Levels Propagation Approach to Image Segmentation: Application to Breast MR Images

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Abstract

Accurate segmentation of a breast tumor region is fundamental for treatment. Magnetic resonance imaging (MRI) is a widely used diagnostic tool. In this paper, a new semi-automatic segmentation approach for MRI breast tumor segmentation called Levels Propagation Approach (LPA) is introduced. The introduced segmentation approach takes inspiration from tumor propagation and relies on a finite set of nested and non-overlapped levels. LPA has several features: it is highly suitable to parallelization and offers a simple and dynamic possibility to automate the threshold selection. Furthermore, it allows stopping of the segmentation at any desired limit. Particularly, it allows to avoid to reach the breast skin-line region which is known as a significant issue that reduces the precision and the effectiveness of the breast tumor segmentation. The proposed approach have been tested on two clinical datasets, namely RIDER breast tumor dataset and CMH-LIMED breast tumor dataset. The experimental evaluations have shown that LPA has produced competitive results to some state-of-the-art methods and has acceptable computation complexity.

Keywords Levels · Propagation · Image segmentation · Breast · MRI · Tumor

Introduction

Breast cancer is the most commonly diagnosed cancer in females worldwide [1] and also the cause of the greatest number of cancer-related deaths among women. According to the World Health Organization (WHO) [2], approximately 627,000 women died from breast cancer in 2018, which is about 15% of all cancer-related deaths among women. For primary assessment of the disease, mammography and ultrasound are often used due to their low cost and ease of use. However, these techniques suffer from several limitations that prevent advanced analysis and diagnosis such as the low quality of the produced images that contain insufficient information about breast tissues [3]. Magnetic resonance imaging (MRI) is another widely used imaging technique in the field of medical radiology [4], it uses the principle of nuclear magnetic resonance

to produce images with high resolution, appropriate for breast abnormalities investigation. In fact, it produces more clear and detailed images of the breast soft tissues than mammography and ultrasound. Thus, MRI is highly recommended for screening purposes to detect suspicious lesions in the breast [5]. However, it generates a large number of data that still need an interpretation by a radiologist, leading to a long interpretation time which can reduce patient compliance [6] and exhausts the radiologist, and the results of the interpretation usually suffer from intra-observer or inter-observer variability [7]. This justifies the clear clinical demand for computer-aided diagnosis (CAD) systems that assist radiologists in the diagnostic reading process. Any CAD system is composed of a series of basic processing steps; one of them is tumor segmentation which is considered crucial [8]. The role of segmentation is to partition a given digital image into multiple sets of pixels having one or more similar features in the goal to simplify the representation of the image into something that is more meaningful and understandable. When the segmentation considers only one particular region to extract such as a tumor region, this latter is commonly referred to as the region of interest (ROI) [9]. Thus, segmentation allows for detection and better representation of the tumor under study and extraction of its features [10]. Nevertheless, extraction of breast tumor from MR images is a challenging

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task due to their considerable shape variations, intensity inhomogeneity, overlap with the normal breast tissue, etc. Several segmentation methods are proposed in the literature to address these issues including contour-based [11–14] and region-based [15–17, 22–27] approaches. Unfortunately, none of the state-of-the-art methods produced rigorous results and the challenge remains open.

In this paper, a new breast tumor segmentation approach for magnetic resonance imaging is introduced. The new approach is inspired by the natural propagation process of a tumor that is initialization, promotion, and progression, and it relies on a new defined organized level propagation to accurately extract the tumor region from the remaining regions of the breast MR image. The introduced novel propagation way has significant advantages over the state-of-the-art methods, including parallelization amplitude, automatic selection and refinement of the threshold, and ability to stop at any desired limit. Furthermore, the proposed approach have been tested on two datasets: RIDER breast MRI dataset and CMH-LIMED breast MRI dataset, and the experimental results have shown that LPA produces accurate segmentation. The remainder of this paper is organized as follows. “[Related Work](#)” is dedicated to give some recent works on MRI breast tumor segmentation. In “[Levels Propagation Approach](#),” the proposed approach is described in detail. The results of experimental evaluations and comparative analysis are reported in “[Experimental Evaluation](#).” Finally, “[Conclusion](#)” summarizes this paper and gives the recapitulations and some future work.

Related Work

MRI breast tumor segmentation has been an active area of research for the last decade, so several approaches have been proposed in the literature. In this section, the main works established in this setting are reviewed and classified into two main classes: *Contour-based* approaches and *Region-based* approaches. For clarity, a comparison study with some criteria of the reviewed works is presented in Table 1.

Contour-Based Approaches

This class of approaches is based on the assumption that intensity discontinuities occur in the boundaries of objects. So, to highlight the boundary of a region of interest, these approaches tend to depict the pixels where intensity discontinuities occur [29]. Shi et al. [11] have proposed a two-stage approach to automatically segment breast masses on DCE-MRI. In the first stage, an initial segmentation of the breast tumor is performed using a K -means clustering algorithm followed by morphological operations. In the second stage, the obtained initial segmentation is refined by

a 3D level set method. Yin and Lu [12] have interest in the 3D reconstruction of the breast tumor from 2D segmented images. The level set method based on energy and gradient is adopted to segment the tumor. But first, the segmentation is preceded with a combination of Otsu thresholding and seeded region growing to discard the breast skin-line region from each image. The results of the segmentation are then processed using the ray casting method to reconstruct a 3D image of the tumor. Liu et al. [13] have proposed a 3D level set approach integrating a new signed pressure function based on a combination of the intensity distribution with pathophysiological basis. Agner et al. [14] have presented a spectral embedding segmentation approach based on an active contour method. Generally, these methods suffer from a sensitivity to the initial contour. Also, the values of their parameters should be set properly so as to yield a good segmentation result. Moreover, they are time consuming and they cannot effectively handle intensity inhomogeneity.

Region-Based Approaches

Region-based approaches rely on an appropriate homogeneity criterion to group pixels into regions [30]. These approaches can be classified into four categories: *thresholding*, *clustering*, *graph-based*, and *other approaches*.

Thresholding-Based Approaches

Al-Faris et al. [15] have proposed a method using a modified automatic seeded region growing based on a variation of the automated initial seed and threshold selection methodologies to segment breast tumors. The method was tested on images from the RIDER breast MRI dataset [39]. The proposed method suffers from a major drawback which consists of the use of a global threshold that is not sufficient to handle the internal heterogeneity characterizing some MRI breast tumors. Cui et al. [16] have proposed a method dedicated to malignant breast lesions segmentation. The introduced method performs a 3D segmentation by segmenting the volume slice by slice using a Gaussian mixture model to select thresholds and generate markers, followed by a watershed method to extract the lesion from the image. Unfortunately, the proposed method uses a complex technique to select thresholds and generate markers. On the other hand, it is based on the conventional watershed that is known to produce excessive over-segmentation which badly affects the accuracy of the segmentation.

Clustering-Based Approaches

Azmi et al. [17] have studied the performance of three clustering method categories called supervised, unsupervised, and semi-supervised on the RIDER breast tumor dataset.

