CHAPTER 5

CAD SYSTEM FOR THE CLASSIFICATION OF PULMONARY TUBERCULOSIS

A CAD system is modelled for the detection and classification of pulmonary TB such as cavitary and miliary TB. The chest CT slices that have already been diagnosed by a radiologist are initially preprocessed, wherein the CT slices are converted into grayscale slices and denoised. The denoised slice is then segmented to extract the lung parenchyma. A region growing algorithm is used to extract the cavities from the segmented lungs. The size of the cavity decides if it is a TB or a non TB cavity. If a CT slice has a TB cavity then it is classified as cavitary TB. All slices without TB cavities are converted into texton images. The texton image is convoluted with the Gabor kernel and only the Gabor phase part is extracted from the convoluted output. The Gabor phase image is quantized and the LXP operator is applied to it, to obtain the LGXP encoded image. The LGXP histogram descriptor is computed for the LGXP encoded image. Statistical texture features are extracted from the LGXP histogram. These features are used to form the feature vector that is used to train the PNN classifier.

When a query slice belonging to any one of the four classes is applied to the CAD system, the processes of preprocessing, segmentation and cavity extraction are performed on all the slices. In case, TB cavities are detected then the query slice is classified as being affected by cavitary TB. If a slice is not affected by cavitary TB then it is converted into a texton image to which the gabor kernel is applied. The gabor phase image is separated,
quantized and the LXP descriptor is applied to obtain the LGXP encoded image. The histogram features that are extracted from the LGXP encoded image are used to form the feature vector. The feature vector is applied to the trained PNN classifier. The classification of miliary TB, normal slice and CT slices affected by other lung diseases is carried out by the classifier based on the training that it has received.

5.1 CAD SYSTEM FOR CLASSIFICATION OF PULMONARY TB

The block diagram of the CAD system for the detection and classification of cavitary and miliary TB from chest CT slices is shown in Figure 5.1. The processes involved in the CAD system are (1) preprocessing, (2) lung segmentation, (3) extraction of cavities, (4) classification of cavitary TB, (5) conversion to texton image, (6) formation of LGXP histogram, (7) feature extraction and (8) classification by PNN.

5.1.1 Preprocessing

Chest CT slices are applied to the CAD system for the diagnosis of two different types of Pulmonary TB. The training dataset consists of cavitary TB, miliary TB, normal and CTs affected by other lung diseases that have already been diagnosed by a radiologist. The CT slices in the training dataset have a dimension of 512 x 512 pixels and are in JPEG format. The size of a pixel is scaled to be 0.27 mm per pixel based on its resolution. The CT slice is transformed to grayscale following which denoising is carried out by applying the CT slice to a Gaussian filter.
Figure 5.1  Block diagram of the CAD system for classification of types of pulmonary TB
Input

Chest CT slice of size 512 x 512 pixels.

Process Logic

The process logic described in Section 4.1.1 is applied to the input chest CT slice.

Output

Denoised chest CT slice.

5.1.2 Lung Segmentation

The denoised lung CT slice is segmented, to extract the left and right lungs so that the pathological regions present in the lungs can easily be delineated (Hu et al 2001). The grayscale lung CT slice is composed of high intensity (white) pixels that are located in the body and low intensity (black) pixels that are present in the lungs and surrounding air. The regions with low density appear as dark regions in the CT while more dense regions appear white. So based on the contrast in intensities between the two types of regions, the lungs are segmented. The numerical value of each pixel can be expressed in HU (Depeursinge et al 2012a). The air that is present in the region surrounding the lung has an average intensity of -1000 HU. Lung tissues have an average intensity in the range of -910 HU to -500 HU. The ribs are denser comparatively and so their average intensity is taken to be greater than -500 HU (Hu et al 2001). The intensity difference between the body pixels and the non-body pixels is very large, so thresholding is a method that provides good separation between the two types of anatomical structures. The Hounsfield units can be converted into grayscale intensity values (Horwood et al 2001) using Equations (5.1) and (5.2).
- 1000 HU = 0 grayscale (Black) \hspace{1cm} (5.1)

+ 1000 HU = 255 grayscale (White) \hspace{1cm} (5.2)

The HU values between -1000 HU and +1000 HU are interpolated to the grayscale range of 0 to 255.

The grayscale slices are first thresholded using iterative thresholding (Ridler & Calvard 1978) to obtain a binary slice. Iterative thresholding is a thresholding technique used to divide the pixels into two classes with values 0 and 1. The pixels whose values are set to zero indicate the non-body pixels and those pixels set to one indicate body pixels.

The conversion of the grayscale slice into the binary slice is done to separate the lung tissue regions from the chest CT. The non-body pixels consist of the lung pixels as well as the background pixels that are connected to the borders of the slice. The background pixels consist of air and other tissues that surround the lungs. These background pixels are to be eliminated. The non-body pixels include the trachea (airways), ribs and intercostal muscles in addition to the lungs. The processes involved in segmentation are: (1) Iterative thresholding, (2) Removal of background pixels, (3) Removal of small connected components and (4) Extraction of left and right lungs.

