

Medical image categorization combining image segmentation and machine learning

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Abstract

The death rate has increased in recent years due to the rising prevalence of encephaloma tumors across all age brackets. Because of their complex structure and background noise, tumors are difficult to detect in medical imaging and require a great deal of time and effort on the part of professionals. This is crucial since locating the tumor early on is key to successful treatment. Scans can detect and even forecast the presence of cancer at a variety of stages. A combination of these scans with segmentation and relegation techniques can aid in a rapid diagnosis, saving valuable time for the treating physician. Due to the complex nature of tumors and the gradual evolution of noise in MR imaging data, physical tumor identification has become a complicated and time-consuming process for medical professionals. Hence, early detection and localization of the tumor site is essential. Using segmentation and relegation techniques, medical imaging can pinpoint cancer tumors at multiple stages for a precise diagnosis. This study presents a machine learning-based method for automatically segmenting and labelling MRI scans of the brain to help in the detection of malignant growths. In addition, this framework employs a number of machine learning algorithms for tasks including image pre-processing, segmentation, feature extraction, and classification, including Nave Bayes, Nearest Neighbours, and Decision Table.

Keywords— Image Segmentation, MRI Images, Machine Learning, Brain Tumor, Feature Extraction.

I. Introduction

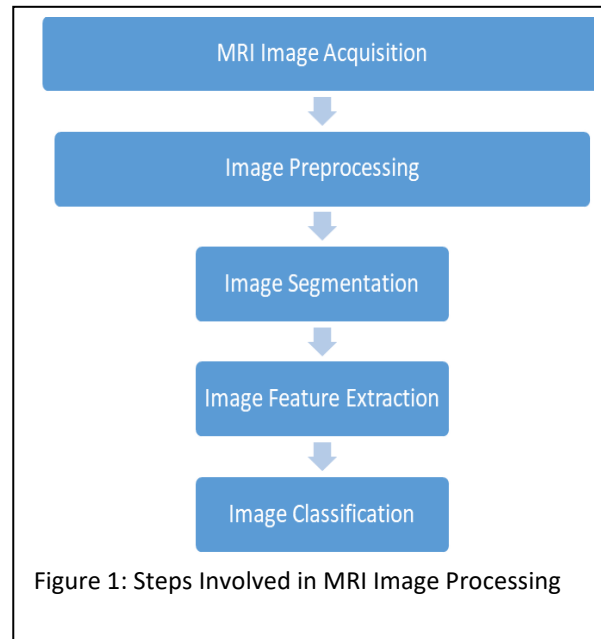
The rising incidence of encephaloma tumors in people of all ages has contributed to a rise in mortality. According to common knowledge, the presence or absence of signs of check growth in the encephalon is diagnostic of a malignant tumor. Tumors are classified as malignant when they exhibit a "non-uniform" growth pattern, indicating the presence of cancerous cells. According to the American Society for Clinical Pathology, benign tumors consist of regularly arranged, non-malignant cells. Tumors are notoriously challenging to visually

recognize in medical imaging due to their intricate structure and underlying noise. Thus, it is crucial to identify the tumor's precise location at an early stage. Employing medical scans, which can be paired with segmentation and relegation methods to provide an early diagnosis, allows for the tracking and prediction of malignant areas at varying levels. [1] [2]

It is a difficult and time-consuming task to segment an MRI image in order to identify brain tumor tissues. Medical photos typically feature a jumble of structures that can only be identified and clinically diagnosed with the aid of segmentation. The radiologist's manual evaluation of the tumor in additional photos increases the likelihood of an incorrect diagnosis. In order to reduce the potential for error, medical image processing and classification had to be automated. [3]

The field of digital image processing encompasses a wide variety of disciplines, such as medicine, microscopy, astronomy, computer vision, and geology. Scientific and medical investigation involve a number of stages. An essential first step, medical imaging paves the way for automated picture segmentation and CAD design. Human-machine interaction is particularly useful for improving surgical treatment planning and accuracy. The method includes the creation of imaging devices and the execution of a treatment strategy, both of which should prove effective in medical diagnosis. The human anatomy was seen in sections using a wide range of diagnostic tools. The most common non-invasive imaging techniques for obtaining images of the human body are magnetic resonance imaging (MRI) and computed tomography (CT). [4] [5]

