

Performance Analysis of EM-MPM and K-means Clustering in 3D Ultrasound Image Segmentation

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Abstract—Breast density is an important indicator for a woman's lifetime risk of breast cancer. A 3D model of breast density can be obtained by taking 3D tomographic ultrasound and then identifying tissue distribution in the breast with 3D medical image segmentation. In this paper, we compare two segmentation algorithms, EM-MPM (Expectation Maximization with Maximization of Posterior Marginals) and K-means clustering using simulated phantoms. The computational phantoms cover various tissue density patterns. A total of twenty volumes of three dimensional synthetic ultrasound breast images were compared. We found that EM-MPM performs better than K-means Clustering on segmentation accuracy because the segmentation result fits the ground truth data very well. The EM-MPM is able to use a Bayesian prior assumption, which takes advantage of the 3D structure and finds a better localized segmentation. EM-MPM performs significantly better especially for the highly dense tissue scattered within low density tissue and for volumes with low contrast between high and low density tissues.

Keywords—3D image segmentation, EM/MPM, K-means Clustering, Tomographic Ultrasound

I. INTRODUCTION

Assessing a woman's lifetime risk of breast cancer at an early stage can help save lives by targeting screening and preventive therapy to the at-risk population. Some studies have shown that a woman's breast density proportion has a relationship to breast cancer risk; the higher the proportion of dense tissue, she is 4-5 times more likely to develop breast cancer [1]. Tomographic Ultrasound is uniquely positioned to identify breast density, since the density is automatically calibrated to water in this imaging mode. In addition, a 3D model of the breast density is available in tomographic ultrasound, in contrast with the projection only available in standard mammogram. Therefore, this study focuses on obtaining a repeatable measure of density proportion using Ultrasound Tomography. In order to get a density map of the data, a process of segmenting this density data to identify the proportion of dense tissue is needed. This research compares two methods of segmentation applied to the synthetic breast data.

To analyze breast density distribution, a good segmentation algorithm is needed. Commonly used segmentation techniques such as filtering, region growing, thresholding, and non-linear edge operations are not effective due to the noise and

attenuation degradation in ultrasound. We choose two robust algorithms, EM-MPM and K-means clustering to compare. First, the Bayesian algorithm combining Expectation Maximization with the Maximization of Posterior Marginals (EM/MPM) is considered effective in many difficult segmentation tasks [2] [3] [4]. This algorithm classifies every pixel in an image by assigning a cost to the number of misclassified pixels, and iteratively finds the best probabilistic solution to fit the data. This method has the advantage of using a 3D neighborhood of pixels as a statistical Bayesian prior, and has the effect of grouping the data similar to the way the tissues are structured. Second, K-means clustering is another commonly used technique [5] in medical image processing, especially in images with noisy data. This algorithm takes n observations and segments them into k clusters in which each observation belongs to the cluster with the nearest mean. The initialization of the k-means algorithm can be critical, and in this case seeds were automatically placed randomly. This K-means algorithm is compared to the EM/MPM performance.

In our paper, the EM-MPM and K-means Clustering are used to process twenty sets of three dimensional synthetic breast ultrasound image stacks. The segmentation results are compared and analyzed for accuracy against the original numerical phantom data. In section 2, we provide a brief introduction explaining the two algorithms used. The detailed segmentation result and accuracy analysis are followed by in section 3. Finally, section 4 concludes that EM-MPM performs better than K-means clustering on the ultrasound image.

II. ALGORITHMS USED IN THE SEGMENTATIONS

A. EM-MPM

The algorithm is divided into two parts: EM (Expectation Maximization) and MPM (Maximization of Posterior Marginals). EM processes for estimation of the mean and variance of Gaussian Statistical models of the segmentation classes. MPM assigns the initial segmentation class for each pixel using a Markov Random Field, with iterative optimization working on a cost function related to the statistics of the image [4].

