CHAPTER 3

METHODOLOGY

3.1 INTRODUCTION

Lung cancer is a widespread disease that constitutes a major health problem. It is a disease that is characterized by the uncontrolled cell growth in the lung tissues. This growth can spread into nearby body parts, or a tissue is known as metastasis. Many cancers that start in the lung are called as primary lung cancers or carcinomas. The major types of lung cancer are,

- Small-Cell Lung Carcinoma (SCLC) - also called as oat cell cancer
- Non-Small-Cell Lung Carcinoma (NSCLC)

The most general symptoms of a lung cancer are shortness of breath, weight loss and coughing. The general cause of lung cancer is long-term exposure to tobacco smoke that leads to 80-90% of lung cancers. Since it is difficult to detect lung cancer in its early stage and it is almost impossible to prevent its growth. Many approaches are utilized for scanning the lung area. CT technique is one of them.

3.1.1 Diagnosing Lung Cancer
A chest X-ray is a basic test that is utilized for diagnosing the lung cancer. Many lung tumors show up on X-rays as a white-gray mass. However, the chest X-rays cannot provide a definitive diagnosis as they frequently cannot differentiate between cancer and other conditions (Zavala 1975).

A Computerized Tomography (CT) is normally carried out after the chest X-ray. A CT utilizes X-rays and a computer to generate detailed images of the body. A Positron Emission Tomography-Computerized Tomography (PET-CT) can be carried out if a CT scan indicates the presence of cancer. (Henschke et al 1999).

As all of these scanning modalities produces images as outputs, image processing techniques can be employed for further understanding of the images. In digital image processing, image segmentation and enhancement techniques are exploited to accomplish the tumor diagnosis more accurately. The lung cancer detection and segmentation follows four basic diagnostic tasks namely, preprocessing, feature extraction, classification and segmentation.

### 3.2 LUNG TUMOR DETECTION AND SEGMENTATION

The main objective of this research work is to scrutinize the exact difference between tumor cells and non-tumor cells along the boundary by segmentation process. Figure 3.1 shows the block diagram of overall processing of lung tumor detection system. It includes tumor detection, segmentation and projection of tumor in 3D. Denoising is done by kernel based non-local neighbourhood with six kernels in preprocessing. The second order histogram is used in feature extraction. Classification is done by the Naive Bayes classifier for the existence of tumor and finally the segmentation is done by using the proposed enhanced level set-active contour model. The contour based segmentation algorithm extracts the tumor slices of the lung.
image. Later, the extracted tumor portion pixels for all slices of the patient datasets are reconstructed in 3D that makes the visualization of tumor more accurate.

![Block diagram of the tumor detection and 3D reconstruction system](image)

**Figure 3.1** Block diagram of the tumor detection and 3D reconstruction system

### 3.3 PREPROCESSING

Image preprocessing is an approach to enhance the data in the images prior to computational processing. Preprocessing and enhancement phase in medical image processing regenerates the input CT lung image into a standard format with enhanced image contrast, sharpened edges, reduced noise through background removal, image filtering and elimination of film artifacts. In the development of automated tumor detection system, the tumor detection depends on the quality of the image. The medical images are usually
complex and noisy in nature. Noise not only reduces the image quality but also cause the feature extraction, analysis algorithm to be unreliable. Hence, an image denoising method is required to preserve the image quality. Preprocessing of images normally involves,

- Removal of low-frequency background noise
- Normalization of individual particle image intensity
- Removal of reflections
- Masking certain portions of images

Denoising approach becomes essential during the modification of the image acquisition process. Many denoising algorithms concentrate on recovering high-frequencies. It is also essential to recover the low-frequencies for high noise levels.

Lung can be separated from the background by searching the object boundary or by utilizing the characteristics of objects like color, texture, shape, brightness and size. Image texture is a set of features that is computed to quantify the perceived texture of the image. Image texture provides data about the spatial arrangement of intensity or color in an image or selected region of an image. Brightness is used to brighten the complete image from the shadows to the highlights equally.

Linear denoising models like Gaussian filter are normally used to minimize the noise. These techniques work well in the flat regions of images. However, a major drawback is that they are unable to conserve edges in a good manner. A nonlinear filter such as a median filter have been used for enhancing the tumor area in the image(Yoshida et al 1996). But it introduces noise into the transformed image. The kernel regression-based framework
uses an implicit local model of the image for the purpose of denoising. In the proposed work, kernel based nonlocal neighbourhood algorithm has been used for denoising the lung image. When a high noise level is present in the image, the algorithm can remove noise and restore features to their near original counterparts.

3.3.1 Denoising Analysis

In Bayesian statistics, the kernel of a probability mass function or probability density function is not the functions of any variable. These factors form the portion of the normalization factor of a probability distribution and are not essential in many situations. For example in pseudo-random number sampling, the normalization factor is ignored. The normalization factors are usually ignored during the computations in Bayesian analysis of conjugate prior distributions. Only the kernel is considered here. The kernel is in closed form in many distributions. In non-parametric statistics, a kernel is utilized as a weighing function. Kernels are utilized in kernel density estimation to evaluate random variable density functions or to measure the conditional expectation of a random variable. It is also used for the estimation of spectral density in the periodogram.

Figure 3.2 demonstrates the process of denoising the lung images. The analysis of tumor detection depends on the region of interest that is noisy and of low contrast. Hence, an image denoising and enhancement is required to preserve the image quality and highlighting image features.
Figure 3.2 Lung Image Preprocessing

The proposed research work uses kernel based non-local neighbourhood denoising for removing the noise. The lung database containing various number of slices is taken as input. The input is denoised by kernel based non-local neighborhood denoising method with different denoising functions such as exponential function kernel, cosine function kernel, flat kernel, gaussian, turkey-bi-weight, wave kernel function and
finally processed with the best kernel function. The analysis of six kernel functions are carried out by the quality parameters and the descriptions of the kernel functions are explained as below:

- **Exponential Kernel**

  The exponential kernel is a set of distribution, which are built using the natural geometry of the distribution space. It can be defined as

  \[
  f(x) = e^{\left(\frac{-x}{\lambda}\right)}
  \]  
  \[ (3.1) \]

- **Cosine Kernel**

  \[
  f(x) = \begin{cases} 
  \cos\left(\frac{x}{\lambda}\right) & 0 < x \leq \lambda \\
  0 & \text{else}
  \end{cases}
  \]  
  \[ (3.2) \]

- **Flat Kernel**

  \[
  f(x) = \begin{cases} 
  \left(\frac{1}{x}\right) & 0 < x \leq \lambda \\
  0 & \text{else}
  \end{cases}
  \]  
  \[ (3.3) \]

- **Gaussian kernel**

  \[
  f(x) = e^{\left(\frac{x^2}{2\lambda^2}\right)}, \text{ for } x > 0
  \]  
  \[ (3.4) \]

- **Wave Kernel**

  \[
  f(x) = \begin{cases} 
  \sin\left(\frac{\pi x}{\lambda}\right) & 0 < x \leq \lambda \\
  0 & \text{else}
  \end{cases}
  \]  
  \[ (3.5) \]

  \(\lambda\)-factor to adjust the decay of the exponential function.
Turkey bi-weight

\[ f(x) = \begin{cases} \frac{1}{2} \left(1 - \left(\frac{x(i,j)}{\lambda}\right)^2\right)^2 & 0 < x \leq \lambda \\ 0 & \text{else} \end{cases} \]  \hspace{1cm} (3.6)

The resulting image quality of each kernel function is being analyzed with two metrics, Mean Squar Error (MSE) and Peak Signal to Noise Ratio (PSNR). The denoising function affords the result with a lesser MSE value and a greater PSNR value is considered as the best function for CT image denoising. Turkey bi-weight kernel function is found to satisfy the above said criteria. Hence Turkey bi-weight function is used for denoising.

