Lung Cancer Detection Using SVM Classifier and MFPCM Segmentation

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Abstract - Lung cancer is most dangerous disease in the world, nowadays. So the early detection of lung cancer is necessary. In this paper, the gray scale converted CT scan image of lung is enhanced since the contrast in all regions are significantly lighter or darker using CLAHE. Then, retrieve the similar and dissimilar regions by Modified Fuzzy Possibilisitic C-Means clustering technique. Extract up to 18 features from Gray Level Co-occurrence matrix and best valued features are selected using sequential forward selection algorithm. According to the selected features, the lung image is classified as normal or abnormal using SVM. If the lung image is abnormal, extract the affected region. The entire processing is done in MATLAB.

Key Words: CLAHE, MFPCM, Lung cancer, Texture features, SVM Classifier, GLCM, CT images.

1. INTRODUCTION

Accurate diagnosis for different types of cancer plays an important role in determining and choosing the proper treatment to the doctors to assist them. By using classification techniques, possible errors that might occur due to unskilled doctors can be minimized. Challenge facing medical practitioners makes this study of a much greater significance. Since symptoms appear only in the advanced stages thereby causing the mortality rate of lung cancer to be the highest among all other types of cancer, challenging the detection of cancer in its early stages [16]. The objective of undertaking this project is to facilitate doctors to provide the best possible treatment by providing useful insights with the help of predictive models through analysis and diagnosis of lung cancer treatments. This technique can also examine medical data in a shorter time and more precisely. The critical task is to define and specify a good feature space that means the type of features which will discriminate between malignant and benign.

Pre-processing the given test image for reducing noise and for enhancing the contrast by Contrast Limited Adaptive Histogram Equalization (CLAHE).To project the affected portion MFPCM technique segmentation is applied. Extract second order textural features from the GLCM matrix and select best valued features for classification. Finally, according to the selected features the image is classified as normal or abnormal using SVM classifier. MATLAB software is used for all these processes.

2. PROPOSED SYSTEM

The proposed system of detection of lung cancer starts with the collection of CT images followed by proposed methodology.

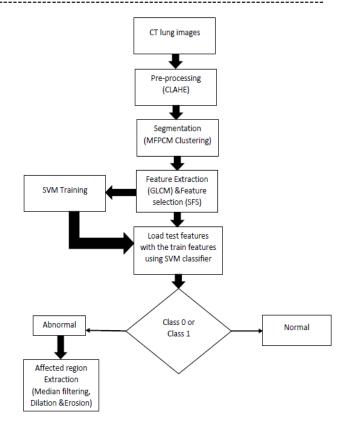


Fig-1: Flowchart of proposed System

2.1 Pre-processing (CLAHE)

The CT images obtained taken as input image is converted into gray scale image. The intensity values are different in the input image, hence CLAHE is applied to equalize the image. In CLAHE, it divide the image into tiles and enhance the contrast in each tile. Bilinear interpolation method is used to eliminate the artificially induced boundaries while combining all the tiles. This helps in making hidden features of the image more visible. Contrast Limited AHE (CLAHE) differs from ordinary adaptive histogram equalization in its contrast limiting. This feature can also be applied to global histogram equalization, giving rise to contrast limited histogram equalization (CLHE), which is rarely used in practice. In the case of CLAHE, the contrast limiting procedure has to be applied for each neighborhood from which a transformation function is derived. CLAHE was developed to prevent the over amplification of noise that adaptive histogram equalization can give rise to. This is achieved by limiting the contrast enhancement of AHE. The contrast amplification in the vicinity of a given pixel value is given by the slope of the transformation function. This is proportional to the slope of the neighborhood cumulative distribution function (CDF) and

therefore to the value of the histogram at that pixel value [7]. CLAHE limits the amplification by clipping the histogram at a predefined value before computing the CDF. This limits the slope of the CDF and therefore of the transformation function. The value at which the histogram is clipped, the so-called clip limit, depends on the normalization of the histogram and thereby on the size of the neighborhood region.

