Diagnosis of Breast Cancer in Digital Mammograms Using Independent Component Analysis and Neural Networks

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Abstract. We propose a method for discrimination and classification of mammograms with benign, malignant and normal tissues using independent component analysis and neural networks. The method was tested for a mammogram set from MIAS database, and multilayer perceptron neural networks, probabilistic neural networks and radial basis function neural networks. The best performance was obtained with probabilistic neural networks, resulting in 97.3% success rate, with 100% of specificity and 96% of sensitivity.

Keywords: Mammogram, breast cancer, independent component analysis, neural networks, computer aided diagnosis.

1 Introduction

Breast cancer is the major cause of death by cancer in the female population. It is known that the best prevention method is early diagnosis, which lessens the mortality and enhances the treatment [1]. Therefore, a great effort has been made to improve the early diagnosis techniques. Among them, the most used is the mammogram, for it is low cost and easy access. However, mammogram has a high error value for medical diagnosis, ranging from 10 to 25%, resulting in a great number of false-positives diagnostics, which causes unneeded biopsies, or false-negatives, which delays the cancer diagnosis. The medical diagnosis using mammography can be aided by image processing and computational vision algorithms, combined with artificial intelligence for features extraction. Those algorithms are able to decrease the error and make the mammograms more reliable [2].

The breast cancer is originated by an exaggerated and disordered cell multiplication, forming a lesion. This lesion is called malignant when its cells have the capacity to cause metastases, that is, invade other healthy cells around them. If those malignant cells reach the blood circulation, they could get into contact with other parts of the body, invading new cells and originate new tumors [3].

On the other hand, the benign lesions do not have this capacity. Their growth is slower, until a maximum fixed size, and they cannot spread to other organs. These kind of lesion is common in the breasts [4].

The mammography of benign tumors are well-defined, circular, with homogeneous texture. The malignant tumors, however, have speculated shape, frequently asymmetric, and less homogeneous than the benign lesions [5].

There are yet structures that can lead to medical misdiagnosis, as calcifications that arise as circular white spots [6].

CAD (Computer-Aided Diagnosis) systems can aid radiologists by providing a second opinion and may be used in the first stage of examination. For this to occur, it is important to develop many techniques to detect and recognize suspicious lesions and also to analyze and discriminate them. Some methods of lesion diagnosis in mammograms images have been reported. In [7], a system based in density-weighted contrast enhancement (*DWCE*) was used, obtaining 82.33% of success. In [8] mammograms are classified by support vector machines (SVM). The system sensibility was 84%. Christoyianni *et al* [9] compared three methods: Gray level histogram moments (GLHM), Spacial Gray Level Dependence Matrix (SGLD) and Independent Component Analysis (ICA). Accordingly to the authors, ICA had a better performance, with 88% of successful discrimination between normal and abnormal lesions, and 79.31% between benign and malignant lesions.

The proposed method is based on feature extraction by Independent Component Analysis. This technique is applied to many situations, as signal processing in cocktail-party environments [10], and pattern recognition in ECG and MEG [11], [12], [13].

Into this work, an image is taken as a linear combination of basis images, mutually statically independents, found using ICA. Such an basis image are extracted through the FastICA algorithm, from a preselected set of region of interest (ROI) of benign, malignant or normal tissues.

The objective of this work is to classify a ROI as normal, benign or malignant from the coefficients (features) extracted using ICA. Then, those features are used as input parameters to a Neural Network do the classification.

We divide this work as follows. Into section 2 we show the techniques for feature extraction and classification of ROI. In Section 3 we present the results and discuss about the application of the techniques under study. Finally, Section 4 presents some concluding remarks.

2 Methods

The block diagram of the proposed method is shown in figure 1. It consists of the selection of ROIs, the extraction of features using ICA, reduction of insignificants features using the *forward-selection* technica and the classification of the ROIs through neural networks.

2.1 Independent Component Analysis

Let us assume that an image is the sum of basis images $s_1, \dots, s_n$, mutually statistically independent. The image is then composed by the combination of n basis images, where we have n coefficients $a_1 \dots a_n$ [9], [14], such that

$$x_i = a_{i1} \cdot s_1 + a_{i2} \cdot s_2 + \dots + a_{in} \cdot s_n \quad \forall_i = 1, \dots, n \quad (1)$$

Fig. 1. Block diagram of the proposed method

$$\text{ROI} = a_{i1} * \text{Basis}_1 + a_{i2} * \text{Basis}_2 + \dots + a_{iN} * \text{Basis}_N$$

Fig. 2. Region of interest as a linear combination of its basis image mutually statistically independent

In equation 1, only the variables x_i are known, and from them we estimate the coefficients a_{ij} and the independent components s_j , that is:

$$X = A.S \quad (2)$$

Where X is an mixture matrix, the columns of A are the basis functions and S are the basis images.

