CLASSIFICATION OF BREAST MASSES AND 3D LOCALIZATION OF MICROCALCIFICATION

PROJECT REPORT

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RADHIKA.S

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(An autonomous institution affiliated to Anna University, Chennai)

COIMBATORE-641049

ANNA UNIVERSITY: CHENNAI 600 025

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BONAFIDE CERTIFICATE

Certified that this project report titled **"CLASSIFICATION OF BREAST MASSES AND 3D LOCALIZATION OF MICROCALCIFICATION"** is the bonafide work of **RADHIKA.S [Reg. No. 13MAE12]** who carried out the research under my supervision. Certified further, that to the best of my knowledge the work reported herein does not form part of any other project or dissertation on the basis of which a degree or award was conferred on an earlier occasion on this or any other candidate.

SIGNATURE

Dr. RAJESWARI MARIAPPAN

PROJECT SUPERVISOR

Department of ECE

Kumaraguru College of Technology

Coimbatore-641 049

SIGNATURE

Dr. RAJESWARI MARIAPPAN

HEAD OF THE DEPARTMENT

Department of ECE

Kumaraguru College of Technology

Coimbatore-641 049

The Candidate with university **Register No. 13MAE12** was examined by us in the project viva –voice examination held on .....

INTERNAL EXAMINER **EXTERNAL EXAMINER**

ABSTRACT

Classification of benign or malignant microcalcification clusters is a major diagnostic challenge for radiologists. Normally the mammogram is available in two views namely Medio Lateral Oblique (MLO) and Cranio Caudal (CC) views. This method deals with the preprocessing of the input images from MLO & CC views. The second step involves the identification of the nipple position based on Region of Interest separately. Then it involves the extraction of the features using Gray level Co occurrence Matrices (GLCM). The next step is the reduction of the dimensions using Principle Component Analysis (PCA). The reduced features are used in the classification of the microcalcifications as normal, benign or malignant. Support vector Machine classifier (SVM) is used for the classification purpose. The main aim of this work is to improve the sensitivity and specificity for early diagnosis of breast cancer. Finally the microcalcifications are located in order to view their positions.

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LIST OF ABBREVIATIONS

2D	Two Dimensions
3D	Three Dimensions
ALOE	Analysis of Local Oriented Edges
BIRADS	Breast Imaging-Reporting and Data System
CAD	Computer Aided Designing
CC	Cranio Caudal
CLAHE	Contrast Limited Adaptive Histogram Equalization
CT	Computer Tomography
DDSM	Digital Database for Screening Mammography
DICOM	Digital Imaging and Communications in Medicine
GLCM	Gray Level Co-Occurrence Matrices
MLO	Medio Lateral Oblique
MPGS	Modified Projective Grid Space
MRI	Magnetic Resonance Imaging
PCA	Principle Component analysis
PET	Positron Emission Tomography
SVM	Support Vector Machine
SVD	Single Value Decomposition
VRMLV	Virtual Reality Modeling Language Viewer

CHAPTER I

INTRODUCTION

Breast cancer has become one of the main causes of cancer deaths among women in the world. In 2013, an estimated 232,340 new cases of invasive breast cancer was diagnosed among women, as well as an estimated 64,640 additional cases of in breast cancer. Approximately 39,620 women are expected to die from breast cancer. More than 2.9 million US women with a history of breast cancer were alive on January 1, 2012. Some of these women were cancer-free, while others still had evidence of cancer and may have been undergoing treatment.

After slowly increasing for many years (0.4% per year from 1975- 1990), breast cancer death rates decreased by 34% from 1990 to 2010. The decline has been faster among women younger than 50 (3.1% per year) than women 50 and older (1.9% per year).From 2001 through 2010, breast cancer death rates declined annually by 1.8% in non-Hispanic whites, 1.7% in Hispanics/Latinas, 1.6% in African Americans, and 1.0% in Asians/Pacific Islanders, but remained unchanged among American Indians/Alaska Natives. The drop in breast cancer mortality has been attributed to both improvements in breast cancer treatment and early detection. However, not all segments of the population have benefited equally from these advances.

In India, according to GLOBACCON (WHO), for the year 2012,144,937 women were newly detected with breast cancer and 70, 218 women died of breast cancer. So roughly, in India, for every 2 women newly diagnosed with breast cancer, one lady is dying of it. India is experiencing an unprecedented rise in the number of breast cancer cases across all sections of society. There is no way we can prevent breast cancer, but we can definitely detect it early and treat adequately. Only with early detection, can we achieve a longer survival.

1.1 Causes & Symptoms

The breast part of the body is made of fibro glandular and fatty tissue. Malignant tumors arise from the glandular tissues. The causes of cancer may be due to family history, late

pregnancy, childlessness, short lactation and overweight. Breast cancer symptoms include lumps, swelling, changes in the nature of skin (etc). Sometimes these symptoms may be due to any infection. Most of the breast cancers do not have any explicit symptoms. Such cancers are identified by doctors through medical imaging techniques like mammography, magnetic resonance imaging (MRI), positron emission tomography (PET), and ultrasound.

1.2 Mammography

Mammograms have more advantages when we compared with X rays because x ray uses a high dose of radiation when compared to mammograms. Also diagnosis of breast using x rays doesn't provide the best information as mammograms do. Since, the radiation cannot spread deeply into the breast tissues. Finally mammogram is the best option for examining the breast tissues with low dose of radiation.

Mammograms are efficient than CT. It is because CT uses the x ray tubes in a circular arc with high level of radiation and it makes difficult to distinguish the micro calcification or the calcium clusters. Mammograms provide the more accurate images than the x rays and CT. High dose of radiation exposure can also be avoided in the mammogram. Also the BIRADS category that defines the stages of breast cancer cannot be obtained in CT.

Mammograms are better when compared to ultrasound because US can detect the lumps or the suspicious that can be felt physically whereas mammograms can diagnose all the lumps that cannot be felt physically. Also studies prove that mammograms are more suitable for both older and younger ages, but US are suitable only for the younger cases. This proves that mammograms are good for the early diagnosis of the breast cancer.

The Cochrane Collaboration states that the mortality rate is best reduced by regular screening of mammograms.

The chances of curing the cancer greatly depend on the early detection of it. Early detection reduces the mortality rate and increases the survival rate. For this, mammography is the mostly used technique. Mammography is a method used for detecting breast cancer. It is an X-ray examination used for detecting any abnormalities present. The image produced is called as

the mammogram. Mammography plays an important role in detecting cancer before the tumor become visible clinically. Using this, micro calcification of size from 0.1mm diameter and tumors from 5mm diameter can be detected. It is approved by the U.S. Food and Drug Administration (FDA) to help screen for breast cancer in women who show no signs of the disease explicitly. A mammogram can show calcifications, masses or other rare conditions. Early detection of these abnormalities results in a higher chance of recovery from the cancer. Mammogram shows these indications even in the early stage and improves the chance of curing.

A mammogram allows the doctor to have a closer look for changes in breast tissue that cannot be felt during a breast exam. In fact, most of these changes are not cancer and are called "benign," but only a doctor can know for sure.

There are two kinds of mammograms:

1. Screening
2. Diagnostic.

1.2.1. Screening mammogram

Screening Mammograms are done for women who have no symptoms. It usually involves two x-rays of each breast. Screening mammograms can detect lumps or tumors that cannot be felt. They can also find micro calcifications or tiny deposits of calcium in the breast, which sometimes mean that breast cancer is present.

