

# Detection of Masses in Digital Mammograms using K-means and Support Vector Machine

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## Abstract

Breast cancer is a serious public health problem in several countries. Computer Aided Detection/Diagnosis systems (CAD/CADx) have been used with relative success aiding health care professionals. The goal of such systems is contribute on the specialist task aiding in the detection of different types of cancer at an early stage. This work presents a methodology for masses detection on digitized mammograms using the K-means algorithm for image segmentation and co-occurrence matrix to describe the texture of segmented structures. Classification of these structures is accomplished through Support Vector Machines, which separate them in two groups, using shape and texture descriptors: masses and non-masses. The methodology obtained 85% of accuracy.

*Key Words:* Mammogram, Computer-Aided Detection, Co-occurrence matrix, K-means, Support Vector Machine.

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## 1 Introduction

Breast cancer is the major cause of cancer-related deaths among the female population. It is well known that the best prevention method is the precocious diagnosis, what lessens the mortality and enhance the treatment [1]. According to the American National Cancer Institute [2], it is estimated that every three minutes, a woman is diagnosed with breast cancer, and every 13 minutes, a woman dies from this disease. It is also estimated that one in eight women will be diagnosed with breast cancer in her lifetime, and 1 in 30 will die from it. Mammography is currently the best technique for reliable detection of early, non-palpable, potentially curable breast cancer [1]. The mortality rate from this disease decreased for the first time in 1995, due in part to the increasing utilization of screening mammography [1]. However, radiologists vary in their interpretation of mammograms. In addition, the interpretation is a repetitive task that requires much attention to minimal details.

With the advances of computer technology, radiologists have an opportunity to improve their image interpretation using computer capabilities that can enhance the image quality of mammograms. Over the past two decades, many attempts have been made by computer scientists to assist the radiologists in detection and

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diagnosis of masses by developing computer-aided tools for mammography interpretation. Image processing and intelligent systems are two mainstreams of computer technologies that have been constantly explored in the development of computer-aided mammography systems.

The main difficulty regarding digital mammogram diagnosis is the detection of suspicious regions. To address this problem, several image-processing techniques have been developed. The principal difficulty in this task is the lack of a general algorithm that produces good results for all images. We can highlight two classes of regions in a digital mammogram, naming them mass and non-mass areas. The mass areas are associated to every region on a mammogram that corresponds to a benign or malignant neoplasy. All regions not associated to a neoplasy are labeled non-mass; i.e., all the normal tissue present on the mammogram is non-mass.

In this paper we intend to investigate the efficacy of a detection methodology that uses textural and shape measures as input features for the K-means clustering algorithm, and a Support Vector Machine, aiming to detecting masses in mammogram images. This work is organized as follows. In Section 2 we present some related works about detection of masses in mammogram images. In Section 3, the techniques for feature extraction, clusterization and classification are presented. Next, in Section 4, the results are shown and the application of the techniques under study are discussed. Finally, Section 5 presents some concluding remarks.

## 2 Related Works

Several works have been formulated aiming to develop computer aided breast cancer detection and diagnosis tools. Tang et al [3] present an overview of recent advances in the development of such tools and related techniques.

Kom et al [4] proposed an algorithm for detection of suspicious masses in mammographic images that exhibits a sensitivity of 95.91% for mass detection, with ROC area of 0.946 when the enhancement of the original image was performed before detection and 0.938 otherwise.

Eltonsy et al [5] showed a technique for the automated detection of malignant masses in screening mammography. The technique is based on the presence of concentric layers surrounding a focal area with suspicious morphological characteristics and low relative incidence in the breast region. Malignant masses were detected with 92%, 88%, and 81% sensitivity of 5.4, 2.4, and 0.6 false positive per image. Rojas et al [6] explores the use of characterization features based on breast-mass contours that are obtained by automated segmentation. The method presented low sensitivity and high specificity values (e.g. 0.6 and 0.8, respectively) since the positive class in the classification experiments is the set of malignant masses.