Over time, abnormal tissues can accumulate to form a tumor in the brain. Despite the fact that these abnormal tissue types interrupt normal tissue development, growth, and death, they nonetheless cause the tissue to multiply and increase at an unchecked rate, these abnormal tissue types are themselves abnormal. Brain tumors can be detected by medical imaging techniques like CT and MRI, with CT being the more common of the two. Magnetic resonance imaging (MRI) and computed tomography (CT) scans are the gold standards for diagnosing and identifying brain malignancies. Radiologists and doctors can employ MRI and CT scans, which provide three-dimensional (3D) images, to diagnose a brain tumor. An expert can save time and get more reliable results if the analysis is performed by a computer, which can recognize the characteristics of a brain tumor and define it in a three-dimensional image. One of the many benefits of automated or semi-automated tumor segmentation is that it frees up medical practitioners to focus on other aspects of patient care planning. [6]. Figure 1 below depicts several stages in the MRI image processing pipeline.



Because of things like background noise, non-brain tissues, and the presence of a bias field, full MRI images cannot be processed immediately. We can use a variety of pre-processing techniques to solve this issue. After the photographs have been properly processed, the next step is the time-consuming pre-processing step of deleting any unnecessary elements. The first step in this direction is known as "image pre-processing" [4]. Grayscale conversion, noise reduction, and image reconstruction are all examples of pre-processing processes. In pre-processing, grayscale conversion is commonplace [1]. After a grayscale image is created, various filtering techniques are used to get rid of the unwanted noise. To get a good result from using the database photographs, noise cancellation is essential. There are major problems with the present approaches to noise reduction.

Segmentation: The scanning technique resulted in several large pictures, which should be easily identifiable by trained medical personnel given enough time. This is a major development. It's crucial in clinical diagnosis, and it's also employed in pre-op preparation and CAS.

Known as "feature extraction," this process entails assigning a feature vector to each character in order to better predict its eventual identity. Both of its ambitious goals—creating a consistent feature set across several occurrences of the same symbol and extracting features that improve the recognition rate with the fewest number of components—are notoriously challenging to realize. Existing feature extraction techniques were unable to select the most crucial characteristics for additional diagnostic work.

In data classification, each piece of information is placed into one of a predetermined number of groups. Differentiating healthy brain tissue from cancerous tissue in images is a frequent use of this method. One of the primary purposes of classification is to correctly guess the intended class for each data point. This is done by classifying images of the brain as either showing a tumor or not. The effective categorization of MRI images is currently undervalued, hence our proposed effort will focus heavily on this step where other methods fall short.

II. LITERATURE REVIEW

1-Preprocessing Techniques

Image processing can be used to examine brain scans. Magnetic resonance imaging (MRI) is used in a wide range of medical settings, both for diagnosis and treatment. The following procedures constitute image pre-processing: less background noise and fewer artifacts after processing. With this picture, we should be able to spot tumors with ease. Suryavamsi et al. [7] offered three approaches for enhancing MRI brain imaging with astrocytoma: "Histogram Equalization," "Adaptive Histogram Equalization," and "Brightness-Preserving Dynamic Fuzzy Histogram Equalization." The effectiveness of these three approaches has been measured quantitatively. MSE, PSNR, and RMSE are all measures of precision.

The MRI data must first be cleaned of unwanted noise before the desired signal can be extracted. Independent component analysis and nuisance regression are utilized in a variety of pre-processing steps. De Blasi and coworkers employ several LD cleaning procedures on healthy individuals and patients with temporal lobe epilepsy to get rid of non-BO LD signals. Improved temporal properties were measured after each preprocessing step, including SNR and power spectrum density in the idle frequency band (0.01-0.1 Hz). The DMN was found via an inspection of the pre-processing pipeline, which was performed as part of the ICA preparation process. These groups and pipelines were able to more accurately characterize the cingulate cortex's posterior region than did other groups and pipelines.

