

Improving the performance of EM and K-means algorithms for breast lesion segmentation

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ABSTRACT

Aims: Breast cancer is the most common type of cancer in women and accounts for a large portion of cancer-related deaths. As in the other types of cancer, the prevention and early diagnosis of breast cancer gain importance day after day. For this purpose, the artificial intelligence-based decision support systems become popular in recent years. In this study, an automatic breast lesion segmentation process is proposed to detect breast lesions in the images taken with magnetic resonance imaging (MRI) protocol.

Methods: Two most popular segmentation methods: expectation maximization (EM) and K-means algorithms are used to determine the region of breast lesions. Furthermore, superpixel based fuzzy C-means (SPFCM) algorithm is applied after EM and K-means methods to improve the lesion segmentation performance.

Results: The proposed methods are evaluated on the private database constructed by the authors with ethical permission. The performances of the utilized methods are analyzed by comparing the lesion areas determined by a radiologist (ground-truth) and areas that are achieved by automatic segmentation algorithms.

Conclusion: Dice coefficient, Jaccard index (JI), and area under curve (AUC) metrics are calculated for performance comparison. According to the simulation results, EM, K-means, EM+SPFCM, and K-means+SPFCM methods provides good segmentation performance on breast MRI database. The best segmentation results are obtained by using EM+SPFCM hybrid method. The results of the EM+SPFCM method are 0,8711, 0,8979, and 0,9981 for JI, Dice, and AUC, respectively.

Keywords: Breast cancer, automatic segmentation, magnetic resonance imaging, image processing

INTRODUCTION

Cancer can be defined simply as abnormal cell formation and uncontrolled proliferation of these cells, beginning in almost any organ or tissue of the body, and can spread to other organs. Since cancer is the second leading cause of death worldwide, cancer research is increasing daily and gaining importance. Among women, the most prevalent cancer types include breast, colorectal, lung, cervical, and thyroid cancers, whereas men commonly encounter lung, prostate, colorectal, stomach, and liver cancers. It's noteworthy that the global incidence and mortality rates of breast cancer are on the rise.¹ Nevertheless, early detection plays a crucial role in reducing the fatality associated with breast cancer, as it does with many other cancer types. Various methods are employed for diagnosing and assessing the progression of breast cancer. Magnetic Resonance Imaging (MRI) is a widely utilized screening technique for breast cancer that offers the advantage of being radiation-free and painless during the imaging procedure.²

In recent studies, the researchers aim to detect breast lesions, segment lesions, and classify them as benign and malignant, automatically. To reach this aim, several image processing, machine learning and deep learning techniques are utilized.³⁻⁶ In this study, our goal is to detect breast lesions and determine lesion region as correct as possible.

Recent segmentation algorithms that are used to determine breast lesions' regions are investigated to show the main contributions of the presented study. According to the literature, the majority of studies conducted in recent years use deep learning techniques. However, deep learning-based techniques require very large databases and high-performance processors because of their computational complexities. So, some of the researchers prefer conventional image processing, machine learning, and pattern recognition methods to reduce computational complexity and also computation time.^{7,8}

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Although there are various studies, the most relevant and effective ones can be summarized as follows: In⁹, the authors propose a CNN-SVM network. In the testing phase of the study, the CNN's labeled output and the grayscale test images are passed through the SVM classifier for segmentation. The database of the study is collected from the Second Affiliated Hospital of Fujian Medical University. DSC, precision, and sensitivity metrics are used to evaluate the performance of the proposed segmentation approach. According to the simulation results, the achieved DSC, precision, and sensitivity values are 0.93, 0.95, and 0.92, respectively. In reference¹⁰, a Res-UNet CNN based automatic segmentation method is used to measure the size and volume of breast masses over MRI database that is constructed by the authors. The DSC metric is calculated to evaluate the segmentation phase of the study. According to the results, improved Res-UNet got the best DSC of 0.89 among different networks. In reference¹¹, a breast tumor segmentation-generative adversary network (BTS-GAN) is proposed to segment breast tumors in MRI scans automatically. The generator of the proposed GAN architecture learns to detect tumors and generates a binary mask; on the other side, the discriminator tries to learn the discriminating ground truth and synthetic mask. The authors use the public RIDER breast cancer MRI dataset and achieve 85% DSC and 93% sensitivity. The highest values of analyzed single and hybrid segmentation methods are 0.90 (DSC), 0.95 (precision), and 0.95 (sensitivity), respectively.

