains facilitates such distinction in most cases. In resection specimens, lung adenocarcinomas are further divided into low-grade (lepidic adenocarcinoma), intermediate-grade (acinar and papillary adenocarcinomas), and highgrade (solid and micropapillary adenocarcinomas) types of prognostic

significance. Significant progress has been made in the understanding of lung cancer biology, due in large part to advancement in the understanding of tumor biology and pathogenesis. Lung cancers are traditionally divided into non-small cell carcinoma (NSCC) and small cell carcinoma (small cell lung carcinoma, SCLC), with the former accounting for 80% of the cases and the latter accounting for the remaining 20%. SCLCs behave aggressively and are treated nonsurgically in most cases, whereas NSCCs are managed by a combination of surgery and adjuvant therapy. Recognition of the diversity of NSCC has led to its subclassification, culminating in the 2004 and 2015 World Health Organization (WHO) classifications.<sup>2,3</sup> Major types of NSCC include adenocarcinoma, squamous cell carcinoma (SSC), and large cell carcinoma (LCC). Thus, subtype of NSCC is specified, whereas the designation “NSCC” is only preserved in certain small biopsies and cytology specimens. Several methods have achieved this segmentations, for example Hongyang Jiang used Frangi filters for enhancement and achieved 80.06% false positivity and 94% of sensitivity. In Using Double Convolution Neural Network for Lung Cancer Stage Detection by Goran Jakimovski, they used CDNN algorithm and trained up with 100 epochs and achieved highest accuracy of 0.9962, whereas the regular CDNN obtained only 0.876 accuracy.

## II. DATA DESCRIPTION

The proposed method takes the input data from Kaggle database. Totally, 86 defected Lung images were taken from the databases.



Fig.1. Sample input CT image that shows lung tumor

## III. PROPOSED METHOD

Initially, the raw CT image may contain noise like salt and pepper noises, which is removed by using Median Filters as shown in Fig.2.

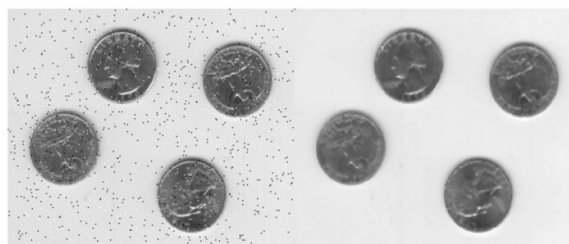


Fig.2. Image contains noise which is removed using filter

Syntax for Median filter for Denoising the noise presented in the CT image of Lung Tumor,

$$B = \text{medfilt2}(A)$$

Gray-Level Co-Occurrence Matrices (GLCM):

A co-occurrence matrix or co-occurrence distribution is a matrix or distribution that is defined over an image to be the distribution of co-occurring values at a given offset. Mathematically, a co-occurrence matrix  $C$  is defined over an  $n \times m$  image  $I$ , parameterized by an offset  $(\Delta x, \Delta y)$ , as:

$$C_{\Delta x, \Delta y}(i, j) = \sum_{p=1}^n \sum_{q=1}^m \begin{cases} 1, & \text{if } I(p, q) = i \text{ and } I(p + \Delta x, q + \Delta y) = j \\ 0, & \text{otherwise} \end{cases}$$

Where  $i$  and  $j$  are the image intensity values of the image,  $p$  and  $q$  are the spatial positions in the image  $I$  and the offset  $(\Delta x, \Delta y)$  depends on the direction used and the distance at which the matrix is computed  $d$ . The 'value' of the image originally referred to the grayscale value of the specified pixel, but could be anything, from a binary on/off value to 32-bit color and beyond. The calculated attributes are,

1. Homogeneity, Angular Second Moment (ASM):

Returns a value that measures the closeness of the distribution of elements in the GLCM to the GLCM diagonal. Range lies between  $[0, 1]$ . Homogeneity is 1 for a diagonal GLCM.

