CHAPTER 3
SYSTEM OUTLINE

3.1. Proposed System

The Computer Aided Diagnosis presented in this work has Liver and Tumor extraction module, Feature Extraction Module and Classifier Module. It does the following functions:

(1) Classifies diffused liver diseases as fatty and cirrhosis liver from CT abdominal images after automatically extracting the liver region from CT abdominal images,

(2) Classifies focal liver diseases as benign and malignant tumor from CT abdominal images after extracting the liver and the tumor region from CT abdominal images,

(3) Classifies focal liver diseases as hepato cellular carcinoma, cholangio carcinoma, hepato cellular adenoma and hemangioma from CT abdominal images after extracting the liver and the tumor region from CT abdominal images and

(4) Classifies ultrasonic liver images into normal liver, fatty liver and cirrhosis liver after selecting the ROI from ultrasonic liver images.

3.2. Methodology

The data used in this work were collected from various hospitals. The areas of interest of the CT abdominal images were captured by SOMATOM Emotion Duo CT Scanner. Plain spiral CT scanning of liver was scanned from the right dome of diaphragm to just below the inferior border of the liver using 8 mm slices at 8 mm interval with 0 mm inter slice gap. 70 mAs technique was used with 110 KVP, field of Vision (foV) of 280 and image matrix of 256 x 256. 100 to 120 cc omnipaque 350 was injected intravenously at the rate of 3 cc per second and post contrast spiral CT scanning was done with 8 mm slices at 8 mm interval and
0 mm inter slice gap. 70 mAs technique was used with 110 KVP, field of Vision (foV) of 280, image matrix of 256 x 256, scan delay of 30 seconds and 20 seconds spiral scanning with a pitch of 1. The ultrasound images were captured by SIEMEN ACUSON ASPEN ultrasound system using convex electronic array multi frequency high density transducers operating from 1.5 MHz to 4 MHz. However, the images were acquired using transducer operating at 3 MHz and 4 MHz. The images are tissue harmonic images.

3.2.1. Liver Extraction from CT abdominal Image

From CT abdominal images, the liver region is extracted by using the anatomic knowledge of the liver, adaptive threshold decision based on histogram analyzer and morphological operations.

CT abdominal image contains the images of the liver and other organs like spleen and stomach. Normally, the liver region is located in the upper left side of the abdomen and takes up the largest area among the various organs included in the image and the liver image maintains a constant intensity throughout. But a fixed threshold is not possible to extract liver region because, the intensity differs according to the patient, slice and the CT machine. Therefore adaptive threshold is chosen for each slice based on histogram analysis of each value.

For the CT abdominal image, a window is fixed by removing the last 30 rows and 50 columns from the right since this area usually does not contain liver region. Then, histogram is drawn and analyzed. The intensities representing background (dark) and bone values (brightest) are removed by making pixel counts to zero. Normally, liver lies in between 100 and 225 intensities range. Since liver area is large compared to other adjacent organs and has constant intensity throughout, the highest pitch corresponds to the liver area. Hence an
intensity range with highest count pixels plus certain margin to accommodate any variance in the liver region pixels is adaptively obtained for each slice. This range represents the liver region pixels.

The pixels in the adaptive threshold range of intensity are extracted. The output looks like scattered sand. It is converted to an object with real area using morphological closing and opening [100]. The liver is extracted along with the fragments of other organs located near to it and with intensity same as that of liver. Since these fragments can affect accurate diagnosis, they can be removed based on area. The area of the liver is large when compared with the fragments of other organs. After removing the fragments, the image obtained is complemented and multiplied with the original image to get the segmented liver in the CT abdominal image.

3.2.2. Tumor Extraction from Liver Images

FCM clustering technique [101, 102] is used to segment the tumor region from the liver region. The pixels in the segmented liver are divided into three clusters. The first cluster includes background pixels, the second cluster includes tumor region pixels and the third cluster includes liver pixels. The tumor region is outputted for further analysis after morphological closing and opening.

3.2.3. ROI Selection from Ultrasonic Liver Images

The square shaped region of interest (ROI) is selected from the liver images. The area is chosen with the help of a radiologist so that the area contains only liver parenchyma.
3.2.4. Biorthogonal Wavelet Based Statistical Texture Feature Extraction

Images contain a large amount of data, but much of which is redundant. From the lowest level of pixel representations, one can gather useful information through a process called feature extraction.

In this work, biorthogonal wavelet based statistical texture features are extracted from the ROI of the CT abdominal images and Ultrasonic liver images. The selection of biorthogonal wavelet was made because of smoothness and their robustness under slight shifts of image components. Texture classification experiments have been performed by Aleksandra Mojsilovic et al. [103] using Haar filters, Daubechies filters and eight different biorthogonal filter pairs. They reported that biorthogonal filters are more suitable for texture analysis.

