An Automated Segmentation Approach for Quantification and Analysis of Brain Tumors from Magnetic Resonance Images

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Abstract

Medical image processing has come to play a key role in diagnosis and planning of treatment modalities. The huge volume of medical data especially in the form of medical images has necessitated the need for automated analysis of the image, especially in the case Magnetic Resonance Imaging (MRI), which is an important ally in the fight against brain tumor. In this paper a tool for automated segmentation of brain tumors from brain MRI is devised. The tool is capable of quantifying the segmented tumors for different types of analysis in order to aid the radiologist. The three different segmentation approaches like K means, Fuzzy C Means Clustering (FCM) and Watershed segmentation are evaluated for their suitability. The results of the segmentation have been evaluated using different evaluation parameters. A Graphical User Interface (GUI) which is designed as part of the tool is also presented.

1. Introduction

Images are considered as one of the most important medium of conveying information. Understanding images and extracting the information from them such that the information can be used for other tasks is an important aspect of Machine learning. The primary objective of image processing is to optimize visualization of particular thematic data set. The type of image processing method and strategy is broadly influenced by the application and its objectives. One of the first steps in direction of understanding images is to segment them and find out different objects in them. Segmentation of an image entails the division or separation of the image into regions of similar attribute. The basic attribute for segmentation is image amplitude-luminance for a monochrome image and color components for a color image. Image

edges and textures [1] are also useful attributes for segmentation. The result of image segmentation is a set of regions that collectively cover the entire image or a set of contours extracted from the image. Segmentation does not involve in classifying each segment. The segmentation only subdivides the image; it does not attempt to recognize the individual segments or their relationships to one another.

Image segmentation is the most critical stage of data processing, because a good classification is dependent on the features extracted from the segmented images. It plays a crucial role in determining the sensitivity of the entire system. Today several different unsupervised classification algorithms are commonly used to cluster similar patterns in a data set based only on its statistical properties [2]. Especially in image data applications, self-organizing methods for unsupervised classification have been successfully applied for clustering pixels or group of pixels in order to perform segmentation tasks. So in order to enhance the accuracy of any classification tool for automated analysis of better morphology, it is imperative for us to design better algorithms that invariably should have better segmentation techniques.

With the advent of multiple imaging procedures there are multitude of tools available for imaging a particular disease. With DICOM standard bridging the different imaging modalities to present their outputs in a universally acceptable format, it is very essential to develop image processing means and tools which can aid in better diagnosis. Better diagnosis is very essential to determine the type of the patient"s disease, the choice of suitable treatment method, and the prognosis: the outcome of the disease. When radiologists are asked to name aspects of their work that are common, time consuming, and could be automated, they usually do not mention detection but rather documentation and quantification. With the increasing volume of medical images, Computer Aided Diagnosis (CAD) systems can go a long way in helping better diagnosis. CAD broadly refers to "the use of computer algorithms to aid the image interpretation process"[3]. The basic concept of CAD is to provide a computer output as a second opinion to assist radiologists image interpretation by improving accuracy and consistency of radiological diagnosis and also by reducing the image reading time. CAD has generally been defined by diagnosis made by a physician who takes into account the computer output based on quantitative analysis of radiological images. The goal of CAD is to improve the quality and productivity of radiologists [4].

This paper explains a CAD systems specifically designed for the purpose of Brain Tumors from MRI. Three different segmentation procedures like K means segmentation, Watershed segmentation and Fuzzy C means segmentation are employed for segmenting the images and the results of segmentation studied and observed. The performance of the segmentation approaches is evaluated using different performance measures they are Probabilistic Rand Index (PRI), Variation of Information (VOI), Global Consistency Error (GCE), PSNR (Peak Signal to Noise Ratio), Dice coefficient (DCE) and Jaccard Distance (JD).

