Computer Aided Diagnosis for Breast Diseases Based on Infrared Images

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Abstract - **In this study, we propose a system to classify thermal images of the breast considering the presence or absence of disease not only tumor and cancer, as most of previous works did. The proposal, at present stage, separates a breast among presenting benign tumor, cancer or being normal and shows how new diagnostic can be included in the data base when a number of proved case of a disease is known. The methodology begins by pre-processing images to be free of those regions that are not of interest for the work before execution of an algorithm for textural features computation, then a set of characteristics is calculated and they are ranged by machine learning classifier, that identity the clinical condition of the patient's breasts. For this classification, a Support Vector Machine (SVM) was used and trained based on already classified diagnosis from two data bases. Tests performed present accuracy above 90%, showing that the proposal is very promising. The project is in the phase of final adjustments and critical use by the medical community for the diagnostic aid. In future work integrations with other examinations is the aim.**

Keywords – **Thermal Images; Textural Features; Breast Cancer; Computer Aided Diagnosis; Genetic Algorithm; Pattern Recognition; Machine Learning.**

I. INTRODUCTION

Cancer does serious damage to the human beings. It affects thousands of people around the world, from the most different age and ethnic groups, being in 2015 the 5th most frequent cause of dead [1]. It is a malignant disease and is characterized by uncontrolled growth of genetically altered cells. On breast cancer, the situation is not different [2]. It is the second most frequent type of cancer, and the most frequent among women [1]. It represents 25% of all cancers in the world, with approximately 1.7 million of new cases and 522,000 deaths; being the most frequent cause of female death [1]. In this context, the use of infrared (IR) or the named thermography appears as possibility of improvements of this scenery [5].

In thermography, the temperature acquired from each point of a body is represented as image in order to be viewed and analyzed [6]. IR is a functional examination that can identify changes in the thermal pattern of the breasts earlier than other medical exams, because most of them are anatomical or structural examinations and not physiological [6]. IR can detect cancer up to 10 years before it can be effectively noted by other approaches like ultrasound, magnetic resonance and x-rays (mammography) [4, 6, 7]. Moreover, unlike other exams, IRs do not emit ionizing radiation, it is not harmful to the patient and is completely non invasible.

This work presents the details of a developed methodology able to receive IR digital images and presents as outcome diagnosis. Moreover, the work intends to contribute to the scientific community through proposition of a methodology to characterize IR digital images of the breast. The steps of a system for breast diagnosis (as normal, benign tumor and cancer) are discussed [23]. In this, machine learning were used allowing the integration of algorithms to generate a product to be used on line. Two hospitals have contributed with examinations and their diagnosis for the approach design. They have projects approved in their ethics committee for this research, did the exams (free of charge for the patients) and asked for a signed consentiment of each person under examination [12].

II. LITERATURE REVISION

The IR is not yet considered as common examination in hospitals and clinics around the world [12]. There is not a complete methodology for classification this as the "Breast Imaging-Reporting and Data System" (BIRADS) used on other traditional breast examinations [8]. This standardization of terms contemplates a universal interpretation of the findings in the images by an uniform definition (using significant terms to the accompanying patient's physician), allowing to present relevant information for treatment in a more simplified way and, assuring consistency in the reporting of the examination. For IR the findings are divided into signs and analyzed based on details defined by at least four established nomenclatures for characterization of breast state. They are known as Marseille, Villa Marie, Hobins and Hoekstra systems [20].

There are a number of works on using pattern recognition techniques to aid in IR image diagnosis [8]. However, two works are much related to ours [9, 10]. Schaefer *et al.* [9] present a methodology for pattern classification and aid medical diagnosis through thermography. The images used were submitted to manual segmentation, because, according to these authors, the automatic segmentation methods developed did not present satisfactory results for the images used in the

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previous published work [9]. The database they have used has one hundred forty-six images; among these twenty-nine correspond to malignant cases and one hundred and seventeen present benign cases. Their methodology contemplates a total of thirty-eight characteristics extracted from images [9]. Such characteristics were generated through the computation of features with statistical bases (moments of histograms, co-occurrence matrix, mutual information and Fourier transform) and presented an accuracy of 79.53% [9].

