# DETECTION OF BRAIN TUMORS USING IMAGE PROCESSING IN MATLAB

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*Abstract*—**In the fast-growing world, the chances of cancerous cells' production in human bodies have also increased in which one of the most dangerous being the brain tumor. This project detects this brain tumor present in the brain. The magnetic resonance imaging (MRI) technique is used to obtain images of brain with tumor which is later used with the technique of biomedical image processing using MATLAB to detect and highlight the tumor.**

INTRODUCTION

A brain tumor is a mass or growth of abnormal cells in your brain. Many different types of brain tumors exist. Some brain tumors are noncancerous (benign), and some brain tumors are cancerous (malignant). Brain tumors can begin in your brain (primary brain tumors), or cancer can begin in other parts of your body and spread to your brain (secondary, or metastatic, brain tumors). Primary brain tumors originate in the brain itself or in tissues close to it, such as in the brain-covering membranes (meninges), cranial nerves, pituitary gland or pineal gland. Primary brain tumors begin when normal cells acquire errors (mutations) in their DNA. These mutations allow cells to grow and divide at increased rates and to continue living when healthy cells would die. The result is a mass of abnormal cells, which forms a tumor. In adults, primary brain tumors are much less common than are secondary brain tumors, in which cancer begins elsewhere and spreads to the brain. Only about 5 to 10 percent of all cancers are genetically inherited, or hereditary. It's rare for a brain tumor to be genetically inherited. The most common treatment for malignant brain tumors is surgery. The goal is to remove as much of the cancer as possible without causing damage to the healthy parts of the brain. While the location of some tumors allows for easy and safe removal, other tumors may be located in an area that limits how much of the tumor can be removed. Even partial removal of brain cancer can be beneficial. In this new technocracy era, the interest in digital biomedical image processing methods takes a most important position in two principal and important areas out of which the most important one is an improvement of pictorial information for human studies and processing of biomedical image data for storage and analysis. A biomedical image sometimes is defined as a two-dimensional function, F (x,y), where x and y are the value or gray level of a biomedical image at a specific point. F are all finite, discrete quantities. An image can be called as a digital image is when it is composed of a finite number of elements, each of which has a particular location and value. Engineers have been actively developing tools to detect various diseases or abnormalities and to process medical images. Medical image segmentation is a powerful tool that is often used to detect tumors. Many scientists and researchers are working to develop and add more features to this tool. Magnetic resonance imaging (MRI) is an imaging technique that produces high quality images of the anatomical structures of the human body, especially in the brain, and provides rich information for clinical diagnosis and biomedical research. The diagnostic values of MRI are greatly magnified by the automated and accurate classification of the MRI images. Wavelet transform is an effective tool for feature extraction from MRI brain images, because it allows analysis of images at various levels of resolution due to its multi-resolution analytic property. However, this technique requires large storage and is computationally expensive. In order to reduce this problem, we have come up with a project which is about detecting Brain tumors from MRI images using image processing and segmentation for detection and support vector machine (SVM) for classification in MATLAB.

## I. DESIGN ASPECTS AND METHODOLOGY

MRI scans of the human brain are transferred and stored in a computer. These are given as input. Detection of tumors take place using MATLAB software. The main principle used here for detection of tumors is image thresholding. The image file is read using imread command and is then converted to black and white image. The tumor would constitute the white part of the image. The image is thresholded by 0.7 pixels which means that image segments with pixel value greater than 0.7 will be converted to white color and below 0.7 pixels will be converted to black color. This is done with the help of im2bw command. Both black and white regions are labelled using bwlabel command. The white region is the one with the tumor. The tumor and the rest of the brain have different solidities (or densities), the tumor is denser and they are also present in different areas of the image. Regionprops command is used to return the solidity and areas of different segments in the image and is stored in two different vectors. We define high dense segments as the segments of the brain having density greater than 0.2. The maximum area with high density is determined using max command. This area is matched with the corresponding element in the area vector

obtained earlier (using the Regionprops command). Checked with the help of ismember command. The tumor is dilated with the help of imdilate command to reduce errors. The code will still work without this command but the percentage of errors is reduced if this command is used. If the maximum area of white region detected is less than 0.1, it might be due to very small regions in the MRI and need not be specified as tumor and tumor is absent. Hence, we print an appropriate message. If maximum area is greater than 0.1, another image is created to indicate the tumor in the input image. A boundary is drawn in for the tumor region using a for loop. The image of the brain is displayed, the image of the tumor in the black and white image is displayed, the tumor is the white part of the image and the image which indicates the tumor is also displayed. These images are displayed in a common window with the help of subplot command and the images are labelled with appropriate titles.

## II. MATLAB CODE

```
close all;
clear all;
clc;
image=imread('2.jpg');
b_w=im2bw(image,0.7);
label=bwlabel(b_w);
stats=regionprops(label,'Solidity','Area');
density=[stats.Solidity];
area=[stats.Area];
high_dense_area=density>0.2;
max_area=max(area(high_dense_area));
if(max_area<0.1)
    print('No tumor detected');
end
if (max_area>=0.1)
    tumor_label=find(area==max_area);
    tumor=ismember(label,tumor_label);
    se=strel('square',5);
    tumor=imdilate(tumor,se);
    figure(2);
    subplot(1,3,1);
    imshow(image,[]);
    title('Brain');
    subplot(1,3,2);
    imshow(tumor,[]);
    title('Tumor');
    [B,L]=bwboundaries(tumor,'noholes');
    subplot(1,3,3);
    imshow(image,[]);
    hold on
for i=1:length(B)
    plot(B{i}(:,2),B{i}(:,1), 'y' ,'linewidth',1.45);
    end

title('Detected Tumor');
hold off;
end
```

