Classification in Dynamic Contrast-enhanced Breast MRI: Comparison of Cluster-based approach and BI-RADS Criteria

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Abstract This study introduces an automatic classification of kinetic patterns on dynamic contrast-enhanced (DCE) breast MR images. We performed k-means cluster analysis technique from real world tumor cases into a reasonable number of reference pattern set that is representative of each cluster. This technique, then, classifies the tumor specific patterns from the given MRI data by measuring vector distances from the reference pattern set. The detections are also compared with color-highlighted texture patterns by reference pattern of BI-RAIDS kinetic criteria. This method will enhance the radiologists’ capability to efficiently identify and characterize the multi-dimensional patterns from tumors on DCE breast MRI.

Key words DCE Breast MRI, Kinetics, K-means Clustering, Breast Imaging Reporting and Data System (BI-RADS)

1. Introduction

Magnetic Resonance Imaging (MRI) in combination with T1 enhancement from gadolinium diethylene triamine pentaacetic acid (Gd-DTPA) [1] is a valuable imaging modality because of its high contrast sensitivity to a large number of characteristics of tissues and body fluids, including T1 relaxation times. Dynamic contrast enhanced MRI (DCE-MRI) is necessary to detect breast lesions, and to help differentiate malignant from benign tumors [2, 3]. Malignant breast lesions tend to enhance more rapidly than benign lesions. Observation of contrast enhancement is typically achieved using dynamic imaging techniques whereby the contrast agent is injected during acquisition of a dynamic image set.

The basis of DCE-MRI is the fact that tumors need many blood vessels to grow, the concentration of the contrast agent at their location will be higher than in surrounding normal tissues and they will consequently appear as brighter areas in the images. Their dynamic and morphological patterns are related to the diffusion of the contrast agent and to the slope, edges, or the internal pattern of the enhancing region [4]. However, there is a considerable overlap between dynamic ad morphological patterns of benign and malignant lesions.

American college of radiology (ACR) breast imaging and reporting data system (BI-RADS) [5] describe the slope from pre-contrast phase to the initial enhancement phase, and the curve change in the delayed phases for kinetic curve assessment. However, BI-RADS kinetic criteria do not consider in detail the intermediate enhancement patterns in the delayed phases. Thus we performed a cluster analysis technique as a part of the role of a computer-aided diagnosis (CAD), for providing the radiologist a second opinion to take into account in difficult cases. Our clustering algorithm was a trial to explore features which are not directly human readable, reaching higher level of accuracy.
In this study, we focused on the differentiation of the kinetic patterns of malignant tumors extracted from DCE-MRI examinations as the first stage and presented the comparative results between k-means clustering and BI-RADS classification analysis.

2. Materials and Methods

2.1. Materials

DCE-MRI images from 13 patients with malignant lesions were acquired by 1.5 T Sonata (Siemens, Erlangen, Germany). First, pre-contrast T1 weighted three dimensional fast low angle shot (3D FLASH) sagittal image was obtained with fat suppression, and four consecutive post-contrast image using the same condition after the injection of 0.1 mmol/kg Gd-DTPA (Magnevist, Schering, Berlin, Germany), respectively. Standard subtraction image (i.e., the image resulted after the first post-contrast image subtracts the pre-contrast image) was acquired as post-processing image.

2.2. Data acquisition

Signal patterns were collected on a voxel by voxel from the enhanced malignant tumor area for each patient. The total number of the signal patterns was 1734 and these signals were used as the training data for the classification of the malignant signal patterns.

2.3. Implementation

In this study, the C++ programming language and Insight Segmentation and Registration Toolkit (ITK) open-source software system sponsored by the National Library of Medicine were used for image analysis.

2.4. K-means clustering

The k-means clustering is a popular method used to divide n patterns \( \{x_i, ..., x_d\} \) in d dimensional space into k clusters. The result is a set of k centers, each of which is located at the centroid of the partitioned dataset. This algorithm can be summarized in the following steps given as Figure 1.

![Figure 1. Steps of k-means clustering algorithm](image_url)