2. Contrast: Returns a measure of the intensity contrast between a pixel and its neighbor over the whole image. Range =  $[0, (\text{size}(\text{GLCM}, 1) - 1)^2]$ . Contrast is 0 for a constant image.

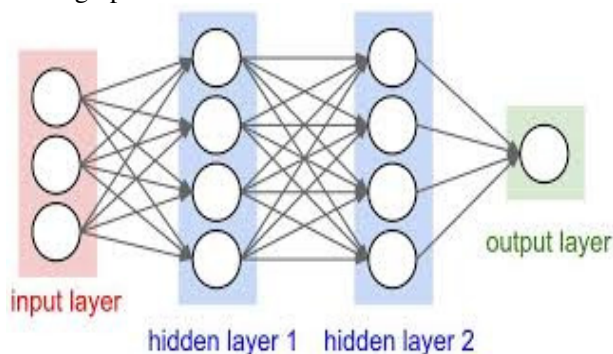
3. Entropy: Inhomogeneous scenes have low first order entropy, while a homogeneous scene has high entropy.  
 4. Correlation: Returns a measure of how correlated a pixel is to its neighbor over the whole image. Range =  $[-1 \ 1]$ . Correlation is 1 or -1 for a perfectly positively or negatively correlated image. Correlation is NaN for a constant image.

5. Energy: It returns the sum of squared elements in the GLCM. Range lies between  $[0 \ 1]$ . Energy is 1 for a constant image.



**Fig.3. CT image after applying GLCM attributes**

Neural networks are typically organized in layers. Layers are made up of a number of interconnected 'nodes' which contain an 'activation function'. Patterns are presented to the network via the 'input layer', which communicates to one or more 'hidden layers' where the actual processing is done via a system of weighted 'connections'. The hidden layers then link to an 'output layer' where the answer is output as shown in the graphic below.



All NN networks have four layers:

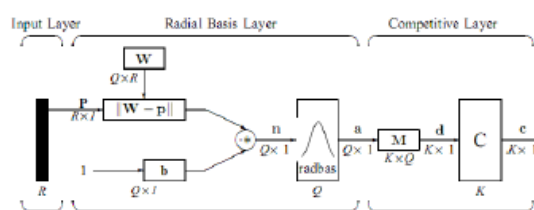
Input layer — there is one neuron in the input layer for each predictor variable. In the case of categorical variables,  $N-1$  neurons are used where  $N$  is the number

of categories. The input neurons (or processing before the input layer) standardize the range of the values by subtracting the median and dividing by the interquartile range.

Hidden layer — this layer has one neuron for each case in the training data set. The neuron stores the values of the predictor variables for the case along with the target value. When presented with the  $x$  vector of input values from the input layer, a hidden neuron computes the Euclidean distance of the test case from the neuron's center point and then applies the RBF kernel function using the sigma value(s). The resulting value is passed to the neurons in the pattern layer.

Pattern layer / Summation layer — The next layer in the network is different for NN networks and for GRNN networks. For NN networks there is one pattern neuron for each category of the target variable. The actual target category of each training case is stored with each hidden neuron; the weighted value coming out of a hidden neuron is fed only to the pattern neuron that corresponds to the hidden neuron's category. The pattern neurons add the values for the class they represent (hence, it is a weighted vote for that category).

Decision layer — The decision layer is different for NN and GRNN networks. For NN networks, the decision layer compares the weighted votes for each target category accumulated in the pattern layer and uses the largest vote to predict the target category.



**Fig.4: output computing method of the proposed system.**

1) Input Layer: The input vector, denoted as  $p$ , is presented as the black vertical bar. Its dimension is  $R \times 1$ . In this paper,  $R = 3$ .