1.2.2. Diagnostic mammogram

Diagnostic mammograms are used to check for breast cancer after a lump or other symptom or sign of breast cancer has been found. Signs of breast cancer may include pain, thickened skin on the breast, nipple discharge, or a change in breast size or shape. This type of mammogram also can be used to find out more about breast changes found on a screening mammogram, or to view breast tissue that is hard to see on a screening mammogram. A diagnostic mammogram takes longer than a screening mammogram because it involves more x-

rays in order to obtain views of the breast from several angles. The technician can magnify a problem area to make a more detailed picture, which helps the doctor make a correct diagnosis.

A digital mammogram also uses x-rays to produce an image of the breast, but instead of storing the image directly on film, the image is stored directly on a computer. This allows the recorded image to be magnified for the doctor to take a closer look.

The goal of mammography is the early detection of breast cancer, typically through detection of characteristic masses and/or microcalcifications. There are several views in mammography but the Cranio-Caudal (CC) view and Medio-Lateral Oblique (MLO) view are commonly used for cancer detection analysis. MLO view covers a larger area than a CC view. The X-ray image which is taken from "head to toe" is CC view whereas MLO is taken from "shoulder to the opposite hip".

The MLO view allows visualization of the largest amount of breast tissue. A technically adequate exam has the nipple in profile, allows visualization of the inframammary fold and includes the pectoral is muscle extending down to the posterior nipple line (an oblique line drawn straight back from the nipple).

The Cranio Caudal (CC) view is the other standard view used in every screening exam. A technically adequate CC view will include as much breast tissue as possible. If you measure straight back from the nipple, the value you get should be within 1cm of measuring the posterior nipple line on the MLO view.

Computer based image analysis aids to detect the abnormal changes in the breast tissues from mammograms. The digital mammogram provides two dimensional images. The 2D view does not give the accurate position of the microcalcifications. Hence, a 3D view of the microcalcification gives a better result for the analysis. 3D visualization is one of the most important aspects of image processing.

3D reconstruction of the tumor allows locating the microcalcification reliably before surgery. It increases the efficiency of diagnosis for breast cancer. The 3D reconstruction reduces the chances of false needle biopsy.

1.3 Microcalcification

Microcalcification clusters are the most important early indicators of breast cancer in X-ray mammograms. A tiny abnormal deposits of calcium salts especially in the breast in the human female is often indicated as Breast cancer. Breast cancer remains a main cause of cancer deaths among women in the world. The classification of bengin and malignant microcalcification clusters posses a considerable diagnostic challenge to radiologists. This work aims a novel algorithm for reconstructing microcalcification clusters in the 3-D uncompressed breast from two mammographic views.

CHAPTER II

LITERATURE SURVEY

[1]Margaret Yam et al developed a method for reconstructing microcalcification clusters in 3D from two mammographic views and it develops a 3-D Breast representation and a parameterized breast compression model which constraints geometrically the possible 3-D positions of a calcification in a two-dimensional image. Initially, breast region, pectoral muscle, nipple are segmented, and microcalcification are detected in each 2-D mammogram. Next a 3D uncompressed breast model is constructed from the information of two views of mammography and a prior geometric model. The microcalcification is approximated as an ellipsoid. Its results are compared with MRI results. It is found that on an average, the volumes estimated from X-ray mammogram are 5.7% less than those computed from MRI data.

[2]Yasuyo Kita et al proposed a method of locating lesions in CC and MLO views. It also allows specialist to point on a lesion in one view (CC/MLO). The corresponding epipolar line is then found. The same lesion is searched in the other to get a match. The CAD system proposed in this method displays the epipolar lines for the match as soon as the lesion in one view is clicked. The 3D location of the lesion is estimated from these inputs. It is assumed that the mammogram has no undesirable deformations. Presence of deformation results in errors in the results obtained. The error achieved is reported as 10-20 mm in the estimation of lesion location and mostly these errors result in the variation in depth direction.

[3]Chun-Rong Huang developed a method to reconstruct 3D locations of microcalcifications from two mammograms without any prior geometric model or X-ray machine information, we proposed a modified projective grid space (MPGS) scheme based on the fundamental matrix and pinhole camera system. To solve the problem of microcalcifications detection, in this paper, three modules are presented. The first module extracts the breast region from mammograms based on K-means clustering based thresholding. Then, the second module detects suspected regions based on blanket method. The third module extracts the real microcalcifications based on the assumption that the average of gray-level of microcalcifications on the mammograms is generally brighter than that of other tissues. As a result, the correct registration accuracy of registration method achieved about 96.7%.

[4]Sheng –Chih Yang et al presented a 3D localization method to register clustered micro calcifications on mammograms from cranio-caudal (CC) and medio-lateral oblique (MLO) views. The method consists of three major steps: registration of clustered micro calcifications in CC and MLO views, 3D localization of clustered micro calcifications and 3D visualization of clustered micro calcifications. The registration is performed based on three features, gradient, energy and local entropy codes that are independent of spatial locations of micro calcifications in two different views and are prioritized by discriminability in a binary decision tree. The 3D localization is determined by a sequence of coordinate corrections of calcified pixels. Finally, the 3D visualization implements a virtual reality modeling language viewer (VRMLV) to view the exact location of the lesion as a guide for needle biopsy. In order to validate the 3D localization system, a set of lesions, which appear both in mammograms and in MR Images is used for experiments where the depth of clustered micro calcifications are verified with the MR images.

[5]Ling Shao proposed a method of automatic segmentation of masses using a region growing approach. A set of seeds are located and merged based on the homogeneity criterion. The dilation operation is then carried out in the neighborhood to obtain the mass. The 3D representation is done using an algebraic technique. It is repeated several times to get the particular shape of the mass. The mass shape is affected by Partial volume effect and is eliminated by applying the partial volume estimation on the initial 2D mass boundary.

[6]This paper performs analysis on mammographic views for detecting the masses. It is based on the experiences that masses and calcifications are present on both CC and MLO views. If a mass/calcification seen in one view is not in other view, it is noted as false positive. Edge flow algorithm is used for image segmentation, which uses an energy propagation technique before thresholding. This technique allows shifting in energy of edges in each iteration. The shifting direction is based on probabilities. For the mass detection step, ALOE texture feature is used. Once the mass is identified in one view then a strip is assigned parallel to the pectoral muscle in the other view. It is assumed that the position of a mass from a tangent drawn parallel to pectoral muscle is same in both the CC and MLO views. There are some variances in the position of the masses. To compensate, the width of the stripe is adjusted. The limitation of this method is that a

malignant mass missed in one view would be unnoticed. It gives a loss of false positive hits of 31%.

[7]R Besar et al gave an identification method for masses in digital mammography. The processing of the mammogram is done to enhance the image quality and to remove the artifacts in the mammogram. For reducing the noise in the image an equalization process called CLAHE (Contrast Limited Adaptive Histogram Equalization) is used. This process is operated on small regions of the image called tiles. The next step in the method is segmenting the suspicious abnormalities. This paper used three techniques for segmentation: threshold technique, K-mean clustering and Otsu's method. After segmenting the suspicious regions, then the next step is feature extraction process, where features are used to distinguish masses and normal tissues. In this paper used processing windows or tiles for determining the masses. The tiles are obtained from dividing the mammogram into small areas. The tiles used are of sizes 32*32, 16*16, 8*8 as in Figure 4. Among the three techniques, it is found that the threshold technique has a true positive (TP) result of 96%; for K –Means clustering the TP rate is 96% and for Otsu's method it is 90%

[8]Charlotte Curtis 2010 proposed a method to estimate the 3D structure of the lesions using only the CC and MLO view of the mammograms. This method is given the input of the CC and MLO features and their undistorted mammograms. It gives an automated and efficient registration procedure for the suspicions. Spatial alignment of the images is done by rotating the CC view by 90^{o} and MLO view to its oblique angle. This alignment aids for the breast model in three dimension. For 3D breast model, its edge contours from the 2D views are used. A series of ellipses are filled along the length to give the 3D model. Then the suspicions are located manually from the 2 views. Back propagation method is used for the 3D rendering of the location of the lesions.

