

# Case-level detection of mammographic masses

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**Abstract.** Breast cancer is one of the most frequent cancerous diseases among women. Currently mammography (X-ray examination) is the most efficient method for early detection. A CAD system for detecting cancer-predicting masses in digitalized mammograms is presented in this paper. Two size classes were defined and different algorithms were used for small and large mass detection. The last processing step was a false mark filtering, based on the comparison of the two views of the same breast. The system was tested with 935 mammographic cases, each containing 4 images.

Keywords: Mammography, mass detection, medical image processing, computer-aided diagnosis (CAD)

## 1. Introduction

Breast cancer is one of the most common forms of cancer in women. Every 12th woman suffers from this disease at least once in her lifetime [1]. According to the World Health Organization, more than 370 000 women worldwide die of breast cancer each year [2]. Since the cause of the disease is unknown, early detection is very important. Of all the diagnostic methods available for detecting breast cancer, currently mammography (X-ray examination of the breast) is the most reliable and practical method. If breast cancer is detected early, the five-year survival rate exceeds 95% [1].

The evaluation of the images taken at screening examinations needs a huge amount of human resource and money. Therefore computer-aided diagnosis (CAD) for mammography has been an active area of research (e.g. [3–11]). The main goals of a CAD system are to increase the accuracy of examination by aiming the radiologists' attention to suspicious locations and to decrease the cost by filtering out normal cases.

In a mammographic session usually two images are taken of both breasts. Left *cranio-caudal* (CC) is a top view, left *medio-lateral oblique* (MLO) is roughly a side view image of the left breast, right CC and right MLO are the same views of the right breast. When analyzing the images, some special signs of cancer – mainly masses and microcalcifications – are looked for. In clinical practice radiologists typically spot suspicious-looking structures in one view and then verify their suspicion by checking the corresponding area of the other view of the same breast.

This paper presents an automated system for detecting cancer-predicting masses in digitalized mammograms. For the recognition of small masses a modified version of a known method was applied. For large masses a new algorithm was developed. The last step of the processing was a false mark filtering, based on the comparison of the CC and MLO views.

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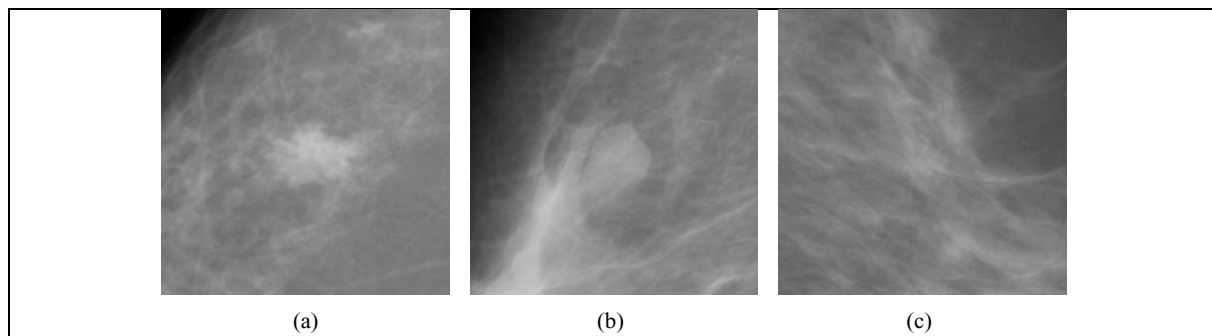


Fig. 1. Mass-like objects in mammograms: a malignant mass (a), a benign mass (b) and a superimposition of normal structures (c).

## 2. The problem

As it is known, tumoral masses are thickenings that appear in mammograms as round or oval objects brighter than the surrounding tissue. The recognition of this structure is a challenging task that needs intelligence, because masses show a great diversity in optical density, shape, position, size and characteristics at the edge. Humans and computer algorithms have to deal with a number of difficulties: for example the boundary can be fuzzy or partially missing, irrelevant objects can overlap the mass, some benign findings (e.g. cysts) also appear as masses, normal architectural structures of the breast superimposed on each other can look like real masses. Figure 1 shows some mass-like objects appearing in real mammograms.

One important question is how to handle the size variability of masses ( $\sim 5$  mm to  $\sim 50$  mm in diameter). The proposed system defines two size classes (“small” and “large”) and uses different methods for small and large mass detection.

## 3. Detection of small masses

For the detection of small masses (smaller than 20 mm in diameter) a variant of the AFUM (Average Fraction Under the Minimum) mass detection algorithm [6] was applied. This algorithm assigns a number from the interval  $[0, 1]$  to a given pixel position of the input image  $(x, y)$ . At first the minimal intensity value at distance at most  $r_1$  from location  $(x, y)$  is computed ( $m_1$ ) and then the fraction of pixels at distance  $r_2$  from  $(x, y)$  that have lower intensity value than the  $m_1$  is measured. This fraction under the minimum (FUM) calculation is done over many scales using a range of  $r_1$  and  $r_2$  values and the average of those calculations yields the average FUM (AFUM) value. Because proportions are averaged, the AFUM value will fall in the range  $[0, 1]$ .

