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MR Brain Image Segmentation Based on Self-Organizing Map and Neural Network

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Abstract: Image segmentation is an important process to extract information from complex medical images. Segmentation has wide application in medical field. The main objective of image segmentation is to partition an image into mutually exclusive and exhausted regions such that each region of interest is spatially contiguous and the pixels within the region are homogeneous with respect to a predefined criterion. The main objective of our project is to develop various segmentation algorithms such as Self organizing map and Neural Network to detect the various tissues like white matter, gray matter and cerebral spinal fluid for a given magnetic resonance image data set and also provide satisfactory results compared to other algorithm in terms of misclassification rate, specificity, sensitivity and correlation.
Keywords: Self-organizing map, Neural Network

I. INTRODUCTION

The brain is the anterior most part of the central nervous system.. Along with the spinal cord, it forms the Central Nervous System (CNS). The Cranium, a bony box in the skull protects it. The structure and function of the brain can be studied noninvasively by doctors and researchers using Magnetic Resonance Imaging (MRI).Magnetic Resonance Imaging (MRI), strongly depends on computer technology to generate or display digital images. Segmentation is an important process in most medical image analysis. It is very difficult to conduct surgery without using image processing techniques. Performance Analysis of Clustering Algorithms in Brain Tumor Detection of MR Images 322Complex medical processes cannot be done without image processing techniques. Structures like tumor, brain tissue and skull cannot be identified without image segmentation. Image Segmentation is needed to extract complex information from images. It takes along time for diagnosis without using image processing techniques. Clustering to Magnetic Resonance (MR) brain tumors maintains efficiency. Clustering is suitable for biomedical image segmentation as the number of clusters is usually known for images of particular regions of the human anatomy. This system uses color-based segmentation method. This system analyses various clustering techniques to track tumor objects in Magnetic Resonance (MR) brain images. The Clustering algorithms used are K-means, SOM, Hierarchical Clustering and Fuzzy C-Means Clustering. A given gray-level MR image is converted into a color space image and clustering algorithms are applied. The position of tumor objects is separated from other items of an MR image by using clustering algorithms and histogram-clustering. In this system we combine, various clustering algorithms one by one and apply Histogram Clustering. After the clustering process, the cluster containing the tumor is selected as the primary segment. To eliminate the pixels which are not related to the tumor pixels, Histogram clustering is applied.The performance analysis is conducted by taking a MRI Brain Tumor image as the input and applying all the four clustering algorithms to the image. The performance of the above four clustering algorithms are found based on the execution time and the number of tumor pixels. A tumor or tumor is the name for a neoplasm or a solid lesion formed by an abnormal growth of cells (termed neoplastic) which looks like a swelling.Tumor is not synonymous with cancer. A tumor can be benign, pre-malignant or malignant, whereas cancer is by definition malignant.types of tumors are benign tumor is a tumor that lacks all three of the malignant properties of a cancer. Thus, by definition, a benign tumor does not grow in an unlimited, aggressive manner, does not invade surrounding tissues, and does not spread to non-adjacent tissues (metastasize). Common examples of benign tumors include moles and uterine fibroids.2) malignant (from the Latin roots mal- = "bad" and -ignis = "fire") is the tendency of a medical condition, especially tumors, to become progressively worse and to potentially result in death. It is characterized by the properties of anaplasia, invasiveness, and metastasis. Malignant is a corresponding adjectival medical term used to describe a severe and progressively worsening disease. The term is most familiar as a description of cancer. Premalignant is a precancerous condition (or premalignant condition) is a disease, syndrome, or finding that, if left untreated, may lead to cancer. It is a generalized state associated with a significantly increased risk of cancer.Magnetic resonance imaging (MRI), or nuclear magnetic resonance imaging (NMRI), is primarily a medical imaging technique used in radiology to visualize detailed internal structure and limited function of the body. MRI provides much greater contrast between the different soft tissues of the body than computed tomography (CT) does,

