Segmentation of Magnetic Resonance Images using K-means and EM Clustering Algorithm

Abstract

Segmentation of images holds an important position in the area of image processing. It becomes more important while typically dealing with medical images where pre-surgery and post surgery decisions are required for the purpose of initiating and speeding up the recovery process Computer aided detection of abnormal growth of tissues is primarily motivated by the necessity of achieving maximum possible accuracy. Manual segmentation of these abnormal tissues cannot be compared with modern day's high speed computing machines which enable us to visually observe the volume and location of unwanted tissues. This paper describes efficient methods for automatic segmentation of magmatic resonance MR images**.**

الخلاصة

المهم من اليوم أصبح . الصورية المعالجة موضوع في مهم دور الصور لتجزئة مع التعامل
الشفاء وسرعة للمرض المسبب لتحديد الجراحية العمليات وبعد قبل الطبية الصور وللحصول
تضاهي الحاسوب استخدام على تعتمد تطبقات وجود تطلب المطلوبة الدقة على التقليدي الاسلوب
. معينة انسجة وموقع حجم لتحديد
مع المغناطيسي الرنين لصور التجزئة في رئيسيتن لطريقتين وصف البحث هذ يتضمن تحديد
للانسجة العزل وامكانية الزمن ناحية من الافضل الطريقة.

1. Introduction

The field known as biomedical analysis has evolved considerably over the last couple of decades. The widespread availability of suitable detectors has aided the rapid development of new technologies for the monitoring and diagnosis, as well as treatment, of patients. Over the last century technology has advanced from the discovery of x rays to a variety of imaging tools such as magnetic resonance imaging, computed tomography, positron emission tomography and ultrasonography. The recent revolution in medical imaging resulting from techniques such as computed tomography (CT) and magnetic resonance imaging (MRI) can provide detailed information about disease and can identify many pathologic conditions, giving an accurate diagnosis. Furthermore, new techniques are helping to advance fundamental biomedical research. Medical imaging is an essential tool for improving the diagnoses,

understanding and treatment of a large variety of diseases [1, 2, 3]. The extraordinary growth experimented by the medical image processing field in the last years, has motivated the development of many algorithms and software packages for image processing. There are also some efforts to develop software that could be easy to modify by other researchers, for example the Medical Imaging Interaction Toolkit, is intended to fill the gap between algorithms and the final user, providing interaction capabilities to construct clinical applications. Therefore, many software packages for visualization and analysis of medical data are available for the research community. Among them we can find commercial and non commercial packages. Usually, the former ones are focused on specific applications or just on visualization being more robust and stable, whereas the latter ones often offer more features to the end user.

2. Basics of Segmentation

Segmentation can be considered the first step and key issue in object recognition, scene understanding and image understanding. Applications range from industrial quality control to medicine, robot navigation, geophysical exploration, and military applications. In all these areas, the quality of the final result depends largely on the quality of the segmentation [4].

Formally, a set of regions $\{R1, R2, \ldots, Rn\}$ is a segmentation of the image R into n regions if:

1. $\bigcup_{i=1}^{n} R_i = R$

2. $R_i \cap R_k = \emptyset, i \neq k$

3. R_i is connected, $i = 1, 2, \ldots, n$

4. There is a predicate P that measures region homogeneity,

   (a) $P(R_i) = \text{TRUE}, i = 1, 2, \ldots, n$

   (b) $P(R_i \cup R_k) = \text{FALSE}, i \neq k$ and R_i adjacent to R_k

The above conditions can be summarized as follows: the first condition implies that every image point must be in a region. This means that the segmentation should not terminate until every point is processed. The second condition implies that regions are non-intersecting, while the third condition determines regions are composed by contiguous pixels. Finally, the fourth condition determines what kind of properties the segmented regions should have, for example, uniform gray levels, and express the

maximality of each region in the segmentation.

During the past years, many image segmentation techniques have been developed and different classification schemes for these techniques have been proposed [4,5].

We have adopted the classification proposed by Fu and Mui, in which segmentation techniques are categorized into three classes: (1) Thresholding or clustering, (2) region-based and (3) boundary-based.