2. Segmentation approaches

Image Segmentation techniques can be classified [5] into the following categories:

Edge-based, Threshold based, Region-based, Neural Network based, Cluster-based, and Hybrid [6]. Image segmentation based on thresholding is one of the oldest and powerful technique, since the threshold value divides the pixels in such a way that pixels having intensity value less than threshold belongs to one class while pixels whose intensity value is greater than threshold belongs to another class [7]. Segmentation based on edge detection attempts to resolve image by detecting the edges between different regions that have sudden change in intensity value are extracted and linked to form closed region boundaries. Region based methods [8], divides an image into different regions that are similar according to a set of some predefined conditions. The different types of Neural Network based image segmentation approaches available in the literature [9] can be primarily classified into two categories: supervised and unsupervised methods. The supervised method requires human input for segmentation in the form of selecting the training data set required for segmenting the images. Unsupervised methods are usually semi or fully automatic but the human intervention is usually necessitated by the need to improve the performance of the methods. Unsupervised segmentation method partitions the images automatically without human intervention. However, these architectures can be executed with help of application specific prior knowledge at design time comprising anatomical, physical or biological knowledge. Clustering is an unsupervised learning technique, where one needs to know the number of clusters in advance to classify pixels [10]. A similarity condition is defined between pixels, and then similar pixels are grouped together to form clusters

2. 1 K-Means Clustering

Specific number of disjoint, flat (non-hierarchical) clusters are generated through K-Means clustering. It is typically suited for creation of globular clusters. The K-Means method can be categorized as numerical, unsupervised, non-deterministic and iterative approach that classifies the input data points into multiple classes based on their distance from one another. The algorithm assumes that the data features form a vector space and tries to find natural clustering in them [10]. K-Means employs least-squares partitioning method which dissects a collection of objects into K distinct groups. The algorithm iterates over these steps:

1.   Compute the mean of each cluster.
2.   Compute the distance of each point from each cluster by computing its distance from the corresponding cluster mean. Assign each point to the cluster it is nearest to.
3.   Iterate over the above two steps till the sum of squared within group errors cannot be lowered any more.

The points are clustered around centroids, which are obtained by minimizing the objective;

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

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

The K means clustering processing can be described as below [11].

- Partitioning the dataset is into K clusters and the assigning data points randomly to create clusters that have roughly the same number of data points.
- For each point of data, calculate the distance (Mahalanobis or Euclidean) between the data point and each cluster.
- If the data point is nearest to its own cluster, then leave the data point where it is or move it into the closest cluster otherwise.
- Repeating the above step until there is no data point moves from one cluster to another and the clusters are stable to end the clustering process.
- The choice of initial partition influences hugely the result, in terms of inter-cluster and intra-cluster distances and cohesion.

The new centroid for each cluster is calculated using

$$\mu_i := \frac{\sum_{i=1}^{m} 1\{C_{(i)} = j\}x^{(i)}}{\sum_{i=1}^{m} 1\{C_{(j)} = j\}} \tag{2}$$

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 μ_i are the centroid intensities.

2. 2 Fuzzy C-means Clustering (FCM)

Fuzzy clustering plays an important role in solving problems in the areas of pattern recognition and fuzzy model identification. A variety of fuzzy clustering methods have been proposed and most of them are based upon distance criteria [12]. One widely used algorithm is the Fuzzy C-means (FCM) algorithm. It uses reciprocal distance to compute fuzzy weights. Fuzzy C-means Clustering (FCM) is also known as Fuzzy ISODATA, is an clustering technique which is separated from hard k-means that employs hard partitioning. The FCM employs fuzzy partitioning such that a data point can belong to all groups with different membership grades between 0 and 1.

FCM is an iterative algorithm. The aim of FCM is to find cluster centers (centroids) that minimize a dissimilarity function.

To accommodate the introduction of fuzzy partitioning, the membership matrix (U) is randomly initialized according to equation (3)

$$\sum_{i=1}^{c} u_{ij} = 1, \forall j = 1,...,n \tag{3}$$

The dissimilarity function which is used in FCM is given equation 4

$$J(U,c_1,c_2,...,c_c) = \sum_{i=1}^{c} J_i = \sum_{i=1}^{c}\sum_{j=1}^{n} u_{ij}{}^m d_{ij}{}^2 \tag{4}$$

u_{ij} is between 0 and 1;
c_i is the centroid of cluster i;

d_{ij} is the Euclidian distance between i_{th} centroid(c_i) and j_{th} data point;
$m \epsilon [1, \infty]$ is a weighting exponent.

