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Breast Cancer Detection using Fuzzy SVMs

Dr. M Raja Sekar¹

¹Dept. Of Computer Science and Engineering, VNR Vigana Jyothi Institute of Engineering And Technology, Hyderabad

Abstract: *Abnormal of growth of the breast is the symptom of the breast cancer. In this paper we designed a systematic methodology that explains the identification of cancer related breast X-ray images. This study is helpful to doctors and medical experts in identification of abnormal growth in the breast X-ray images. Breast cancer X-ray image sequence is deeply analyzed with fuzzy support vector machines. Fuzzy support vector machines play an important role in the preprocessing phase of the classification of breast cancer X-ray images. Preprocessing step performs data cleaning in which noise data is removed and also highlights the essential components of the breast cancer images. In the second step of this formulated methodology convolutional generative adversarial networks (CGANs) are used to divide the regions of interest which consists of cancer cells. The regions of interest may be in the form of circular disproportion, density, eccentricity, circularity and circular density. Angular radial descriptor, Zernike random descriptor are used to the asses the region shapes with the help of fuzzy support vector machines. All the brain X-ray images are divided on the basis of masses present in the mammogram image sequence. The designed methodology shows the accuracy rate of 97%.*

Key words: *Convolutional generative adversarial networks (CGANs), support vector machines, geostatistic functions and breast cancer images.*

I. INTRODUCTION

From the past few years, various researchers have been published articles to identify breast cancer textures in mammograms images. These researchers developed an automated system with help of computers to detect breast cancer tissues. Developed automated systems are useful to the doctors as a reliable source of information and also saves the precious time. The accuracy of implemented system relies on the attribute extraction and segmentation of the regions of interest. Our study offers a computer aided procedure to assist an expert to identify abnormal growth in breast cancer images. In this method we used cellular non linear networks for segmenting mammogram image regions and which are useful to obtain the attributes from mammogram images. Angular radial descriptor, Zernike random descriptor functions are used to understand the texture in breast cancer images. In the final phase of this procedure, supervised SVMs are used to categorize obtained sample areas of the brain images into masses or non masses. There are three possible forms mass in the extracted region namely benign, neoplasm and malignant. The significant role of this study is explaining the importance of CNN to divide the doubtful regions in the breast cancer images. This study also describes about the usage of geostatistical functions in the identification mass present in mammograms. The results of this study are useful to an expert in assessing the intensity of breast cancer when visualization is very hard.

In this study, section 2 explains about brief description of literature survey. Section 3 explains the methods for identification, categorization, authentication of features which are extracted from mammograms and recommended procedure and its assessment. Section 4 explains the results of this study and purpose of methods which are used. Section 5 describes conclusion of this study.

II. LITERATURE SURVEY

Several procedures are formulated that can helpful to identify breast cancer in mammogram images. Various algorithms were suggested for identifying masses in mammogram images ([1-5]). These algorithms accomplished sensitivity ranging from 77% to 88%, and false positive is 0.43 to 5.1 per an image. In this study we used publicly available breast cancer image database like DDSM [6-10] and MIAS [11-13]. CNNs are exclusively used in various applications to process mammogram images [14-15]. Rekeczky et al.[16] formulated methods for the categorization of medical images especially mammogram images. Medical images may be MRI images, CT images and ultrasonic images. Chua et al. [17-19] used CNNs to verify the features of mammograms. The accuracy of Support vector machines and Linear Discriminant analysis are compared by Costa et al. [20- 22], categorized 200 regions into 100 normal tissues, 50 malignant issues and 50 benign tissues and these images are collected from MIAS and DDSM database which consists of huge set of mammogram images. The accuracy of the results in the case of MIAS database is 85% for LDA and 97% for Support vector machines respectively. The accuracy of the results in the case of DDSM database is 89.2% for LDA and 99.6% for Support vector machines respectively. Hence SVMs shows superior performance compare to Linear

Discriminant Analysis.