3.3.1.1 Turkey bi-weight kernel function

The Turkey bi-weight kernel function is expressed as

\[ f(x) = \begin{cases} \frac{1}{2} \left(1 - \left(\frac{x(i,j)}{\lambda}\right)^2\right)^2 & 0 < x \leq \lambda \\ 0 & \text{else} \end{cases} \]  \hspace{1cm} (3.7)

In Equation 3.7 \( \lambda \) represents a factor to adjust the decay of exponential function and \( x \) indicates the coefficient value. From the above equation, the coefficient value is computed and this filter replaces the intensity value at each pixel in an image by a weighted average intensity values from nearby pixels.

\[ x(i,j) = \|v(N_i) - v(N_j)\|_{2a}^2 \]  \hspace{1cm} (3.8)

In Equation 3.8 \( a \) is the standard deviation of the Gaussian kernel, \( N_i \) and \( N_j \) denotes a square neighborhood of fixed window sizes 3x3 centered at pixel \( i \) and \( j \). \( v(N_i) \) and \( v(N_j) \) denotes the intensity gray values of \( N_i \) and
The existing technique provides image smoothness by using 5x5 filter coefficient to perform an image noise reduction. The image obtained after preprocessing is blurred and not clear. In order to reduce this effect, a Turkey bi-weight filter is introduced. In this filter, the filtering coefficient value is altered and 3x3 coefficient matrix is used to get a better result.

3.3.1.2 Pseudo code for denoising

**Input:** Raw Lung Image Slice ‘I’

**Output:** Preprocessed Image

**Step 1:** Initialize window size (3x3).

**Step 2:** For i=1 to r //r – Row size of image

**Step 3:** For j=1 to c //c – Column size of image

**Step 4:** Initialize x and y 3x3 matrix

**Step 5:** temp = I (i-1: i+1, j-1: j+1); //Project window over image matrix

**Step 6:** Extract Turkey bi-weight linear, T //Using Eqn. (3.7)

**Step 7:** Y(i, j) = T*temp(i, j); //Update output Image matrix

**Step 8:** End loop ‘i’

**Step 9:** End loop ‘j’

Mean Squared Error (MSE) of an estimator is one of the techniques to find the difference between the values that are implied by an estimator and true values of the quantity being estimated. The average of the squares of the errors is measured by MSE. MSE is the second moment of the error and thus includes both the bias of the estimator and its variance. It consists of the same units of measurement as the square of the quantity estimated. It is equal to the
sum of the squared bias and variance of the estimator. Mean Square Error (MSE) of each kernel function for the input lung image is determined by,

$$MSE = \frac{1}{n \times m} \sum_{i=1}^{n} \sum_{j=1}^{m} (x_{i,j} - y_{i,j})^2$$  \hspace{1cm} (3.9)

where \( n \), \( m \) denotes the dimensions of the image. \( x_{i,j} \) is the original image and \( y_{i,j} \) is a distorted image.

### 3.3.1.3 Peak Signal to Noise Ratio

Peak Signal to Noise Ratio (PSNR) is defined as the ratio between the maximum possible signal power and the power of a corrupting noise affecting the fidelity of its representation. As many signals have a wide dynamic range, PSNR is normally expressed in terms of logarithmic decibel scale. PSNR is used for the measurement of the reconstruction quality of the image. PSNR is easily defined via the mean squared error.

The Peak Signal to Noise Ratio (PSNR) value for each denoised image is evaluated using equation 3.10 as,

$$PSNR = 20 \log_{10} \frac{255}{\sqrt{MSE}}$$  \hspace{1cm} (3.10)

where, MSE is the mean square error. Turkey bi-weight denoising function furnishes lesser MSE and a higher PSNR. The PSNR and MSE values of Turkey bi-weight kernel are 34.119 and 25.21 respectively. Originally, the lung image is acquired from the dataset and the labels and marks on the images are removed. Preprocessing stage generates a noise reduced, filtered edges of a given input lung image which is used for feature extraction.
3.4 FEATURE EXTRACTION

Feature extraction is defined as the transformation of input data into a set of features. It plays a vital role in a computer assisted diagnosis system to provide an accurate result. During the analysis of medical images, a major problem is the number of variables involved for analysis. Analysis of a large number of variables requires a large amount of computation power and memory. One of the important factors that affect the classification result is feature extraction. Researchers spent much time to find the features that will improve the classification. It is known that some features used for classification are irrelevant or redundant. The irrelevant features used for any classifier may cause cost problem and also affect the classification rate. The process of feature extraction helps the researchers to improve the classification accuracy and minimize the computation time.

Feature extraction is the process of acquiring higher level information of an image such as color, shape and texture. Color is a virtual attribute that results from the light they emit or transmit or reflect. It provides information to distinguish various physical causes for color variations. It can be derived from a histogram of the image. Color features are used in biomedical image processing for cell classification, cancer cell detection (Siew et al 1988). The shape is defined as the geometrical information that remains when location, scale and rotational effects are filtered out from an object. The shape of an object is determined by external boundary. The image texture is defined as a variation in pixel intensities. It is an important virtual cue in identifying the homogeneous region of an image. Texture features are useful in biomedical image processing such as classification of pulmonary diseases (Suttan & Hall 1972) using texture features.
Feature extraction can be described in two steps such as feature selection and feature construction. Feature selection is performed to select relevant and informative features to improve the prediction accuracy. A number of feature selection procedures have been proposed. Some of the popular feature selection algorithms are sequential forward selection, sequential backward selection, genetic algorithm and particle swarm optimization. Feature construction is the process of obtaining high level features from the available features. The aim of the feature construction is to group the efficient features for making predictions powerful. There are a number of feature construction methods such as clustering (Bekkerman et al 2003) and principal component analysis.

3.4.1 Texture Feature Extraction

The texture is one of the important feature used for identifying the region of interest in the image. A texture may be fine coarse, smooth or grained depending on its tone and structure. The tone is the pixel intensity property whereas structure defines the spectral relationship between the pixels. As an image is made up of pixels, texture can be defined as an entity consisting of mutually related pixels. The texture of the image is determined by the distribution of the gray level over the pixels in the region. Tuceryan & Jain (1998) classified the methods for texture feature extraction into four based on the type of approach,

- Statistical approach
- Structural approach
- Model based approach
- Transform based approach
In the case of a statistical approach, texture is represented by a set of statistically extracted features in multidimensional feature space. The feature vector generated from the pattern is assigned to their class by probabilistic or deterministic decision algorithm. This technique is one of the first methods in machine vision (Tuceryan & Jain 1988). The statistical methods can be used to a spatial distribution of gray values. Based on the number of pixels defining the local features, the statistical features can be classified into the first order, second order or higher statistics. The most popular second order statistical feature was derived from the co-occurrence matrix (Materka & Strzelecki 1998).

