



An Automatic Approach for Brain Tumor Detection Using Fuzzy Local Information C-Means Clustering

Abhishek Govindu¹, Sandeep Kumar Mekapothula²

¹PG Scholar, Department of ECE, RISE Krishna Sai Gandhi Group of Institutions, Ongole
abhishekgovindu@gmail.com

² Assistant Professor, Department of ECE, RISE Krishna Sai Gandhi Group of Institutions, Ongole
sandeepmekapothula@gmail.com

ABSTRACT

Clustering approach is widely used in biomedical applications particularly for brain tumor detection in abnormal magnetic resonance (MRI) images. Fuzzy clustering using fuzzy local information C-means algorithm proved to be superior over the other clustering approaches in terms of segmentation efficiency. As it is known, brain tumor is inherently serious and life-threatening because of its character in the limited space of the intracranial cavity (space formed inside the skull). Most Research in developed countries show that the number of people who have brain tumors were died due to the fact of inaccurate detection. Generally, CT scan or MRI that is directed into intracranial cavity produces a complete image of brain. This image is visually examined by the physician for detection & diagnosis of brain tumor. However this method of detection resists the accurate determination of size of tumor. This method allows the segmentation of tumor tissue with accuracy and reproducibility comparable to manual segmentation. In addition, it also reduces the time for analysis. At the end of the process the tumor is extracted from the MR image and its exact position and the shape also determined. The graph based on pixel value is drawn taking the various points from the tumor cells lies in the original position from the affected region. Here the affected region is considered as ellipsoid shape and the volumes have been calculated from it. In this system the mean has been found from the volumes grown in the affected region (tumor area). The experimental results show that 97% brain tumor growth and volume can be measured by the advanced diameter Technique.

Keywords- MRI, Imaging, FLICM, Brain tumor, Segmentation, Graph based technique, Diameter Technique.

1. INTRODUCTION

Now a day's brain abnormality mainly brain tumors are one of the most common brain diseases, so detection and quantification of tumor in MRI are important in medical diagnosis. Through past many researchers have prepared important research in the field of brain abnormality segmentation but still now it is very important research fields due to the large number of variation of MRI of brain. The accurate segmentation of internal structures of the brain is of great interest for the study and very helpful for the treatment of tumors. It aims at reducing the mortality and improving the surgical or radio therapeutic management of tumors. The most important aim of medical image analysis in general

and brain MRI analysis in particular, is to extract clinical information that would improve diagnosis and treatment of disease. The aim is to provide information associated to anatomical structures as well as potential abnormal tissues necessary to treatment planning and patient follow-up. There are different brain tumor detection and segmentation methods to detect and segment a brain tumor from MRI images. The measurement of brain tumor volume can assist tumor staging for brain tumor volume measurements is developed which overcome the problem of inter-operator variance, besides partial volume effects and shows satisfactory performance for segmentation, thus segmentation is very important for volume calculation. Different segmentation techniques such as thresholding based segmentation methodology, Region Growing based segmentation, K-nearest neighbors (KNN), Bayesian approach, Markov Random Field Models, Expectation maximization (EM), Support vector machine (SVM), Fuzzy c-means algorithms, K-means algorithms, Morphology-based segmentation, Atlas-guided based segmentation, Knowledge based segmentation, Texture-based segmentation, Artificial neural networks (ANNs), Fusion-based, Fuzzy connectedness, Watershed Methods, Level set based segmentation, Hybrid Self Organizing Map (SOM), SOM, Graph Cut based segmentation, Fractal-based segmentation, Parametric deformable models (snakes), Boundary based methods, Geometric deformable model, The Combination of Watershed and Level Set segmentation, Spatio-Temporal Model, Hidden Markov Model, Genetic algorithms based segmentation, Kohon-en Self Organizing Map (SOM) with a common phase pre-processing and segmentation and its steps are shown below.