In this study, an automatic breast lesion segmentation process based on two most popular segmentation methods: EM and K-means algorithms are used to determine the region of breast lesions. Then, SPFCM algorithm is applied after EM and K-means methods to augment the lesion segmentation performance.

The main contributions of the study can be summarized as follows:

- i. Breast MR database used in the study is a private database that is built to design a decision support system for breast lesion segmentation. The database includes various types of benign and malignant lesions.
- ii. The segmentation performances of the two popular methods are investigated.
- iii. Performance improvement is achieved by utilizing SPFCM algorithm as a post processor.
- iv. Three common metrics are calculated to evaluate the success of the proposed segmentation methods.

The study is organized as follows: The utilized methods are introduced in Section 2. The experimental results of the study are shown in Section 3. Finally, the main contributions of the study are discussed in Section 4.

METHODS

The study was carried out with the permission of the Sakarya University Non-interventional Ethics Committee (Date: 21.12.2016, Decision No: 201-7). All procedures were carried out in accordance with the ethical rules and the principles of the Declaration of Helsinki. In addition, the proposed single and hybrid segmentation algorithms are explained to better understand the background of the study.

Database

RI serves to enhance our understanding of the suspicious regions identified through mammography, ultrasonography, or palpation. In this particular investigation, Dynamic Contrast-Enhanced MRI (DCE-MRI) is conducted by using a 1.5 Tesla GE Healthcare-Signa Voyager machine, equipped with a specialized breast surface coil. To begin the examination, T2-weighted spin-echo sequences in the axial plane is acquired. Subsequently, a T1-weighted sequence is captured following the administration of a Gadolinium-based contrast agent, dosed at 0.1 mmol/kg with a flow rate of 1.5 ml/s. For each patient, ensuring a temporal resolution of at least 30 seconds, resulting in the acquisition of approximately 5000 images, five scans are utilized. The dynamic T1 series' parameters included a repetition time (TR) of 7.2 ms, a scan-specific echo time (TE) of 2.0 ms, a flip angle (FA) of 11 degrees, a slice thickness of 1.4 mm, and a field of view (FOV) frequency of 35.0 along with a FOV phase of 1.0. The imaging process produced a maximum of 1618 slices, each with a pixel size of 0.9×1.2 . We used a single excitation (NEX 1.0) and a matrix size of 192×300 . It's important to note that these parameter values may be adjusted for individual patients based on their structural characteristics. The radiologist carefully selected the most appropriate slices that would aid in accurately delineating the lesion's location to ensure the most informative results.

Lesion Segmentation

Before performing lesion segmentation process, the left and right breast regions were separated according to the location of hearth. In the lesion segmentation step, two single algorithms: EM and K-means are employed to determine the lesion area as correct as possible. These methods are selected according to their segmentation performances on the breast MRI database. Then, a hybrid model was constructed by performing SPFCM method after K-means and EM algorithms, respectively. **Figure 1** shows the lesion segmentation process.