In the case of a structural approach (Haralick 1979), texture is defined by well-defined primitives and a hierarchy of spatial arrangements. For those primitives describing the texture, it is needed to define the primitive and the placement rule. The structural method provides a symbolic description of the image that is more useful in image synthesis than analysis task and not suitable for natural texture since there is no clear distinction between micro and macro texture.

The model based approaches such as Fractal and Markov model (Cross 1983) describe an image as a probability model or as a linear combination of a set of basic functions. The fractal model is useful for modeling certain natural texture that have a statistical quality of roughness at different scales. The fractal model can be used for texture analysis and discrimination but not suitable for describing local image structures as it lacks orientation selectivity (Pentland 1984).

In a transform based approach, the texture is described by frequency and size. Some methods of transform based approach for texture analysis are Fourier (Rosenelfeld & Weszka 1980), Gabor (Bovik et al 1990)
and wavelet transform (Lu et al 1997). Wavelets are best suited for texture analysis for a specific application. The problem with wavelet transform is that it is not translation invariant.

Comparing the above mentioned four approaches, the methods based on second order statistics show higher discrimination rate than the transform based methods and structural methods (Weska et al 1976). In the present work second order statistical features have been considered for diagnosis of the lung tumor.

3.4.1.1 First order statistical features

The features are described to quantify properties of an image by exploiting space relation underlying the gray level distribution of a given image. The features generated by first order statistics provide information related to the gray level distribution of the image. However, they do not give any information about the relative position of the various gray levels within the image (Namita Agarwal & Agarwal 2012). The histogram of the intensity level is the summary of the statistical information contained in the image. The features such as mean, variance, skewness and kurtosis are considered. The mean is the average level of intensity of the image. Variance is the histogram width. Skewness is a measure of the degree of histogram asymmetry around the mean. Kurtosis is a measure of the flatness of the histogram.

3.4.1.2 Second order statistical features

The second order histogram is defined as the co-occurrence matrix \( h_{\theta}(i,j) \). The co-occurrence matrix is a function of parameters such as distance measured in pixel number \( d \) and its orientation \( \theta \). These features are estimated based on the second order joint density function \( p(i, j \mid d, q) \) for \( q = 0^\circ, 45^\circ, 90^\circ \) and \( 135^\circ \) (Haralick 1973). The function \( p(i, j \mid d, q) \) is the
probability of two pixels located in an inter sample distance $d$ and orientation $\theta$, having gray level $i$ and $j$. The graphical representation of this co-occurrence matrix is shown in Figure 3.3

**Figure 3.3 Co-occurrence Matrix**

The co-occurrence matrix can be constructed by counting the number of occurrence of pixel pairs at a given displacement. Non-normalized frequencies of the co-occurrence matrix as functions of $0^\circ, 45^\circ, 90^\circ$ and $135^\circ$ is defined in equations 3.11 to 3.14.

$P(i,j,d,0^\circ) = \#\{((k,l),(m,n)) \in (L_x \times L_y) \times (L_x \times L_y) | k - m = 0, |l - n| = d, I(k,l) = i, I(m,n) = j\}$

(3.11)

$P(i,j,d,45^\circ) = \#\{((k,l),(m,n)) \in (L_x \times L_y) \times (L_x \times L_y) | k - m = d, |l - n| = -d, I(k,l) = i, I(m,n) = j\}$ or $\{((k,m) = -d, l - n = -d), I(k,l) = i, I(m,n) = j\}$

(3.12)

$P(i,j,d,90^\circ) = \#\{((k,l),(m,n)) \in (L_x \times L_y) \times (L_x \times L_y) | k - m = 0, |l - n| = d, I(k,l) = i, I(m,n) = j\}$

(3.13)
where \# denotes the number of elements in the set, \( I \) is the image, \( d \) represents the distance, \( I \) and \( j \) are gray tone. \( L_x \) and \( L_y \) are horizontal and vertical spatial domains, respectively. The set \((L_y, L_x)\) is the set of resolution cells of the image. \( k, l, m \) and \( n \) denotes the number of iterations.

3.5 EXTRACTION OF FEATURES IN LUNG IMAGE

The image feature extraction phase is substantial in working with image processing techniques that uses various procedures and techniques to detect and isolate distinctive portions or shapes of the image. In this proposal, the characteristics of an image such as contrast, energy, entropy, variance and homogeneity are considered that paves the way for appropriate classification results. The noise-free image attained from denoising process is fed into the second order histogram based feature extraction, which represents the relative frequency of incidence of various gray levels in an image.

The GLCM is a matrix that defines how often the different combinations of pixel gray levels occur in an image. Gray level co-occurrence matrix have been used for extracting the image features of the human lung. Since, the human visual system uses second order distribution gray levels in identifying features. The feature based on the co-occurrence matrix can capture characteristics of texture such as entropy, energy, contrast and others. The present work uses GLCM to extract the lung features. Haralick et al (1973) suggested the use of gray level co-occurrence matrices that have been used for extracting second order statistical features. In this research, twelve different texture features such as contrast, correlation, cluster prominence, cluster shade, dissimilarity, energy, entropy, homogeneity, homogeneity
based probability, maximum probability, sum of squares, variance and autocorrelation are extracted from the image by using GLCM technique.

- **Contrast**

  The contrast estimates the local variations in the GLCM. It is the basic measure of contrast between an intensity of a pixel and its adjacent pixels over the entire images.

  \[
  C_r = \sum_{a}^{N} \sum_{b}^{N} (a - b)^2 P(a, b) \tag{3.15}
  \]

- **Correlation**

  It is a measure of gray level linear dependence between the pixels at the specific positions that is closely correlated with each other.

  \[
  C_r = \sum_{a}^{N} \sum_{b}^{N} \frac{P(a, b) - \mu_x \mu_y}{\sigma_x \sigma_y} \tag{3.16}
  \]

- **Cluster Prominence**

  It is a measure of asymmetry. When the cluster prominence \(C_p\) is high, the image has less symmetric, or else there has a peak in the GLCM matrix around the mean value. And also a low cluster prominence denotes a small variation in the gray-scale.

  \[
  C_p = \sum_{a=0}^{N-1} \sum_{b=0}^{N-1} \left\{(i + j - \mu_x - \mu_y)^4 \right\} \times P(a, b) \tag{3.17}
  \]

- **Cluster Shade**
It is an estimation of the skewness of the matrix and is believed to gauge the perceptual concepts of uniformity. This cluster shade \( C_s \) is estimated as,

\[
C_s = \sum_{a=0}^{N-1} \sum_{b=0}^{N-1} \left( a + b - u_x - u_y \right)^3 P(a, b) \tag{3.18}
\]

- **Dissimilarity**

It mainly estimates the variations of the gray level image pairs in the image. This dissimilarity \( D \) is estimated as,

\[
D = \sum_{a,b=1}^{N} C_{a,b} |a - b| \tag{3.19}
\]

