Brain Tumor Segmentation Using Kernel Support Vector Machine

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Abstract- Segmentation of brain tumors from magnetic resonance imaging (MRI) data sets is of great importance for improved diagnosis, growth rate prediction and treatment planning. In this paper, we introduce a new methodology that combines K means clustering and Principal Component Analysis for automated segmentation of the gliomas from multimodal volumetric MR images. We propose a fully automatic segmentation method based on K means clustering algorithm. We use Linear transformation and Discrete Wavelet Transformation method to remove the noise such as salt and pepper noise and the Gaussian noise. Principal Component analysis is used to calculate the accuracies present in the tumor and K means clustering algorithm is used to segment the tumor from the MRI image. Kernel Support Vector Machine is used to classify the tumor either as Benign or Malignant tumor based on the training sets that has been provided to the system.

I. INTRODUCTION

Gliomas are the brain tumors with the highest mortality rate and prevalence. Glioma is a brain tumor class triggered in glial cells of the brain, which are supporting cells of Central Nervous System. These tumors can be graded into Low Grade Gliomas and High Grade Gliomas with the low grade gliomas being less aggressive and removable whereas the high grade gliomas are more aggressive and leads to short life expectancy. Even under treatment patients do not survive more than 12 months after diagnosis. According to the World Health Organization (WHO) glioma is classified into 4 grades (I to IV). The term high grade glioma is used to describe grades III and Iv. The low grade glioma is used to describe grades I and II.

Firstly for diagnosis and monitoring the tumors progression, then for treatment planning and afterwards for assessing the effect of treatment various neuro imaging techniques are employed.

Over the past years, automatic segmentation of brain tumor tissues, despite not being used in clinical routines yet, has proven to be a viable and robust method to overcome the large costs of human resources and the intra and inter-rater variabilities associated with manual segmentation. The need to develop a fast and accurate image segmentation method for brain tumors is of high interest for diagnosis, radiotherapy and surgery planning. MRI plays a prominent role in providing the needed information to determine brain tumor tissues.

This however requires accurate delineation of the tumor, which proves challenging due to its complex structure and appearance, the 3D nature of the MRI images and the multiple MR sequences that need to be consulted in parallel for informed judgement. These factors make manual delineation time-consuming and subject to inter and intra rater variability.

Automatic segmentation systems aim at providing an objective and scalable solution. Representative early works are the atlas-based outlier detection and the joint segmentation registration framework, often guided by a tumor growth model. The past few years saw rapid developments of machine learning methods, with kernel based being more successful. Therefore, tumor inhomogeneity, overlapping signal intensity with surrounding tissues and uneven tumor growth make the segmentation a difficult task. Additionally magnetic resonance images are influenced by poor radio frequency (RF), inhomogeneous static field and others. Methods for intensity normalization and bias field correction are widely known, and areas still in research, but information is still lost in the process. The multiple configuration choices for a system influence not only performance but also its behavior. For instance, different, models may perform better with different types of pre-processing. Consequently, when investigating their behavior on a given task, findings can be biased. Finally, a configuration highly optimized on a given database may be an over-fit, and not generalize to other data or task.

II. RELATED WORK

Several methods for tumor segmentation tend to combine the maximum amount of information, from different sources, to obtain amore accurate classification of the brain tumor. The majority of these methods are still based on generative models which detect growth or the atrophy of some regions, for instance trough atlas registration. This class of

models is based on prior information of the different tissue types.

In the case of atlas registration, the main work is to model the anatomy of the patient in order to detect tumor boundaries through joint probability distribution of target variables and the observed intensities. The location of the tumor is computed since the abnormal tissues cause a considerable deviation from the expected tissue and its distribution. Most of the generative models require a registration stage to guaranty spatial alignment between images. Statistical methods, such as these are more vulnerable to noise, inter subject ratter differences and dependent on their initialization. Allied to these restraints, image information from different modalities is more difficult to be captured by a single statistical model and the registration is challenging to perform. To avoid initialization errors, some methods of use human interaction to place markers so that the spatial prior contains tumor specific appearance, or include tumor growth models embedded in the model. However, various approaches obtained promising results and good generalization.

