GLCM Features

1. autoc (Autocorrelation):

$$\rho(x,y) = \frac{1}{(L_x - |x|)(L_y - |y|)} \int_{-\infty}^{\infty} I(u,v) I(u+x, v+y)\, du\, dv$$

$$\frac{1}{L_x L_y} \int_{-\infty}^{\infty} I^2(u,v)\, du\, dv \qquad |x| < L_x \text{ and } |y| < L_y.$$

2. Contr (Contrast): It is a measure of the intensity contrast between a pixel and its neighbor over the whole image.

$$\sum_{i,j=0}^{G-1} (i-j)^2 P(i,j)$$

3. corr (Correlation): It is a measure of gray level linear dependence between the pixels at the specified positions relative to each other.

$$\sum_{i=0}^{G-1} \sum_{j=0}^{G-1} \frac{\{i \times j\} \times P(i,j) - \{\mu_x \times \mu_y\}}{\sigma_x \times \sigma_y}$$

4. cprom (Cluster prominence):

$$\sum_{i=0}^{G-1} \sum_{j=0}^{G-1} \{i + j - \mu_x - \mu_y\}^4 \times P(i,j)$$

5. cshad (Cluster shade): It is a measure of skewness of the matrix.

$$\sum_{i,j=0}^{G-1} (i + j - \sigma_I - \sigma_J)^3 P(i,j)$$

6. dissi (Dissimilarity): It gives the measure of much dissimilar are of two neighboring pixels.

$$\sum_{i,j=0}^{N-1} P_{i,j} |i - j|$$

7. energy (Energy):

It is also known as uniformity of ASM (angular second moment) which is the sum of squared elements from the GLCM. Range = [0 1] Energy is 1 for a constant image.

$$\sum_{i,j=0}^{G-1} P(i,j)\, 2$$

8. entro (Entropy):

It is a measure of randomness. Entropy measures the loss of information or message in a transmitted signal and also measures the image information.

$$-\sum_{i=0}^{G-1} p(z_i) \log_2 p(z_i)$$

9. homom (Homogeneity):

It returns a value that measures the closeness of the distribution of elements in the GLCM to the GLCM diagonal.

$$\sum_{i=0}^{G-1} \sum_{j=0}^{G-1} \frac{1}{1 + (i-j)^2} P(i,j)$$

10. maxpr (Maximum probability):

This simple statistic records in the centre pixel of the window the largest P_{ij} value found within the window.

$$\max(i,j) P(i,j)$$

3.4 Tumor classification

After extracting GLCM features of images, tumor classification is carried out. For this, we have used SVM (Support vector machine) classifier. This classifier must be trained first. For training we have used 6 images out of which first 3 images are of 'benign' type and next 3 are of 'malignant' type tumor. The GLCM features are given as input to SVM. Each image is assigned a class i.e. for benign, class 0 and for malignant, class1.

Here, two class SVM classifier is used. An SVM classifies data by finding the best hyperplane that separates all data points of one class from those of the other class. The best hyperplane for an SVM means the one with the largest margin between the two classes. Margin means the maximal width of the slab parallel to the hyperplane that has no interior data points. The hyperplane is defined by the equation:

$(w.\ x) + b = 0$

Where, w= weight vector

x= feature vector

B= bias

The value of bias 'b' is found to be -0.3481.

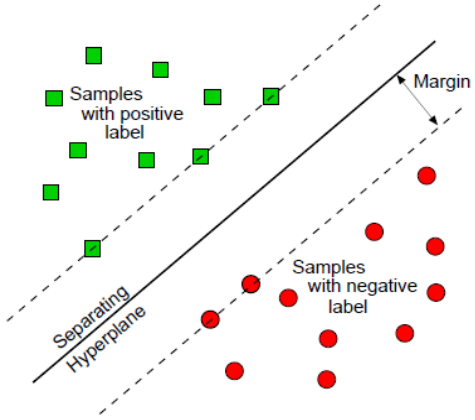


Figure 2: SVM classifier

The vectors closest to the boundaries are called support vectors and the distance between the support vectors and hyper plane is called margin [8]. SVM first maps the input feature vectors into higher dimensional feature space and then perform classification.

1. Training the classifier

In the training phase, known data is given and the classifier is trained. Here, six images are used for training out of which 3 are benign and 3 are malignant and are assigned class 0 for benign and class 1 for malignant. The training points satisfy the following conditions.

$(w.x_i) + b \geq +1$ for $y_i = +1$

$(w.x_i) + b \leq -1$ for $y_i = -1$

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)

The sign of this function decides the class of the test image. Here, if it is positive, then result will be 'malignant' and if it is negative, then result will be 'benign'.

