

## PROCESSING OF MRI IMAGES FOR DETECTION OF BRAIN TUMORS

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**Abstract.** We used the MRI technique to achieve a dataset of ten images: five healthy brain images and five images of brains with tumors. To highlight tumor development, the images were preprocessed using OpenCV, converted into grayscale, then underwent contrast changes, resizing, and Gaussian blur. The feature extraction stage involved binarizing images in well-defined values and extracting the tumor contour using the "find\_contours" and "grab\_contours" functions. The segmentation stage added the contour to a copy of the resized image, highlighted it with endpoints, and cropped the image to the edges of the contour. The results showed the changes in the tumor area after contrast and well-defined tumor tissues after feature extraction and segmentation.

**Keywords:** MRI, brain tumor, segmentation, features, pre-processing

### Introduction

Medical imaging information can be provided by various methods, such as magnetic resonance imaging (MRI), computed tomography (CT), and positron emission tomography (PET). Although these medical images can provide exceptional anatomical views of organs, their detection, segmentation, and identification of organ pixels or lesions in the images continues to be among the most difficult endeavors in the field of medical image analysis [1].

This paper focuses on processing tomographic images made by MRI in the brain to identify the occurrence of brain tumors.

The topic was chosen because brain tumors are one of the most difficult to treat and have a high incidence rate. The annual, global, age-standardized incidence of primary malignant brain tumors is approximately 3.7 per 100,000 men and 2.6 per 100,000 women [2].

Brain tumors result from the uncontrolled proliferation of neural or glial tissue cells. Therefore, to apply an optimal treatment method, it is essential to identify the structure and origin of the tumor [3].

### Detection methods

With the advancement of medical imaging, imaging modalities play an essential role in evaluating patients with brain tumors and significantly impact patient care. For patients suspected of having a brain tumor, the recommended evaluation typically involves an MRI with and without gadolinium contrast, which is considered the gold standard. However, in emergency department settings, some patients with progressive clinical signs and symptoms of a brain tumor may receive a CT scan without contrast medium instillation [4].

#### Image pre-processing

Most algorithms rely on some pre-processing to prepare and enhance the image. Denoising an image is a standard preprocessing task for MRI. Several denoising methods have been proposed for MRI images to reduce noise and improve the contrast between regions: anisotropic diffusion filtering and independent component analysis [5]. Various denoising algorithms were evaluated for their

effectiveness in brain tumor segmentation. The findings revealed that while these algorithms reduced image noise, many of them introduced artifacts that had a detrimental impact on the segmentation process. The normalization of intensity is a crucial step in MRI, particularly when classification methods are employed for segmentation. However, this task becomes more challenging in images containing tumors due to confounding effects arising from differences in tumor appearance compared to healthy patient images [4].

#### *Feature extraction*

The most common features used for brain tumor segmentation are image intensity (different tissues have different gray levels) and local image textures (other tumor areas exhibit different textural patterns). They can be calculated according to different strategies. Alignment-based features make use of prior spatial knowledge. Intensity gradients or edge-based elements can evolve a tumor edge contour.

#### *Segmentation*

Typically, brain tumor segmentation methods are broadly categorized into three main types: manual, semi-automatic, and fully automatic segmentation approaches. In addition, there are several segmentation algorithms, for example, region or edge-based method, classification and clustering, classification, and clustering with additional constraints [4].

#### *Post-processing [5]*

### **The method implemented**

The data set consists of the ten images made by the MRI technique (5 images taken on a healthy patient and another five taken on a tumor patient). To highlight tumor development, the first step was to load them into the Spyder growth medium. For this, the OpenCV package is used, calling the `cv2` method. In the pre-processing stage, the images undergo contrast changes using the `convertScaleAbs` function. Next, resizing images is done with the `resize` function, with the resized image, size, and interpolation attributes. This stage also includes the transformation of RGB images into grayscale images. For this step, the `cvtColor` method is called, with the details: image converted to shades of gray, color code `COLOR_RGB2GRAY`. Finally, a Gaussian blur was applied to the image with the function `GaussianBlur` with the attributes: blurred vision, kernel size 5x5, and standard deviation in the x direction (sigma).

The feature extraction stage starts with binarizing the images in a narrow, well-defined range of values. This is done with the `threshold` function, which has the attributes: binarized idea, truncation interval, and binary method.

Its purpose is to delimit the range of values representative of the intensity of the tumor from the rest of the brain tissue because the tumor has much lighter shades compared to the rest of the brain surface. First, two erosion iterations are performed to eliminate small noise areas, followed by another two dilations performed with the `erode` and `dilate` functions. Next, the tumor's contour is identified on the support image using a `findContours` process, with the attributes: copy of the binarized, eroded, and dilated image, the choice of `EXTERNAL` and `SIMPLE` contour type. The `EXTERNAL` type of contour identifies an external contour, which, together with the `SIMPLE` attribute, identifies a contour with a minimum number of points to reduce the memory used.

The next step extracts the tumor contour with the `grab_contours` function. To differentiate healthy patients' images from those of pathologies, the next step is performed only if a tumor outline is found. This phenomenon is checked using a `try` block.