On the contrary, discriminative approaches define a learning technique model to infer voxel labels conditioned on intensity distribution. This kind of models require a set of features, frequently intensity based, in order to segment brain tumor tissues. In this type of approaches, image data pre-processing is mandatory, since the intensity plays an important role. Discriminative models employ classifiers to assign a class to each of the testing voxels, the advantages of these methods is the capability to handle high dimensional features diminishing the initial impact of intensity information. Nevertheless, segmentation algorithms consider the voxels independent and identically distributed, which may result in isolated misclassified voxels or small clusters. Therefore, the sampling and training stages are key factors that strongly impact the classifier performance.

In brain tumor segmentation, there are several methods that develop two types of probabilistic model either as parametric probabilistic model or non-parametric probabilistic model for the underlying data.

These models include the functions related to their associations and also to their corresponding observations. Incase of abnormalities the tumor can be segmented as thin layers of tissues with respect to their shape and their connectivity. In case of brain tumors, during the segmentation time the atlas must be estimated in accordance with the shape and location of neoplasms. Growth models of the tumor can be used to estimate the effect of the growth of the tumor. The voxels obtained by using the calculation is used to provide useful information for obtaining smoother segmentations. There are different class of methods learns a distribution directly from the data. The training stage can be a disadvantage of these methods which can be a brain tumor patterns which do not follow a specific model. This considers voxels as an individual element and which the information is introduced through features. Some of the isolated clusters or small voxels may be mistakenly classified with the wrong class, sometimes in physiological and anatomically unlike locations. To overcome this problem, they include the information of the probabilistic prediction information of the classifier into a Conditional Random Field.

A variety of features such as, encoding text, first-order and fractals-based texture, gradients, brain symmetry and physical properties.

Another method that has been used in recent times was the usage of Deep Learning which is used to provide automatic learning with a hierarchy of increasing complex features directly from data. The major aim of deep learning is to introduce the architectures instead of developing the handcrafted features. Convolutional Neural Network operates over the patches using the kernels. It uses shallow CNN with two convolutional layers which are separated by max-pooling technique followed by two layers such as fully connected layer and soft max layer. Some of the proposals evaluated the three-dimensional filters where the majority of the proposals used the two-dimensional filters.

In accordance with the cancer treatment and cancer research it is important to include the subregions by using segmentation of healthy and pathological brain tissues from the Magnetic Resonance Images (MRI). Nowadays, in clinical practice, in order to delineate the tumor and its subregions from MRI images of the head has used four different MRI modalities. The hierarchical approach adds robustness and speed by allowing to apply different levels of regularization at different stages.

The proposed approach is able to integrate the Principal Component Analysis and the Kernel Support Vector Machine which is abbreviated as KSVM is used to obtain the type of tumor form the MRI image that is loaded into the support vector machine. The MRI image is loaded into the system by using the Graphical User Interface (GUI) and the loaded image is led into the preprocessing system where the noise such Gaussian noise and the Salt and Pepper noise is removed using the Discrete Wavelet Transformation method. The noise removed MRI image is normalized by using the Linear Transformation technique. The Normalized image is sent to the Segmentation phase in which the tumor is

segmented separately by using Principal Component Analysis method where the K-Means algorithm is used in which the dissimilar objects are grouped separately from the similar objects. The grouped dissimilar objects are identified as tumor and the segmented groups are sent to the Feature extraction and Feature reduction phase where the threshold values are provided in which the value is used to identify the type of the tumor either it is Benign or Malignant type.

III. METHODS

The flowchart of the proposed method is shown in Fig.1. In this proposed system, the brain tumor segmentation is started with the removal of noise such as Gaussian noise and Salt and Pepper noise which is removed using Discrete Wavelet Transform method in which the noises are removed and the MRI image is normalized using the Linear Transformation method.
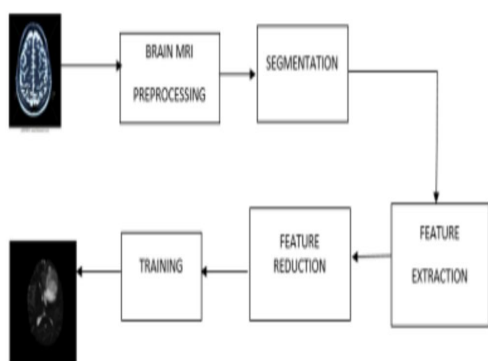