Table 1 Comparative table of MRI breast tumor segmentation according to some criteria

Classes	Sub-classes	Criteria		Tasks	Features	Dimensions	Evaluation (metrics and results)
		Works					
Contour-based approaches	/	Shi et al. [11] (2008)		Segmentation	Automatic	3D	One metric (<i>mean ± std</i>): •Overlap measure for pre-chemotherapy = (0.81 ± 0.13) . •Overlap measure for post-chemotherapy = (0.70 ± 0.22) .
		Yin and Lu [12] (2015)		Segmentation and Reconstruction	Automatic	3D	Five metrics (<i>average</i>): •TPF = 91.09%. •FNF = 08.91%. •FPF = 01.23%. •TNF = 98.77%. •TT = 88.60%.
		Liu et al. [13] (2014)		Segmentation	Semi-automatic	3D	Seven metrics (<i>mean ± std</i>): •VOR = (79.55 ± 12.60) . •Accuracy = (99.35 ± 0.44) . •Precision = (93.59 ± 5.21) . •Specificity = (99.75 ± 0.37) . •Sensitivity = (84.65 ± 11.55) . •MCC = (88.36 ± 6.01) . •Time(s) = (5.30 ± 2.54) .
		Agner et al. [14] (2013)		Segmentation and Classification	Automatic	2D	Three metrics (<i>mean ± std</i>): •MAD = (2.31 ± 2.26) . •DSC = (0.74 ± 0.21) . •HD = (5.64 ± 5.04) .
Region-based approaches	Thresholding-based	Al-Faris et al. [15] (2014)		Segmentation	Automatic	2D	Five metrics (<i>mean ± std</i>): •TPF = (0.82 ± 0.10) . •TNF = (0.90 ± 0.10) . •STVF = (1.73 ± 0.10) . •RO = (0.75 ± 0.09) . •MCR = (0.18 ± 0.10) .
		Cui et al. [16] (2009)		Segmentation	Semi-automatic	3D	One metric calculated regarding the manual segmentations R1 and R2 (<i>average</i>): •VOR for R1 = 62.6%. •VOR for R2 = 61%.
	Clustering-based	Azmi et al. [17] (2011)		Segmentation	Semi-automatic	2D	Five metrics (<i>mean ± std</i>): •TPF = (0.79 ± 0.19) . •TNF = (0.83 ± 0.15) . •STVF = (1.61 ± 0.21) . •RO = (0.68 ± 0.17) . •MCR = (0.21 ± 0.12) .
		Moftah et al. [22] (2014)		Segmentation	Automatic	2D	Three metrics were applied to three image samples. To be brief, the results obtained on one sample are given only: •Accuracy (<i>average</i>) = 89.47%. •Texture-based (entropy = 0.9973, std = 0.4996, mean = 0.5307). •Shape-based (circularity = 0.4291, orientation = -25.6164 , solidity = 0.7908).
		Hassanien et al. [23] (2014)		Segmentation and classification	automatic	2D	Three metrics were applied to three image samples. To be brief, the results obtained on one sample are given only: •Accuracy (<i>average</i>) = 95.1%. •Texture-based (entropy = 0.9636, std = 0.4874, mean = 0.3882). •Shape-based (circularity = 0.1723, orientation = 2.7775, solidity = 0.6061).

Table 1 (continued)

Classes	Sub-classes	Criteria		Tasks	Features	Dimensions	Evaluation metrics and results
		Works					
	Graph-based	McClymont et al. [24] (2014)		Segmentation	Automatic	2D	Four metrics were applied to two Test sets (<i>median</i>): 1) Test set 1: •DSC = 0.76. •FPVF = 0.20. •FNVF = 0.21. •Sensitivity (<i>average</i>) = 100%. 2) Test set 2: •DSC = 0.75. •FPVF = 0.31. •FNVF = 0.11. •Sensitivity (<i>average</i>) = 100%.
		Yu et al. [25] (2015)		Segmentation	Automatic	2D	Five metrics (<i>mean</i>): •DSC = 0.83. •Accuracy = 0.96. •VOC = 0.72. •MAD = 0.79. •MHD = 11.71.
	Other approaches	Jayender et al. [26] (2014)		Segmentation	Automatic	2D	Three metrics were calculated according to two references: 1) Radiologist's segmentation: •Accuracy (<i>average</i>) = 90%. •Sensitivity (<i>average</i>) = 100%. •DSC (<i>mean</i>) = 0.77. 2) CADstream output: •Accuracy (<i>average</i>) = 82%. •Sensitivity (<i>average</i>) = 100%. •DSC (<i>mean</i>) = 0.72.
		Maicas et al. [27] (2017)		Segmentation	Automatic	2D	Two metrics (<i>mean</i>): •DSC = 0.77. •Time(s) = 7.78.

The supervised methods were the K -nearest neighbor algorithm (K-NN) [18], support vector machine (SVM) [19], and Bayesian classifier [20]. The unsupervised category was tested using the fuzzy C -means algorithm (FCM) [21]. And finally, the semi-supervised category included self training and improved self training (IMPST) [17]. The authors have found that the supervised and semi-supervised methods produce a satisfactory accuracy. However, these methods highly require initially labeled data. This fact constitutes one of the significant disadvantages of the methods. On the other hand, the unsupervised methods need no initial data but they produce actually a poor segmentation. Moftah et al. [22] have presented a segmentation method focused on identification of target objects on MRI breast images using an adaptation of the K -means clustering algorithm. The method is simple but it exhibits a loss of accuracy. Hassanien et al. [23] have proposed a segmentation and classification framework. The segmentation is performed by an adaptive ant-based clustering algorithm which is an improved version of the classical algorithm and the classification is done by the multilayer perceptron neural networks classifier. Unfortunately, the proposed framework suffers from a long searching time and a large amounts of calculations.

Graph-based approaches

McClymont et al. [24] have used mean-shift to produce an initial segmentation of the MR image. The resulting regions were next used to construct a region adjacency graph which was segmented by the graph-cuts partitioning algorithm. Yu et al. [25] have proposed a segmentation framework which incorporates mean-shift smoothing, superpixel-wise classification, pixel-wise graph-cuts partitioning, and morphological refinement. Graph-based approaches are easy to implement. However, the accuracy of such methods is highly related to the number of edges that are in the graph to segment. Specifically, the more edges to process, the more accurate segmentation to obtain. Hence, by considering the fact that the complexity of these methods increases with the increase of the number of the edges of the graph, it is obvious that a high accuracy requires a high complexity.

Other Approaches

Jayender et al. [26] have presented a method dedicated to breast invasive cancer segmentation. The idea behind their

contribution is to model the underlying dynamics of the tumor by a linear dynamics system and use the system parameters to segment the cancer. Maicas et al. [27] have proposed a method based on a globally optimal inference in a continuous space using a shape prior computed from a semantic segmentation produced by a deep learning model. Despite the fact that the presented state-of-the-art methods are based on strong theoretical foundations, they actually generate a large amount of computations per final output.

Levels Propagation Approach

This section is dedicated to the presentation of the contribution, so-called *levels propagation approach (LPA)*. First, its initial bio-inspiration is justified. Then, for a better understanding of the essential details, the methodology flowchart and the pseudo-algorithm of the core of the approach are given. Finally, some of its points of strength compared to a resembling and well-known state-of-the-art method which is *seeded region growing (SRG)* are illustrated.

Origin of LPA

A tumor is a population of abnormal cells (tumor cells) that are issued from a single tumor cell originating from the mutation of a normal body cell [31]. The mutated cell initiates continuous and uncontrolled replications that induce the growth of the tumor in all directions around the tumor-initiating cell [32]. Figure 1 is inspired by Scott et al. [33] and shows the different steps of this tumor growing: initiation, promotion, and progression.