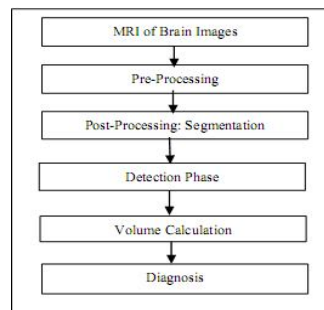


Fig: 1.1 Segmentation process

Thus accurate segmentation over full field of view is another very much problem but during the segmentation procedure verification of results is another source of difficulty. Statistical classification may not allow differentiation between non-enhancing tumor and normal tissue due to overlapping intensity

distributions of healthy tissue with tumor and surrounding edema. Manually segmenting brain tumors from MR imaging is generally time consuming and difficult. An automate segmentation method is desirable because it reduces the load on the operator and generates satisfactory results. The region growing segmentation is used to segment the brain tumors due to its wide range of applications and automatic features. After taking the image of the tumorous brain there is a need to process it. The image clearly shows the place of the tumorous portion of the brain. The image does not give the information about the numerical parameters such as area and volume of the tumorous portion of the brain. After segmentation the desired tumor area is selected from the segmented image. This selected region is used to calculate the area and volume of the tumor present in the MR image.

2. LITERATURE SURVEY

The previous methods for brain tumor segmentation are tresholding, region growing & clustering. Tresholding is the simplest method of image segmentation. From a grayscale image, tresholding can be used to create binary images. During the tresholding process, individual pixels in an image are marked as "object" pixels if their value is greater than some threshold value (assuming an object to be brighter than the background) and as "background" pixels otherwise. This convention is known as threshold above. Variants include threshold below, which is opposite of threshold above; threshold inside, where a pixel is labeled "object" if its value is between two thresholds; and threshold outside, which is the opposite of threshold inside. Typically, an object pixel is given a value of "1" while a background pixel is given a value of "0." Finally, a binary image is created by colouring each pixel white or black, depending on a pixel's labels.

The major drawback to threshold-based approaches is that they often lack the sensitivity and specificity needed for accurate classification. The first step in region growing is to select a set of seed points. Seed point selection is based on some user criterion (for example, pixels in a certain gray-level range, pixels evenly spaced on a grid, etc.). The initial region begins as the exact location of these seeds. The regions are then grown from these seed points to adjacent points depending on a region membership criterion. The criterion could be, for example, pixel intensity, gray level texture or colour. Since the regions are grown on the basis of the criterion, the image information itself is important. For example, if the criterion were a pixel intensity threshold value, knowledge of the histogram of the image would be of use, as one could use it to determine a suitable threshold value for the region membership criterion.

3. BRAIN MRI IMAGE PREPROCESSING

In order to improve the visual effects of the image for further image recognition, MRI image pre-processing is needed, mainly including colour image grayscale, image

smoothing and sharpening and so on. Image smoothing is to eliminate noise and improve image quality. The purpose of image sharpening is to make the tumor edges, contour lines and image details clearer. Same process will be applied to the real target image.

3.1 MRI ANALYSIS

Given a brain MRI image, the first step enhances the image, the second step segments the brain tumor image and in the third step post processing using morphological operations and windowing technique takes place. As a result of these steps, we get a final brain tumor detected image. The diagnosis was confirmed pathologically in each patient. All participants in this study remained Blinded as to the arms to which any patients had been assigned. Each MRI study was performed according to a standardized protocol that included pre-and post contrast T1-weighted imaging in multiple planes, as well as a high - resolution (3- or 1.5-mm slice thickness) gradient echo acquisition. Clinical data, such as Patient survivals, treatment parameters, and so on, are not described in this report because they are not relevant to the main focus of this work, the reproducibility of the measurement techniques. The following fig1 shows the MRI images.