Belloti et al [7] presented an automatic computational tool for mass detection. The authors used an edge-based segmentation algorithm in order to separate suspicious regions. Second order measures obtained from co-occurrence matrices were used to describe the texture of each region. Finally, artificial neural networks were used in the classification step. The results showed a sensitivity of 80% and 4.23 false positives per image. Chan et.al [8] proposes a CAD system based in tridimensional mammograms obtained from a tomosynthesis process. The area under the ROC curve was 0.91, with standard deviation of 0.03. The CAD tool obtained a sensitivity of 85%, with 1.32 false positives per image.

Martins et al [9] presented a mass detection method that use Growing Neural Gas algorithm to perform the segmentation step. For each segmented region, shape measures are computed in order to discard bad mass candidates and texture measures are obtained from Ripley's K function. The classification step is performed using a SVM classifier. The method provides an accuracy rate of 89.30%. Campanini et al [10] presented an approach for detection of masses in digital mammograms that reaches a sensitivity around 80%, with a false-positive rate of 1.1 marks per image. The work used images coming from the DDSM database.

Also, in Martins et al [11], rates of about 86.85% are reached to classify regions of mammograms into benign, malignant and normal using a Bayesian Neural Network. A Support Vector Machine together with Independent Component Analysis was used in [12] to classify mammogram tissues, reaching 99.6% of accuracy. Braz et al [13] reaches an accuracy of 98.36% employing geostatistical functions and SVM.

In [14], the authors proposed a method for discrimination and classification of mammograms with benign, malignant and normal tissues using independent component analysis and multilayer neural networks. The best performance was obtained with probabilistic neural networks, resulting in a success rate of 97.3%, 100% of specificity and 96% of sensitivity.

We may observe that there is a need for methodologies that provide support to automatic detection of lesions in mammogram images with little or no specialist participation. Such objective is a great challenge for the segmentation methods, because this is a problem that strongly depends on the characteristics of objects.

### 3 Material and Methods

The methodology proposed in this work intends to classify breast tissues on mammograms into mass and non-mass groups. This methodology is based on three steps: Images Database formation; structures segmentation using K-means and texture descriptors; structures classification using texture and shape descriptors submitted to the Support Vector Machine classifier.

The first step is the construction of the image database, which is done by obtaining mammograms from a public available database. After this, we perform a clustering step using characteristics based on co-occurrence matrix to describe the texture of the mammography tiles and the K-means algorithm to cluster the tiles representing breast structures in the mammography, like fat regions, muscles, mass, calcifications, etc. In the last step, the extraction of texture characteristics from structures is done using co-occurrence matrix and shape descriptors and their classification as mass or non-mass through the Support Vector Machine classifier.

#### 3.1 Image Database

For the development and evaluation of the proposed methodology, we used the Digital Database for Screening Mammography (DDSM) [15] that is a publicly available database of digitized screen-film mammograms. It contains 2620 cases acquired from Massachusetts General Hospital, Wake Forest University, and Washington University in St. Louis School of Medicine. The data are comprised of studies of patients from different ethnic and racial backgrounds. The DDSM contains descriptions of breast lesions in terms of the American College of Radiology's breast imaging lexicon called the Breast Imaging Reporting and Data System (BI-RADS) [15]. Mammograms in the DDSM database were digitized by different scanners depending on the institutional source of the data.

A subset of the DDSM cases was selected for this study. Cases with mass lesions were selected through the reports that only included the BI-RADS descriptors for mass margin and mass shape. From 2620 cases, 433 images were selected based on these criteria.

#### 3.2 Texture Descriptors

Textures represent tonal variations in the spatial domain and determine the overall visual smoothness or coarseness of image features. They reveal important information about the structural arrangements of the objects in the image and their relationship to the environment. Consequently, texture analysis provides important discriminatory characteristics related to variability patterns of digital classifications.