To reach a minimum of dissimilarity function there are two conditions. These are given in Equation 5 and Equation 6.

$$c_i = \frac{\sum_{j=1}^{n} u_{ij}^{m} x_j}{\sum_{j=1}^{n} u_{ij}^{m}} \tag{5}$$

$$u_{ij} = \frac{1}{\sum_{k=1}^{c} \left(\frac{d_{ij}}{d_{kj}}\right)^{2/(m-1)}} \tag{6}$$

Detailed algorithm of fuzzy c-means proposed by Bezdek in 1973[13]. This algorithm determines the following steps [14].

Step 1. Randomly initialize the membership matrix (U) that has constraints in Equation 3.
Step 2. Calculate centroids (c_i) by using Equation 5.
Step 3. Compute dissimilarity between centroids and data points using equation 4. Stop if its improvement over previous iteration is below a threshold.
Step 4. Compute a new U using Equation 6. Go to Step 2.

By iteratively updating the cluster centers and the membership grades for each data point, FCM iteratively moves the cluster centers to the "right" location within a data set.

2. 3 Watershed Segmentation

The concept of watershed is based on visualizing an image in three dimensions: two spatial coordinates and intensity [15]. We consider three types of points:
1.   The points belonging to the local minimum.
2.   The points where a drop of water, if placed at the locations of these points, would fall to a single local minimum. It is called *catchment basin* or *watershed*.
3.   The points where water would be equally likely to fall to more than one local minimum. They are similar to the crest lines on the topographic surface and are termed *divide lines* or *watershed lines*.

The two main properties of watershed segmentation result are continuous boundaries and over-segmentations. As we know, the boundaries that made by the watershed algorithm are exact the watershed lines in the image. Therefore, the numbers of region basically will be equal to the numbers of minima in the image.
The following figures illustrate the mechanism to construct dam.
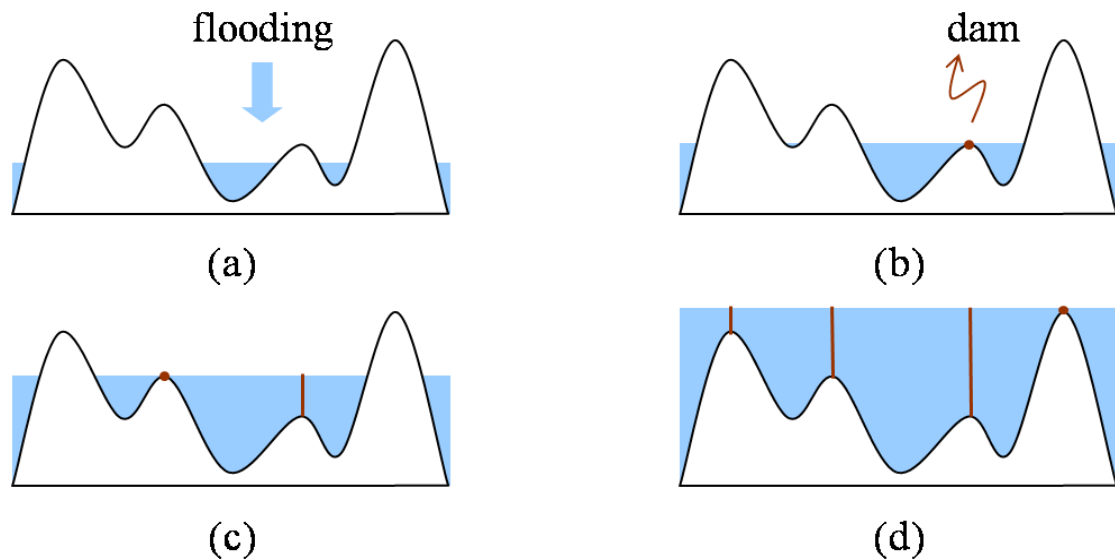
Figure (1) (a) ~(d) Watershed algorithm.