International Journal for Research in Applied Science & Engineering Technology (IJRASET)

making it especially useful in neurological (brain), musculoskeletal, cardiovascular, and oncological (cancer) imaging. Unlike CT, MRI uses no ionizing radiation. Rather, it uses a powerful magnetic field to align the nuclear magnetization of (usually) hydrogen atoms in water in the body. Radio frequency (RF) fields are used to systematically alter the alignment of this magnetization. This causes the hydrogen nuclei to produce a rotating magnetic field detectable by the scanner. This signal can be manipulated by additional magnetic fields to build up enough information to construct an image of the body.

II.   EXISTING SYSTEM

In the Existing System, the task was to produce a binary segmentation of the (heterogeous) tumor and edema region, with ground truth defined by an expert radiologist. Our data set consisted of 10 patients with brain tumors covering4 different types of tumors. With Edema and MRI combined with the fact that we performed inter-patient testing on makes this a very difficult scenario, where this existing methods proposed to perform this task will perform poorly.To quantify the quality of the segmentations, we used the similarity measure between the ground truth and the segmentation results interms of true positives (tp), false positives (fp), and false negative (fn) pixels of the image but results poor in quality.

III.   PROPOSED SYSTEM

In this proposed system brain tumors have been segmented with the help of four methods. The execution time for K-means Clustering and SOM were less compared to the other clustering methods. With calculating the number of tumor pixels, K-means clustering and Hierarchical clustering gave a better result than the other methods. The four clustering algorithms were tested with a database of 100 MRI brain images.K-means and Hierarchical clustering achieved about 95% result. SOM and FCM achieved a result of about 80%. In this system, the axial view of the human brain is taken for tumor detection. The system can be extended to detect tumors on other views of the brain. This system considers the color and luminosity parameters for tumor detection. The texture can be taken as an additional parameter for tumor detection.

A.   Related Work

Two ideas struck me as plausible ways to find k, given nothing but a sample, although both of them relied on using standard deviation. The first algorithm sorts the examples in the combined sample and simply iterates over each of them, adding examples to a new working sample if they are within three standard deviations of the current mean, since about 99 percent of the points in a given normal distribution should be within that range.   When an example falls outside that range, another working sample is created, and the process continues. When all the examples have been iterated over, the function returns the number of working samples it used. Further, it assumes a minimum of 50 examples in each sample (to calculate the initial mean and standard deviation), and this parameter can be varied depending on knowledge of the data. The Java source code for this function (or the entire experiment) is available upon request.The second algorithm takes the standard deviation of a sample, and recursively calls itself using smaller ones as the standard deviation decreases. Since it is easier to understand a recursive function by viewing it as opposed to reading a description from the source code .At first glance it looks like the function expects an initial standard deviation, but in fact, it is used such that on the first run, that parameter is initialized to -1. Therefore, it will calculate the initial standard deviation based on the entire sample. Within it there is a variable, tolerance, which is used to indicate how close the smaller samples standard deviation should be to the last standard deviation to continue splitting the sample. This value is chosen arbitrarily, and it is likely the experiment results could have been better had I attempted to let the program "learn" a good value to use.

B.   Algorithm For Detecting Brain Tumor

Input: MRI of brain image.

Output: Tumor portion of the image.

Step1:- Read the input color or grayscale image.

Step2:- Converts input colour image in to grayscale image which is done by forming a weighted sum of each three (RGB) component, eliminating the saturation and hue information while retaining the luminance and the image returns a grayscale colour map.

Step3:- Resize this image in to 200 × 200 image matrix.

Step4:- Filters the multidimensional array with the multidimensional filter. Each element of the output an integer or in array, then

International Journal for Research in Applied Science & Engineering Technology (IJRASET)

output elements that exceed the certain range of the integer type is shortened, and fractional values are rounded.