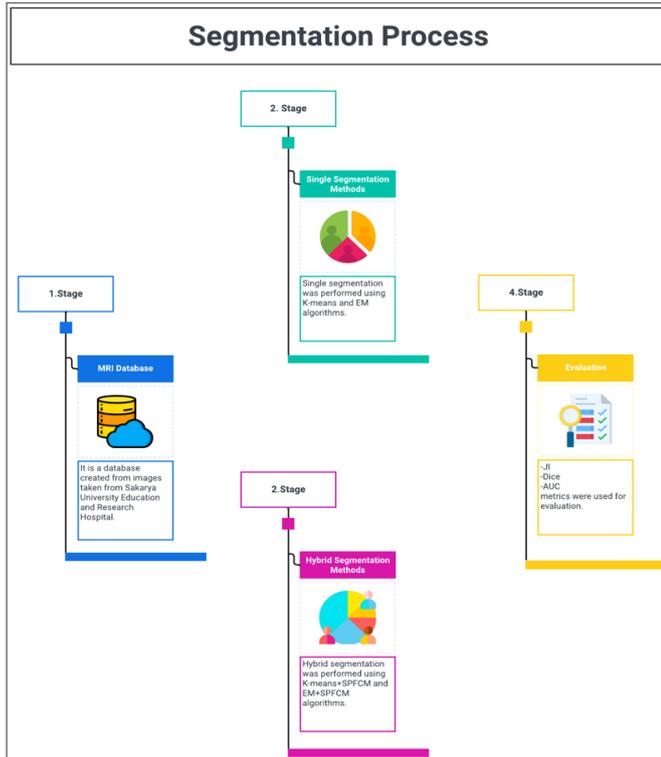


Figure 1. Breast lesion segmentation process of the study.

The main steps of the utilized algorithms are given in the following subsections.

Expectation maximization: Maximum likelihood estimation (MLE) is a statistical method that is used to predict the parameters of an assumed probability distribution under adequate number of observations. The EM algorithm is also a statistical technique which is based on MLE and used to segment images. EM method constructs a likelihood function and tries to maximize this function according to the given problem. However, maximizing the likelihood function according to the parameters in many real-world problems is a challenging task.

The EM algorithm solves this problem by degrading the problem to two simple small steps referred as expectation (E) and maximization (M). The E is the expectation of the unknown underlying variables. On the other side, M step provides a new estimate of the parameters. Steps E and M are performed consecutively until convergence is achieved.¹² EM algorithm can be summarized as follows:

Assume that, n training data points having d attributes $\{x_1, x_2, \dots, x_n\} \in R^d$ are observed. In this case, for the sake of simplicity, it is supposed that the observations are generated by a Gaussian Mixture Model (GMM) of which parameters are needed for algorithm initialization. The probability density function of GMM is expressed as follows:

$$f(x|\theta) = \sum_{i=1}^K \alpha_i f_i(x|\theta_i) \quad (1)$$

In Equation (1), K shows the number of Gaussian distributions in the model and α_i is the weight of the mixture. Each Gaussian in the mixture is characterized by its mean μ_i and variance σ_i^2 . The probability density function of Gaussian distribution can be expressed as follows

$$P(x|\theta_i) = \frac{1}{\sqrt{2\pi\sigma_i}} \exp\left\{-\frac{(x-\mu_i)^2}{2\sigma_i^2}\right\} \quad i = 1, 2, \dots, K. \quad (2)$$

where $\theta_i = (\mu_i, \sigma_i)$ is the Gaussian mixture distribution parameter. In this stage, the target is to find $\varphi = \alpha_1, \alpha_2, \dots, \alpha_k, \mu_1, \mu_2, \dots, \mu_K, \dots, \sigma_1^2, \sigma_2^2, \dots, \sigma_K^2$ parameters. So, MLE approach must be carried out. But, because of the high computational complexity of MLE, EM algorithm is preferred.

After parameter initialization, the posterior probabilities given in Equation (3) are calculated.

$$\varphi(i|x_j, \theta) = \frac{p_i f_i(x_j|\alpha_i)}{\sum_{k=1}^K p_k f_k(x_j|\alpha_k)} \quad (3)$$

In Equation (3), i and j are the data point and Gaussian component indices, respectively. The posterior probability of j th Gaussian component of each data point is estimated by performing E-step. The likelihood of observations is maximized by re-estimating all the parameters to achieve a better parameter estimation. So, M-step updates the prior p_i and parameters with Equations (4-6).