2.1 Thresholding or Clustering Segmentation
2.1.1 Thresholding
The most basic segmentation procedure that may be carried out is thresholding of an image (see [6]). This method consists on comparing the measure associated to each pixel to one or some thresholds in order to determine the class which the pixel belongs to. The attribute is generally the grey level, although color or a simple texture descriptor can also be used. Thresholds may be applied globally across the image (static threshold) or may be applied locally so that the threshold varies dynamically across the image.

Under controlled conditions, if the surface reflectance of the objects or regions to be segmented are uniform and distinct from the background and the scene is evenly illuminated then the resulting image will contain homogenous regions with well defined boundaries that generally lead to a bimodal or multi-modal histogram.

Finding the modes determines the partitions of the space and hence the segmentation.

Be an image composed by a bright object on a darker background, thus the histogram is bimodal, similar to the example shown in Figure 1.a. The two peaks correspond to the relatively large number of points inside and outside the object.

The dip between the peaks corresponds to the relatively few points around the edge of the object. The threshold is then placed in the valley between both peaks, then pixels with a grey level higher than the threshold t will be associated to the object, while the remaining pixels to the background. Figure 1.b illustrates a multi-modal histogram.

Nevertheless, in many cases the background level is not constant, and the contrast of objects varies within the image. In such cases, a threshold that works well in one area of the image might work poorly in other areas. Thus, it is convenient to use a threshold that is slowly varying in function of position in the image. A dynamic threshold was proposed by Chow an Kaneko, which divides the image up into
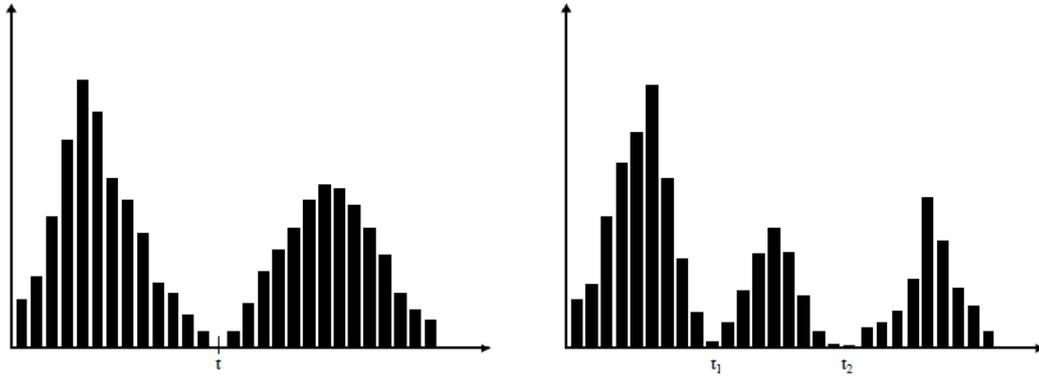
Figure 1: Histogram examples. (a) Bimodal histogram, (b) multi-modal histogram.

rectangular subimages and computes the threshold for each subimage. However, a subimage can fail to have a threshold if its gray-level histogram is not bi-modal, and then such sub-images receive interpolated thresholds from neighboring subimages. Finally, the entire picture is thresholded by using the separate thresholds for each subimage.
The success of this approach hinges on whether suitable thresholds exist and whether they may be inferred from the image histogram. Various methods have been proposed for determining an appropriate threshold [8]. However, this is only possible with a restricted set of images under the assumption of a controlled environment i.e. industrial applications. As methods to tackle natural images, where variation of illumination, noise and texture are present, they become inadequate.

2.1.2 Clustering
Clustering is a process whereby a data set is replaced by clusters, which are collections of data points that "belong together". It is natural to think of image segmentation as clustering, grouping those pixels that have the same colour and/or the same texture. Clustering methods [9] can be divided into two basic types: hierarchical and partitional clustering. Within each of the types there exists a wealth of subtypes and different algorithms for finding the clusters.
Hierarchical clustering proceeds successively by either merging smaller clusters into larger ones (agglomerative algorithms), or by splitting larger clusters (divisive algorithms). The clustering methods differ in the rule by which it is decided which two small clusters are merged or which large cluster is split. The final result of the algorithm is a tree of clusters called a dendogram, which shows how the clusters are related. By cutting the dendogram at a desired level, a clustering of the data items into disjoint groups is obtained.
On the other hand, partitional clustering attempts to directly decompose