The block diagram of the segmentation process is illustrated in Figure 5.2.
Figure 5.2 Processes in segmentation of lung parenchyma

5.1.2.1 Iterative thresholding

Iterative thresholding (Ridler & Calvard 1978) is a process in which a threshold $T$ is selected to separate the object from the background. The initial threshold $T$ is computed using Otsu’s method (Otsu 1979). The initial threshold value is selected in such a way that the intra-class variance is minimal. This selected threshold $T$, groups the pixels in the slice into two classes: one group of pixels $G_1$ with grayscale values below the threshold and another group of pixels $G_2$ with grayscale values greater than or equal to the threshold. Let the mean value of the pixels in $G_1$ be $\mu_a$ and the mean value of the pixels in $G_2$ be $\mu_b$. The mean value of $\mu_a$ and $\mu_b$ is computed as the new threshold value using Equation (5.3).
The next new threshold is calculated from the average values of the pixels in both the classes. The process of computing the new threshold continues iteratively until consecutive threshold values from 2 successive iterations converge.

Input

Denoised chest CT slice (Output of the Preprocessing process).

Process Logic

Step 1: Compute the initial threshold using Otsu’s technique (Otsu 1979). The threshold separates the pixels in the slice into two classes of pixels. The first class of pixels has intensity values that are greater than or equal to the threshold. The second class of pixels have intensity values lesser than the threshold.

Step 2: Compute the average intensity values, for both the classes of pixels and determine a new threshold by computing the mean of these two values.

Step 3: Using the newly computed threshold, repeat the Steps 1 and 2 until the thresholds obtained in successive iterations converge.

Step 4: Convert pixels whose intensity values are greater than or equal to the converged threshold value, to white. Convert pixels with intensity values lesser than the converged threshold to black.

Output

Binary chest CT slice.
5.1.2.2 Removal of background pixels

All the non-lung pixels, connected to the borders of the slice are referred to as background pixels. The background pixels that are black correspond to air, that is present in the body cavity and the body tissues surrounding the lungs. The background is not needed for further processing, so it is eliminated by clearing the pixels that touch the borders of the slice using morphological clearing operations (Tolouee et al 2011).

Input

Binary chest CT slice (Output of the iterative thresholding process).

Process Logic

Step 1: Complement the thresholded slice. This is the mask image that constrains the transformation.

Step 2: Create a marker image with the same dimensions as the mask image. The marker image is completely filled with zeros except along the image borders. At the borders, the marker image is equal to the mask image. The marker image is the starting point of the transformation.

Step 3: Clear all pixels at the border of the CT slice using the morphological clear border operation. This operation causes all the structures that are lighter than their surroundings and those that are connected to the border of the slice to be suppressed.

Output

Binary slice without the background pixels.
5.1.2.3 **Removal of small connected components**

All non lung components like the trachea and airways have to be separated from the lungs. The connected components with an area between 500 and 800 pixels are removed using morphological operations. The edges of the lungs are then detected using the Canny edge detector (Canny 1986).

**Input**

Binary slice without the background pixels (Output of the removal of background pixels process).

**Process Logic:**

**Step 1:** Compute the total number of connected components in the binary slice based on the 8-connectivity of neighboring pixels (Rosenfield & Kak 1982) and label them.

**Step 2:** Eliminate the trachea and any other small connected component by filling with zeroes the connected component, whose area lies between 500 and 800 pixels using a morphological open operation.

**Step 3:** Detect the edges of the lungs using the Canny edge detector (Canny 1986).

**Output**

Edge detected output slice.

5.1.2.4 **Extraction of lung regions**

The edge detected slice contains holes that are not connected to the border of the slice. So they are not eliminated when the border pixels are
cleared. Therefore the holes are filled using a morphological fill operation. If the pathological regions are at the periphery of the lungs, then the shape of the lung border gets changed. The lung borders are reconstructed using the convex hull morphological operations.

**Input**

Edge detected output slice (Output of removal of small connected components process).

**Process Logic**

**Step 1:** Set all the regions outside the lung to zero as the disease is not located outside the lung.

**Step 2:** Fill the holes that are present inside the lung regions.

**Step 3:** Apply the convex hull operator to the CT slice to reconstruct and obtain the complex shape of the lung border (Tolouee et al 2011).

**Step 4:** Replace each white pixel present in the region by its original grayscale value and leave all black pixels unchanged.

**Output**

Grayscale slice containing the right and left lungs.

**5.1.3 Extraction of Cavities**

The pathological regions in the slice are the ROIs. The presence of cavities in the lung regions is the hallmark of post primary TB. A cavity is defined as a parenchymal cyst that is nearly spherical in shape, with a diameter that is greater than 1 cm and lesser than 6 cm, containing either air
or fluid or both (Shen et al 2010, Xu & Cheng 2011 and Bagci et al 2012a). The radiologic patterns of cavities are usually annular rings with thick and irregular wall thickness. The cavities have a darkened area within the lung parenchyma and they may be surrounded by a consolidation which may be thick or thin.

In the experimental setup as each pixel has been scaled to 0.27 mm, the smallest cavity is estimated to have a diameter equal to or greater than 38 pixels and the diameter of the largest cavity is lesser than or equal to 222 pixels. The gray level intensity of the cavity region is found to lie approximately between 0 and 60. The region growing technique is used to extract the cavities. This technique groups pixels that are spatially close, as those pixels will have similar gray level intensity and texture values. The pixel having the minimum grayscale value in the segmented lung region is determined to be the seed pixel if its intensity level lies below 60 and all pixels that are the 8-neighbors of the seed pixel are first added to the region, if they satisfy the threshold conditions. A neighboring pixel can be added to a region if its intensity value lies within the range of 0 to 60. So pixels are constantly added to the region surrounding the seed pixel, if they lie within this range and if they are connected to the pixels in the region by 8-connectivity. The region keeps growing until no further pixels satisfy the intensity and connectivity conditions.

