DETECTION OF BREAST MASSES USING WATERSHED AND GLCM TEXTURE FEATURES

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ABSTRACT

Nowadays, breast cancer is the primary cause of the increase in the rate of death among women in both developed and developing countries. Examining mammograms to find signs of breast lesions is a challenging task that radiologists have to perform often. Thus, it is crucial to implement image analysis techniques to detect and outline breast lesions, as they provide essential morphological data that can assist in ensuring an accurate diagnosis. In this paper, we propose an efficient split-and-merge approach for tumor segmentation in digital mammogram images, using a watershed algorithm and texture features. First, we adopt the median filter technique to reduce noise and enhance the quality of the mammograms. Second, we apply Contrast-Limited Adaptive Histogram Equalization (CLAHE) to improve the interpretability of texture analysis results. Third, we exploit the watershed algorithm to split the image into homogenous subregions. Finally, we use the Gray Level Co-occurrence Matrices (GLCM) technique to localize the suspected subregions and merge these subregions to detect and outline breast lesions. The mini-MIAS database is used to evaluate the efficiency of the proposed approach. The experimental results demonstrate that the proposed hybrid method achieves a highly satisfactory success rate compared to state-of-the-art breast lesion segmentation methods in mammogram images.

Keywords: *Digital mammogram, tumor segmentation, Watershed algorithm, texture features, Split-and-Merge*

1. INTRODUCTION

Breast cancer is considered a public health problem and the most common cancer among women in the world. The World Health Organization estimates that in 2020, there were 2.26 million new cases of breast cancer and 685,000 deaths in the world [1]. According to data from Globocan (2020) [2], in Morocco, breast cancer is the most common cancer among women (38.9%) and the second cause of death by cancer (10.5%).

According to studies, a patient's chance of survival is greatly increased by the early detection of breast cancer [3],[4]. Screening mammography is presently the most cost-effective method for detecting breast cancer. It recognizes breast anomalies at an early stage, which considerably improves the chance of successful treatment [5]. In mammographic diagnosis, it is possible to mistake benign lesions or normal breast disturbances for breast cancer [6]. In addition, radiologists detect only about 70% of breast cancers [7], [8]. Therefore, computer-aided detection systems (CAD) have been developed to help radiologists accurately detect and classify breast cancers.

Breast tissue lesions of different kinds are created when cells proliferate abnormally, giving birth to breast cancer. These include the formation of microcalcifications (MCs), masses of varied sizes and forms, distortion of the tissue's normal architecture, and asymmetries between the left and right breasts [9]. Breast mass is one of the most recognizable indicators for the diagnosis of breast cancer, and its border information reveals the growth

pattern and biological properties. In general, benign masses have regular forms with smoothed boundaries, but malignant ones may have irregular forms and a spiculated boundary. Therefore, the classification of the masses as benign or malignant will depend on how well the masses are segmented.

Mass segmentation is a crucial step in breast cancer CAD to facilitate early detection and treatment of the cancer. However, breast masses vary in size and form, and have ill-defined borders, making correct segmentation a challenging and pressing problem in CAD system [10], [11]. For this reason, several researchers have been creating algorithms particularly for the detection of breast masses in mammography [12], [13].

Despite these efforts, existing segmentation methods face significant challenges. Deep learning-based approaches, such as U-Net, rely heavily on extensive annotated datasets, which are often unavailable in clinical settings. Traditional techniques, including active contours and k-means clustering, struggle to accurately segment masses with blurred or low-contrast boundaries. Additionally, while the Watershed algorithm is effective in detecting edges, its sensitivity to noise and tendency toward over-segmentation limit its application in clinical environments.

To overcome these limitations, this study explores how integrating texture features derived from GLCM can enhance the performance of Watershed segmentation. It also investigates whether combining GLCM-guided labeling with post-segmentation fusion can produce a robust and accurate method for segmenting masses in challenging mammographic images, ultimately providing clinicians with a reliable tool for early diagnosis.

