A Random-Walk Based Breast Tumors Segmentation Algorithm for Mammograms

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Abstract

Mammography is a commonly performed imaging study for screening breast cancer. One of the crucial elements of the mammogram processing is an accurate segmentation of the breast tumor region from a mammogram because it directly influences the subsequent analyzing accuracy and the processing speed of the mammogram. The goal of this paper is to propose an accurate and efficient algorithm of breast tumor extraction from the medio-lateral oblique (MLO) mammograms. The proposed algorithm adapts the modified gradient vector flow (MGVF) snake to determine the breast region from a mammogram image, and uses Otsu thresholding and multiple regression analysis to delete the pectoral muscle from the breast region. It further utilizes upper outlier detection and texture complexity analysis to segment the initial breast tumor regions, and finally, segments the final breast tumor image from the initial breast tumor regions by using random walk scheme. The proposed algorithm is tested on the digital mammograms from the Mammogram Image Analysis Society (MIAS) database. The experimental results show that the tumor extracted by the presented algorithm approximate accurately to the actual tumor regions confirmed on the biopsy results of MIAS.

Keywords: Breast cancer, mammogram, breast tumor.

1. Introduction

Breast cancer is one of the most common cancers [1-5] in women. Screening and early detection is essential for better outcomes in breast cancer treatment. For screening of breast cancer, mammography has been utilized widely in various clinical settings for many years. With regards to the mammogram processing, extracting the region of interest (the breast tumour) accurately from a mammogram is one kernel stage of the mammogram processing. It significantly influences the overall analysis accuracy and processing speed of the mammogram.

Segmenting the breast tumor region is frequently difficult due to the wide variation of tumor size, shape and relative location within the mammogram. In the meantime, the low contrast and poor definition of tumor edge, and the surrounding fatty tissues and veins are also contributing to the difficulty of tumor segmentation [6]. However, the tumor regions often have different texture patterns and gray scale levels from the normal tissues which make it possible to be segmented from a mammogram by utilized conventional image segmentation schemes [7].

A lot of schemes have been proposed to segment the tumor regions in mammograms [5-13]. These segmentation schemes can be classified into two main categories: (i) region-based tumor segmentation schemes and (ii) edge-based tumor segmentation schemes. Region-based segmentation schemes search pixels that satisfy a given homogeneity criterion, and collect these pixels to estimate the region of interest. For region-based tumor segmentation schemes, Jiang et al. [11] first utilized a Gaussian filter to remove image noise and a gamma correction on a region of interest (ROI) to improve its contrast. They then applied the principle of maximum entropy and selected optimal thresholds to obtain initial segmented tumor regions. Finally, they conducted a morphologic dilation operation on the initial tumor regions to obtain the tumor. Xu et al. [12] used the iterative thresholding scheme to extract suspicious regions. They then used 3-level discrete wavelet transform to decompose the suspicious area into four sub-bands to locate centers of the tumors. Finally, they utilized the region growing scheme to merge adjacent regions to extract tumors.

Edge-based segmentation schemes detect the edge of the region of interest directly without processing the actual image content. While it is computationally fast, but the edge detection frequently fails to enclose the region of interest completely. To enhance the edge detection, Yuan et al. [8] applied a radial gradient index (RGI)-based segmentation scheme to generate an initial contour. Song et al. [9] used plane fitting and dynamic programming techniques to detect the optimal contour of a tumor from the candidate edge pixels.

To propose an accurate and efficient algorithm of breast tumor segmentation on medio-lateral oblique (MLO) mammograms is this paper's goal. The proposed algorithm consists of four stages: (i) Employing modified gradient vector flow (MGVF) snake to determine the breast region, (ii) applying Otsu thresholding and multiple regression analysis to delete the pectoral muscle region from the breast region, (iii) using upper outlier detection and texture complexity analysis to extract the initial breast tumor region, and (iv) utilizing random walk scheme on the initial tumor regions to accurately segment the final breast tumor region. The proposed algorithm is

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tested on digital mammograms from the Mammogram Image Analysis Society (MIAS) database. The remainder of this paper is organized as following: Section 2 introduces the brief outline of the proposed segmentation algorithm, the breast region extracting scheme of using modified gradient vector flow (MGVF) snake, the pectoral muscle deletion scheme using Otsu thresholding and multiple regression analysis, and the breast tumors segmenting scheme utilizing outliers detection and texture complexity analysis. Section 3 presents the experimental results. Finally, the conclusion is presented in Section 4.