Through LPA, it is aimed to propose a new region-based segmentation approach that tries to reconstruct the development of a tumor which starts often from a given point (tumor-initiating cell) and propagates in all directions around the initiated cell to progressively reach a given level of surface area contamination. For this, a new concept of *level* that serves in the definition of a novel propagation way that characterizes LPA is introduced. In the contribution, a level is a set of pixels that surround a predefined pixel called *origin* in a specific way. Specifically, in this paper,

Fig. 2 A representation of four nested levels that surround the origin pixel

it is assumed that the origin is designated interactively from the core of the tumor area through an interface and each level is square shaped and placed in a manner that the origin is superposed with the centroid of the square. Thus, the levels are nested and non-overlapping. To better explain the introduced concept, four nested levels that surround the origin pixel are presented in Fig. 2. Each level is highlighted with a closed path passing through all its pixels. The principle of LPA is to process each level independently by starting from the closest level to the origin and to sequentially propagate to upper levels following the increasing order of the distances of the levels from the origin. The propagation stops as soon as a stopping predicate is satisfied.

Description of LPA

As it is mentioned above, LPA is inspired by a natural tumor development. It starts from a single pixel that belongs to the core of the tumor area and shifts progressively toward the boundary in an organized strategy. In other words, LPA tries to reconstruct the progression of the tumor by progressively processing different nested levels

Fig. 1 Tumor growing steps: initiation, promotion and progression [33]

that surround the origin. LPA proceeds in three main steps: *initialization*, *segmentation*, and *post-segmentation*. The general LPA framework is summarized in the methodology flowchart presented in Fig. 3 and the pseudo-algorithm of the core of LPA is given in Algorithm 1.

Initialization Step

This phase serves to prepare the parameters and data to be processed in the next step. Here, a minor human intervention is needed. Indeed, according to the shape and location of the tumor in the image, the user selects the origin pixel. Since the location of the origin is important in the measure that it affects the distances between the origin and the pixels which belong to the boundary of the tumor, it is a key factor in

determining the number of levels that are needed to process in order to reach the first level that is completely outside the tumor area. It is obvious that an optimal location of the origin would minimize that number of levels. Accordingly, such a location would be in fact the gravity center point of the tumor area. Thus, it is recommended to select it approximately around this point.

Segmentation Step

Just after the origin pixel is passed to LPA, the processing of levels starts. In this step, the levels are treated sequentially, starting from the closest level to the origin and propagating to upper levels until the stopping level is reached. Each level L_k , $k \geq 2$ is processed with an associated threshold Th_k^α which is automatically obtained from the processing of its previous level L_{k-1} , where α is a parameter to fix depending on the feature of the tumor in the MR image to analyze. Since the first level L_1 is too close to the origin which is supposedly near the gravity center of the tumor area, it is assumed that all its pixels are tumorous pixels. The remaining levels are processed one by one respecting the ascendent order of their distance to the origin. The processing of each level consists in differentiating its contaminated pixels (or in the process of being contaminated) from its safe pixels and this is done by analyzing all of its pixels with respect to the origin by starting from the top left corner pixel and pursuing the clockwise rotation. Specifically, the processing of the k -th level L_k , $k \geq 2$ is done in two steps: in the first step, the distance in terms of intensity between every pixel P_i^k , $i = 1, \dots, 8k$ of the level L_k and the origin O is calculated using the following formula: $d(P_i^k, O) = |I(P_i^k) - I(O)|$, where $8k$ is the number of pixels of level L_k and $I(P_i^k)$ (resp. $I(O)$) is the intensity of the pixel P_i^k (resp. O). In the second step, for every couple of neighboring pixels P_i^k and P_j^k of the level L_k , a test which consists in using the distances $d(P_i^k, O)$ and $d(P_j^k, O)$ (calculated in the first step) is performed to decide whether the two pixels are (in the process of being) contaminated or not. Thereby, if $d(P_i^k, O) \leq Th_k^\alpha \vee d(P_j^k, O) \leq Th_k^\alpha$, then it is considered that P_i^k and P_j^k are contaminated (or in the process of being contaminated), otherwise they are not. The associated threshold Th_k^α of the level L_k is obtained simply by using the greatest distance in term of intensity among the distances which are calculated for the contaminated pixels of the previous level L_{k-1} . The exact formula is the following:

$$Th_k^\alpha = \frac{1}{10} \left(\max_{i \in \mathcal{I}(L_{k-1})} \{d(P_i^{k-1}, O)\} + e^{\frac{1}{k}} \max_{i \in \mathcal{I}(L_k)} \{d(P_i^{k-1}, O)\} - \alpha \right), \quad (1)$$

Fig. 3 Flowchart of the proposed LPA

where $\mathcal{I}(L_{k-1}) = \{i \in \mathbb{N} : P_i^{k-1} \in L_{k-1}\}$, and α is a parameter related to the feature of the tumor in the MR image to analyze, such that

$$\alpha = \begin{cases} 0.8, & \text{if the image to process contains a tumor that} \\ & \text{expresses an enhancement after the injunction} \\ & \text{of the product of contrast;} \\ 0.95, & \text{otherwise.} \end{cases}$$

It is worth noting that the most important term in the formula (1) of the threshold Th_k^α is the term $\frac{1}{10}(e^{\frac{1}{10} \max_{i \in \mathcal{I}(L_k)} \{d(P_i^{k-1}, O)\}} - \alpha)$ which follows with enough fidelity the variation of the tumor through the different levels that characterize the LPA approach. However, the term $\frac{1}{10} \left(\max_{i \in \mathcal{I}(L_{k-1})} \{d(P_i^{k-1}, O)\} \right)$ is added in the formula (1) to play a smoothing role in the threshold Th_k^α estimation during the progression in the processing of the levels of LPA. More details, illustration, and discussion on the threshold Th_k^α will be given in “Threshold Discussion.”

Once all the pairs of neighboring pixels of the level L_k are verified, the same processing is applied to the pixels of the level L_{k+1} which is situated above the level L_k . The levels are treated one by one, producing therefore an organized propagation way that stops as soon as a specific level having a stopping condition is processed. Actually, it is worthwhile to note that the best level at which the propagation should stop has the feature that it is the closest level to the origin having all of its pixels outside the tumor area. Unfortunately, this situation is improbable and may not occur due to the noise that is present in the breast MR image. Specifically, the processing of a level that is completely outside the tumor area containing noisy pixels may result a small segmented component formed in each locality where a noisy pixel is present in that level. In this case, each noisy pixel erroneously generates a small segmented component composed of a successive supposed contaminated pixels. To overcome this issue, it is more convenient to stop the propagation at the first processed level which contains components of a tolerated size. For this purpose, the sum of pixels of each resulted component after the processing of each level is computed, and the propagation stops at the first level that produces components having at maximum three pixels. Note that this latter size is justified by the fact that the smallest size of a component generated by a noisy pixel with LPA is supposed to be equal to three.

Post-segmentation Step

Post-segmentation step is used to clean the image obtained from the previous step. In fact, the resulted segmented image does not only contain the tumor segment but also few disconnected small components around the component

of interest which is in this case the tumor area. These components can be understood as tumorous regions. However, generally it is not the case. Actually, they are formed from the noise and speckles that are present in the MR image. Therefore, it is more significant to remove them to guarantee a good segmentation accuracy. In order to keep the tumor component only, a mathematical morphology opening operation is used to remove the unwanted small components. By using this operation, all the segments which have a sum of pixels that does not exceed a fix threshold are removed.