The Gaussian segmentation class means and variances are represented by the vector: $\theta=(\mu_1, \sigma_1, \dots, \mu_k, \sigma_k)$. The EM algorithm is used to estimate this vector, based on the best log-likelihood probability that a particular pixel belongs to one of the k classes. The EM function is as follows, where

$f(y|x, \theta)|Y, \theta_{p-1}$ is the posterior (Gaussian) distribution and $p(x|\theta)|Y, \theta_{p-1}$ is the prior distribution, after p iterations it will converge to the optimum solution.

$$Q(\theta, \theta_{p-1}) = E[\log f(y|x, \theta)|Y, \theta_{p-1}] + E[\log p(x|\theta)|Y, \theta_{p-1}]$$

The MPM algorithm segments the pixels into N class labels, using the estimated parameter vector from EM. This is accomplished by choosing a class label for every pixel in the estimate of X which maximizes the marginal probability mass functions in the equation below, where β is weighting factor for amount of spatial interaction, C is clique of X , y is source image, μ and σ are mean and variance for each class.

$$P_{x_t|Y}(x_t|y, \theta) = \prod_{s \in S} \frac{1}{\sqrt{2\pi\sigma^2}} \exp \left\{ -\frac{(y_s - \mu_s)^2}{2\sigma_s^2} - \sum_{[r,s] \in C} \beta t(x_s, x_r) \right\}$$

B. K-means Clustering

K-means clustering is a method of cluster analysis. It aims to partition n observations into k clusters in which each observation belongs to the cluster with the nearest mean, m [5]. Given a set of observations (x_1, x_2, \dots, x_p) , k-means clustering partitions the n observations into k sets ($k \leq p$) $S = \{S_1, S_2, \dots, S_k\}$. The algorithm proceeds by repeating two steps:

1) Assignment step: Assign each observation to the cluster with the closest mean, Where each x_p goes into exactly one $S_i^{(t)}$.

$$S_i^{(t)} = \{x_p : \|x_p - m_i^{(t)}\| \leq \|x_p - m_j^{(t)}\| \forall 1 \leq j \leq k\}$$

2) Update step: Calculate the new means to be the centroid of the observations in the cluster.

$$m_i^{(t+1)} = \frac{1}{|S_i^{(t)}|} \sum_{x_j \in S_i^{(t)}} x_j$$

The algorithm is converged when the assignments no longer change, which produces a separation of the objects into groups that the metric to be minimized and calculated.

III. RESULT AND DISCUSSIONS

In this section, we compare and analyze the segmentation result from EM-MPM and K-means clustering, using Tanimoto coefficient and Parenchyma Percentage. The test data used here are twenty sets of 3-D synthetic breast ultrasound images with various densities, which is represented by different gray level. The numerical phantom is first processed through a tomographic ultrasound simulation [7] and an ultrasound volume is produced. This ultrasound volume contains noise and tomographic imaging artifacts, and also has a limited resolution, therefore the segmentation cannot perfectly represent the numerical phantom. In the original numerical phantom, the dense part includes the pixels of various density indicated by the gray scale. These phantoms were produced to simulate the variation of anatomical tissues in the breast, such as fat, parenchyma, and dense tissues. When comparing, the

densest 3 gray levels in the phantom are compared with the one densest segmented class with the highest gray value.

A. Tanimoto Coefficient

Given two images, A and B , the Tanimoto coefficient is used for comparing the similarity between them [6]. It is defined as the size of the intersection divided by the size of the union of the sample sets, which is expressed as:

$$T = \frac{\sum_i (A_i \cap B_i)}{\sum_i (A_i \cup B_i)}$$

Where A_i and B_i represent the i th pixel of images A and B . $\sum_i (A_i \cap B_i)$ represents the total number of pixels that both in image A and B , on i th position, is the target object. $\sum_i (A_i \cup B_i)$ represents the total number of pixels of either in A or in B , are the target object. The perfect segmentation would be $T=1.0$. Normally very good segmentations are above $T=0.6$, and can depend on the noise and distortion in the images.

B. Parenchyma Percentage

Parenchyma percentage is calculated by dividing the volume of high density segmented tissue by the total volume of the tissue. The result of the segmentation image is compared with the one from the numerical phantom original image. The aim is to produce a measurement similar to the original numerical phantom:

$$P = \frac{V_{\text{dense}}}{V_{\text{total}}}$$

C. Results Comparison

From Fig 1 to Fig 3, image (a) represents the numerical phantom; image (b) is the simulated synthetic ultrasound image that is produced with the phantom as the input; image (c) is the resulting EM-MPM segmentation with the ultrasound simulation as input, and image (d) is the K-means algorithm result with ultrasound input. The dense tissue from the ground truth image has gray values of 191, 202 and 223, which corresponds to the edge (skin), the intersection lines (connective tissue) and bright areas (dense tissues) within breast.