- **Energy**

It is the summation of squared elements in the GLCM and the values range between 0 and 1. The energy \( E \) is evaluated as,

\[
E = \sum_{a=0}^{N} P^2(a, b) \tag{3.20}
\]

- **Entropy**

Entropy estimates the randomness of the image texture i.e. intensity distribution. This entropy is high when all the Homogeneity probabilities \( P(a, b) \) are equal and is low when the entries in \( P(a, b) \) are unequal.

\[
Ent = \sum_{a=0}^{N} \sum_{b=0}^{N} P(a, b) \log (P(i, j)) \tag{3.21}
\]

- **Homogeneity**
It is the measurement of the closeness of the elements distribution in the GLCM and its value ranges between 0 and 1.

\[ C_n = \sum_a \sum_b \frac{P_d[a,b]}{1+|a-b|} \]  \hfill (3.22)

- **Homogeneity based probability**

It is estimated according to the absoluteness of \( a \) and \( b \) by using the following equation.

\[ \text{Homop} = \sum_a \sum_b \frac{1}{1+\text{abs}(a-b)} P_{ij} \]  \hfill (3.23)

- **Maximum probability**

It indicates the largest entries in the matrix, and the strongest response. The maximum probability (\( \text{maxprob} \)) is estimated as,

\[ \text{maxprob} = \max_{a,b} P_d[a,b] \]  \hfill (3.24)

- **Variance**

Variance has relatively high weights on the elements that differ from the average value of \( p(a, b) \). It generally refers to the gray-level variability of the pixel pairs and is a measurement of heterogeneity.

\[ \text{Var} = \sum_{i=0}^{N-1} \sum_{j=0}^{N-1} (i - u_x)^2 . P(a, b) + \sum_{i=0}^{N-1} \sum_{j=0}^{N-1} (j - u_y)^2 . P(a, b) \]  \hfill (3.25)

- **Autocorrelation**
This autocorrelation ($AC$) analyzes the regularity and coarseness of texture. It is evaluated by using the below equation,

$$AC = \frac{XY}{(X-a)(Y-b)} \cdot \frac{\sum_{a=1}^{X-n} \sum_{b=1}^{Y-m} f(a,b) f(a+m,b+n)}{\sum_{a=1}^{X-n} \sum_{b=1}^{Y-m} f^2(a,b)}$$

(3.26)

Here, $f(a,b)$ is similar to $P$, where $f(a,b)$ is the coefficient matrix. The entire feature that are estimated from the preprocessed lung image, convey some important information regarding lung tumor. This information is very helpful to detect lung as normal or abnormal.

Table 3.1 Values for Various Texture Features of Lung Image

<table>
<thead>
<tr>
<th>Lung Image</th>
<th>$C_1$</th>
<th>$C_r$</th>
<th>$C_p$</th>
<th>$C_t$</th>
<th>$D$</th>
<th>$E$</th>
<th>$Ent$</th>
<th>$C_h$</th>
<th>Homop</th>
<th>maxprob</th>
<th>Var</th>
<th>AC</th>
</tr>
</thead>
<tbody>
<tr>
<td>Normal values</td>
<td>1.02</td>
<td>0.88</td>
<td>499.31</td>
<td>44.49</td>
<td>0.42</td>
<td>0.17</td>
<td>2.35</td>
<td>0.84</td>
<td>0.84</td>
<td>0.31</td>
<td>14.14</td>
<td>13.73</td>
</tr>
<tr>
<td>Normal values</td>
<td>1.01</td>
<td>0.88</td>
<td>494.88</td>
<td>44.27</td>
<td>0.42</td>
<td>0.17</td>
<td>2.35</td>
<td>0.84</td>
<td>0.84</td>
<td>0.31</td>
<td>14.14</td>
<td>13.73</td>
</tr>
<tr>
<td>Normal values</td>
<td>1.02</td>
<td>0.88</td>
<td>496.24</td>
<td>44.47</td>
<td>0.42</td>
<td>0.17</td>
<td>2.35</td>
<td>0.84</td>
<td>0.84</td>
<td>0.31</td>
<td>14.14</td>
<td>13.73</td>
</tr>
<tr>
<td>Normal values</td>
<td>1.04</td>
<td>0.87</td>
<td>484.68</td>
<td>43.83</td>
<td>0.43</td>
<td>0.17</td>
<td>2.36</td>
<td>0.83</td>
<td>0.83</td>
<td>0.32</td>
<td>14.20</td>
<td>13.78</td>
</tr>
<tr>
<td>Abnormal values</td>
<td>1.05</td>
<td>0.88</td>
<td>498.19</td>
<td>41.91</td>
<td>0.44</td>
<td>0.16</td>
<td>2.46</td>
<td>0.85</td>
<td>0.84</td>
<td>0.32</td>
<td>15.11</td>
<td>14.69</td>
</tr>
<tr>
<td>Abnormal values</td>
<td>1.05</td>
<td>0.88</td>
<td>499.53</td>
<td>42.01</td>
<td>0.44</td>
<td>0.16</td>
<td>2.47</td>
<td>0.85</td>
<td>0.84</td>
<td>0.32</td>
<td>15.11</td>
<td>14.69</td>
</tr>
<tr>
<td>Abnormal values</td>
<td>1.04</td>
<td>0.88</td>
<td>500.71</td>
<td>41.92</td>
<td>0.43</td>
<td>0.16</td>
<td>2.46</td>
<td>0.85</td>
<td>0.84</td>
<td>0.31</td>
<td>15.13</td>
<td>14.71</td>
</tr>
<tr>
<td>Abnormal values</td>
<td>1.04</td>
<td>0.88</td>
<td>501.55</td>
<td>42.07</td>
<td>0.43</td>
<td>0.16</td>
<td>2.45</td>
<td>0.85</td>
<td>0.84</td>
<td>0.32</td>
<td>15.14</td>
<td>14.72</td>
</tr>
<tr>
<td>Abnormal values</td>
<td>1.04</td>
<td>0.88</td>
<td>502.81</td>
<td>42.21</td>
<td>0.43</td>
<td>0.16</td>
<td>2.45</td>
<td>0.85</td>
<td>0.84</td>
<td>0.32</td>
<td>15.13</td>
<td>14.71</td>
</tr>
</tbody>
</table>

Table 3.2 Parameter Descriptions

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>$C_1$</td>
<td>Contrast value</td>
</tr>
<tr>
<td>$N$</td>
<td>Number of gray levels</td>
</tr>
<tr>
<td>$P$</td>
<td>Co-occurrence matrix</td>
</tr>
<tr>
<td>a and b</td>
<td>Gray levels</td>
</tr>
<tr>
<td>Parameter</td>
<td>Description</td>
</tr>
<tr>
<td>-----------</td>
<td>-------------</td>
</tr>
<tr>
<td>$\mu_x, \mu_y$</td>
<td>Mean values of gray levels at x and y sizes</td>
</tr>
<tr>
<td>$\sigma_x, \sigma_y$</td>
<td>Standard deviation of gray levels at x and y sizes</td>
</tr>
<tr>
<td>$\gamma$</td>
<td>Correlation value</td>
</tr>
<tr>
<td>$C_p$</td>
<td>Cluster Prominence</td>
</tr>
<tr>
<td>$C_s$</td>
<td>Cluster shade</td>
</tr>
<tr>
<td>D</td>
<td>Dissimilarity</td>
</tr>
<tr>
<td>E</td>
<td>Energy</td>
</tr>
<tr>
<td>X</td>
<td>Input image</td>
</tr>
</tbody>
</table>

Table 3.1 represents the values of various texture feature, which are obtained from the lung image. This table includes normal and abnormal values for each texture features. From this table, the normal and abnormal images of the lung are identified. The parameter descriptions for the texture features in GLCM are depicted in table 3.2. After the estimation of the twelve different texture features, the Feature Set (FS) are arranged for training and testing stages.