There are methods which are based on SOM (Self Organizing Maps) to detect mammogram images [20]. Oliveira et al. [14] formulated a method based on GNG (Growing Neural Gas) to divide the mass sample regions and Ripley’s values associated with support vector machines to identify textures in breast cancer images. They worked extensively on DDSM image databases and obtained remarkable accuracy in classifying breast cancer images. Nunes et al. [20] formulated a procedure for identify the texture which uses clustering algorithms to divide mammogram image regions. The formulated procedure was examined with 650 breast cancer images collected from the DDSM database and obtained 83% of classification accuracy.

Wang et al. [11] formulated a methodology for identification of masses in breast cancer images by applying pixel based approach. In this approach measurements like gradient, standard deviation, average, invariant momentum and gradient related boundary calculations are used. Attributes like sphericity, density, circularity and Fourier descriptors are also used in the assessment of masses present in mammogram images. They used 192 mammograms used for training and 150 mammograms for testing. This algorithm accomplished 78.6% of accuracy rate and the value of 3.6 false positive per image. Pereira et al. [12] examines the identification of masses using ridgelet transforms, oblique views and craniocaudal methods. They used DDSM mammogram database from which 300 images were selected for training 154 mammogram images for testing. This procedure accomplished an accuracy of 79%.

From this related work, we can realize the significance of identifying masses in the mammogram images. Various methods of machine learning are used to enhance the classification of texture in the brain image into masses and normal. Hence, it appears to be very useful to use cellular networks to classify breast cancer related images by extracting different features from mammograms.

III. DESIGNED PROCEDURE

This section explains the procedure to identify masses in breast cancer images. There are various phases in the proposed methodology like attainment, cleaning, dividing the texture regions, attribute acquisition, selection of attribute and categorization of textures in mammograms into non masses and masses.

The first phase of this proposed procedure is obtaining mammogram image and subsequent phases are cleaning, dividing the regions in to segments and obtaining attributes. In the phase of cleaning, noise data is eliminated by clustering algorithms, Hough’s transform, histograms, operators related to erosion and Cranny’s filter. CNNs are used to identify mammograms with textures, hence subsequent phases operate within the desired region.

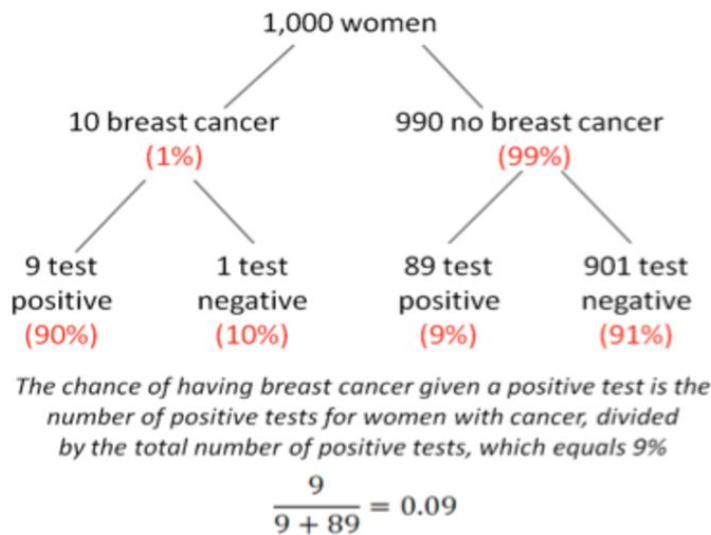


Fig 1. Images collected for the study

The attributes are obtained with help of shapes like circular density, circularity, eccentricity, compactness, circular disproportion and methods like Angular radial descriptor, Zernike random descriptor. Conclusively, the support vector machines are used to

remove the non masses from given set of breast cancer images.

