Breast MRI Multi-Tumor Segmentation Using 3D Region Growing: Preliminary Results

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Abstract

Breast tumor analysis is essential to diagnose breast cancer. Accurate 3D segmentation of breast tumors from medical images is essential for comprehensive disease analysis. This paper presents an automated pipeline for segmenting multiple breast tumors from Magnetic Ressonance Imaging (MRI) scans. Utilizing a 3D region growing algorithm, the study addresses challenges in detecting multiple tumors and seed point selection. Successful segmentation of four tumors highlights the potential of this approach for automatic multi-tumor segmentation, suggesting compatibility with a classification model based on the segmented structural features.

1 Introduction

Breast cancer is a major global health concern with high mortality rates, emphasizing the importance of early detection, which has been shown to improve the quality of life and survival rates [3]. Computer-aided Diagnosis (CAD) systems aid in breast mass detection through detection, segmentation, and classification stages [1]. However, automatic breast tissue segmentation faces challenges due to varying breast sizes and shapes, intensity inhomogeneities, image artifacts, and other noise errors. Tumor classification relies on distinctive characteristics, with malignant tumors being often irregularly shaped and surrounded by spicules, whereas benign tumors tend to have more rounded or elliptical shapes [1]. This study addresses limitations in Pelicano et al. [3] segmentation pipeline, focusing on the automatic seed point selection and the segmentation of multiple tumors. The paper outlines an overview of related works, a description of the materials and methods, and the presentation of the results, followed by a discussion of the findings and main conclusions of this work.

2 Literature Review

Accurately identifying tumor boundaries is essential for treatment assessment, but challenges arise due to variable shapes and intensity distributions of breast lesions. Traditional methodologies use the intensity values of the entire image, however, when dealing with heterogeneous structures, these methods result in a poor segmentation of the tumor volume. Researchers have proposed various solutions, such as specifying seed points and threshold values to distinguish lesion and non-lesion regions.

Wang et al. [6] proposed a deep learning model for micro-calcifications detection in mammograms. They segmented images into small clusters to analyze micro-calcification characteristics and larger clusters for surrounding tissue analysis. In [5], authors employed machine learning to detect breast tumors in mammograms, utilizing geometric and texture features, such as roundness, entropy and energy, for tumor localization. Melouah et al. [2] proposed mammogram segmentation using a threshold determined from row-wise pixel values and seed point selection using statistical features, yielding strong single-tumor detection but limited multi-tumor performance. Shrivastava et al. [4] introduced automatic seed point identification and threshold calculation using seeded region growing. More recently, Pelicano et al. [3] introduced a semi-automatic 3D region growing technique for the successful segmentation of heterogeneous tissues. Although it requires manual seed selection, the method excels at segmenting varying tissue heterogeneity. However, it struggles to identify multiple tumors.

Existing tumor segmentation methods present several limitations. Some prioritize accuracy over efficiency, incurring high computational costs. Certain approaches demand substantial human input, like seed position and threshold selection, hindering their implementation. Conversely, others attain high accuracy but struggle with multi-tumor segmentation.

3 Materials and Methods

In this exploratory analysis, two MRI scans from different patients were used, containing a total of six tumors: five in one scan and one in the other. Patients were scanned using a Siemens MAGNETON Vida MRI machine and a specialized Siemens Breast 18 coil. Images were collected under clinical protocols CES/44/2019/ME (2019) and CES/34/2020/ME (2020) at Hospital de Luz Lisboa. The collected MRI sequences included DCE-fl3D and T1-w Dixon. DCE-fl3D images enhanced tumor visibility using a gadolinium contrast agent, and Pelicano et al. [3] performed digital subtractions for better tumor highlighting. This study also utilized SUB-DCE-fl3D images for effective tumor segmentation.

The pre-processing followed the pipeline proposed in [3], comprising bias field correction, data normalization, and image filtering. Bias field artifacts were corrected using SimpleITK N4BiasFieldCorrectionImage filter. Data normalization scaled voxel values using Min-Max approach. Regarding image filtering, a median filter was used to remove Salt-and-Pepper noise and smooth intensity variations.

3.1 Tumor Segmentation

To address inaccuracies in segmenting heterogeneous tumors with varying intensity values, a 3D region growing algorithm was utilized. This algorithm starts from a seed point, and expands the region by adding adjacent voxels within a specified threshold range.

3.1.1 Threshold Selection

The 3D region growing algorithm's threshold was derived statistically from non-zero values. The threshold was set at three standard deviations above the mean to differentiate tumors from surrounding tissue effectively, as suggested in [3].

3.1.2 Seed Selection

The initial stage of the tumor segmentation process involved the selection of a seed point. To address this, an automatic seed detection algorithm was developed:

1. Subsampling: Image division into non-overlapping regions using a 5-point step size in both axes, optimizing computational efficiency while retaining information.

2. Points of Interest: Analyzing each point in the reduced set for each transverse cut to identify potential regions of interest using the 3D region growing method. This step identifies points where surrounding voxel intensities align with threshold-defined intervals. The order in which the cuts are processed was determined based on the number of points of interest identified in each cut, prioritizing high-intensity areas for efficient tumor detection.

3. Regions of Interest: K-means clustering groups high-intensity points by spatial location, separating isolated points from actual regions of interest. Single-point clusters are discarded, focusing on multi-voxel clusters.

4. Region Segmentation: Applying the 3D region growing algorithm to each group's centroid segments regions of interest, with the process continuing across cuts without re-segmentation. This results in a comprehensive mask encompassing the structures identified across cuts.