### 3.6 CLASSIFICATION

Tumor classification systems provide the basis for diagnosis of the tumor and patient therapy. It provides a critical foundation for epidemiological and clinical studies. The aim of the classification approaches is to adhere to the principles of reproducibility and simplicity to reduce the amount of homogeneous unclassifiable lesions and clinical significance. Classification is a technique to group all the pixels in the image into many classes. The classification discriminates multiple images from each other. It is done on the basis of spectrally defined features. The features may be density, texture, etc.

#### 3.6.1 Normal Distribution
The normal distribution or Gaussian distribution is suitable for features that have common distributions in each class. The Naive Bayes classifier evaluates a separate normal distribution for each class by calculating the standard deviation and mean of the training data in that class.

### 3.6.2 Multinomial Distribution

The multinomial distribution is suitable when all the features denote counts of a set of words or tokens, sometimes known as the "bag of words" model. The Naive Bayes model works on the assumption that the total length is independent of the response class. For the multinomial option, each feature denotes the count of one token. The set of a relative token probabilities is then counted by the classifier separately for each class.

The classifier characterizes the multinomial distribution for each row by using the vector of probabilities for the corresponding class, and by the total token count for that row. Categorization depends on the relative frequencies of the tokens.

### 3.6.3 Kernel Distribution

The kernel distribution is suitable for the features that consist of a continuous distribution. It does not require a strong assumption like the normal distribution and it is used in cases where the distribution of a feature is skewed or consists of multiple peaks or modes. It requires more calculation time and higher memory than the normal distribution. The naive Bayes classifier calculates separate kernel density estimation for every class, depending on the training data for that class.

### 3.6.4 Classification of Lung Image
The features extracted in feature extraction stage are given as input for classification, to distinguish the normal and abnormal status of the lung image. The lung image is classified by exploiting multivariate multinomial distributed Bayes classification. In multivariate distributed Bayes classification, the distributed data are classified corresponding to multivariate distributions. Precisely, multiple features that appear in the training data are chosen and made an assumption of each variable as a binary valued vector. The multivariate decision rule in each class chases the non-occurrence of features, whereas decision rule based on a multinomial classification neglects the non-appearing feature. The classification algorithm evaluates both the models.

In the training phase the naive Bayes classifier estimates the parameters of a probability distribution using the training samples, by making the assumptions of conditionally independent features. In the prediction phase, it estimates the posterior probability of unseen test sample and then distinguished the test sample based on greatest posterior probability. The ultimate goal of classification is to examine the accuracy rate of generating results. For that purpose, accuracy metrics like sensitivity, specificity, error rate, correct rate, last error rate, last correct rate, classified rate, prevalence, and the positive / negative likelihood are validated.

3.6.4.1 Naive Bayes classifier

A naive Bayes classifier is a probabilistic classifier that depends on the application of Bayes theorem with naive independence assumptions. The structure of the naive Bayes classifier is shown in Figure 3.4. In naive Bayes classifier, the presence or absence of a specific feature is not related to the presence or absence of another feature. The naive Bayes classifier estimates a separate set of probabilities for the set of extracted feature levels in each class,
whereas the naive Bayes classifier is applicable when features are independent of one another within a class.

The naive Bayes classifier supports kernel, normal (Gaussian), multivariate multinomial distributions. It is possible to utilize distinct distributions for distinct features. The classification is performed in two steps.

- Training step
- Prediction step

Training Step: With the training samples, this step computes the metrics of the probability distribution with an assumption that features are conditionally independent.

Prediction Step: For classifying unseen test image, the step estimates posterior probability value of that image belonging to each defined class. Further, the unseen image is classified by the largest posterior probability value.
Figure 3.4 Naive Bayes classifier

- Multivariate multinomial distributed bayes classification

The multivariate multinomial distribution is congruous for categorical features. The feature categories are sometimes known as feature levels. A separate set of probabilities is computed by the naive Bayes classifier for the set of feature levels for every class.

Multinomial distributed Bayes classification is one of the Naive Bayes variants used in image classification, which holds the algorithm for multinomial distributed data. For each class $X$, the distribution framework is represented by vectors $\theta_x = (\theta_{x1}, ..., \theta_{xk})$, where $k$ denotes the total number of features in lung image classification, $\theta_{xi}$ implies the probability $P(w_i|x)$ of feature $i$ present in a sample belonging to class $X$. $\theta_x$ is the metrics measured by a smoothened version of maximum likelihood.

$$\theta_{xi} = \frac{R_{xi} + \alpha}{R_x + \alpha k}$$ (3.27)

where, $R_{xi} = \sum_{w \in T} W_{iw_i}$ denotes the number of times the feature $i$ reflects in the training set $(T)$, $R_x = \sum_{i=1}^{[r]} R_{xi}$ implies the total count of all features for class $X$ and $\alpha$ is a constant in Equation 3.27.

In multivariate distributed Bayes classification, distributed data is classified corresponding to multivariate distributions. Accurately, multiple features appear in the training data are chosen and made an assumption that each variable as a binary valued vector. The classification rule for multivariate distributed Bayes classification is as follows,

$$P(w_i|x) = P(i, w_i|x, w_i)(1 - w_i) - P(i|x)(1 - w_i)$$ (3.28)
The multivariate decision rule in a class x explicitly chases the non-occurrence of a feature i, whereas the decision rule based on the multinomial classification neglects a non-appearing feature. The classification algorithm used in this work evaluate both the above models.

The classification performance analysis is validated by its accuracy rate. The result of accuracy rate is predicted by the formation of inverted L-shaped curve in ROC graph. A complete sensitivity, specificity report is generated for diagnostic test evaluation. The proposed classification system maximizes the accuracy rate by distinguishing the lung image as a tumor or normal. Positive Predictive Value (PPV) or precision rate is defined as the proportion of positive test results that are true positives. Negative Predictive Value (NPV) is known as the proportion of subjects with a negative test result which are diagnosed accurately. NPV is utilized to describe the performance of a diagnostic testing approach. NPV and PPV can be estimated by using data from a cross-sectional study. Likelihood ratios are utilized for the value assessment of performing a diagnostic test as given in equations 3.29 and 3.30. It uses specificity and sensitivity of the test to find whether the test result alters the probability of a condition to exists.

\[
Likelihood \, ratio \, positive = \frac{Sensitivity}{1 - Specificity} \quad (3.29)
\]

\[
Likelihood \, ratio \, negative = \frac{1 - Sensitivity}{Specificity} \quad (3.30)
\]

Sensitivity or true positive rate measures the proportion of actual positives that are accurately identified positively, indicating that the person has the disease. Sensitivity relates to the ability of the test to recognize positive results. Specificity is the probability that a diagnostic test is negative, indicating that the person does not have the disease (Achrya et al 2008).
relates to the ability of the test for identifying negative results. Prevalence is defined as the proportion of the population found to have a condition.