$$p_i^{new} = \frac{1}{N} \sum_{j=1}^N \varphi(i|x_j, \theta^{old}) \quad (4)$$

$$\mu_i^{new} = \frac{\sum_{j=1}^N x_j \varphi(i|x_j, \theta^{old})}{\sum_{j=1}^N \varphi(i|x_j, \theta^{old})} \quad (5)$$

$$\sigma_i^{2,new} = \frac{\sum_{j=1}^N \varphi(i|x_j, \theta^{old}) (x_j - \mu_i^{new})(x_j - \mu_i^{new})^T}{\sum_{j=1}^N \varphi(i|x_j, \theta^{old})} \quad (6)$$

Steps E and M are performed consecutively until the difference between the new and old parameter values is smaller than the predetermined error quantity.

$$||\theta^{new} - \theta^{old}|| \leq \varepsilon \quad (7)$$

The details of the EM algorithm can be investigated with reference.¹²

K-Means: K-means is a known unsupervised clustering method that aims to reach locally optimal solutions that provides minimum clustering error. As aimed in the most clustering based segmentation methods, K-means tries to group homogenous data points in a given image or data set. Each group constitutes a region where the object's density is locally different from other regions. Suppose that the vector $X = \{x_1, x_2, \dots, x_N\}$, $x_n \in R^d$ is the data set. The aim of the K-means clustering algorithm is to obtain k partitions (clusters) which optimizes the clustering objective function. K-means algorithm's steps are explained as follows:

- i. Divide n data into k clusters and randomly determine the centers of clusters C_1, C_2, \dots, C_k .
- ii. Measure the Euclidean distance between each data point and cluster center.
- iii. Assign each data point to the nearest cluster.
- iv. Calculate the value of objective function J with Equation (8). Note that, to reach the best clustering performance J must be minimized.

$$J = \sum_{i=1}^k \sum_{X_j \in C_i} \|X_j - C_i\|^2 \tag{8}$$

- v. Assign the mean of each cluster as a new centroid by calculating means with the Equation (9).

$$C_i = \frac{1}{n_i} \sum_{j=1}^{n_i} X_j \quad (i = 1, 2, \dots, k) \tag{9}$$

- vi. Repeat steps (ii-v) to reach the determined convergence criterion.

If the value of objective function converges to zero, it can be said that the best clustering performance is achieved. In other words, the ideal J value is zero. In addition, the convergence criterion mentioned in Step (vi) can be either the number of iterations or the value of J.¹³

Super pixel fuzzy C-means: Superpixels arise from perceptual grouping of image pixels and carry more information than pixels. The use of superpixels becomes popular in image processing applications, as it can significantly reduce the complexity of post-processing tasks.

A superpixel must have main properties to be implemented in the FCM algorithm, which assigns each pixel in an image to a cluster. A superpixel extraction algorithm must be fast and simple to overcome time consuming problem. Once superpixels are constructed, information such as the number of pixels of each superpixel, and the adjacent relationship between the superpixels is stored for the next clustering process. The steps of the SPFCM algorithm is given below:

Superpixel objective function J is generated by the information obtained from the original image.

$$J = \sum_{i=1}^C \sum_{j=1}^Q \gamma_j u_{ij}^m \|\zeta_j - v_i\|^2 + \frac{\alpha}{N_R} \sum_{i=1}^C \sum_{j=1}^Q u_{ij}^m (\sum_{S_r \in N_j} \gamma_r \|\zeta_r - v_i\|^2) \tag{10}$$

In Equation (10), Q denotes the number of image superpixels, γ_j and ζ_j are the number of pixels in superpixel and the average color value of superpixel S_j , respectively. u_{ij} is the membership of superpixel S_j to the i th cluster. N_j shows the set of neighboring superpixels adjacent to S_j . N_R stands for the cardinality of N_j . v_i , is the i th cluster center. $\|\cdot\|$ presents the Euclidean distance between pixels and cluster centers. The parameter inspects the effect of the neighbor element.

The cluster centroids ($v_i, i = 1, 2, \dots, C.$) are obtained.