Improved pre-processing techniques developed by Poornachandra and Naveena allow for accurate glioma tumor separation [9]. Medical imaging for brain tumors has just recently been created utilizing state-of-the-art Deep Learning methods. Researchers with a deeper understanding of brain tumors can detect the disease and provide patients with therapy alternatives thanks to superior segmentation results.

Controversy has arisen about whether or not MR imaging of the brain can be used to detect and segment the anatomy of a tumor. The uniformity of the image makes segmentation challenging. The Region Scalable Fitting method for image segmentation was enhanced by Setyawan Widyarto et al. [10] to incorporate pre-processing prior to a region-based active contour model. Intensity data models are employed in specific regions. In preprocessing, the 2D sigmoid function is imposed at the tumor margin. An additional 2D-sigmoid function was applied during image preprocessing to boost contrasts in the brain MRI scan.

2- Feature extraction techniques

One of the most critical steps in tumor segmentation Extraction of relevant attributes is a crucial stage in tumor segmentation systems. [11] Jui et al. improved the accuracy of brain tumor segmentation by using a feature extraction component that accounts for the compression and distortion of intracranial structures brought on by tumor growth. The LaV area of the brain is distorted in 3D using non-rigid registration and deformation modeling. Classification techniques like k-means can be used to verify and enforce LaV deformation feature data on brain tumor segmentation. The author conducted both quantitative and qualitative analyses, and found the proposed component to be effective.

To diagnose AD using longitudinal structural MR images, Jun Zhang devised an extraction method based on landmarks, eliminating the need for nonlinear registration or tissue segmentation at the application stage. We use a fast landmark identification strategy that can accurately identify landmarks in test images without resorting to time-consuming and inaccurate methods like nonlinear registration or tissue segmentation. We next use these points of reference to characterize the spatial absorption of the brain in terms of broad statistical characteristics and broad longitudinal factors. Using the Alzheimer's Disease Neuro imaging Initiative database, we discovered that our suggested method achieved a classification accuracy of 88.30% for AD and MCI, outperforming other methods in both performance and efficiency. [12]

3- Segmentation techniques

An automatic segmentation strategy using Convolution Neural Networks (CNN) that analyzes the modest 3 x 3 kernels was proposed by Sérgio Pereira et al. [15]. Fewer weights in the network not only aid in preventing over fitting, but also permit the development of more intricate architectures. Although this pre-processing step is not typically used in CNN-based segmentation algorithms, it proved to be extremely successful for brain tumor segmentation in MRI images when combined with data augmentation.

By leveraging the higher resolution images possible with ultrahigh field (7 T) MRI, Jinyoung Kim et al. [16] developed a semi-automatic segmentation method. Edge information from several structural MRI modalities was used to complement each other in this technique. It bridges the gap between susceptibility-, T2-, and diffusion-weighted MRI and presents a novel edge indicator function that is derived from all three. Knowledge of the form and organization of the subcortical structures can facilitate the development of geometric active surfaces. Oversegmentation was punished by a non-overlapping penalty at the borders of nearby structures, which was segmented in a series of iterations.

Antonios Makropoulos et al. [17] propose dividing the brain into 50 different sections from the early preterm period up till term-equivalent age. Here, the structural hierarchy and anatomical constraints are factored into a novel segmentation approach to modeling intensity over the whole brain. In comparison to standard atlas-based methods, this strategy enhances label overlaps for manually referenced segmentations, which is where it truly shines. The results of the experiments reveal that the proposed approach is highly reliable from 24 weeks' gestation to term-equivalent age.

III. METHODOLOGY

Image enhancement is the first step in the pre-processing steps, and it entails performing a set of operations that are required for better subsequent processing. These include histogram equalization to boost contrast (we'll refer to the image as X in this step), followed by linear contrast stretching (the result will be Y) to whiten the image. The state of the pixels in the output image depends on the correlation of the input image with its neighbor similar pixels in the morphology operation. Working on this image is dependent on the shape, size of the structure component, and the number of pixels removed or replaced added.