2.2 Segmentation (MFPCM)

Segmentation is a technique of unsupervised classification that arranges pattern in the clusters or regions. The first method is to partition the image based on abrupt changes in intensity, such as edges in an image. The second method is based on partitioning the image into regions that are similar according to a predefined criterion.

The MFPCM algorithm attempts to partition a finite collection of elements $X=\{x1, x2, x3, ..., xn\}$ into a collection of c fuzzy clusters with respect to some given criterion. Given a finite set of data, the algorithm returns a list of c fuzzy clusters with respect to some given criterion. Given a finite set of data, the algorithm returns a list of c cluster centers V, such that V=vi, i=1, 2, 3, ..., c. And a partition matrix U such that U=uij,i=1,2,3, ..., c, j=1,2, ..., n Where uij is a numerical value in [0, 1] that tells the degree to which the elements xj belongs to the i-th cluster. Defines a family of fuzzy sets {Ai, i=1, 2, 3, ..., c} as a fuzzy c partition on a universe of data points X, [17].

The steps of MFPCM algorithm given below [14]:

1. The objective function of the MFPCM can be formulated as follows:

$$J_{MFPCM} = \sum_{i=1}^{c} \sum_{j=1}^{n} \left(\mu_{ij}^{m} w_{ji}^{m} d^{2m}(x_{j,v}) + t_{ij}^{\eta} w_{ji}^{\eta} d^{2\eta}(x_{j,v_{i}}) \right)$$

- 2. Fix the number of clusters(c). The value of m should be always greater than one.
- 3. Calculate U = $\{\mu_{ij}\}$ represents a fuzzy partition matrix, is defined as:

$$u_{ij} = \left[\sum_{k=1}^{c} \left(\frac{d^2(x_j, v_i)}{d^2(x_j, v_k)}\right)^{\frac{2m}{(m-1)}}\right]^{-1}$$

4. Calculate T = $\{t_{ij}\}$ represents a typical partition matrix, is defined as :

$$t_{ij} = \left[\sum_{k=1}^{n} \left(\frac{d^2(x_j, v_i)}{d^2(x_j, v_k)}\right)^{\frac{2\eta}{(\eta-1)}}\right]^{-1}$$

5. Calculate V = {v_{ij}} represents c centers of the clusters [4], is defined as:

$$\boldsymbol{v}_{ij} = \frac{\sum_{j=1}^{n} \left(\boldsymbol{\mu}_{ij}^{m} \boldsymbol{w}_{ji}^{m} + \boldsymbol{t}_{ij}^{\eta} \boldsymbol{w}_{ji}^{\eta} \right) * \boldsymbol{x}_{j}}{\sum_{j=1}^{n} \left(\boldsymbol{\mu}_{ij}^{m} \boldsymbol{w}_{ji}^{m} + \boldsymbol{t}_{ij}^{\eta} \boldsymbol{w}_{ji}^{\eta} \right)}$$

2.3 Feature extraction and selection

Feature extraction is a crucial step for the CAD system. It uses different methods and algorithms for feature extraction from the segmented image. The extracted ROI can be distinguished as either cancerous or not using their texture properties. Use GLCM (Gray level co-occurrence matrix) for the texture feature extraction form CT scan image. Feature extraction is a dimensionality reduction. Transforming input data into set of features. A statistical method that considers the spatial relationship of pixels is the gray-level cooccurrence matrix (GLCM), also known as the gray-level spatial dependence matrix [7]. The toolbox provides functions to create a GLCM and derive statistical measurements from it. The gravcomatrix function creates a gray-level co-occurrence matrix (GLCM) by calculating how often a pixel with the intensity (gray-level) value i occurs in a specific spatial relationship to a pixel with the value *j*. Each element (*i*, *j*) in the resultant glcm is simply the sum of the number of times that the pixel with value *i* occurred in the specified spatial relationship to a pixel with value *i* in the input image. Because the processing required to calculate a GLCM for the full dynamic range of an image is prohibitive, graycomatrix scales the input image. The gray-level cooccurrence matrix can reveal certain properties about the spatial distribution of the gray levels in the texture image, [14][15]. In this process, total 18 textural features of all images in the database are extracted using GLCM (Gray level co-occurrence matrix). Then these features are used for tumor classification, example of four state space is shown in fig 2.