The classification procedure follows the steps,

- The essential lung features are extracted from the preprocessed lung image by feature extraction process. The extracted lung features are given as an input for classification.

- The multivariate multinomial distributed Bayes classification Classifies the lung image as normal or abnormal based on training and classification analysis.

- The abnormal images are given to the segmentation process to extract the tumors for further process.

### 3.7 SEGMENTATION

Segmentation is the process of dividing the image into regions with similar properties. The properties of the image may be a gray level, color, texture, brightness, contrast. Segmentation extracts structures of interest automatically by the segmentation process. The selection of the segmentation technique depends on the characteristics of image type. Texture based segmentation can be performed on sonographic images. Edge-based segmentation searches for discontinuities in the image intensity. Region-based segmentation looks for uniformity within a sub-region, depending on the desired property, i.e., intensity, texture and color.

The major objectives of the segmentation in medical images are as follows,

- Obtaining the information about the anatomical structure of the organs.
• Identifying the Region Of Interest (ROI) to locate the tumor, lesion and other abnormalities.

• Estimating the tissue volume to measure the growth of the tumor.

3.7.1 Contour Based Segmentation

Contour based approaches generally start with a stage of edge detection followed by a linking process to exploit curvilinear continuity. It also deforms an initial curve so that it separates foreground from the background based on the means of the two regions. In active contour models the user specifies a first guess of the contour, which is stimulated by image-driven forces to the boundaries of the preferred objects. Two types of forces are measured. One is the internal force and another is the external force. The internal forces are defined in the curve and considered to keep the model smooth during deformation. The external forces are computed from the original image and defined to progress the contour towards the object boundary within the image. One direction of describing the curve is, using an unambiguous parametric form, which is the technique used in snakes (Bakos 2007).

3.7.1.1 Traditional active contour model

The active contour is an energy-minimizing spline that is guided by external constraint forces and also it is influenced by image forces, which pull it toward features such as edges and lines. In the active contour models, an edge-detector is used, relying on the gradient of the image to stop the
evolving curve on the boundary of the desired object. The active contour model (Chan & Vese 2001) is represented as,

\[
J_1(C) = \alpha \int_0^1 |C'(s)|^2 ds + \beta \int_0^1 |C''(s)| ds - \lambda \int_0^1 \left| \nabla u_0(C(s)) \right|^2 ds \tag{3.31}
\]

In equation 3.31, \(\alpha\), \(\beta\) and \(\lambda\) are positive parameters. \(\alpha\) and \(\beta\) control the smoothness of the contour (the internal energy), whereas \(\lambda\) attracts the contour towards the object in the image (Bakos 2007). By minimizing the energy, the curve is located at the points of maximal \(\left| \nabla u_0 \right|\), which is acting as an edge-detector to keep the smoothness in the curve (object boundary). Based on the equation 3.31, the minimization problem is stated in the Equation 3.32,

\[
\inf_{C} J_2(C) = 2 \int_0^1 |C'(s)| . g(\left| \nabla u_0(C(s)) \right|) ds \tag{3.32}
\]

The path of minimal new length is found by solving the minimization problem in the above equation. The minimizer \(C\) will be obtained when \(g(\left| \nabla u_0(C(s)) \right|)\) vanishes, i.e., when the curve \(C\) is on the boundary of the object. A level set model can perform a numerical computation that contains curve and surfaces without parameterizing the object. Since all the active contour models rely only on edge-function, which is depending on the image gradient \(\left| \nabla u_0 \right|\) to stop the curve evolution, these models can determine only objects with edges defined by the gradient. Hence, by acquiring level set equations with active contour modeling, contour formation for segmentation is more appropriate, with respect to the cancer mass.

3.7.2 The Level Set Method
The level set technique is an arithmetic and theoretical technique for propagating the boundary. In image processing, the level set technique is normally used as a segmentation tool through the propagation of a contour by using the properties of the image. One of the initial application was to detect edges in the image, although in recent applications shapes, colors, textures etc., can be identified. In the level set technique, an interface \( C \) is symbolized completely as a level set of a function \( \varnothing \), called the level set function, of higher dimension (Sifakis et al 2002). The geometric characteristics and the movement of the front are calculated with this level set function. The interface is characterized implicitly as the zeroth level set or contour of this scaling function. Over the rest of the image space, this level set function is defined as the signed distance function from the zeroth level set. Particularly, given a closed curve \( C \), the function is zero if the pixel lies on the curve itself, or else, it is the signed minimum distance from the pixel to the curve. Through convention, the distance is observed as negative for pixels outside \( C \) and positive for pixels inside \( C \). The level set function \( \varnothing \) of the closed front \( C \) is estimated using the equation 3.33,

\[
\varnothing(i,j) = \pm e((i,j), C)
\]  

where, \( e((i,j), C) \) is the distance from point \((i,j)\) to the contour \( C \), and the sign plus are selected if the point \((i,j)\) is inside or outside of interface \( C \). The interface is now symbolized implicitly as the zeroth level set of this scaling function.

\[
C = \left\{ \frac{\varnothing(i,j)}{e((i,j), C)} = 0 \right\}
\]  

Moreover, an implicit representation of \((i,j)\) in equation 3.34 contains frequent advantages over a parametric approach. The most prominent
example is topological, it usually occurs during the propagation. For example, when two flames burn the evolving interfaces mutually combine into one particular propagating front. The function $\varnothing$, that varies with space and time is then developed using a limited differential equation, including terms that are either parabolic or hyperbolic in nature.

An arithmetical active contour model based on the mean curvature motion is given in equation 3.35,

$$\frac{\partial \varnothing(i,j)}{\partial s} = |\nabla \varnothing(i,j)| \epsilon n(\varnothing(i,j)) + v$$  \hspace{1cm} (3.35)

The constant $v$ is an alteration term. The quantity $(v + \epsilon n(\varnothing(i,j)))$ always remains positive. This constant may be defined as a force pushing the curve toward the object while the curvature becomes null or negative. In addition, $v > 0$ is a restriction on the area within the curve, where, $n$ represents the mean curvature of the level set function given by,

$$n(\varnothing(i,j)) = div\left(\frac{\nabla \varnothing}{|\nabla \varnothing|}\right)$$  \hspace{1cm} (3.36)

$$n(\varnothing(i,j)) = \frac{\varnothing_{ij}^2 - 2 \varnothing_i \varnothing_{ij} + \varnothing_{ii}^2}{\varnothing_{ii}^2 + \varnothing_{ij}^2}$$  \hspace{1cm} (3.37)

where, $\varnothing_{i}$ and $\varnothing_{ii}$ indicate the first and second-order partial derivatives of $\varnothing(i,j)$ value to $i$, and $\varnothing_{j}$ and $\varnothing_{ij}$ denote the similar respect values to $j$ in equations 3.36 and 3.37. An additional term, called stopping function is added to the speed function in the geometric active contour model. It is given by,

$$\frac{\partial \varnothing(i,j)}{\partial s} = f(X(i,j)) \epsilon n(\varnothing(i,j)) + v |\nabla \varnothing(i,j)|$$  \hspace{1cm} (3.38)
where, $f(X(i,j))$ in equation 3.38 and 3.39 denotes the stopping function, which is a constructive and a decreasing function of the image gradient.

$$f(X(i,j)) = \frac{1}{1+|\nabla X(i,j)|}$$  \hspace{2cm} (3.39)

The contours progress in the normal direction with a speed of $f(X(i,j))(\nu + \varepsilon n(\partial(i,j)))$ and discontinues on the edges, where $f(\cdot)$ disappears. The curvature term $n$ continues the regularity of the contours while the constant term $\nu$ speeds up and remains the contour evolution by minimizing the enclosed area.