2. Proposed Breast Tumor Segmentation Algorithm

In order to construct an accurate breast tumor segmentation algorithm for digital mammograms, several schemes are used in this paper to achieve the goal. The presented breast tumor segmentation algorithm has four phases: (i) breast region extracted using modified gradient vector flow (MGVF) snake, (ii) pectoral muscle deletion using the iterative Otsu thresholding and multiple regression analysis, (iii) breast tumor regions initially segmented utilizing dynamic threholdings and texture complexity analysis, and (iv) breast tumor regions further refined utilizing random walk scheme. The details of these phases used in the presented breast tumor segmentation algorithm are illustrated in the following subsections. And the flow chart of the proposed breast tumor segmentation algorithm is shown in figure 1.

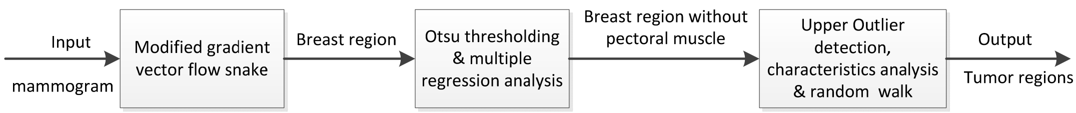


Figure 1. The flow chart of the proposed breast tumor segmentation algorithm.

2.1 Breast Region Segmentation Using Modified Gradient Vector Flow Snake [14]

The accuracy and efficiency of the segmenting algorithm can be improved by segmenting the breast region from the rest of the mammogram in the initial step. The breast region segmentation algorithm must be fully automated and give correct results for all digital mammograms. The MGVF snake is employed in this paper - it was introduced in our previous paper: a breast segmentation scheme for digital mammograms using gradient vector flow snake [9]. The proposed breast region extracting algorithm integrated the median filtering step, the scale down step, the binarization processing step, the morphological erosion processing step and novel gradient adjusting step. The median filter step was used to filter out the noise in a mammogram, the scale down step was used to resize down the mammogram size to speed up the breast region segmentation. The binarization processing step and the morphological erosion processing step were used to find a rough breast border. The novel gradient adjusting step was applied to get a modified edge map; and then the gradient vector flow snake (GVF snake) was employed to obtain an accurate breast border from the initial breast border. This breast segmentation scheme can output the corresponding accurate breast region from an input digit mammogram, and the output breast region will be used in the following phase to detect the pectoral muscle.

2.2 Pectoral Muscle Deletion [15]

In the breast region of a mammogram, the gray scale intensity and texture of the pectoral muscle region can be similar to the breast tumor regions. The appearance of pectoral muscle in the medio-lateral oblique (MLO) views of mammograms can increase the false positive in computer aided detection (CAD) of the breast cancer. For this reason, pectoral muscle has to be segmented from the breast region before further analysis. In order to construct an accurate pectoral muscle segmentation algorithm for digital mammograms, several schemes are used in this paper to achieve the goal. The overall pectoral muscle segmentation algorithm for digital mammograms consists of three main stages: (i) breast region extracted by using modified gradient vector flow (MGVF) snake, (ii) rough pectoral muscle region detection by using the iterative Otsu thresholding scheme, (iii) pectoral border modified by utilizing multiple regression analysis.