2) Radial Basis Layer: In Radial Basis Layer, the vector distances between input vector  $p$  and the weight vector made of each row of weight matrix  $W$  are calculated. Here, the vector distance is defined as the dot product between two vectors [8]. Assume the dimension of  $W$  is  $Q \times R$ . The dot product between  $p$  and the  $i$ -th row of  $W$  produces the  $i$ -th element of the

distance vector  $\|W-p\|$ , whose dimension is  $Q \times 1$ . The minus symbol, “-”, indicates that it is the distance between vectors. Then, the bias vector  $b$  is combined with  $\|W-p\|$  by an element-by-element multiplication. The result is denoted as  $n = \|W-p\| \cdot b$ . The transfer function in NN has built into a distance criterion with respect to a center. In this paper, it is defined as  $\text{radbas}(n) = 2 \cdot e^{-n^2}$ . Each element of  $n$  is substituted into Eq. 1 and produces corresponding element of  $a$ , the output vector of Radial Basis Layer. The  $i$ -th element of  $a$  can be represented as  $a_i = \text{radbas}(\|W_i - p\| \cdot b_i)$  (2) where  $W_i$  is the vector made of the  $i$ -th row of  $W$  and  $b_i$  is the  $i$ -th element of bias vector  $b$ .

Some characteristics of Radial Basis Layer:

The  $i$ -th element of  $a$  equals to 1 if the input  $p$  is identical to the  $i$ th row of input weight matrix  $W$ . A radial basis neuron with a weight vector close to the input vector  $p$  produces a value near 1 and then its output weights in the competitive layer will pass their values to the competitive function. It is also possible that several elements of  $a$  are close to 1 since the input pattern is close to several training patterns.

### 3) Competitive Layer:

There is no bias in Competitive Layer. In Competitive Layer, the vector  $a$  is firstly multiplied with layer weight matrix  $M$ , producing an output vector  $d$ . The Competitive function, denoted as  $C$  in Fig. 2, produces a 1 corresponding to the largest element of  $d$ , and 0's elsewhere. The output vector of competitive function is denoted as  $c$ . The index of 1 in  $c$  is the number of tumor that the system can classify. The dimension of output vector,  $K$ , is 5 in this paper.

## IV. EXPERIMENT SETUP

Once the network weights and biases are initialized, the network is ready for training. The multilayer feed forward network can be trained for function approximation (nonlinear regression) or pattern recognition.

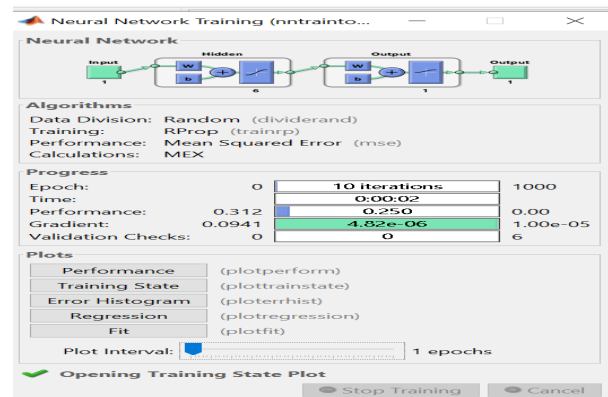


Fig.5: Training progress of the network

The process of training a neural network involves tuning the values of the weights and biases of the network to optimize network performance, as defined by the network performance function  $\text{net}$ . The default performance function for feed forward networks is mean square error  $\text{mse}$ —the average squared error between the networks outputs and the target outputs  $t$ . It is defined as follows:

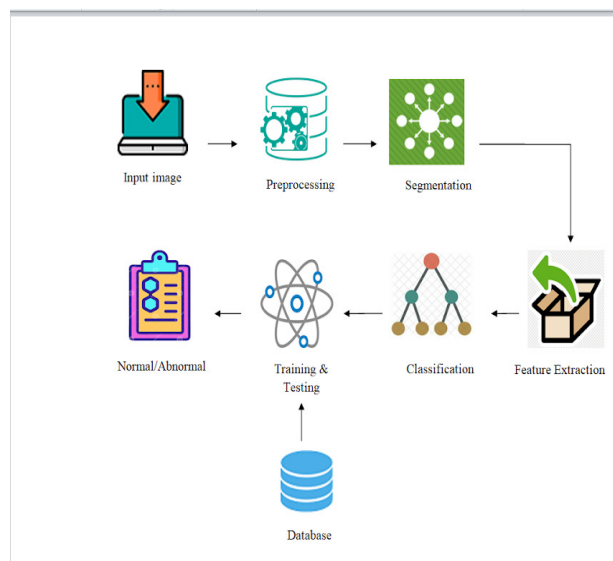
$$F = \text{mse} = \frac{1}{N} \sum_{i=1}^N (e_i)^2 = \frac{1}{N} \sum_{i=1}^N (t_i - a_i)^2$$