3.1.3 Structure Characterization

After segmentation, structures underwent analysis by calculating volume, circularity, and compactness measures. The volume was calculated by voxel count multiplied by voxel size (1mm x 1mm x 1mm), providing structural size information. The circularity was computed by multiplying the volume by 4π and then dividing it by the square of the surface area, providing circularity values between 0 and 1. The compactness was calculated by multiplying the square of the volume by 36π, and then dividing the result by the cube of the surface area, yielding compactness values between 0 and 1.

4 Results

The results showcase the application of the proposed methodology to MRI scans: one with multiple tumors (1 malignant, 4 benign), another with a single malignant tumor. One transverse cut was chosen for demonstration. The 3D region-growing algorithm applied in the centroids of the k-means clustering, successfully segments tumors based on intensity thresholds. In Figure 1, the left side shows the yellow segmented tumor mask on the transverse cut. The right side displays the same mask in three dimensions, confirming accurate segmentation.

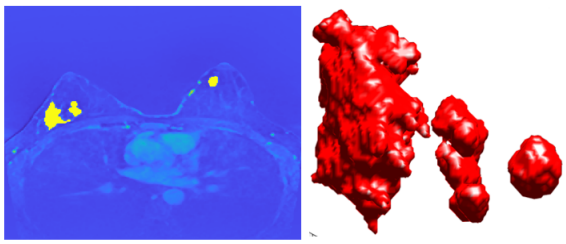

Figure 1: Left: Output of the 3D region-growing, represented in yellow. Right: Representation, in three dimensions, of the application of the yellow mask on the left.

The segmentation was expanded to all transverse cuts, yielding a complete mask. In Figure 2, on the left, four tumors were well-segmented, and an irregular artifact appeared. One benign tumor was missed, likely due to parameter constraints when detecting small volumes. For the other scan (Figure 2, on the right), the algorithm struggled with a large, irregular tumor, suggesting the need for parameter tuning for better results.

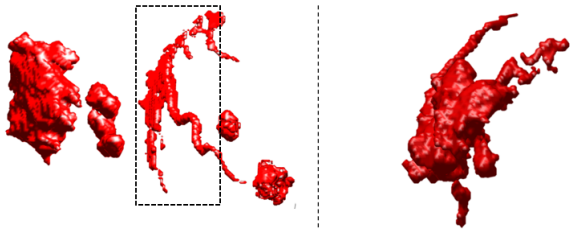

Figure 2: Left: Representation of the final 3D mask obtained for the multi-tumor MRI exam. Right: Representation of a poorly-segmented tumor obtained for the single-tumor MRI exam.

Masks were segmented into individual structures for analysis: five in the first exam and one in the second. The resulting structures were label based on their position in Figure 2, numbered from 1 to 5 from left to right, and characterized by their volume, compactness, and circularity.

Table 1 reveals that malignant tumors exhibited larger volumes (11.682 mm^3 and 12.259 mm^3 for the first and second exams, respectively) than benign tumors. Malignant tumors showed lower circularity (0.0067 and 0.0035) and compactness (0.1502 and 0.0586), indicating irregular and less rounded shapes. In contrast, benign tumors (structures 2, 4, and 5) demonstrated higher circularity and compactness, indicating their round and compact shapes. The third structure - an artifact - had the lowest compactness (0.0167) and ranked second lowest in volume and circularity (845 mm^3 and 0.0037, respectively). These findings align with the expected characteristics of malignant and benign tumors, enhancing the pipeline accuracy in distinguishing non-tumor structures.

Table 1: Characterization of the structures according to their volume, compactness, and circularity. The classification was based on medical records and human expert inspection.

Structure	Volume	Compactness	Circularity	Classification
1 (MRI1)	11682	0.1502	0.0067	Malignant
2 (MRI1)	1938	0.2016	0.0148	Benign
3 (MRI1)	845	0.0167	0.0037	Not Tumor
4 (MRI1)	763	0.8451	0.0526	Benign
5 (MRI1)	1813	0.2602	0.0180	Benign
1 (MRI2)	12259	0.0586	0.0035	Malignant

5 Discussion and Conclusions

Our novel approach overcomes previous methods' limitations by utilizing k-means clustering for automatic multi-tumor segmentation with multiple seed selection. Visual inspection suggests promising results, but due to the absence of direct comparisons, effective evaluation is challenging. The algorithm successfully segmented irregular and large structures resembling malignant tumors and also round and small structures corresponding to benign tumors. However, limitations arise from parameter choices, leading to missed benign tumors and false non-tumor identification. Adjusting the threshold value may impact the segmentation performance as a lower value might include non-tumor regions, whereas a higher value may exclude them. Moreover, variations in the parameter k would change the grouping, impacting the seed point identification and consequently the resulting mask. Further analysis involved characterizing structures through volume, compactness, and circularity. Malignant tumors had larger volumes and lower compactness and circularity, aligning with expected characteristics, whereas benign tumors were round and compact. These insights can enhance differentiation of malignant and benign tumors, suggesting the potential integration of features into classification machine learning algorithms for improved performance.

In conclusion, our automated methodology for breast MRI multi-tumor segmentation successfully achieved the objectives of automatic seed selection and multiple tumor segmentation. Despite promising results, limited sample size restricts generalization, underscoring the importance of expanding the dataset for validation. In summary, our study presents a promising approach with potential for improvement through parameter tuning and integration with a classification model based on segmented structure characteristics.

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