CHAPTER III

IMAGE DATABASES

Two image databases are used for the project. They are

1. DDSM
2. INBREAST

3.1 DDSM DATABASE

The Digital Database for Screening Mammography (DDSM) is a resource for use by the mammographic image analysis research community. Primary support for this project was a grant from the Breast Cancer Research Program of the U.S. Army Medical Research and Materiel Command. The DDSM project is a collaborative effort involving at the Massachusetts General Hospital, the University of South Florida, and Sandia National Laboratories. Additional cases from Washington University School of Medicine were provided by Peter E. Shile, MD, Assistant Professor of Radiology and Internal Medicine. Additional collaborating institutions include Wake Forest University School of Medicine Departments of Medical Engineering and Radiology, Sacred Heart Hospital and ISMD, Incorporated. The primary purpose of the database is to facilitate sound research in the development of computer algorithms to aid in screening. Secondary purposes of the database may include the development of algorithms to aid in the diagnosis and the development of teaching or training aids.

The database contains approximately 2,500 studies. Each study includes two images of each breast, along with some associated patient information (age at time of study, ACR breast density rating, subtlety rating for abnormalities, ACR keyword description of abnormalities) and image information (scanner, spatial resolution ...) Images containing suspicious areas have associated pixel-level "ground truth" information about the locations and types of suspicious regions. Also provided are software both for accessing the mammogram and truth images and for calculating performance figures for automated image analysis algorithms.

The Digital Database for Screening Mammography is organized into "cases" and "volumes." A "case" is a collection of images and information corresponding to one mammography exam of one patient. A "volume" is simply a collection of cases collected

together for purposes of ease of distribution. All volumes are available on 8mm tape. Normally all (or almost all) volumes are also available on-line.

Each volume is a collection of cases of the corresponding type. Normal cases are formed from a previous normal screening exam (pulled from a file) for a patient with a normal exam at least four years later. A normal screening exam is one in which no further "work-up" was required. Cancer cases are formed from screening exams in which at least one pathology proven cancer was found.

Benign cases are formed from screening exams in which something suspicious was found, but was determined to not be malignant (by pathology, ultrasound or some other means). The term benign without callback is used to identify benign cases in which no additional films or biopsy was done to make the benign finding. These cases, however, contained something interesting enough for the radiologist to mark. A small number of cancer cases may contain, in addition to one or more regions that are path-proven malignant, one or more regions that are unproven. These are suspicious regions for which there is no path result.

3.2 INBREAST DATABASE

The image matrix was 3328 x 4084 or 2560 x3328 pixels, depending on the compression plate used in the acquisition (according to the breast size of the patient). Images were saved in the DICOM format. All confidential medical information was removed from the DICOM file, according to Supplement 55 of the DICOM standard; the correspondence between images of the same patient is kept with a randomly generated patient identification and collected from which 90 have two images (MLO and CC) of each breast and the remaining 25 cases are from women who had a mastectomy and two views of only one breast were included. This sums to a total of 410 images. Eight of the 91 cases with 2 images per breast also have images acquired in different timings. The database includes examples of normal mammograms, mammograms with masses, mammograms with calcifications, architectural distortions, asymmetries, and images with multiple findings and their bi-rads rating.

BI-RADS is an acronym for Breast Imaging-Reporting and Data System, a quality assurance tool originally designed for use with mammography.

BI-RADS Assessment Categories are:

Category 0: Incomplete

Category 1: Negative

Category 2: benign findings

Category 3: probably benign findings

Category 4: suspicious findings

Category 5: a high probability of malignancy and

Category 6: proved cancer

In case of categories 4 and 5, a biopsy is needed to exclude or confirm malignancy.

CHAPTER IV

PROPOSED WORK

The proposed work has the following process flow:

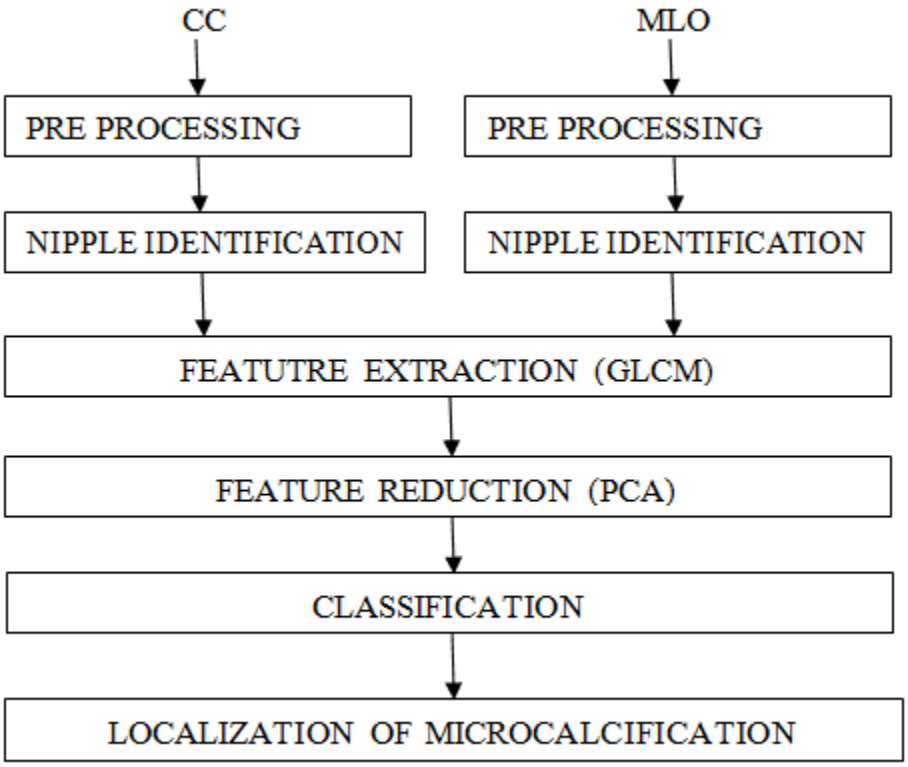

Figure 4.1 Process flowchart

The image which is taken from Cranio Caudal and Medio Lateral Oblique views. Then the images are preprocessed separately. The pre processing steps includes label removal and pectoral muscle removal. Then it involves identifying the nipple position separately and the GLCM features are extracted. Then the features are fed into the classifier which classifies the microcalcification as normal, benign or malignant. Finally the microcalcifications are located in order to view their positions.

4.1 Pre processing

Digital mammograms are medical images that are difficult to be interpreted, thus a preparation phase is needed in order to improve the image quality and make the segmentation results more accurate. It aims at separating the breast tissue from the background of the mammogram and it includes two independent segmentations. The first segments the background region which usually contains annotations, labels and frames from the whole breast region, while the second removes the pectoral muscle portion (present in Medio Lateral Oblique (MLO) views) from the rest of the breast tissue.