2.1.1 FastICA Algorithm

The FastICA algorithm is used to solve the blind source separation (BSS) problem, where we want to estimate the basis images and the basis functions of the image X . This algorithm is based on fixed-point iteration [15], [16], [17]. In [15], a fixed-point algorithm was introduced using kurtosis, and in [16]-[17], the FastICA algorithm was generalized for general contrast functions [16]. For sphered data, the one-unit FastICA algorithm has the following form:

$$w(k) = E\{x.g(w(k-1)^T.x)\} - E\{g'(w(k-1)^T.x)\}w(k-1) \quad (3)$$

Where the weight vector w is also normalized to unit norm after every iteration, and

$$w^{-1} = A \quad (4)$$

The function g is the derivative of the function G used in the general contrast function in equation 5.

$$J_{G(y)} = \left| E_y\{G(y)\} - E_v\{G(v)\} \right|^p \quad (5)$$

Where ν is a standardized Gaussian random variable, y is assumed to be normalized to unit variance, and the exponent $p=1,2$ typically. The subscripts denote expectation with respect to y and ν .

The basic form of the FastICA algorithm is as follows [14]:

1. Choose an initial (e.g. random) weight vector $\mathbf{w}$.
2. Let $w^+ = E\{xg(w^T x)\} - E\{g'(w^T x)\}w$
3. Let $w = \frac{w^+}{\|w^+\|}$
4. If not converged, go back to 2.

The expectations are estimated, in practice, using sample averages over a sufficiently large sample of the input data. Units using this FastICA algorithm can then be combined, just as in the case of neural learning rules, into systems that estimate several independent components. Such systems may either estimate the independent component one-by-one using hierarchical decorrelation (deflation), or they may estimate all the independent components [16]-[17].

2.2 Neural Networks

In this work, we use a Multilayer Perceptron Neural Network (MLP), Probabilistic Neural Network (PNN) and Radial Basis Functions Neural Network (RBFNN) to classify malignant, benign and normal tissues.

2.2.1 Multilayer Perceptron Neural Networks

The Multilayer Perceptron (MLP), a feed-forward back-propagation network, is the most frequently used neural network technique in pattern recognition [18], [19].

Speaking, MLPs are supervised learning classifiers that consist of an input layer, an output layer, and one or more hidden layers that extract useful information during learning and assign modifiable weighting coefficients to components of the input layers. In the first (forward) pass, weights assigned to the input units and the nodes in the hidden layers and between the nodes in the hidden layer and the output, determine the output. The output is compared with the target output. An error signal is then back propagated and the connection weights are adjusted correspondingly. During training, MLPs construct a multidimensional space, defined by the activation of the hidden nodes, so that the three classes (malignant, benign and normal tissue) are as separable as possible. The separating surface adapts to the data.

2.2.2 Probabilistic Neural Network

The probabilistic neural network (PNN) is a direct continuation of the work on Bayes classifiers. The PNN learns to approximate the *pdf* of the training examples [19].

More precisely, the PNN is interpreted as a function which approximates the probability density of the underlying example

The PNN consists of nodes allocated in three layers after the inputs:

- *pattern layer*: there is one pattern node for each training example. Each pattern node forms a product of the weight vector and the given example for classification,

where the weights entering a node are from a particular example. After that, the product is passed through the activation function:

$$\exp[(\mathbf{x}^T \mathbf{w}_{ki} - 1) / \sigma^2] \quad (6)$$

Where

- $\mathbf{x}$: Data input
- $\mathbf{W}_k$: Weight
- σ : Smothing adjust

- *summation layer*: each summation node receives the outputs from pattern nodes associated with a given class:

$$\sum_{i=1}^{N_k} \exp[(\mathbf{x}^T \mathbf{w}_{ki} - 1) / \sigma^2] \quad (7)$$

- *output layer*: the output nodes are binary neurons that produce the classification decision

$$\sum_{i=1}^{N_k} \exp[(\mathbf{x}^T \mathbf{w}_{ki} - 1) / \sigma^2] > \sum_{i=1}^{N_j} \exp[(\mathbf{x}^T \mathbf{w}_{kj} - 1) / \sigma^2] \quad (8)$$

2.2.3 Radial Basis Functions Neural Networks

Successful implementation of the Radial Basis Functions Neural Network (RBFNN) can be achieved using efficient supervised or unsupervised learning algorithms for an accurate estimation of the hidden layer [20]-[21].

In our implementation, the k-means unsupervised algorithm was used to estimate the hidden layer weights from a set of training data containing the features from malignant, benign and normal tissue. After the initial training and the estimation of the hidden layer weights, the weights in the output layer are computed using Wiener-filter, for example, by minimizing the mean square error (MSE) between the actual and the desired output over the set of samples.

The RBFNN have a faster learning rate and have been proved to provide excellent discrimination in many applications.

2.3 Selection of Most Significant Features

Our main objective is to identify the effectiveness of a feature or a combination of features when applied to a neural network. Thus, the choice of features to be extracted is important.

Forward selection is a method to find the "best" combination of features (variables) by starting with a single feature, and increasing the number of used features, step by step [22]. In this approach, one adds features to the model one at a time. At each step, each feature that is not already in the model is tested for inclusion in the model. The most significant of these feature is added to the model, so long as P-value is below some pre-selected level.