Algorithm 1 Pseudo-algorithm of the core of LPA.

Input: MRI breast image, Origin pixel $O(x, y)$, parameter α .

Output: Segmented tumor.

```

1:  $k \leftarrow 1$ ;
2:  $max \leftarrow 0$ ;
3: for each pixel  $P_i^1, i = \overline{1, 8}$  of the level  $L_1$  do
4:  $d(P_i^1, O) \leftarrow |I(P_i^1) - I(O)|$ ;
5: if ( $max < d(P_i^1, O)$ ) then
6:  $max \leftarrow d(P_i^1, O)$ ;
7: end if;
8:  $P_i^1$  is a contaminated pixel;
9: end for;
10: repeat
11:  $k \leftarrow k + 1$ ;
12: Compute the threshold  $Th_k^\alpha$  associated to the level  $L_k$ 
    using formula (1);
13:  $max \leftarrow 0$ ;
14: for each pixel  $P_i^k, i = \overline{1, 8k}$  of the level  $L_k$  do
15:  $d(P_i^k, O) \leftarrow |I(P_i^k) - I(O)|$ ;
16: end for;
17: for every couple of neighboring pixels  $P_i^k$  and  $P_j^k$  of
    the level  $L_k$  do
18: if ( $d(P_i^k, O) \leq th_k^\alpha \vee (d(P_j^k, O) \leq th_k^\alpha)$ ) then
19:  $P_i^k$  and  $P_j^k$  are contaminated (or in the process of being
    contaminated);
20: if ( $\max \{d(P_i^k, O), d(P_j^k, O)\} > max$ ) then
21:  $max \leftarrow \max \{d(P_i^k, O), d(P_j^k, O)\}$ ;
22: end if;
23: end if;
24: end for;
25: Find the largest contaminated component  $C_k$  of the
    level  $L_k$ ;
26: until ( $|C_k| \leq 3$ );

```

Threshold Discussion

This subsection is devoted to discuss the properties of the function (1), especially the role of the parameter α in the threshold Th_k^α . And this, by taking into consideration two

Fig. 4 Example showing the impact of the value of the parameter α on the final extraction of a non-enhanced tumor

kinds of breast MRI images: an image containing a non-enhanced tumor (see Fig. 4a) and an image containing an enhanced tumor (see Fig. 6a). For each image, the results obtained by processing it with LPA by considering the two values of the parameter α were compared. The main conclusions of this comparison are given as follows.

- Figure 4 shows the impact of the two values of the parameter α on the final extraction of a non-enhanced tumor. From Fig. 4a, one can easily notice that a non-enhanced tumor has a close intensity mean to that of its surrounding normal tissue. Therefore, to extract such tumors, the threshold has to be sufficiently harsh when processing the levels to distinguish between tumorous pixels and safe pixels. This statement is illustrated in Fig. 4b and c, and Fig. 5. Actually, as it is shown in Fig. 5, when the threshold function is initialized with $\alpha = 0.95$, it returns low threshold values (approximately vary from 0.0145 to 0.0159), compared to those returned when it is initialized with $\alpha = 0.8$ (approximately vary from 0.0165 to 0.0180). In fact,

Fig. 5 Variation of the threshold values through the levels for the image of Fig. 4a according to $\alpha = 0.8$ and $\alpha = 0.95$

when $\alpha = 0.8$, the produced threshold values which are relatively large induce to exceed the real border of the tumor. This is the reason for which the tumor extraction which is illustrated in Fig. 4c (extracted with $\alpha = 0.95$) is considerably more accurate than the one that is shown in Fig. 4b (extracted with $\alpha = 0.8$). Thus, the sharp threshold values produced when $\alpha = 0.95$ cope well with the issue of intensity overlapping between the tumor and its surrounding healthy tissue in the case of a kind of image containing a non-enhanced tumor. Hence, the border of the tumor of an image of a such type is more precisely delineated when $\alpha = 0.95$ instead of $\alpha = 0.8$.

- Analogously, Fig. 6 shows the impact of the two values of the parameter α on the final extraction of an enhanced tumor. As one can see from Fig. 6a, an enhanced tumor region tends to be more bright than its surrounding normal tissue. Consequently, it is more easy to differentiate it from the latter, comparing it with the case of a non-enhanced tumor. Furthermore, generally enhanced breast tumors are characterized with high internal intensity heterogeneity. Thus, in order to extract such kind of tumors in an accurate way, a sufficiently high threshold is needed to consider when processing the levels to deal well with the inner intensity inhomogeneity of the tumor region as well as its border. As illustrated in Fig. 7, the application of the threshold function with $\alpha = 0.8$ to the enhanced tumor of the image of Fig. 6a produces adequately high enough threshold values (approximately vary from 0.021 to 0.024) which are more suitable in delineating the border of the tumor and also are less sensitive to the intensity changing within such a kind of tumor (see Fig. 6b). However, when $\alpha = 0.95$, the produced threshold values which are significantly low produce an under segmentation of the tumor which is characterized by the net presence of some areas having the characteristic as if they are not contaminated inside the tumor zone and does not reach its real border (see Fig. 6c). Thus the tumor extraction which is illustrated

Fig. 6 Example showing the impact of the value of the parameter α on the final extraction of an enhanced tumor

in Fig. 6b (extracted with $\alpha = 0.8$) is clearly more accurate than the one that it is shown in Fig. 6c (extracted with $\alpha = 0.95$). Hence, the area of the tumor of an image of such type is more precisely determined when $\alpha = 0.8$ instead of $\alpha = 0.95$.

Comparison Between LPA and SRG

Seeded region growing (SRG), which was introduced by Adams and Bischof [34], is a frequently applied image segmentation method in the literature. Moreover, it is widely used to extract tumors in medical images. Specifically, due to its ease of implementation, SRG have been applied in several works that addressed the segmentation of different breast pathologies such as cancer, mastitis, and cyst in a variety of imaging techniques. For example, in ultrasound by Malek et al. [35], in mammography by Shrivastava et al. [36], and in MRI by Al-Faris et al. [15].

Fig. 7 Variation of the threshold values through the levels for the image of Fig. 6a according to $\alpha = 0.8$ and $\alpha = 0.95$

LPA is based on a resembling principle to that of SRG. However, it differs from it in different features, mainly in the propagation way. In the conventional method, the process starts from an initial pixel that belongs to the ROI and propagates in the image in an anarchic manner. Then, basing on a threshold to decide whether two pixels are similar or not, it attracts to the ROI other pixels which are similar to the initial pixel, so that to extract at the end the ROI from the remaining part of the image. Unlike SRG, LPA comes up with the concept of levels that allows to establish a defined and organized propagation strategy. This characteristic is important in the measure that it offers to LPA possibilities to overcome issues that are limiting SRG in one hand and the state-of-the-art methods in the other hand. Some features of LPA are given below:

- At first glance, LPA is inherently suitable to parallelization. Actually, the way by which the levels are defined and the propagation strategy of LPA guarantee independence in the levels processing. Therefore, it is adaptable to parallelization with minimal changes. This is a considerable feature of LPA, notably when the approach is extended to segment 3D MRI breast tumor for which the need for methods having improved real-time performance is clear. Despite the benefits of parallel programming on dealing with the large amount of data which are generated in the MR exam, to the best of our knowledge, no previous attempts have been devoted to parallel or 3D parallel MRI breast tumor segmentation.
- Furthermore, in the majority of MRI breast tumors cases, tumors appear as heterogeneous regions. Therefore, it is more interesting to develop segmentation methods which are able to easily accommodate variations that may occur in the intensity distribution to ensure a good extraction of the tumor region. LPA is designed with a novel technique which is both simple and efficient, allowing it to adapt to any changing in intensity that may happen within the ROI. Indeed,

the information collected during the processing of a given level allows to LPA to learn about the evolution of the intensity distribution within the tumor region, in order to refine and adapt the threshold to the processing of the next level. By relying on this technique, the threshold automatically changes through the levels to better deal with the heterogeneity characterizing the tumor. Contrary to the state-of-the-art methods which tend to seek the optimal value of threshold by trial and error or analyze the histogram of the image. This is time consuming and lead generally to unsatisfactory results [28].