Supposed that figure 1 is the image of input, and the height of the "mountain" is proportional to intensity values input image. We start to flood water from below by letting water rise through the holes at a uniform rate. Figure (b) we see that water now has risen into the first and second catchment basins. So we will construct a dam to stop it to overflowing, and do the same motion step by step.Direct application of the watershed segmentation algorithm in the form discussed in the previous section generally leads to *over segmentation* due to noise and other local irregularities of gradient.

An approach used to control over segmentation is based on the concept of markers [15]. We have *internal* markers, associated with objects of interest, and *external* markers. A procedure for markers selection typically will consist of two principal steps:

(1)   Preprocessing (usually smoothing).
(2)   Definition of a set of criteria that markers must satisfy (to do edge detection for every small region).

3. The CAD Tool – Graphical User Interface

A comprehensive tool capable of performing segmentation and different analysis as required by the user is designed. The tool is proposed to be in the form of a Graphical User Interface (GUI) which enables the user to have ease of operation in loading the image, segmenting it and analyzing it. The tool is coded using Matlab Version 12. A Graphical User Interface enable the user to have seamless use and flexibility of operation. The implementation is carried out in a system having Core 2 Duo processor cloaking at a speed of 2 GHz with a RAM of 2GB. The screen shot of the tool is given in the figure (2)
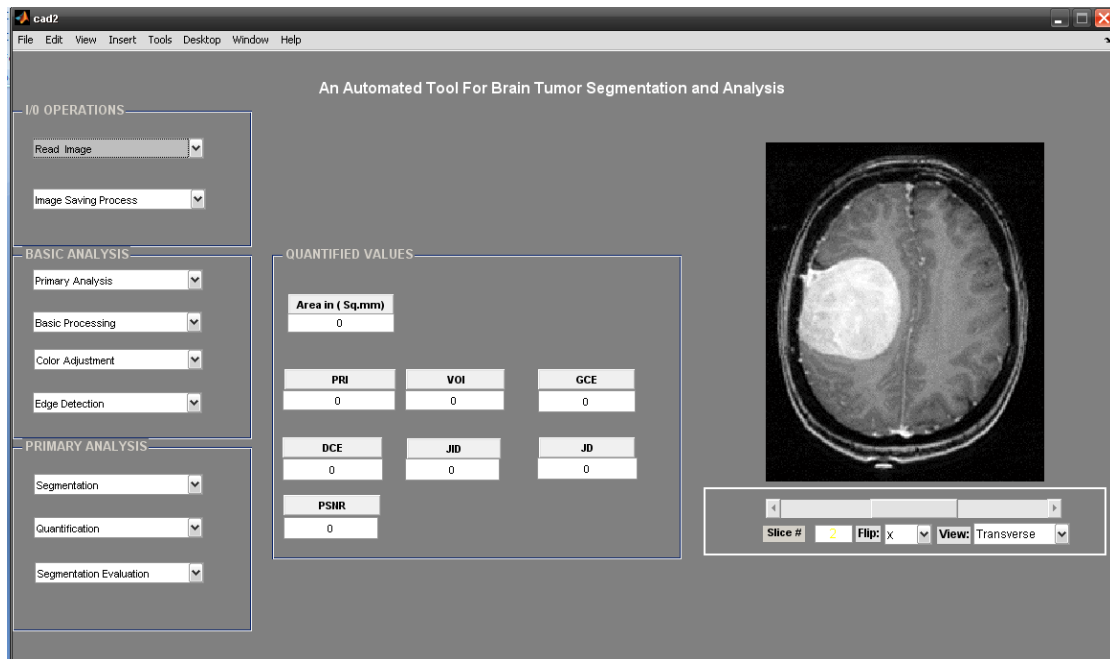
Figure (2) : The Screen shot of the CAD tool

The tool as such can be demarcated in to 5 different functional regions. Each region has specific functional and analysis elements inbuilt in to them.