the data set into a set of disjoint clusters. An objective function expresses how good a representation is, and then the clustering algorithm tries to minimize this function in order to obtain the best representation. The criterion function may emphasize the local structure of the data, as by assigning clusters to peaks in the probability density function, or the global structure. Typically the global criteria involves minimizing a measure of dissimilarity for the samples within each cluster, while maximizing the dissimilarity between different clusters. The most commonly used partitional clustering method is the K-means algorithm, in which the criterion function is the squared distance of the data items from their nearest cluster centroids.

Clustering methods, even as thresholding methods, are global and do not retain positional information. The major drawback of this is that it is invariant to spatial rearrangement of the pixels, which is an important aspect of what is meant by segmentation. Resulting segments are not connected and can be widely scattered.

Some attempts have been made to introduce such information using pixels coordinates as features. However, this approach tends to result in large regions being broken up and the results so far are no better than those that do not use spatial information. The need to incorporate some form of spatial information into the segmentation process, led to the development of methods where pixels are classified using their context or neighborhood.

2.2 Region-based Segmentation

The region approach tries to isolate areas of images that are homogeneous according to a given set of characteristics. We introduce in this section two classical region based methods: region growing and split-and-merge.

2.2.1 Region Growing

Region growing [10] is one of the most simple and popular region-based segmentation algorithms. It starts by choosing a (or some) starting point or seed pixel.

The most habitual way is to select these seeds by randomly choosing a set of pixels in the image, or by following a priori set direction of scan of the image. However, other techniques of selection based on boundary information will be discussed in next section.

Then, the region grows by successively adding neighboring pixels that are similar, according to a certain homogeneity criterion, increasing step by step the size of the region. This criterion can be, for example, to require that the variance of a feature inside the region does not exceed a threshold, or that the difference between the pixel and the average of the region is small. The growing process is continued until a pixel not

sufficiently similar to be aggregated is found. It means that the pixel belongs to another object and the growing in this direction is finished. When there is not any neighboring pixel which is similar to the region, the segmentation of the region is complete. Monitoring this procedure gives on the impression of regions in the interior of objects growing until their boundaries correspond with the edges of the object.