The technique introduced in this work is based on split-and-merge segmentation methodology. The split-and-merge method involves recursively splitting an image into homogeneous and smaller subregions, then merging those subregions into homogeneous and larger regions. Our approach is mainly divided into two successive parts: the splitting and the merging steps. In the splitting step, we propose the Watershed algorithm to divide the image into homogeneous subregions. In the merging step, we suggest using texture analysis to merge the homogenous subregions acquired from the splitting procedure into bigger regions.

The rest of this paper is organized as follows: Sections 2 and 3 describe related works and the proposed materials and methods, respectively. Then, the experimental results are detailed and presented in Section 4. Finally, the discussion and conclusion are presented in Section 5.

2. RELATED WORK

In the past few decades, several methods of breast lesion segmentation have been proposed for mammogram images. Hamed Pezeshki[14]developed a breast tumor segmentation method focusing on spiculated regions, where pixels exhibit a linear arrangement, and pixels within lesion core areas share similarities. The approach utilizes differences between a pixel and its surrounding pixels to identify these regions. The method involves employing three thresholds to eliminate unnecessary pixels from both the lesion core and spiculated portions, resulting in a segmented tumor. Azmeera Srinivas et al. [15] proposed a CAD system for early-stage cancer detection using Adaptive Kernel-Based Fuzzy Cuckoo Search Optimization Clustering applied to digital mammography. The authors implemented kernel-based fuzzy c-means clustering with a cuckoo search optimization to find the best cluster centers for the KFCM algorithm used in the preprocessing stage in order to improve the accurate detection of the lesions and segmentation accuracy from mammograms. In the second stage, a level-set technique is introduced for reducing boundary leakages. Abdul Qayyum et al. [16] proposed a methodology consisting of three stages for automatic breast segmentation and cancer detection in mammograms using the SVM algorithm, breast region segmentation, pectoral muscle suppression, and classification of normal and pathological breast muscle tissues. The canny edge detection technique and Otsu's thresholding are used to remove the pectoral muscle region. Then, the Gray Level Co-occurrence Matrices (GLCM) are applied for texture feature extraction, and the SVM classifier is carried out to distinguish between normal and abnormal tissues. Jiaming Luo et al. [17] developed a novel framework for breast mass segmentation in mammogram images. The authors employed the MLP-based segmentation model known as U-shaped Sparse-MLP (USMLP), which has a U-shaped architecture. The proposed framework combines CNN layers and sparse MLP (sMLP) blocks. S. Vidivelli et al. [18] proposed a new system for breast cancer detection in mammography. In the pre-processing stage, RGB-Grey scale conversion is employed, and in the second stage, a fuzzy entropy model is carried out in the segmentation process. The features are then determined, including fractal

properties like lacunarity, fractal dimension, and texture features such as proposed Local Binary Patterns (LBP) and the Grey Level Co-occurrence Matrix (GLCM). Then, Support Vector Machine (SVM), Optimized CNN, and Neural Network (NN) are used to classify the extracted features. J. Anitha et al. [6] developed an automatic identification of suspicious tumor regions in four stages, beginning with image enhancement using the median filter technique, followed by thresholding and morphological operations to identify the breast profile, followed by pectoral boundary extraction using the single-seeded region growing technique, and finally tumor segmentation using the adaptive global and local thresholding technique. Arnab Chattaraj et al. [19] proposed a marker-controlled watershed segmentation method for mammograms to more clearly identify suspicious regions. It is a morphological process that uses the input image's topographic representation to produce watershed lines. G. R. Jothilakshmi et al. [20] introduced an automated system for segmenting mammogram images using a seed point and a split and merge methodology, which is based on a region-based segmentation approach. This method utilizes morphological operations to digitally reduce noise, enhancing image clarity. The system then applies region split and merge techniques to differentiate between normal and abnormal areas within the mammograms, aiming to improve the accuracy and efficiency of mammogram analysis. VAGSSA et al. [21] developed a computer-aided diagnostic (CAD) system for the early detection and classification of breast lesions in mammogram images. The system uses a 2D median filter to eliminate noise and artifacts from the images. After preprocessing, Hough's algorithm is applied for pectoral muscle suppression, followed by the watershed algorithm to extract tumor boundaries. In the final stage, features are extracted using wavelet transform and the Gray-Level Co-occurrence Matrix (GLCM). These features are then classified as normal or abnormal using the Support Vector Machine (SVM) algorithm. Pratap S. Vikhe et al. [22] presented an enhanced marker-controlled watershed technique for segmenting and identifying abnormal regions in mammograms. The proposed approach employs morphological operations and a threshold method to suppress artifacts and the pectoral area in the images. The authors computed the magnitude gradient to obtain lesion edges. To separate the suspicious region, internal and external markers were identified, and the watershed transform was then applied to the modified gradient image. Dhungel Neeraj et al. [23] developed a CAD system for tumor detection and