Acharya *et al.* [10] present a methodology for breast cancer detection based on thermal images using texture characteristics and support vector and machine (SVM). They create an image database with fifty records. Half of these, twenty-five, are from patients diagnosed with breast cancer and the other half from patients diagnosed with normal breast. 72% of these images was used to create the training base (36 images, 18 normal). The remaining 14 images, also half of each class, were used to assemble the test base. These images were provided by Singapore General Hospital. In this work, sixteen texture features were used, however, according to the authors, only four of these are considered significant: the first and third geometric moment (or moment of area), the Run Length Percentage (RLP) and Grayscale Non-Uniformity (GNU). All characteristics are normalized. They reached an accuracy of 81.07% [10].

III. PROPOSED METHODOLOGY

The developed methodology has the objective to aid in diagnosis on real time. They are composed of two stages: the learning stage and the examination stage. In the first stage we used images with proved diagnosis for Knowledge Discover from Database (KDD). Then this knowledge can be used for similar images with unknown diagnosis that when submitted to the same analyses and having similar features have their diagnostic provided by the KDD process. Both parts of the process present an image preparation and then their transformation in features. Such features are used by the KDD techniques also for the learning stage using known results or after using the knowledge to suggest the diagnosis. We name "datasets" both: the step of construction of "the rules", as well as the step of use "these rules" to images with unknown classification. This denomination allows us to describe our methodology in the same manner to construct the system and to use the system, turning easy a continuous improvement of the system with the existence of new diagnosis, as well as the inclusion of new class for the diagnosis when the number of proved cases of some disease is enough for it.

Figure 1. Work flow of proposed methodology.

Figure 1 shows in four steps the proposed and used system. Although this ensemble of learning and use of the knowledge can seem very strange at first view, it makes possible the current system classification in normal, cancer and tumor (that became from a former one where it is possible to classify only normal breast and cancer, to a second version where there are normal, tumor and cancer, and maybe to future when type of cancer and other breast problems like cysts can be considered).

In the methodology, first, the images are pre-processed where the Regions of Interest (ROI) are delimited by the segmentation. Once segmented, the images are processed for feature extraction creating a feature vector for each one. After that, what is used for the rest of the analysis is no more the image but its feature vector. So, each examination of a patient is transformed to this vector, which can be used in the same manner to improve the system, when there is proved diagnosis (for a disease), or to suggest one in case it does not happen. Images with proved diagnosis are used to compose a database that will be used for KDD. When the diagnosis is known it is used for training of classifiers that after testing and validation will be used to identify diseases of new images of the same type. These four steps are better described in the following subsections.

A. *Pre Processsing*

At this stage, the data used are pre-processed to eliminate regions that are not of interest to the study, such as annotations, arms, neck, head and abdomen. A preliminary step uses a tool from the IR camera (FLIR T640) to transform the temperatures in grey scale image [11]. Then it is segmented to achieve the region of interest (ROIs) using a manual segmentation performed by a specialist. To segmentation we considered the same points pointed by [12, 14] (Figure 2: lower, lateral and superior limits of the breast) and improves the output asking for a manual definition of such limits.

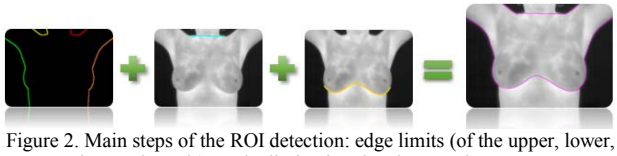

Figure 2. Main steps of the ROI detection: edge limits (of the upper, lower, and upper bounds), neck elimination, low breast edges [12, 14]

B. *Extraction Features*

After segmented, the images are processed to the feature extraction algorithm. In other words: their visual properties will be replaced by a vector of number representing them. This can be done through several ways: but adequate definition of the characteristic used is fundamental for a good representation of the images in process [2, 5, 7-10, 15-17, 23]. This turns possible a definition of a correspondence among each element of the used "datasets" and its images. In other word: it establishes a bijection or a one-to-one correspondence between them [18]. A feature in this context will be the values calculated from each image, according to a certain type of features and the dimension or number of elements of this array. The set of characteristics of an image, or instance of the dataset, will be used to determine patterns for each class that, when analysed in the next step (i.e. the KDD), allow to define or find a label related to clinical state of the patient's breasts.