A. Breast Image Extraction

This study is carried out by making use of publicly available database DDSM (Digital database for screening mammography). This database is built by Washington University, Massachusetts General Hospital, Washington University, Wake Forest University and St. Louis school of medicine. This database contains huge set of freely available of mammogram images. MLO view and CC view of breast cancer images are collected by considering the parameters like number of difficulties, pathological variations, person age and time of study. The design of DDSM also consider the number of bits per pixel, sequence, kind of film, digitalization time and types of digitizer. Logical and physical design and implementation of DDSM is based on the information supplied by specialists. In our study we have been used 898 mammogram images from this database. These mammogram images are chosen arbitrarily from DDSM. While choosing the mammogram images from DDSM, criteria followed was that each mammogram must have only one mass.

B. Preprocessing

Preprocessing is a phase in which an inconsistent mammogram images are transformed into consistent mammogram images collected from DDSM. In this stage noise data, invalid data and incomplete data is removed. Noise may be in the form of background of mammogram, defects in the image, problems in digitalization and difficulties in individual breast identification. The internal structure of breast is enhanced by eliminating the unnecessary stuff from mammogram which leads to obtain the significant and useful information. This can be seen in the Fig. 2. In the preprocessing, initially mammogram image size is reduced to the size of 1000x1000, which can be seen in Figure 3(a).



Fig 2 Image is with noise elements



Fig. 3 Noise removal process of mammogram image

Reduction of mammogram is needed to speed up the preprocessing time. As a second phase of the preprocessing, boundaries of the mammogram images are eliminated. As a consequence of this phase quality of mammogram images are enhanced.

Background of the mammogram is removed with well known K-means clustering algorithm by using pixel intensity information. As a consequence of this phase, all gray level intensity pixels which are closely associated with block color are eliminated which can be

seen in Figure 3(b). This K-means clustering algorithms separates regions of mammogram into two groups in which one group consists of pixels with less intensity and another group with high intensity. Pixels with high intensity represents identification marks of the mammogram and whereas pixel with low intensity represents noise and background. Lower intensity pixels (background and noise related pixels) are removed by changing their values to zero which is shown in Fig. 3(c). After this preprocessing step also there are few more noise and back ground pixels exists in the mammogram images which can be eliminated by using region growing algorithms [12]. These regions growing algorithms are used to select appropriate breast are by separating mutually exclusively regions which can be seen in Fig. 4.

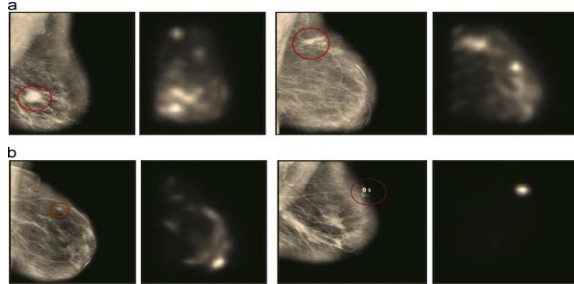


Fig. 4 Segmentation process of mammogram image

Visualization and structure of the mammograms are significantly improved by histogram equalization algorithms which is shown in Fig. 5. Chest muscles in MLO viewed mammograms removed in the final phase of the preprocessing methodology. Chest muscles are identified by calculating average intensity values of the divided mammogram image as shown in Fig. 5. Mammogram image boundaries are identified by Canny's filter [22] and removed all these detected boundaries with the help of morphological operators. Hough transform is used to remove the noise in the borders of mammogram images as shown in Fig.4.

C. Segmentation

This phase is useful to detect mammogram images with masses with cellular non linear networks [20]. In this