### 3.7.3 Proposed Enhanced Level Set -Active Contour Model

An Enhanced Level Set-Active Contour Model (ELS-ACM) is proposed to segment the tumor mass of the lung image. It is the combination of both active contour and level set model. The basic idea of the active contour is to start with initial boundary shapes, which is represented in the form of closed curves known as contours. The contours can be iteratively modified by applying the shrink or expansion operations according to the image constraints. That shrink or expansion operations can be termed as contour evolution. The level set is a powerful mathematical and computational tool for tracking the evolution of curves or surfaces along the image sequences. The level set method evolves a curve by updating the level set function at fixed coordinates through time instead of tracking a curve through time.

A model for ELS-ACM implemented is mentioned as $J_1(c)$ in Equation 3.43. In this equation, the contour generated entrusts on the Internal
Mean (IM), External Mean (EM) and the Attraction Force (AF) of contour towards the object for curve evolution. A curve is evolved and is subjected to constraints in terms of discovering objects from the given input image. These constraints in active contour modeling are formulated by exploiting the level set equations.

Traditional active contour models used an edge detector to halt the curve evolving on the boundaries of the desired object. The contour models can converge to an incorrect boundary if the initial contour is not close to an adequate amount of the preferred boundary (Somkantha et al 2011). In Active contour without edges (Chan & Vese 2001) the parameter used to stop the curve evolution was formed by two regions namely piecewise constant, the intensity of distinct value. This criterion produced multiple force term and multiple minimizer terms. Moreover, the initially formulated curve was not accurate to facilitate accuracy in curve evolution and it required to be adjusted under certain constraints that paved the way for the multiple minimizer terms. Hence this research work surmounts the aforementioned minimization problem by exploring one force term and one minimizer term.

The contour initialization is done by using the level set function and distance transform of a binary image. It computes the Euclidean distance transform of the binary image. For each pixel in the binary image, the distance transforms assign a number that is the distance between the current pixel and the nearest non-zero pixel of the binary image. This nearest neighbor transform returns a label matrix where each element of label matrix has the linear index of the nearest nonzero pixel of the binary image.

The Euclidean distance $E_d$ between the pixels $(x_1, y_1)$ and $(x_2, y_2)$ is calculated using the Equation 3.40,
\[ E_d = \sqrt{(x_1 - x_2)^2 + (y_1 - y_2)^2} \]  

(3.40)

3.7.3.1 Pseudo code for contour initialization

The pseudo code for contour initialization is given below:

**Step 1:** Initialize k=0; //Initialize iteration limit

**Step 2:** Initialize v [0] =0; //Initialize temporary variable for image index

**Step 3:** \[ z = E_d \] // Euclidean distance for binary image matrix where finding the distance from present x and y intensity with nearest of ‘1’ pixel in a binary image. Here x and y represent the location of pixel in row and column respectively.

**Step 4:** for q = 1 to size of image then

**Step 5:** \[ s = \frac{(f(q) + q^2) - (f(v[k]) + v[k]^2)}{(2q - 2v[k])} \] // Weight updation of image (f(q)) at every index of ‘v’ and ‘q’ iteration of image input

**Step 6:** if \[ s \leq z[k] \] then //Checking for maximum range of weight, ‘s’

**Step 7:** s = z[k] //Update s.

**Step 8:** end if

**Step 9:** k = k+1;

**Step 10:** v [k] = q //Update index

**Step 11:** z [k] = s; //Update weight array

**Step 12:** End loop q //End step 4 loop

**Step 13:** k=0; //Initialize iteration
Step 14: for q = 0 to n-1 //Loop up to image size where n – maximum size of image

Step 15: L=0 //Initialize iteration

Step 16: while z [L+1] < q //Index loop upto size of image matrix

Step 17: L=L+1; //Increase ‘L’ iteration

Step 18: k = k + 1; //Increase ‘k’ iteration

Step 19: \[ D_f(q) = (q - v[k])^2 + f(v[k]) \] // Location for ROI over input image for the index of ‘q’ and v[k].

Step 20: Extract Binary mask of D_f image region. //From D_f, the binary formation is extracted which is represented as binary mask output. This can be represented as M_{x,y}

Step 21: End while //Ending step 14 loop

Step 22: End for q //Ending step 15 loop

Step 23: Provide contour over the mask of image.

The above algorithm can be represented as,

\[
y_a = \begin{cases} 
E_o, & \frac{((f(q)+q^2)-(f(v[k])+v[k]^2))}{(2q-2v[k])} \geq (E_d+D_f(q)) \\
\frac{((f(q)+q^2)-(f(v[k])+v[k]^2))}{(2q-2v[k])} & \text{else} 
\end{cases}
\]  

(3.41)

where, q is the number of horizontal parabola, v[k] is the left of S in the q parabola and z[k] is the lower envelope of q parabola, for k= 1,2,3,…size of image
The initial binary masking is formed by applying the Equation 3.41 to the original input image. The formation of binary masking leads to the development of the active contour model. The binary images which are also called as Region Of Interest (ROI) is given as input for the segmentation process. In ROI, the edge information, represented as $\xi$, are extracted from the tumor slices. The value of $\xi$ varies continuously for the $q^{th}$ and $k^{th}$ iteration.

The extracted $\xi$ value has the background and foreground region, where foreground is considered as updated ROI. Euclidean distance ($E_d$) is computed for the nearest region of foreground pixels. Based on the Euclidean distance, weight value is updated for every iteration of $q$ and $k$. From the updated weight value, index of each iteration is obtained and finally ROI is updated as $D_t$. In the Equation 3.41, if the ROI distance is lesser than or equal to the weight value, then the value of Euclidean distance is updated on the initial masking parameter $y_{ij}$. From the obtained initial masking value, $\xi$ is updated. The proposed ELS-ACM is represented in the Equation 3.42.

\[
I_s(C) = \sum_{(x,y)} \xi(r, C) \left( \frac{I_{x,y}(i)}{\text{length}(i) + \varepsilon} \right) + \sum_{(x,y)} \xi(r, C) \left( \frac{I_{x,y}(e)}{\text{length}(e) + \varepsilon} \right) \{[I_{\text{index}} - \text{IM}]^2 - [I_{\text{index}} - \text{EM}]^2 \}
\]

(3.42)