2.2.2 Split-and-Merge

As has been above defined, one of the basic properties of segmentation is the existence of a predicate P which measures the region homogeneity. If this predicate is not satisfied for some region, it means that that region is inhomogeneous and should be split into subregions. On the other hand, if the predicate is satisfied for the union of two adjacent regions, then these regions are collectively homogeneous and should be merged into a single region.
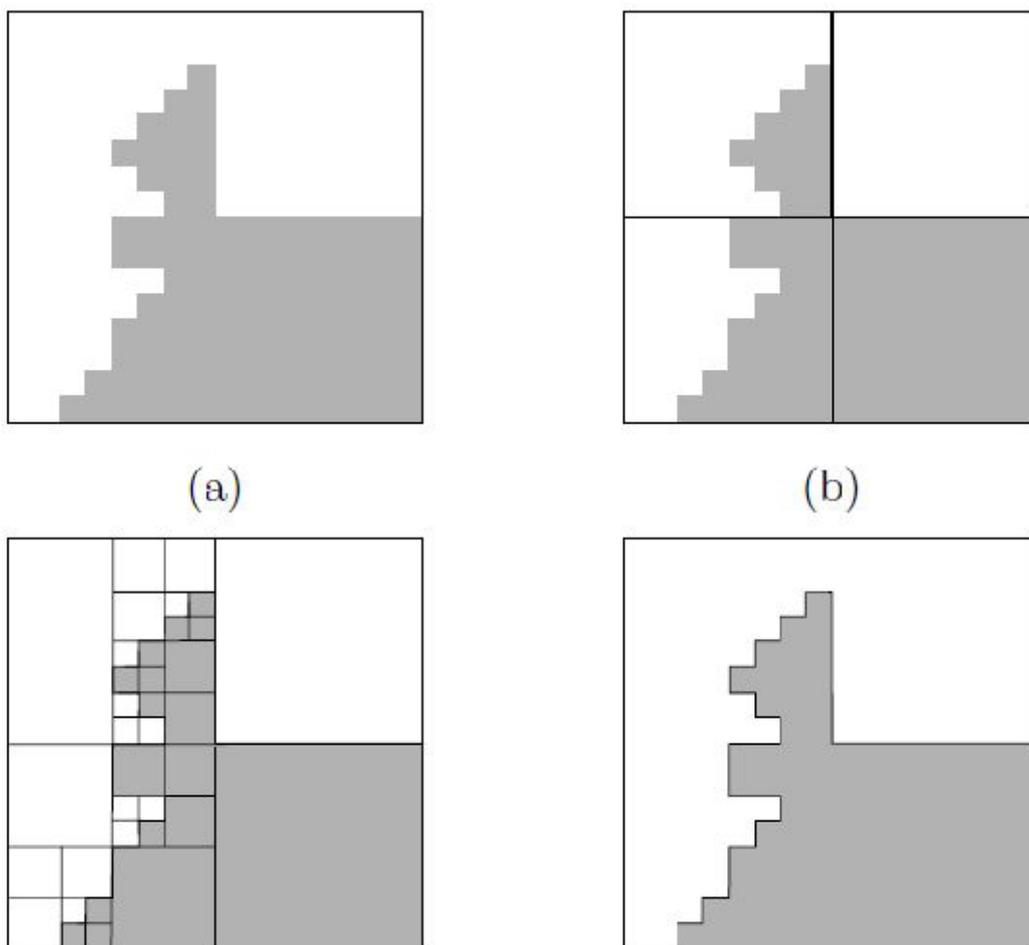
Figure 2: Split-and-merge segmentation. (a) Original image, (b) initial split in four squared blocks, (c) splitting of the image in homogenous blocks and (d) final segmentation after the merging.

A way of working toward the satisfaction of these homogeneity criteria is the split-and-merge algorithm. This technique consists, as their name denotes, of two basic steps. First, the image is recursively split until all the regions verify a homogeneity criterion. Next, in a second step, all adjacent regions are reassembled of way that resulting regions satisfy the homogeneity criterion.

A quad-tree structure is often used to effect the step of splitting: it is based on the recursive decomposition of the regions that does not verify the homogeneity criterion into four squared subregions, starting from the whole image. Therefore, an inverse pyramidal structure is builded. The merging step consists on merging the adjacent blocks which represent homogeneous regions but have been divided by the regular decomposition. The different steps are depicted in Figure 2.

2.3 Boundary-based Segmentation

The last class of methods for image segmentation are related to the detection of the luminance transitions between regions, i.e. the boundaries (lines or edges).

The fundamental importance of line and edge information in both biological and Computer Vision systems has long been recognized. Indeed, the biological evidence showing edge-detection playing a central role in the early stages of visual perception in mammals (low level vision), such as the Human Visual System, has often been the motivation for its adoption by researchers in image processing. Local features, such as lines and edges, can describe the structure of a scene relatively independently on the illumination. For example, a cartoon drawing consisting only of lines is often enough for humans to interpret a scene. Image segmentation techniques based on edge detection have long been in use, since the early work of Roberts in 1965. Although a variety of methods of edge detection have been suggested, there are two basic local approaches: first and second order differentiation. The bane of all these methods, however, is noise. Edges, by definition, are spatially rapidly varying and hence have significant components at high spatial frequencies. This is also, unfortunately, the characteristic of noise, and therefore any gradient operator that responds well to the presence of an edge will also respond well to the presence of noise or textures thus signaling false edges.

2.3.1 First order

In the first case, a gradient mask is convolved with the image to obtain the gradient vector associated with each pixel. Edges are the places

where the magnitude of the gradient vector is a local maximum along the direction of the gradient vector . For this purpose, the local value of the gradient magnitude must be compared with the values of the gradient estimated along this orientation and at unit distance on either side away from the pixel. After this process of non-maxima suppression takes place, the values of the gradient vectors that remain are thresholded, and only pixels with a gradient magnitude above that threshold are considered as edge pixels [11].