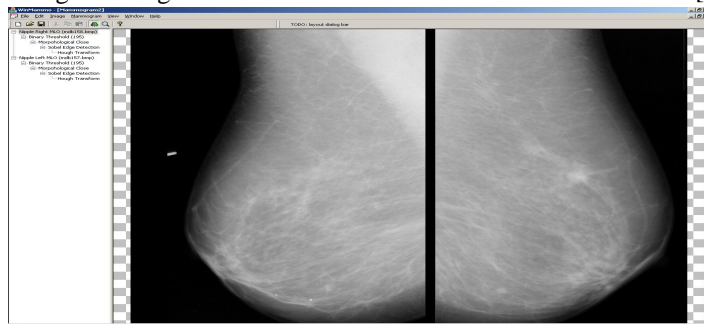


Fig. 4 Improvement of mammogram image

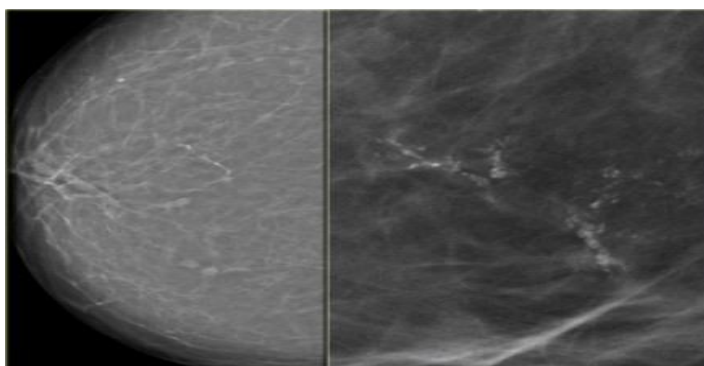


Fig. 5 Algorithm generated image

CNNs are constructed by Cartesian coordinate system with the help of rectangular matrix of order $m \times n$ using the following formula

$$a_j^k = a^k(x_k - z_j^k)(1)$$

$$K(x, z) = \prod_{k=1}^n a^k(x_k - z_j^k)(2)$$

In the above formula u indicates number of steps in particular iteration and s is the radius of the identified cell which is useful CNNs. The parameters y, z, v and a are treated as state, input mammogram image, out put mammogram image and threshold value of cell $c(j, k)$ respectively. In equation1, B denotes feedback involution operator and C denotes syntactic weighted input. Mammogram image pixel intensity values are calculated by v_{im} which is to be normalized between -1 and +1.

There are two types of templates which are used in this study in which first one is Textudier[18] to separate masses from mammogram image and second one is Blur[19] to enhance the processing speed. Empirical calculation of these mammogram images. Blur and Textudi are used to remove duplication with help of logical operator. Region growing methods are used to remove the candidate mammograms which are not satisfying size criteria as shown in Fig.5.

D. Feature Extraction

In this phase, the goal is to obtain significant attributes from the mammogram images which are processed in the previous phase. The resultant mammogram images are used to generate feature vector space which consists of attributes like texture and feature. There are five significant attributes which are used in this study are circular density, compactness, eccentricity, circular disproportion and circularity. The procedure used in this phase uses shape information of the mammogram images instead of pixels' intensity information. Concentric rings [22] are formed with the help of Replay's mapping to identify texture of the mammogram images. ROIs in the mammogram images are calculated using Grey index and Moran's index.

Formula for Replay's mapping is

$$Maxw(\delta_k) = \sum_{k=1}^n \beta_k - \frac{1}{2} \sum_{i,j=1}^l \beta_i \beta_j x_i x_j K(x_i, x_j)(3)$$

here L represents Replay's mapping, s is the radius of the concentric ring, B represents are of the concentric ring, j is the sample pixel, e is the distance function, j, k represents pixel position with respect to origin.

$$f(x) = Sign(b_0 + \sum_{j=1}^m \beta_j y_j K(x, x_j)(4)$$

$$\frac{\partial L(w, b, \eta, \gamma)}{\partial w} = w - \sum_{i=1}^l \alpha_i y_i z_i = 0(5)$$

$$\frac{\partial L(w, b, \eta, \gamma)}{\partial b} = w - \sum_{i=1}^l \alpha_i y_i z_i = 0(6)$$

$$\frac{\partial L(w, b, \eta, \gamma)}{\partial \xi} = w - \sum_{i=1}^l \alpha_i y_i z_i = 0(7)$$

Equation 4 represents Greary's index and equation 5 represents Moran's index in which o represents number of mammogram imgs, X represents weight of the mammogram images. These indexes are calculated with the angles 0, 45, 90 and 135 degrees. In this study we used 450 vectors representing mass classes and 3000 vectors representing mammogram images with non masses.

