

Extraction and Identification of Tumor Regions from MRI using Zernike Moments and SVM

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Abstract: Brain tumor is a serious type of malignancy that is caused by the abnormal cell formation within the brain. The brain tumor identification and further analysis from the Magnetic Resonance Imaging (MRI) is a tough process and this paper proposes an effective method for identifying the tumor regions within brain. For the MRI preprocessing High Pass Kernel filter along with a median filter and for the effective segmentation K-means clustering and Watershed segmentation are used. Here we propose Zernike moments for the extraction of features and Support Vector Machine (SVM) classifier is used for the identifying the tumor regions in the brain. The identification of the tumor using the proposed method yields better results.

Keywords: Magnetic Resonance Imaging (MRI), K-means Clustering, Zernike Moments, Support Vector Machine (SVM) classifier

1. INTRODUCTION

Brain tumor is a deadly disease which occurs due to the abnormal cell growth with in the brain. The cell multiplication process sometimes occurs in an uncontrollable manner which leads to serious consequences in the health conditions of the patient. As technology has advanced various methods are available for the identification and analysis of brain tumors. It includes Computed Tomography, Skull X ray, Spinal Tap, Myelogram and Magnetic resonance Imaging. The Magnetic Resonance Imaging (MRI) has the ability to change the contrast of images and also it is able to change the imaging plane without moving the patient. Diagnoses of brain tumor are usually done using MRI scanning and are confirmed by a biopsy test. Some of the basic properties that are possessed by the normal brain images produced by an MRI are that they will appear equal in proportion on both sides of the image on the paper and each section of the brain images will be equal in size and coloration dimension. Depending on the medical illnesses of the patient the abnormal brain images produced by the MRI will vary since the illness will affect various parts of the brain and this will be represented in particular regions of the brain. One of the noticeable differences is that there exist obvious inequalities between the two sides of the brain. When the image shows a larger-sized portion on the left side of the brain than the right side then this shows a clear case of abnormality.

There exist color variations in the abnormal images. Suppose if there exist white color at some portions of the brain in the MRI image then it may be an abnormal image. Instead of muted shades of gray the abnormal MRI images are much darker in certain portions. Figure 1(a) shows the normal MRI brain axial, sagittal and coronal images and Figure 1(b) shows the abnormal MRI brain axial, sagittal and coronal images. MRI is more preferred over CT (Computed Tomography) since MRI produces no ionizing radiations.

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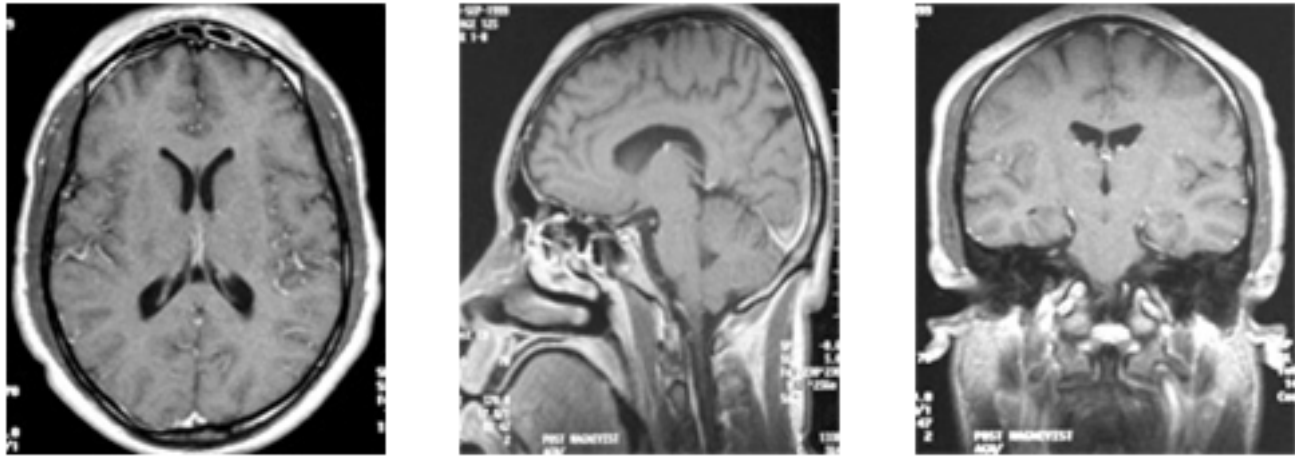