classification in mammogram images. Their approach utilized a random forest algorithm and a cascade of deep learning models for mass detection. Following segmenting the masses using active contour models, they extracted partial images from the detected tumors. Finally, a deep learning model was used for lesion classification. Volkan Müjdat Tiryaki [24] introduced a novel deep-learning model for segmenting and classifying lesions using mammograms from a breast cancer digital repository. The study utilized cascaded deep transfer learning (DTL)-based segmentation techniques to segment mass lesions. Initially, deep learning-based breast segmentation was employed to eliminate noise from the mammogram background. The study evaluated the performance of various models, including a five-layer U-net and U-nets pretrained with weights from VGG16, ResNet50, and Xception networks in the encoding phase. Additionally, the effectiveness of attention U-net, residual U-net, MultiResUnet, DeepLabV3Plus, and Unet++ architectures was investigated. The study recommended using Xception network weights in the encoder section of the Unet++ model. To estimate mass lesion characterization using DTL, the mass segmentation model predictions were applied by the author.

According to the state of the art of medical images, the shape of a lesion stands out as one of the key factors crucial for distinguishing between malignant and benign masses. However, it is important to emphasize that accurately extracting lesion boundaries relies heavily on the quality of segmentation. In our study, we propose a novel approach for extracting the limits of breast masses from the region of interest (ROI) in mammogram images. This approach is based on the watershed algorithm, texture features, and split and merge technique.

3. MATERIALS AND METHODS

This section of the paper describes each module employed in the study for detecting mass borders on mammograms, including pre-processing, watershed segmentation, texture feature extraction, and breast mass detection. Figure 1 provides an overview of the proposed workflow.
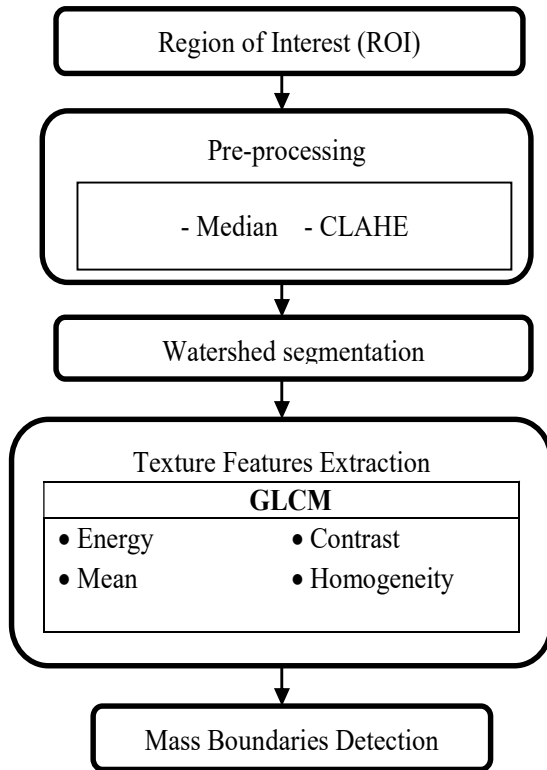
Figure 1: Workflow diagram illustrating the process of mass detection

4.1 Digital Mammogram Database

The mini-MIAS database [25] was employed for the experiments, consisting of 322 mammographic images taken from the left and right breasts of 161 patients. These patients include both healthy individuals and those with various lesions such as benign or malignant tumors and calcifications.