3.5 Tumor segmentation

Clustering is a process for classifying objects or patterns in such a way that samples of the same group are more similar to one another than samples belonging to different groups. Here fuzzy C-means algorithm is used for tumor segmentation. Fuzzy clustering is basically a multi valued logic that allows intermediate values i.e., member of one fuzzy set can also be member of other fuzzy sets in the same image. In the proposed FCM, 3 clusters are taken and maximum number of iterations is 100. The algorithm is an iterative clustering method that produces an optimal c partition by minimizing the weighted within group sum of squared error objective function J_{FCM} [6].

$$J_{FCM} = \sum_{k=1}^{n} \sum_{i=1}^{c} (u_{ik})^q \, d^2 (x_k, v_i) \quad \ldots(1)$$

The membership function defines the fuzziness of an image and also to define the information contained in the image. These are three main basic features involved in characterized by membership function. They are support, Boundary. The core is a fully member of the fuzzy set. The support is non membership value of the set and boundary is the intermediate or partial membership with value between 0 and 1. This clustering algorithm allows one piece of data may be member of more than one clusters. It is based on reducing the equation 2,

$$Y_m = \sum_{i=1}^{N} \sum_{j=1}^{C} M_{ij}^{m} \left\| x_i - c_j \right\|^2 \quad \ldots. (2)$$

Where,
m- Any real number greater than 1.
Mij- Degree of membership of X; in the cluster j
xi- Data measured in d-dimensional.
Cj - Dimension centre of the cluster.
‖Xi-Cj‖²- Induced norm (Euclidean norm)
This system uses two level segmentation i.e. for two levels of thresholding, image is divided into 3 clusters and maximum number of iterations is 100.

3.6 System flowcharts

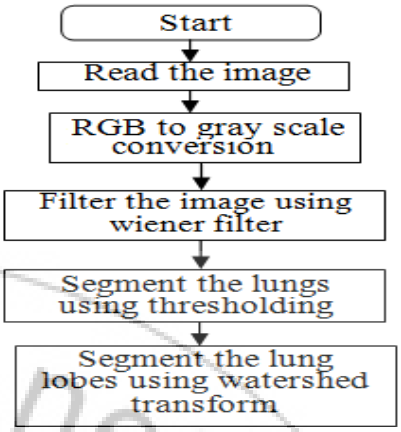


Figure 3: Flowchart for lobe segmentation

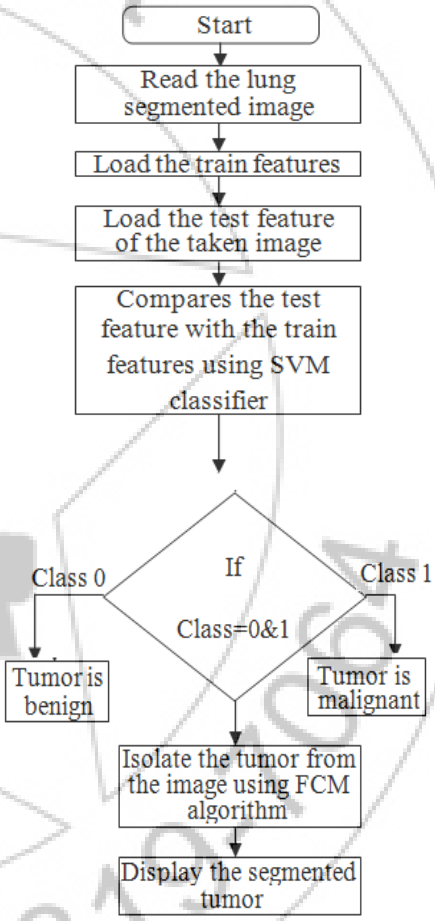


Figure 4: Flowchart for tumor classification and segmentation

3.7 Database

We have taken the database of 51patients which are lung CT scan images from web link http://lola11.com/Details. All these images are of size 256*256 and are in JPEG format. Some images from the database are shown in following figure:

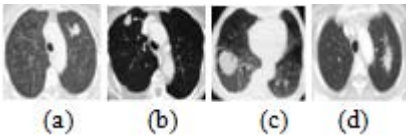
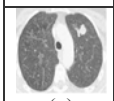
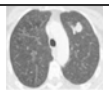
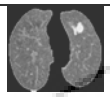
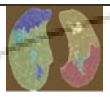
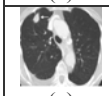
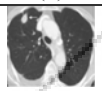
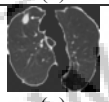
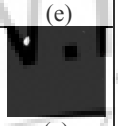
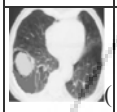
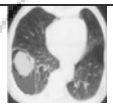
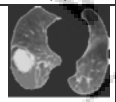
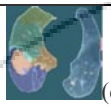
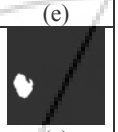
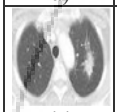
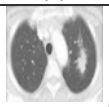
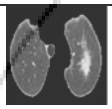
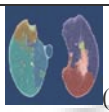


Figure 5: Images from database

4. Results of Experimentation

In this section, the results of the proposed system are shown for four images from the database.

