

# Image Processing Techniques for Brain Tumor Extraction from MRI Images using SVM Classifier

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**Abstract**— Brain tumor extraction and analysis of it are challenging tasks in medical image processing by the use of Magnetic resonance imaging (MRI) because brain image and its structure is complicated that can be analyzed only by expert radiologists. Normally, to produce images of soft tissue of human body, MRI images are used by experts. It is used for analysis of human organs to replace surgery. A tumor may lead to cancer, which is a major leading cause of death and responsible for around 13% of all deaths world-wide. Magnetic Resonance images are used to find the presence of brain tumor in brain. Magnetic resonance imaging (MRI) is an imaging technique that has played an important role in neuro science research for studying brain images. In this paper we propose an automatic brain tumor detection that can detect and localize brain tumor in magnetic resonance imaging. The proposed method work in follows manner: Firstly we extract the feature of an image and then classifies it. First stage is used to extract the features from images using Grey level Co-occurrence matrix. In the second step the features which are extracted are used as input for Support Vector machine (SVM).

**Keywords**— Brain tumor detection, Imaging technique, brain tumor, medical image processing, MRI images.

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## I. INTRODUCTION

Normally, the anatomy of brain tumor can be examined by MRI scan or CT scan. The main advantage of MRI over CT scan is, it is not contain any radiation. MRI provide accurate visualize of anatomical structure of tissues. Because of that's MRI not affect human body. So fundamentally MRI is better compared to CT scan. MRI is a one type of scanning device, which use magnetic field and radio waves. It is also use computer to create images of the brain on film [1]. Due to the complex structure of brain tissues such as white matter (WM), gray matter (GM) and cerebrospinal fluid (CSF) in the brain images, extracting of useful feature is a fundamental task [1]. Tumor is defined as the abnormal growth of the tissues. Brain tumor is an abnormal mass of tissue in which cells grow and multiply uncontrollably, seemingly unchecked by the mechanisms that control normal cells. Brain tumors can be primary or metastatic, and either malignant or benign. A metastatic brain tumor is a cancer that has spread from elsewhere in the body to the brain [2].

Usually Image processing system includes treating images as two dimensional signals while applying already set signal processing methods to them. Brain tumor is caused by an abnormal growth of cell in brain. Normally brain tumor emerges from brain cells, blood vessels or nerves that are present in the brain. Early detection of brain tumor is necessary as death rate is higher among humans having brain tumor. Nowadays there are several methodologies for classifying MR images, which are fuzzy methods, neural networks, atlas methods, knowledge based techniques, shape methods, variation segmentation. MRI consists of T1 weighted, T2 weighted and PD (proton density) weighted images and are processed by a system which integrates fuzzy based technique with multispectral analysis [2]. The following figure embraces the fundamental steps in image processing system.

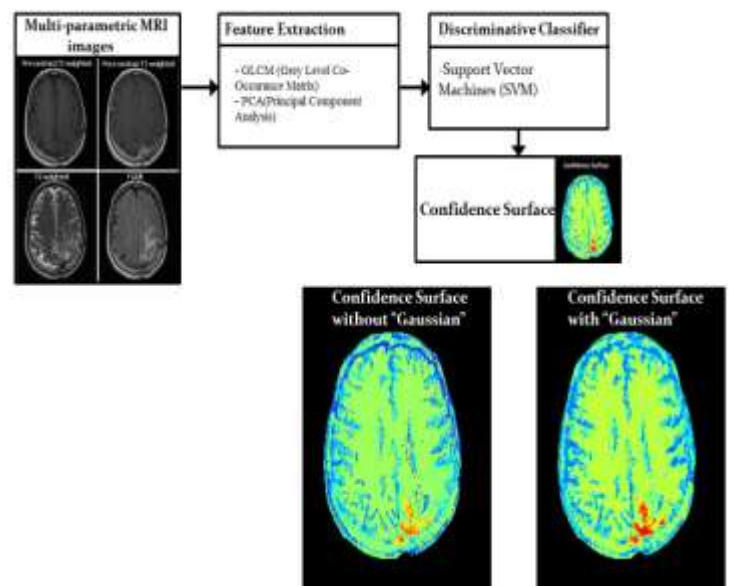


Fig. Steps in digital image processing

## II. MAGNETIC RESONANCE IMAGE

Magnetic resonance imaging (MRI) is a type of scanner which is used to form scans a particular part of human body. In the MRI system uses magnetic fields and also uses the radio waves for producing the detailed images of the part of the human body. An MRI scanner consists from a large tube that contains powerful magnetic fields. Human is lie inside the MRI systems tube during the scanning of human body part. By the MRI scanner we can scan the every part of the human body like the: Spinal cord bones, brain, joints breasts heart and blood vessels internal organs etc. The output of an MRI scan is in the form of an image. By analyzing the MRI image we can

identify the abnormalities and also it can help in diagnose conditions for any diesis.