Figure 1 (a): normal brain MRI Images

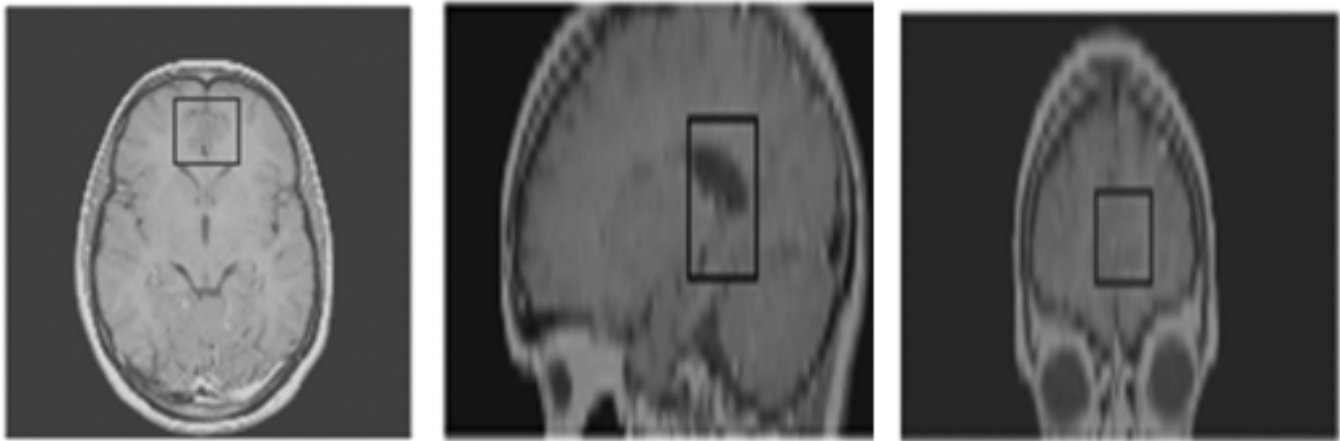


Figure 1 (b): abnormal brain MRI Images

In this paper we propose the usage of various enhanced image processing techniques for the brain tumor identification. MRI Preprocessing includes the usage of High Pass Filter Kernel followed by a median filtering. K-means Clustering algorithm and watershed segmentation are effectively used for MRI segmentation. The feature extraction and selection is carried out by Zernike moments. SVM classifier is used for identification of tumor in MRI images.

This paper is organized as follows: Section II describes the proposed methodology which includes various techniques used and proposed block diagrams. Section III describes the experimental results obtained and finally concludes with section IV.

2. METHODOLOGY

The brain tumor detection from Magnetic Resonance Images involves a series of processes which are discussed in the following sections.

2.1. Proposed Block diagram

The existing method such as Region growing method can be used for the identification of brain tumors. It is a simple pixel based image segmentation method. It includes the selection of initial seed points. The segmentation carried out by region growing method examines the neighboring pixels of the initial seed points and then the decision is taken whether to add the pixel neighbors to the region. This method is an iterative procedure.

The main highlighting merit of region growing method is that, by this approach the regions can be effectively separated which is having the same properties that are defined earlier. However there are some major defects with this method. This approach is computationally expensive and is sensitive to noise. Here we propose an effective method for the identification of brain tumors.

The figure 2(a) shows the proposed block diagram for brain tumor identification. Here the input MRI image is preprocessed firstly to enhance the image. The preprocessing of MRI uses a High Pass Kernel filter and a median filter. After preprocessing the image segmentation is done by threshold values through K-means clustering and for enhancing the quality of segmented image watershed method is used. Then from the segmented image the useful features are extracted by using Zernike moments. Eventually the tumor regions are identified using Support Vector Machine.