The contour whose area is maximum is chosen using the `max` function with the attributes: list of shapes and sizes under the contour. The extreme points of the outline are found by finding the minimum and maximum values on the vertical and horizontal, respectively, and put in 4 tuples.

For the segmentation step, the contour found on a resized image is added using the `drawContours` function, which has the attributes: copy of the resized image, maximum area contour, `-1` indicating to take the entire contour, line color, and thickness. To highlight the contour maxima,

the four endpoints are added using the "circle" function with the attributes: the image to draw on, the coordinates of the center of the circle, the radius and color of the circle, and the option to fill the contour. The final step of the segmentation is represented by cropping the image by choosing all the points between the edges of the contour.

If no outline is found in the "try" block, it goes directly to the "except" block intended for images that do not show tumor conditions.

## **Results**

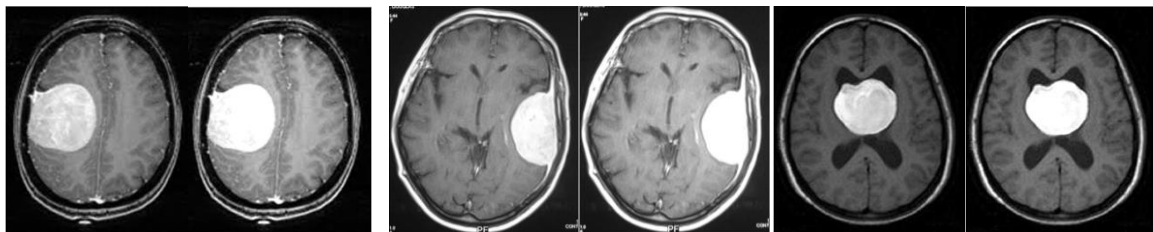
The project results are presented in stages through analyzed images captured during the changes.

### *Pre-processing*

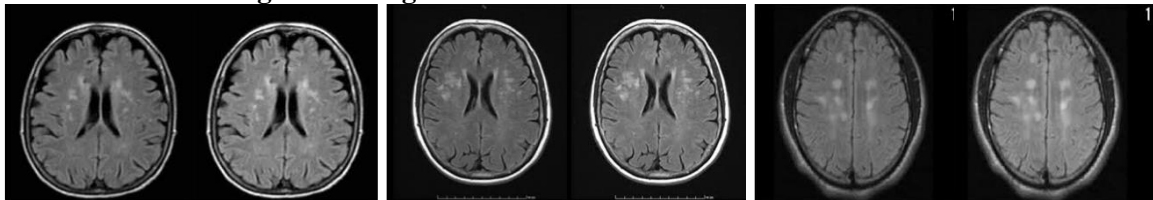
The image contrast is changed according to equation (1), where  $\alpha = 1.25$  and  $\beta = 0$  were chosen.

$$g(i, j) = \alpha \cdot f(i, j) + \beta \quad (1)$$

Following the application of the contrast, a highlighting of the tumor area is observed in the case of the images belonging to the patient with pathological conditions. And in the case of the images of the physiologically healthy patient, the application of contrast does not produce significant changes.



**Figure 1. Images with a tumor before and after contrast**



**Figure 2. Images without tumor - before and after contrast**

After changing the difference, the new images are brought to the size of (255, and 255) and are interpolated using the "INTER\_CUBIC" method. For further processing, they are converted to grayscale images using "cvtColor". A Gaussian blur is applied to remove high-frequency noise.

### *Features extraction*

In this step, the binarization of the images is created by choosing the value 195 as a cutoff range. So, all values below 195 take the value 0 (black), and all above 195 become 255 (white). The erosion was carried out twice to eliminate the noise, followed by a series of 2 dilations. Next, the tumor contour is extracted, and the tumor tissue is well-defined on the images.

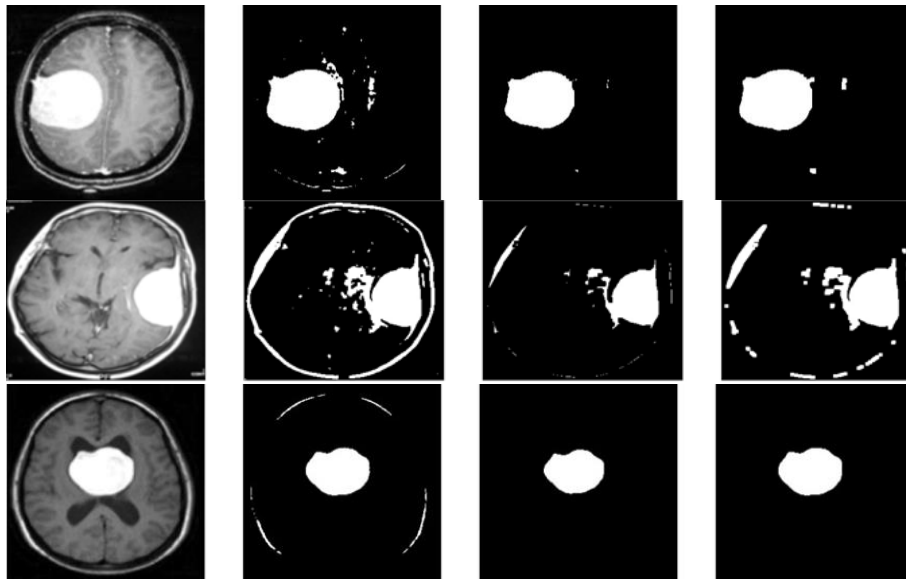


Figure 3. Images with tumors - before and after binarization, erosion, and dilatation