Steps

Preprocessing stage consists of three steps.

- Contrast enhancement
- Label removal
- Pectoral muscle removal

4.1.1. Contrast enhancement

The first part involves the contrast enhancement of the images in CC and MLO views, if required. The DDSM database has low contrast images and is in need of contrast enhancement. Histogram Equalization technique is used for contrast enhancement.

4.1.2. Label removal

The next part is the removal of labels from the images. The label is removed, based on the area of the individual objects in the image. The areas of such objects are then calculated. The labels occupy only smaller area than the breast portion is removed by considering the maximum area condition. Thus the breast portion having maximum area is only present in the output image. Based on the area calculation, the desired part occupying larger area is separated out.

4.1.3. Pectoral muscle removal

The final stage involves the pectoral muscle removal. Pectoral muscles are the regions in mammograms that contain brightest pixels. These regions must be removed before detecting the

tumor cells so that mass detection can be done efficiently. The Pectoral muscles located at the left top corner or right top corner which depends on the left or right view of the image. The label removal output is given to the input of pectoral muscle. Initially the pectoral muscles are detected before removing it. For this searching for non zero pixels and zero pixels in the image. It is done by calculating the values of first five rows and last five rows and comparing them. By assigning a first five rows are greater than the last five rows then it is assumed that the breast region is right oriented otherwise it is left oriented and it is to be converted into right. Then the starting and ending point of the breast region is found and it is joined by using a straight line. Then the space above the line is covered by pectoral muscle and which is removed by assigning zero pixels to those values. The resulting image contains the pectoral muscles are removed from the original image.

4.1.4 Nipple Detection

Identifying the nipple position for Cranio Caudal and Medio Lateral Oblique view individually. The nipple detection algorithm steps are follows as

Step 1: Setting the threshold of the image, and calculating the image parameters

Step 2: Selecting the proper region for that particular image, so that selection of the centroid term in the image will be provided

Step 3: From the Selected centroid region we will be tracking for the selection of Region of Interest region in the boarder of the image area

Step 4: The Same Process is repeated till it reach the border of the image, and the separate region is flipped so that boundary at both the region will be detected

Step 5: Now the calculation of the average value throughout the region will be estimated through

$$x_c = \frac{1}{M}\sum_{i=1}^{n} x_1 m_i \quad (1)$$

Step 6: Nearer Closest point is acquired from the result and it is plotted

CHAPTER V

FEATURE EXTRACTION

Feature Extraction is a method of capturing visual content of images for indexing & retrieval. Primitive or low level image features can be either general features, such as extraction of color, texture and shape or domain specific features. It involves simplifying the amount of resources required to describe a large set of data accurately. When performing analysis of complex data one of the major problems stems from the number of variables involved.

Analysis with a large number of variables generally requires a large amount of memory and computation power or a classification algorithm which over fits the training sample and generalizes poorly to new samples. Feature extraction is a general term for methods of constructing combinations of the variables to get around these problems while still describing the data with sufficient accuracy. Texture analysis aims in finding a unique way of representing the underlying characteristics of textures and represent them in some simpler but unique form, so that they can be used for robust, accurate classification and segmentation of objects.

This work uses gray level co-occurrence matrix (GLCM) to extract second order statistical texture features. In statistical texture analysis, texture features are computed from the statistical distribution of observed combinations of intensities at specified positions relative to each other in the image. According to the number of intensity points (pixels) in each combination, statistics are classified into first-order, second-order and higher-order statistics.

The Gray Level Co-occurrence Matrix (GLCM) method is a way of extracting second order statistical texture features. The approach has been used in a number of applications. Third and higher order textures consider the relationships among three or more pixels. These are theoretically possible but not commonly implemented due to calculation time and interpretation difficulty.

A GLCM is a matrix where the number of rows and columns is equal to the number of gray levels, G, in the image. It is obtained by calculating how often a pixel with gray-level (grayscaleintensity) value ‘i’ occurs horizontally adjacent to a pixel with the value ‘j’. Each element (i,j) in glcm specifiesthe number of times that the pixel with value ‘i’ occurred horizontally adjacent to a pixel with value ‘j’. If the image is a binary image, GLCM scales the image to two gray-levels. If the image is an intensity image, GLCM scales the image to eight gray-levels as shown in Figure 5.1

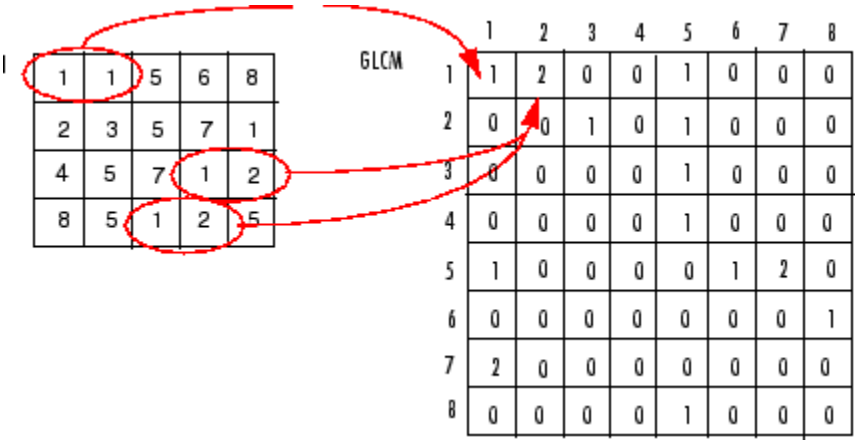

Figure 5.1 GLCM generation

Gray-level co-occurrence matrix (GLCM) is the statistical method which computes the numerical features of textures. The co-occurrence matrix is often formed using a set of offsets sweeping through 180 degrees (i.e. 0, 45, 90 and 135 degrees) at the same distance to achieve a degree of rotational invariance. Transforming the input data into the set of features is called feature extraction. It is a type of dimensionality reduction. Large sized images are difficult to process so it is transformed to set of feature so it is easy to process. Almost 20 parameters are considered for feature extraction. It includes GLCM features and Gray co-level features. The GLCM features computed are contrast, correlation, energy and homogeneity. The Gray co-level features such as autocorrelation, contrast, correlation, cluster Prominence, cluster shade, dissimilarity energy, entropy, homogeneity, homogeneity positive, maximum probability, sum of squares, sum of squared variance , Sum average, sum variance, sum entropy, difference variance,

difference entropy, information measure of correlation1, information measure of correlation2, inverse difference, inverse difference normalized and Inverse difference moment normalized are also calculated.

Contrast

It returns a measure of the intensity contrast between a pixel and its neighbor over the whole image.

$\sum_{i,j} |i-j|^2 p(i,j)$ (2)

Contrast is 0 for a constant image.

Correlation

It returns a measure of how correlated a pixel is to its neighbor over the whole image.

Range = [-1 1]

Correlation is 1 or -1 for a perfectly positively or negatively correlated image.

$$\sum_{i,j} \frac{(i-\mu i)(j-\mu j)p(i,j)}{\sigma_i \sigma_j} \quad (3)$$

Energy

It returns the sum of squared elements in the GLCM. Range is between [0 1]. Energy is 1 for a constant image.

$$\sum_{i,j} p(i,j)^2 \quad (4)$$

Homogeneity

It returns a value that measures the closeness of the distribution of elements in the GLCM to the GLCM diagonal. Range is between [0 1]. Homogeneity is 1 for a diagonal GLCM.

$$\sum_{i,j} \frac{p(i,j)}{1+|i-j|} \quad (5)$$

Autocorrelation

It resembles to the information provided by the GLCM correlation.