The membership of superpixel is updated by using Equation (11)

$$u_{ij} = \left(\sum_{k=1}^C \left(\frac{\gamma_j \|\zeta_j - v_i\|^2 + \frac{\alpha}{N_R} \sum_{S_r \in N_j} \gamma_r \|\zeta_r - v_i\|^2}{\gamma_j \|\zeta_j - v_k\|^2 + \frac{\alpha}{N_R} \sum_{S_r \in N_j} \gamma_r \|\zeta_r - v_k\|^2} \right)^{1/(m-1)} \right)^{-1}$$

Equation (12) calculates the new cluster centroids as follows:

$$v_i = \left(\sum_{j=1}^Q u_{ij}^m (\gamma_j \zeta_j \frac{\alpha}{N_R} \sum_{S_r \in N_j} \gamma_r \zeta_r) \right) \left(\sum_{j=1}^Q u_{ij}^m (\gamma_j + \frac{\alpha}{N_R} \sum_{S_r \in N_j} \gamma_r) \right)^{-1} \tag{12}$$

Finally, steps ii-v are repeated until the difference between the new and old parameter values is smaller than the given error value ϵ .

$$\|V^{new} - V^{old}\| \leq \epsilon$$

According to the database, modifications such as inserting a bias parameter can be required to generate the objective function.¹⁴

In the presented study, K-means and EM single segmentation algorithms are applied to breast MR images to perform given lesion segmentation task. Then, to improve the performance of these algorithms SPFCM method is used as a post processing step. In the following section, the performances of the EM, K-means, EM+SPFCM, and K-Means+SPFCM segmentation algorithms is evaluated by calculating three performance metrics.

RESULTS

In this section, our goal is to show the success of the proposed methods on the constructed private dataset. For this purpose, several MR images are analyzed that include benign and/or malignant breast lesions. Dice coefficient, JI, and AUC metrics are used for performance evaluation.

At first, pixel-level confusion matrix must be obtained to calculate performance metrics. The lesion area determined by the radiologist (manual segmentation) is compared with the lesion area determined by the applied segmentation method (automatic segmentation) when constructing the pixel-level confusion matrix. The manual segmentation region selected by the expert is assumed as the ground truth lesion region. For example, with a segmentation algorithm, pixels that are claimed to be in the lesion area and are actually in the lesion area, according to the expert, are evaluated as true positive (TP). True negative (TN), false positive (FP), and false negative (FN) assessments are done similarly. After obtaining the pixel-level confusion matrix, the metrics can be calculated to evaluate segmentation algorithm.

The JI is a statistic used to measure similarity and diversity. The JI can be expressed in terms of TP, FP, and FN as:

$$JI = \frac{TP}{TP+FP+FN} \tag{13}$$

The Jaccard similarity coefficient of two sets A and B (also known as intersection over union or IoU). In our study, A is the lesion region manually selected by the radiologist and B shows the lesion region determined by the proposed segmentation methods. The Dice coefficient is a statistic used to measure similarity and can be calculated as follows:

$$Dice = \frac{2*JI}{1+JI} \tag{14}$$

The AUC represents the degree or measure of separability. In **Table 1**, the proposed breast lesion segmentation methods are compared by means of three criteria. Note that, the highest values of JI, Dice, and AUC metrics are 1.

The rows of the **Table 1** give JI, Dice coefficient, and AUC values, respectively. According to the table, EM+SPFCM hybrid method provides the best segmentation results. The values of JI, Dice, and AUC for EM+SPFCM are 0,8177, 0,8979, and 0,9981, respectively. On the other hand, K-Means+SPFCM hybrid method gives 0,7805, 0,8756, and 0,9986 for JI, Dice, and AUC, respectively. As can be seen from the table, hybrid methods perform the segmentation task more successful than single methods. So, applying SPFCM method after K-Means and EM algorithms improves the segmentation ability of methods.