**Input**

Segmented grayscale slice containing the right and left lungs (Output of extraction of the left and right lungs process).
**Process Logic**

**Step 1:** Determine the pixel with minimum grayscale intensity in the segmented lung, as the seed pixel or seed point, as the cavity (filled with air) has a lower intensity compared to the lung tissues.

**Step 2:** Add pixels to this seed point if the absolute difference in intensity between the neighboring pixel and the seed pixel is lesser than or equal to the threshold. The threshold value is taken to be 60, as this is the maximum grayscale value of the cavity region. The pixel that is added to a region should be 8-connected to the neighboring pixel in the region.

**Step 3:** Check the absolute difference in grayscale intensity between the neighboring pixel and the seed pixel. If it is greater than the threshold, then that pixel is not added to the region.

**Step 4:** Repeat Steps 2 and 3 for all pixels in the slice until no further pixels can be added to the region. At this point the region growing stops.

**Step 5:** Eliminate all regions other than the ROIs (which are the cavity regions formed by region growing), using morphological erosion and dilation operations.

**Output**

Extracted cavities (ROIs).

**5.1.4 Classification of the Extracted ROI**

The ROIs obtained are the cavities that have been extracted as a result of applying region growing technique. Next the cavities are analyzed
based on the condition that the diameter of a TB cavity lies between 38 and 222 pixels. If a cavity satisfies this condition, it is classified as a TB cavity.

**Input**

Extracted cavities (Output of the Extraction of ROI process).

**Process Logic**

**Step 1:** Label all cavities that are extracted.

**Step 2:** Compute the area of all the labeled regions. This gives the number of pixels within each cavity.

**Step 3:** Compute the diameter of each cavity using Equation (5.4).

\[
Diameter = 2\sqrt{\frac{Area}{\pi}}
\]

**Step 4:** If the diameter of the ROI is within the range 38 pixels (small cavity) to 222 pixels (large cavity) then the ROI is treated as a TB cavity, otherwise it is a non-TB cavity.

**Step 5:** If the ROI is a TB cavity then the CT slice is classified as affected with cavitary TB. Otherwise the slice is further processed.

**Output**

Classification of the CT slice as affected with cavitary TB.

5.1.5 **Detection of Miliary TB**

All CT slices that have not been diagnosed with cavitary TB are processed next to determine if they are miliary TB, normal or CT slices with
other diseases since CT slices that have not been diagnosed with cavitary TB belong to the other three classes. Miliary TB occurs in 2–6% of primary TB and also occurs with more frequency in reactivation TB (Jeong & Lee 2008). The characteristic radiographic and HRCT findings of miliary TB consist of innumerable, 1 to 3-mm diameter nodules that look like millet seeds and are randomly distributed in both the lungs. A texton-based LGXP technique is used to extract the features from CT slices belonging to the three classes (miliary TB, normal and other diseases).

5.1.5.1 Conversion of segmented lung to a texton image

All CT slices from which the cavities were not extracted could either be miliary TB, normal lung or CT slices affected by other diseases. These slices are now transformed into texton images to retain the spatial relationships between the pixels (Liu & Yang 2008; Julesz 1981; Leung & Malik 2001). The dimensions of an image can be reduced if the image can be decomposed and represented using textons. Hence in this feature extraction scheme, textons are used to reduce the dimensions of the CT slice. Five textons $T_1$, $T_2$, $T_3$, $T_4$ and $T_5$ are identified in the segmented lung slice (Liu & Yang 2008). All the pixels in the segmented lung slice corresponding to $T_1$ are arranged to form the texton component $TC_1$. Similarly the remaining four texton components are identified. Then all the texton components are combined to form a single texton image $I(x,y)$. Pixels that are not identified as textons are replaced by zeros in the texton image. The algorithm used to convert the segmented lung CT slice to a texton image is explained below.

Input

All grayscale slices containing the segmented lung regions that have not been classified as cavitary TB (Output of the classification of the extracted ROI process).
Process Logic

Step 1: Create five 2 x 2 texton masks to identify five types of textons in the segmented lung slice. They are

\[ M_1 = \begin{bmatrix} 1 & 0 \\ 1 & 1 \end{bmatrix}; M_2 = \begin{bmatrix} 0 & 1 \\ 1 & 1 \end{bmatrix}; M_3 = \begin{bmatrix} 1 & 1 \\ 0 & 1 \end{bmatrix}; M_4 = \begin{bmatrix} 1 & 1 \\ 1 & 0 \end{bmatrix} \text{ and } M_5 = \begin{bmatrix} 1 & 1 \\ 1 & 1 \end{bmatrix} \]

Step 2: Shift the mask \( M_1 \) through the input grayscale slice, starting from the top left and proceed to the right.

Step 3: Repeat the above process until the entire slice is covered by the mask from the top to the bottom of the slice. The mask \( M_1 \) detects the locations of all the \( T_1 \) textons in the slice. The texton pixels that are identified correspond to the texton component \( TC_1 \) and should have identical grayscale values and should also occur in the same position as the mask \( M_1 \).