4.2 Selection of Regions of Interest (ROI)

The region of interest (ROI) is crucial for identifying abnormalities, as it directs algorithms to specific areas where issues such as tumors or calcifications are likely to be found. Using the region of interest enhances the accuracy of diagnostic algorithms and improves computational efficiency, leading to more reliable and timely detection of breast cancer. In the mini-MIAS database, each image measures 1024×1024 pixels. To reduce computation costs, we propose using regions of interest of 174×174 pixels instead of the full mammogram images. The size of 174×174 pixels is selected because it accommodates the largest detected masses [26].

4.3 Pre-processing

Pre-processing is considered a crucial stage in mammography image processing techniques. The accuracy of this stage significantly influences the success of subsequent stages like segmentation and classification. The primary goal of this approach is to improve image quality through noise reduction and contrast enhancement. A median filter [27] is a nonlinear filter known for effectively reducing impulse noise, pepper noise, and Gaussian noise. This filter is adept at noise reduction while preserving image quality and maximizing information content. In our proposed method, we employed a median filter with a sliding window size of 3x3 to achieve optimal results. Additionally, to improve the contrast of mammograms, we introduced the contrast-limited adaptive histogram equalization (CLAHE) approach. This method is widely preferred in image enhancement thanks to its simplicity and superior performance across various image types compared to alternative techniques [26]. Figure 2 indicates that the median filter is effective at reducing salt-and-pepper noise while preserving sharp edges. It can be seen that CLAHE greatly improves the overall image contrast.
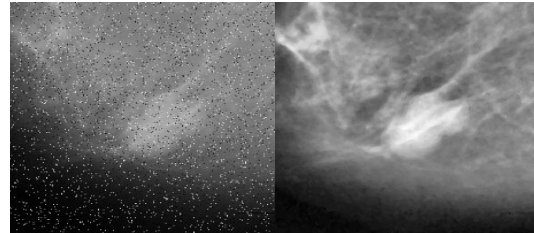
Input   *Output*
Figure 2: pre-processing step

4.4 Watershed segmentation

Watershed [29] is an image segmentation method derived from mathematical morphology which considers a grayscale image as a topographic relief undergoing simulated flooding. In this concept, the image is viewed as a three-dimensional surface where homogeneous zones are watersheds associated with minima. Starting from these minima, the watershed algorithm floods the basins so that water fills the basins from these minima until the basins assigned to different minima meet at the watershed lines. The minima are generally chosen as local image minima. Figure 3 provides a simple explanation of the watershed concept. The filling of the basins begins from the minima, resulting in three regions (green, orange, and yellow). The watersheds (in red) are placed between these regions.
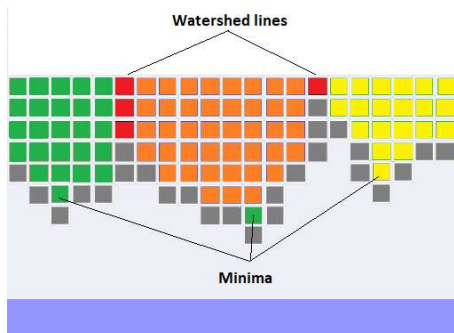
Figure 3: Representation of watershed lines and minima for a one-dimensional signal

After the pre-processing step, we applied the watershed transformation technique to produce an initial segmentation of the pre-processed mammogram image, followed by a fusion step. Figure 4 shows the result of segmentation using the watershed method, with the blue lines representing the watershed lines.
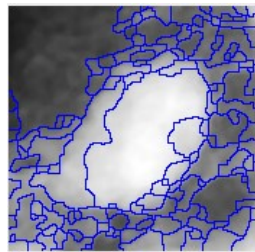

Figure 4. Result obtained using watershed

4.5 Mass Boundaries Detection

At this stage, any two similar and neighboring subregions are merged by following these steps:

- Constructing the Region Adjacency Graph (RAG)

After applying the watershed transform, the resulting partitioned image is utilized to construct the Region Adjacency Graph (RAG), which serves as input for the region merging procedure. The RAG is a standard data structure used to depict neighborhood relationships among segmented regions in an image. Each node in the RAG represents a region from the over-segmented image. An edge labeled (Ri, Rj) exists between adjacent regions "Ri" and "Rj". Two regions are considered neighbors if they share at least two adjacent pixels. Figure 5 illustrates this scenario: regions R3 and R4 are neighbors, but R1 and R4 are not.
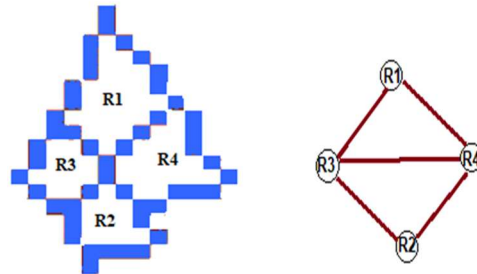
- Filtering small regions

Figure 5: Four partitions of an image and the corresponding RAG

After performing the watershed method, the resulting image may contain numerous small regions that cannot hold a window of size 8x8. To address this, we filter out these small regions using a size threshold. Regions smaller than a predefined constant are merged with neighboring regions that are similar. Figure 6 illustrates the result after filtering out small regions.
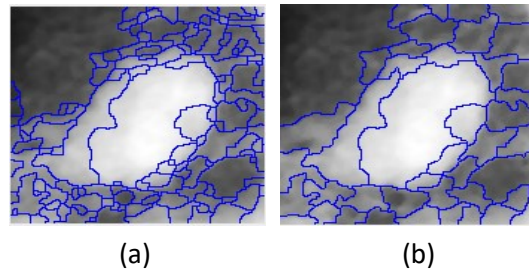

(a)   (b)

Figure 6: Small regions filtering result: (a) before filtering, (b) after filtering

- Texture Features Extraction

After performing the initial segmentation using the watershed technique, the subsequent step involves examining the texture features for each region of the resulting image. This is crucial because abnormal tissue textures often exhibit distinct characteristics compared to normal breast tissues [13]. In this study, we utilize an 8x8 window size to extract four texture features (Mean, Homogeneity, Energy, and Contrast) out of the 16 proposed by Harlick [30]. The Gray Level Co-occurrence Matrix (GLCM) is employed as a statistical method for feature extraction. The 8x8 size represents the smallest area that can encompass the masses.