Fig. 1 Flowchart of the proposed system

Preprocessing

Digital data will not be changed even when it is reproduced number of times such that it replaces the originality of the data. There are various techniques such as Neural Network based image processing, statistical approach for texture analysis, segmentation in color and B/W images, expert system based Image Processing, application of object oriented programming techniques in Image Processing environments, shape in machine vision, multispectral classification techniques, auto focusing techniques for MRI images, threshold techniques for finding contours of objects, sequential segmentation technique to find out thin vessels in medical imaging and hair line cracks in NDT, fractal method for texture classification, data compression techniques using fractals and Discrete Cosine Transformers, image restoration methods using Point Spread functions and Wiener filter.

Strong, uniform and steady magnetic fields are provided to the MRI systems using superconducting magnets. These super conducting magnets produce very high magnetic field and its cooled to liquid helium temperature the signal to noise ratio of the received signals and image quality are better than using conventional magnets in MRI image processing systems.

MRI images are altered by bias field distortion. This makes the intensity of the same tissues to vary across the image. However, this is not enough to ensure the intensity distribution of a tissue type is in a similar intensity scale across different subjects for the same MRI sequence., which is an explicit or implicit assumption in most segmentation methods.

The intensity is normalized using the linear transformation method. This linear transformation is used to normalize the intensity across the whole side of the image.

The MRI images are mostly affected by two types of noise such as salt and pepper noise and another type of noise known as Gaussian noise. The salt and pepper noise is the black and white dots that occur in the MRI image during the transformation.

In order to make the contrast and intensity ranges more similar across patients and acquisitions, we apply the intensity normalization methods which is a linear transformation method.

The MRI image is converted into the gray scale image at first during the preprocessing stage using the formula in MAT lab software such as
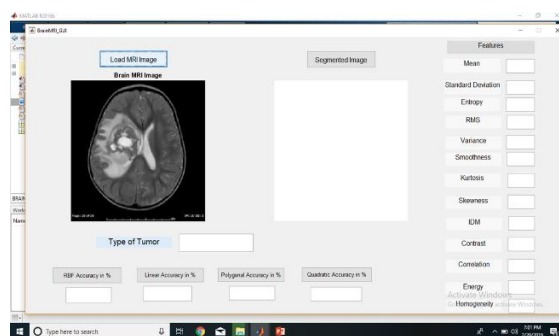
I=handles.ImgData;
Gray = rgb2gray(I)

Fig. 2 MRI image is loaded

Intensity images are also called as gray scale images. 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.

The figure 1 shows architecture of the proposed work, the MRI image which is given as input is lead to the preprocessing step in which the noise such as salt and pepper noise and gaussian noises are removed and the intensity is normalized. The normalized image is sent to the segmentation phase where the tumor image is segmented. The next step such as feature reduction and extraction is used to calculate the accuracies of the tumor identified.

Noise presented in the image can reduce the capacity of region growing filter to grow large regions or may result as a fault edge. When faced with noisy images, it is usually convenient to pre-process the image by using weighted median filter. Weighted Median (WM) filter have the robustness and edge preserving capability of the classical median filter. WM filters belong to the broad class of nonlinear filters called stack filters. This enables the use of the tools developed for the latter class in characterizing and analyzing the behavior and properties of WM filters, e.g. noise attenuation capability. The fact that WM filters are threshold functions allows the use of neural network training methods to obtain adaptive WM filters (Schiff and Roberts, 1990). A weighted median filter is implemented as follows:

W(x, y) =median {w1 x x1…wn x wn}

x1…..xn are the intensity values inside a window cantered at (x,y) and w x n denotes replication of x, w times. There are several types of noise that influences images like salt and pepper noise, Gaussian noise, shot noise, quantization noise, anisotropic noise etc,. But the noise that influence the MRI images is salt and pepper noise.
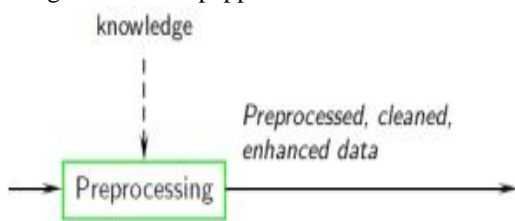