- Moreover, the application of LPA to an image containing a tumor consists in successively analyzing levels starting from the initial level L_2 to the terminal level L_{max} . The level L_{max} which represents the smallest envelope of the image that contains the tumor, by starting from O , is of utmost importance. In fact, L_{max} targets in a precise manner the tumor area. This is exactly with a significant importance; on one hand, it allows to LPA to considerably reduce the area of the image to analyze; on the other hand, it prevents it to reach the skin-line region which reduces the accuracy of the segmentation operation. Actually, as reported by Solves et al. [37] and Al-Faris et al. [38], in the majority of MRI breast cases, the skin-line region has relatively the same intensity level as the tumor region. Thus, the skin-line region can be easily considered as a part of the ROI leading to an erroneous segmentation result. Figure. 8 is given to visually illustrate the fact that in a breast MRI image, the skin-line region is closely similar in intensity to the tumor region. In the previous works such as in the method of Al-Faris et al. [15], this issue has been approached by a thinning operation which consist in the use of pre-processing techniques to exclude the undesired region before applying the segmentation operation. Despite the fact that performing the exclusion by using a pre-processing procedure can reduce the area to be processed, unfortunately, it is an additional step that increases the running time and considerably affects the final segmentation result, since any skin-line exclusion failure would reduce the segmentation accuracy. LPA supports the exclusion strategy, however, in a lightweight manner. Indeed, instead of using an additional pre-processing procedure, it relies on the levels to exclude the skin-line region from being processed. In fact, the stopping level has two roles: reducing the computation complexity of LPA by targeting only the main area where the ROI is and halting the propagation as soon as the main area is left, so as to prevent LPA to reach the skin-line region.

Fig. 8 An example of an image from the RIDER breast tumor MRI dataset in which the intensity of the skin-line region is closely similar to the intensity of the tumor region

Experimental Evaluation

This section is devoted to the evaluation of the proposed approach LPA. For this aim, two features are analyzed, namely segmentation accuracy and computation complexity. To do this, we present the differently used evaluation metrics, then we report the obtained results induced from the comparison of LPA with concurrent methods in the literature on two datasets. Lately in the section, the computation complexity of LPA is estimated.

Accuracy Analysis

The proposed approach was developed in MATLAB R2015b, performed on an Acer Aspire 5732Z, with Intel Pentium (R) dual-core CPU 2.20 GHz, 2 GB RAM, on a 32-bit Windows 8.1 Professional platform. For the experiments, two clinical datasets of breast tumors are used: a public dataset and a dataset which we have constructed in collaboration with a specialized radiology service of a well-reputed hospital. Each of the latter contains MRI images with benign and malignant breast tumors, as well as ground truth images that are used as a benchmark to evaluate the accuracy of the obtained segmentation.

Evaluation Metrics

To evaluate the accuracy of the new approach LPA, a set of five metrics is used to compare the obtained segmentation

results with their associated ground truths. Accordingly, two parameters should be found: the first parameter is the number of pixels that constitute the segmented region, while the second parameter is the number of pixels of the ground truth region that is delineated by the expert radiologists. These two parameters are used to calculate the following metrics: the true positive fraction (TPF), the true negative fraction (TNF), the sum of true volume fraction (STVF), the relative overlap (RO), and the misclassification rate (MCR). The formulas of the metrics can be found in [15, 17].

A good segmentation is indicated, on one side, by high values of TPF, TNF, STVF, and RO and, on the other side, by a low value of MCR.

RIDER breast MRI Dataset: Results and Discussion

The first dataset on which the validation studies of the proposed approach are carried out is the *Reference Image Database to Evaluate Therapy Response* (RIDER) breast MRI dataset which belongs to the US National Cancer Institute. The dataset is publicly available for download from the Cancer Imaging Archive (TCIA) [39]. It contains coffee break repeat dynamic contrast-enhanced magnetic

resonance imaging (DCE-MRI) data of five subjects diagnosed with primary breast tumors. The collection includes also ground truth segmented images that have been manually identified by expert radiologists. All the ground truth images are 288×288 pixels and made for the axial slices of the breast MR images only.

For the evaluations on RIDER breast MRI dataset, LPA has been applied to forty randomly selected images from the dataset. The obtained overall segmentation results are compared to the ones of previous works. Specifically, six different segmentation methods were chosen for the purpose; five of them have been stated in the comparative study of Azmi et al. [17], namely K-Nearest Neighbor (K-NN), Support Vector Machine (SVM), Bayesian, Fuzzy C-Means (FCM), and Improved Self-Training (IMPST). Whilst, the sixth method is Modified Automatic Seeded Region Growing (MASRG) which is proposed by Al-Faris et al. [15]. The choice of these methods is motivated by the fact that all of them have been tested on the same dataset (RIDER breast MRI dataset) and evaluated by adopting the same evaluation metrics that were introduced in “Evaluation Metrics”. The experimental results are summarized in Table 2 and an example of the application of LPA to two images is shown

Table 2 Segmentation accuracy results for the proposed approach and concurrent approaches for RIDER breast MRI dataset

Methods	Statistics	TPF	TNF	STVF	RO	MCR
MASRG	Mean	0.82	0.90	1.73	0.75	0.18
Al-Faris et al. [15]	Std	0.10	0.10	0.10	0.09	0.10
	Max	0.99	0.99	1.87	0.88	0.48
	Min	0.52	0.65	1.46	0.49	0.01
IMPST	Mean	0.79	0.83	1.61	0.68	0.21
Azmi et al. [17]	Std	0.19	0.15	0.21	0.17	0.12
	Max	0.96	0.99	1.88	0.89	0.62
	Min	0.38	0.58	1.18	0.34	0.04
K-NN,	Mean	0.73	0.75	1.49	0.60	0.27
Fix and Hodges [18]	Std	0.13	0.15	0.19	0.12	0.10
	Max	0.87	0.97	1.75	0.76	0.58
	Min	0.42	0.99	1.85	0.36	0.13
SVM	Mean	0.75	0.71	1.46	0.60	0.25
Yao et al. [19]	Std	0.19	0.21	0.31	0.19	0.12
	Max	0.94	0.99	1.85	0.86	0.70
	Min	0.30	0.17	0.67	0.26	0.06
Bayesian	Mean	0.76	0.59	1.34	0.56	0.24
Wu et al. [20]	Std	0.19	0.25	0.35	0.17	0.08
	Max	0.95	0.97	1.76	0.77	0.70
	Min	0.30	0.09	0.69	0.22	0.05
FCM	Mean	0.82	0.42	1.24	0.59	0.18
Chen et al. [21]	Std	0.27	0.55	0.71	0.25	0.08
	Max	0.99	0.96	1.83	0.84	1.00
	Min	0	−0.73	−0.19	0	0.01
LPA,	Mean	0.90	0.79	1.70	0.90	0.11
The proposed approach	Std	0.04	0.12	0.13	0.38	0.13
	Max	0.97	0.96	1.89	1.89	0.85
	Min	0.77	0.49	1.32	0.51	0.02