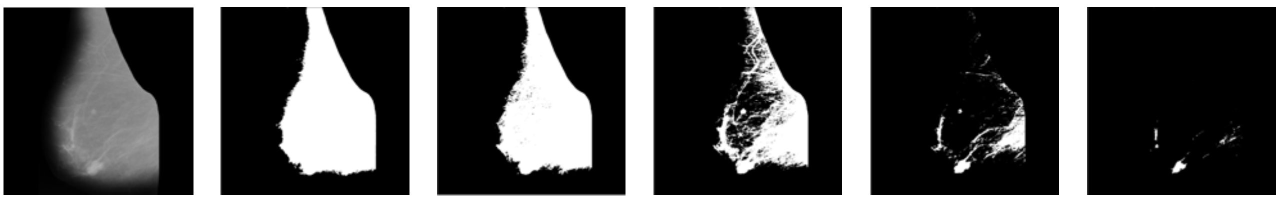
2.3 Breast Tumors Segmentation

The goal of this phase is to extract one or more suspicious areas from the pectoral muscle deleted breast region (PMDBR). After pectoral muscle deleting, next phase is to partition separate the suspicious areas that may contain tumors from the PMDBR, which is to separate the PMDBR of a mammogram into several non-overlapping areas, then extract and locate several areas as the suspicious tumor candidates. Edge-based segmentation schemes are frequently difficult to determine their boundary due to some ill-defined edges. Region-based segmentation schemes are more suitable for mammograms since a suspicious region is always brighter than its surrounding tissues, has an almost uniform density, has a regular shape with varying size, and has a fuzzy boundary [16]. There are many region-based segmentation schemes such as region growing, watershed, and thresholding algorithms. In this paper, region segmentation based-thresholding scheme is utilized for extracting suspicious breast tumors from a pectoral muscle deleted breast region.

For obtaining a better initial segmentation of breast tumors from a pectoral muscle deleted breast region, the proposed algorithm repeatedly utilizes the upper outlier detection scheme with different thresholds to binarize the pectoral muscle deleted breast region into a black-white image. The binarization procedure shall be terminated while the area ratio of white area to the black area is within in the interval [0.01, 0.1] and the absolute difference ratio of white area between two adjacency iterations is less than 5%. Then the white regions are taken as the breast tumor candidates. And the morphological erosion processing, area value filter, main-axes ratio filter and texture analysis are applied in series on these breast tumor candidates to find the real breast tumors. Some steps are illustrated in the following subsections.

2.3.1 Upper Outlier Detection

The binarization step is used to locate suspicious areas in the mammogram from the pectoral muscle deleted breast region. On the other hand, the grayscale value of the real tumor is always higher than that of the remainder of the tissue within a mammogram. The fact means that the breast tumors shall be in the outliers of the gray values distribution of the pectoral muscle deleted breast region. So, the presented algorithm repeats the outlier determination scheme with different threholds to binarize the breast region to determine the breast tumor candidates. In statistics an outlier is defined as an observation that deviates substantially from the other observations that it is considered generated by a different system. Outliers frequently have an effect on the parameters estimating a model being fitted to the data. This could cause inaccurate predictions and mistaken conclusions. In many cases, outliers are frequently removed to improve the accuracy of the estimators. To define the outliers of a data set, let $\bar{x}$ be the mean and let σ be the standard deviation of the data set. One observation is declared a lower outlier if it is no more than $\bar{x}-k\sigma$, and declared as an upper outlier if it is no less than $\bar{x}-k\sigma$, and the others are declared as inliers, where the value of upper-outlier parameter (UOP) k is usually taken as no more than 3 and no less than 1.



(a) (b) (c) (d) (e) (f)

Figure 2. The detected outliers of a PMDBR for different upper-outlier parameters, (a) Original PMDBR, (b) UOP = 1, (c) UOP = 1.5, (d) UOP = 2, (e) UOP = 2.5, (f) UOP = 3.

The brightest areas in a grayscale PMDBR are the breast tumor candidates. These bright regions are always located in the upper outliers of the pixel value distribution of a PMDBR. It should be reasonable and effective that the proposed algorithm calculate the mean and standard deviation of a grayscale PMDBR by taking the upper outlier points of the PMDBR as the breast tumor candidates. For obtaining real breast tumors from the

PMDBR, the presented algorithm will apply the morphological operation and connected component scheme on the upper outlier regions (suspicious breast tumors) to extract the real tumors in following processes. Figure 2 shows an example of the outlier detection of a PMDBR with different upper-outlier parameters; the example shows that the detected outlier area is smaller when the upper-outlier parameter is higher.

2.3.2 Breast Tumor Characteristics Analysis

The presented upper outlier detection scheme although can effectively determine the breast tumor candidates. However, the detected breast tumor candidates may contain other regions of higher grayscale value such as dense tissue, calcifications, and various kinds of noise, etc. On the other hand, a breast tumor is usually a localized area and has some shape and texture characteristics [17, 18]. There are several qualitative and quantitative schemes for characterizing the shape of tumors in a mammogram. The shape feature of tumors contains the geometric parameters such as area, area ratio, perimeter, circularity, mean and standard deviation of radial distance, eccentricity, and orientation moment invariants, etc [19]. In this paper, area, area ratio, and ratio of two main axes are taken as criteria to evaluate whether a suspicious breast tumor is a real tumor or not. For obtaining a better and simple binary image of breast tumors, the presented algorithm applies the Sobel gradient mask on each suspicious breast tumor to acquire the tumor's texture characteristic. The Sobel gradient mask is one of popular edge detection methods. Figure 3 shows the Sobel gradient mask; Figure 3(a) is a mask type, Figure 3(b) and Figure 3(c) are the values of masks that are used for detecting the horizontal and vertical edge, respectively.