In the first stage, the GLCM is used to calculate the mean value for each window. If this mean value exceeds 210, the window is selected as a suspicious area. In the second stage, the other three texture descriptors are extracted to further evaluate the windows categorized as suspicious (Figure 7).
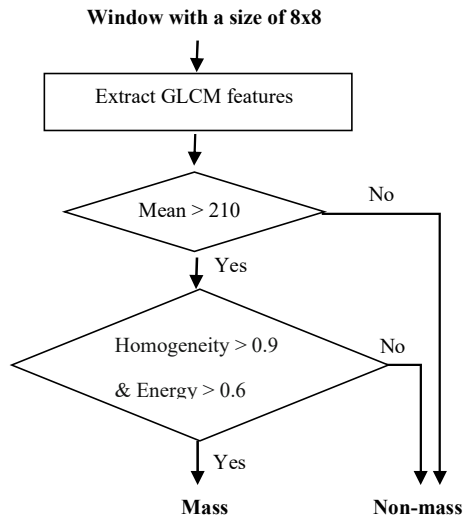
Window with a size of 8x8

```
Extract GLCM features
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Mean > 210 — No

Yes

Homogeneity > 0.9 & Energy > 0.6 — No

Yes

Mass   **Non-mass**

Figure 7: Decision tree for classifying the window of 8x8 size using GLCM features

• Region Merging

The result of the first segmentation step using the watershed technique produces an over-segmented image where each small region is classified as either mass or non-mass. In this step, we propose to merge any pair of adjacent regions belonging to the same class (mass or non-mass) to determine the precise boundary of the mass. For instance, Figure 8 illustrates the outcome of applying our segmentation approach.
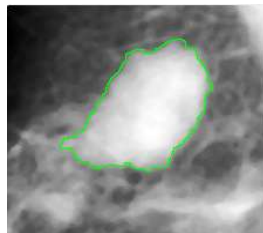

Figure 8: Final Result

4. EXPERIMENT RESULTS

This section presents the experimental results and evaluates the performance of the proposed breast mass segmentation approach. In this study, we used a testing data set of 2O mammography images from the mini-MIAS database to test and evaluate the suggested approach's performance. The performance was evaluated by comparing the mass contour obtained by the proposed method with the mass contour outlined by three radiologists.

4.1 Qualitative Evaluation of the Proposed Approach

Qualitative evaluation of segmentation methods often involves comparing the outputs of different algorithms to a ground truth or reference standard. In this study, we propose to compare the outputs of our segmentation approach to a ground truth. Figure 9 shows examples of breast mass segmentation on a few tests' mammogram images. In this Figure, we can see that the contours extracted by our approach are much closer than the contours marked by the radiologists.
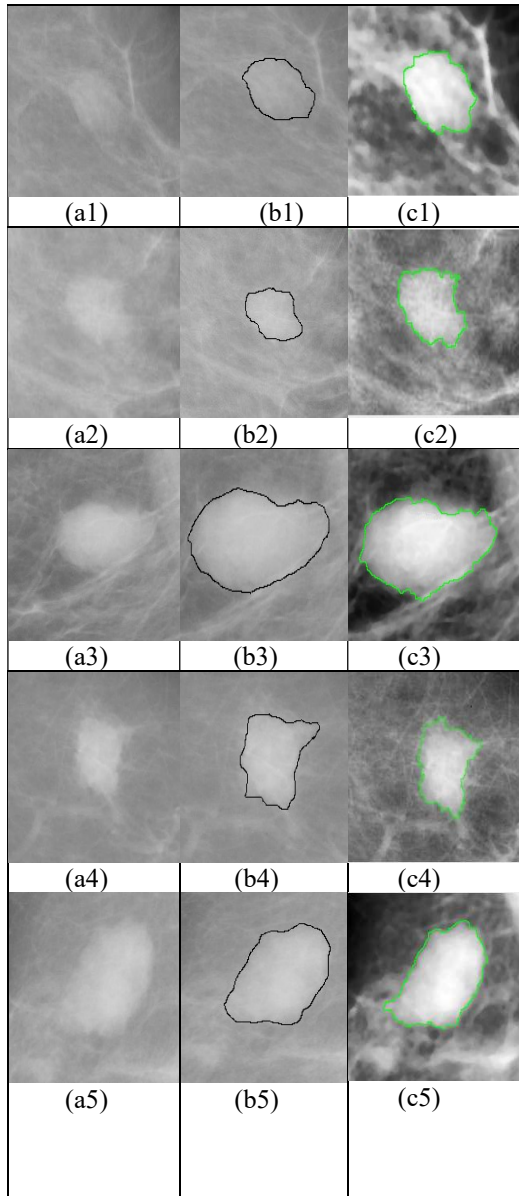
Figure 9: Experimental results: (a1) -(a5) Original images, (b1) -(b5) The ground truth, (c1) -(c5) Results by the proposed method

4.2 Quantitative evaluations of the Proposed Approach

To evaluate the efficiency of the segmentation approach, various performance metrics were assessed. For the proposed method, metrics such as accuracy, sensitivity, specificity, and overlap were calculated using formulas involving True Positives (TP), True Negatives (TN), False Positives (FP), and False Negatives (FN). Figure 10 illustrates TP, FP, TN, and FN. These terms are defined as follows:
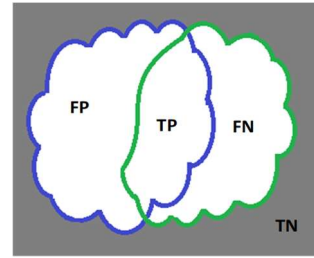

Figure 10: An illustration of TP, FP, TN and FN: The Green Contour: Lesion Outlined by a Radiologist. The Blue Contour: Lesion Outlined by a System

-True Positive (TP): Correctly identified mass regions.

-True Negative (TN): Correctly identified non-mass regions.

-False Positive (FP): Non-mass regions incorrectly identified as mass.

-False Negative (FN): Mass regions incorrectly identified as non-mass.

- Accuracy

Accuracy measures the overall correctness of the segmentation approach. It is calculated as the ratio of correctly identified mass and non-mass regions to the total number of regions. It is calculated using the following formula:

$$\text{Accuracy} = \frac{TP+TN}{TP+TN+FP+F} \times 100 \qquad (1)$$

- Specificity