Texture processing algorithms are usually divided into three major categories: structural, spectral and statistical [16]. Structural methods consider textures as repetitions of basic primitive patterns with a certain placement rule [17]. Spectral methods are based on the Fourier transform, analyzing the power spectrum [17]. The third and most important group in texture analysis is that of statistical methods, which are mainly based on statistical parameters such as the Spatial Gray Level Dependence Method (co-occurrence matrices), the Gray Level Difference Method, and Gray Level Run Length Matrices [18], [19].

In this work we use co-occurrence matrix, which displays the gray level spatial-dependency along different angular relationships, horizontal, vertical and two diagonal directions on an image, to calculate textural

measures. A co-occurrence matrix is specified by relative occurrence frequencies  $P(i, j, d, \Theta)$  of two pixels, separated by distance  $d$ , along the direction of angle  $\Theta$ , one with gray level  $i$  and the other with gray level  $j$ . A co-occurrence matrix is therefore a function of the distance  $d$ , the angle  $\Theta$  and gray levels. The co-occurrence matrix can be calculated for the whole image, but by calculating it in a small window which scans the image, the co-occurrence matrix can be associated with each pixel.

Based on [20] we may define non-normalized frequencies  $P_{i,j}$  of the co-occurrence matrices for a defined window  $M \times N$ , the distance  $d$  and angles of  $0^\circ$ ,  $45^\circ$ ,  $90^\circ$  and  $135^\circ$  by

$$P(i, j, d, 0^\circ) = \#\{((k, l), (m, n)) \in (M \times N) \times (M, N) : k - m = 0, |l - n| = d, I(k, l) = i, I(m, n) = j\} \quad (1)$$

$$P(i, j, d, 45^\circ) = \#\{((k, l), (m, n)) \in (M \times N) \times (M, N) : (k - m = d, l - n = -d) \text{ or } (k - m = -d, l - n = d), I(k, l) = i, I(m, n) = j\} \quad (2)$$

$$P(i, j, d, 90^\circ) = \#\{((k, l), (m, n)) \in (M \times N) \times (M, N) : |k - m| = d, l - n = 0, I(k, l) = i, I(m, n) = j\} \quad (3)$$

$$P(i, j, d, 135^\circ) = \#\{((k, l), (m, n)) \in (M \times N) \times (M, N) : (k - m = d, l - n = d) \text{ or } (k - m = -d, l - n = -d), I(k, l) = i, I(m, n) = j\} \quad (4)$$

where  $\#$  denotes the number of elements. It is observed that the co-occurrence matrix is symmetrical because  $P(i, j, d, \Theta) = P(j, i, d, \Theta)$ .

Based on the co-occurrence matrix, many different texture descriptors may be computed. To reduce the computational complexity, only some of these features were selected. The descriptions of the four most relevant descriptors that are widely used in literature [21] and also in this work are:

1. Contrast:

$$\sum_{i,j} |i - j|^k (P_{ij})^\lambda \quad (5)$$

2. Energy:

$$\sum_{i,j} P_{ij}^2 \quad (6)$$

3. Entropy:

$$\sum_{i,j} P_{ij} \log P_{ij} \quad (7)$$

4. Inverse Difference Moment:

$$\sum_{\substack{i,j \\ i \neq j}} \frac{(P_{ij})^\lambda}{|i - j|^k} \quad (8)$$

### 3.3 Shape Descriptors

The shape descriptors are used as additional information about the object. Shape descriptors must supply important information to discriminate mass and non-mass [22], because masses commonly have shapes similar to a circle.

In this work we propose the use of the following shape descriptors:

### 3.3.1 Eccentricity

The eccentricity defines how the object is spatially distributed along his axis. It is calculated using central moment functions as

$$\frac{(\mu_{02} - \mu_{20})^2 + 4\mu_{11}}{A} \quad (9)$$

where  $A$  is the object area, and the central moments  $\mu$  can be calculated by

$$\mu_{pq} = \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} (x - \bar{x})^p (y - \bar{y})^q \quad (10)$$

with  $p + q > 1$

### 3.3.2 Circularity

Circularity shows how circular a certain object is, being calculated by

$$\frac{4\pi A}{P^2} \quad (11)$$

where  $A$  is the area of the object and  $P$  the convex perimeter.