Step 4: Repeat Steps 2 and 3 with the texton masks \( M_2, M_3, M_4 \) and \( M_5 \) to detect the locations of the textons \( T_2, T_3, T_4 \) and \( T_5 \) in the slice and to form the texton components \( TC_2, TC_3, TC_4 \) and \( TC_5 \).

Step 5: Combine all the five texton components that are formed in Step 3 and 4 to form the final texton image. The texton image has the same dimensions as the original grayscale slice.

Step 6: At any pixel position, check if any one of the five texton components has non-zero values. Then the pixels at those positions in the texton image will also have the same non-zero value.

Step 7: Replace all other pixels in the texton image with zeroes.

Output

Texton image.
5.1.5.2 Local gabor XOR pattern descriptor

The texton image $I(x, y)$ that is formed is convoluted with the Gabor kernel. The Gabor kernel (Xie et al 2010) given by $\Psi_{\mu, v}(x, y)$ and having spatial coordinates $(x, y)$, standard deviation $\sigma$, orientation $\mu$ and scale $v$ is given by Equation (5.5).

$$\Psi_{\mu, v}(x, y) = \frac{\|k_{\mu, v}\|^2}{\sigma^2} e^{-\frac{\|k_{\mu, v}\|^2 I(x, y)}{2\sigma^2}} e^{i\frac{\|k_{\mu, v}\|^2 I(x, y)}{\sigma^2}}$$

(5.5)

where $k_{\mu, v}$ is the wave vector, $\Psi_{\mu, v}(\cdot)$ denotes the Gabor kernel and $\|\cdot\|$ denotes the norm operator.

The pixels of the texton image $I(x, y)$ are convoluted with the Gabor kernel given by Equation (5.5) and the resultant image (Xie et al 2010) $G_{\mu, v}(x, y)$ is computed using Equation (5.6).

$$G_{\mu, v}(x, y) = I(x, y) * \Psi_{\mu, v}(x, y)$$

(5.6)

where $*$ is the convolution operator.

When the Gabor kernel is convoluted with the texton image $I(x,y)$, a complex number is formed. This complex number has a real part $\text{Re}_{\mu, v}(x,y)$ and an imaginary part $\text{Im}_{\mu, v}(x,y)$. The phase part $\Phi_{\mu, v}(x,y)$ at each pixel can be computed from this complex number, using Equation (5.7) (Xie et al 2010).

$$\Phi_{\mu, v}(x, y) = \arctan\left(\frac{\text{Im}_{\mu, v}(x, y)}{\text{Re}_{\mu, v}(x, y)}\right)$$

(5.7)
The Gabor phase part is considered as it has better discriminative properties compared to the Gabor magnitude part. It is also called the Gabor phase pattern map and has values between $0^\circ$ and $360^\circ$. The Gabor phase pattern map is divided into $m$ number of $3 \times 3$ non-overlapping sub-blocks. The quantizer block compares the phase of each of the 8 neighbors in the $3 \times 3$ sub-block with the phase of the center pixel $(x, y)_c$ and quantizes the phase values into four ranges based on the four quadrants. So the $0^\circ$ to $360^\circ$ range of phase values, are grouped into four phase ranges and these are quantized as 0, 1, 2 and 3 respectively based on Equations (5.8) and (5.9) (Xie et al 2010).

\[
\frac{360 \cdot i}{b} \leq \Phi_{j,i}(\bullet) < \frac{360 \cdot (i+1)}{b}, i = 0,1,...,b-1
\]  \hfill (5.8)

\[
q(\Phi_{j,i}(\bullet)) = i
\]  \hfill (5.9)

where $b$ is the number of phase ranges considered (here $b=4$) and $\Phi_{j,i}(\bullet)$ denotes the phase, ‘$i$’ is the $i^{th}$ phase range and $q(\bullet)$ is the quantization operator. For example, when $i = 0$, then the phase range is $0 \leq \Phi_{j,i}(\bullet) < 90^\circ$. Thus all phase values in the range from $0^\circ$ to less than $90^\circ$ are quantized as ‘0’.

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(a) 3 x 3 phase pattern
(b) grid after quantizing the phase into 4 intervals
(c) grid after XORing each of the 8-neighbors in (b) with the center pixel

**Figure 5.3 Illustration of the LGXP technique**
Figure 5.3 illustrates the LGXP technique for a sample 3 x 3 sub-block of the image $G_{ij; \lambda} (x, y)$, after convoluting the texton image with the Gabor kernel to which the LXP operator is applied. Figure 5.3 (a) is the 3 x 3 Gabor phase pattern sub-block that is considered. Figure 5.3 (b) shows how the phases are quantized into the four ranges based on Equations (5.8) and (5.9). The quantized grid has labels 0, 1, 2 and 3. The LXP operator is then applied to the quantized grid. The 8-neighboring pixels $(x, y)_i$ (unshaded pixels) from Figure 5.3 (b) are then XORed with the center pixel $(x, y)_c$ (shaded pixel) (Xie et al 2010) as shown in Figure 5.3 (c). This computation is performed using the Equation (5.10).

$$c \otimes d = \begin{cases} 0, & \text{if } c = d \\ 1, & \text{otherwise} \end{cases}$$ \hspace{1cm} (5.10)

where $\otimes$ is the LXP operator. Equation (5.10) is modified to compute the phase code of the quantized image. Then the XOR pattern calculated between $(x,y)_c$ and its neighbors $(x,y)_i$ is calculated using Equation (5.11).