## III. OBSERVATIONS

The MRI's from the MRI machine is scanned in a computer and the scans are saved as images. These images are passed as input to the Matlab code and are processed using various image processing techniques and the detected tumor is also highlighted and indicated in the image. Some example outputs are shown below.
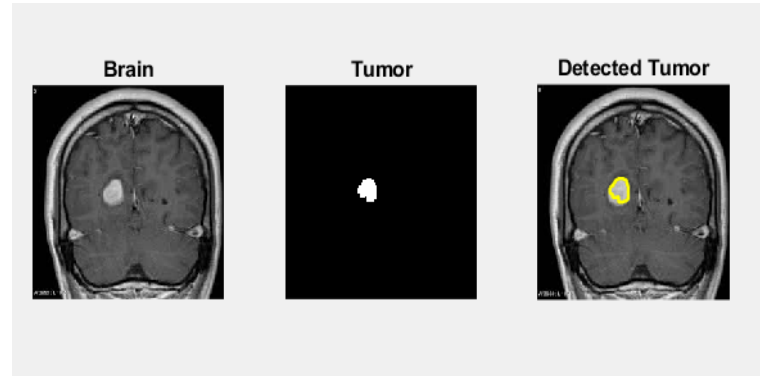
## IV. RESUTS

First image – It is an MRI image of a brain containing tumor.

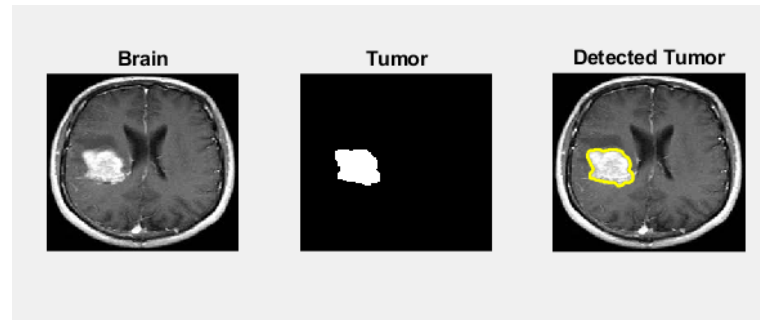Second image- It is the image of the detected tumor in white on a black background.

Third image – It is the image of the tumor outlined with a yellow boundary actually located in the brain.

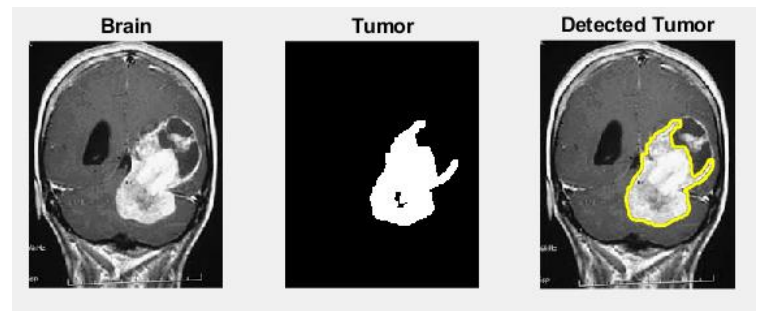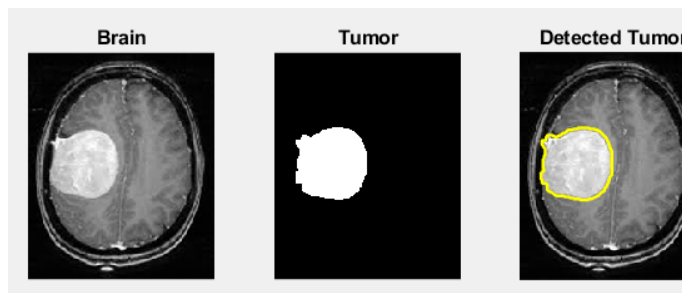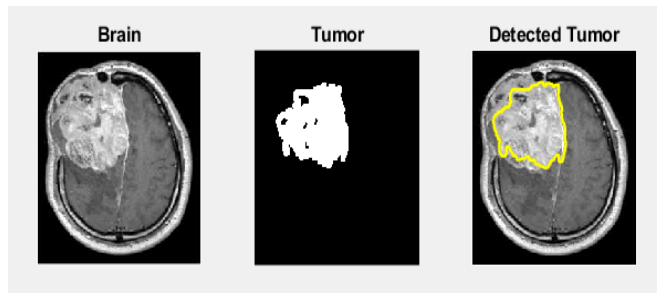The five cases of brain tumor recorded are as follows:

Case-1



Case-2



Case-3

Case-4



Case-5



## V. CONCLUSION

The tumor and cancerous cells present in the brain using MRI image is detected using biomedical image processing using MATLAB. This technique can be used to detect even small quantities of tumor which can later be very harmful.

This technique is proved to be very helpful and important invention as it detects the tumor which can later be removed by surgery and can make the affected person healthy.

## VI. RECCOMEDATIONS AND SCOPE

The MRI machine can be directly interfaced with the MRI machine and the MRI images can directly be passed as input to MATLAB and the output can be easily determined. This saves time and gives output directly.

Recommendations on how to go about this project might include adding classification of tumors using MATLAB and SVM (Standard Vector Machines) can be used for this purpose. Instead of performing image processing for detection of tumors, we can use discrete wavelet transforms. This method is more efficient and yields more accurate results.

This can be implemented in laboratories and an expert is not needed to check the images. This also helps in confirming the results.

Other software's can also be used instead of MATLAB but MATLAB is found to give the best results. GUI can also be included. It reduces the complexity of passing inputs and viewing outputs. The code need not run every time.

## VII. ACKNOWLEDGMENT

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## VIII. REFERENCES

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