### 3.3.3 Convexity

Convexity is the relative difference between an object and a convex hull containing it. It is calculated starting from the ratio between the perimeter of the o convex hull of the object and the perimeter of the object. It is defined by

$$\frac{P_{ch}}{P_{img}} \quad (12)$$

where  $P_{ch}$  is the perimeter of the convex hull of the object, and  $P_{img}$  is the perimeter of the object.

## 3.4 K-means Algorithm

Clustering algorithms can be applied to solve the segmentation problem. They consist in choosing an initial pixel or region that belongs to one object of interest, followed by an interactive process of neighborhoods analysis, deciding if whether each neighboring pixel belongs or not to the same object. In this work we use the K-means to resolve the mass detection task on mammograms using texture information obtained from Haralick's descriptors. The K-means algorithm is one of the simplest non-supervised learning algorithms class that solves the clustering segmentation problem [23].

The method follows the usual steps to satisfy the primary objective: clustering all the image objects into  $K$  distinct groups. First,  $K$  centroids are defined, one for each group, being their initial position very important to the result. After that, it is determined a property region for each centroid, which groups a set of similar objects. The interactive stage of the algorithm is started, in which the centroid of each group is recalculated in order to minimize the objective function. This function, for K-means, is the minimum square method, calculated by

$$J = \sum_{j=1}^k \sum_{i=1}^n \|x_i^{(j)} - c_j\|^2 \quad (13)$$

where  $\|x_i^{(j)} - c_j\|^2$  is the distance metric from any point  $x_i^{(j)}$  to the group centroid  $c_j$ . Thus, the  $J$  (objective function) represents the similarity measure of the  $n$  objects contained in their respective groups.

### 3.5 Support Vector Machine

In this section we briefly sketch the Support Vector Machine (SVM) algorithm and the reasons for using it. A more detailed description of SVM can be found in [24].

The SVM is a method to estimate the function that classifies data into two classes. SVM is based on the idea of minimizing the generalization error when the classifier is applied to test samples that do not exactly match any training sample used to train the classifier. In comparison, most classifiers (e.g., neural networks) try to minimize the training error, and tend to "overfit the training data.

The basic concepts we want to use are the following: there are two classes (mass e non-mass),  $y_i \in \{-1, 1\}$ , and there are  $N$  labeled training examples:  $(x_i, y_i), \dots, (x_N, y_N)$ ,  $x \in R^d$  where  $d$  is the dimensionality of the vector.

If two classes are linearly separable, then one can find an optimal weight vector  $w^*$  such that  $\|w^*\|^2$  is minimum; and

$$\begin{aligned} w^* \bullet x_i - b &\geq 1, \text{ if } y_i = 1 \\ w^* \bullet x_i - b &\leq -1, \text{ if } y_i = -1 \end{aligned} \quad (14)$$

Training examples that satisfy the equality are termed support vectors. The support defines two hyperplanes, one that goes through the support vector of one class and another one that goes through of the support vector the other class. The distance between two hyperplanes defines a margin and this margin is maximized when the norm of the weight vector  $\|w^*\|$  is minimum. This minimization can be performed with the maximization of the following function with respect to the variables  $\alpha_j$ .

$$W(\alpha) = \sum_{i=1}^N \alpha_i - 0.5 \sum_{j=1}^N \alpha_i \alpha_j (x_i \bullet x_j) y_i y_j \quad (15)$$

subject to the constraint:  $0 \leq \alpha_i$  where it is assumed there are  $N$  training examples,  $x_j$  is one of the training vectors, and  $\bullet$  represents the dot product. If  $\alpha_j \geq 0$  the  $x_j$  is termed a support vector. For an unknown vector  $x_j$  classification then corresponds to finding

$$F(x_j) = \text{sign}\{w^* \bullet x_j - b\} \quad (16)$$

where

$$w^* = \sum_{i=1}^r \alpha_i y_i x_i$$

and the sum is over the  $r$  nonzero support vectors.