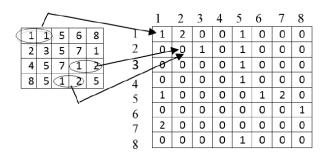


Fig-2: Gray level co-occurrence matrix

Contents of the GLCM is used to calculate the texture features to give a measure of the variation in intensity at the pixel of interest. From the co-occurrence matrix obtained, extracted the 18 different statistical features, are Energy, Contrast, variance, Correlation, maximum probability, entropy, homogeneity, cluster shade, cluster prominence, dissimilarity, sum average, sum entropy, sum variance, ,Difference entropy, information measure of correlaton1, information measure of correlaton2,Inverse difference moment, autocorrelation. Feature selection algorithms helps in recognising and classifying systems. If a feature space with large dimension is used, there are chances of decrease in classifier performance in connection to execution time and recognition rate. For determining the best feature subset in same case, automatic feature selection technique can be used for completion of feature space, by varying the number of selected features from 1 to m. By using sequential forward selection algorithm, best features can be easily extracted. After selecting the final feature subset will be sent to classifier for the classification. It is an empty matrix for storing features from SFS [6].

2.4 Classification

Next phase in the proposed system is the classification of occurrence and non-occurrence of cancer nodule for the supplied lung image. The classifier used is Support Vector Machine. The aim of classification is to group items that have similar feature values into groups. Classifier achieves this by making a classification decision based on the value of the linear combination of the features. SVM is a binary classification method that takes as input labelled data from two classes and outputs a model file for classifying new unlabelled/labelled data into one of two classes.

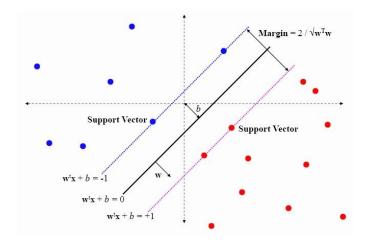


Fig 3: SVM Classifier

Training an SVM involves feeding known data to the SVM along with previously known decision values, thus forming a finite training set. It is from the training set that an SVM gets its intelligence to classify unknown data. In SVM, for two class classification problem, input data is mapped into higher dimensional space using RBF kernel. Then a hyper plane linear classifier is applied in this transformed space utilizing those patterns vectors that are closest to the decision boundary, [16], shown in fig-3.

Consider the pattern classifier, which uses a hyper plane to separate two classes of patterns based on given examples {x (i), y (i)}, i=...n.Where (i) is a vector in the input space I=Rk and y (i) denotes the class index taking value 1 or 0. A support vector machine is a machine learning method that classifies binary classes by finding and using a class boundary the hyper plane maximizing the margin in the given training data. The training data samples along the hyper planes near the class boundary are called support vectors, and the margin is the distance between the support vectors and the class boundary hyper planes. The SVM are based on the concept of decision planes that define decision boundaries.

1. Training the classifier

In the training phase, known data is given and the classifier is trained. Given training data (xi, yi) for $i = 1 \dots N$, with $xi \in Rd$ and $yi \in \{-1, 1\}$. The training points satisfy the following conditions.

$$F(\mathbf{x}) = \boldsymbol{W}^{T} \mathbf{x}_{i} + \mathbf{b} \ge +1 \text{ for } \mathbf{y}_{i} = +1$$
$$F(\mathbf{x}) = \boldsymbol{W}^{T} \mathbf{x}_{i} + \mathbf{b} \le -1 \text{ for } \mathbf{y}_{i} = -1$$

2. Testing of data

In testing phase, unknown data are given and the classification is performed using trained classifier. Classification is done by using following decision function.

$$F(x, \{w, b\}) = sign(w.x+b)$$

Every input x is initially mapped into a higher dimension feature space F, by $z=\varphi(x)$ through a nonlinear mapping φ : Rn \rightarrow F. W is the normal to the line, x is the feature vector and b the bias. W is known as the weight vector and b is bias.