The Sobel operator introduced a weighting of local averages measures at both sides of the central pixel. Several works have looked for the optimization of this weighting factor. Canny proposed the derivative-of-Gaussian filter as a near optimal filter with respect to three edge-finding criteria: (a) good localization of the edge, (b) one response to one edge and (c) high probability of detecting true edge points and low probability of falsely detecting non-edge points. Deriche [12], based on Canny's criteria, implemented a filter with an impulse response similar to that of the derivative of Gaussian, but which lends itself to direct implementation as a recursive filter.

2.3.2 Second order

In the second-order derivative class, optimal edges (maxima of gradient magnitude) are found by searching for places where the second derivative is zero. The isotropic generalization of the second derivative to two dimensions is the Laplacian.

However, when gradient operators are applied to an image, the zeros rarely fall exactly on a pixel. It is possible to isolate these zeroes by finding zero crossings:

places where one pixel is positive and a neighbor is negative (or vice versa). Ideally, edges should correspond to boundaries of homogeneous objects and object surfaces.

Having obtained an edge map, there is usually a second stage to boundary based segmentation, which is to group the boundary elements to form lines or curves. This is necessary because, excepting the simplest noise free images, the edge detection will result in a set of fragmented edge elements. There are three main approaches to this problem: local linking techniques [13], global methods, such as Hough Transform (HT) methods , or combined approaches, such as the hierarchical HT and the MFT based methods. The local linking methods use attributes of the edge elements, such as magnitude, orientation and proximity, to grow the curves in the image. In the HT methods, the edge elements are transformed to a parameter space, which is a joint histogram of the parameters of the model of line or curve being detected.

The peaks in this histogram then indicate the presence and location of the

lines or curves being detected.

3. Algorithms

3.1 K-means Clustering Algorithm
K-Means algorithm is an unsupervised clustering algorithm that classifies the input data points into multiple classes based on their inherent distance from each other. The algorithm assumes that the data features form a vector space and tries to find natural clustering in them. The points are clustered around centroids $\mu_i \forall i = 1 \ldots k$ which are obtained by minimizing the objective

$$V = \sum_{i=1}^{k} \sum_{x_j \in S_i} (x_j - \mu_i)^2$$

where there are k clusters $S_i, i = 1, 2, \ldots, k$ and μ_i is the centroid or mean point of all the points $x_j \in S_i$

As a part of this project, an iterative version of the algorithm was implemented. The algorithm takes a 2 dimensional image as input. Various steps in the algorithm are as follows:

1. Compute the intensity distribution(also called the histogram) of the intensities.
2. Initialize the centroids with k random intensities.
3. Repeat the following steps until the cluster labels of the image does not change anymore.
4. Cluster the points based on distance of their intensities from the centroid intensities.

$$c^{(i)} := \arg \min_j \left\| x^{(i)} - \mu_j \right\|^2$$

5. Compute the new centroid for each of the clusters.

$$\mu_i := \frac{\sum_{i=1}^{m} 1\{c_{(i)} = j\} x^{(i)}}{\sum_{i=1}^{m} 1\{c_{(i)} = j\}}$$

where k is a parameter of the algorithm (the number of clusters to be found), i iterates over the all the intensities, j iterates over all the centroids and μi are the centroid intensities.[14]

3.2 EM Algorithm
Expectation Maximization(EM) is one of the most common algorithms used for density estimation of data points in an unsupervised setting. The

algorithm relies on finding the maximum likelihood estimates of parameters when the data model depends on certain latent variables. In EM, alternating steps of Expectation (E) and Maximization (M) are performed iteratively till the results converge.The E step computes an expectation of the likelihood by including the latent variables as if they were observed, and a maximization (M) step, which computes the maximum likelihood estimates of the parameters by maximizing the expected likelihood found on the last E step[1]. The parameters found on the M step are then used to begin another E step, and the process is repeated until convergence.

Mathematically for a given training dataset $\{x_{(1)}, x_{(i2)}, \ldots x_{(m)}\}$ and model p(x; z) where z is the latent variable, We have:

$$l(\theta) = \sum_{=1}^{m} \log p(x; \theta)$$

$$= \sum_{i=1}^{m} \log \sum_{z} p(x, z; \theta)$$

As can be seen from the above equation, The log likelihood is described in terms of x, z and θ. But since z, the latent variable is not known, We use approximations in its place.