Entropy

The entropy measure from the pixel intensity distribution is given by

$$-\sum_i \sum_j p(i,j)\log\left(p(i,j)\right) \tag{6}$$

Cluster Prominence

Cluster Prominence is a measure of asymmetry is given by

$$\sum_{i=0}^{Ns-1} \sum_{j=0}^{Ns-1} \left(i + j - u_x - u_y\right)^4 p(i,j) \tag{7}$$

Cluster shade

Cluster shade is a measure of skewness of the matrix is given by

$$\sum_{i=0}^{Ns-1} \sum_{j=0}^{Ns-1} \left(i + j - u_x - u_y\right)^3 p(i,j) \tag{8}$$

Dissimilarity

The dissimilarity measure weights increase linearly (0, 1, 2, 3 etc.). Dissimilarity equation is

$$\sum_{i,j=1}^{N} P_{i,j} \ |i - j| \tag{9}$$

Sum Average

Sum Average is calculated by

$$\sum_{i=1}^{2G-2} iP_{x+y}\ (i) \tag{10}$$

Sum Entropy

Sum Entropy is found by

$$\sum_{i=1}^{2G-2} iP_{x+y}(i)\log i(P_{x+y}(i)) \quad (11)$$

Difference Entropy

Difference Entropy is calculated by

$$-\sum_{i=1}^{G-1} P_{x+y}(i)\log\left((P_{x+y}(i)\right) \quad (12)$$

Inverse Difference Moment

It is also called the Homogeneity. If weights decrease away from the diagonal, the result will be larger for windows with little contrast. Homogeneity equation is

$$IDM = \sum_{i=1}^{G}\sum_{j=1}^{G}\frac{P(i,j|\Delta x,\Delta y)}{1+(i-j)^2} \quad (13)$$

Sum of variance

The sum of Variance is given by

$$SOV = \sum_{i=1}^{G}\sum_{j=1}^{G}(i-\mu)^2 P(i,j) \quad (14)$$

Correlation Maximum

It is initialized as zero. It is given by

$$corm(k) = \sum_{k}\sum_{i}\sum_{j} corm(k) + \left(\left((i) - u_{x(k)}\right) * \left((j) - u_{y(k)}\right) * glcm(i,j,k)\right) \quad (15)$$

Correlation Positive

It is initialized as zero. It is given by

$$corrp(k) = \sum_{k}\sum_{i}\sum_{j}\frac{corrp(k) - u_{x(k)} * u_{y(k)}}{s_{x(k)} * s_{y(k)}} \quad (16)$$

CHAPTER VI

DIMENSIONALITY REDUCTION

In machine learning and statistics, dimensionality reduction is the process of reducing the number of random variables and it can be divided into feature selection and feature extraction. Feature selection approaches try to find a subset of the original values (features). Feature extraction involves simplifying the amount of resources required to describe a large set of data accurately. When performing analysis of complex data one of the major problems stems from the number of variables involved. Analysis with a large number of variables generally requires a large amount of memory and computation power or a classification algorithm which overfits the training sample and generalizes poorly to new samples. Feature extraction is a general term for methods of constructing combinations of the variables to get around these problems while still describing the data with sufficient accuracy.

Feature reduction transforms the data in the high dimensional space to a space of fewer dimensions. In the reduced space, data analysis such as classification and regression can be done more accurately. The data transformation is performed in both linear and nonlinear approaches. A different approach to nonlinear dimensionality reduction is through the use of auto encoders, a special kind of feed-forward neural networks with a bottle-neck hidden layer. The training of deep encoders is typically performed using a greedy layer-wise pre-training that is followed by a fine tuning stage based on back propagation.

For high-dimensional datasets (i.e. with number of dimensions more than 10), dimension reduction is usually performed prior to applying a Single Value Decomposition (SVD) in order to avoid the effects of the curse of dimensionality. Dimensionality reduction methods can be categorized into stand alone and hybrid approaches. The dimensionality reduction methods are used in applications such as electrocardiogram signal analysis and gene expression analysis for cancer detection. The stand alone method utilizes a single criterion from either supervised or unsupervised perspective. Many dimension reduction techniques do the reduction once for all. Adaptive dimension reduction combines dimension reduction and unsupervised learning (clustering) together to improve the reduced data (subspace) adaptively.

Principal component analysis (PCA) is a mathematical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components. The number of principal components is less than or equal to the number of original variables. PCA is the simplest of the true eigenvector-based multivariate analyses. PCA is mathematically defined as an orthogonal linear transformation that transforms the data to a new coordinate system such that the greatest variance by any projection of the data comes to lie on the first coordinate (called the first principal component), the second greatest variance on the second coordinate, and so on.

Principal Component Analysis (PCA) can be used to find a subspace whose basis vectors correspond to the maximum-variance directions in the original space. Let W represent the linear transformation that maps the original t-dimensional space onto f-dimensional feature subspace where normally $f << t$. The new feature vectors $yi \in Rf$ are defined by $WTxi$, $i=1, 2…N$. The columns of W are the eigen values ei obtained by solving the eigen structure decomposition by the term $\lambda iei = Qei$, where $Q = XXT$ is the covariance matrix and λi is the eigen value associated with the eigenvector ei. It is less sensitive to noise and it is used for reconstructing training datasets. It is not effective for some datasets.

CHAPTER VII

CLASSIFICATION

The extracted feature values are fed to the classifier for classification to classify whether it is cancerous or non cancerous.

7.1 Support Vector Machine

Support Vector Machine is an unsupervised or self organized neural network. SVM have recently found considerable attention in classification problems due to its generalization capabilities. These classifiers maximize the distance (margin) between the training examples and the decision boundaries by mapping the training examples to higher dimensional space [II]. The dimension of the new space is considerably larger than that of the original data space. Then the algorithm finds the hyper plane in the new space having the largest margin of separation between the classes of the training data using an optimization technique known as the risk minimization. For a binary classification problem where there are only two classes in the training data = $\{-1,1\}$, a hyper plane can be defined as:

$$W.x + b = 0 \quad (17)$$

where W is the normal to the hyper plane and b / W is the shortest distance of the plane from the origin. For a good classification model, the positive and negative examples of the training data should fulfill the following two conditions:

$$(W.x_i) + b > 0 \quad \text{if } Y_i = 1 \quad (18)$$

$$(W.x_i) + b < 0 \quad \text{if } Y_i = -1 \quad (19)$$

These inequalities can be combined into one set of Inequalities

$$y(W.x + b) \geq 1 \text{ for all i} \quad (20)$$

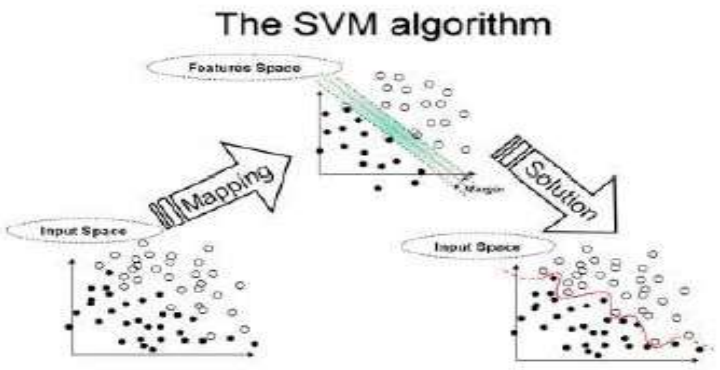

Figure 6.1 SVM Algorithm

The SVM finds an optimal hyper plane responsible for the largest separation of the two classes by solving the following optimization problem subject to the condition.