The original image I is represented by a set of sub images at several scales after biorthogonal wavelet transform: \( \{ L_d, D_{ni} \}_{i=1,2,3, n=1...d} \) is a multiscale representation of depth d and scale n of the image I. Since each wavelet coefficient \( D_{ni}(bi,bj) \in R \) and the co occurrence matrix or SGLDM is defined for an image with a countable number of gray levels, the co occurrence matrix \( C_{ni}^{d_\theta} \) can be defined for each detail image. The element \((j, k)\) of the co occurrence matrix \( C_{ni}^{d_\theta} \) is defined as the joint probability that a wavelet coefficient \( D_{ni} = j \) co occurs with a coefficient \( D_{ni} = k \) on a distance \( d \) in direction \( \theta \). Usually small \( d \)-values for \( d \) are used since most relevant correlation between pixels exists on small distance. Hence, from these three detail images three SGLDM or co occurrence matrixes \( C_{11}^{d\theta}, C_{12}^{d\theta} \) and \( C_{13}^{d\theta} \) are constructed with 1 for \( d \) and 0, 45, 90 and 135 degrees for \( \theta \) and averaged. Then second order statistical features are extracted in horizontal, vertical and diagonal directions (total of 42 features). For ultrasonic liver images also, all the 14 features from
these three detail images and hence 42 features are extracted. The feature values are normalized by subtracting minimum value and dividing by maximum value minus minimum value. Maximum and minimum values are calculated based on the training data set. In the test data set, if the feature value is less than minimum value, it is set to minimum value. If the feature value is greater than maximum value, it is set to maximum value. Then values are normalized and are optimized by feature selection algorithm.

3.2.5. Feature Selection

The feature selection problem involves the selection of a subset of ‘d’ features from a total of ‘D’ features, based on a given optimization criterion. The D features are denoted uniquely by distinct numbers from 1 to D, so that the total set of D features can be written as $S = \{ 1, 2, \ldots, D \}$. $X$ denotes the subset of selected features and $Y$ denotes the set of remaining features. So, $S = X \cup Y$ at any time. $J(X)$ denotes a function evaluating the performance of $X$. $J$ depends on the particular application. Here $J(X)$ denotes the classification performance of tumor region as benign or malignant using the set of features in $X$. In this work, Sequential Forward Search (SFS), Sequential Backward Search (SBS), Sequential Forward Floating Search (SFFS) and Genetic Algorithm (GA) techniques are used.

3.2.5.1. Sequential Forward Search Algorithm:

1. $X = \emptyset$;
2. $Y = \{ i \mid 1 \leq i \leq D \}$
3. repeat
   
   Choose the most significant feature $y$ in $Y$ such that $J(X \cup \{y\})$ gives maximal classification performance. Move $y$ to $X$. 

71
until J(X) gives optimal classification performance

4. End

3.2.5.2. Sequential Backward Search Algorithm:

1. Y = \emptyset;
2. X = \{ i \mid 1 \leq i \leq D \};
3. repeat

Choose the least significant feature x in X such that J(X - \{x\}) gives maximal classification performance. Move x to Y.

until J(X) gives optimal classification performance

4. End

3.2.5.3. Sequential Forward Floating Search Algorithm:

1. X = \emptyset;
2. Y = \{ i \mid 1 \leq i \leq D \};
3. k = 0 // initialization
4. while (k < d) {

find the most significant feature y in Y and add to X.

find the least significant feature x in X

while (J(X_k - \{x\}) > J(X_{k-1})) {

X_{k-1} = X_k - \{x\};

k = k - 1;

find the least significant feature x.

}
The most and least significant feature is selected based on the classification performance, $J(X)$, of PNN classifier for identifying benign and malignant tumor.

3.2.5.4. Genetic Algorithm

$\text{GA\_select()}$

\[
\begin{aligned}
&\{ \\
&\text{Initialize population } P; \\
&\text{repeat } \{ \\
&\quad \text{select two parents } p1 \text{ and } p2 \text{ from } P; \\
&\quad \text{offspring} = \text{crossover}(p1, p2); \\
&\quad \text{mutation}(\text{offspring}); \\
&\quad \text{replace}(P, \text{offspring}); \\
&\} \text{ until (stopping condition);} \\
&\}
\end{aligned}
\]

A binary digit represents a feature, values 1 and 0 meaning selected and removed, respectively. As an example, chromosome 00101000 means that the third and fifth features are selected. That is, the chromosome represents $X = \{3,5\}$ and $Y = \{1,2,4,6,7,8\}$. The initial population is generated by random function.

Initial population:

\[
\begin{aligned}
&\text{for } (i = 1 \text{ to } |P|) \\
&\quad \text{for (each gene } g \text{ in } i^{\text{th}} \text{ chromosome) } \\
&\quad \quad \text{if (random()} < \text{d/D}) \text{ } g = 1; \text{ else } g = 0;
\end{aligned}
\]
The evaluation is straightforward since a chromosome represents a selected feature subset, \( X \), and the evaluation function is clear. In order to force a feature subset to satisfy the given subset size requirement, the size value, \( d \), is taken as a constraint and a penalty is imposed on chromosomes breaking this constraint. The fitness of a chromosome \( C \) is defined as

\[
\text{fitness}(C) = J(X_c) - \text{penalty}(X_c),
\]

where \( X_c \) is the corresponding feature subset of \( C \), and 
\[
\text{penalty}(X_c) = w \times (|X_c| - d)
\]
with a penalty coefficient \( w \). The chromosome selection for the next generation is done on the basis of fitness. The selection mechanism should ensure that fitter chromosomes have a higher probability survival. So, the design adopts the rank-based roulette-wheel selection scheme. If the mutated chromosome is superior to both parents, it replaces the similar parent. If it is in between the two parents, it replaces the inferior parent; Otherwise, the most inferior chromosome in the population is replaced. The selected feature set based on the test data set is used to train the Neural Network Classifier for classifying the liver diseases to select the optimum feature set.

3.2.6. Neural Network Classifiers

In this work, three classifiers namely Probabilistic Neural Network (PNN), Learning Vector Quantization (LVQ) Neural Network and Back Propagation Neural Network (BPN) are considered for classification of the diseases. Neural Network classifiers are compared with Minimum Distance classifier.