Specificity evaluates the segmentation approach's ability to accurately identify non-mass regions, minimizing false positives. It is calculated using the following formula:

$$\text{Specificity} = \frac{TN}{(FP+FN)} \times 100 \qquad (2)$$

- Sensitivity

Sensitivity measures the segmentation approach's ability to accurately identify mass regions, minimizing false negatives. It is calculated using the following formula:

$$\text{Sensitivity} = \frac{TP}{TP+FN} \times 100 \qquad (3)$$

- Overlap

The overlap metric measures the extent to which the segmented mass overlaps with the ground truth mass. It is calculated using the following formula:

$$\text{Overlap} = \frac{TP}{TP+FP+FN} \times 100 \qquad (4)$$

Table 2: Comparison with Other Approaches

Paper Reference	Results			
	Overlap	*Specificity*	*Sensitivity*	*Accuracy*
Proposed	91.4%	92.5%	94%	93.2 %
[31]	80,30 %	94,35 %	91 %	91.15 %
[32]	80.92 %	73.41 %	96.16 %	95.06 %
[33]	0,91 %	0,97 %	0,83 %	0,79 %

Table 1: Performance Results

Data	Quantitative evaluation metrics			
	Overlap (%)	*Specificity (%)*	*Sensitivity (%)*	*Accuracy (%)*
20 images	90.4	92.5	94	93.2

Table 1 presents the quantitative evaluation metrics obtained by the suggested method. Table 2 presents the comparison of the results obtained by the proposed approach against the results obtained by state-of-the-art methods for breast mass segmentation.

5. DISCUSSION AND CONCLUSION

This paper introduces a novel method for segmenting breast masses in mammography images, aiming to assist radiologists in identifying lesions. The method utilizes the watershed algorithm and GLCM texture features and has been validated using 20 images from the mini-MIAS dataset. Quantitative analysis results, presented in Table 1, and qualitative results, shown in Figure 9, highlight the effectiveness of the proposed methodology. When compared to other approaches, as illustrated in Table 2, the proposed method demonstrates superior performance across most metrics. A significant advantage of this technique is its much shorter runtime compared to the method described in [33]. Moreover, it produces fine and continuous mass contours without requiring any expert parameterization.

Several studies have proposed methods for breast mass segmentation, including deep learning approaches like U-Net and traditional methods such as active contours and k-means clustering. However, these techniques often require large annotated datasets or struggle with low-contrast and blurred masses. Our method improves upon these approaches by combining Watershed segmentation with GLCM texture features, addressing the sensitivity of Watershed to noise and over-segmentation. This results in more accurate and reliable segmentation, particularly for challenging cases, and makes the method more applicable in clinical environments with limited annotated data.

However, the present method has some limitations. First, the segmented object is already part of the ROI images, which were pre-selected from full mammograms. Second, the method was tested on a limited set of 20 images from the mini-MIAS database. While this allowed us to assess its feasibility, the small dataset restricts the generalization of the results. Future work should focus on validating the method on larger and more diverse datasets, including complete mammograms.

In future work, the segmented mass will be analyzed to obtain more descriptive and useful information for determining whether the tumor is cancerous or benign.

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