Various morphological processes use the Dilation and Erosion method to deal with objects within the image. Dilation is a technique that adds pixels to the borders of objects in an image, whereas erosion removes some of the unnecessary pixels from the object borders. The proposed system attempts to scan the image and use these two techniques to extract the white shapes within the image while ignoring the black ones by adding or removing pixels from the shape borders as needed.

The proposed system attempts to scan the image vertically from top to bottom, registering the highest pixel values from each cell region into a specific list before repeating the process horizontally. The final

list now contains all of the necessary information about the objects in the image. This method improves processing efficiency and makes the next step easier to complete. The performance of the classifier chosen has a significant impact on feature selection mechanisms, and vice versa. To obtain robust and powerful classifications, the features must be sufficient to perfectly describe all MRI subgroups while also keeping these MRI isolated from one another. The system we propose generates an N-dimensional table of texture, shape, and intensity features are all represented by feature vectors. After extracting the significant features from each MRI, data vectors are named after that feature [24][25][26][27][28]. Following that, the feature vectors are converted into a collection of attributes used by the classifier procedures. To deal with the WBC identification process, various classification techniques are used. The authors begin by presenting the criteria (Mean absolute error, Relative absolute error, Correlation coefficient, Root-mean-square deviation, and Root relative squared error) as well as the sensitivity, accuracy and specificity used to generate the output[29][30][31][32][33][34]. The correlation coefficient, which measures the firmness and trend of a linear correlation, is the first criterion. involving two variables This criterion's values range from 0 to 1. The closer the absolute value is to one, the more solid the relationship. Zero indicates a poor relationship between the variables.

A small procedure was written to create a data set. For the results from each shape features, statically features and texture features are extracted and written inside a Microsoft excel file. As a result, a featureset of 22 features is created and is considered as an input to the classification systems.

After extracting the significant feature from the MRI brain tumor images, a new data vector called Feature Vector is created. The next step is a transformation of the feature vector into a set of classes by using a device or algorithm called Classifier [33]. The classification technique is a systematic approach to design classification models from an input data set. In this paper, the focus will be on Naïve Bayes, Nearest Neighbours, and Decision Table algorithms which are different techniques to solve the Brain Tumor classification problem. Each technique adopts a learning algorithm to identify a model that best fits the relationship between the feature set and class label of the input data. The procedure of the classification algorithm is shown in figure 3.

There are a total of 22 input characteristics, which we refer to as the features vector. The features that are deemed important to represent an image of MRI image are retrieved and gathered in the vector. Neural networks are then used to solve the Brain tumor classification problem by converting the features vector into a set of classes. This method uses a learning algorithm to choose a model

that most closely matches the relationship between the input data's feature set and class label. Input Layer the size of the input features determines how many neurons are present in the input layer. In this case, the author tested the 22 features we extracted for each.