Haralick *et al* [15] use features mainly based on the Gray Level Co-occurrence Matrix (GLCM). The GLCM matrix can be understood as an array of probabilities, where, for every

two values of gray intensity (two pixels on analysis), the probabilities of being involved by a particular spatial relation are stored (Fig. 3). Using the GLCM a bijection is obtained between image to the probability of occurrence of the intensities of the tones *i* and *j* in two pixels of such an image [17]. Moreover, in order to establish a representation of the image by a vector of numbers, a set of 14 values calculated from the co-occurrence matrix is used [15]. These values are called the descriptors of the GLCM according to an aspect of interest [16, 19] and form a 14-dimensional array representing the image. This promotes a reduction of space from N x N to a 14 x 1 for each image to be processed and stored in a database and for used in KDD. Of course, the usage of good features are of greater relevance. This work considers some statistical features from those computed in [23].

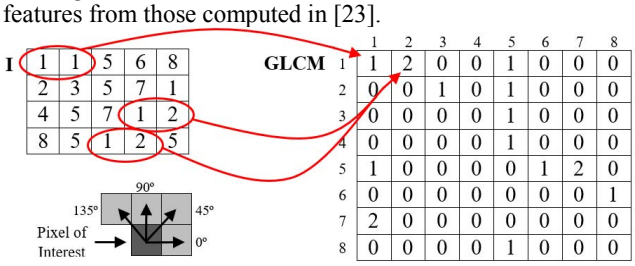

Figure 3. Example of how from a small images of 4x5 pixel (left) to obtain the GLCM (right) considering one pixel and its horizontal neighbor.

We used 48 features for each patient, 24 for each breast. They came from the 6 more-important features computed from the GLCM acquired in 4 directions considering one pixel and its neighbor. These features have been used to compose a vector or array to represent an exam in the rest of the computations. With these features, datasets are created representing the breasts (see Figure 1) of the patients. The elements of these dataset are normalized between the 0 and 1 in order to avoid that feature with high values overlap those with smaller values, impairing learning. Such a dataset is used for diagnosis when the state of the breast is unknown, when the breast state is known it is used in KDD learning process to acquire knowledge, as described in next section.

C. *Acquisition of Knowledge from Proved Cases*

This work uses a supervised method of machine learning to acquire rules for classification from the dataset. We use the called Support Vector Machines (SVM), our implementation is based on the LibSVM version [21] of this. We choose SVM because empirically it shows good outcomes and it is parameterizable. Decision based in an SVM considers the construction of one or more hyperplanes in an n-dimensional space of the feature vectors to separate the classes represented by them. The dimension of this space is related to the number of features used in the vectors. It is expected that in these hyperplanes a more efficient separation of classes is achieved. This construction finds for possible hyperplanes that maximize the margins between group of data [23] corresponding to the class of elements of the dataset. The LibSVM presents four different kernels, defined as Linear, Sigmoidal, Radial e Polynomial. Their differences are in how the data separation plans are outlined in hyper plane's space. We have used a kernel based on a Radial function. This kind of kernel can generate circular and semicircular cutting planes.

D. *Validation of the Acquired Knowledge*

The process of KDD must be validated by some metric in order to see its degree of confidence and to compare with other works, as well. For this a number of approaches can be used as the holdout, cross validation and leave-one-out.

The holdout approach divides the dataset in disjoints sub sets. One of them is used for training and the other for testing. Usually this is division used the relations 70-30% or 66-34% for acquire knowledge and training, respectively [26].

The cross validation also divides the dataset in disjoints subsets. One of them is used for training and the other for testing, as in the holdout approach, but now it is repeated a number of times. The degree of success of an approach is computed from the average of all these results in the technique performed [26].

The leave-one-out is a special case of the cross validation where the training set presents N-1 elements and the testing set is the subset not yet used for training. The approach is repeated N times until all subsets are tested, because in each time a different subset is selected for test [26].