IV. CLASSIFICATION OF MAMMOGRAM

A. Images

In the phase of classification, mammogram images are classified into two groups in which first one is training mammogram images

and second one testing mammogram images. Support vector machines are used to classify mammogram images into two groups one with masses and another with non masses.

$$L_p = \frac{1}{2} \|w\|^2 + c \sum_{i=1}^n \chi_i [y_i (wx_i + b) - \sum_{i=1}^n \eta_i] \quad (8)$$

Here k is biased parameter, v is the weight and h is the linear combination of variables.

This can be represented in the form Wolf programming with conditions.

Here v and δ are part of objective function. Conditions which are represented in equation 7 are known as Kuntucker conditions.

Equation 8 is another form of equation 6 which is useful to formulating hyper plane in support vector machines.

$$\varphi(dx) \equiv \psi(dx) \quad (9)$$

$$\beta(x, x_i) = q(x)r(x_i)s(x, x_i) \quad (10)$$

Equation 9 and 10 are useful for finding optimal hyper plane which optimally separates the given set of mammogram image into two sets one with masses and another with non masses.

Equation 11 and 12 are useful to build desired kernel in the support vector machine algorithm. In this study, the support vector machines are used with different kernels which are formed with help of equation 6 to equation 12.

$$j(x, x_i) = \exp \left(-\frac{\|x - x_i\|^2}{\pi^2} \right) \quad (11)$$

$$g_{ij}(x) = \frac{1}{\mu^2} \delta_{ij} \quad (12)$$

V. RESULTS AND DISCUSSION

Methodology which is presented in this paper is evaluated by performing various tests with different test cases. In this phase results of several procedures are discussed.

In the initial phase, we arbitrarily selected 732 mammogram images which contains one mass from DDSM data base. These images are divided into ROIs which gives 4302 regions with textures. Out of these 4302 regions 3300 are non masses related mammograms and 1002 are mass related mammograms. This segmentation is not successful in the case 41 mammogram images which degrade the performance. As a result of this, we optimized the parameters of the mammogram images as shown in Table1 and Table2.

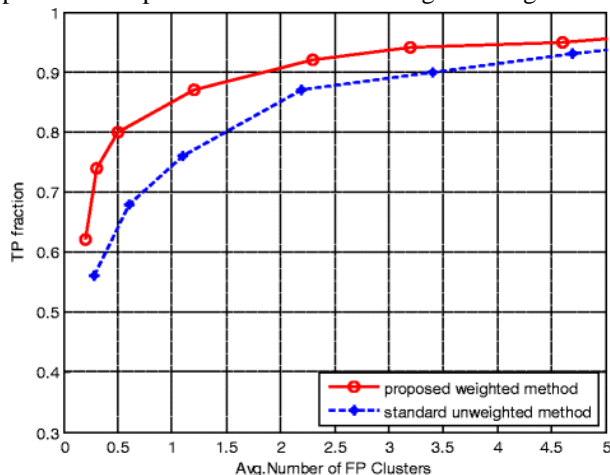


Fig. 6 ROC curve for mammogram images

The 623 mammogram images are correctly divided into segments with the accuracy 92%. The results proven that mammogram image segmentation phase significantly improved the efficiency of accuracy. Classification of mammogram images are performed in two stages in which first stage analysis is done without reducing the attributes and in second stage performed with reducing the attributes. In our work total set of mammogram images are classified into 10 major groups. Bias in the image classification is avoided by training and testing all the groups under consideration. In our study, we used two procedures in which first one uses texture and shape information of mammogram image to classify as non-masses and masses. Such results indicate that the combination of shape descriptors, Angular radial descriptor, Zernike random descriptor provides a good tool to characterize regions suspect of containing masses.