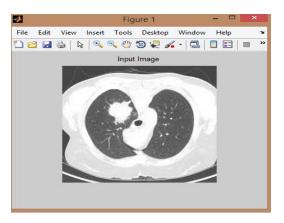


Fig-4: Input Lung CT image

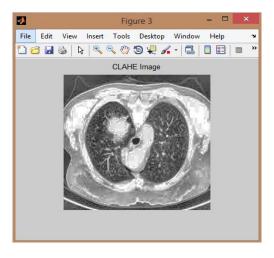


Fig-5: Pre-processed image

2.5 ROI Extraction

The final phase in the proposed system is the extracting the affected region using median filtering, dilation and erosion.

To remove noise from images median filtering is a nonlinear method used. It is widely used as it is very effective at removing noise while preserving edges. It is particularly effective for removing 'salt and pepper' noise. Working of median filter is by moving through the image pixel by pixel, replacing each value with the median value of neighboring pixels [2].

Dilation and erosion are two basic operators in the area of mathematical morphology. The dilation operator need two pieces of data as inputs. First is an image which is to be dilated and second is a small set of coordinate points known as a structuring element [6].



Fig-6: Segmented image using MFPCM

Area opening removes small objects from binary image. That is, it removes from a binary image all connected components (objects) that have fewer than P pixels, producing another binary image. This operation is known as an area opening.

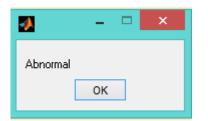


Fig-7: SVM classifier outputs supplied input CT Lung image as 'Abnormal'.

Consider each of the foreground pixels in the input image in turn to compute the erosion of a binary input image by structuring element. The origin of the structuring element coincides with the input pixel coordinates by each foreground pixel (which we will call the input pixel) superimpose with the structuring element on top of the input image [6].

3. EXPERIMENTAL RESULTS

Here, the input images are chest CT scan images that contain tumors. First image selected from the file specified by the string filename, shown in fig-4. Then each image is resized to 250*250.

The contrast limited adaptive histogram equalization algorithm separates the images into contextual regions and applies the histogram equalization to all, shown in fig 5. This evens out the allocation of applied gray values and thus makes hidden features of the image more visible by reducing noise and by enhancing the contrast.

The MFPCM segmentation is performed for determining the cancer nodules in the lung. This phase will help identify the Regions of Interest (ROI) in the lung nodule that can help identify the cancerous region in fig 6.

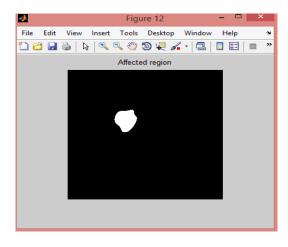


Fig -8: Extracted cancer region

Then create a GLCM matrix from the images and calculates the statistics specified in properties from the gray-level cooccurrence matrix. After extracting GLCM features of images, features selected are correlation, energy, cluster prominence and Dissimilarity using sequential Forward Selection algorithm [9] and tumor classification is done.

For this, we have used SVM (Support vector machine) classifier. This classifier is trained first. Here, two class (class1 as abnormal in fig 7 and class 2 as normal) SVM classifier is used. An SVM classifies data to separate all data points of one class from those of the other class, by finding the best hyperplane.

To extract the cancerous part from the lung if it is abnormal, applied median filtering, dilation, erosion and area opening shown in fig 8.

Performance is measured by accuracy, specificity, sensitivity, Mean squared error and time taken, shown in Fig-9.



Fig-9: Analysis of performance

4. CONCLUSION

The proposed system is able to detect both benign and malignant tumors more correctly. Thus, it can be concluded that the SVM used for tumor classification have accuracy of 100% and handle better complex classifications. SVM uses more parameters and have very large feature spaces. MFPCM is faster and noise pixels can be easily predicted with better accuracy and less error rate for MFPCM.

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