$$LGXP_{ij; \lambda}^{p} = q(\Phi_{ij; \lambda}(x, y)_c) \otimes q(\Phi_{ij; \lambda}((x, y)_i)), i = 1, 2, 3, ..., P$$ \hspace{1cm} (5.11)

where $q(\bullet)$ is the quantization operator used to obtain the code of the quantized image, $\Phi_{ij; \lambda}(\bullet)$ is the phase, $(x,y)_c$ is the center pixel, $\otimes$ is the LXP operator, $(x,y)_i$ is the neighboring pixel, $i$ is the position of the neighboring pixel and $P$ is the size of the neighborhood (here $P=8$) which depends on the size of the sub-image. The computed values are next concatenated to obtain the binary value of the center pixel (Xie et al 2010) (shaded block in Figure 5.4(c)) using Equation (5.12).

$$LGXP_{ij; \lambda}((x, y)_c) = [LGXP_{ij; \lambda}^{p_1}, LGXP_{ij; \lambda}^{p_2}, ..., LGXP_{ij; \lambda}^{p_8}]_{\text{binary}}$$ \hspace{1cm} (5.12)
where \((x,y)_c\) is the center pixel and \(P\) is the size of the neighborhood. The decimal value of each center pixel is computed using Equation (5.13).

\[
LGXP_{\mu,v}((x,y)_c) = \left\lfloor \sum_{i=1}^{P} 2^{i-1} LGXP_{\mu,v}^i \right\rfloor_{\text{decimal}}
\] (5.13)

The histogram of each individual 3 x 3 sub-block is next computed. Then the histograms of all the individual \(m\) sub-blocks are concatenated to form the LGXP descriptor (Xie et al 2010) of the lung CT slice using Equation (5.14).

\[
H = [H_{\mu,1,v,1}^1, \ldots, H_{\mu,1,v,1}^m; \ldots; H_{\mu,1,1,v,s}^1, \ldots, H_{\mu,1,1,v,s}^m]
\] (5.14)

where, \(H_{\mu,v,i}(i=1, \ldots, m)\) refers to the histogram of the \(i^{th}\) sub-block of the LGXP map with scale \(\mu\) and orientation \(v\) (\(v\) is the orientation with \(s\) levels).

**Algorithm to extract the LGXP Histogram Descriptor**

**Input**

Texton image (Output of the conversion of segmented lung to a texton image process).

**Process Logic**

**Step 1:** Convolute the texton image with the Gabor kernel of Equation (5.5) to obtain the Gabor image \(G_{\mu,v}(x,y)\) as in Equation (5.6).

**Step 2:** Compute the Gabor phase image \(\Phi_{\mu,v}(x,y)\) from the Gabor image \(G_{\mu,v}(x,y)\), using Equation (5.7). The Gabor phase image has values from \(0^\circ\) to \(360^\circ\).
Step 3: Divide the Gabor phase image into 3 x 3 non-overlapping sub-blocks.

Step 4: Quantize each element in the sub-block to a new value depending on which quadrant it belongs to, using Equations (5.8) and (5.9). The total phase range (0° to 360°) is divided into 4 phase ranges based on the four quadrants.

Step 5: Quantize all phase values that lie in the first quadrant (0° to < 90°) as ‘0’, all phase values that lie in the second quadrant (90° to < 180°) as ‘1’, those that lie in the third quadrant (180° to < 270°) as ‘2’ and finally all phase values that lie in the fourth quadrant (270° to < 360°) as ‘3’.

Step 6: XOR the center pixel in each 3 x 3 quantized sub-block with each of its 8-neighbors using Equation (5.11).

Step 7: If the quantized phase value of the neighboring pixel is identical with that of the center pixel, then the value of the neighboring pixel is changed to ‘0’. If the quantized phase value of the neighboring pixel and the center pixel value is not identical then its value is changed to ‘1’.

Step 8: Encode the center pixel, by concatenating the values of the neighboring pixels to obtain an eight bit binary value using Equation (5.12).

Step 9: Convert the value of the center pixel obtained in Step 8 into its equivalent decimal value using Equation (5.13).

Step 10: Repeat Steps 4 to 9 for all the remaining sub-blocks. All the pixel values in each of the sub-blocks now consist of the decimal encoded LGXP values.
Step 11: Compute the histograms of each of the non-overlapping sub-blocks.

Step 12: Concatenate the histograms of all the sub-blocks to form the LGXP histogram descriptor using Equation (5.14).

Output

LGXP histogram descriptor of the texton image.

5.1.5.3 Histogram feature extraction

The LGXP histogram is computed for all the CT slices that have not been classified as cavitary TB. The statistical texture features (Gonzalez & Woods 2002) like mean, variance, skewness, kurtosis and energy are computed, based on the intensity values, from the LGXP histogram. These statistical features are computed using Equations (5.15) to (5.19).

Input

LGXP histogram of the texton image (Output of the LGXP histogram extraction algorithm).

