K-Means and Active Contour Approach to Detecting and Segmenting Masses in Breast MR Images

Justin Kennedy and Dr. William Hsu*

* Department of Bioengineering, UCLA

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I. Introduction

While the five-year relative survival rate for women with stage 0 or stage I breast cancer is 100%, the survival rate of cancers caught at stage III and stage IV drops to 72% and 22%, respectively[1]. Effective methods for early detection, particularly in high risk women with extremely dense breasts, can significantly improve patient outcomes. As a systematic, non-invasive approach to examining the malignancy potential of masses in magnetic resonance (MR) images, image quantification has proven to be an effective method for evaluating MR images and efficiently scaling results to multiple series and patients. Among providing an additional lense for viewing images, implications for accurate segmentation could potentially improve the effectiveness of treatment planning and resource-heavy procedures such as biopsy scheduling.

For lesion segmentation in breast images, Chen et al.[1] proposed a fuzzy k-means approach that utilizes a procedure based on human selection of a region of interest in a breast MR image followed by image enhancement through thresholding and connected component labelling and a k-means based segmentation. Through application of their method to an external image data set, they were able to segment 97% of lesions correctly and the results of a paired t-test comparing their segmentation algorithm to manual delineation showed no significant difference.

Lucas-Quesada et al.[2] proposed two alternative approaches to lesion segmentation including a method utilizing temporal correlation to create a similarity map based on comparing pixel values to a region of interest through temporal similarity as well as a method using multi-spectral analysis to derive features from the pre/post contrast pixel intensity value scatterplots. The results of their study revealed the temporal correlation-based method to outperform the mutli-spectral technique in regards to segmentation speed and accuracy.

In this work, we explore the use of machine learning approaches such as k-means clustering and active contours to automatically detect and segment masses in breast MR images. To evaluate the efficacy of the algorithm, we compare the algorithm's performance to human annotations of the same studies. Our goal is to create an effective supplemental tool for clinical decision making in regards to the evaluation of breast MR images.

II. METHODS

The images used in this study were MR dynamic contrast enhanced (MR-DCE) images from the Cancer Imaging Archive (TCIA) dataset (n=87)[2]. The cases contained high-risk normals, ductal carcinoma in situ (DCIS), fibroids, and lobular carcinomas acquired using 3 or more distinct MR pulse sequences on a Phillips 1.5T scanner. Specifically, the sequences labelled BLISS were processed and used for training and testing the algorithm. BLISS is an MR technique that improves fat suppression and achieves high spatial resolution of the breast. Contrast is injected to improve the visibility of tumors and other inflammations in the MRI scan. The volume of Bayer gadolinium contrast injected into the brachial vein is amount based on 10% of the patient's weight in pounds, and the injection is 6 or 7 seconds at a rate of 3cc per second. The first dynamic sequence is started 1 minute after the injection is started.