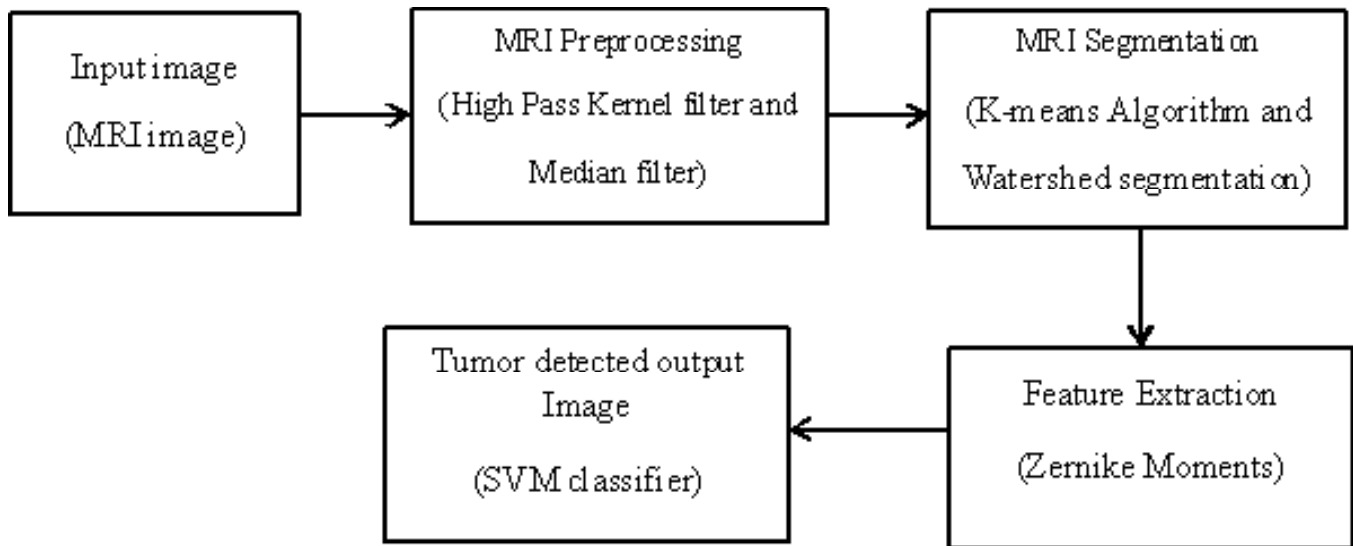


Figure 2 (a): Proposed Block Diagram for brain tumor identification

2.2. Preprocessing of MRI

The MRI preprocessing is a technique for enhancing the relevant information about the tumor. It involves the conversion into a digital format, and performs some operations in it, in order to extract the tumor details from it. The image preprocessing will provide the characteristics associated with the MRI. Here the MRI input image is firstly converted into gray scale for extracting features related to tumor, since from an RGB image the features cannot be extracted. The gray scale converted image undergoes a filtering process.

Here a High Pass filter kernel is used to make the image to appear sharper. The high pass filters emphasize on finer details of MRI. After the High pass filtering of MRI a median filtering is done. It is a non-linear process used for the eradication of impulsive noise and salt and pepper noise. It is also useful for preserving the edges in an image while reducing the random noise. Hence the net result obtained by preprocessing is enhanced tumor regions in the MRI input image.

2.3. MRI Segmentation

Image segmentation is the process of partition of a digital image into multiple segments. These multiple segments are actually a set of pixels which are called as super pixels. The major goal of segmentation is to alter the representation of an image into something meaningful and it makes the analysis easier. Image segmentation locates the objects and boundaries. In the field of bio-medical imaging the important applications of segmentation includes the location of tumor regions and other pathologies, diagnosis and surgical planning.