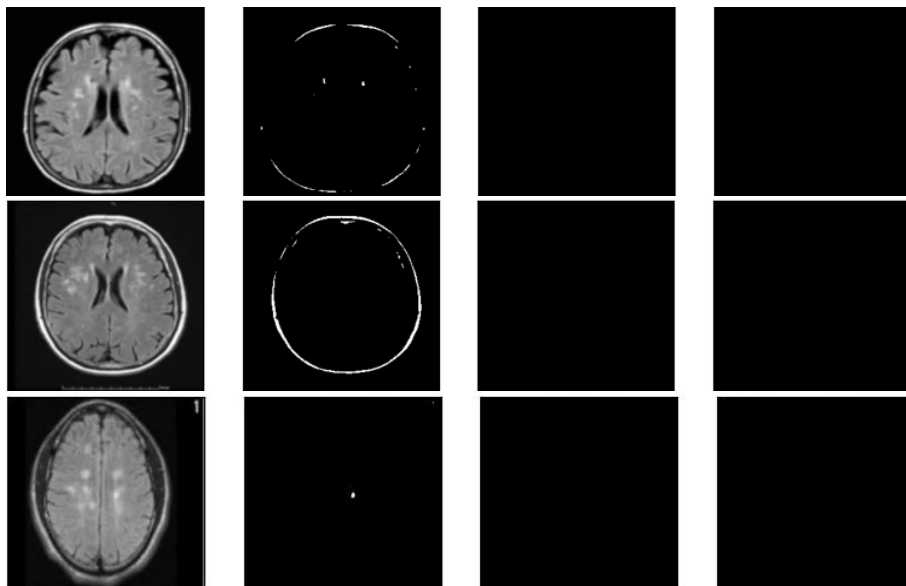


Figure 4. Images without tumors - before and after binarization, erosion, and dilation

*Segmentation stage*

In the segmentation stage, the algorithm aims to extract tumors in the context of images belonging to pathological cases. If they do not contain tumor areas, the original image is returned. Figure 5 shows the four stages from the original image to find the tumor which can be observed. After this step, the extreme points of the contour are established, following the cutting of the images, strictly including the identified tumor.

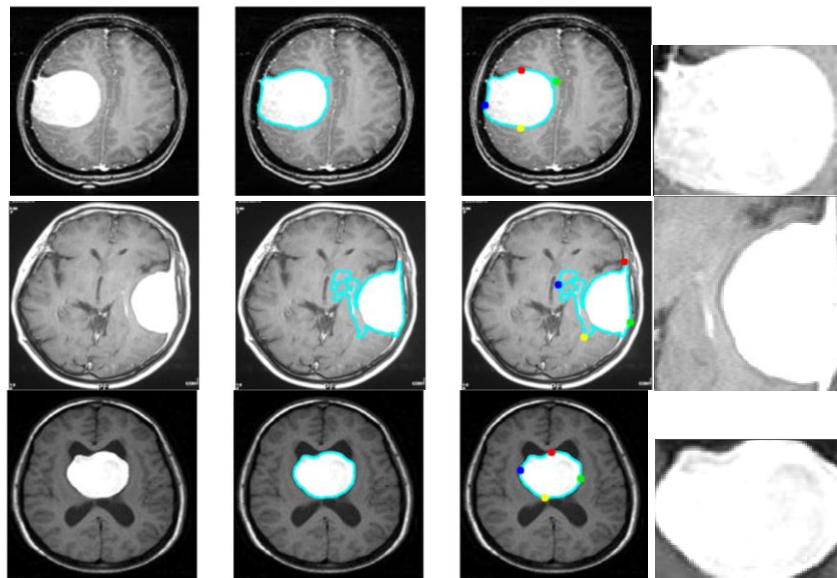


Figure 5. Images with tumors - identification

### Conclusions

In the supporting project, data obtained by the MRI technique is analyzed, the subjects being healthy patients or patients presenting a brain tumor. The analysis approaches the classification of images in health diagnosis, or tissue showing tumor developments, through the segmentation technique, with the four steps used in this algorithm as a model. The project addresses the first three steps, so the pre-processing, feature extraction, and segmentation steps are performed. Finally, the results were displayed, in graphic form, based on images generated using the "matplotlib. pyplot" library. These representations help to quickly highlight the presence of tumors by extracting them based on intensity and edges because tumors appear in lighter gray tones in the original MRI images.

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