Z1	Z2	Z3
Z4	Z5	Z6
Z7	Z8	Z9

(a)

-1	-2	-1
0	0	0
1	2	1

(b)

-1	0	1
-2	0	2
-1	0	1

(c)

Figure 3. The Sobel gradient mask, (a) the mask pixels (b) $f_x(x,y)$ **(c)** $f_y(x,y)$

2.3.3 Final breast tumor Segmentation

For image segmentation, random walk scheme is a semi-automated interactive algorithm proposed by Grady [20, 21]. The main steps are: The original image is first presented with its corresponding weighted graph G= (V, E ,W), in which each pixel is the vertex V, and W is the weight between the neighbor vertices. The weight is defined by the Gaussian weight function:

$$w(\upsilon_i,\upsilon_j)=\exp(-\beta(g(\upsilon_i)-g(\upsilon_j))^2), \qquad (1)$$

where $g(\upsilon_i)$ is the intensity of the pixel υ_i and β is a free parameter.

For the weighted graph, all vertices are divided into a marked vertices set V_M , and an unmarked vertices set V_U , such that $V_M \bigcup V_U = V$ and $V_M \bigcap V_U = \phi$.

Finally, due to the probability problem for a random walk is the same as a Dirichlet problem, and Dirichlet problem can be evaluate from the graph Laplacian matrix defined as the follows.

$$L(i,j)=\begin{cases}\sum_{\upsilon_i} w(\upsilon_i,\upsilon_j), & \upsilon_i=\upsilon_j\\ w(\upsilon_i,\upsilon_j), & \upsilon_i \text{ and } \upsilon_j \text{ are adjacent vertices.}\\ 0, & \text{otherwise}\end{cases} \qquad (2)$$

So the image segmentation with random walk is transformed to the Dirichlet problem and the image segmentation results are obtained by solving the corresponding Dirichlet problem. In the random walk step, the mass center of a selected candidate breast tumor is taken as the corresponding source seed, and the middle pixel between the candidate breast tumor and the nearest neighbor candidate breast tumor is taken as the sink seed, respectively.

3. Experimental Results

For evaluating the effectiveness of the proposed algorithm, the presented tumor segmentation scheme was applied on Mammogram Image Analysis Society (MIAS) database [22]. This MIAS database has 322 mammograms of right and left breast taken from 161 patients. The size of mammogram is 1024*1024 and bit-depth of 8 bits ([0, 255]), and each pixel is 50um. In the database, 51 mammograms were diagnosed as having malignant lesions, 64 mammograms were diagnosed as having benign lesions and 207 mammograms were diagnosed as normal. And different classes of abnormal tissues in mammograms are indicated as ill-defined masses, well-defined circumscribed masses, speculated masses, architectural distortion, calcification, asymmetry and normal. Each of these diagnosis has been further compared with the biopsy results.

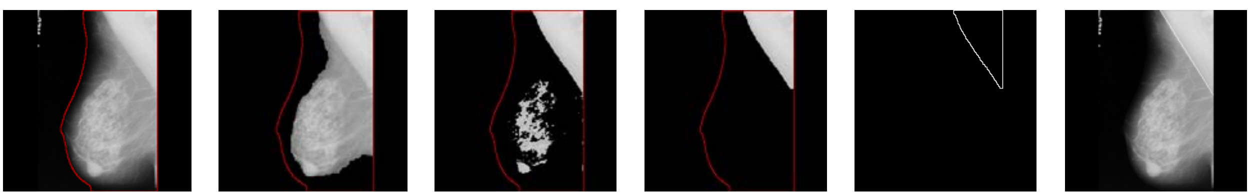
The experimental results show that the breast border extrapolated by the phase 1 of the presented tumor segmentation algorithm with average of mean error function is 2.2818, average of misclassification error is 0.0144, and average of relative foreground area error is 0.0166 [14]. This means that the breast border extrapolated by our proposed scheme approximately follows the breast border extrapolated by an expert radiologist. Figure 4 shows an example of the output of each step in phase 1 of the presented algorithm.