These approximations take the form of E & M steps mentioned above and formulated mathematically below.

E Step, for each i:

$$Q_i(z^{(i)}) := p(z^{(i)}|x^{(i)}; \theta)$$

M Step, for all z:

$$\theta := \arg\max_{\theta} \sum_{i} \sum_{z^{(i)}} Q_i(z^{(i)}) \log \frac{p(x^{(i)}, z^{(i)}; \theta)}{Q_i(z^{(i)})}$$

where Qi is the posterior distribution of z(i)'s given the x(i)'s. Conceptually, The EM algorithm can be considered as a variant of the K Means algorithm where the membership of any given point to the clusters is not complete and can be fractional.[15]

4. Experimental Results
We did experiments on a set of MR images shown in figure 3, the dataset consist of 7 different MR images. These images are tested for both Kmeans
and EM algorithms and the results are shown in figure 4 and figure 5 respectively.
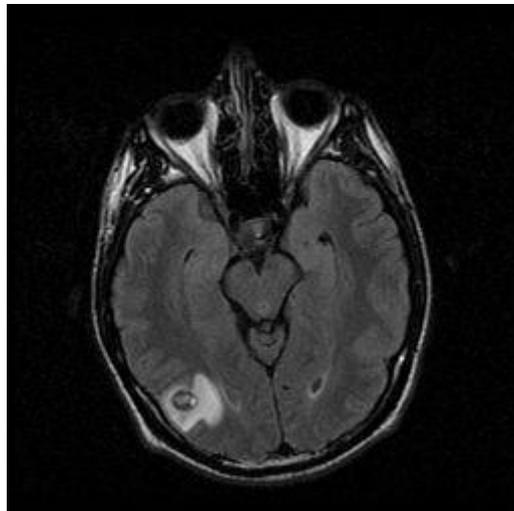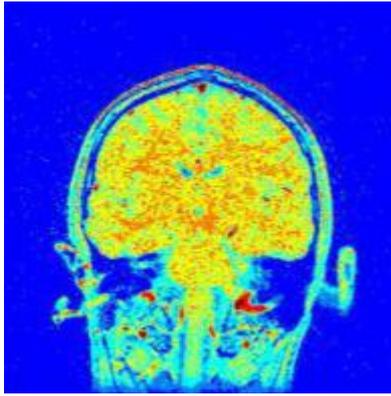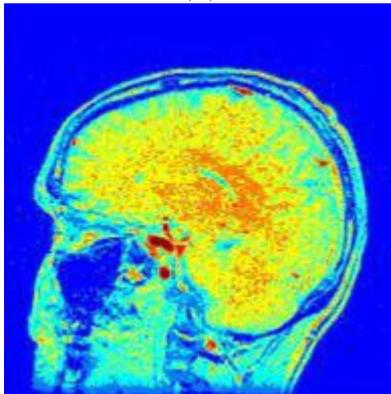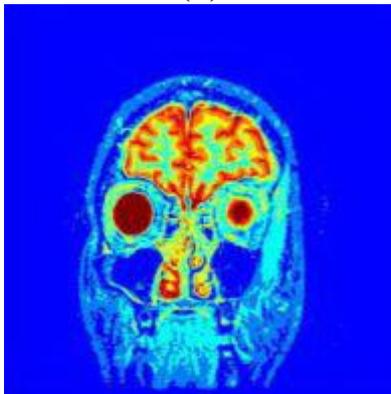
(a)

(b)