in Fig. 9 in which Fig. 9a (resp. Fig. 9d) is an original breast MRI image that contains a tumor, Fig. 9b (resp. Fig. 9e) is the ground truth image that is delineated by expert radiologists from Fig. 9a (resp. Fig. 9d), and finally Fig. 9c (resp. Fig. 9f) is the extracted tumor from Fig. 9a (resp. Fig. 9d) using LPA. As it can be seen in Fig. 9, LPA has accurately extracted the tumor regions from the original images. Furthermore, the experimental results have shown that in general LPA has yielded competitive segmentation results to the concurrent state-of-the-art methods and has shown the potential to be successfully applied to breast tumor extraction from MR images. Specifically, LPA has had the best TPF mean score of all the evaluated methods, it has achieved a score of 0.90 which is by far higher than the one achieved by both MASRG and FCM. Furthermore, the RO mean score of LPA, which is 0.90, is significantly higher than the best RO mean of the remaining methods. LPA also has reached a MCR mean of 0.11 which is much less than the MCR mean of MASRG and FCM. Thus, LPA has had the best MCR mean of all the evaluated methods. The good results yielded by LPA are justified by the use of the novel thresholding technique that ensures a simple and accurate solution to overcome the issue of intensity inhomogeneity of breast tumors. Actually, the new thresholding technique proceeds by taking advantage from the organized propagation which characterizes LPA to progressively learn about the changes that occur in the intensity distribution within the tumor region. Therefore, it exploits the acquired knowledge to gradually refine the threshold value through the levels in order to deal with the intensity changes. In addition, LPA

delimits the tumor area by examining at each time a pair neighboring pixels, this is more accurate than examining one by one pixels, because it is less sensitive to intensity alternations.

However, LPA has yielded less favorable results regarding two evaluation metrics. Actually, it have produced the third-best TNF mean score and the second best STVF mean score of all the tested methods. This comes down to the fact that LPA slightly exceeds the border of a tumor, because it is based on the evaluation of pairs neighboring pixels. Consequently, the pixels which are adjacent to the tumor's border pixels (contaminated pixels) are considered by LPA as being pixels that are in the process of being contaminated and are therefore added to the tumor area during the segmentation process. As a result, the region extracted by LPA exceeds the border that is delimited by expert radiologists in the ground truth image by one pixel all around the border of the tumor.

CHM-LIMED Breast MRI Dataset: Results and Discussion

The second dataset on which LPA is evaluated is the *Chahids Mahmoudi Hospital-Laboratory of Medical Informatics* (CMH-LIMED) breast MRI dataset, which contains fat-saturated T1-weighted images of eighteen patients having different types of tumors that vary in shape and location. The images of the dataset were collected in the radiology service of Chahids Mahmoudi Hospital (<https://hcm-dz.com>) in Tizi Ouzou, Algeria on September 2018, using a General Electric (GE) MRI device. Furthermore,

Fig. 9 Example of segmentation results of LPA on RIDER dataset. With (b) and (c) (resp. (e) and (f)) are the ground truth and the extracted tumor of (a) (resp. (d))

Fig. 10 Example illustrating the segmentation results of a non-enhanced tumor using MASRG, Level set, and LPA. With **a** is the original MRI image, **b** is the ground truth, **c** is the segmented image by MASRG, **d** is the segmented image using Level set, and **e** is the segmented image by LPA

all the medical imaging data of the dataset were totally anonymized before provision, and the dataset itself contains ground truth mask images that were made with the help of Dr Farid Kechih who is a confirmed expert radiologist and the head of the radiology service of the hospital. Both the original and ground truth images are 512×512 pixels. Moreover, it is noteworthy to mention that this study was approved by the head of the radiology service of the establishment.

In addition to what we have done previously, LPA has been tested on the CMH-LIMED breast MRI dataset and its results are compared against MASRG [15] which is region-based and the most recent method among the concurrent methods previously used for RIDER breast MRI dataset,

as well as the golden standard Level set [40] that is a contour-based method.

However, unlike the first dataset, this second dataset is split into two sub-datasets, CMH-LIMED 1 and CMH-LIMED 2, according to two kinds of tumors, non-enhanced and enhanced tumors. More specifically, CMH-LIMED 1 is constituted of a set of twenty-four images from eight patients having non-enhanced tumors and CMH-LIMED 2 is constituted of a set of thirty images from ten patients with enhanced tumors. This would allow principally to have more precise and clear conclusions about the performance of the evaluated methods regarding the two kinds of tumors.

An example of the segmentation results of LPA and its concurrent methods for non-enhanced tumors is shown

Table 3 Segmentation accuracy results for MASRG, Level set, and LPA for CMH-LIMED 1 breast MRI dataset

Methods	Statistics	TPF	TNF	STVF	RO	MCR
MASRG Al-Faris et al. [15]	Mean	0.4622	−30.0527	−29.5905	0.0292	0.5395
	Std	0.4069	29.1071	29.1562	0.0388	0.4180
	Max	1.0000	−1.6749	−1.6749	0.1522	1.0000
	Min	0	−89.0161	−88.7972	0	0
Level set Li et al. [40]	Mean	0.7441	0.7706	1.5442	0.6369	0.2683
	Std	0.1675	0.2464	0.2749	0.1664	0.1731
	Max	0.9389	1.0000	1.8664	0.8754	0.6939
	Min	0.3061	0.2500	0.8397	0.2804	0.0611
LPA, the proposed approach	Mean	0.8632	0.6345	1.4977	0.6518	0.1368
	Std	0.1116	0.2498	0.2818	0.1388	0.1116
	Max	1.0000	0.9312	1.8387	0.8493	0.3878
	Min	0.6122	0.0469	0.9389	0.3822	0

Table 4 Segmentation accuracy results for MASRG, Level set and LPA for CMH-LIMED 2 breast MRI dataset

Methods	Statistics	TPF	TNF	STVF	RO	MCR
MASRG	Mean	0.7810	0.7655	1.5464	0.6611	0.2190
Al-Faris et al. [15]	Std	0.1701	0.4169	0.3655	0.1593	0.1701
	Max	0.9875	1.0000	1.8805	0.8829	0.6849
	Min	0.3151	−0.6526	0.3319	0.2774	0.0125
Level set	Mean	0.7105	0.8250	1.5295	0.6022	0.2796
Li et al. [40]	Std	0.2118	0.1747	0.2100	0.1713	0.2093
	Max	0.9917	1.0000	1.8318	0.8498	0.8178
	Min	0.1822	0.3435	1.0844	0.1743	0.0083
LPA,	Mean	0.8422	0.8445	1.6868	0.7443	0.1578
the proposed approach	Std	0.1337	0.2281	0.2356	0.1369	0.1337
	Max	0.9875	1.0000	1.9063	0.9108	0.5418
	Min	0.4582	0.0688	0.9168	0.3481	0.0125

in Fig. 10. From Table 3 which reports the experimental results for CMH-LIMED 1, it is easy to deduce that LPA has produced encouraging results for non-enhanced tumors. In fact, it has achieved a high TPF mean score, around 0.86, which is far better than the TPF scores of the Level set and MASRG. In addition, it approximately yielded an RO mean score of 0.65 and an MCR mean score of 0.13 which are considered as the best scores among those of all the tested methods. However, LPA has achieved the second best mean scores in TFN and STVF metrics for which the best mean scores are obtained by level set. The

worst scores for this sub-dataset are produced by MASRG. This is justified by the fact that the method uses the pixel having the highest intensity in the MRI image as a seed to initiate region growing. This technique is more suitable for enhanced tumors cases, because in such situations, the tumor region has the maximum mean intensity of all the regions of the MRI image. Unfortunately, considering the fact that after the injection of the contrast product, this latter is transported in the blood which passes through the heart inducing an enhancement of the corresponding region in the MRI image. Consequently, when the tumor region is not