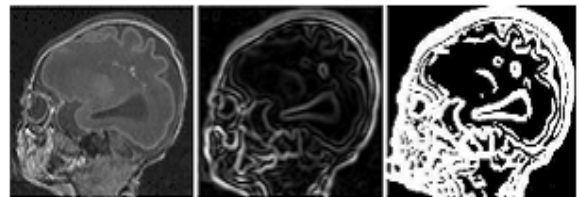


Fig: 3.1 Brain Images

3.2 Grayscale

In photography and computing, a gray-scale or grayscale digital image is an image in which the value of each pixel is a single sample, that is, it carries only intensity information. Images of this sort, also known as black-and-white, are composed exclusively of shades of gray, varying from black at the weakest intensity to white at the strongest. Grayscale images are distinct from one-bit black-and-white images, which in the context of computer imaging are images with only the two colors, black, and white also called bi-level or binary images. Grayscale images have many shades of gray in between. Grayscale images are also called monochromatic, denoting the absence of any chromatic variation. Grayscale images are often the result of measuring the intensity of light at each pixel in a single band of the electromagnetic spectrum e.g. Infrared, visible light, ultraviolet, etc, and in such cases they are monochromatic proper when only a given frequency is captured. But also they can be synthesized from a full color image. The intensity of a pixel is expressed within a given range between a minimum and a maximum, inclusive. This range is represented in an abstract way as a range from 0 means total absence, black and 1 means total presence, white with any fractional values in between. Another convention is to employ percentages, so the scale is then

from 0% to 100%. This is used for a more intuitive approach, but if only integer values are used, the range encompasses a total of only 101 intensities, which are insufficient to represent a broad gradient of grays. Also, the percentile notation is used in printing to denote how much ink is employed in half toning, but then the scale is reversed, being 0% the paper white or no ink and 100% a solid black or full ink. In computing, although the grayscale can be computed through rational numbers, image pixels are stored in binary, quantized form. Some early grayscale monitors can only show up to sixteen (4-bit) different shades, but today grayscale images as photographs intended for visual display both on screen and printed are commonly stored with 8 bits per sampled pixel, which allows 256 different intensities i.e., shades of gray to be recorded, typically on a non-linear scale. The precision provided by this format is barely sufficient to avoid visible banding artifacts, but very convenient for programming due to the fact that a single pixel then occupies a single byte. Technical uses in medical imaging or remote sensing applications often require more levels, to make full use of the sensor accuracy typically 10 or 12 bits per sample and to guard against round off errors in computations. Sixteen bits per sample (65,536 levels) is a convenient choice for such uses, as computers manage 16-bit words efficiently. The TIFF and the PNG among other image file formats supports 16-bit grayscale natively, although browsers and many imaging programs tend to ignore the low order 8 bits of each pixel. No matter what pixel depth is used, the binary representations assume that 0 is black and the maximum value 255 at 8 bpp, 65,535 at 16 bpp, etc. is white, if not otherwise noted [1].

3.3 Converting Color to Grayscale

Conversion of a color image to grayscale is not unique; different weighting of the color channels effectively represents the effect of shooting black-and-white film with different-colored photographic filters on the cameras. A common strategy is to match the luminance of the grayscale image to the luminance of the color image [1]. To convert any color to a grayscale representation of its luminance, first one must obtain the values of its red, green, and blue (RGB) primaries in linear intensity encoding, by gamma expansion. Then, add together 30% of the red value, 59% of the green value, and 11% of the blue value these weights depend on the exact choice of the RGB primaries, but are typical. Regardless of the scale employed 0.0 to 1.0, 0 to 255, 0% to 100%, etc., the resultant number is the desired linear luminance value; it typically needs to be gamma compressed to get back to conventional grayscale representation [1]. This is not the method used to obtain the luma in the Y'UV and related color models, used in standard color TV and video systems as PAL and NTSC, as well as in the L*a*b color model. These systems directly compute a gamma-compressed luma as a linear combination of gamma compressed primary intensities, rather than use linearization via gamma expansion

and compression [1]. To convert a gray intensity value to RGB, simply set all the three primary color components red, green and blue to the gray value, correcting to a different gamma if necessary.