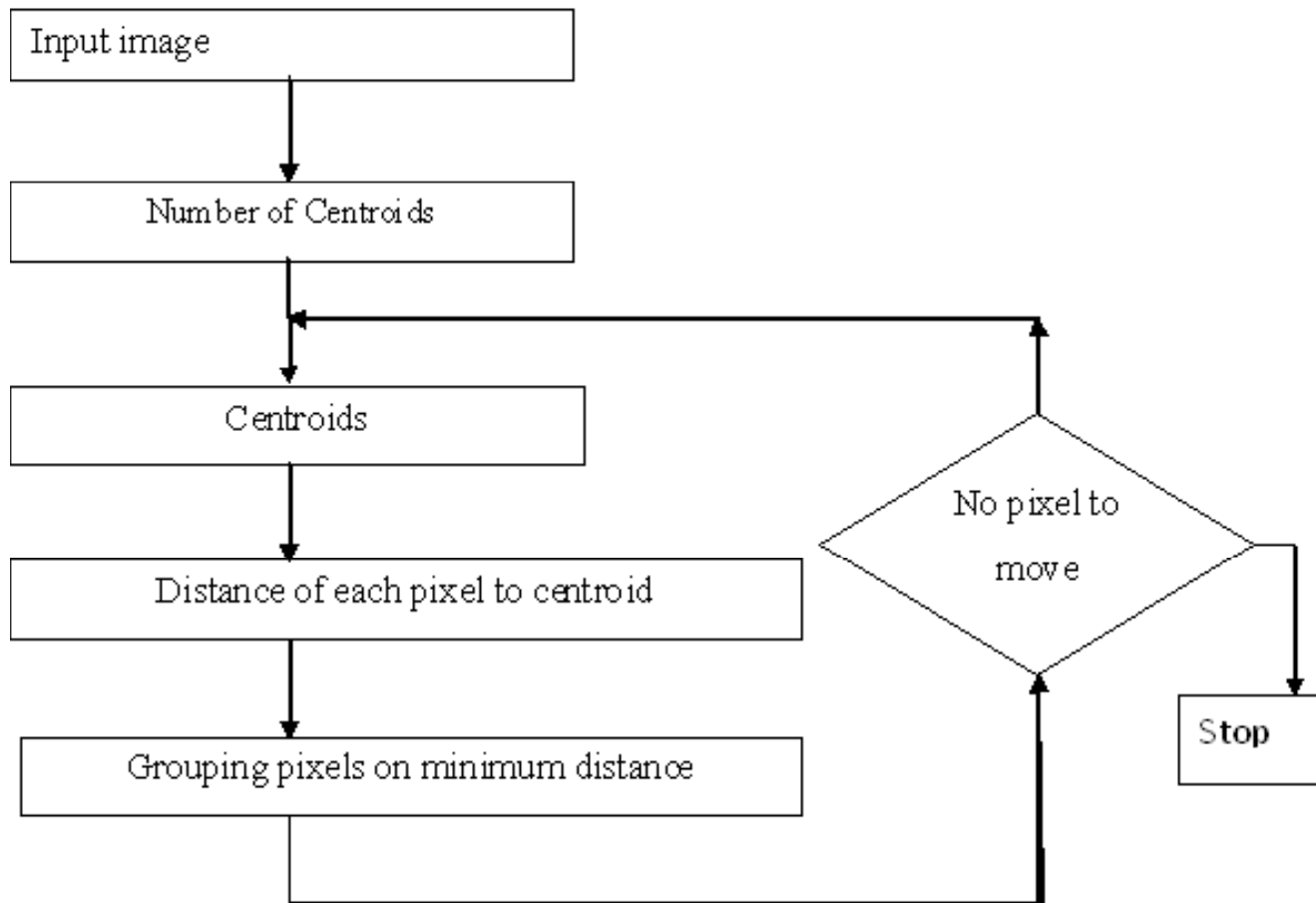


Figure 2 (b): K-means clustering algorithm

For the threshold segmentation of MRI, K-means clustering algorithm is used. Thresholding segmentation is a simple method for image segmentation. The selection of a threshold value is the key point in this method. The major goal of K-means clustering algorithm is the partitioning of n observations into K clusters and here each observation belongs to the cluster with the nearest mean. The steps involved in the K-means clustering algorithm are shown in the figure 2(b).

The various steps involved in K-means clustering algorithm are explained as follows:

Step1: Pick K cluster centers, either randomly or based on some heuristics.

Step 2: Assign each pixels in the image to the cluster that minimizes the distance between the pixel cluster centers.

Step 3: Recompute the cluster centers by averaging all of the pixels in the cluster.

