

Abstract

We will work on brain tumor detection using several sample images without using learning-based method (machine learning, deep learning).

As we know, medical image processing is one of the most important tasks in computer vision. Image processing for disease detection, such as tumor identification, is challenging without using deep learning and machine learning methods. In this section, we focus solely on using filters to first detect and then locate tumors. This process is part of the preprocessing steps and even algorithms used in image processing and classification.

There is a technique called augmentation used in learning methods to prepare images for feature extraction. However, as mentioned, we will focus solely on analyzing a few MRI images.

Tumor segmenting

Here, we analyze given MRI images to determine whether they contain a brain tumor.

Binary thresholding is commonly used to simplify images and focus on specific areas (such as edge detection or regions with certain brightness levels). In this method, pixel values are divided into two states of zero and one (or black and white). Binary thresholding is useful for detecting specific features or areas of interest, like tumor regions, as it highlights differences more clearly. However, this method may lose a lot of details and is less suitable for finer analyses.

Since our goal here is to detect and locate the tumor region, we applied binary thresholding by first converting the images into binary format. Next, we split each image in half. To remove as much of the shared borders in the image as possible, we subtract one half from the other. This approach is not entirely accurate because our images are not perfectly symmetrical. In the function, you can uncomment the relevant line to see the result of this subtraction.

After completing this step, if an area exceeds a specific threshold with pixel values of 255, the function will likely conclude that the image contains a tumor.

One example of the output is:

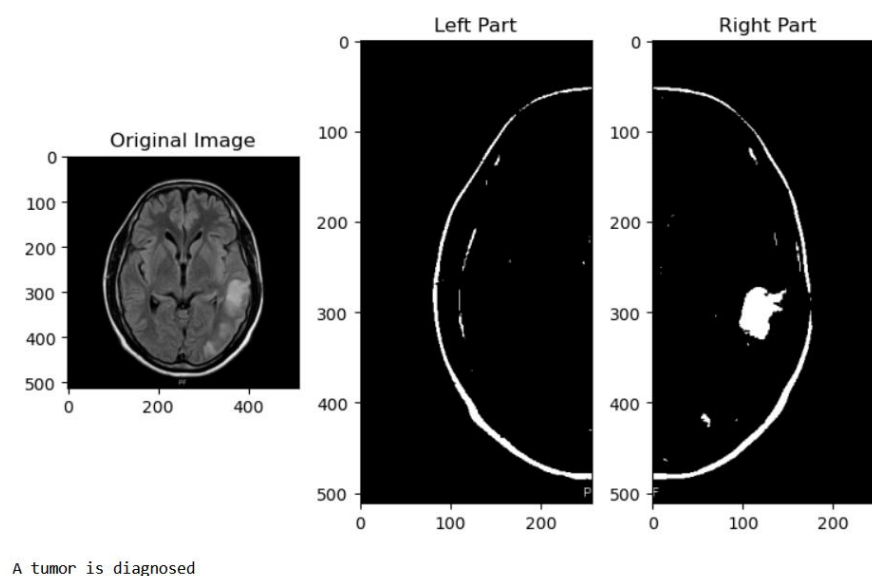


Figure 8 (Output example of tumor diagnosing)

Here, we used three threshold. One of them is for binary thresholding of the image. Since we used a custom function, we can adjust the threshold value ourselves, allowing flexibility because the color of brain cells varies in this dataset. The third threshold is used to determine the area of contiguous white pixels to detect a tumor.

There is another threshold method we did not use. This threshold involves calculating the histogram of the binary image. We compute the histograms of the two halves of the image and then find the difference between them. If the difference exceeds a certain threshold, we can then determine that the image likely contains a tumor.

Now we turn to tumor segmentation. In this section, we also use the binary method.

First, we perform preprocessing on the image. There are various filters available for this purpose, such as median blur, Gaussian blur, etc., and here we use the Gaussian blur method. This filter is

based on the Gaussian distribution. The fundamental concept of the filter involves using a kernel, which is a matrix of odd size. The larger this filter is, the more blurred the image will be, resulting in fewer details and reduced noise; however, this also makes the image processing heavier and leads to the loss of finer details. Each element in this kernel has a specific weight assigned to the surrounding pixels of the central pixel when the filter is applied. Essentially, it is this kernel that determines the new pixel value by multiplying and summing the values of the surrounding pixels.

After applying this filter, we convert the image to binary. Then we use morphological operations. For this purpose, we create another unit kernel. This kernel is used for the opening operation, which is employed to remove noise. This process eliminates small noise artifacts, leaving only the main and larger regions in the image. Additionally, by setting iterations equal to 2, this operation is repeated twice to have a greater impact on the image.

Finally, we establish a threshold to identify regions that contain more or fewer white pixels than a specified number. We outline these regions to indicate the tumor areas. An example of this is shown below.

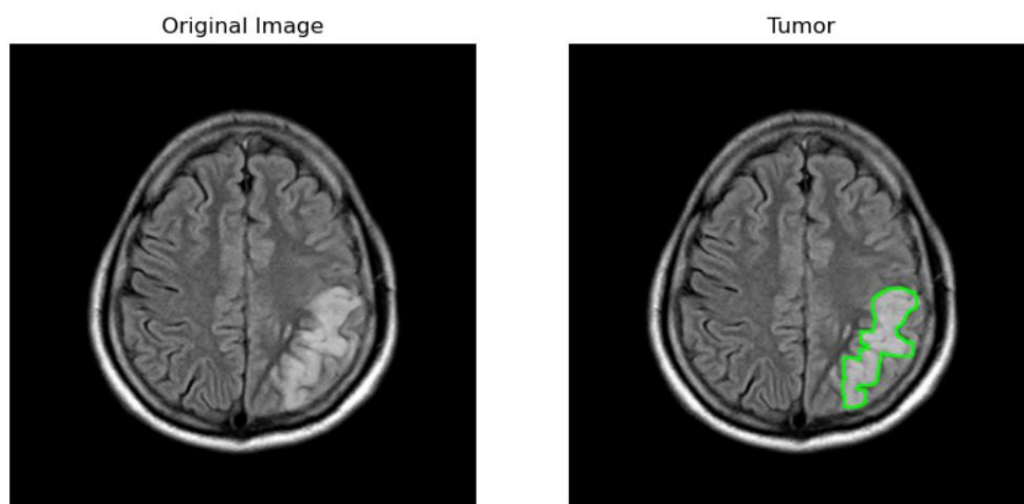


Figure 9 (output example of segmenting tumor)

The output of all images can be found in Part5/output.