Region 1: This is the Input / Output section of the tool. The tool is capable of handling images in normal image formats like,. jpg,. bmp,. tiff and also it is capable of handling DICOM images. Using the tool a series of DICOM images can also be fed as input for 3D Visualization. In the output section, function elements here enable to save the image in current display window for further analysis. The output section also has the capability to save 3D volume information in the case of series images being read.

Region 2: This section helps the user in performing basic analysis of the images; the image can be either the MRI image of the whole brain or the segmented image as obtained by the tool. This section has 4 sub functional sections like;

Initial Analysis: This includes, Histogram Analysis, Pixel Profile of a particular region of the image and a specific tool for adjusting the image intensity for better visualization.

Basic Processing: This incorporates analysis like, Image adjusts for smoothening, histogram equalization, and wiener smoothening and morphology based analysis.

Color Adjustment: This has the option of viewing the image in different color spaces like, hot, gray and jet. This helps in better visualization of images.

Edge Detection: Different edge detection operations like, Prewitt, Sobel, Canny, Log, Roberts and Zero crossing operators are implemented for edge analysis.

Region 3: This is the primary analysis section in which the segmentation, quantification and evaluation of segmentation is carried out.

Segmentation: K means segmentation, Watershed segmentation; Fuzzy c means

segmentation based segmentation are implemented here

Quantification: The area of the segmented Brain tumor is calculated using this functional icon

Segmentation Evaluation: The performance of the segmentation approaches is evaluated using different performance measures they are Probabilistic Rand Index (PRI), Variation of Information (VOI), Global Consistency Error (GCE), Peak Signal to Noise Ratio(PSNR), Dice coefficient(DCE) and Jaccard Distance (JD).

Region 4: This visual representation of the different analysis and processing is displayed here. It has the capability to handle both 2D and 3D images.

Region 5: The quantified results are presented here. This includes the value for the estimated tumor area and the value for different parameters used for evaluation segmentation.

4. Results and Discussion

In order to illustrate the different segmentation approaches implemented in this tool and other aspects of the tool the following image is considered as a test image. The image slice and its corresponding histogram are given in the figure (3) below.
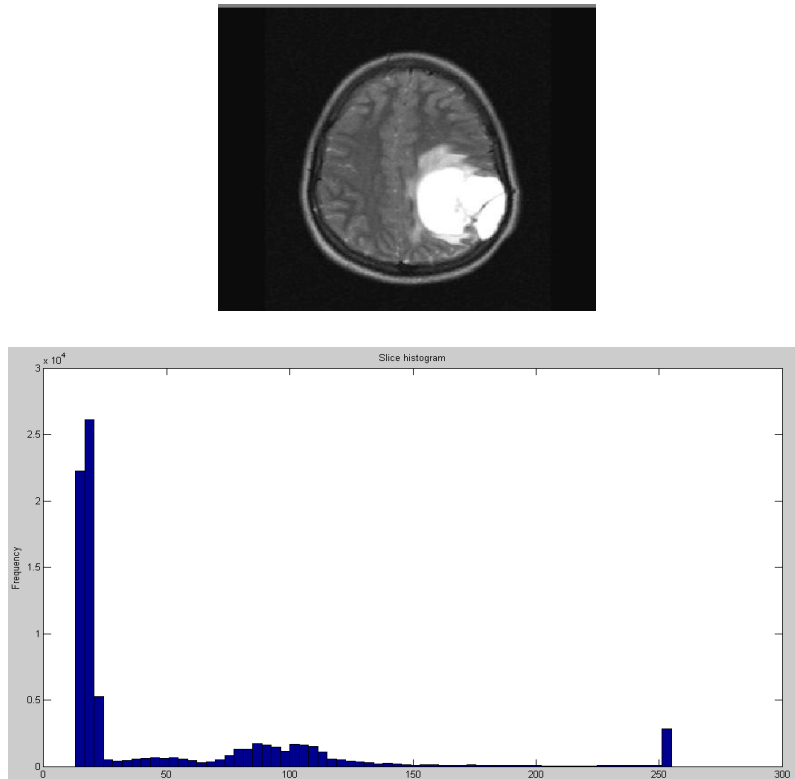

Figure (3) : Input Brain MRI and its Histogram.