	MI-1	MI-2	MI-3	MI-4	MI-5
Geary	52	65	55	2.0	0.58
Moran	74	66	52	2.61	0.65
Happy	71	56	55	1.9	0.67
Moran + Geary	68	73	76	1.3	0.79
Shape	78	63	67	1.1	0.80
Angular	89	58	70	1.1	0.98

Table1. Results with Angular radial descriptor

	MI-1	MI-2	MI-3	MI-4	MI-5
Geary	62	75	55	2.5	0.68
Moran	84	76	72	2.81	0.75
Happy	77	59	58	2.3	0.67
Moran + Geary	78	83	88	1.67	0.79
Shape	78	63	67	1.7	0.83
Zernik	89	88	77	1.8	0.96

Table2. Results with Zernike random descriptor

Training data forms the basis to identify support vectors which are useful for constructing decision surface. Number of vectors for non-mass and masses are identified as 1600 and 200 respectively.

Another important remark is the performance of the analysis involving only the texture descriptors (Angular radial descriptor, Zernike random descriptor), which achieved an accuracy of 81.66%, sensitivity of 81.75% and specificity of 81.86%, with average rates of false positives and false negatives per image of 1.06 and 0.18, respectively, and an area under the ROC curve of 0.861 as shown in Table3 .

Despite the good results obtained, several aspects of the methodology can be improved, allowing for even better results. One of these aspects is the performance of the segmentation stage, where nearly 9.15% of the original masses were lost.

We also observed that the objects classified as masses have areas smaller than the area informed by the DDSM (overlay index below 0.4, on average). This did not constitute a problem, but it indicates that larger masses can be divided into smaller ones, which might impact texture analysis, causing the mass to be classified as a false negative. Additional studies must be carried out to determine to what extent and how often this happens.

Another problem found in segmentation is the large number of regions of interest selected (566 regions containing masses and 3305 with healthy tissue). This numerical disproportion between the two classes ends up influencing the classifier, since much more information is available about one class in relation to the other. This has led to the need to use different weights for SVM training, in order to reach a balance between sensitivity and specificity. A solution can be obtained through parameter optimization algorithms (genetic algorithms, fuzzy systems) to find a single template that can reduce the amount of false candidates and increase the

proportion of masses found.

D-SVM		MI-1	MI-2	MI-3
	SVM-1	0.73	0.45	0.654
	SVM-2	0.540	0.513	0.6256
F-SVM	SVM-1	.92	0.87	.89
	SVM-2	0.75	0.98	0.87
	NNH	0.95	0.83	0.93
F-SVM		MI-1	MI-2	MI-3
	SA+SVM Linear	0.85	0.654	0.82
	SA+SVM RBF	0.87	0.82	0.81
DV-SVM	SA+SVM Poly	0.456	0.543	0.62
F-SVM	Geary	MI-1	MI-2	MI-3
	Frequency Count	0.85	0.83	0.81
	TF-IDF	0.4509	0.4737	0.588
V-SVM	Geary	MI-1	MI-2	MI-3
	Frequency Count	0.67	0.76	0.37
	TF-IDF	0.75	0.473	0.5872
F-SVM	Geary	MI-1	MI-2	MI-3
	NCRA	0.95	0.92	0.96
	TF-IDF	0.87	0.93	0.97

Table 3. Comparison of F-SVM with other SVMs

VI. CONCLUSION

The algorithm discussed in the previous section shows significant performance in the context of mammogram image classification with respect to regions of interest. In the sample of 1000 mammogram images 980 mammogram images regions are divided accurately and achieved accuracy of 97%. The categorization of mammogram images achieved precision of 86%, sensitivity of 88%, false negative 0.6 and 0.9 false positive per image.

These results prove that the use of descriptors like Geary's descriptor, Moran's indicator and Ripley's function gives significant performance in the classification masses of mammogram images. There are few limitations in this study like segmentation phase in which original masses were not properly classified, handling false negative images, handling large number of regions, identifying different weights for training the support vector machine. These problems can handle with the help of the algorithms like fuzzy algorithm and genetic algorithms.

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