Figure 1 represents an ultrasound which contains strong contrast of dense structure (with high gray value) with normal tissue (with low gray value). Here, the EM-MPM performs similarly to K-means clustering, where both of them can identify the dense part. However, under low contrast circumstances, as in Fig 2 and Fig 3, the EM-MPM performs better than K-means clustering. EM-MPM finds the dense part clearly compared to ground truth. K-means clustering has confused the dense tissue with the semi-dense background and clusters them together in high density part (Fig 2), or has omitted some dense pixels in high density case (Fig 3).

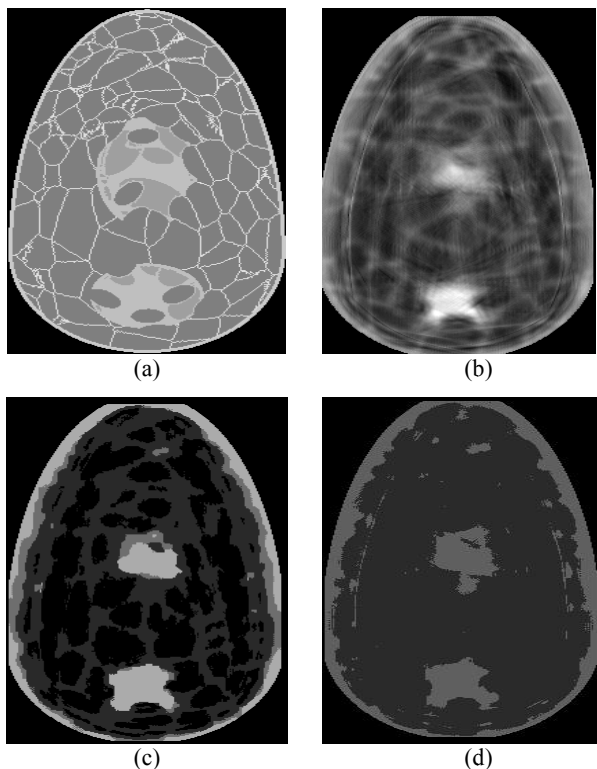


Fig. 1 High contrast, low density case (a) Numerical phantom ground truth (b) Synthetic ultrasound tomography image from phantom (c) EM-MPM segmentation on ultrasound image (d) K-means segmentation on ultrasound image

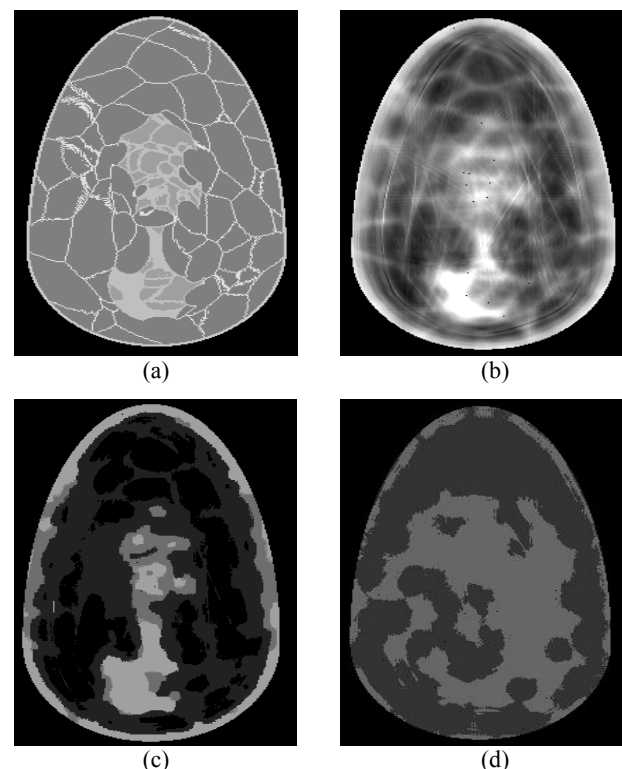


Fig. 2 Low contrast, low density case (a) Numerical phantom ground truth (b) Synthetic ultrasound tomography image from phantom (c) EM-MPM segmentation on ultrasound image (d) K-means segmentation on ultrasound image