With reference to the manually demarcated pectoral muscle regions, the segmented regions provided by the proposed scheme resulted in low average mean error function, misclassification error, and relative foreground area error with 1.7188, 0.0083 and 0.0056, respectively [15]. The experimental results show that the pectoral muscle extracted by the phase 2 of the presented algorithm approximately follows that extracted by an expert radiologist. Figure 5 shows an example of the output of each step in phase 2 of the presented algorithm.

Successful tumor segmentation is defined as that the overlapping area between the algorithm's extracting area and the area labeled by a biopsy in MIAS is larger than 80%. 15 mammograms with abnormal masses selected from MIAS are tested by the proposed algorithm, and the number of successful tumor segmentation is 14 mammograms. Figure 6 shows an example of the output of each step in phase 3 of the presented algorithm, and figure 7 shows the output of the presented algorithm applying on mdb005 in MIAS database with random walk after iteration 5, 80, and 120, respectively.

(a) (b) (c) (d) (e)

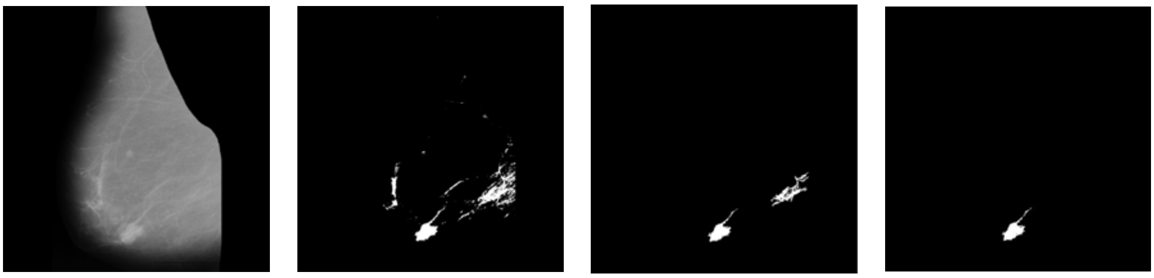
Figure 4. The output of each step in phase 1 of the presented algorithm, (a) Original mammogram, (b) after binarization, (c) After non-breast objects removal, (d) Initial breast border segmentation, (e) final breast region extracted by using MGVF snake.



(a) (b) (c) (d) (e) (f)

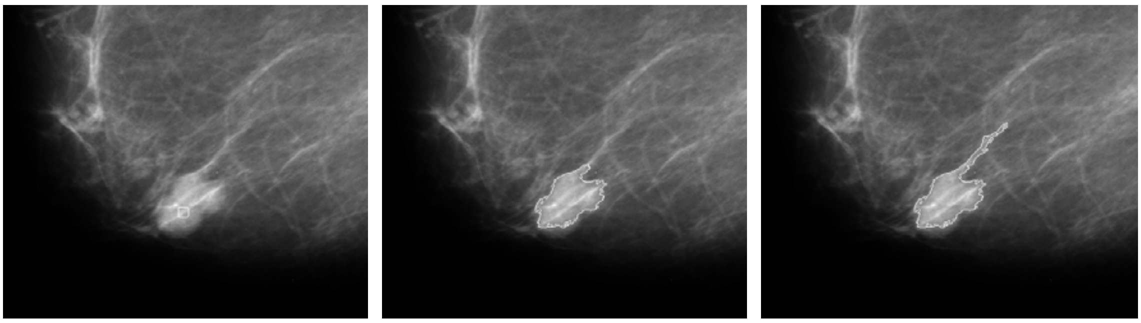
Figure 5. The output of each step in phase 2 of the presented algorithm, (a) breast region extracted by using

MGVF snake, (b) after Otsu threholding and morphological processing one time, (c) after Otsu threholding and morphological processing two times, (d) after position detecting, (e) extracted pectoral muscle rough border, (f) final extracted pectoral muscle.



(a) (b) (c) (d)

Figure 6. The output of each step in phase 3 of the presented algorithm, (a) an input pectoral muscle deleted breast region (PMDBR), (b) after outlier detection with UOP = 2.75 , (c) after breast tumor size and shape characteristics analysis, (d) after breast tumor texture characteristics analysis.



(a) (b) (c)

Figure 7. The close-up view output of the presented algorithm applying on mdb005 in MIAS database with random walk after iteration (a) 5, (b) 80, (c) 120.