3.4 Filtering an Image

Image filtering is useful for many applications, including smoothing, sharpening, removing noise, and edge detection. A filter is defined by a kernel, which is a small array applied to each pixel and its neighbors within an image. In most applications, the center of the kernel is aligned with the current pixel, and is a square with an odd number 3, 5, 7, etc. of elements in each dimension. The process used to apply filters to an image is known as convolution, and may be applied in either the spatial or frequency domain. Within the spatial domain, the first part of the convolution process multiplies the elements of the kernel by the matching pixel values when the kernel is centered over a pixel.

The elements of the resulting array which is the same size as the kernel are averaged, and the original pixel value is replaced with this result. The CONVOL function performs this convolution process for an entire image. Within the frequency domain, convolution can be performed by multiplying the FFT of the image by the FFT of the kernel, and then transforming back into the spatial domain. The kernel is padded with zero values to enlarge it to the same size as the image before the forward FFT is applied. These types of filters are usually specified within the frequency domain and do not need to be transformed. IDL's DIST and HANNING functions are examples of filters already transformed into the frequency domain. Since filters are the building blocks of many image processing methods, these examples merely show how to apply filters, as opposed to showing how a specific filter may be used to enhance a specific image or extract a specific shape. This basic introduction provides the information necessary to accomplish more advanced image-specific processing. Filters can be used to compute the first derivatives of an image.

3.5 Median filter

Median Filter remove the noise with high frequency components from MRI without disturbing the edges and it is used to reduce salt and pepper noise. This technique calculates the median values i.e. Set median value pixels values of the surrounding pixels to determine the new denoised value of the pixel. A median is calculated by Sorting all pixel values by their size, then selecting the median value as the new value for the pixel. The basic function for median image is written below in equation, where $f(x,y)$ output median and $g(x,y)$ is the original values.

$$\hat{f}(x,y) = \text{median}_{(i,j) \in N} \{g(i,j)\}$$

Before filtering if the intensity values are 46, 58, 47, 49, 41, 45, 42, 55, and 59. So the ascending orders of the pixel

intensity values are 41, 42, 45, 46, 47, 49, 55, 58, and 59. So the median value is 47 and this 47 replace the value 41 in the actual output of the median filter.

46	58	47
49	41	45
42	55	59

(a)

46	58	47
49	47	45
42	55	59

(b)

Fig: 3.2 Median Filtering Masks

4. FUZZY C MEANS ALGORITHM

The goal of a clustering analysis is to divide a given set of data or objects into a cluster, which represents subsets or a group. The partition should have two properties:

1. Homogeneity inside clusters the data, which belongs to one cluster, should be as similar as possible.
2. Heterogeneity between the clusters: the data, which belongs to different clusters, should be as different as possible.

The membership functions do not reflect the actual data distribution in the input and the output spaces. They may not be suitable for fuzzy pattern recognition. To build membership functions from the data available, a clustering technique may be used to partition the data, and then produce membership function from the resulting clustering. Clustering is a process to obtain a partition P of a set E of N objects X_i ($i=1, 2, \dots, N$), using the resemblance or disresemblance measure, such as a distance measure d. A partition P is a set of disjoint subsets of E and the element P_s of P is called cluster and the centers of the clusters are called centroid or prototypes. Many techniques have been developed for clustering data. In this report c-means clustering is used. It's a simple unsupervised learning method which can be used for data grouping or classification when the number of clusters is known. It consists of the following steps.