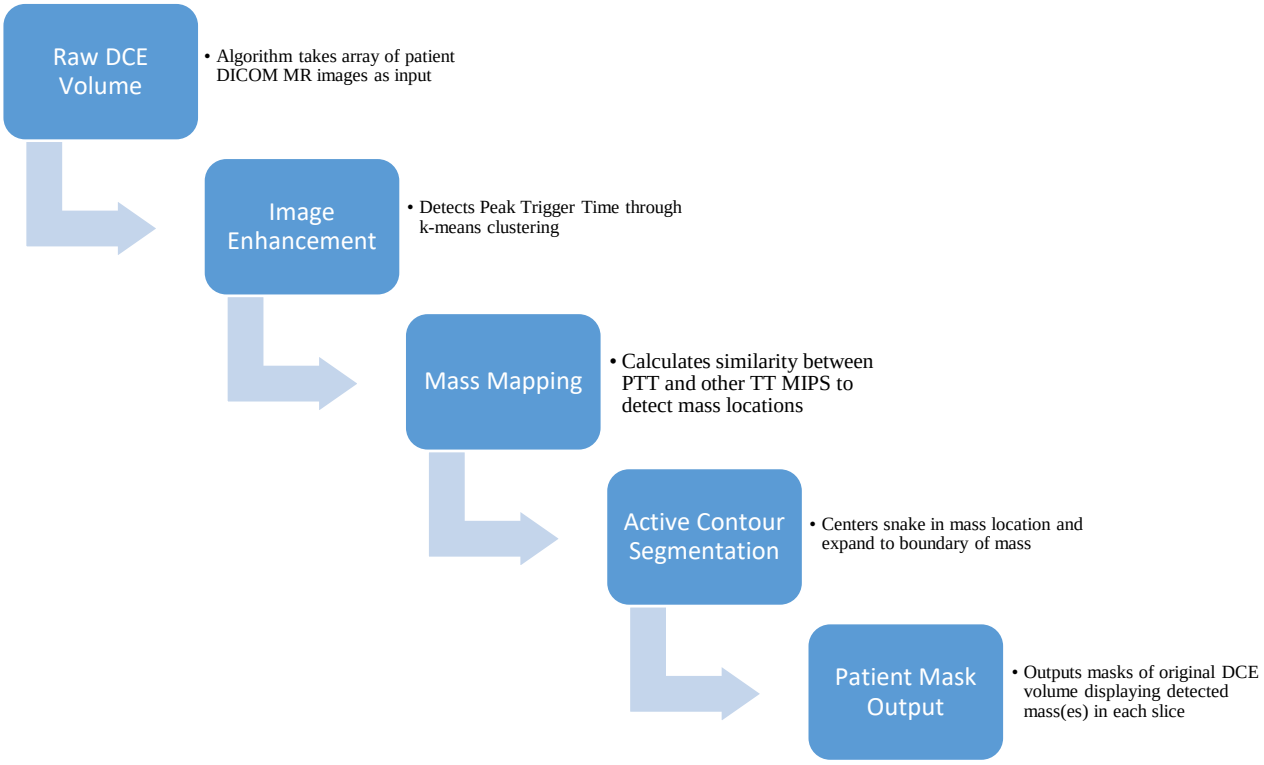


Figure 1. Diagram for proposed active contouring-based segmentation algorithm.

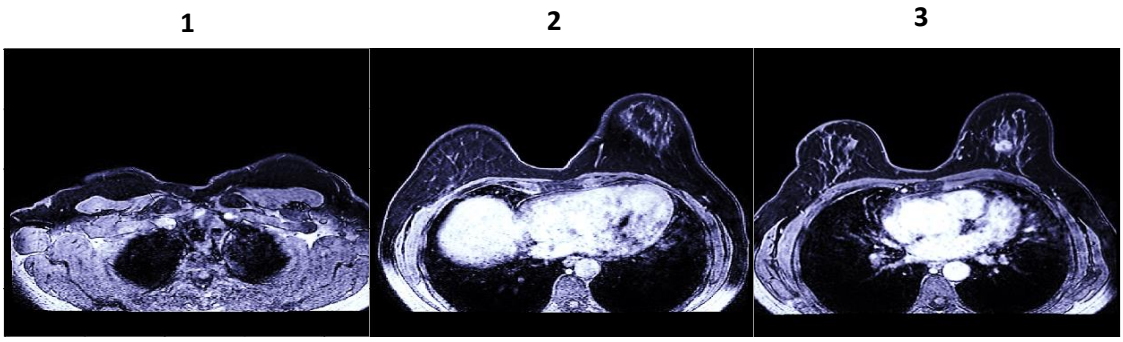


Figure 2. The input DICOM image is represented as an array of different sequences, separated by Trigger Time (e.g., time after contrast is injected)

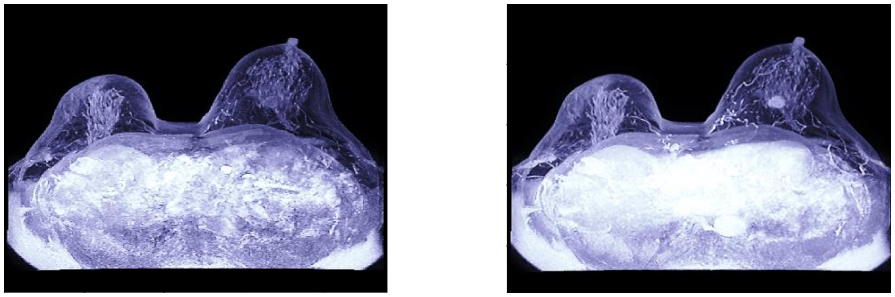


Figure 3. The MIP is then taken for each trigger time array to find the 'peak trigger time', or when the resolution with contrast shows the greatest difference with the previous trigger time. In this case (b) is the Peak Trigger Tine (PTT) MIP and (a) is the MIP of the trigger time before it.