Step5:- Add step2, step4 image and a integer value 45 and pass it in to a median filter to get the resultant enhanced image.

Step6:- Computes a global threshold that can be used to convert an intensity image (Step5) to a binary image with a normalized intensity value which lies in between range 0 and 1.

Step7:- Compute watershed segmentation by matlab command watershed (step6 image).

Step8:-Compute the morphological operation by two matlab command imerode and imdilate and strel with arbitrary shape.

Step9:- Store the size of the step 8 image into var1 and var2 i.e no. Of rows and column in pixels by [var1 var2]=size(step8 image)

Step10:- For i=1:1:var1

Step11:- For j=1:1:var2 do Step12:- If step8 image (i,j) == 1do

Step13:- step2 image (i,j) = 255 Step14:- Else do

Step15:- step2 image (i,j) = step2 image (i,j) * 0.3 Step16:- End If

Step17:- End For

Step18:- End For

Step19:- Convert in to binary image and traces the exterior boundaries of objects, as well as boundaries of holes inside these objects, in the binary image and into an RGB color image for the purpose of visualizing labeled regions.

Step20:- Show only tumor portion of the image by remove the small object area. **Step21**:- Compute edge detection using sobel edge detection technique.

C. Algorithm For Area Calculation

Input: Tumor portion of the image. **Output:** Area of the tumor.

Step1:- Read the input color or grayscale image.

Step2:- Converts input colour image in to grayscale image which is done by forming a weighted sum of each three (RGB) component, eliminating the saturation and hue information while retaining the luminance and the image returns a grayscale colour map and store it into variable I. **Step3**:- Compute numbers of rows and column in pixels by [r2 c2] = size (I) Step4:- Initialize a variable a=0

Step4:- For i=1:1:r2

do Step4:- For j=1:1:c2

Do Step4:- If I (i,j)==255

Do Step4:- a=a+0 Step4:- Else do

Step4:- a=a+1 Step4:- EndIF

Step4:- EndFor

Step4:- End For

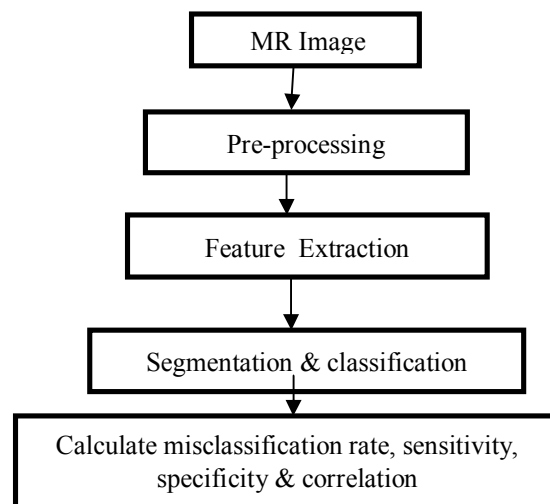Step4:- Display the area

D. Flow Diagram

Fig 1: Flow diagram of the segmentation

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E.   Methodology

The main objective was to identify the principal stressors affecting biotic integrity in each of the three states evaluated in the present report. Grouping the sites with similar types of stressors and compare these with the biotic integrity in each homogeneous group was important in order to identify those that showed a major influence. The stressor and biological indices data were available in different databases that are explained later in the present report. SOM were the tool used to identify the clusters or homogenous groups of stressors and they are explained in detail in the present report. Basically, SOM are a tool to organize highly dimensional data in homogeneous groups or clusters in which the data belonging to these groups are as similar as possible. The SOM were used in two different ways:

1) *SOM followed by multiple range tests within clusters: The* SOM were run using all the chemical and physical environmental variables and habitat metrics. A number of optimum clusters was then found. Subsequently, the distributions among clusters of the available indices of biotic integrity (fish for Minnesota and Ohio and benthic for Maryland) were plotted and a multiple range test among clusters was performed to determine if the differences within the clusters were statistically significant. A 95% confidence interval was used. The different statistically significant homogeneous group's distribution was obtained. The same process was then repeated for each one of the variables used in the clustering process and the distribution of the homogeneous groups was then compared to the distribution of the biotic indices. Those metrics that showed equal or similar distributions were considered to be the most important for biotic integrity.

