# Breast Tissue Classification Using Gabor Filter, PCA and Support Vector Machine

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**Abstract** – Analysis of medical images is done by using image processing as it is one of the prominent tools. It is also used in the breast cancer detection. This experiment focuses towards the identification of relevant, representative and more important, discriminate image features for analysis of medical images. The features from mammogram images representing normal tissues or benign and malign tumors are extracted using Gabor wavelets. These features with large dimensions (1024x1024) are then applied to Principal Component Analysis (PCA) to reduce data dimensionality and converted into 140x140 pixel size images. Finally, the extracted features are classified using the proximal support vector machines as classifier. The features with orientations of 0,  $\pi/4$ ,  $3\pi/4$ , and  $\pi/2$  and also with all orientations of Gabor filters are combined with low frequency and high frequency filters and compared for Recognition rate are calculated. The Gabor filter with low frequency with all orientation gives the highest recognition rate.

**Keywords**: Breast cancer, Mammography, Gabor wavelets, PCA, SVM

## I. Introduction

Mammography is at present the best available technique for early detection of breast cancer. The most common breast abnormalities that may indicate breast cancer are masses and calcifications. Early detection and treatment are considered as the most promising approaches to reduce breast cancer mortality. Mammogram image is considered as the most reliable, low cost, and highly sensitive technique for detecting small lesions. The radiologists are searching for signs of abnormality, but the signs of early disease are often small or subtle. One of the main points that should be taken under serious consideration when implementing a robust classifier for recognizing breast tissue is the selection of the appropriate features that describe and highlight the differences between the abnormal and the normal tissue in an ample way. Feature extraction is an important factor that directly affects the classification result in mammogram classification. Most systems extract features to detect and classify the abnormality as benign or malignant from the textures. A particular image type is given by mammographic images that are typically X-ray captures of breast region displaying points with high

intensities density that are suspected of being potential tumors. Early diagnostic and screening is crucial for having a appearing in the mammogram images could indicate a potential presence of a benign or malignant tumor.

## II. Image pre-processing

The experimentation is done with the database images taken from Mammographic Image Analysis Society (MIAS), which contains 322 samples belonging to three different categories as normal, benign and malign. The database consists of 208 normal images, 63 benign and 51 malign cases, which are considered abnormal [13]. These database images are of  $1024 \times 1024$  pixel size and having background information like breast contour, therefore the pre-processing of these images is required and therefore the images are cropped into patches of  $140 \times 140$  pixels as shown in figure 1. The cropping does not affect on the information residing in the image. Database is then divided into two sets. First set is having 80% database images of whole database with known classes,

normal, benign and malign. Whereas the second set is with 20% database images which are the test images and are having unknown classes.

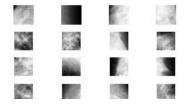


Fig. 1. Training images (Abnormal patches 140x141)

To reduce the computations during the further processing the images are down sampled to the size of 30x30 pixels as shown in figure 2. The cropping of image and also the down sampling is carried out by statistical calculations of pixels from original image.

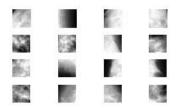


Fig. 2. Training images (Abnormal patches 30x30)

## III. Feature Extraction

III.1.Gabor Wavelets

A 2-D Gabor function is a Gaussian modulated by a sinusoid. It is a non orthogonal wavelet. Gabor filters exhibits the properties as the elementary functions are suitable for modeling simple cells in visual cortex [12] and gives optimal joint resolution in both space and frequency, suggesting simultaneously analysis in both domains. The definition of complex Gabor filter is defined as the product of a Gaussian kernel with a complex sinusoid. A 2D Gabor wavelet transform is defined as the convolution of the image I (z).

$$J_{k}(z) = \int \int I(z') \psi_{k}(z - z') dz'$$
 (1)

with a family of Gabor filters (functions):

$$\Psi_k(z) = k^T k / \sigma^2 \exp((-k^T k / 2\sigma^2) * z^T z) (\exp(ik^T z) - \exp(-\sigma^2 / 2))$$

where z = x, y and k is characteristic wave vector:

 $K = (k_v \cos \varphi_u \quad k_v \sin \varphi_u)^T$  (3)

with

$$Kv = 2 - v + \frac{2}{2}\pi, \phi_{\mu} = \mu \frac{\pi}{8},$$
 
$$v = 0, 1, 2, 3, 4, \quad \mu = 0, \pi/4, \pi/2, 3\pi/4 \tag{4}$$

The results obtained by extracting the features with Gabor filters are as shown in Figure 3 and 4. Fig. 3 shows the magnitude response of features with low frequency Gabor filter bank whereas Fig. 4 shows the magnitude response of high frequency filter bank.