Our modification on the original algorithm is that we drop pixels closer than  $r_1$  to  $(x, y)$  and define  $m_1$  as the minimal intensity at distance  $r_1$  from  $(x, y)$ . The reason of this modification is that we wanted to handle masses with small dark dots inside. However the modification turned out to be not very important, because the dark dot situation is quite rare in the testing database.

We did not define yet the set of  $(r_1, r_2)$  pairs, for which the FUM calculation should be made. This can be done e.g. by giving the possible values of  $r_1$  and fixing the distance between  $r_1$  and  $r_2$  (The same scheme is used in [6].) If  $r_1 = R_{\min}, \dots, R_{\max}$  and  $r_2 = r_1 + D$ , then the AFUM value calculation can

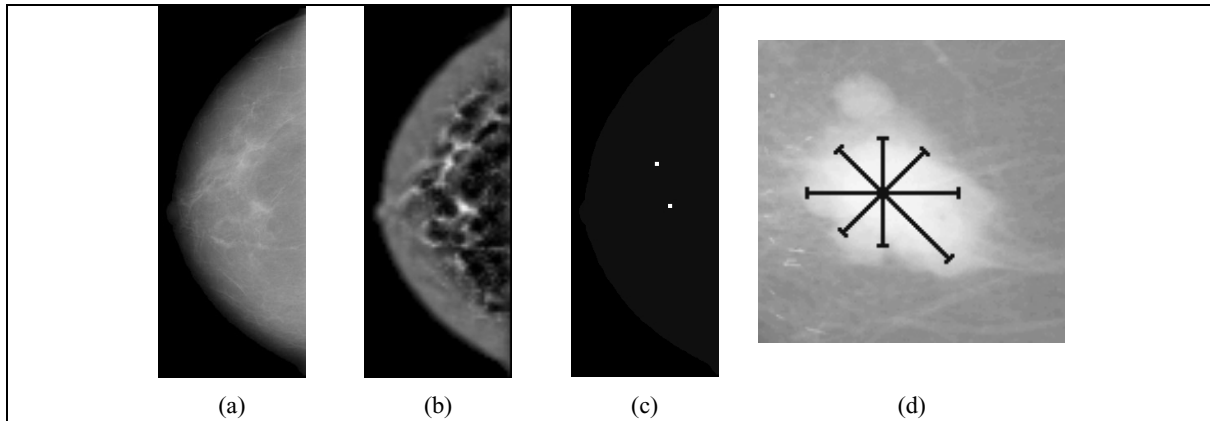


Fig. 2. Small and large mass detection. The first three subfigures show a mammogram containing a small mass (a), the result of AFUM filtering (b) and the locations returned by the small mass detector. The last subfigure (d) illustrates the mass boundary estimation step of large mass detection.

be written as:

$$AFUM = \frac{1}{R_{\max} - R_{\min} + 1} \cdot \sum_{r_1=R_{\min}}^{R_{\max}} FUM(r_1, r_1 + D) \quad (1)$$

Parameters  $R_{\min}$ ,  $R_{\max}$  and  $D$  should be fixed in advance, based on some a priori knowledge of the problem. An advantage of this algorithm is simplicity and therefore computational efficiency. A nice property of the algorithm is invariance to any monotonically increasing intensity transformation of the input image, since only logical operators (minimum finding and comparison) are applied to the intensity values.

Whole mammograms (Fig. 2a) are processed by running the AFUM algorithm for each pixel of the breast (Fig. 2a). Then the resulting AFUM map is thresholded and continuous regions are identified by a region-filling algorithm. Regions with a too high perimeter to area ratio are excluded from further examinations. The location of the maximal AFUM value is computed for each region, and an “energy” value is assigned for each maximum location based on the AFUM value of that position and its neighboring pixels. A structure is accepted as a mass if this energy is higher than a limit. (The energy limit parameter can be used to adjust the sensitivity of the small mass detector.) Finally the locations of the  $N$  highest energy maxima are returned (Fig. 2c).