For the non-separable case, training errors are allowed and we now must minimize

$$\|w^*\|^2 + C \sum_{i=1}^N \xi_i \quad (17)$$

subject to the constraint

$$y_i(w^* \bullet x_i - b) \leq 1 - \xi, \xi \geq 0$$

$\xi$  is a slack variable and allows training examples to exist in the region between the two hyperplanes that go through the support points of the two classes.

## 4 Results and Discussion

This section intends to investigate the efficiency of using shape and textural descriptors for detection of masses in digital mammograms using K-means and SVM.

## 4.1 Clustering

In this step we group breast structures (fat, mass, calcification, etc.). We just intend to group similar regions of the mammography irrespective of identifying mass and non-mass structures.

The proposed method uses a  $4 \times 4$  sliding window to allow co-occurrence calculation and extraction of descriptors. For each pixel  $p$  in the input image, the sliding window is positioned so that its first cell (0,0) matches the position of  $p$  in the image. A co-occurrence matrix is computed inside the window, the four Haralick's descriptors shown in Section 3.2 are computed based on it and associated to pixel  $p$ . This is done using the gray level co-occurrence already presented before. The sliding window size was chosen because, after some experiments, we observed that this size is the one that best fits the shape characteristics of the mass. It was observed that this window size is adequate because we want to detect masses in a range of dimensions from 3 mm to 30 mm.

We considered as parameters for co-occurrence matrices the four directions ( $0^\circ$ ,  $45^\circ$ ,  $90^\circ$  and  $135^\circ$ ) and three distances ( $d = 1, 2$  and  $3$ ). As we computed four Haralick's descriptors for each co-occurrence matrix, we obtained a set of 48 descriptors ( $4$  directions  $\times 3$  distances  $\times 4$  descriptors) for each sliding window. These descriptors are defined as the textural descriptors for each specific sliding window.

The next step, in the proposed scheme, is the grouping of similar sliding windows performed with the K-means algorithm, which generates the segmentation of input image.

The set of textural descriptors are submitted to the K-means algorithm which them in accordance with texture similarity. We use the number of K groups equal to 4, 5 and 6. Finally, the various connected windows returned from K-means are considered as segmented structures. It is important to highlight that in this step we just group breast internal structures (fat, mass, calcification, etc.) without performing a classification of these structures, leaving this task to the next step.

In the next phase we analyze each segmented structure (a set of connected windows from the previous phase) individually, based on their shape and texture descriptors, and use SVM to classify them as mass and non-mass.

We used 433 mammogram images from our image database, each one containing at least one mass. Applying texture descriptors and K-means algorithm we obtained 60.06% of accuracy. From this set of 433 images, we verified that 260 contained a mass structure between the set of structures grouped by the clustering algorithm. This verification was performed based on DDSM metadata. This set of 260 mammograms, with segmented structures composed of mass and non-mass regions is considered as the new sample set for the next step, the classification of structures as mass or non-mass.

Figure 1 presents a mammography that generates an incorrect segmentation of a structure represented as mass. For more specific information, analyzing the cases on which the K-means presented problems, it was verified that they were related to mammograms that have high density tissue; i.e., dense breast. In Figure 1b the mass cannot be defined with the clustering algorithm due to the great similarity between the mass region and the neighboring structures. Thus, the K-means algorithm was not capable of making the distinction (inadequate gray level) or did not search the separation (inadequate number K for the image).

Figure 2b presents a result of correct segmentation of the mass on Figure 2a. In this mammogram image we notice that the gray level of the mass is much more intense than that of other structures in the breast and it is not connected to other dense structure, where the K-means could recognize the mass as an isolated breast structure.

## 4.2 Mass Classification

In this step we used 250 segmented structures defined as mass obtained from the previous step. Ten segmented structures, defined as mass in the previous step, were discarded because they were connected to other segmented structures defined as non-mass. We also included 927 random non-mass segmented structures in our new sample to test the classification performance.