Fig. 3 preprocessing of image

K-means clustering for segmentation

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. In this method segmentation is carried out using k- means clustering algorithm for better performance. This enhances the tumor boundaries more and is very fast when compared to many other clustering algorithms. In this algorithm the similar objects are neglected and dissimilar objects are collected. Those collected objects are stored in separate array for future classification.
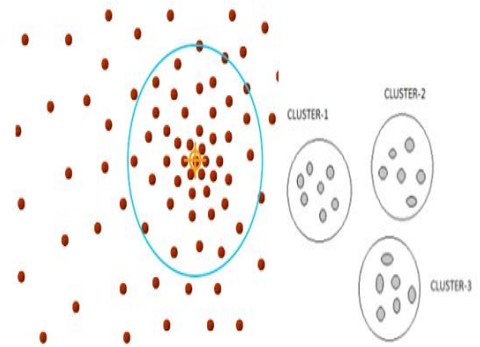

Fig. 4 clustering of dissimilar objects

The noise removed image and the intensity normalized image is provided into the segmentation phase in which the gray scale image which now normalized with intensity and the removal of noise from the image is now given as an input to the segmentation phase.

In this phase the image is divided into 3X3 matrix and the matrices are indicated with the values of 0 and 1.

K-means is one of the simplest unsupervised learning algorithm that is used to solve all kinds of clustering problem. The dataset is provided as a matrix format with certain number of clusters with a fixed apriori.. This methods first finds the K center from each clusters which is represented with a matrix format. These centers must be placed in a way such that change in the location must not produce a difference in the value.

These K center points are taken and it is associated to the nearest center. The recalculation of new centroids also takes place simultaneously. This usage of K-means clustering is fast and robust and is easier to understand. It is relatively efficient where n objects and k clusters and d dimension of each object and t iterations gives the best result when the data are distinct and are well separated from each other.

Algorithmic steps for K-means clustering

Let X={x1,x2,x3,….,xn} be the set of data points obtained from the matrices and V={v1,v2,…….vc} be the set of centers.

1. Randomly select the cluster centers obtained from the matrix after performing certain calculations.
2. Calculate the distance between each data points and the cluster centers obtained from the calculation.
3. Assign the data point to the cluster center whose distance from the cluster center is minimum of all the cluster centers.
4. Recalculate the new cluster center using the formula, v=(1/c)
5. Recalculate the distance between each data point and new obtained cluster centers.
6. If no data point is reassigned then separate the dissimilar data points from the similar data points.
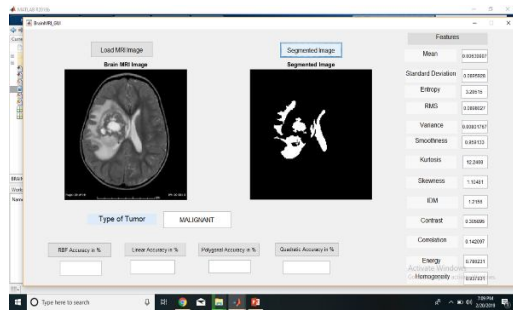

Fig. 5 segmented image

Principal Component Analysis

PCA is a mathematical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components. The number of principal components is less than or equal to the number of original variables. This transformation is defined in such a way that the first principal component has the largest possible variance (that is, accounts for as much of the variability in the data as possible), and each succeeding component in turn has the highest variance possible under the constraint that it be orthogonal to (i.e., uncorrelated with) the preceding components. Principal components are guaranteed to be independent only if the data set is jointly normally distributed. PCA is sensitive to the relative scaling of the original variables. Depending on the field of application, it is also named the discrete Karhunen–Loève transform (KLT), the Hotel ling transform or proper orthogonal decomposition (POD).