We used a combination of techniques. For the dataset from database 1, with 164 elements a stratified cross validation technique with 4-fold is used, because this strategy is the most indicated to datasets with more samples in a class than in others. For the dataset from database 2, with 80 elements equally distributed in each class: a holdout technique with 70% of dataset in training step end 30% of dataset in test, is used, this strategy is more indicate to balanced datasets (same number of cases in each subclass).

To measure the efficiency of the KDD, we must consider the number of correct evaluated cases with correct diagnosis (in comparison of a ground true of proved cases), this is named True Positive (TP) and True Negative (TN) cases. In case of wrong evaluated cases they are named: False Negative (FN) and False Positive (FP). These numbers will compose the confusion matrix showed in Table I. Where, TP is the case positive correctly classified as positive, TN is the number of cases negative correctly classified as negative, FP is the case of negative for some disease classified as positive, and FN is cases positive (with disease) but classified as negative, i.e. wrong or false classification.

TABLE I. CONFUSION MATRIX

		Real Positive	Real Negative
Predicted	Positive	TP	FP
	Negative	FN	TN

By comparing 2 possibilities, that is from tables like Table I, it is possible to compute some number to compare approaches.

If a curve is constructed using the rate of TP (TPR) and the FP rates (FPR), it represents the Receiver Operating Characteristics (ROC) and the performance of the classifier can be measured. A TPR shows the number of correct results. Otherwise, FPR evaluates the rate of incorrect results in a test:

$$TPR = TP / (TP + FP), FPR = FP / (FP + TN)$$

An important analysis from this curve is the computation of the area under the curve ROC (AUC), also known as a-prime. In this aspect, bigger area represents better performance of the classifier. The AUC joints these 2 values (TPR and FPR) in one. Moreover, AUC (as well as the ROC curve) considers the correct evaluation of the classifier and the misevaluations. So, the AUC represents more properly the performance of an approach for unbalanced datasets.

E. Feature Selection

The purpose of attribute selection is to find the smallest set that can result in satisfactory prediction performance. It is often necessary and recommended to limit the amount of input attributes for having good predictive model. In addition, performance can be improved using a small subset of attributes from the entire base [27]. The literature exposes several proposed heuristic measures to estimate the relative importance or contribution of input attributes to the output of the system [25]. Attribute selection algorithms are designed to learn which attributes are most appropriate for making decisions. More attributes should, in theory, result in a greater discriminating power. In practice, adding irrelevant attributes often confuses the machine learning system [26].

A solution is to select features by unvaried feature selection that works by selecting a percentile of the best features based on statistical tests of single variable that can be false positive rate or false discovery rate. This technique is called Percentile (PERC). Another technique is to implement a Genetic Algorithm (GA) to perform the feature selection. We used both: PERC and GA. A GA is a kind of evolutionary algorithm that generates solution to search for optimizing on biological inspired concepts natural evolution. Basically is composed by 3 parts: objective function (evaluation), selection method and reproduction (crossover). Figure 4 shows these parts with intermediate steps.

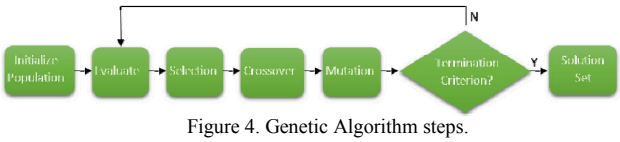

Figure 4. Genetic Algorithm steps.

We have implemented GA based on Figure 4. First, the Initial Population is defined, in the "Initialize Population" step, where at random 140 elements or genes are created. Each gene consists of 48 attributes and each attribute has an on/off flag. When a flag for a particular attribute is off, this attribute is not used for classification. Each gene the population is different because the attributes on/off can be different.

In the "Evaluate" step in Figure 4, the average AUC is used to evaluate the performance of the population. 10 preconfigured classifiers based on tests are used in this one. Each classifier performs the classification of two classes at a time because the SVM is best indicated to be executed in this way. There are strategies for using SVM with multi-classes, but this will be better explored in future. At the end, for each classifier there is a population of 140 individuals and everyone has its performance computed considering the AUC for it.