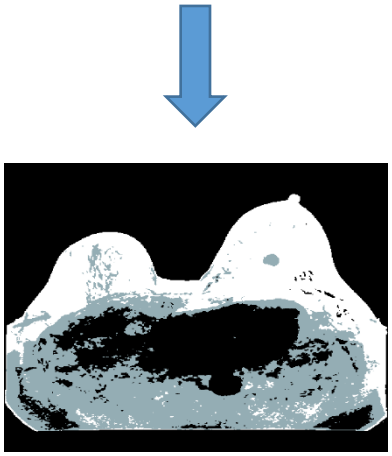


Figure 4. The PTT MIP is then clustered using k-means clustering (k=4) with three feature vectors to better isolate potential masses from the rest of the breast and chest cavity. This MIP is then compared to the segmented MIPs of the previous trigger times to derive a coordinate-based location and radius for the mass(es).

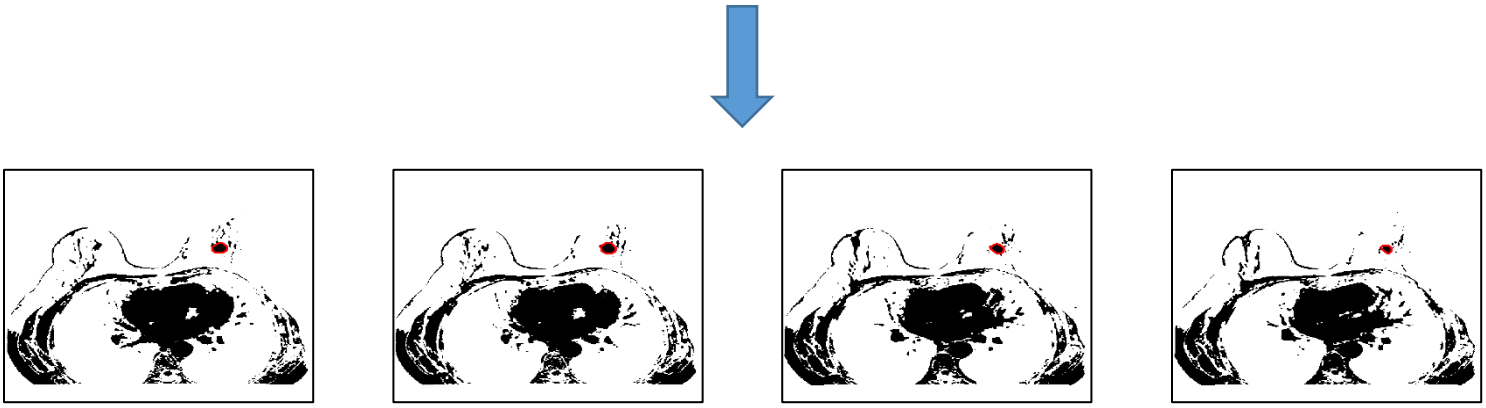


Figure 5. The PTT MIP is then clustered using k-means clustering (k=4) with three feature vectors to better isolate potential masses from the rest of the breast and chest cavity. This MIP is then compared to the segmented MIPs of the previous trigger times to derive a coordinate-based location and radius for the mass(es).

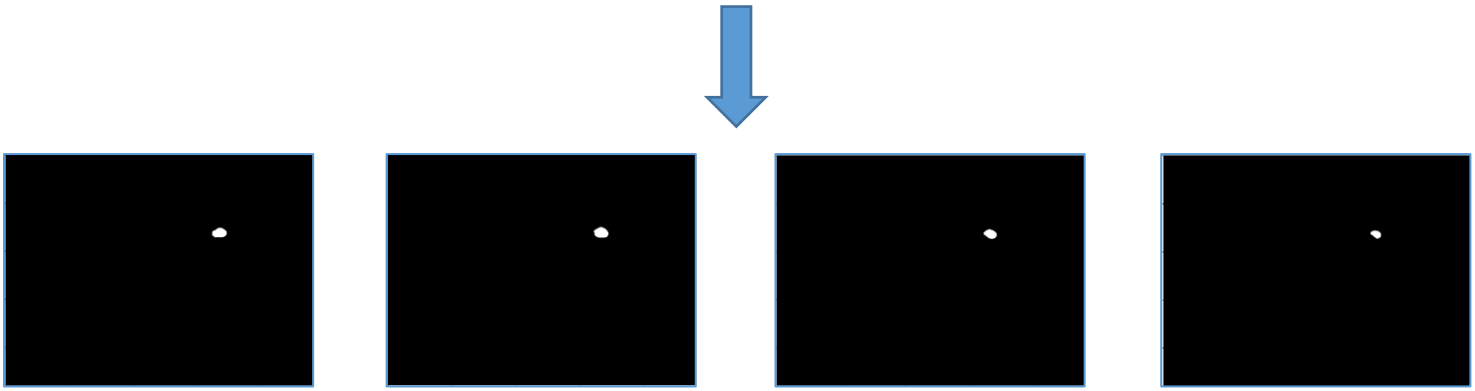


Figure 6. The resulting mass segmentations are converted to binary output images.