1. Choose the number of clusters k and input a dataset of n patterns \( X=\{x_1, ..., x_n\} \). Randomly select the initial candidates for k cluster centers matrix \( V^{(0)} \) from the dataset.
2. Assign each pattern to the nearest cluster using a distance measure. For each pattern \( x_i \), computer its membership function \( m(C_j|x_i) \) in each cluster \( C_j \). The membership function \( m(C_j|x) \) defines the proportion of pattern \( x \) that belongs to the \( j \)th cluster \( C_j \). The k-means algorithm uses a hard membership function, that is the membership \( m(C_j|x) \in \{0, 1\} \). If the pattern \( x_i \) is closest to cluster \( C_j \) (i.e., the distance between \( x_i \) and cluster center \( v_j \) is minimal), then \( m(C_j|x_i)=1 \); otherwise \( m(C_j|x_i)=0 \).
3. Recompute the centroids (centers) of these k clusters to find new cluster centers \( v_j \), and compute the sum of square error \( E \).
   \[
   v_j = \frac{\sum_{i=1}^{n} m(C_j|x_i)x_i}{\sum_{i=1}^{n} m(C_j|x_i)} \quad \text{for } j=1, ..., k. \tag{1}
   \]
   \[
   E = \sum_{j=1}^{k} \sum_{x \in C_j} \| x_i - v_j \|^2 \quad \text{for } i=1, ..., n; \quad j=1, ..., k. \tag{2}
   \]
4. Repeat step 2 and 3 until convergence. Typical convergence criteria are: no more reassignment of
patterns to new clusters, the change in error function $E$ fails below a threshold, or a predetermined number of iterations have been reached.

Table 1. Notation used in our algorithm

<table>
<thead>
<tr>
<th>$k$</th>
<th>The number of clusters</th>
</tr>
</thead>
<tbody>
<tr>
<td>$n$</td>
<td>The number of patterns in a dataset</td>
</tr>
<tr>
<td>$x_i$</td>
<td>The $i$th data element (pattern)</td>
</tr>
<tr>
<td>$d$</td>
<td>The number of dimensions</td>
</tr>
<tr>
<td>$v_j$</td>
<td>The centroid of the $j$th cluster</td>
</tr>
<tr>
<td>$C_j$</td>
<td>The $j$th cluster</td>
</tr>
</tbody>
</table>

Figure 2. Ten centroid signals computed from 1734 kinetic curves in malignant tumors

Table 1 shows the notation used in describing the algorithm. Figure 2 shows the 10 centroids computed finally through k-means clustering.

2.5. Approach to BI-RADS kinetic classification

Tumor regions were detected based on the analysis contrast enhancement properties of the tissue as an approach of BI-RADS kinetic criteria. The pharmacokinetic properties of the tumor were quantified by computing percentage enhancement (PE) and signal enhancement ratio (SER) at each pixel, defined as followings.

$$PE = \frac{s_1 - pre}{pre}$$ (3)

$$SER = \frac{s_1 - pre}{s_2 - pre}$$ (4)

where $S_0$, $S_1$ and $S_2$ are the precontrast (baseline), early postcontrast and late postcontrast signal intensities.

Figure 3 shows voxel classification scheme based on PE and SER values.

2.6. Classified image mapping

The centroids of the signal patterns computed through k-means clustering analysis were used for classifying random dynamic breast MR kinetic patterns within a malignant lesion. The criterion of k-means classification is to assign each pattern extracted from the MR image to the nearest reference centroid using distance measure. In this study, the number of clusters, $k$ was 10, which was selected empirically. The voxels corresponding to the position of each signal patterns were highlighted with different colors reflecting likelihood of malignancy and the type of reference pattern on a 3D volume display. On the other hand, the voxels classified by BI-RADS kinetic approach were also highlighted in the same method based on PE and SER values.

2.7. Intensity, distance and size threshold

Intensity threshold was performed in order to remove contribution into input patterns of noise and background intensities. Moreover, kinetic patterns were considered as normal tissue over a fixed distance from reference patterns in the course of k-means classification, and by threshold of PE in BI-RADS classification. Finally, size threshold was used to remove all connected components that had fewer than the number of pixels in a tumor region.

3. Results
Figure 4. An example of the results from (a) the k-means and (b) BI-RADS classification

Our classification results were displayed on an image as the texture with difference colors for each reference pattern within a malignant tumor. The various classes within a malignant tumor could be visually identified. The use of k-means clustering could subdivide as more reference patterns than with the existing BI-RADS criteria and was able to provide information for more detailed cancer diagnosis. Classification by the k-means clustering reflected the rim enhancement within a tumor better than by BI-RADS kinetic criteria. Figure 4 shows an example detected by k-means and BI-RADS classification from DCE breast MR kinetic patterns of a patient with a single breast cancer.

4. Discussion and conclusion

In this study, we presented the experimentation of k-means classifier for automatic detection of tumor specific patterns, considering the intermediate kinetic patterns in the delayed phases. Such experimentation strategy can discriminate the heterogeneous patterns within malignant tumor and characterize the multi-dimensional patterns in detail. Also, it enables to analyze diagnostic accuracy by comparing texture patterns with the result of BI-RADS kinetic approach.

There are several ways we plan our future work:

1. The short-term goal is to enrich the set of kinetic features used by the classifiers and try to improve the classification of contrast-enhancement patterns. In addition, other advanced classifiers need to be tested.

2. The long-term goal is to introduce morphological analysis. The combination with morphological analysis makes possible the comparison with the fully ranked classification by BI-RADS criteria for better differentiating benign from malignant lesions.

5. References