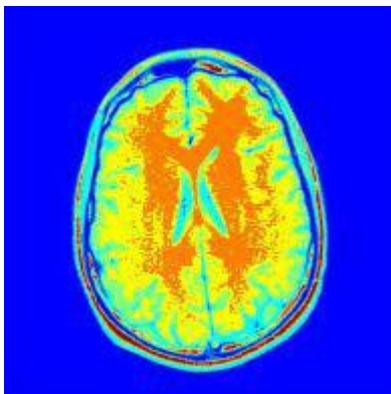

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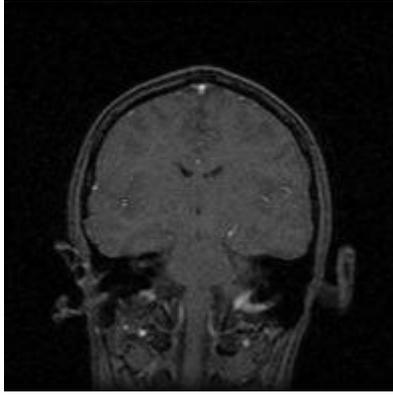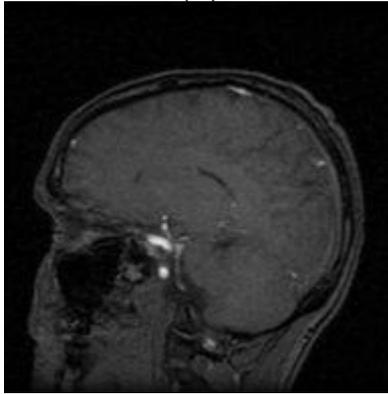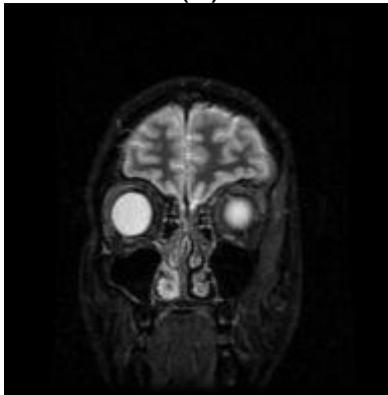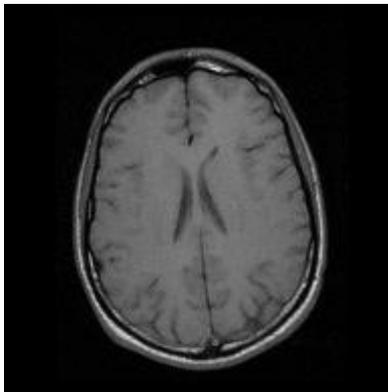
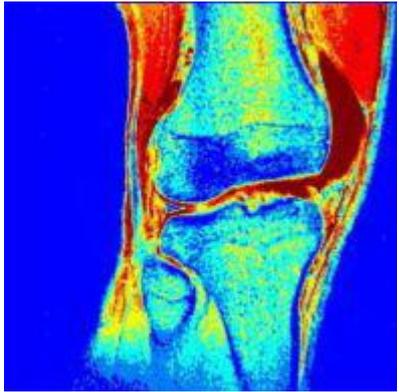
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Figure 3 The dataset used in our experiments

(a)

(b)
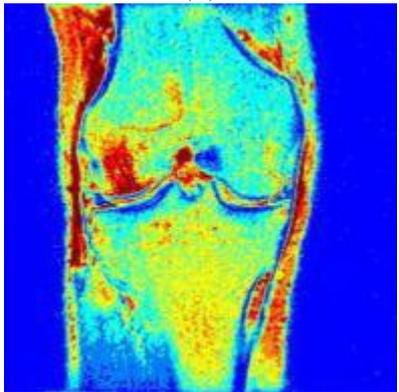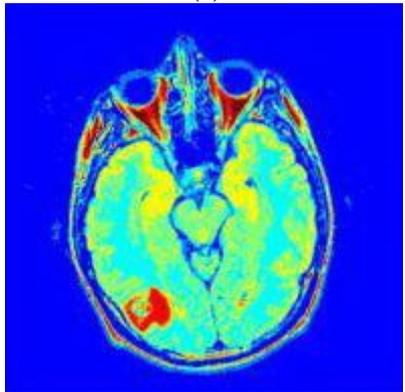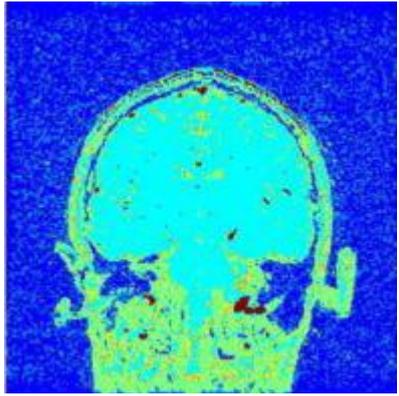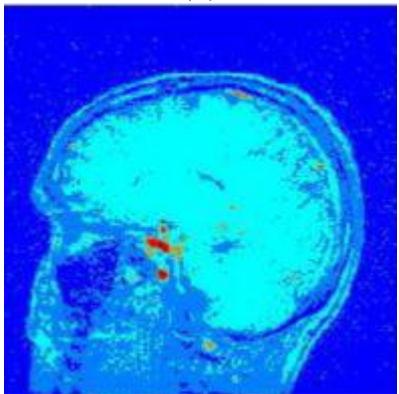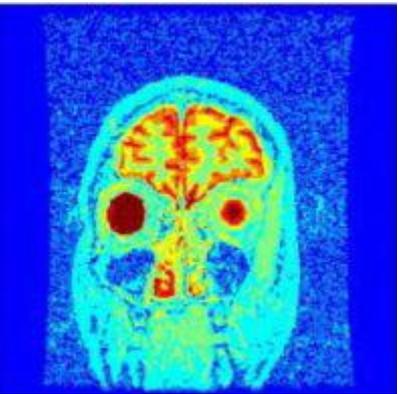