Step 1:

Choose the number of clusters - K

Step 2:

Set initial centers of clusters $c_1, c_2 \dots c_k$;

Step 3:

Classify each vector

$x [x_1, x_2, \dots, x_n]^T$ into the closest centre c_i by

Euclidean distance measure

$$\|x_i - c_i\| = \min \|x_i - c_j\|$$

Step 4:

Recomputed the estimates for the cluster centers c_i

Let $c_i = [c_{i1}, c_{i2}, \dots, c_{in}]^T$

c_{im} be computed by,

$$c_{im} = \frac{\sum x_i \in \text{Cluster}(i) x_{im}}{N_i}$$

Where, N_i is the number of vectors in the i -th cluster.

Step 5:

If none of the cluster centers ($c_i = 1, 2, \dots, k$) changes in step- 4 stop; otherwise go to step 3.

5. IMPLEMENTATION OF FLICM

The original MRI image of brain is as follows

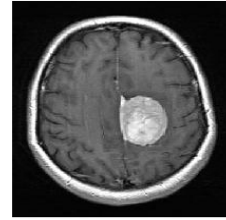


Fig: 5.1 Original MRI

Original MRI image is filtered by using median filter. The filtered image is shown below.

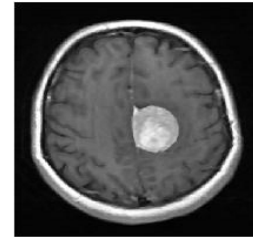


Fig: 5.2 Filtered image

The algorithm of fuzzy c-means (fuzzy c-means) is a classification algorithm based on fuzzy optimization of a quadratic criterion of classification where each class is represented by its center of gravity. The algorithm requires knowing the number of classes in advance and generates classes through an iterative process minimizing an objective function. Thus, it provides a fuzzy partition of the image by giving each pixel a degree of n belonging to a given region. Segmentation of anatomical structures is a critical task in medical image processing, with a large range of applications going from visualization to diagnosis. For example, to delineate structures in the mid sagittal plane of the brain in the context of a pre-operative planning, an accurate segmentation of the hemispheres, and especially of their internal faces, is needed. In such a task, the main difficulties are the non-homogeneous intensities within the same class of tissue, and the high complexity of anatomical structures such as white and gray matter as well as their large variability. The filtered image is converted to grey in preprocessing and FLICM is applied to it gives the segmented tumor.



Fig: 5.3 Segmented tumor

6. System Overview

In this study the tumor growth has been measured by graph based technique. Here input is the MRI image which is divided into four sections by one horizontal and vertical line shown in fig.

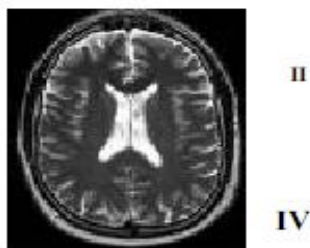


Fig: 6.1 MRI Sections-I affected area

Region growing group’s pixels or sub regions into larger regions based on predefined criteria. The basic idea is to start with a pixel or a group of pixels and examine the neighboring pixels. If a neighboring pixel meets a certain criteria, it is added to the group and if it does not meet the criteria, it is not added. This process is continued until no more neighboring pixels can be added to the group. Thus, a region is defined. In the divided four sections of the MRI have been denoted as I, II, III and IV. The MRI image divided into 4 sections that is I, II, III, and IV. If the affected region lies in section the graph has been drawn from it. This type of approach is better than other approaches because this system has been taken by only the affected region. The graph has been drawn based on the daily report from the MRI dataset as shown in below fig.

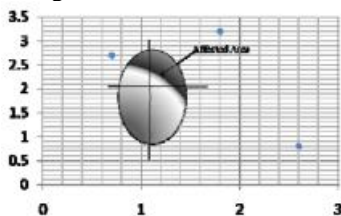


Fig: 6.2 MRI Sections-I affected area

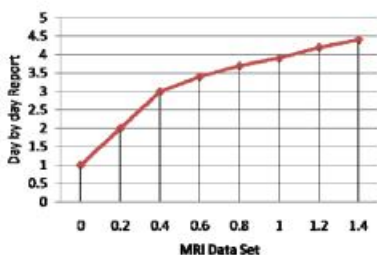


Fig: 6.3 MRI Section-I Glioma Growth

Here the First step is to mark the affected region in section-I Now takes the affected region from the MRI data and matches it with the graph as shown in fig. After matching them, from the affected regions the points have been selected and using them the graph has been drawn as shown in following fig.