The pixel distribution profile anlaysis fucntion available in the tool box helps in identifying the distribution of pixel and inference of regions having sudden change in

the pixel intensity. The user upon selection of this option will prompted to draw a line across the image for which the user intends to identifty the pixel profile.
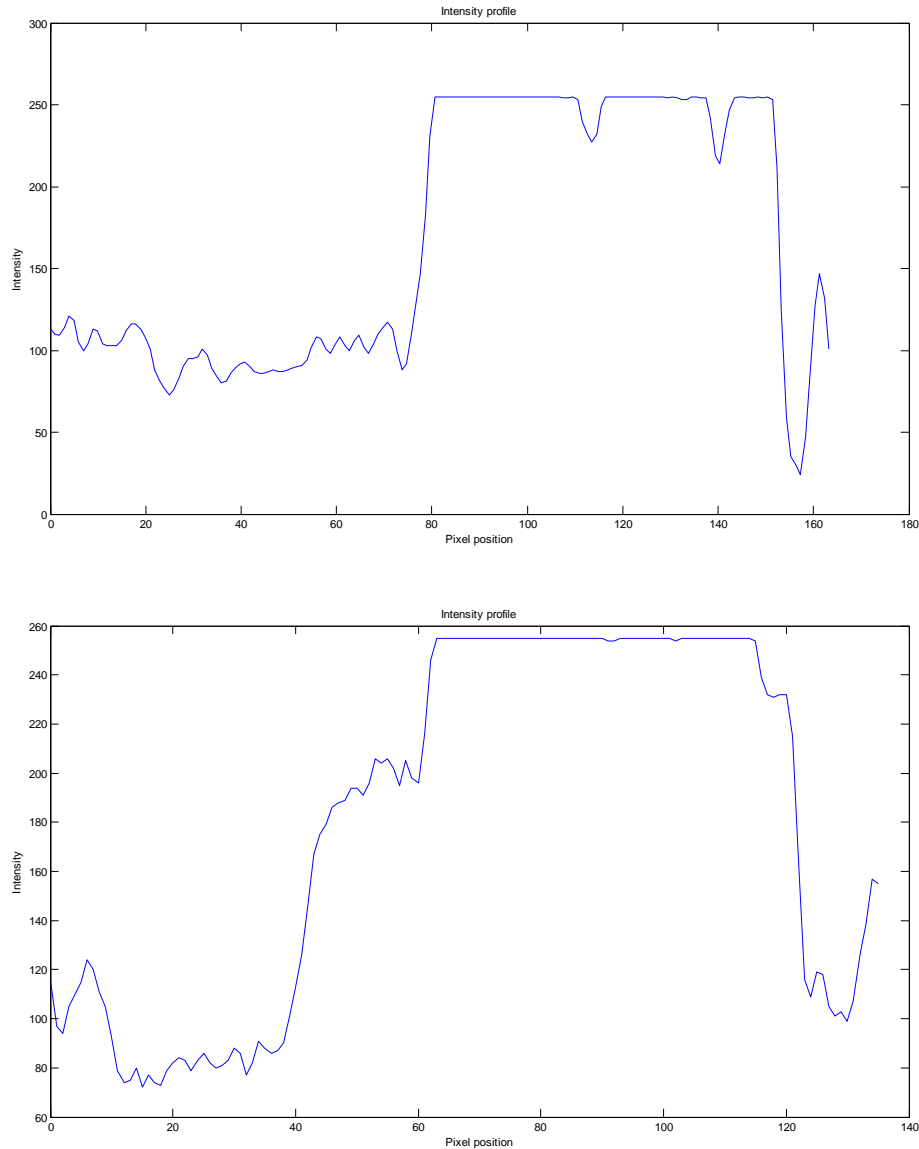
Figure (4) : Intensity Profile Horizontal and Vertical crossing through the Tumor.

The figure (4) illustrates the pixel profile when the analysis is done for horizontal row and vertcial coloumn as it pass through the tumor. It can be clearly be identified a change in pixel profiel is clearly visible on the either side of the tumor and is clearly indicative of a morphological change with a varying intensity profile than the background.