We analyzed individually each of the 1177 (250 masses and 927 non-masses) segmented structures. To do that, were calculated the Haralick's descriptors and the three shape descriptors described respectively in

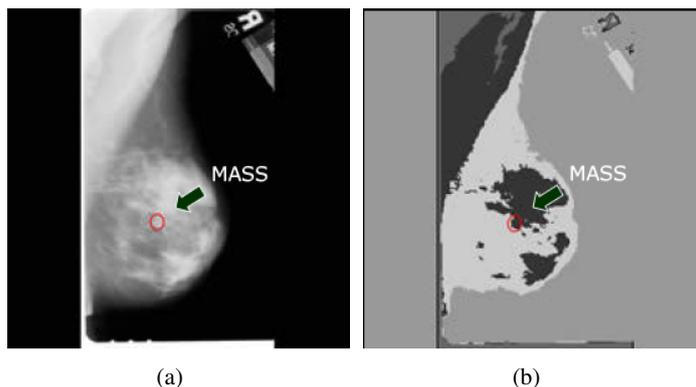


Figure 1: (a) Original mammogram. (b) Clustered mammogram with segmentation error.

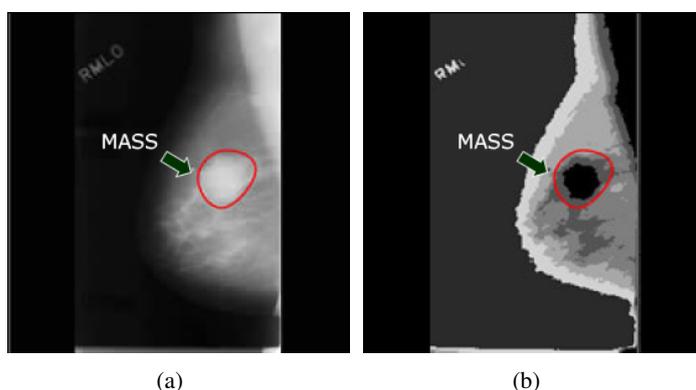


Figure 2: (a) Original mammogram. (b) Clustered mammogram with correct segmentation.

Section 3.2 and 3.3. These sets of descriptors compose the new feature vector for a segmented structure that is composed of several sliding windows grouped in accordance with the similarity with each other. Now, we intend to classify the resulting segmentation structure into two classes: mass or non-mass. For the computed Haralick's descriptors, we considered four directions ( $0^\circ$ ,  $45^\circ$ ,  $90^\circ$  and  $135^\circ$ ), six quantizations of gray levels (8, 16, 32, 64, 128 and 256) and three distances ( $d=1$ , 2 and 3) totalizing a feature vector composed of 360 texture descriptors. Also, we included in this feature vector the three shape descriptors (eccentricity, circularity and convexity). However, to make the computation feasible, we need to select from all the obtained descriptors which was the minimum set that had the power of discriminating mass from non-mass elements. Thus, we used the stepwise discriminant analysis [25] that reduced the number of variables. This technique reduced the number of variables to 9 (6 of texture and 3 of shape). Initially all segmented structures will be considered as mass until our classification technique verifies the opposite.

The samples (1177 segmented structures) were separated randomly into two sets: 960 samples for training and 217 samples for tests. Then, the training set was composed of 200 masses and 760 non-masses samples. The testing set contains 50 samples related to mass regions and 167 non-masses samples.

A Library for SVM, called LIBSVM [26], was used for training and testing. We used Radial Basis Function as kernel and the parameters values used were  $C = 8192$  and  $\gamma = 0.5$ . Table 1 shows the training and tests results of the SVM classifier, using as metric True Positive (TP), True Negative (TN), False Positive (FP), False Negative (FN), Sensitivity (SE), Specificity (SP) and accuracy (AC) .

The experimental results show that in the training set, 85% of the mass are classified correctly and 95.39% of non-mass are labeled accurately. For tests, these values are 86% for the masses and 94.61% for non-mass objects. The global accuracy, considering both training and test sets, is equal to 93.11%.