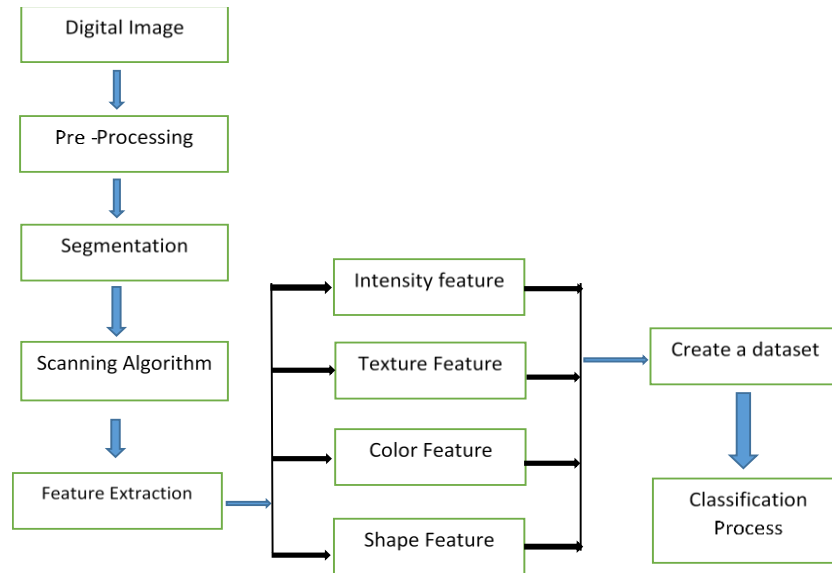


Figure 2 Flowchart of proposed method

IV. RESULT ANALYSIS

Our group has evaluated the Harvard Clinical College of Architecture and Planning's "Dataset-160" and "Data-255" For this study, we examined datasets 160, 255, and 35, which contained, for example, 20 "Normal" MR256x256 axial aircraft encephalon images and 140 "Abnormal" images. In "Dataset-265," Irregular Encephalon Magnetic Resonance metaphors reflect eleven separate symptoms and connect to "Dataset-160" via ties between the aforementioned seven illnesses. Cases of Huntington's disease, Alzheimer's disease, and sarcoidosis are among those in "Dataset-160," along with agnosia, glioma, meningioma, Pick's infection, and sarcoma. Dataset-255 documents four rare diseases, including herpes encephalitis, chronic subdural hematoma, and several types of sclerosis. "Dataset-255". The ratio of accurately anticipated observations to the total number of observations is known as accuracy, and it is the most straightforward performance metric. One would reason that since our model is quite accurate, it must be the best. Accuracy is an excellent indicator, but only when the number of false positives and false negatives in a dataset are about equal. As a result, different

metrics will have to be considered as you assess your model's efficacy.

The precision of a prediction is the percentage of positive observations that were actually positive. This measure provides a response to the question, "How many of the passengers who were marked as having survived actually did survive?" The rate of false positives is low when accuracy is high.

Recall (Sensitivity) is the proportion of true positives over all observations. How many passengers did we actually label? This is the question we need to answer to find out how many people made it off the plane alive.

Known as a "weighted average" of "Precision" and "Recall," the "F1 Score" measures overall model performance. To that end, this score considers the possibility of both false positives and false negatives. F1 is usually more valuable than accuracy, especially if you have an uneven class distribution, although it is not as intuitive to grasp. If the price of a false positive or negative is about the same, then accuracy is maximized. Both Precision and Recall should be considered if the costs of false positives and false negatives differ significantly.

Based on the result of the F1 score metric shown in figure 4 of the mentioned method shown that the Naïve Bayes is better than other methods. The accuracy, Recall, and precision of the proposed methods shown in the figure 5, 6, and 7, and it show the Naïve Bayes also better than other mentioned methods.