Steps:

1. Find the mean value for each one dimensional image by dividing sum of pixel values and number of pixel values.
2. Find the difference matrix for each images by [A]=(Original pixel intensity of 1D image) – (mean value)
3. Find the covariance matrix L

The Principal Component Analysis method is used to find the accuracies present in the tumor such as Polygonal accuracy, Linear accuracy, Quadratic accuracy which is used to find the type of the tumor either as Benign or Malignant the graph is plotted according to the accuracy of the tumor that has been calculated.
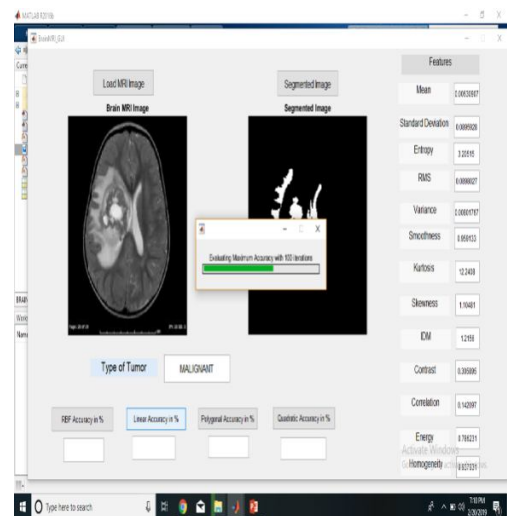

Fig. 6 calculating accuracy

Kernel Support Vector Machine

Kernel methods are a class of algorithms for pattern analysis, whose best known member is the support vector machine. The general task of pattern analysis is to find and study general types of relations (for example clusters, rankings, principlecomponents, correlations,classifications) in datasets. In the simplest form , the kernel trick means transforming data into another dimension that has a clear dividing margin between classes of data. For many algorithms that solve these tasks , the data in raw representation have to be explicitly transformed into feature vector representations via a user- Specified feature map: in contrast,kernel methods require only a user- specified kernel i.e., similarity function over pairs of data points in raw representation. Kernel methods owe their name to the use of kernel functions,which enable them to operate in high dimensional ,implicit feature space without ever computing the coordinates of the data in that space,but rather by simply computing the inner products between the images inpair of data in the feature space.

Using the feature extracted we use SVM classifier and SVM trainer for classifying the tumor as benign or malignant tumor. Where benign is a non-cancerous type of tumor which does not spread easily and it can also be removed at the earlier stage. Whereas the Malignant tumor is a cancerous type of tumor and it spreads easily. This type of tumor can not be removed and it leads to short life expectancy.
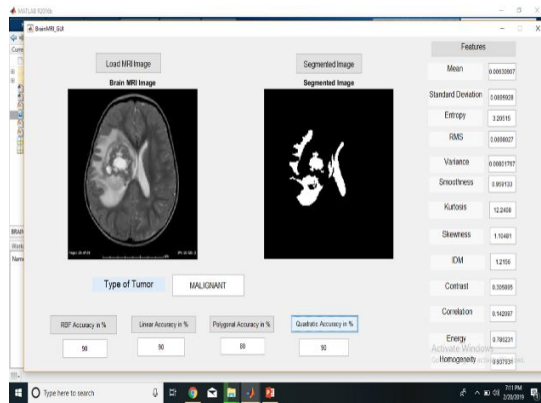

Fig. 7 Detected the type of tumor

The graph is plotted according to the accuracies whose values are calculated and displayed. The feature such as entropy, standard deviation, Mean, Energy, variance, smoothness, correlation are calculated and it also has been displayed in the graphical user interface.

IV. CONCLUSION

In summary, we propose a novel K-means clustering method for segmentation of brain tumors in MRI images. We start by a pre-processing stage consisting of bias field correction, intensity and patch normalization. After that, during feature extraction stage, the edges based and threshold based patches are extracted for segmentation process. During the Segmentation process, K-means clustering technique is applied where the clusters are divided into 2 x l rows and columns and the tumor patches are identifies and segmented. During the post processing stage the type of tumor is identified and accuracy percentage with the original MRI image is identified when compared to the segmented tumor. Also the entire algorithm is executed in the GUI format so that it will be easy for any person to identify the tumor location, type of tumor and accuracy percentage of identified tumor. Thus the proposed technique shows better segmentation and also user friendly environment.

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