Step 4: Repeat steps 2 and 3 until the convergence is attained that is no pixels change cluster.

The minimization with in cluster sum of squares is given by the following function

$$\text{Arg}_s \min \sum_{i=1}^k \cdot \sum_{x \in S_i} \|x - \mu_i\|^2 \quad (1)$$

Where, set of observations (x_1, x_2, \dots, x_n) , μ_i is the mean of points in S_i , K is number of clusters and S_i is set of clusters.

After performing K-means clustering, Watershed segmentation algorithm is used for the segmentation. The water segmentation is performed by the usage of sobel Filter. The sobel filter is also known as sobel operator. It is used in the various image processing especially in edge detecting algorithms.

2.4. Feature Extraction by Zernike Moments

The extracted features from the images are supposed to contain the useful information from the input data. In feature extraction the amount of resources which are needed to describe a large set of data. Feature extraction is the process of transformation of the input data into a set of features.

In this paper we propose Zernike Moments for feature extraction. For this purpose Zernike Moment polynomials are used here. Zernike moments are based on complex polynomials that form a complete orthogonal set on a unit circle. The Zernike moments over the unit circle.

$$V_{nm} = V_{nm}(\rho, \theta) = R_{nm}(\rho) e^{im\theta} \quad (2)$$

Where, n is a non-negative integer and m is a non-zero integer. Zernike radial polynomials in polar coordinates and are defined by

$$R_{nm}(\rho) = \sum_{s=0}^{(n-|m|)/2} (-1)^s \frac{(n-s)!}{s! \left(\frac{n+|m|}{2} - s\right)! \left(\frac{n-|m|}{2} - s\right)!} \rho^{n-2s} \quad (3)$$

Polynomials in above equation are orthogonal and according to orthogonality condition

$$\iint V_{nm}(x, y) dx dy = \frac{\pi}{n+1} \delta_{nm} \quad (4)$$

Zernike moment for order n and repetition m is given by

$$A_{nm} = \frac{n+1}{\pi} \iint f(x, y) V_{nm}^*(\rho, \theta) dx dy \quad (5)$$

If $f(x, y)$ is a digital image, we replace the integral by summations to get Zernike moments for the image. Then in this case, reduces to

$$A_{nm} = \frac{n+1}{\pi} \sum_x \cdot \sum_y f(x, y) V_{nm}^*(\rho, \theta) \quad (6)$$

Let us assume that $f(x, y)$ is the image formed by the complex Zernike moments value and $b(x, y)$ is the image pixels located at the center boundary of image. The average value of the pixel $b(x, y)$ located at the center boundary of the image can be calculated. Average pixel value is calculated using following equation

$$Avgvalue = \frac{1}{N} \sum_{x=0}^{x=x-1} \cdot \sum_{y=0}^{y=y-1} b(x, y) \quad (7)$$

Where, N is the total number of pixels located at the center boundary of the image.

2.5. Brain Tumor Detection using SVM

Support Vector Machines falls under the category of supervised learning models. They are associated learning algorithms that are used for the analysis of data and to recognize patterns. It is a non-probabilistic binary linear classifier. SVM is basically a good classifier for binary classification of images, in which the exact answer is obtained such as yes or no. here in tumor detection SVM is chosen due to its admirable feature in classification to derive the fact that whether the input MRI is having tumor or not. Moreover SVMs are used for solving various real world problems. The classification of images can also be done using SVMs. Experimental results show that SVMs achieve significantly higher search accuracy than traditional methods. In the field of medical science SVMs are employed to classify proteins. It is most widely used binary classifier and it provides high accuracy.

3. EXPERIMENTAL RESULTS

The description of the experimental results obtained is shown in this section. Figure 3(a) shows an input MRI image. The figure 3(b) shows the preprocessing output images. The figure 3(c) represents the MRI segmentation output and also the Zernike moment values obtained. The figure 3(d) shows the tumor detected region using SVM classifier.