The algorithm takes an array of DICOM breast MR Images of a patient as an input. Then for each patient, the image sequences are separated by trigger time (time after contrast is injected). The maximum intensity projection (MIP) image is then taken for each trigger time array and is used as a comparison tool for finding the 'peak trigger time', or the first place where the resolution with contrast shows the greatest difference with the previous trigger time. To calculate the MIP, the algorithm finds the highest intensity value at each pixel location from the set of images, and in this way 'projects' the entire image set to one clearer resolution image that highlights the high intensity features of the data set. The MIP also provides a method of comparison for differentiating between images in the set actually containing the breasts to those higher/lower in the sequence only showing parts of the chest. The reason for segmenting by trigger time is that in the image dataset tested, a few of the patient image sequences exhibited properties that would interfere with the algorithm's detection protocol, such as fat developments. These abnormalities would be mistakenly clustered the same as the masses by the k-means segmentation and thus shroud the masses from being detected. By isolating one peak trigger time where a mass first occurs, the noise caused by contrast permeation over time is reduced and consequently the image is processed more optimally for segmentation.

The MIP pixel values of the peak trigger time are then clustered using k-means clustering (k=4) to segment the image and better isolate potential masses from the rest of the breast and chest cavity. K=4 was chosen as the optimal number of clusters through experimentation with the patient training set. Greater than 4 clusters appeared to create too much noise within the MR segmentation while less than 4 clusters consistently caused the apparent masses to be clustered similarly to other features in the MR image. The clustering implementation uses three feature parameters representing the location of the pixel, its intensity value, and the pixel values of its neighbors. The segmented MIP of the peak trigger time is then compared to the segmented MIPs of the previous trigger times to derive a coordinate-based location and radius for the mass(es). The location and radius of the masses detected are then used as inputs for the morphological snake active contouring algorithm. The morphological snake technique, as described by Alvarez et al.[4] is a form of active contouring that works by seeking a contour boundary for separating an image into a foreground and background through solving a system of partial differential equations on a binary circle level set. The PDE system is based on the general form:

$$\frac{\partial u}{\partial t} = |\nabla u| \left(\mu \operatorname{div} \left(\frac{\nabla u}{|\nabla u|} \right) - \nu - \lambda_1 (I - c_1)^2 + \lambda_2 (I - c_2)^2 \right).$$

where morphological operators on lambda and smoothing term inputs are used to solve the system of PDEs, where *v* is the morphological balloon parameter, *u* is the level set embedding function, μ is the number of repetitions of the smoothing step in each iteration, λ_1 is a scalar representing the relative importance of the inside pixels against λ_2 (relative importance of the outside pixels), *I* is the background image pixels, while c1 and c2 are determined constants.

The boundary-seeking algorithm starts at the center of the detected mass and expands outward until detecting the mass' boundary. Using the resulting mass boundary, the original DICOM input images are then looped through to find which of the images contain the mass outlined in the MIP by calculating the similarity in pixels between the MIP mass area and the original images. The output of the algorithm for each patient is then an array of the mass segmentations in binary format of all the DICOM images where a mass is detected.

A subset of 10 BLISS MR sequences was used for training the algorithm. 6 patient cases were randomly selected from the TCIA dataset for testing. From the 6 patient test cases, 26 slices were identified by the algorithm to contain masses. Manual segmentations of the masses were generated by the outlining of a single annotator. The algorithm's accuracy was determined through comparison with the manual segmentations of the 26 slices using the Sorensen-Dice Coefficient, a statistic commonly used to measure the similarity between binary data sets.

$DSC = \frac{2|X \cap Y|}{|X| + |Y|}$, where X and Y are the pixels within each segmented region.