The "Selection" step in Figure 4 is performed after the "Evaluate", in this the new population is composed of the survivors in an elitist strategy, where it is selected the 20 best organisms of the generation. The best individuals should remain in the population as they tend to continue improving and contributing to the adaptation to a high-performance gene (fewer attributes and higher AUC value).

"Crossover" step is shown in Figure 4 where the reproduction is performed by sexual strategy that 2 individuals generate 2 new individuals. 40 new organisms are generated, 20 being by an *elitist* strategy (20 best crossing each other) and 20 other organisms coming from the top 10 crosses with the 10 worst individuals in the population. Use of worst individuals can insert some noise on search that avoids local minimum. There is only one randomly selected crossover point that defines the size of each part of the genetic material of each parent. 74 individuals are randomly generated.

In case of such a performance does not improve the next generation (repeat the same AUC result for 5 consecutive times for the best individual) a disturbance is inserted in the generation of the population, in which only the best individual survives and all the rest are generated randomly.

In the "Mutation" step, 6 mutations are performed, 2 mutations in the elite (10 better); 2 mutations among the 10 worst; 2 mutations among the rest of the population. For each mutations, how many genes will be mutated and which genes will undergo mutation are chosen randomly. Since the individual is composed of active and inactive genes, the mutation process only reverses the gene's state.

In the end of the process, the "Termination Criterion" step in Figure 4, the AG stops after 100 generations. Then, the set of attributes with better performance, measured according to AUC is used. Even though the AUC is used as a performance measure, the other measures presented in section *D* are also calculated for a more complete analysis of the experiments.

F. Configurations of the Experiments Performed

The two used databases were assembled in the dataset as already mentioned and represented by their features. The two datasets were kept separate during all the analysis to see if the type of camera and resolutions present any influence. The strategy of joining their features is elementary and can be easily used. The used images are segmented with and without axillar regions, to verify the influence of linfonods (that can be present in such a region) has in disease identification. The database 1 has 164 images. From database 2, 80 images, 40 with cancer and 40 normal, was used. Table II shows them.

TABLE II. DATABASE COMPOSITION

Database	Normal	Benign	Cancer	All
Database 1	60	66	38	164
Database 2	40	-	40	80

IV. DISCUSION ABOUT THE PERFORMED TESTES

Table III presents our results on percentage of accuracies (ACC) using database 1 and those from other authors. The 2 types of segmentations (i.e. inclusion of axillar area or not in the ROI) do not show considerable differences in this case of comparing normal versus cancer diagnosis, and need more tests in order to promote a more conclusive statement. We

used in this table the denomination of the authors under comparison. Comparing the results obtained by Scheafer *et al.* [9] (cancer *x* normal) and Acharya *et al.* [10] (cancer *x* no cancer) with the results obtained in our approach using the set of features from database 1, we can state that the application of the methodology here proposed presents significantly better accuracy than those from such works [9,10]. To compare our work to the methodologies proposed in [9, 10] we reimplemented the literature proposals and applied the two datasets used in this work because we did not get the datasets described in [9,10].

TABLE III. COMPARISON OF OUR METHOD WITH [9,10].

Methodologies	**ACC (%)**
Database 1 - with axilla	91.77
Database 1 - without axilla	92.60
Database 2 - with and without axilla	**94.87**
Schaefer *et al*. [9]	79.53
Acharya *et al*. [10]	81.07

We also evaluated the performance of the classification comparing the diagnosis. In this case, three combinations of diagnostic pairs were created (Normal, Benign and Cancer) and the results can be seen in Table IV. This evaluation can not be compared to the other authors because only tests between Normal x Cancer diagnoses were pointed out in their studies. The results show the ROI with axilla presents slightly better values than ROI without axilla. For instance, on Benign x Cancer the outcome is 91.86% against 82.94% to segmentation without and with axilla, respectively. We can say that this way is better trained for the discrimination between normal and cancer because shows high accuracy values (ACC) and area under the curve (AUC): 86.74% and 82.94% respectively for images from segmentation with axilla and 86.34% and 91.86% respectively for segmented images without axilla. Images with a benign tumor were not used in the analysis of the database 2 because the database does not have a significant number of proved diagnostic for this type of breast problem.