Process

Step 1: Compute the mean (m) which is used to measure the average intensity level of the histogram descriptor.

\[ m = \sum_{i=0}^{L-1} r_i p(r_i) \]  

(5.15)

where \( r \) is a discrete random variable representing the discrete gray-levels in the range 0 to \( L-1 \), \( L \) is the number of gray levels and \( i=0,1,2,\ldots, L-1 \) and \( p(r_i) \) is the histogram.
Step 2: Compute the second order moment called the variance. It is a measure of the contrast in the gray levels in the neighborhood of a pixel.

\[ \mu_2(r) = \sum_{i=0}^{L-1} (r_i - m)^2 p(r_i) \]  
(5.16)

where \( \mu_2(r) \) is the second order moment.

Step 3: Compute the third order moment called the skewness, which is a measure of the skewness of the intensity values of the histogram.

\[ \mu_3(r) = \sum_{i=0}^{L-1} (r_i - m)^3 p(r_i) \]  
(5.17)

where \( \mu_3(r) \) is the third order moment.

Step 4: Compute the fourth order moment called the kurtosis which is a measure of the relative flatness of the histogram.

\[ \mu_4(r) = \sum_{i=0}^{L-1} (r_i - m)^4 p(r_i) \]  
(5.18)

where \( \mu_4(r) \) is the fourth order moment.

Step 5: Compute the energy which is the angular second moment which measures the uniformity of the intensity level distribution of the histogram.

\[ \text{energy} = \sum_{r_i} p^2(r_i) \]  
(5.19)
Output

Statistical features of the LGXP histogram.

The histogram statistical features that are computed, are normalized to have values in the range between 0 and 1 (Depeursinge et al 2012b) and the normalized features are concatenated to form a five dimensional feature vector which is applied to the classifier.

5.1.5.4 Probabilistic neural network classifier

A PNN is used as the classifier (Haykin 1998) to classify the CT slices into three classes namely miliary TB, normal and other diseases. PNN calculates the error during the forward propagation to the output and propagates the error back to the input. The weights are adjusted so that the error is minimized to the maximum extent possible. The PNN is implemented as a three layer network. The normalized histogram statistical feature vectors are applied to the input layer consisting of five input nodes, which correspond to the five histogram features computed in Section 5.1.5.3. The feature vectors are given to train the PNN. There are three output nodes corresponding to the three output classes into which the dataset has to be classified.

The PNN is implemented using an input matrix and a target matrix. The input matrix is of the order M x N, where M equals 5 rows representing the feature vectors and N equals the number of segmented lung slices that do not have cavitary TB. The output layer consists of 3 output nodes corresponding to three output classes representing miliary TB, normal lung and all other diseases which are set as the target. The weights are assigned automatically and are continuously updated during the training process to achieve the target outputs that are set by the target matrix. P x Q is the target
matrix where P refers to the three output classes and Q corresponds to the number of segmented lung slices that have to be classified. In the columns of the target matrix representing miliary slices, the first element in the column is represented by a one and the other two elements in the column are filled with zeros. The columns in the target matrix representing normal CT slices are filled with a one in the second element and the remaining elements are filled with zeros. Finally the class, other chest diseases, is represented by a one in the third element and the remaining elements in the column being filled with zeros. Nearly 70% of the slices in the database are used as training samples during training, while the remaining slices are used for testing.

During the training process of the classifier, the weights of each layer are varied iteratively for each training slice so that the PNN learns the features of the training set of slices corresponding to a particular class and can thus minimize the errors while classifying the test slices. Hence, larger the number of training samples, smaller the error. During the testing process, when the feature vectors of the test slices are applied to the trained PNN, based on its training, classification into the three classes is done.

5.2 RESULTS AND DISCUSSION

The proposed scheme is tested using 906 CT slices taken from 150 CT scans of patients as shown in Table 5.1. This dataset consists of cavitary TB, miliary TB, normal lung CT scans and other chest CT slices Out of the dataset of 906 CT slices, nearly 70 percent of the chest CT slices are used as the training dataset while the remaining CT slices are used for testing. The 2D CT slices are obtained in JPEG format of size 512 x 512. The CAD system has been implemented using MATLAB 2011(a) software.
Table 5.1 Dataset used for testing the CAD system

<table>
<thead>
<tr>
<th>Class Type</th>
<th>Scans</th>
<th>Slices</th>
</tr>
</thead>
<tbody>
<tr>
<td>Normal</td>
<td>75</td>
<td>300</td>
</tr>
<tr>
<td>Other Slices</td>
<td>30</td>
<td>209</td>
</tr>
<tr>
<td>Cavitary TB Slices</td>
<td>40</td>
<td>247</td>
</tr>
<tr>
<td>Miliary TB Slices</td>
<td>20</td>
<td>150</td>
</tr>
<tr>
<td>Total Slices</td>
<td>150</td>
<td>906</td>
</tr>
</tbody>
</table>

The different processes involved in the segmentation of the lung parenchyma are illustrated in Figures 5.4 to 5.11. The input 2D CT slices of cavitary TB, miliary TB and normal lung are illustrated in Figure 5.4.

(a) Cavitary TB slice  (b) Miliary TB slice  (c) Normal Lung slice

Figure 5.4 Input CT slices

The CT slices are denoised and converted to grayscale. The histogram of the gray scale slices is first computed. The histogram is bimodal of which the first peak corresponds to the low intensity pixels in the lung and the second peak corresponds to the high intensity body pixels as illustrated in Figure 5.5. From the histogram it is inferred that the lung and its background can be easily separated by using a thresholding technique.
The selected threshold should lie in the valley between the two peaks of the histogram. The initial threshold is fixed by Otsu’s thresholding.
process, which is followed by iterative thresholding. Iterative thresholding results in a binary slice as shown in Figure 5.6.