Fig. 11 Example showing the segmentation results of an enhanced tumor using MASRG, Level set, and LPA. With **a** is the original MRI image, **b** is the ground truth, **c** is the segmented image by MASRG, **d** is the segmented image using Level set, and **e** is the segmented image by LPA

Table 5 Segmentation accuracy results for MASRG, Level set and LPA for CMH-LIMED breast MRI dataset

Methods	Statistics	TPF	TNF	STVF	RO	MCR
MASRG	Mean	0.6535	−11.5618	−10.9083	0.4084	0.3433
Al-Faris et al. [15]	Std	0.3259	23.6899	23.8146	0.3367	0.3285
	Max	1.0000	1.0000	1.8805	0.8829	1.0000
	Min	0	−89.0161	−88.7972	0	0
	Mean	0.7255	0.8026	1.5360	0.6176	0.2745
Level set Li et al. [40]	Std	0.1924	0.2067	0.2387	0.1685	0.1924
	Max	0.9917	1.0000	1.8664	0.8754	0.8178
	Min	0.1822	0.2500	0.8397	0.1743	0.0083
	Mean	0.8515	0.7512	1.6027	0.7032	0.1485
LPA, the proposed approach	Std	0.1237	0.2581	0.2717	0.1441	0.1237
	Max	1.0000	1.0000	1.9063	0.9108	0.5418
	Min	0.4582	0.0469	0.9168	0.3481	0
	Mean					

sufficiently enhanced, the seed pixel is chosen among the pixels of the heart region leading to the segmentation of this latter instead of the tumor region, as in the case of Fig. 10c.

Concerning the validation studies for enhanced tumors, the experimental results for CMH-LIMED 2 sub-dataset are outlined in Table 4. From the latter, one can observe that LPA has produced the best mean scores for all the evaluation metrics. Thus, it outperforms its concurrent state-of-the-art methods. Specifically, it has yielded a TPF mean of approximately 0.84, a TNF mean which is around 0.84, a STVF mean that is about 1.68, an RO mean of approximately 0.74, and, finally, an MCR mean approximating 0.15. Figure 11 illustrates a sample of segmentation results of an enhanced tumor by MASRG, Level set, as well as LPA.

Finally, to make a concluding statement about the overall performance of the proposed approach LPA, a summarization of the validation study for the whole CMH-LIMED breast MRI dataset is given in Table 5. In general, LPA has achieved a satisfying performance and exhibited the ability to be successfully applied to segment both non-enhanced and enhanced tumors as can be seen from Table 5. This is justified by the fact that LPA is outperformed by its concurrent methods in one evaluation metric only, namely TNF in which Level set has reached a mean score that is around 0.80 exceeding the TNF mean obtained by LPA with approximately 0.05. Nevertheless, the best mean scores for the remaining metrics are obtained by LPA.

Despite the advantages of LPA over the state-of-the-art methods and its yielded good results, it is worth to mention in this discussion that it has a limitation. Actually, it is true that the human intervention is minor when the MRI image to process presents one tumor. However, it gets higher with the increase in the number of tumors to segment in the same image.

Computation Complexity Analysis

In this subsection, the complexity of LPA is analyzed. Here, the complexity is estimated in terms of the number of operations done through the processing of the levels from L_2 to L_{max} . Consequently, there are $m = max - 1$ levels to which the same processing is applied and each level L_k contains exactly $8k$ pixels. Thus, it is easily to deduce that the total number of operations performed by LPA is $NO = NO(L_2) \times \frac{1}{2} \sum_{i=2}^{m+1} i$, where $NO(L_2)$ is the number of operations performed in the level L_2 . Hence it is obtained that $NO = NO(L_2) \times \frac{m(m+3)}{4}$. Accordingly, the complexity of LPA is quadratic that is $O(m^2)$.

Conclusion

In this paper, a new region-based semi-automatic approach for the segmentation of breast tumors from MR images is developed. The presented approach is named Levels Propagation Approach (LPA) and takes inspiration from the natural development of a tumor. Actually, a tumor originates from a mutation of a normal body cell which initiates continuous and uncontrolled replications inducing the growth of the tumor in all directions around that abnormal cell. LPA tries to reconstruct this natural development process to segment breast tumors. To do so, the processing starts from a specific pixel called the origin which is manually selected from the core of the tumor area. Then, relying on nested and non-overlapped levels, it propagates respecting an organized way in all directions around the origin until reaching all the contaminated surface area. LPA is endowed with several features including a high potential for parallelization, a simple technique for the automatic selection of the threshold, and its refinement to deal with the

issue of overlapping intensity between non-enhanced breast tumors and their surrounding healthy tissue, as well as the internal heterogeneity of enhanced breast tumors. Moreover, LPA is designed to stop at any desired limit. This feature is important specifically to avoid reaching the skin-line region which is considered to be an issue that compromises the segmentation results.

Furthermore, the performance of the new approach has been studied over images from two different clinical datasets, RIDER breast tumor dataset, and CMH-LIMED breast MRI dataset. Experimental results have shown the effectiveness of LPA and its applicability to accurately segment both enhanced and non-enhanced breast tumors.

As future works, it is intended to focus on improving the performance of LPA and extending it to a fully automatic approach by adding further implementations such as an automatic technique for the automatic selection of the origin pixel. Also, it is interesting to use the levels for the aim of tumor classification to distinguish whether an extracted tumor is benign or malignant for diagnosis purposes. Furthermore, it is planned to extend it to a 3D parallel approach.