TABLE IV. ANALYSIS BETWEEN NORMAL, BENIGN TUMOR AND CANCER.

ROI type	**Type Analysis**	**ACC (%)**	**AUC (%)**
With axilla	Normal x Benign (NxB)	86.74	87.30
	Benign *x* Cancer (BxC)	82.94	81.86
	Normal x Cancer (NxC)	91.77	91.14
Without axilla	Normal x Benign (NxB)	86.34	86.90
	Benign x Cancer (BxC)	91.86	91.17
	Normal x Cancer (NxC)	92.60	92.70

Probably the results from database 2 are better because the number of cases from each group in this base is balanced, the Database 1 (although larger) is very unbalanced presenting much more normal and benign than cancer diagnosis in their images. The outcomes presented are obtained after feature selection. Table V shows results with and without feature selection step showing the improvement achieved with the genetic selection, where the GA presents better results always.

TABLE V. OUTCOMES: NO FEATURE SELECTION, PERCENTILE AND GENETIC ALGORITHM.

AUC %		No selection	PERC	GA
With Axilla	N x B	75.79	65.83	87.30
	N x C	80.20	75.00	91.14
	B x C	74.01	59.37	81.86
Without Axilla	N x B	70.63	79.16	86.90
	N x C	80.72	90.62	92.70
	B x C	74.19	60.41	91.17

Table VI shows outcomes of feature selection with images from database 2. The results from GA are always better than others strategies.

TABLE VI. OUTCOMES OF FEATURE SELECTION FROM DATABASE 2

AUC %	No selection	PERC.	GA
With axilla N x C	80.12	81.94	94.87
Without axilla N x C	83.97	66.66	94.87

At this stage of the work, variables related to the computational complexity of the developed algorithms were not considered and their times were not measured.

V. FINAL DISCUSSION AND CONCLUSIONS

The use of features based on the gray levels co-occurrence matrix allows to present relevant and competitive results in comparison to other works present in the literature. The features used to compose the presented method are bases on two databases that could be used in the classification.

The SVM classifier proved to be effective when applied in this context obtaining good results on the aid of medical diagnosis of the breasts. The results show that the methodology proposed in this work is not conditioned to only one style of capture or to images captured by a single camera model, since the work used images from two hospitals with different acquisition protocols and camera models. Also, based on these results, it is possible to prove the feasibility of the use of statistical measures as descriptors of thermal images of the breast.

The best results reached are 94.87% of accuracy and were obtained from the analysis between patients whose breasts were diagnosed with cancer or normal from the set of images of the database 2. Using the set of database 1, the best result of accuracy between normal and cancer was 92.70%. It was 86.90% and 91.17% in the analysis between normal and benign; and benign and malignant, respectively for images segmented without axilla.

The algorithms developed in this work could be integrated into a computational tool that assists the doctor in obtaining breast diagnoses. Although it is a relatively low-cost examination, thermography is still not used because it is a relatively new examination and because of the lack of computational tools that aid in the analysis of the images.

From the diagnosis obtained in the thermography the doctor may suggest, if necessary, more examinations that show structures inside the breast. It is hoped that the results of this research can contribute to this reality and new clinics will begin to adhere to thermography as an examination to aid in the detection of breast cancer.

Finally, this type of system using IR imaging identifies whether there is thermal change in the region under study and or there is a possible benign or malignant tumor (cancer). In future we intend to get feedback from experts to validate the implemented system. As system usability evaluation tool, we will apply the System Usability Scale (SUS) [22]. SUS is a ten-item scale that gives a view of subjective assessments of system usability resulting in a score from 0 to 100. An acceptable result is above 70 [22]. Such a feedback will allow continuous improvements. Besides, we intend to analyze the feedback of physicians, including their opinion related to diagnosis support provided. We intend to perform system validation in clinical setting and getting feedback from physicians concerning the quality of the developed software. Therefore, we wish to implement adjustments based on such feedbacks promoting continuous improvements and a development centered in users of the system.

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