The figure (5) presents the results of segmentation of three different approaches like K means segmentation, Watershed segmentation; Fuzzy c means segmentation. Image processing is a subjective analysis and more so in the case of medical image processing, it can be observed from the figure, K means based clustering provides a better segmentation of the image when compared to the other two approaches for this particular image. Even though watershed segmentation clearly demarcates regions, the design of this tool is such that the segmented results are used for

quantification of the area of the tumor. In such a circumstance the K means algorithm is capable of providing much better quantification when comapred to the other aprroaches.
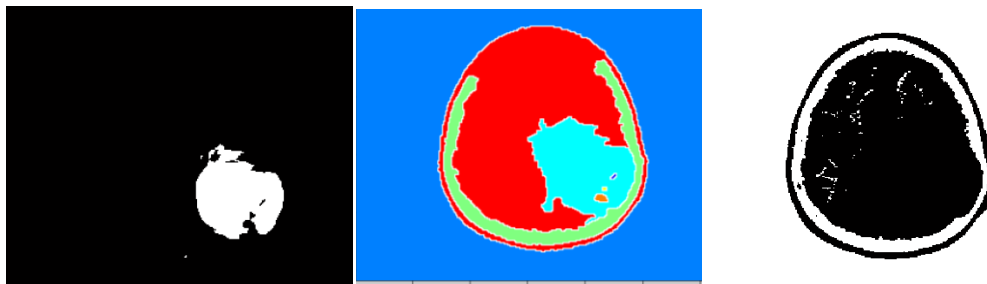
**Figure (5) : Segmentation results of K means, Watershed and FCM methods**

The quantification of the segmented tumor is done by estimating the area of all of the high value pixels of a binary image. Area of an individual pixel is determined by looking at its 2-by-2 neighborhood. The following table (1) illustrates the area as quantified by different segmentation approaches. The wide variation can be attributed to the different results of segmentation.

Table (1) : Area of the tumor quantified.

| Method	Actual	K Means	Water Shed	FCM
Area (Sq. mm)	54. 2	40. 3088	830. 76	830. 76

It can be observed from the table that k means is much suited for automated quantification than the other two approaches. K means produces a result which is much closer to the actual value in comparison with FCM and Water shed.

The segmentation is evaluated by comparing it with a ground truth obtained using manual segmentation of the tumor in the image. In view of the wide variation in the segmentation of the watershed and FCM to have a realistic comparison, the segmentation evaluation of K means is only presented here. The figure (6) presents the image segmented manually and the segmented image obtained using K means segmentation approach.
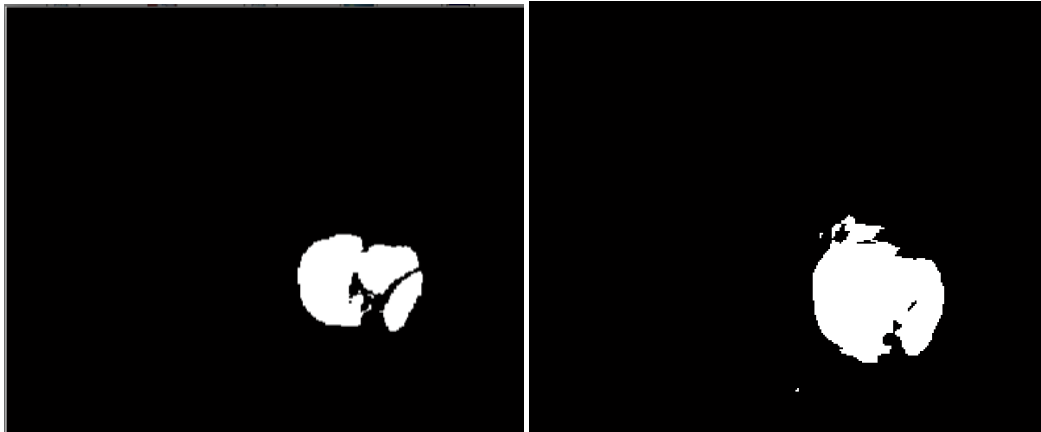
Figure (6) : Image segmented manually and through K means