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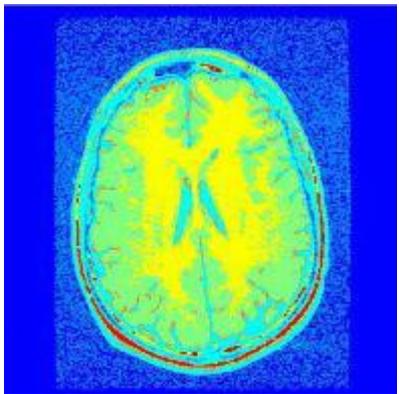Figure 4 The results of applying K-means algorithm (Number of segmentation levels=8)

(a)

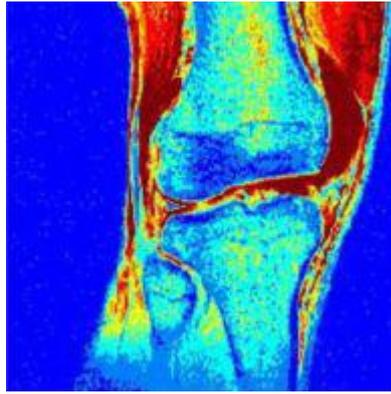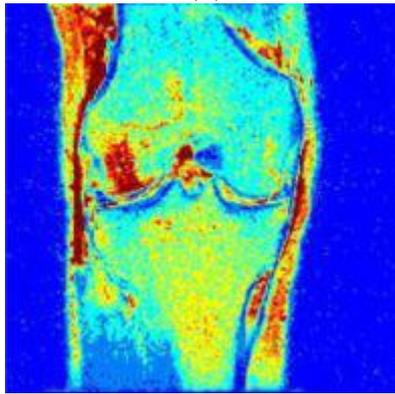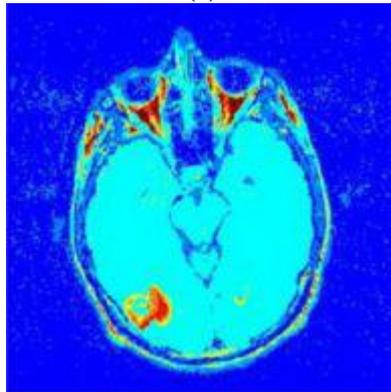
(b)

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Figure 5 The results of applying EM algorithm (Number of segmentation levels=8)

5. Conclusions

After the dataset shown in figure 3 were used to test K-mean and EM algorithms the following points are concluded:

· k-mean algorithm is faster than EM algorithm (0.33 second, and 10 seconds respectively)

· K-mean shows segments that never been appear in the results of EM algorithm (see figures 4.b and 5.b as an example)

· EM has higher sensitivity to noise rather than K-mean (see figures 4.c and 5.c as an example)

Finally, we recommend using k-means algorithm for segmenting MR images.

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