$$Min\ w, b \quad \frac{1}{2}\ W^T W \tag{21}$$

The quadratic optimization problem can be solved using a langrangian function

$$Lp(w, b, \alpha) = \frac{1}{2}\ W^T W - \sum_{i=1}^{m} \alpha i(yi(Wxi + b) - 1) \tag{22}$$

where αi is the constant known as langrage multipliers. The solution for αi determines the parameters w and b of the optimal hyper plane. Thus a decision function for the binary classification is formulated as

$$f(x) = sgn(\sum_{i=1}^{m} yi\ \alpha i(x, xi) + b) \tag{23}$$

In any classification task only a few langrangian multipliers αi tend to be greater than zero and the corresponding training vectors are the closest to the optimal hyper plane and are called the support vectors. In nonlinear SVM, the training samples are mapped to a higher dimensional space with the help of a kernel function K (xi ,xj) instead of the inner product <xi , xj> . Some of

the famous kernel functions are the polynomial kernels, radial basis function kernels, and sigmoid kernels.

7.2 Performance Measure

Accuracy

Accuracy is the measure of number of correctly identified examples to the total number of test examples

$$\text{Accuracy} = \frac{(TP+TN)}{(TP+TN+FP+FN)} \quad (24)$$

Where,

TP - True Positive

TN - True Negative

FP - False Positive

FN - False Negative

Sensitivity

Sensitivity measures the proportion of the positives, which are correctly identified by the classifier. Numerically sensitivity is the number of true positives results divided by the sum of true negatives and false positives.

$$\text{Sensitivity} = \frac{TP}{(TP+FN)} \quad (25)$$

Specificity

Specificity measures the proportion of negatives, which are correctly identified by the classifier. Numerically specificity is the number of true negatives results divided by the sum of true negatives and false positives.

$$\text{Specificity} = \frac{TN}{(TN+FP)} \quad (26)$$

With all the three parameters the classifiers efficiency can be calculated.

CHAPTER VIII
LOCALIZATION OF MICROCALCIFICATION

Using mammograms images with the tumor in the breast will result in two sub images, each showing the cluster from a different viewing angle in both vertical and oblique. Each microcalcification results in a point in each sub image detected area. To reconstruct the position of a microcalcification it is neccessary to backtrack the projection beam from each sub image. If more than one point appear within a (y,z) plane an unique reconstruction is not possible and additional points may fake positions of not existing microcalcifications.

If the interest point of the image is not exactly aligned the projection beams do not intersect and therefore no reconstruction can be performed. The subimages are shifted until the beams intersect, until every microcalcification in the rest subimage found its counterpart in the second subimage. The best shift will be the one with the most beam crossings.

Tumor affected with three microcalcifications a, b and c. The viewing angle between the subimages is arbitrary, here 90 degree. For a correct reconstruction, the two projections b1 and b2 should align and the projection lines should intersect in b. Both projection lines mount a plane, obviously containing b1 and b2. All projected points stretch such planes parallel to each other. Therefore all projected points in subimage 1 left from b1 are located left from b2 in subimages 2. We could use this fact by moving one subimage along the other step by step to compute a quality value. The best quality value should be computed for the best offset, which means a maximum overlap of microcalcifcation positions.

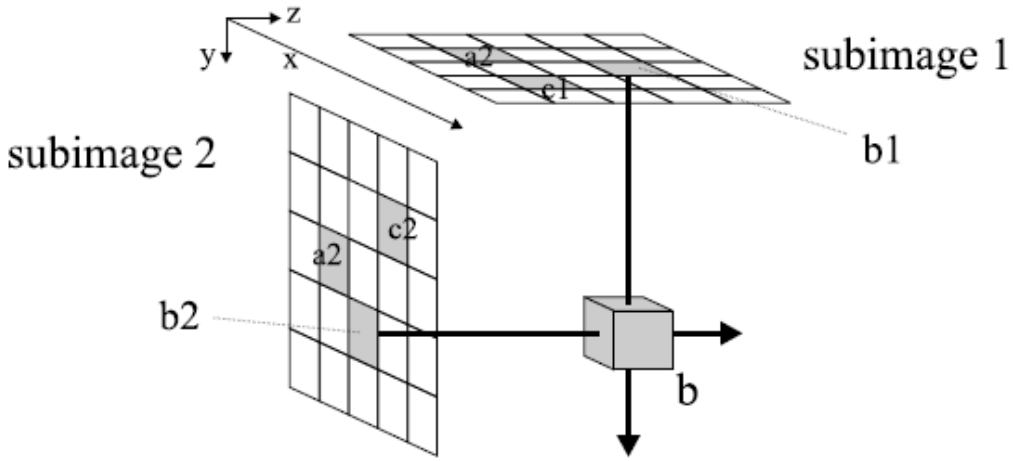

Figure 8.1 Alignment of two projections of a simple cluster containing three microcalcifications

To compute the overlap it is enough to know whether two corresponding microcalcifications are located in the same plane like b1 and b2, the best offset of sub images can now be calculated along the x-axis by using a correlation function. In additon only the x-axis offset is of interest. The y-axis and z-axis offset is not needed, because it would only change the location of the reconstructed cluster. It has no effect on the spatial distribution of microcalcifications and the shape of the cluster.

$$\text{Quality value qv(x)} = \sum_{i=-\infty}^{\infty} f(i).g(x+i) \qquad (27)$$

Where f(x) is the number of microcalcifications in the upper image and
g(x) is the number of the lower one in column x.

CHAPTER IX

MATLAB

MATLAB (**mat**rix **lab**oratory) is a numerical computing environment and fourth-generation programming language. Developed by Math Works, MATLAB allows matrix manipulations, plotting of functions and data, implementation of algorithms, creation of user interfaces, and interfacing with programs written in other languages, including C, C++, Java, and FORTRAN. Although MATLAB is intended primarily for numerical computing, an optional toolbox uses the MuPAD symbolic engine, allowing access to symbolic computing capabilities. An additional package, Simulink, adds graphical multi-domain simulation and Model-Based Design for dynamic and embedded systems.

MATLAB Compiler compiles a MATLAB application into a standalone application or software component. The act of compiling this code is sometimes referred to as building. Building with MATLAB Compiler enables we to run our MATLAB application outside the MATLAB environment. It reduces application development time by eliminating the need to translate our code into a different language. If we are building a standalone application, MATLAB Compiler produces an executable for our end users. If we integrate into C or C++, MATLAB Compiler provides an interface to use our code as a shared library. If we integrate into other development languages, MATLAB builder products (available separately) let us package our MATLAB applications as software components. We are able to use Java classes, .NET components, or Microsoft Excel add-ins. It provides good platform for performing image processing operations.

Image Processing Toolbox provides a comprehensive set of reference-standard algorithms and graphical tools for image processing, analysis, visualization, and algorithm development. We can perform image enhancement, image deblurring, feature detection, noise reduction, image segmentation, spatial transformations, and image registration. Many functions in the toolbox are multithreaded to take advantage of multicore and multiprocessor computers.Image Processing Toolbox supports a diverse set of image types, including high dynamic range, gigapixel resolution, ICC-compliant color, and tomographic images. Graphical

tools let us explore an image, examine a region of pixels, adjust the contrast, create contours or histograms, and manipulate regions of interest (ROIs). With the toolbox algorithms we can restore degraded images, detect and measure features, analyze shapes and textures, and adjust the color balance of images.