(a) Thresholded slice of Cavitary TB
(b) Thresholded slice of Miliary TB
(c) Thresholded slice of Normal lung

Figure 5.6 Thresholded CT slices
The thresholded CT slice is complemented and the background pixels are then removed. This is followed by the removal of small connected components like the airways by morphological open operations as illustrated in Figures 5.7 and 5.8.

(a) Cavitary TB slice with background pixels removed

(b) Miliary TB slice with background pixels removed

(c) Normal slice with background pixels removed

Figure 5.7 Background removal
Figure 5.8 Removal of airways

Holes that are present in the lung regions which are not connected to the borders of the CT slice are filled using morphological fill operation as shown in Figure 5.9.
Figure 5.9 Filling of holes

The holes filled left and right lungs in Figure 5.9 are replaced by the original grayscale slice pixels as illustrated in Figure 5.10.
Figure 5.10 Segmented lungs

The cavity regions are extracted from the segmented lung, using the region growing technique. As the miliary TB and normal lung CT slices do not contain cavities, they do not yield any results when region growing algorithm is applied. Region growing technique extracts the cavity from
Figure 5.10 (a). The extracted cavity is shown in Figure 5.11. The extracted cavity is tested to determine if it is a TB or a non TB cavity based on which the CT slice is classified as affected with Cavitary TB.

![Extracted cavity region](image)

**Figure 5.11 Extracted cavity region**

All the CT slices that did not yield cavities are converted into texton images. The texton image is convoluted with the Gabor kernel from which the Gabor phase component is separated. The Gabor phase image is divided into $3 \times 3$ sub-blocks. The phase values of the pixels in the sub-blocks are next quantized into four values based on the four quadrants in which each phase component occurs. The center pixel in each of the $3 \times 3$ quantized sub-blocks is then XORed with its 8-neighbors. The center pixel value is then encoded by concatenating the values of the neighboring XORed pixels to obtain an eight bit binary value. The eight bit binary value of the center pixel is then converted into its equivalent decimal value. All the pixel values in each of the sub-blocks now consist of the decimal encoded LGXP values. The histograms of each of the non-overlapping sub-blocks are computed. Finally the histograms of all the sub-blocks are concatenated to form the LGXP descriptor as illustrated in Figures 5.12 and 5.13.
Figure 5.12 LGXP histogram of a normal lung CT slice

Figure 5.13 LGXP histogram of a miliary TB CT slice

The TP, TN, FP and FN values are tabulated in Tables 5.1 and 5.2 which are the confusion matrices for cavitary and miliary TB during the testing process. In Table 5.2 the confusion matrix is computed between cavitary TB CT slices and all the other CT slices (miliary TB, normal and other disease CT slices) in the CT slice dataset. The performance measures for cavitary TB are compared with another technique in which the cavities have been extracted using active contours.
Table 5.2 Confusion matrix of cavitary TB CT slices

<table>
<thead>
<tr>
<th>Actual</th>
<th>Classified</th>
<th>Cavitary TB (247 slices)</th>
<th>Others (659 slices)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cavitary TB</td>
<td>229 (TP)</td>
<td>18 (FN)</td>
<td></td>
</tr>
<tr>
<td>Others</td>
<td>15 (FP)</td>
<td>644 (TN)</td>
<td></td>
</tr>
</tbody>
</table>

Table 5.3 Confusion matrix of miliary TB CT slices

<table>
<thead>
<tr>
<th>Actual</th>
<th>Classified</th>
<th>Miliary TB (45 slices)</th>
<th>Others (147 slices)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Miliary TB</td>
<td>39 (TP)</td>
<td>6 (FN)</td>
<td></td>
</tr>
<tr>
<td>Others</td>
<td>7 (FP)</td>
<td>140 (TN)</td>
<td></td>
</tr>
</tbody>
</table>

In Table 5.3 the confusion matrix is computed between miliary TB CT slices and all the other CT slices (cavitary TB, normal and other disease CT slices). The lung CT slices are segmented and the LGXP operator is directly applied to the segmented lung. The confusion matrix of miliary TB when only the LGXP technique is used is shown in Table 5.4. The performance results when the texton based LGXP operator is applied and when only LGXP is applied is computed in Table 5.5. The performance metrics are computed using Equations 3.1 to 3.10 from Chapter 3. The results demonstrate the effectiveness of the texton based LGXP feature extraction system over the LGXP based feature extraction system.
Table 5.4 Confusion matrix of miliary TB CT slices using LGXP technique

<table>
<thead>
<tr>
<th>Actual</th>
<th>Classified</th>
<th>Miliary TB (45 slices)</th>
<th>Others (147 slices)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Miliary TB</td>
<td>35 (TP)</td>
<td>10 (FN)</td>
<td></td>
</tr>
<tr>
<td>Others</td>
<td>12 (FP)</td>
<td>135 (TN)</td>
<td></td>
</tr>
</tbody>
</table>

The performance of the proposed texton based LGXP feature extraction technique is compared with the feature extraction system that uses only the LGXP technique in Table 5.5. Also the results for Cavitary TB using region growing algorithm are compared with Active Contour method.