As an illustration of how the training works, consider the simplest optimization algorithm — gradient descent. It updates the network weights and biases in the direction in which the performance function decreases most rapidly, the negative of the gradient. One iteration of this algorithm can be written as,

$$\mathbf{x}_{k+1} = \mathbf{x}_k - \alpha_k \mathbf{g}_k$$

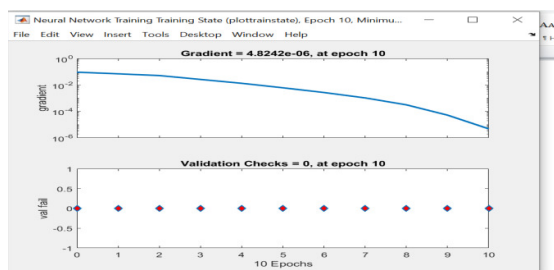
Where  $\mathbf{x}_k$  is a vector of current weights and biases,  $\mathbf{g}_k$  is the current gradient, and  $\alpha_k$  is the learning rate. This equation is iterated until the network converges.





**Fig.6. Architecture diagram of proposed system**

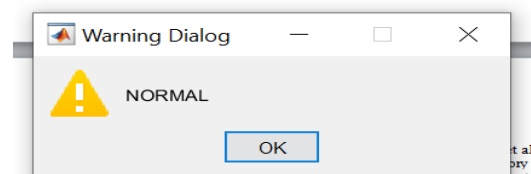
In this project, lung images of a patient are taken as input. The images are pre-processed and segmented and then classified for the required feature. Then feature Extraction is done for the images by GLCM features. Fuzzy C means clustering algorithm is applied in order to identify the affected portion of tumor. Here the threshold required for segmenting adjusts itself according to the segmented area and position. Finally, classification applied through neural networks then results in the image that will be compared with the dataset images and it will display whether the tumor is normal or abnormal.



**Fig.7. Gradients and Validations on Training**

If the input images are color images means we are convert to gray scale from that color images. A median filter is more effective than convolution when the goal is to simultaneously reduce noise and preserve edges. The back propagation neural network concept for training the image and testing the image with the help of weight estimating classifier. The result image will

compared with the dataset images and it will display whether it is normal or abnormal.



**Fig.8. The Resultant Dialogue box after determining the given CT image of Lung Tumor is Normal or Abnormal**

## V. RESULTS

The deep learning and machine learning algorithms are developed using Mat lab The Image Acquisition Toolbox's is a collection of functions that extend the capability of the MATLAB numeric computing environment. Many of the toolbox functions are MATLAB M-files. You can extend the capabilities of the Image Acquisition Toolbox by writing your own M-files, or by using the toolbox in combination with other toolboxes, such as the Image Processing Toolbox and the Data Acquisition Toolbox. Fig.7 shows the performance of GLCM technique in terms of Gradients and Validation. Fig.8 shows the performance of DNN algorithm in terms of Back propagation technique. This system produces the result with the accuracy of 94.73%.

## VI. CONCLUSION

In this paper, we study a general inference framework for extracting lung tumors from medical image sequences. A collaborative formulation of tumor segmentation is discussed by jointly integrating region and boundary information. Here we used the Fuzzy c means clustering algorithm is used in order to segment the portion of defected areas. We used to establish the neural network concept for training the image and testing the image with the help of weight estimating classifier. The result image will compared with the dataset images and it will display whether it is normal or abnormal.

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