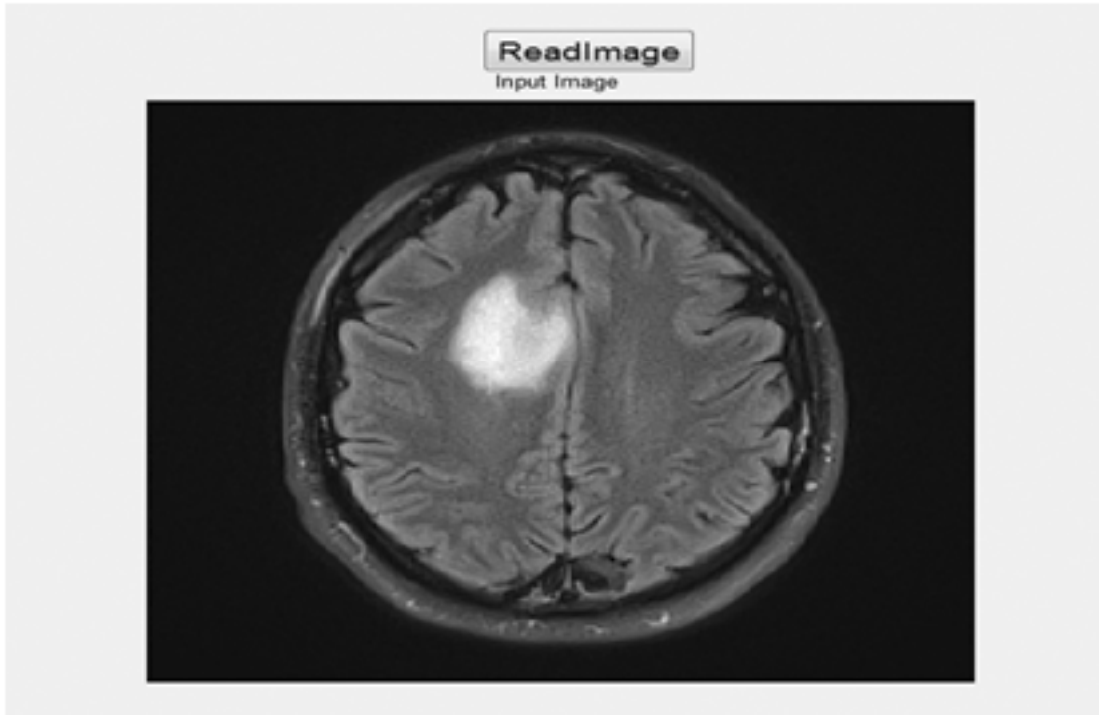


Figure 3 (a): Input MRI Image

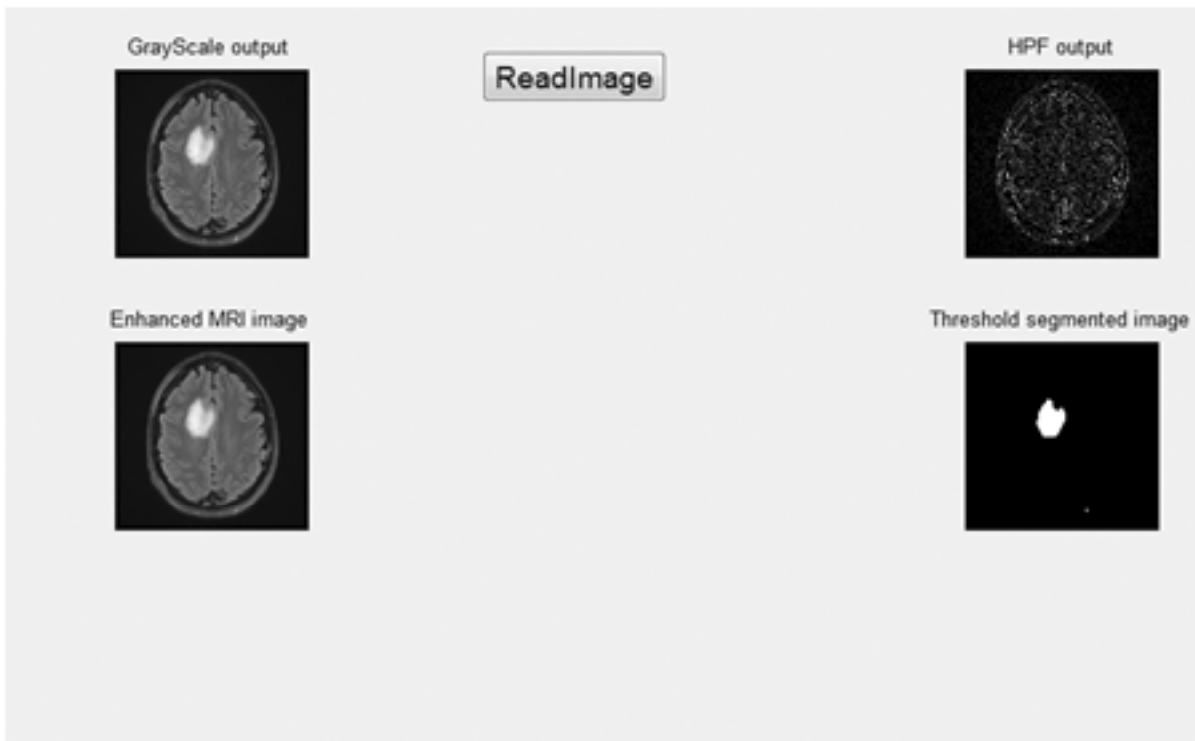


Figure 3 (b): MRI Preprocessing output images

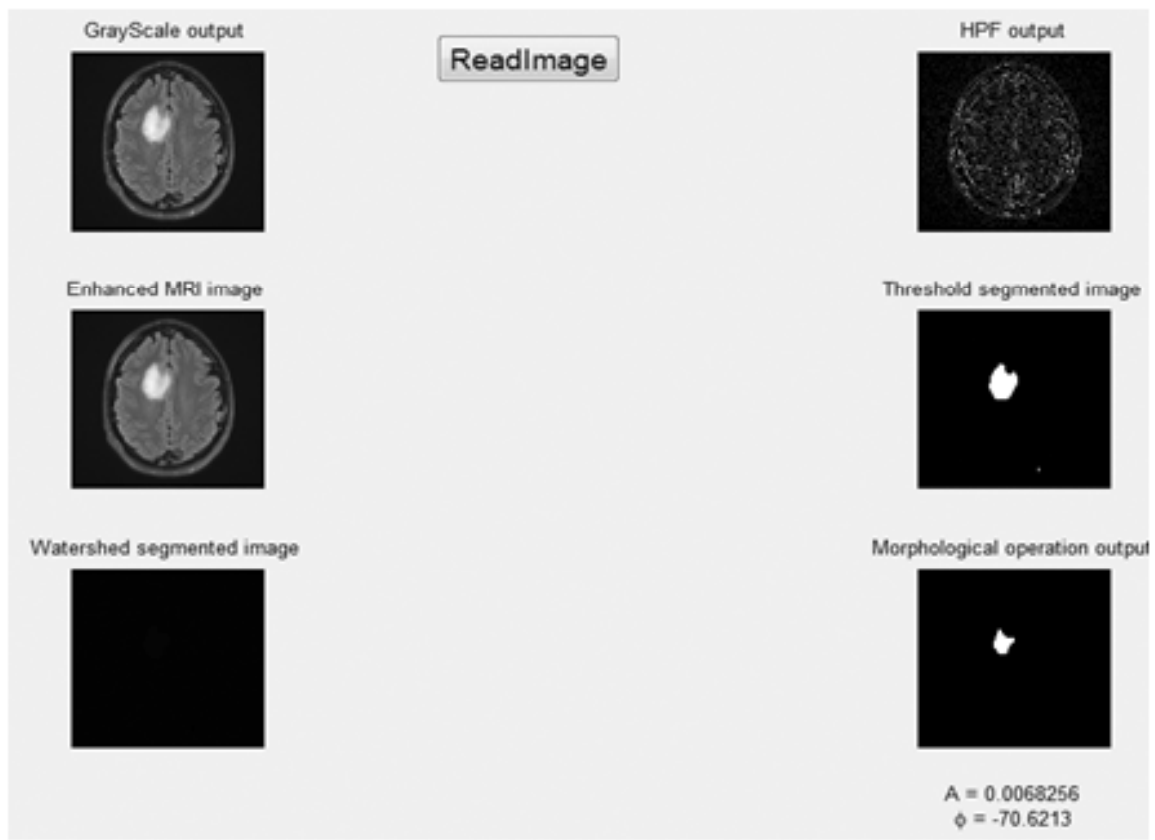


Figure 3 (c): MRI Segmentation and Zernike moments output Images