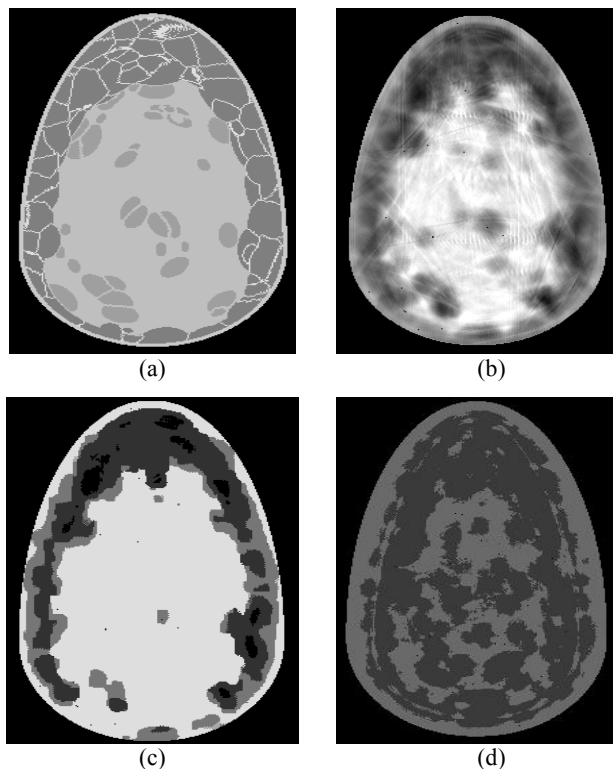


Fig. 3 Low contrast, high density case (a) Numerical phantom ground truth (b) Synthetic ultrasound tomography image from phantom (c) EM-MPM segmentation on ultrasound image (d) K-means segmentation on ultrasound image

Fig 4 illustrates the Tanimoto Coefficient of EM-MPM compared to K-means Clustering. The test cases are arranged by ascending sequence of the density. It is seen that EM-MPM has higher segmentation accuracy than K-means, and as the tissue density increases, the accuracy increases compared to K-means clustering.

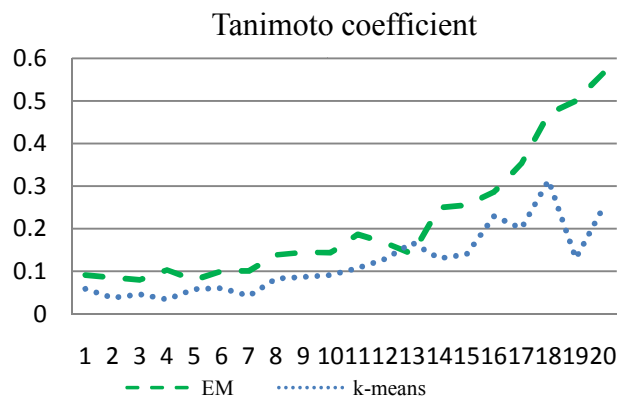


Fig. 4 Tanimoto Coefficient

Parenchyma percentage is shown in Fig 5. It is clear that the segmentation result from EM-MPM fits very well with the original ground truth data, which means it accurately finds the dense tissue proportion as defined in the original phantom picture. However, K-means Clustering does not track the

original RGB and for low density volumes total density is low, it overestimates the proportion of parenchyma.

study. Our future work will focus on applying this technique to clinical data.

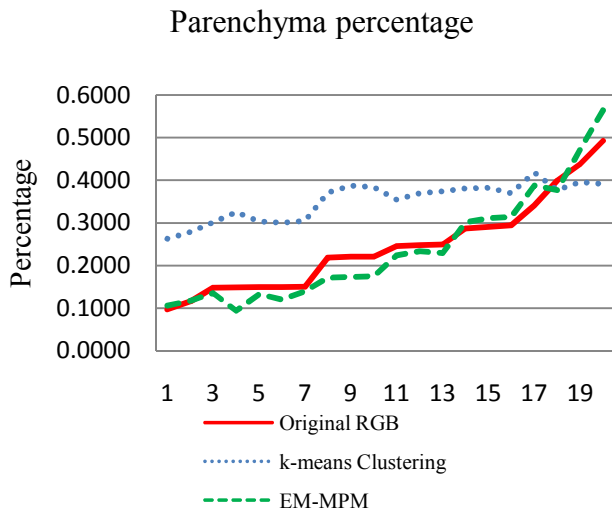


Fig. 5 Parenchyma percentage of segmentation compared to ground truth numerical phantom.

IV. CONCLUSION

In this paper, we compared and analyzed the segmentation performance of EM-MPM and K-means Clustering, using synthetic medical image sets. After comparison of the segmentation result, Tanimoto Coefficient and Parenchyma Percentage, it is shown that EM-MPM outperforms the K-means clustering in both segmentation accuracy (superior Tanimoto coefficient) and in the measure of Parenchyma percentage. Especially in the cases with high density, the segmentation accuracy of EM-MPM is high, which means EM-MPM could greatly help on the dense proportion – cancer risk

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