2) *SOM neuron-analysis:* In this case we considered the neurons as the minimal, most homogeneous group of environmental values. In a SOM, one neuron groups a few sites with very similar characteristics. The values of each environmental variable and the biotic index in each neuron were averaged. The neuron-based environmental variables were then regressed against the neuron-based biotic index. Those variables with highest correlation were considered the most important for biotic integrity. Subsequently, we analyzed the relationships among different environmental variables, especially the relationships between off-stream and in-stream habitat parameters as well as the relationships between physical variables and chemical quality values. This was done by a simple neuron-based regression among the different variables.

F.   Methods

1) *Pre-processing:* According to the need of the next level the pre-processing step convert the image. It performs filtering of noise and other artifacts in the image and sharpening the edges in the image. RGB to grey conversion and Reshaping also takes place here. It includes median filter for noise removal.

2) *Segmentation:* Segmentation is carried out by advanced K-means and Fuzzy C-means algorithms.

3) *Feature extraction and approximate reasoning:* The feature extraction is extracting the cluster which shows the predicted tumor at the FCM (Fuzzy C-means) output. The extracted cluster is given to the threshold process. It applies binary mask over the entire image. In the approximate reasoning step the tumor area is calculated using the binarization method.

G.   Modeling Techniques

1) *K-Means clustering:* The corresponding cluster centroid. Thus the purpose of k-means clustering is to cluster the data. A cluster is a collection of objects which are similar between them and are dissimilar to the objects belonging to other clusters. Clustering is an unsupervised learning method which deals with finding a structure in a collection of unlabelled data. A loose definition of clustering could be the process of organizing objects into groups whose members are similar in some way. K-means clustering is an algorithm to group objects based on attributes/features into k number of groups where k is a positive integer. The grouping (clustering) is done by minimizing the Euclidean distance between data set.

H.   K-Means Algorithm

The purpose of k-means algorithm is to cluster the data. K-means algorithm is one of the simplest partitions clustering method's-Means is the one of the unsupervised learning algorithm for clusters. Clustering the image is grouping the pixels according to the some characteristics. In the k-means algorithm initially we have to define the number of clusters k. Then k cluster centre are chosen randomly. The distance between the each pixel to each cluster centers are calculated. The distance may be of simple Euclidean function. Single pixel is compared to all cluster centers using the distance formula. The pixel is moved to particular cluster which has shortest distance among all. Then the centroid is re estimated. Again each pixel is compared to all centroids. The process continuous until the center converges.For a given cluster assignment *C* of the data points, compute the cluster means for a current set of cluster.

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Algorithm:
1) Give the no of cluster value as k.
2) Randomly choose the k cluster centers
3) Calculate mean or center of the cluster
4) Calculate the distance between each pixel to eachcluster center
5) If the distance is near to the center then move tothat cluster.
6) Otherwise move to next cluster.
7) Re-estimate the center.