Set	TP	TN	FP	FN	SE (%)	SP (%)	AC (%)
Training	170	725	35	30	85	95.39	93.23
Test	43	158	9	7	86	94.61	92.63

Table 1: Detailed analysis of the mass vs. non-mass characterization.

To measure the effectiveness of separation of abnormalities in medical images, an evaluation by an expert or radiographs technician is required, in order to indicate whether or not the algorithm separated the suspected region from the rest of the image. The DDSM, used in this study, provides the location of the abnormality in cases where it exists.

The experimental results show that in the training set, 85% of the mass is correctly classified and 95.39% of non-mass is accurately labeled. For tests, these values are 86% for the masses and 94.61% for non-mass structures. The global accuracy, considering both training and test sets, is equal to 93.11%.

Table 2 shows a comparative view among several mass detection methods, including the proposed method, by examining the sensitivity of each method and their rate of false positives per image.

Method	Sensitivity (%)	Fp/Image
Belloti et al. [7]	80	4.23
Chan et al. [8]	85	1.32
Eltonsy et al. [5]	88	2.4
Campanini et al. [10]	80	1.1
Lim and Er [27]	62	1.81
Martins et al. [9]	89.3	0.93
New method	86	1.2

Table 2: Performance results for mass detection methods.

Examining the results presented in 2, we can observe that the method proposed in this paper provides support for detection of masses in digitalized mammograms in a similar way as the other methods available in research literature.

Our method is based on the use of techniques (K-means, SVM) and characteristics (co-occurrence matrix, eccentricity, circularity and convexity) for detection of masses. These techniques are consecrated in the literature, making their reproducibility easier.

In order to perform the clustering we used the K-means algorithm, which needs a previous definition of the number of clusters, other than a more robust one, such as the Growing Neural Gas [28], on which the number of clusters varies in an incremental manner. This choice is based on the performance, as with K-means we obtained a satisfactory processing time (approximately 20 seconds per image).

The use of geometrical and texture measures in the characterization of the segmented objects presents some advantages in relation to other approaches. Usually, just the texture information isn't enough to completely describe the mass, since a great part of its characterization can come from its shape. Besides, the use of texture measures discards most of the objects that represent healthy tissues.

Among the classifiers available in the literature, SVM comes off since it deals with sets of high dimensionality non-linear data with much accuracy and computational efficiency. Another advantage in comparison to other classifiers, such as Artificial Neural Networks (ANN) is the reduced number of parameters. So, after several tests and due to the large number of input variables used in this work, we concluded that SVM is the best candidate to perform the task of classification in the problem under discussion.

Thus, through the analysis of the results, it is possible to conclude that the proposed methodology proved to be effective in detecting masses in screening mammograms. The presented results allow us to infer that the use of the K-means algorithm in the task of segmenting screening mammograms provides a good rate of correct segmentation of mass structures. Similarly, the use of the co-occurrence matrix allows describing textures

and shape descriptors in an efficient way, thus contributing to the correct recognition of segmented structures. Furthermore, the SVM classification provides good generalization, also contributing to the effectiveness of the methodology during the classification of segmented structures.

## 5 Conclusion

The use of computational tools to aid detection and diagnosis of breast masses has grown and gained increasing acceptance in recent years, as a kind of "second readers" of medical images. These tools have been contributing to increase the early detection rates for breast cancer.

This paper presented a methodology for detection of masses in digital screening mammograms, which can also be used in the development of a CAD tool. Such methodology used for both purposes is subdivided into preprocessing, segmentation through K-means algorithm, reduction of mass candidates, and classification of segmented structures into mass or non-mass, based on co-occurrence matrix, shape descriptors (eccentricity, circularity and convexity) and Support Vector Machine classification.

The results indicate that the use of these techniques in the detection of masses is promising, since it achieves accuracy rates of over 85%. This will lead to a natural development of a CAD system capable of assisting health professionals in the painstaking task of tracing mammograms in search of mass abnormalities.

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