Naturally the human body is made from water molecules, these molecules consist form the atoms of hydrogen and oxygen. The center of every hydrogen atom contains a proton. A proton is type of a subatomic particle. When the particular part of human body is examine in the powerful scanner magnets, the protons which in human body are line up in the same direction. When the radio waves are turned off, the protons send out radio signals, which are picked up by receivers. These signals give the information about the exact location of the protons in the body. It also helps to differentiate between the many types of tissue in the body of human. By this process an image is created on computer screen, and finally we get a detailed image of inside of the human body. This is the widely-used method for the medical imaging of high quality. This is specially used for human brain for identifying or finding the abnormalities by the experts.

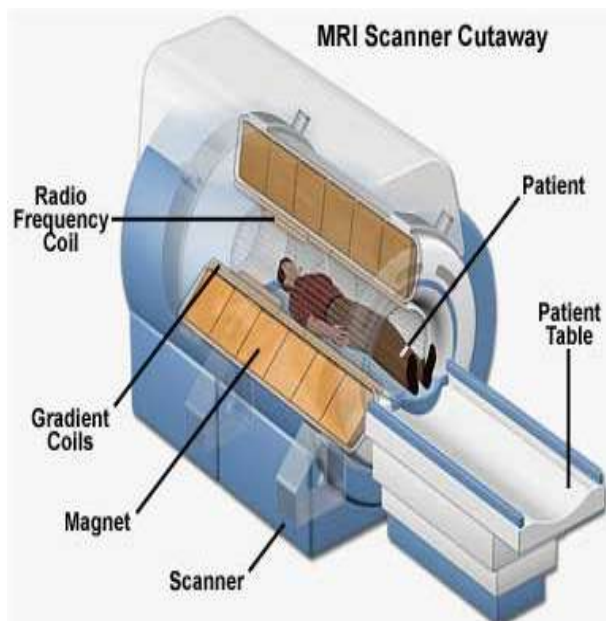


Fig: Block Diagram for MRI System

### III. METHODOLOGY

In the methodology part of this paper we describe our method which is used for detection of tumor in human brain using SVM. The proposed work mainly gives a review that what steps are performed throughout the entire process to detect tumor from MRI of brain. Detection of brain tumor involves different stages such as image preprocessing, segmentation, feature extraction and classification. In the Image pre-processing we can significantly increase the reliability of an optical inspection. After the image preprocessing we will segment the image. By the image segmentation we can partition a digital image into multiple segments (sets of pixels, also known as super pixels). And then extract the feature of image by using the GLCM and PCA algorithms. And at the end the extracted features are feed as input to the Support Vector Machine (SVM). The SVM classified the image by using its classes. Class 1 indicates that

the MRI image is non- cancerous and class 2 shows that MRI image is cancerous.

All the focus of our research is mainly work on two steps or phases. In the first phase textural features are extracted from MRI and in the second phase tumor is classified as cancerous or non-cancerous. The proposed method is shown below graphically in the flowchart.

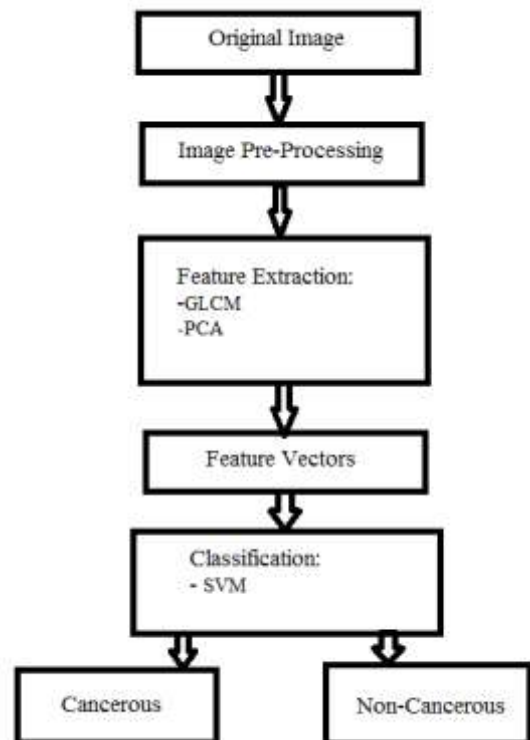


Fig: Flowchart

### IV. GLCM

The Gray level Co-Occurrence matrix (GLCM) is a method to extract statistical texture features [3]. The GLCM gives the information of how a pixel with gray-level value  $i$  occurs either in vertical direction , horizontal direction, or diagonally to adjacent pixels with the value  $j$  where  $i$  &  $j$  are the values of gray levels of an image. The Second-order statistics are observe the gray values pairs which are occurred at the endpoints of a needle of random length placed in the image at a random location and orientation. [4].