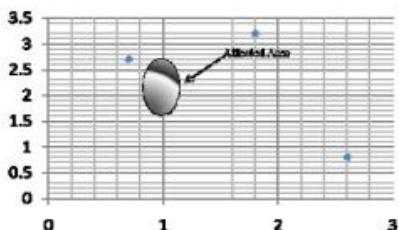


Fig: 6.4 MRI Sections-I affected area lies in graph

7. DIAMETER METHOD FOR VOLUME CALCULATION

Diameters were manually measured on MRI films with calipers (dividers). In each case where a second lesion was present, or the shape of the lesion was best characterized by two ellipsoids, a second set of three diameters was also recorded, and the volumes were summed. If one or more necrotic or cystic areas were thought to be present, additional diameters for the cystic component were recorded, and the computed cystic volume was Subtracted from the overall volume. Readers were not aware that an end point of this study was the determination of how many sets of diameters (one v two v three diameter measurements) were thought to be required to accurately characterize the lesion volume. The formula used to compute volumes was the standard volume of an ellipsoid, as follows:

$$V = 4/3 \pi (a * b * c) \quad (2)$$

An ellipsoid is a closed type of quadric surface. If all three radii are equal, the solid body is a sphere; if two radii are equal, the ellipsoid is a spheroid:

- if $a=b=c$ then shape sphere
Volume= $4/3 \pi abc$
 - if $a=b > c$ then shape Oblate spheroid (disk-shaped)
Volume = $(axbxc) \times 8/3 \sqrt{3}$
 - if $a=b < c$ then shape Prolate spheroid (like a rugby ball)
Volume = $(axbxc) \times 8/3 \sqrt{3}$
 - if $a > b > c$ then Scalene ellipsoid ("three unequal sides")
Volume= $8xaxbxc$
- Mean $V1+V2...+Vn$
Mean: Result (volume)

Where $a, b,$ and c are the three radii (half the diameters). In addition to the total volume, the individual diameters were also recorded to allow analysis on a single- or dual-diameter basis, ie, diameter or area rather than a volume estimate.

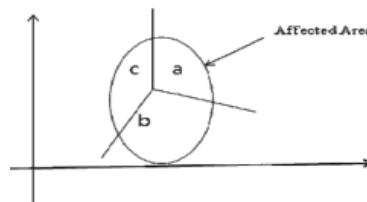


Fig: 6.5 Ellipsoid method

This result will produce out the volume of brain tumor. Again this same diameter method has been used and has found out the volume -2 up to N times. N is a number of steps to determine the volume by different parameters as shown in fig. The mean has been measured from these volumes using formula-3 which is equal to average of volumes calculated using different parameters. From this mean the volume of glioma has been determined from day by day MRI report. The graph shows the brain tumor growth affected in brain cells.

$$\text{Mean} = V_1 + V_2 \dots + V_n \quad (3)$$

Where v_1, v_2 are the volumes it has been calculated from dataset-1 and dataset-2