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References

- Hecht F, Pessoa CF, Gentile LB, Rosenthal D, Carvalho DP, Fortunato RS: The role of oxidative stress on breast cancer development and therapy. *Tumor Biol* 37:4281–4291, 2016
- World Health Organization (2018) Available at <http://www.who.int/en/>. Accessed on October 20th
- Banaie M, Soltanian-Zadeh H, Saligheh-Rad HR, Gity M: Spatiotemporal features of DCE-MRI for breast cancer diagnosis. *Comput Methods Programs Biomed* 155:153–164, 2018
- Ferreira A, Gentil F, Tavares JMR: Segmentation algorithms for ear image data towards biomechanical studies. *Comput Methods Biomech Biomed Engin* 17:888–904, 2014
- Mughal B, Sharif M: Automated detection of breast tumor in different imaging modalities: A Review. *Current Medical Imaging Reviews* 13:121–139, 2017
- Scoggins M, Dogan B, Ma J, Wei W, Song JB, Candelaria RP, Litton JK, Arun B: Short breast MRI screening trial in women at high-risk for breast cancer. *J Clin Oncol* 35:e13049, 2017
- Ma Z, Tavares JMR, Jorge RN, Mascarenhas T: A review of algorithms for medical image segmentation and their applications to the female pelvic cavity. *Comput Methods Biomech Biomed Engin* 13:235–246, 2010
- Singh SP, Urooj S: An improved CAD system for breast cancer diagnosis based on generalized pseudo-Zernike moment and Ada-DEWNN classifier. *J Med Syst* 40:105–118, 2016
- Jida S, Aksasse B, Ouanan M (2017) Face segmentation and detection using Voronoi diagram and 2D histogram. In: *Intelligent systems and computer vision*, Fez, 1–5
- Oliveira RB, Mercedes Filho E, Ma Z, Papa JP, Pereira AS, Tavares JMR: Computational methods for the image segmentation of pigmented skin lesions: a review. *Comput Methods Programs Biomed* 131:127–141, 2016
- Shi J, Sahiner B, Chan HP, Paramagul C, Hadjiiski LM, Helvie M, Chenevert T: Treatment response assessment of breast masses on dynamic contrast-enhanced magnetic resonance scans using fuzzy c-means clustering and level set segmentation. *Med Phys* 36:5052–5063, 2009
- Yin D, Lu RW (2015) A method of breast tumour MRI segmentation and 3D reconstruction. In: *7th International conference on information technology in medicine and education*, Huangshan, 23–26
- Liu H, Liu Y, Zhao Z, Zhang L, Qiu T: A new background distribution-based active contour model for three-dimensional lesion segmentation in breast DCE-MRI. *Med Phys* 41(8), Part 1, 2014
- Agner SC, Xu J, Madabhushi A: Spectral embedding based active contour (SEAC) for lesion segmentation on breast dynamic contrast enhanced magnetic resonance imaging. *Med Phys* 40(3), 2013
- Al-Faris AQ, Ngah UK, Isa NAM, Shuaib IL: Computer-aided segmentation system for breast MRI tumour using modified automatic seeded region growing (BMRI-MASRG). *J Digit Imaging* 27:133–144, 2014
- Cui Y, Tan Y, Zhao B, Liberman L, Parbh R, Kaplan J, Theodoulou M, Hudis C, Schwartz LH: Malignant lesion segmentation in contrast-enhanced breast MR images based on the marker-controlled watershed. *Med Phys* 36:4359–4369, 2009
- Azmi R, Anbiaee R, Norozi N, Salehi L, Amirzadi A: IMPST: a new interactive self-training approach to segmentation suspicious lesions in breast MRI. *J Med Signals Sensors* 1:138–148, 2011
- Fix E, Hodges JL (1951) Discriminatory analysis, nonparametric discrimination: Consistency properties, Technical Report 4, USAF School of Aviation Medicine, Randolph fields TX
- Yao J, Chen J, Chow C: Breast tumor analysis in dynamic contrast enhanced MRI using texture features and wavelet transform. *IEEE J Sel Top Sign Proces* 3:94–100, 2009
- Wu Q, Salganicoff M, Krishnan A, Fussell DS, Markey MK (2006) Interactive lesion segmentation on dynamic contrast enhanced breast MRI using a markov model. In: *Proc. SPIE medical imaging: Image processing*, 6144, San Diego
- Chen W, Giger ML, Bick U: A fuzzy c-means (FCM)-based approach for computerized segmentation of breast lesions in dynamic contrast-enhanced MR Images. *Acad Radiol* 13:63–72, 2006
- Moftah HM, Azar AT, Al-Shammari ET, Ghali NI, Hassanien AE, Shoman M: Adaptive K-means clustering algorithm for MR breast image segmentation. *Neural Comput Appl* 24:1917–1928, 2014
- Hassanien AE, Moftah HM, Azar A T, Shoman M: MRI breast cancer diagnosis hybrid approach using adaptive ant-based segmentation and multilayer perceptron neural networks classifier. *Appl Soft Comput* 14:62–71, 2014
- McClymont D, Mehnert A, Trakic A, Kennedy D, Crozier S: Fully automatic lesion segmentation in breast MRI using mean-shift and

- graph-cuts on a region adjacency graph. *J Magn Reson Imaging* 39:795–804, 2014
25. Yu N, Wu J, Weinstein SP, Gaonkar B, Keller BM, Ashraf AB, Jiang Y, Davatzikos C, Conant EF, Kontos D (2015) A superpixel-based framework for automatic tumor segmentation on breast DCE-MRI. In *Proc. SPIE medical imaging: Computer-aided diagnosis*, 9414, Orlando
 26. Jayender J, Chikarmane S, Jolesz FA, Gombos E: Automatic segmentation of invasive breast carcinomas from dynamic contrast-enhanced MRI using time series analysis. *J Magn Reson Imaging* 40:467–475, 2014
 27. Maicas G, Carneiro G, Bradley AP (2017) Globally optimal breast mass segmentation from DCE-MRI using deep semantic segmentation as shape prior. In: *14th international symposium on biomedical imaging*, Melbourne, 305–309
 28. Zaheeruddin Z, Jaffery ZA, Singh L (2012) Detection and shape feature extraction of breast tumor in mammograms. In: *Proceedings of the world congress on engineering*, London, pp 719–724
 29. Xie X, Yeo SY, Mirmehdi M, Sazonov I, Nithiarasu P: Image gradient based level set methods in 2D and 3D. In: González HM, et al Eds. *Deformation Models*, Netherlands, 2013, pp 101–120
 30. Pavlidis G (2017) Segmentation of digital images. In: *Mixed Raster Content. Signals and communication technology*, Singapore, 213–260
 31. Nowell PC: The clonal evolution of tumor cell populations. *Science* 194:23–28, 1976
 32. Visvader JE: Cells of origin in cancer. *Nature* 469:314–322, 2011
 33. Scott RE, Wille JJ, Wier ML: Mechanisms for the initiation and promotion of carcinogenesis: a review and a new concept. *Mayo Clin Proc* 59:107–117, 1984
 34. Adams R, Bischof L: Seeded region growing. *IEEE Trans Pattern Anal Mach Intell* 16:641–647, 1994
 35. Malek AA, Rahman WEZWA, Haris MHM, Jalil UMA: Segmenting masses in ultrasound images by using seed based region growing and mathematical morphology. *Adv Sci Lett* 23:11512–11516, 2017
 36. Shrivastava A, Chaudhary A, Kulshreshtha D, Singh VP, Srivastava R (2017) Automated digital mammogram segmentation using dispersed region growing and sliding window algorithm. In: *2nd international conference on image, vision and computing*, Chengdu, pp 366–370
 37. Solves LJ, Monserrat C, Rupérez MJ, Naranjo V, Alajami M, Feliu F, García M, Lloret M: MRI skin segmentation for the virtual deformation of the breast under mammographic compression. *Stud Health Technol Inform* 173:483–489, 2012
 38. Al-Faris AQ, Isa NAM, Ngah UK, Shuaib IL (2015) Automatic exclusion of skin border regions from breast MRI using proposed combined approach. In: *2nd international conference on biomedical engineering*, Perlis, pp 1–6
 39. Meyer CR, Chenevert TL, Galbán CJ, Johnson TD, Hamstra DA, Rehemtulla A, Ross BD (2015) Data from RIDER-Breast-MRI. The cancer imaging archive. <http://doi.org/10.7937/K9/TCIA.2015.H1SXNXL>
 40. Li C, Huang R, Ding Z, Gatenby J, Metaxas DN, Gore JC: A level set method for image segmentation in the presence of intensity inhomogeneities with application to MRI. *IEEE Trans Image Process* 20:2007–2016, 2011