Table 5.5 Comparison of the performance metrics of the texton based LGXP technique and the LGXP technique

<table>
<thead>
<tr>
<th>Performance Measures</th>
<th>Results for Cavitary TB with Active Contour</th>
<th>Results for Cavitary TB with Proposed Technique</th>
<th>Results for Miliary TB using LGXP</th>
<th>Results for Miliary TB using Proposed Technique</th>
</tr>
</thead>
<tbody>
<tr>
<td>Accuracy</td>
<td>91.50</td>
<td>96.36</td>
<td>88.54</td>
<td>93.23</td>
</tr>
<tr>
<td>Specificity</td>
<td>94.39</td>
<td>97.72</td>
<td>91.84</td>
<td>95.24</td>
</tr>
<tr>
<td>Precision</td>
<td>84.84</td>
<td>93.85</td>
<td>74.47</td>
<td>84.78</td>
</tr>
<tr>
<td>Sensitivity</td>
<td>83.81</td>
<td>92.71</td>
<td>77.78</td>
<td>86.67</td>
</tr>
<tr>
<td>FPR</td>
<td>5.61</td>
<td>2.28</td>
<td>8.16</td>
<td>4.76</td>
</tr>
<tr>
<td>FNR</td>
<td>16.19</td>
<td>7.29</td>
<td>22.22</td>
<td>13.33</td>
</tr>
<tr>
<td>NPV</td>
<td>93.96</td>
<td>97.28</td>
<td>93.10</td>
<td>95.89</td>
</tr>
<tr>
<td>FDR</td>
<td>15.16</td>
<td>6.15</td>
<td>25.53</td>
<td>15.22</td>
</tr>
<tr>
<td>PLR</td>
<td>15.11</td>
<td>40.73</td>
<td>9.53</td>
<td>18.20</td>
</tr>
<tr>
<td>NLR</td>
<td>0.17</td>
<td>0.07</td>
<td>0.24</td>
<td>0.14</td>
</tr>
</tbody>
</table>
It is observed from Table 5.5 that the PLR for Cavitary TB is 40.7317, and for Miliary TB is 18.2 which indicates that the CAD system has an improved possibility of identifying the disease i.e. it improves the TPs. Similarly the NLR for Cavitary TB is 0.074572 and the NLR for Miliary TB is 0.14. As the NLR value decreases below 0.01 the significant contribution of the CAD system will be to lower the probability of misclassifying a diseased slice as a normal slice i.e. it reduces the FN.

5.2.1 Performance Comparison between Texton based LGXP Technique and only LGXP Technique

The performance of the system is compared based on the performance metrics computed in Table 5.5. For an ideal CAD system, the sensitivity, specificity, precision, accuracy, NPV and PLR value should be close to 100% while the FPR, FNR, FDR, MR and NLR should be close to 0%. Figure 5.14 (a) and (b) illustrate the comparison in the performance of the cavitary TB detection using GICOV and region growing algorithms. Figure 5.15 (a) and (b) illustrate the comparison in the performance of the texton based LGXP CAD system and the CAD system with only LGXP.

In Figure 5.14 it is observed that the CAD system for the classification of cavitary TB using region growing performs better than the system that uses the active contour technique. This is because some of the contours are not properly placed when ACM is used leading to those cavities not getting detected. In Figure 5.15 texton based LGXP technique has good performance characteristics in comparison with the CAD system that uses only the LGXP technique. This is because textons not only help in dimension reduction, but they are also rotation and translation invariant. They take every pixel in the image into account and hence give better results. For the performance metrics illustrated in Figure 5.14 (a) and 5.15 (a) such as specificity, sensitivity, accuracy, precision, NPV and PLR, the proposed
system has higher values while as illustrated in Figure 5.14 (b) and 5.15 (b) the proposed system has reduced FPR, FNR, FDR and NLR.

Figure 5.14 (a) and (b) Comparison of classifier performance of cavitary TB CT slices with active contour and region growing algorithms
Figure 5.15  (a) and (b) Comparison of classifier performance of miliary TB CT slices with texton based LGXP and with only LGXP.
5.2.2 Receiver Operating Characteristics Curve

The ROC curve (Fawcett 2006) is a plot of the TPR against the FPR for the different threshold values of the diagnostic test. The ROC curve indicates that the test is more accurate if it follows the Y axis and the top border of the ROC space. The area under the curve (AUC) for both cavitary and miliary TB is very close to 1 as indicated in Figures 5.16 and 5.17.

Figure 5.16 ROC curves for cavitary TB
5.3 CONCLUSION

A CAD system for the classification of cavitary and miliary TB is modeled with a new feature extraction scheme. The CAD system achieved an average accuracy of 94.79%. The CAD system has been implemented to aid the radiologists in the diagnosis of pulmonary TB from lung CT slices. Compared to radiographs, chest CT has an improved accuracy as many of the cavities that go undetected in radiographs (Husen et al 1971) can easily be detected and diagnosed using CT especially when the cases are complicated by fibrosis. In the existing works cavity detection in TB has been carried out using CXRs, whereas in this work the results have improved as CT has been used. The results have improved when a texton based LGXP technique was used for feature extraction compared to when only the LGXP technique was used. The false positives have also reduced by more than 3% in this work compared to the scheme that uses only the LGXP technique.