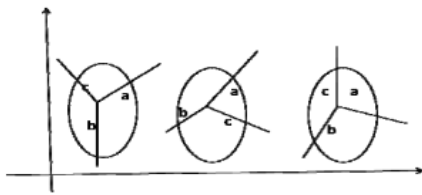


Fig: 6.6 Volume measurements

8. RESULTS

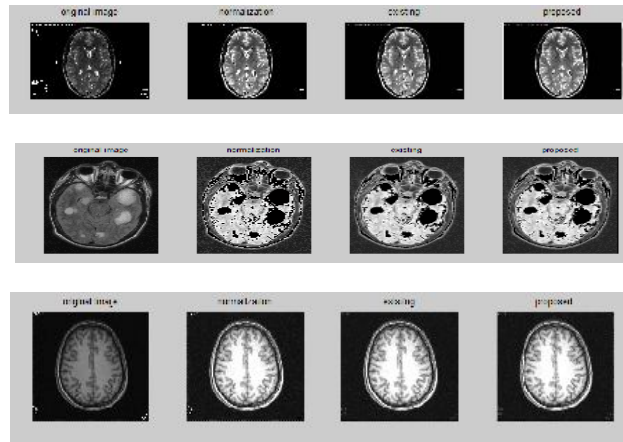


Fig: 8.1 Experimental Results on different brain images

8.1 Graph for output images:

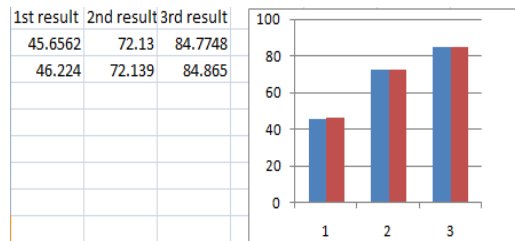


Fig: 8.1 Graph corresponding to Experimental Results

9. CONCLUSION

Imaging plays a central role in the diagnosis and treatment planning of brain tumor. In this project, a novel robust fuzzy local information c-means algorithm for image clustering was introduced. Also, the algorithm is relatively independent of the type of the added noise, and as a consequence, in the absence of prior knowledge of the noise. Tumor volume is an important diagnostic indicator in treatment planning and results assessment for brain tumor. The measurement of brain tumor volume can assist tumor staging for brain tumor volume measurements is developed which overcome the problem of inter-operator variance, besides partial volume effects and shows satisfactory performance for segmentation. This method is applied to 8-tumor contained

MRI slices from 2 brain tumor patients data sets of different tumor type and shape, and better segmentation results are achieved. In this study a new approach has been discussed to detect the volume of brain tumor using diameter and graph based method to find the volume. Here the affected region is considered as ellipse shape and the volumes have been calculated from it. In this system the mean has been found from the volumes grown in the affected region. The experimental results show that 97% brain tumor growth and volume can be measured by graph and diameter method.

REFERENCES

[1] S Roy, S Nag, I K Maitra, S K. Bandyopadhyay, "A Review on Automated Brain Tumor Detection and Segmentation from MRI of Brain," IJARCSSE, Vol 3, Issue 6, June 2013, pp. 1706-1746.

[2] Mohamed Lamine Toure "Advanced Algorithm for Brain Segmentation using Fuzzy to Localize Cancer and Epilepsy Region", International Conference on Electronics and Information Engineering (ICEIE 2010), Vol. no 2.

[3] S.Karapagam and S.Gowri, "Detection of Glioma(Tumor) Growth by Advanced Diameter Technique using MRI data," Medical Proceedings of the World congress on Engineering 2011 Vol I WCE 2011, July 6 - 8, 2011, London, U.K.

[4] S.Karpagam and S. Gowri "Detection of Glioma (Tumor) Growth by Advanced Diameter Technique Using MRI Data"

AUTHORS



Abhishek Govindu received his B.Tech, Degree in Electrical and Electronics Engineering and currently pursuing M.Tech at Rise Krishna Sai Gandhi Group of Institutions, Ongole, Andhra Pradesh, INDIA. His main research interest includes Enhancement, Pattern Recognition and

Image Processing.



Sandeep Kumar Mekapothula is working as Assistant Professor in the department of ECE at Rise Krishna Sai Gandhi Group of Institutions, Ongole, Andhra Pradesh, INDIA. He has received B.Tech, Degree in Electronics and Communication Engineering. His main research

interest includes Segmentation, Image Enhancement, Pattern Recognition and Image Processing.