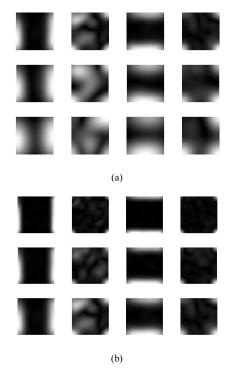


Fig. 3. Magnitude responses of filtering operation with Gabor filter bank a) Low frequency b) High frequency

# IV. Principal Component Analysis

PCA involves the calculation of the Eigen value decomposition of a data covariance matrix or singular value decomposition of a data matrix, usually after mean centering the data for each attribute. The results of a PCA are usually discussed in terms of component scores and loadings. PCA is the simplest of the true eigenvectorbased multivariate analyses. Often, its operation can be thought of as revealing the internal structure of the data in a way which best explains the variance in the data. If a multivariate dataset is visualized as a set of coordinates in a high-dimensional data space, PCA supplies the user with a lower-dimensional picture, a "shadow" of this object when viewed from its most informative viewpoint. PCA is closely related to factor analysis; indeed, some statistical packages deliberately conflate the two techniques. True factor analysis makes different

assumptions about the underlying structure and solves eigenvectors of a slightly different matrix. 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 the second greatest variance on the second coordinate, and so on [4]. PCA is theoretically the optimum transform for given data in least square terms. For a data matrix, XT, with zero empirical mean (the empirical mean of the distribution has been subtracted from the data set), where each row represents a different repetition of the experiment, and each column gives the results from a particular probe.

Given a set of points in Euclidean space, the first principal component (the eigenvector with the largest Eigen value) corresponds to a line that passes through the mean and minimizes sum squared error with those points. The second principal component corresponds to the same concept after all correlation with the first principal component has been subtracted out from the points. Each Eigen value indicates the portion of the variance that is correlated with each eigenvector. Thus, the sum of all the Eigen values is equal to the sum squared distance of the points with their mean divided by the number of dimensions. PCA essentially rotates the set of points around their mean in order to align with the first few principal components. This moves as much of the variance as possible (using a linear transformation) into the first few dimensions. The values in the remaining dimensions, therefore, tend to be highly correlated and may be dropped with minimal loss of information. In this way, the PCA is used in this experiment for dimensionality reduction. Fig. 4 shows 10 Eigen images resulted from PCA.

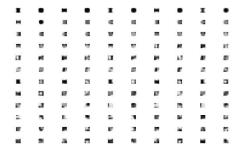


Fig. 4. 10 Eigen images obtained by applying PCA for the Matrix Xke (Training dataset)

## V. Support Vector Machine

Support vector machines (SVMs) are a set of related supervised learning methods that analyze data and recognize patterns, used for classification and regression analysis. The standard SVM is a non-probabilistic binary linear classifier, i.e. it predicts, for each given input, which of two possible classes the input is a member of. Since an SVM is a classifier, then given a set of training examples, each marked as belonging to one of two categories, an SVM training algorithm builds a model that predicts whether a new example falls into one category or the other. Intuitively, an SVM model is a representation of the examples as points in space, mapped so that the examples of the separate categories are divided by a clear gap that is as wide as possible. New examples are then mapped into that same space and predicted to belong to a category based on which side of the gap they fall on.

Multiclass SVM aims to assign labels to instances by using support vector machines, where the labels are drawn from a finite set of several elements [10]. The dominating approach for doing so is to reduce the single multiclass problem into multiple binary classification problems. Each of the problems yields a binary classifier, which is assumed to produce an output function that gives relatively large values for examples from the positive class and relatively small values for examples belonging to the negative class. Two common methods to build such binary classifiers are where each classifier distinguishes between (i) one of the labels to the rest (one-versus-all) or (ii) between every pair of classes (one-versus-one). Classification of new instances for one-versus-all case is done by a winner-takes-all strategy, in which the classifier with the highest output function assigns the class (it is important that the output functions be calibrated to produce comparable scores). For the oneversus-one approach, classification is done by a maxwins voting strategy, in which every classifier assigns the instance to one of the two classes, then the vote for the assigned class is increased by one vote, and finally the class with most votes determines the instance classification. The figure 5 shows the classification result, the abnormal area is shown with more cross points and circles.

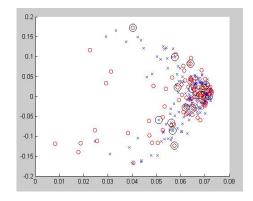


Fig. 5 . Classification result obtained by using proximal support vector machine.

Table I: Recognition Rate for Different combinations of Gabor and PCA with different orientations.

Features	Frequency range	Orientation	RR (%)
Gabor filter and PCA	Low frequency range	0	65.62
		$\pi/4$	67.18
		$\pi/2$	68.75
		$3\pi/4$	64.06
		All	84.375
Gabor filter and PCA	High frequency range	0	65.62
		$\pi/4$	64.06
		$\pi/2$	71.87
		$3\pi/4$	64.06
		All	68.75

#### VI. Conclusion

The system works on two filter banks, low frequency and high frequency. At first original images are cropped into size of 140x140 pixels. Then the most discriminating features from images are extracted. The images are passed through 12 different Gabor filters. The features are obtained by convolving patches representing tumor or tumor-free areas with several Gabor filters and are employed for recognition purpose. As the extracted features are having large dimensions and it will increase the number of computations, these are given to PCA to reduce the dimensionality. As shown in the result table the recognition rate obtained by the Gabor filter with low frequency and all orientation is the highest, 84.37%, compared to other results.

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