In the process of segmentation evaluation, the ground truth and segmented image using k means are superimposed over one another to have a visual interpretation of segmentation results. The overlap image is presented in the figure (7) below.
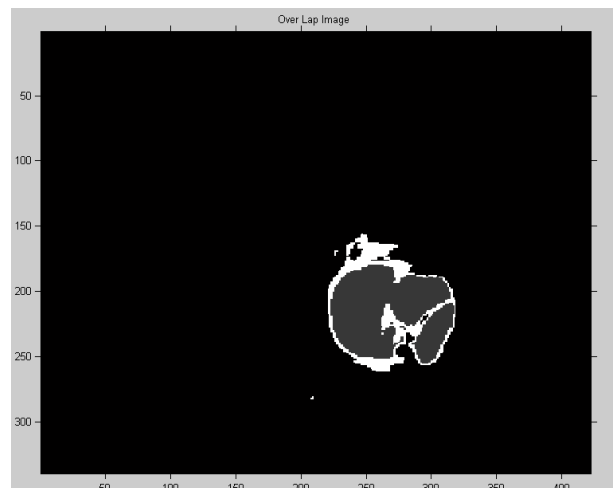
Figure (7) : Overlap image obtained by superimposing ground truth and segmented image.

The following table (2) tabulates different evaluation parameters of segmentation for the K means clustering approach

Table (2) : Quantified Segmentation Evaluation Parameters.

Method	PRI	VOI	GCE	PSNR	DCE	JD
K-means	0. 8923	0. 3620	0. 165	32. 274	8. 923e-08	0. 54145

a)   The Probabilistic Rand Index (PRI) counts the fraction of pairs of pixels whose labeling are consistent between the computed segmentation and the ground truth, averaging across multiple ground truth segmentations to account for scale variation in human perception.

b)   The Variation of Information (VoI) metric defines the distance between two segmentations as the average conditional entropy of one segmentation given the other, and thus roughly measures the amount of randomness in one segmentation which cannot be explained by the other.

c)   The Global Consistency Error (GCE) measures the extent to which one segmentation can be viewed as a refinement of the other. Segmentations which are related in this manner are considered to be consistent, since they could represent the same natural image segmented at different scales.

d)   The Peak Signal to Noise Ratio (PSNR) is used to find the deviation of segmented image from the original image. Equation (i) represents the PSNR. In this equation mean squared error (MSE) for two M * N monochrome images f and z and it is given by Equation (ii). MaxBits gives the maximum possible pixel value (255) of the image. PSNR can be considered as one of the most important parameters that can be used to quantify the quality of segmentation.

$$PSNR = 10 \log_{10} \frac{MaxBits^2}{MSE} \qquad (i)$$

$$MSE = \frac{1}{MN} \sum_{x=0}^{M-1} \sum_{y=0}^{N-1} \big(f(x, y) - z(x, y)\big)^2 \qquad (ii)$$

e)   The Dice coefficient (DCE) measures the spatial overlap between two segmentations. Conceptually that DCE is also a special case of the kappa statistic commonly used in reliability analysis

f)   Jaccard Distance (JD) which measures *dis*similarity between sample sets is complementary to the Jaccard coefficient and is obtained by subtracting the Jaccard coefficient from 1. The Jaccard index, also known as the Jaccard similarity coefficient is a statistic used for comparing the similarity and diversity of sample sets.

5. Conclusion

In this paper we have presented a CAD system that can be a useful tool in providing quality secondary opinion to the radiologist. The tool has different features that can help in having differential diagnosis. It can be observed from the discussion the subjective nature of medical imaging makes it very difficult to have a particular method prefixed for an analysis. In this case it can be clearly observed that the k means segmentation approach is suitable for this type of CAD systems which involves quantification of tumors as well. The results of segmentation evaluation also prove this fact. Even though K means segmentation provides better results for this particular scenario it cannot be safely stated that, it will be the case for other images and scenario.

This fact impresses the need to have better segmentation approaches that can be generic to a higher extend.

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