I. *Fuzzy C Means Algorithm*

Clustering is an unsupervised classification of objects (data instances) into different groups. In particular we are talking about the partitioning of a dataset into subsets (clusters), so that the data in each subset (ideally) share some common property. This property is usually defined as proximity according to some predefined distance measure. The goal is to divide the dataset in such a way that objects belonging to the same cluster are as similar as possible, whereas objects belonging to different clusters are as dissimilar as possible. The computational task of classifying the data set into k clusters is often referred to as k-clustering. Although estimating the actual number of clusters (k) is an important issue we leave it untouched in this work. Fuzzy clustering in contrast to the usual (crisp) methods does not provide hard clusters, but returns a degree of membership of each object to all the clusters. The interpretation of these degrees is then left to the user that can apply some kind of a thresholding to generate hard clusters or use these soft degrees directly. All the algorithms that we consider here are partitional, deterministic and non-incremental (based on the taxonomy defined in . The property that we want to change using fuzzy methods instead of crisp clustering is exclusiveness, as there are cases in which algorithms constructing overlapping partitions of set of documents perform better than the exclusive algorithms.We devote the majority of space to the hard c-means, fuzzy c-means and possibilities c-means. For the other methods we provide just a short description, as we did not find them appropriate for our needs.All algorithms described here are based on objective functions, which are mathematical criteria that quantify the quality of cluster models.

IV.   SIMULATION RESULTS

We have mapped the resultant tumor image onto the original grayscale image for presentation purposes.
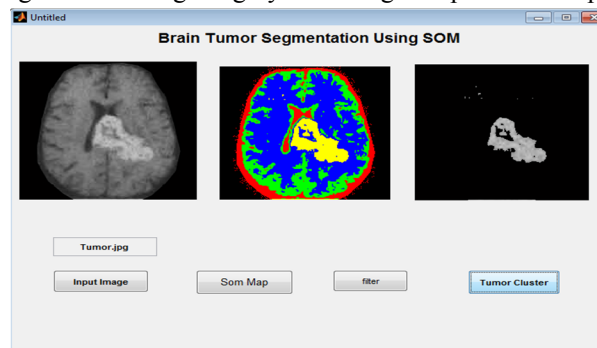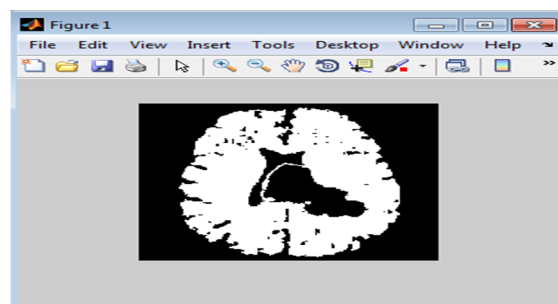

Fig 2: Output Image for Tumor Cluster

Fig 3: Area calculation output

528

International Journal for Research in Applied Science & Engineering Technology (IJRASET)
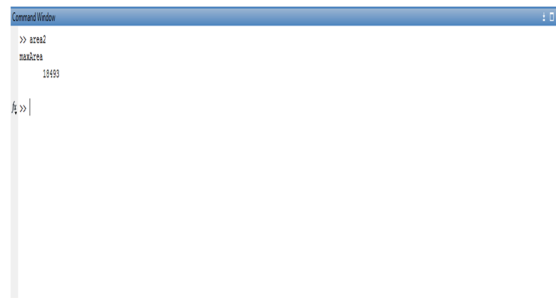

Fig 4: area calculation output in command window

V.   CONCLUSION

We have discussed the performance of the MRI image in terms of weight vector, execution time and tumor pixels detected. We have described several methods in medical image processing and discussed requirements and properties of techniques in brain tumor detection .our project is used to give more information about brain tumor detection and segmentation. The target area is segmented and the evaluation of this tool from the doctor, whom the project is cooperated with, is positive and this tool helps the doctors in diagnosis, the treatment plan making and state of the tumor monitoring. In future, the system should be improved by adapting more segmentation algorithm to suit the different medical image segmentation. Using color based image segmentation; it is possible to reduce the computational cost avoiding feature calculation for every pixel in the image. We have proposed a system for MR image of brain tumor, based on Self-organizing map and fuzzy C-mean Algorithm. Artificial vision aims to replace the human vision in various areas. Image analysis and interpretation represent an essential phase in the chain of the vision process by computer the design of the system depends on the Self-organizing map and fuzzy C mean algorithm to detect brain tumor, the efficiency have been proved by the results obtained from our project.

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