Key Features

- Image enhancement, filtering, and deblurring
- Image analysis, including segmentation, morphology, feature extraction, and measurement
- Spatial transformations and image registration
- Image transforms, including FFT, DCT, Radon, and fan-beam projection
- Workflows for processing, displaying, and navigating arbitrarily large images
- Modular interactive tools, including ROI selections, histograms, and distance measurements
- ICC color management
- Multidimensional image processing
- Image-sequence and video display
- DICOM import and export

MATLAB supports standard data and image formats, including JPEG, JPEG-2000, TIFF, PNG, HDF, HDF-EOS, FITS, Microsoft Excel, ASCII, and binary files. It also supports the multiband image formats BIP and BIL, as used by LANDSAT for example. Low-level I/O and memory mapping functions enable us to develop custom routines for working with any data format.

CHAPTER X

SIMULATION RESULTS

10.1. Original images

The proposed work uses two databases viz., Digital Database for Screening Mammography (DDSM) and INBREAST database. It uses an image set of 65 pair images from DDSM database and 28 pair images from INBREAST database. These image databases have both the CC and MLO view images with normal, benign and malignant categories.

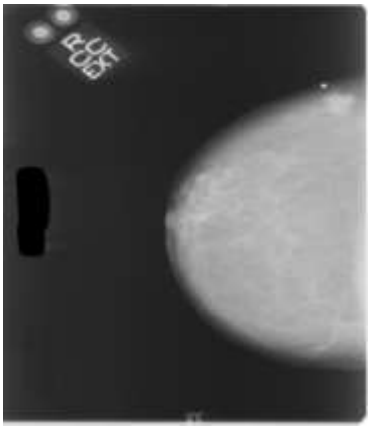

Figure 10.1 Original CC image-benign

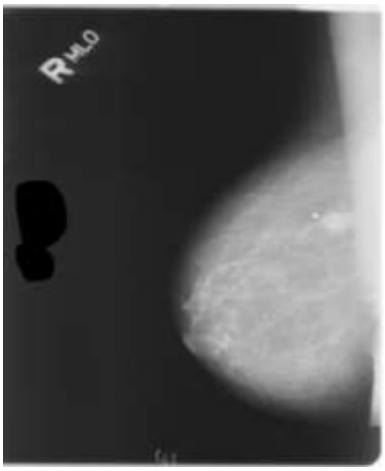

Figure 10.2 Original MLO image-benign

10.2. PREPROCESSING - Label removal

The next part is the removal of labels from the images. The labels occupy only smaller portion in the image. Based on the area calculation, the desired part occupying larger area is separated out.