2.4 Evaluation of the Classification Method

Sensitivity and specificity are the most widely used statistics to describe a diagnostic test. Sensitivity is the proportion of true positives that are correctly identified by the test and is defined by $S = TP/(TP+FN)$. Specificity is the proportion of true negatives that are correctly identified by the test and is defined by $TN/(TN+FP)$. Where **FN** is false-negative, **FP** is false-positive, **TN** is true negative and **TP** is true positive diagnosis.

3 Experimental Results and Discussions

Here are describe the results obtained using the method proposed in the previous section.

3.1 Mammogram Database

The database used into this work is the *Mammographic Institute Society Analysis* (MIAS) [23]. The mammograms have a size of 1024 x 1024 pixels, and resolution of 200 micron. This database is composed of 332 mammograms of right and left breast, from 161 patients, where 53 were diagnosed as being malignant, 69 benign and 206 normal. The abnormalities are classified by the kind of found abnormality (calcification, circumscribed masses, architectural distortions asymmetries, and other ill-defined masses) .

This database contains a file lists the mammograms in the MIAS database and provides appropriate details, for example, the class of abnormality, xy image-coordinates of centre of abnormality, and approximate radius (in pixels) of a circle enclosing the abnormality.

From this database, we selected 100 abnormal (50 benign and 50 malignant mammograms) and 100 normal from each group, summing up 200 mammograms. To each mammogram, a ROI was manually selected, containing the lesion, in the case of the benign and malignant mammograms. The ROIs was found through of xy images coordinates of centre of abnormality, contained in file list of MIAS database . To the normal mammograms, was randomly selected the ROI. Only the pectoral muscle was not considered as a possible ROI, although tissue and fatty tissue were. If the tissues had different sizes, it was rescaled each ROI. Therefore, they were resized to 24x24 *pixels*. Figure 3 exemplifies the ROI selection of a mammogram diagnosed as benign, malignant and normal, respectively.

3.2 ICA Application

X of Equation 2 was represented using the chosen ROIs. The images with ROI were rescaled and transformed into a one-dimensional vector

$$P = P_x \times P_y \quad (9)$$

where P_x is a rows and P_y is a columns of P and P has dimension 1x 576.

Fig. 3. Chosen region of interest (ROI) of mammograms diagnosed as benign (a), malignant (b) and normal (c)

Each sample represents one row of the mixture matrix. The matrix $\mathbf{X}$ is represented by the samples into the dimension of $\mathbf{P}$, that is, 1×576 . Thus, each row of the matrix $\mathbf{A}$ correspond to a ROI, and each column correspond to an attributed weight to a base image, i.e., an input parameter to the neural network [9].

Using the FastICA algorithm and the matrix $\mathbf{X}$, we obtain the basis function matrix $\mathbf{A}$, which contains the features of each sample.

Figure 4 exemplifies the basis image found using the basis functions of the malignants, benigns and normal ROIs, respectively. We can clearly observe the differences between the basis images of each kind. Thus, the basis functions of the benign tissue are different of those of the malignant tissue.

Fig. 4. Basis image sample produced from the ROIs basis functions for normal, benign and malignant tissue

3.3 Neural Networks

Using the *forward-selection* algorithm, basis functions were selected as being the most significant features. The chosen features (a_i) are the input to the Neural Network. For each Neural Networks (MLP, PNN, RBFNN) the algorithm selected the most significant features.

We carried out tests with different Neural Network architutures to find the bests MLP, PNN and RBF Neural Networks.

In order to carry out the tests, we divided a sample in 200 ROIs: 100 for training and 100 for tests.

3.4 Results

Table 1 shows the Neural Networks architecture, the performance of the application of the ICA technique with each Neural Network for discrimination tissues (ROI).

Table 1. Neural Networks architecture and classification of malignant, benign and normal ROI

N.Networks	Arquiteture	TP	TN	FP	FN	(%)		
						Specificity	Sensitivity	Accuracy
PNN	50:76-3:1	96	$\frac{10}{0}$	0	4	100	96	97.3
RBF	44:15-3:1	93	98	2	7	98	93	94.6
MLP	44:21:3	90	98	2	9	98	90.91	92.6

Based on the Table 1, the best results was obtained with Probabilistic Neural Networks. The PNN obtained a success rate of 97.3 % on discriminating malignant, benign and normal tissues. The found specificity was 100 % and the sensitivity, 96%. The PNN obtained 96 true positives diagnosis, 100 true negatives, 0 false positives and 4 false negatives.

4 Conclusion

The presented results demonstrate that Independent Component Analysis and Neural Networks is a useful tool to discriminate malignant, benign and normal tissues.

Furthermore, the Probabilistic Neural Network obtained the best performance, classifying those tissues, with a success rate of 97.3%, specificity of 100 % and sensitivity of 96%. It can decrease the number of unneeded biopsies and late cancer diagnosis.

Based on these results, we have observed that such features provide significant support to a more detailed clinical investigation, and the results were very encouraging when tissues were classified with ICA and Neural Networks.

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