In the traditional active contour model, weight updation was carried out by considering the internal and external energies, where the energy lies between 0 and 1. In the proposed ELS-ACM the internal and external energy are replaced by internal and external mean. The size of the active contour is computed by applying the attractive force. Internal Mean (IM) is defined as a sum of the product of ratio between input image intensity with row length and a constant relative accuracy $\varepsilon$. Similarly, External Mean (EM) is defined as a
sum of the product of ratio between the initial masking with row length and a constant relative accuracy \( \varepsilon \). When the internal mean exceeds the external mean, the active contour shrinks \((J_1(c))\) towards the centroid. When the external mean exceeds the internal mean, active contour grows \((J_1(c))\) outwards i.e. away from the centroid. The updation of \(J_1(c)\) based on the difference in attractive force, where the attractive force can be defined as the difference from square distance between input intensity and internal mean and square difference between input intensity and external mean for respective row and column size, which is given in Equation 3.50.

\[
IM = \sum_{(x,y)} \xi(r,c) \left( \frac{I(x,y)i}{\text{length}(i) + \varepsilon} \right)
\]  

(3.43)

\[
EM = \sum_{(x,y)} \xi(r,c) \left( \frac{I(x,y)e}{\text{length}(i) + \varepsilon} \right)
\]  

(3.44)

The energy minimization equation is framed to accomplish minimized energy to evolve the contour. The interior and exterior mean calculations drawn in Equation (3.43) (3.44) and curvature information from the image will support the force of attraction computations. In Equation 3.43 and 3.44 \(IM\) and \(EM\) are the interior and exterior means, \(i\) is interior points, and \(e\) is exterior points. \(i\) and \(e\) are computed from \(I_{\text{Mask}}\), which is a binary representation of distance metric \(I_{\text{dist}}\). It is calculated from the \(E_d\) of the binary image. \(I_{bw}\) represents the average difference between the intensity of each image pixel. The value of \(\varepsilon\) is 2.2204e-016 and \(I\) denotes the image.

\[
i = \{ I_{\text{Mask}} \leq 0 \}
\]  

(3.45)

\[
e = \{ I_{\text{Mask}} > 0 \}
\]  

(3.46)

\[
I_{bw} = \begin{cases} 1 & I_{x,y} > \text{Avg}(I_{x,y}) \\ 0 & \text{else} \end{cases}
\]  

(3.47)
\[ I_{\text{dist}} = E_d(I_{bw}(x,y)) \] (3.48)

\[ I_{\text{Mask}} = I_{\text{dist}} - I_{\text{dist}}(1 - I_{bw}(x,y)) + (I_{bw}(x,y) - 0.5) \] (3.49)

The values generated from Equation 3.45 to 3.49 estimate and update the interior and exterior forces of attraction for contour updation. Then the force of attraction and curvature value is subjected to compute the energy to be minimized. This force of attraction is necessary to hold the contour in an intact position. The force of attraction and curvature value is subjected to compute the energy to be minimized.

\[ AF = [(I_{(x,y)} - iM)]^2 - [(I_{(x,y)} - EM)]^2 \] (3.50)

where the index value ranges from \( \text{index} = \{1.2 \geq i_{\text{mask}} \leq -1.2\} \) with fixed threshold value.

In the level set algorithm, in place of using image gradient, curve evaluation is implemented with the help of internal and external energy supportive parameters. The level set equation for the proposed ELS-ACM is given in Equation 3.51.

\[
\frac{\partial \phi}{\partial t} = \left( \frac{\phi_x^2 + \phi_y^2}{(1 + (\phi_x^2 + \phi_y^2)^{\gamma})} \right) + \left( \frac{AF_{\text{argmax}(\text{absolute}(AF))} \ast \alpha \ast C}{\max(\text{ME})+\varepsilon} \ast \text{ME} \right)
\] (3.51)

where \( \alpha = 0.2 \) and \( C \) is the curvature level of the tumor slice in evolution. The curvature level \( C \) is computed by taking the edges of the curve and depends on external properties like gray level intensity and intrinsic curvature properties. Regularly, the positions of the curvature points are checked and
the value of curvature is computed from the Equation (3.53) for t limitation. This finally brings contour region, which fits the tumor slice.

The minimization energy and curvature are estimated as

\[
ME = \frac{AF}{\arg\max (\text{abs}(AF))} \times \alpha \times C
\]  

(3.52)

\[
C = \frac{\left(\frac{d^2 I}{d t^2}\right)}{\left(1 + \left(\frac{d I}{d t}\right)^2\right)^{\frac{3}{2}}}
\]  

(3.53)

In Equation (3.51), (3.52), and (3.53) \(AF\) denotes an attractive force, \(ME\) is the minimization energy and \(C\) is curvature. When the differentiation is equal to the divergence in the curvature, the minimized energy value is manipulated with the automatically generated mask to initialize the evolution of the contour. The contour evolution is formulated using the Equation 3.54.

\[
CE = M_{(x,y)} + D \times ME
\]  

(3.54)

\[
M_{x,y} = I_{bw}
\]  

(3.55)

where, \(CE\) = curve evolution, \(M\) = mask image, \(D\) = experimental constant whose value is 0.4. The binary mask is updated for every iterations of contour formations from CE. Mask image is obtained by acquiring the differentiation between repetitions of pixels (tumor pixels and tissue pixels) from the image. To view the three dimensional volumetric reconstruction of tumor slices from the 2D CT segmented lung, some of the basic steps are needed to be performed. The segmented tumor slices are viewed in 3D for volume estimation which is described in chapter 4.
Figure 3.5 shows the formation of contour using the proposed ELS-ACM method. The segmented contour region is shown in Figure 3.6. In the existing traditional active contour and level-set algorithms, separate functions were used to update the contour formation over image. The equations used in the traditional system provided an evolving curve on the boundary of the image. The complexity of the system was increased due to the presence of a large number of parameters. To reduce this complexity the proposed ELS-ACM method employs the weight updation equation by estimating the pixel variation in the input image.

The performance of the ELS-ACM is evaluated using Hausdorff distance. The segmentation time taken for all the three dataset are estimated and is compared with the existing Average Edge Vector Field Edge Following
algorithm (AEVFEF) and other traditional contour models. The results are discussed elaborately in chapter 5.

3.8 SUMMARY

In this research work, a model is developed to segment the lung tumor. The initial denoising process removes the noise by kernel based non-local neighbourhood algorithm with six kernels. Among the six kernels it is found that the turkey kernel produces higher PSNR value of 34.1 Hence the system proceeds with the turkey kernel for denoising the lung CT images. The feature extraction and classification processes are carried out to classify the lung image as tumor image or normal lung image. The accuracy of the classification process has been evaluated in terms of specificity, sensitivity, accuracy and found to be 98%, 99% and 99.7% respectively. The tumor from the images are segmented by the proposed ELS-ACM. It initiates the contour along with the acquired level set equations. It uses internal mean, external mean and attractive force to evolve the contour. The average segmentation time taken for segmenting the lung tumor is 48.24 seconds. The lower segmentation time and higher accuracy indicates the proposed ELS-ACM improves the lung tumor diagnosis system with less computation cost.

CHAPTER 4

3D RECONSTRUCTION

4.1 INTRODUCTION