Table 2: (a) Input image, (b) Wiener filtering, (c) Thresholding, (d) Watershed transformation, (e) FCM

Input image	Filtered image	Segmen-ted lungs	Lung lobes segme-nted image	Extracted tumor
 (a)	 (b)	 (c)	 (d)	 (e)
 (a)	 (b)	 (c)	 (d)	 (e)
 a)	 (b)	 (c)	 (d)	 (e)
 (a)	 (b)	 (c)	 (d)	 (e)

Similarly, the results for all 51 images in the database are obtained.

4.1 Classification Results and Analysis

When the above images were given to the SVM classifier for testing, we obtained the following outputs.

Table 3: SVM outputs and accuracy parameters

Image No.	*Expert's opinion*	*Experimental results*	*SVM output*	*Parameter*
1	Benign	Benign	Class 0	TP
2	Benign	Malignant	Class 1	FP
3	Malignant	Malignant	Class 1	TN
4	Malignant	Benign	Class 0	FN

Where,
TP- predicts benign as benign.
FP- predicts benign as malignant.
TN- predicts malignant as malignant.
FN- predicts malignant as benign.

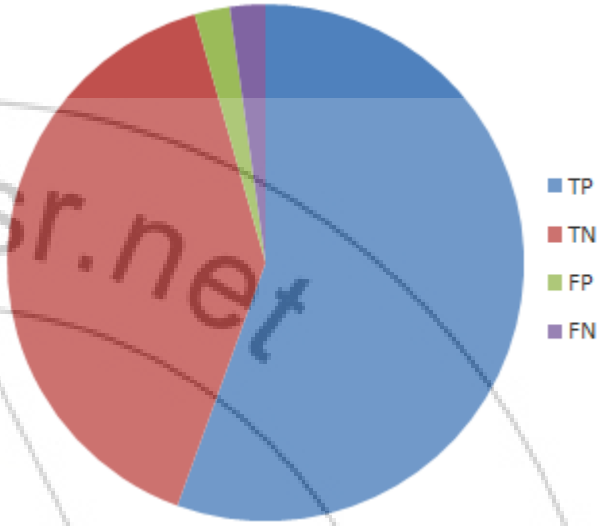
4.2 Performance measures

The following parameters are calculated on the basis of the results obtained for all the images in database.

1) Accuracy (AC) = (TP+TN) / (TP+TN+FP+FN)
= (25 + 18) / (45)
=0.9556
Accuracy in % = 95.56%

2) Sensitivity (SE) = TP / (TP+FN)
= 25 / (25+ 1)
= 0.9615
Sensitivity in % = 96.15%

3) Specificity (SP) = TN / (TN+FP)
= 18 / (18 + 1)
= 0.9473
Specificity in % = 94.73%



Graph 1: Accuracy parameters

Thus, from the results we found that our proposed system has achieved 95.56% accuracy, specificity of 94.73% and better sensitivity i.e. 96.15% that means our system has higher accuracy for the classification of benign type of tumor as compared to malignant tumor.

5. Conclusions

Thus it can be concluded that the proposed method performs well and is robust against anatomical variations of the lungs. The system gives results within few seconds. The SVM used for tumor classification has improved accuracy. Thus, this approach is a potential for developing an algorithm to segment lung, lobes and tumor identification for surgical planning of treating lung disease and it will assist radiologist as second opinion for the better diagnosis of lung cancer. The SVM classifier achieved an average accuracy of 95.56%.

6. Future Scope

The automatic lobe segmentation and tumor classification has very wide scope since it reduces manual work and also computational time. Also it can be useful for diagnosis of other lung diseases. Further it can be performed for 3D images in future. The million order dataset can be selected and image classification can be done on larger dataset. With increased size of dataset various issues such as uploading data, managing feature set, increased execution time of classification algorithms etc. can be considered. More image features can be extracted for better classification. Various combinations of pre-existing features can be used to correctly classify medical data.

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