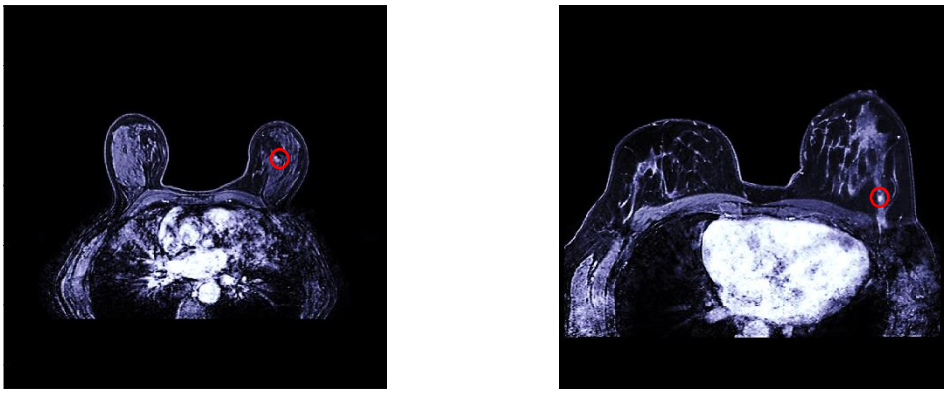
III. Results

Patient	Segmentation Accuracy Results (DICE Coefficients)						
BreastDx-01-0008	0.95	0.94	0.87				
BreastDx-01-0012	0.93	0.94	0.95	0.93			
BreastDx-01-0018	0.92	0.91					
BreastDx-01-0020	0.93	0.93	0.92	0.96	0.96	0.97	0.91
BreastDx-01-0030	0.85	0.77	0.84				
BreastDx-01-0068	0.9	0.95	0.89	0.83	0.83	0.77	0.82

Table 1. Results of mass segmentations for proposed method (n=26).

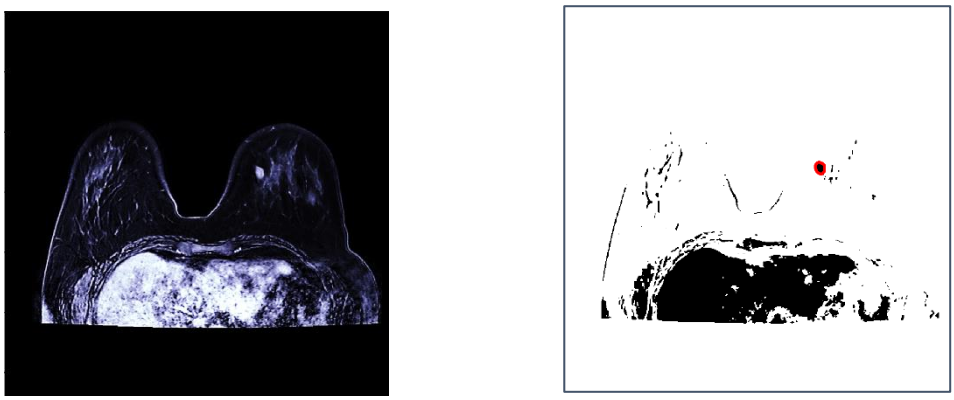
	TCIA Dataset	
	DICE AVG	DICE STDEV
Proposed	**0.90**	**0.06**

Table 2. Summary of algorithm's segmentation results (n=26).



(a) *(b)*

Figure 3 Examples of DICOM images where the contained masses were not detected by the algorithm.



(a) *(b)*

Figure 4 Example of a DICOM image slice where the contained mass was detected and segmented by the algorithm.

IV. Discussion

The results of the segmentation comparisons showed the algorithm was effective at segmenting the breast MR masses it detected. A current limitation of the algorithm is a difficulty in detecting smaller masses not as visible to the naked eye in the original DICOM images.

For future work, with the help of radiologists to identify more common features of tumors, the algorithm can be trained to better detect masses of smaller size, specifically in adjusting the clustering component. Currently, the clustering component utilizes feature vectors based off pixel value, neighboring pixel value, and location. Features based off contiguity and shape, for instance, could be added to improve mass detection.

Furthermore, in being able to better differentiate mass tissue versus extraneous tissue such as fat through the addition of insightful features, the algorithm's performance can be improved, particularly on masses more heavily shrouded by excess tissue. Through testing the performance of the algorithm on more patient cases, we will be able to make adjustments in both the detection and segmentation procedures and increase the confidence in the efficacy of our algorithm.

Additionally, quantitative features such as shape and texture can be extracted from the resulting 3-D segmentations of the algorithm to create models predicting probabilities of malignancy for the detected masses. Our hope is to be able to provide an accurate, robust algorithm that can be used as a supplemental tool for radiologists to consider and potentially compare results to.

V. Acknowledgements

We would like to thank Dr. Stephanie Lee-Felker for providing helpful feedback on identifying characteristics of tumors and trigger time properties in MR Images.

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