#### 4. Detection of large masses

The a priori parameters of the AFUM algorithm ( $R_{\min}$ ,  $R_{\max}$  and  $D$ ) could not be set to deal with arbitrary mass size. At the resolution of 400 microns  $R_{\min} = 0$ ,  $R_{\max} = 6$  and  $D = 12$  proved to be a good choice but worked well only for masses smaller than 20 mm in diameter. For the detection of larger masses the following simple and fast algorithm was developed: At a given pixel position 8 lines are started from the center (vertically, horizontally and diagonally) and a mass boundary point is estimated for each direction (Fig. 2d). Then a “conspicuousness” value can be obtained from line lengths ( $l_i$ ), average intensity along the lines (Brightness) and average contrast at the end of the lines (Contrast).

$$\text{Conspicuousness} = \min_i l_i \cdot \text{Brightness} \cdot \text{Regularity} \cdot \text{Contrast} \quad (2)$$

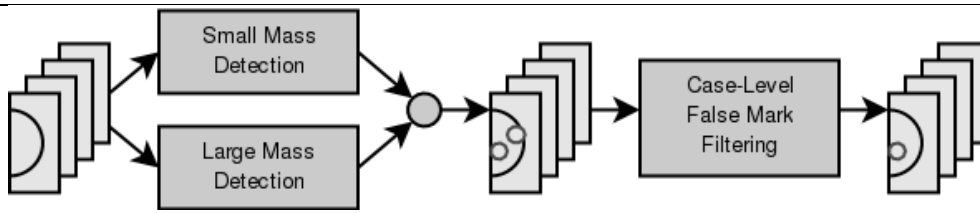


Fig. 3. Block diagram of the proposed system.

$$\text{Regularity} = \min_i l_i / \max_i l_i \quad (3)$$

Since the detection of large masses is easier than that of the small ones, the large mass detector returns only the location of the highest conspicuousness value, when processing a whole mammogram. Obviously, a threshold for the conspicuousness value can be applied to control the sensitivity of the large mass detector.

### 5. Case-level false mark filtering

Human experts always work with mammographic cases and not with individual images. Comparing views is an important part of their decision making process. For example, if they notice a cancerous-looking mass in an image, then they check the corresponding area of the other view of the same breast to verify their suspicion. The proposed system follows this approach, currently in a simplified way: if any of the CC or MLO views contains no mass candidates then all mass candidates are deleted from the other view.

Figure 3 shows the block diagram of the proposed mass detection system.

### 6. Evaluation scheme

A current retarding factor of computer-aided breast cancer detection research is the lack of standard large datasets and a common evaluation scheme. The comparison of the algorithms and experimental CAD systems published in this field is usually very difficult, because different training and testing datasets are used and different performance parameters are measured [12].

Our suggestion is that the standard datasets should be extracted from DDSM [13]. This public database contains more than 2500 annotated four-view cases. The images were acquired by scanning analog films at sampling rate  $\sim 50$  microns. DDSM is not the perfect mammogram database (e.g. it is not easy-to-use, the quality of the images is worse than analog films), but has the best overall features among the publicly available databases (e.g. it is the largest and the most detailed one). Currently most of the researchers use the DDSM database, but usually small and different parts of it.

We recommend to measure sensitivity (cancer recognition) and specificity (healthiness recognition) at case-level, and not at image- or patch-level as it is quite common in the literature. In terms of masses a case is malignant if it contains at least one malignant mass and normal if it does not contain any type of masses. A malignant case should be counted as recognized if one of the mark positions returned by the system is located inside the radiologist-drawn boundary of any malignant mass in the case. A normal case should be counted as recognized if the mass detector returns no mass candidates. Note that this

Table 1

Test results

	Sensitivity (Malignant Case Recognition)	Specificity (Normal Case Recognition)	# False Marks/Image
Without Case-Level False Mark Filtering	90.3 %	0.4 %	3.6
With Case-Level False Mark Filtering	89.7 %	6.3 %	3.5

scheme is not a two-class classification, therefore the usage of concepts true positive (TP), false positive (FP), true negative (TN) and false negative (FN) is problematic. (Consider the situation when a case contains a malignant mass and the system marks locations that are not inside the expert-drawn boundary of that mass. This case is not an FP, because it is not a negative case classified as positive, but it is neither a TP.) Beyond the malignant and normal case recognition we suggest the average number of false marks per image as the third performance parameter.

## 7. Results and conclusions

The proposed mass detection system was tested with 935 cases ( $935 \bullet 4 = 3740$  images) of the DDSM database [13]. 475 cases contained malignant masses, 460 cases were normal (contained no masses). The performance of the system was measured with and without case-level false mark filtering (Table 1).

It can be seen that the normal case recognition rate could be significantly increased at the cost of a minimal degradation in sensitivity even with the applied primitive case-level false mark filtering. Further improvements could be achieved with a more sophisticated case-level analysis.

The comparison with other mass detection algorithms is difficult, because currently very few are available that measure case-level parameters. An exception is [10] that uses an evaluation scheme similar to ours (without normal case recognition). Their system was tested with a smaller and different dataset containing 144 malignant and 50 normal cases. They achieved a specificity of 90% at 3 false marks per image.

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