	EM	EM+SPFCM	K-Means	K-Means+SPFCM
JI	0.7149	0.8177	0.6821	0.7805
Dice	0.8264	0.8979	0.8062	0.8756
AUC	0.9937	0.9981	0.9933	0.9986

Furthermore, to illustrate the lesion area determined by the utilized segmentation algorithms **Figure 2** is drawn. In **Figure 2**, original MR image, the images obtained by applying single and hybrid segmentation methods, binary images, and ground truth image are illustrated from left to right. **Figure 2** is given to show the performances of the utilized segmentation methods on an MR image exist in the database. According to the figure it is clear that the hybrid methods determine the lesion are more compact and correct than single methods.

Finally, **Table 2** is built to compare utilized segmentation approaches with the recent studies that are performed to segment breast MR images. **Table 2** shows the lesion segmentation results of references^{9,10} and our higher-performance methods. In **Table 2**, the comparison is made

with only Dice metric which is the common metric used in our study and compared studies. According to the table the proposed method achieves the breast lesion task better than the compared studies with respect to Dice coefficient.

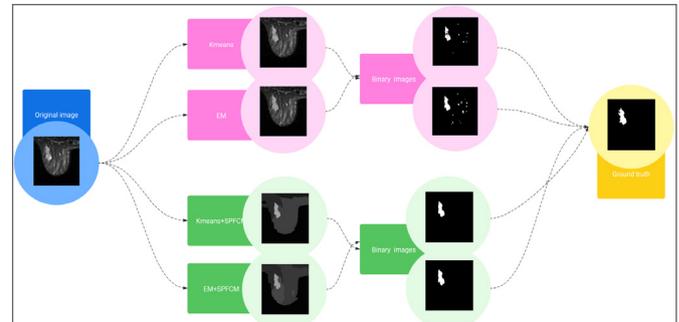


Figure 2. Illustration of detected lesion areas achieved by utilized methods

Method	Dice
[9]	0.93
[10]	0.89
Proposed	0.90

DISCUSSION

In this study, at first, two popular segmentation methods; EM and K-means are applied to MR images to determine the breast lesions' regions. Then SPFCM algorithm is utilized to improve the performance of these segmentation methods.

In the presented study, **Table 1** and **Figure 2** are given to show the segmentation results of the methods. **Table 1** compares the performances of single and hybrid methods with respect to JI, Dice coefficient, and AUC criteria. The higher Dice coefficient and JI values imply that the breast lesion region determined by the automatic segmentation algorithms are very close to that of manual segmentation performed by an expert radiologist. As can be seen from **Table 1**, the proposed single and hybrid segmentation methods provide good performance on the constructed database. Furthermore, the performances of EM and K-means methods increase by carrying out SPFCM algorithm after these methods. K-means+SPFCM and EM+SPFCM provide the most successful segmentation results. So, K-means+SPFCM and EM+SPFCM hybrid methods can reliably be used to determine the breast lesion region in MR examinations.

Figure 2 illustrate the determined lesion region for ductal carcinoma in situ malignant lesion type. **Figure 2** give an idea about the segmentation ability of all performed methods. According to the figure, hybrid methods give a more distinct and compact lesion region than single methods. Thus, the lesion area determined by hybrid methods is closer to the manually determined area.

Finally, **Table 2** compares the proposed study with recent studies that are performed to segment breast MR images. **Table 2** shows the lesion segmentation results of references^{9,10} and our higher-performance methods. According to the table the proposed method performs the breast lesion task better than the compared studies with respect to Dice coefficient.

CONCLUSION

In addition, the proposed segmentation process needs a shorter computation time than deep learning based segmentation methods and does not require high-performance processors. In our future studies, our goal is to use deep learning based segmentation methods by modifying them to decrease the computational load. For this purpose, also the constructed database must be extended. The main limitation of the study is the size of constructed database. The number of MR images will be increased and various benign and malignant lesion types will be included to the database to obtain more reliable results.

ETHICAL DECLARATIONS

Ethics Committee Approval: The study was carried out with the permission of the Sakarya University Non-interventional Ethics Committee (Date: 21.12.2016, Decision No: 201-7).

Informed Consent: Written informed consent form was obtained from participating in this study.

Referee Evaluation Process: Externally peer-reviewed.

Conflict of Interest Statement: The authors have no conflicts of interest to declare.

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