By the analysis of GLCM directions we get the following  
1. The angle of Horizontal is  $0^\circ$  or  $180^\circ$ . 2. The angle of Vertical is  $90^\circ$  or  $270^\circ$ . 3. The angle of Right Diagonal is  $45^\circ$  or  $225^\circ$ . 4. The angle of Left diagonal is  $135^\circ$  or  $315^\circ$  [4].

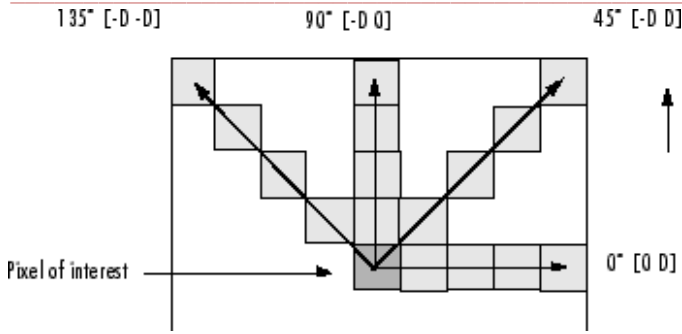


Fig. Directional analysis of GLCM

The some GLCM Features used in this work are:

#### • Contrast

The term contrast are related from the intensity. By this we can measure the intensity of contrast between a pixel and its neighbor in the whole image.

$$\sum_{i,j=0}^{N-1} P_{ij} (i - j)^2$$

For any constant image contrast is always 0.

#### • Correlation

The term contrast are related from the correlation of pixels. By this term we can measure how correlated a pixel is to its neighbor over the whole image.

$$\sum_{i,j=0}^{N-1} P_{ij} \frac{(i - \mu)(j - \mu)}{\sigma^2}$$

For a perfectly positively or negatively correlated image the correlation is 1 or -1.

#### • Energy

The energy we can calculate the sum of squared elements which is in the GLCM.

$$\sum_{i,j=0}^{N-1} (P_{ij})^2$$

For a constant image the Energy is 1.

#### • Homogeneity

The term homogeneity used for measuring the looseness of the distribution of elements from a GLCM to the GLCM diagonal. For a diagonal GLCM Homogeneity is 1.

$$\sum_{i,j=0}^{N-1} \frac{P_{ij}}{1 + (i - j)^2}$$

$P_{ij}$  = Where  $i, j$  are the element of the normalized symmetrical GLCM.

$N$  = Number of gray levels in the image.

$\mu$  = The GLCM mean, calculated as:

$$\mu = \sum_{i,j=0}^{N-1} iP_{ij}$$

$\sigma^2$  = The variance of the intensities of all reference pixel in the relationships that contributed to the GLCM, calculated as:

$$\sigma^2 = \sum_{i,j=0}^{N-1} P_{ij} (i - \mu)^2$$

### V. PRINCIPAL COMPONENT ANALYSIS

Principal Component Analysis PCA is a powerful technique for extracting structure from possibly high dimensional data sets. It is readily performed by solving an Eigen value problem or by using iterative algorithms which estimate principal components. PCA is an orthogonal transformation of the coordinate system in which we represent our data. The new coordinate values by which we represent out data are called principal components. It is often the case that a small number of principal components is sufficient to account for most of the structure in the data. These are sometimes called the factors or latent variables of the data.

Listed below are the 6 general steps for performing a principal component analysis, which we will investigate in the following sections.

- Take the whole dataset consisting of  $d$ -dimensional samples ignoring the class labels
- Compute the  $d$ -dimensional mean vector (i.e., the means for every dimension of the whole dataset)
- Compute the scatter matrix (alternatively, the covariance matrix) of the whole data set
- Compute eigenvectors and corresponding eigenvalues
- Sort the eigenvectors by decreasing eigenvalues and choose  $k$  eigenvectors with the largest eigenvalues to form a  $d \times k$  dimensional matrix  $W$  (where every column represents an eigenvector)
- Use this  $d \times k$  eigenvector matrix to transform the samples onto the new subspace. This can be summarized by the mathematical equation:

(where  $x$  is a  $d \times 1$  -dimensional vector representing one sample, and  $y$  is the transformed  $k \times 1$  -dimensional sample in the new subspace.)