The breast tumor segmentation results are analyzed according the normalized performance metrics to show the different performance features of the segmentation algorithms. These normalized performance metrics are misclassification error (*ME*) function, relative foreground area error (*RFAE*), accuracy, extraction error rate (*EER*), and non-uniformity (NU) [14, 15, 21]. *ME, RFAE, Accuracy*, and *EER* are varying from 0 for a perfectly correct segmentation to 1 for a completely error case. These performance measures are defined as the follow.

$$ME = 1 - \frac{TP + TN}{TP + FN + TN + FP} = \frac{FN + FP}{TP + FN + TN + FP}, \quad (3)$$

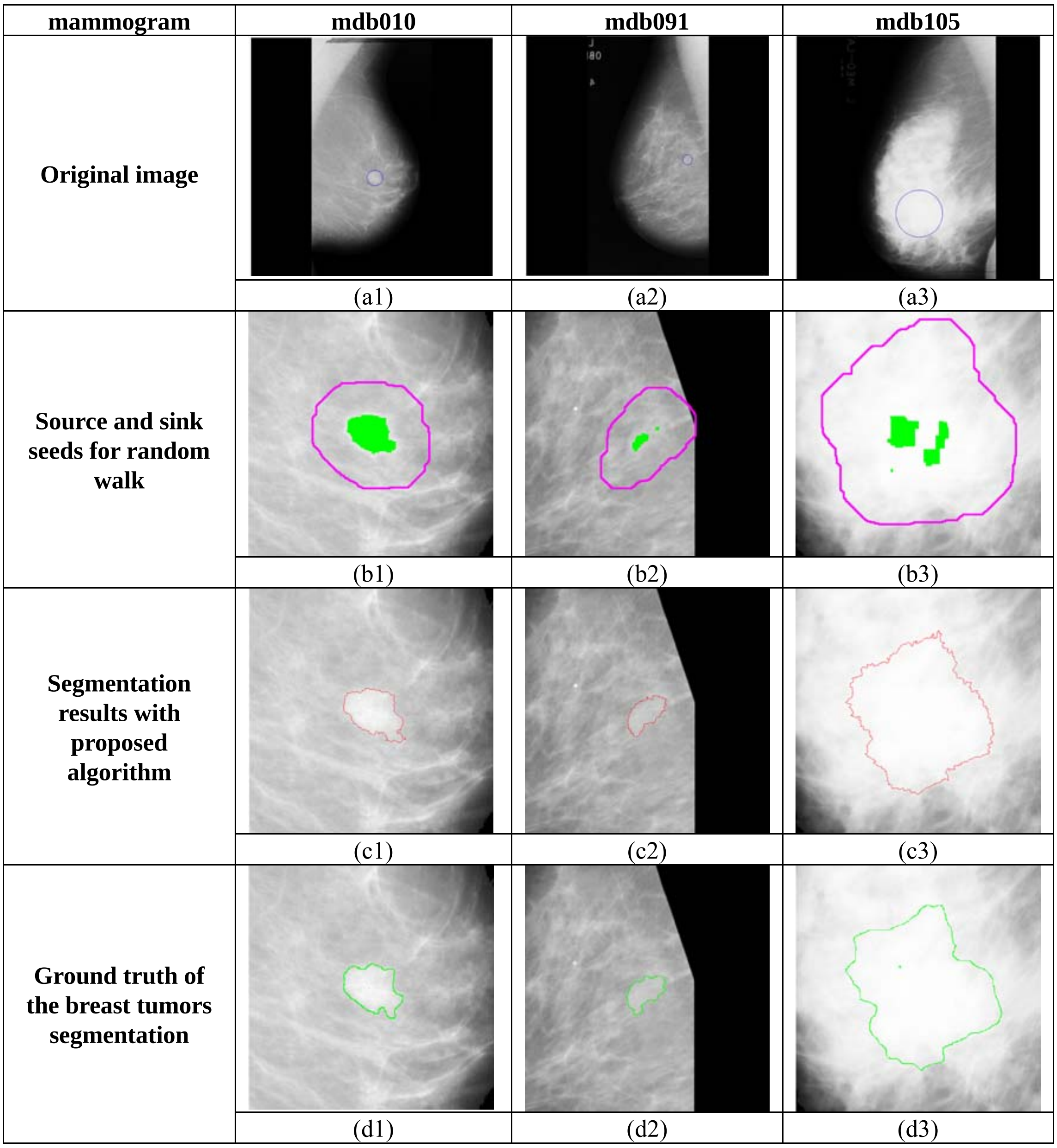
$$RFAE = \begin{cases} \dfrac{(TP + FN) - (FP + TP)}{TP + FN} = \dfrac{FN - FP}{TP + FN} & if \ (FP + TP) < (TP + FN), \\ \dfrac{(FP + FN) - (TP + FN)}{FP + TP} = \dfrac{FP - FN}{FP + TP} & if \ (FP + TP) \geq (TP + FN) \end{cases} \quad (4)$$