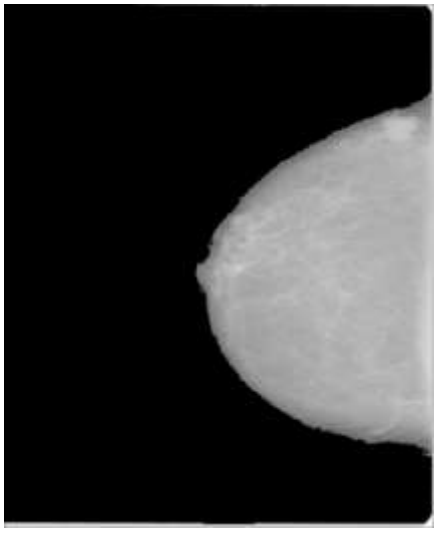

Figure 10.3 Label removed CC image

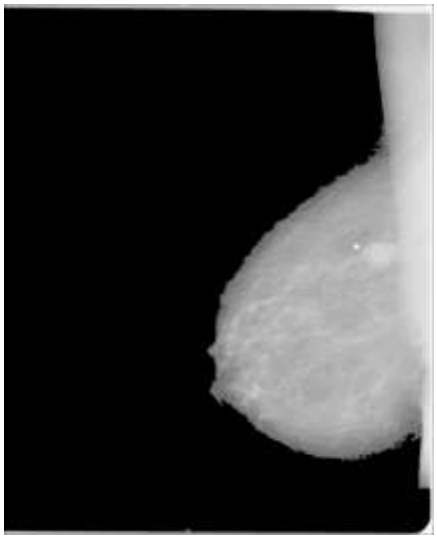

Figure 10.4 Label removed MLO image

10.3. PREPROCESSING - Pectoral muscle removal

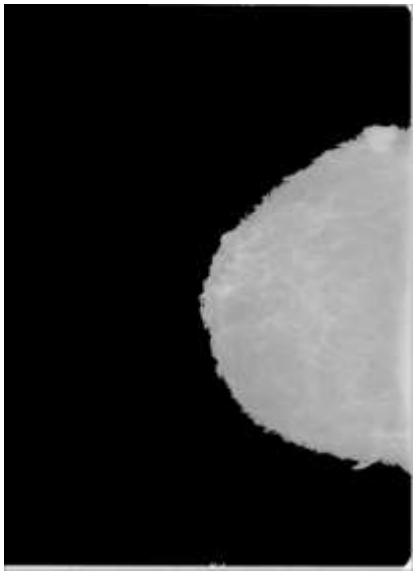

Figure 10.5 Pectoral muscle removed CC image-DDSM

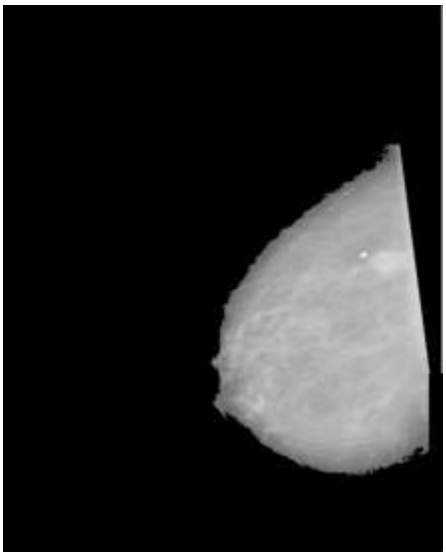

Figure 10.6 Pectoral muscle removed MLO image-DDSM

10.4 Nipple Identification

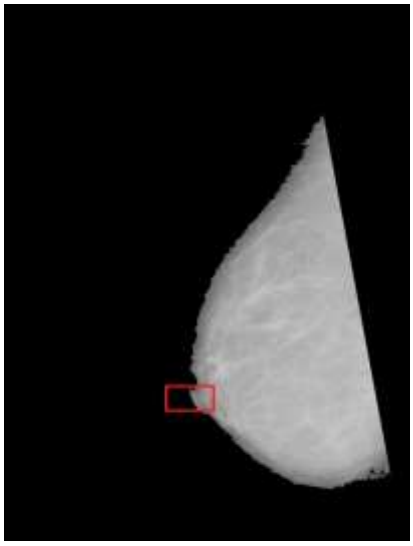

Figure 10.7 Nipple identified image DDSM

10.5 Original MLO images from INBREAST

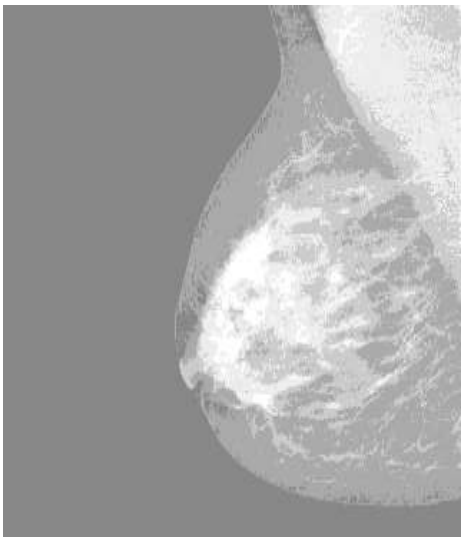

Figure 10.8 Original image from MLO malignant-INBREAST

10.6 Pectoral muscle removal-INBREAST

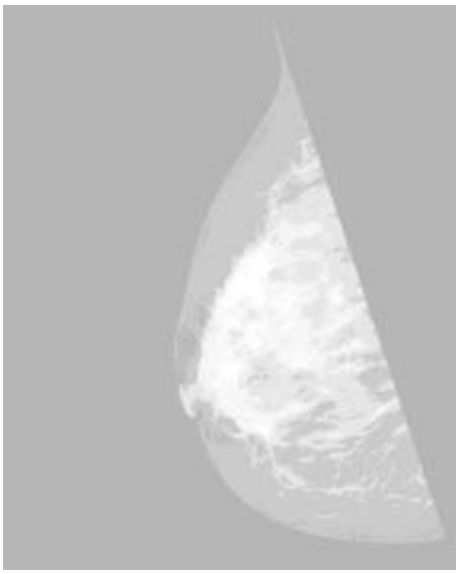

Figure 10.9 Pectoral muscle removed from MLO-INBREAST

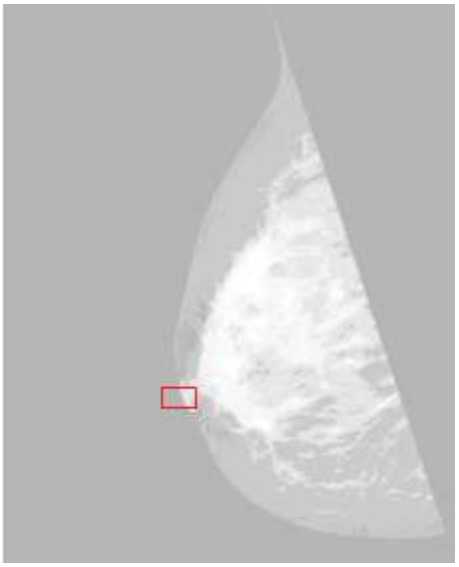

Figure 10.10 Nipple identified image from INBREAST

Texture features are extracted from the nipple identified image. Texture analysis helps in determining a unique way of representing the characteristics of textures. It is used for robust, better classification of objects. GLCM is used to calculate these texture features. Totally 20 features are extracted for each image.

Features	Benign	Malignant
Contrast	0.041093	0.18344
Correlation	0.995731	0.978879
Energy	0.44743	0.305749
Homogeneity	0.983637	0.969611
Autocorrelation	1715.501	2827.615
Correlation maximum	0.203323	0.227812
Correlation Positive	0.203323	0.227812
Cluster Prominence	5273797	13779128
Cluster Shade	-9544.78	22858.45
Dissimilarity	47.76686	42.49147
Entropy	8.660527	9.166383
Homogeneity maximum	0.056297	0.060954
Homogeneity Positive	0.021559	0.023291
Maximum Probability	0.000264	0.000175
Sum of Squares	750.9928	1915.929
Sum Average	92.20082	107.8579
Sum Variance	9188.62	12888.29
Sum Entropy	5.043947	5.274412

Table 10.1 Texture features extracted from DDSM Database

Features	Benign	Malignant
Contrast	0.015317	0.016486
Correlation	0.976368	0.984314
Energy	0.46615	0.443879
Homogeneity	0.992341	0.991757
Autocorrelation	4052.983	4088.093
Correlation maximum	-0.00216	-0.02233
Correlation Positive	-0.00216	-0.02233
Cluster Prominence	17812856	17690964
Cluster Shade	1922.638	2183.966
Dissimilarity	42.80553	43.61005
Entropy	9.700954	9.701548
Homogeneity maximum	0.061917	0.060828
Homogeneity Positive	0.023847	0.023325
Maximum Probability	8.16E-05	7.80E-05
Sum of Squares	5252.094	5322.44
Sum Average	127.4022	128.3909
Sum Variance	17619.28	17837.43
Sum Entropy	5.350778	5.347318

Table 10.2 Texture features extracted from INBREAST Database

10.7 Performance Evaluation

Based on the features extracted, the masses are classified as benign, malignant or normal tissue. The proposed work uses Support Vector Machine (SVM) for the classification of the suspicions. SVM algorithm is a supervised learning method. The obtained accuracy results are compared in CC, MLO and combined CC&MLO views.

Parameters	DDSM DATABASE	INBREAST DATABASE
Sensitivity	**71.9%**	**95.3%**
Specificity	**60.5%**	**51.7%**

Table 10.3 Comparision results of Sensitivity and Specificity

Mammographic views used in classification	Accuracy	
	DDSM DATABASE	INBREAST DATABASE
CC view	**82.1%**	**83.6%**
MLO view	**85.8%**	**82.4%**
CC &MLO view	**93.2%**	**92.6%**

Table 10.4 Comparision results of Accuracy

10.8 Localization of Microcalcification

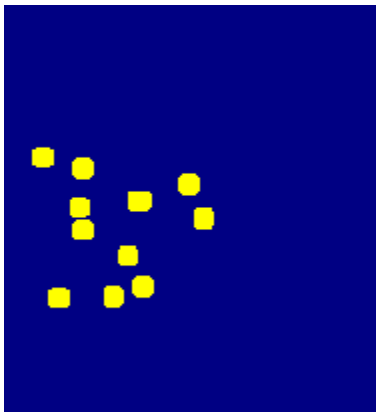

Figure 10.11 Location of microcalcification

CHAPTER XI

CONCLUSION AND FUTURE WORK

The images are taken from two data bases such as DDSM and INBREAST database. In the first step labels and pectoral muscles are removed. Pre processing step is necessary in order to improve the image quality and make the results more accurate. The image consists of label name such as hospital name or date. Such labels are removed from image. Then identification of the nipple position based on the Region of Interest separately. Then it involves the extraction of the features using Gray level Co occurrence Matrices (GLCM). Then reducing the dimensions using Principle Component Analysis (PCA). The reduced features are used in the classification of the microcalcifications as normal, benign or malignant by using Support vector Machine classifier (SVM). Finally the microcalcifications are located in order to view their positions. The future work can be reconstructing the microcalcifications in 3D and extracting the 3D features of microcalcification.

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LIST OF PUBLICATIONS

JOURNAL

- Published a paper "**Detection and 3D Reconstruction of Tumor Based on Mammographic Images: A Survey***"* in **International Journal of Applied Engineering Research,** ISSN 0973-4562, Volume 9, Number 20, 2014.

CONFERENCE

- Presented a paper titled "**Detection and 3D reconstruction of tumor based on mammographic images: A Survey**" in International Conference on Pattern Recognition and Multimedia Signal Processing at Annamalai University, Chidambaram.

- Presented a paper titled "**Three Dimensional Reconstruction of Microcalcification Clusters from CC and MLO views**" in 2nd International Conference on Electronics and Communication Systems on 26th and 27th February, 2015 organized by Department of Electronics and Telecommunication Engineering at Karpagam College of Engineering