### VI. SUPPORT VECTOR MACHINE

The Support Vector Machine (SVM) was first proposed by Vapnik and has since attracted a high degree of interest in the machine learning research community. Support Vector Machines (SVM) have recently gained prominence in the field of machine learning and pattern classification [6]. Classification is achieved by realizing a linear or non-linear separation surface in the input space. In Support Vector classification, the separating function can be expressed as a linear combination of kernels associated with the Support Vectors as [7]

$$f(x) = \sum_{x_j \in S} \alpha_j y_j K(x_j, x) + b$$

where  $x_i$  denotes the training patterns,  $y_i \in \{+1, -1\}$  denotes the corresponding class labels and  $S$  denotes the set of Support Vectors [6].

#### LINEAR SVM:

The linear SVM are those SVM in which the training patterns are linearly separable. This is the simplest case of SVM classifier. In the Linear SVM a linear function is used. The function is in the form of:  $f(x) = w^T x + b$  (1)

There are two different classes of the training examples. Each class is separated by the hyperplane

$$f(x) = w^T x + b = 0,$$

in the above equation the  $w$  is the unit vector and  $b$  is a constant.

In the given training set, many number of hyperplanes can be exists that maximize the margin between the two classes which are separate from each other, In the below figure shows that the SVM classifier is based on the hyperplane that maximizes the separating margin between the two classes.

More simply we can say that in the SVM the hyperplane provide the separation between the decision function values for the "borderline" examples from the two classes. In below Figure shows that the SVM classifies by a hyperplane that minimizes the separating margin between the two classes. These classes are indicated as "X" s and "O"s. Support vectors are elements of the training set that lie on the boundary hyperplanes of the two classes.

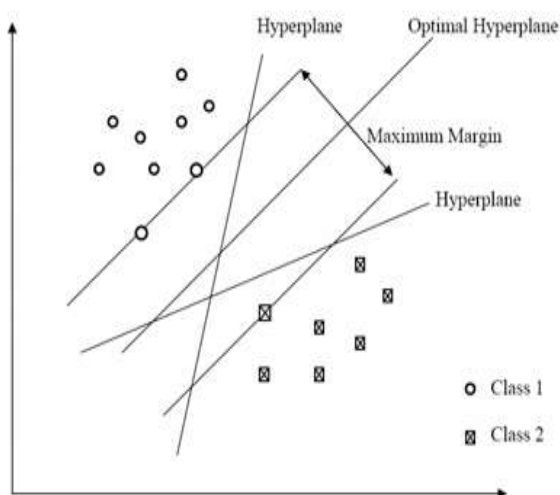


Fig: Linear SVM Classification

#### NON-LINEAR SVM:

In the above case of SVM classifier shows that a straight line or hyperplane is used for differentiate the two classes of SVM. But in many cases datasets or data points are not

separate from each other by a straight line between two classes. For example the data points or data set are not separate from each other in below fig. So for the separation of both the classes Kernel functions are used with SVM classifier.

The basic functionality of Kernel function is to provide the connection between non-linear to linear SVM. The kernel function maps the low dimensional data into the high dimensional feature in which data points are linearly separable.

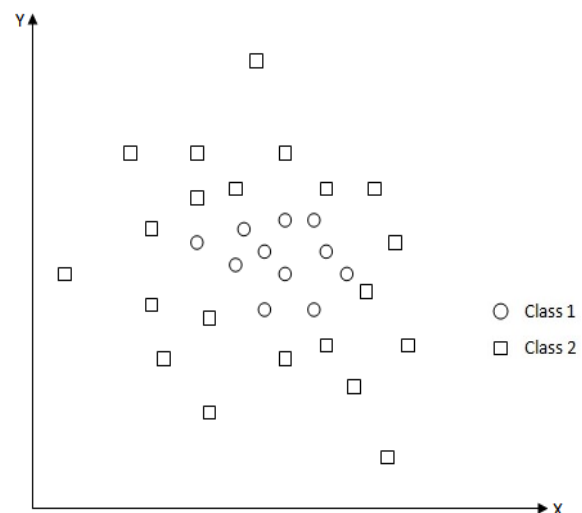


Figure: Non-linear data points

#### VII. CONCLUSION

In this paper we proposed an approach of classification using Support Vector Machine Classifier which has very good in working and also in efficiency. It generates the correct and useful results as compare to other classifiers. So the SVM classifier can more accurately and effectively detect the tumor of human brain by the analysis of MRI images.

#### VII. FUTURE WORK

The proposed approach in this paper is more effective and provides good result. By this approach in the future we can examine the more specific results from the MRI images. In the future of this research we can fully examine the abnormalities in human brain and also diagnose the abnormalities by expert systems by provide the better training set.

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