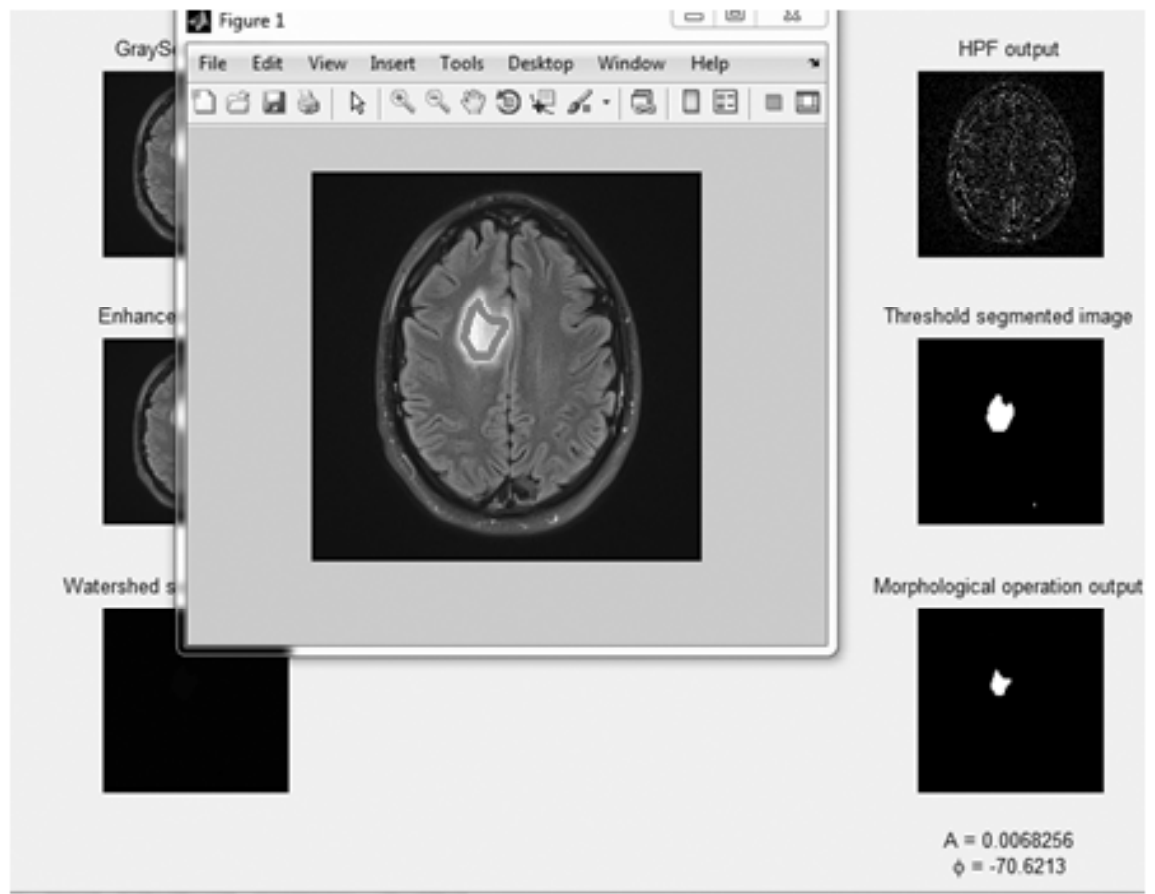


Figure 3 (d): Tumor Detected by SVM classifier

4. CONCLUSION

It is observed from the work that the proposed extraction and identification of the tumors using techniques namely Zernike moments and Support Vector Machines yields better results. This work can be extended for detailed classification of tumors and also classification based on different grades of tumors.

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