$$Accuracy = (TP + TN)/(TP + TN + FN + FP), \tag{5}$$

$$EER=OER+UER=(FP/(TP+FN))+(FN/(TP+FN)), \tag{6}$$

$$NU=((TP+FP)/((TP+FP)+(TN+FN)))*(\sigma_e^2/\sigma^2), \tag{7}$$

where *TP*, *TN*, *FP* and *FN* represent the areas of true positive, true negative, false positive and false negative, respectively. σ_e^2 is the variance of extracted object and σ^2 is the variance of original image. Three experimental examples are rearranged in figure 8, and the corresponding normalized performance metrics are illustrated in table 1. The experimental results show that the tumor extracted by the presented algorithm approximate accurately to the actual tumor regions confirmed on the biopsy results of MIAS.



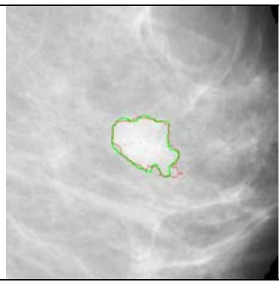
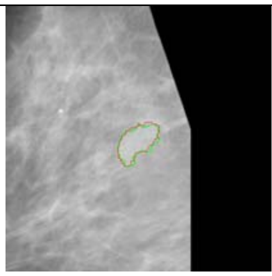
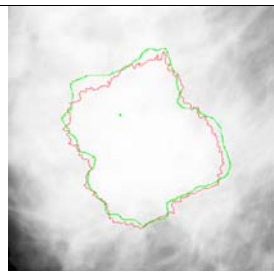
Comparison between the proposed algorithm and the ground truth			
	(e1)	(e2)	(e3)

Figure 8. Some experimental examples; (a) Row a shows the original mammograms, (b) Row b represents the close-up view of source and sink seeds for random walk, (c) Row c shows the close-up view of the proposed algorithm's segmentation results, (d) Row d shows the close-up view of the ground truth of the breast tumors, (e) Row e shows the close-up view of the segmentation comparison between the proposed algorithm and the ground truth.

Table 1: The corresponding normalized performance metrics of figure 8

Mammogram	ME	RFAE	Acc	EER	NU
Mdb010	0.00142	0.0067	0.9986	0.132	0.000695
Mdb091	0.00179	0.0024	0.9982	0.169	0.000043
Mdb105	0.01005	0.0410	0.9900	0.131	0.000990

4. Conclusions

Breast cancer is one of the most common cancers in women. Screening and early detection is essential for better outcomes in breast cancer treatment. For screening of breast cancer, mammography has been utilized widely in various clinical settings for many years. With regards to the mammogram processing, extracting the region of interest (the breast tumour) accurately from a mammogram is one kernel stage of the mammogram processing. It significantly influences the overall analysis accuracy and processing speed of the mammogram.

The main goal of this paper is to propose an accurate and efficient algorithm of breast tumor extraction on the medio-lateral oblique (MLO) mammograms. The proposed algorithm adapts breast region extracted by using modified gradient vector flow (MGVF) snake to determine the breast region from a mammogram image, uses Otsu thresholding and multiple regression analysis to delete the pectoral muscle from the breast region, utilizes upper outlier detection and texture complexity analysis to segment the initial breast tumor regions, and takes random walk scheme on the initial tumor regions to accurately segment breast tumors. The presented algorithm is tested on the digital mammograms from the Mammogram Image Analysis Society (MIAS) database. The experimental results show that the tumor extracted by the presented algorithm approximately follows that extracted by the biopsy of MIAS. In the future we will develop a high performance breast mass analysis based on accurate breast tumor segmentation to power the computer aided detection of breast cancer.

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