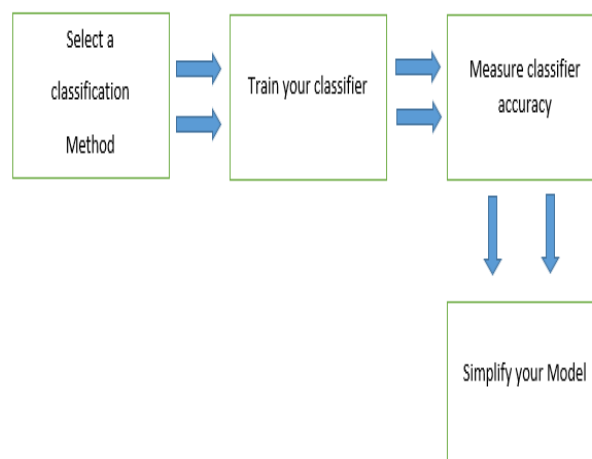


Figure 3 The block diagram of the classification process

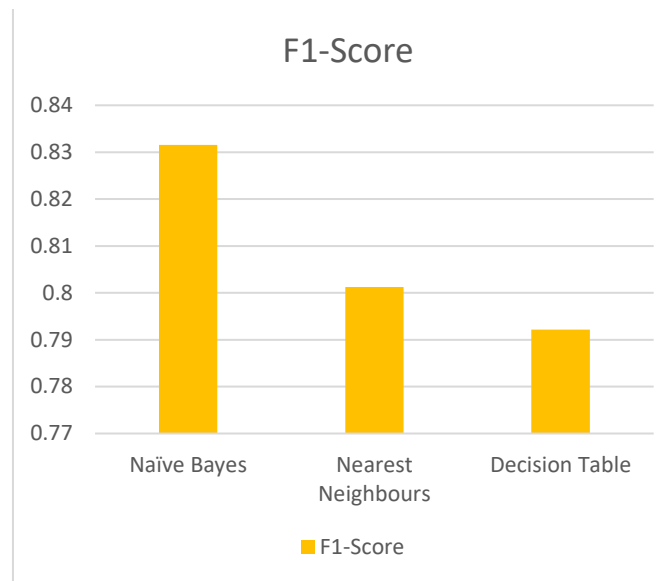


Figure 4: F1 score of Naïve Bayes, Nearest Neighbors, and decision tree.

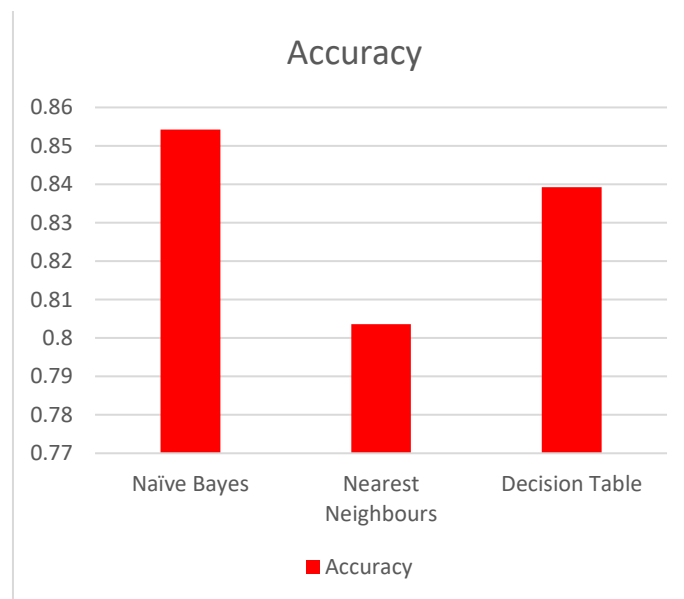


Figure 5 Accuracy of Naïve Bayes, Nearest Neighbors, and decision tree.

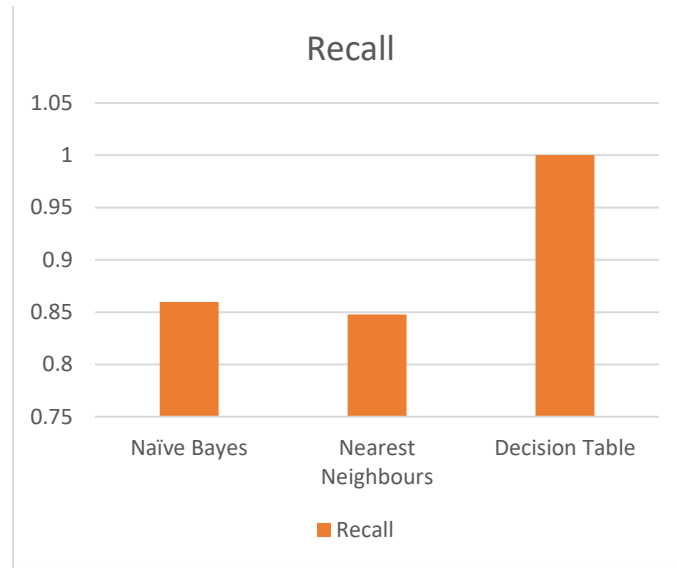


Figure 6 Recall of Naïve Bayes, Nearest Neighbors, and decision tree

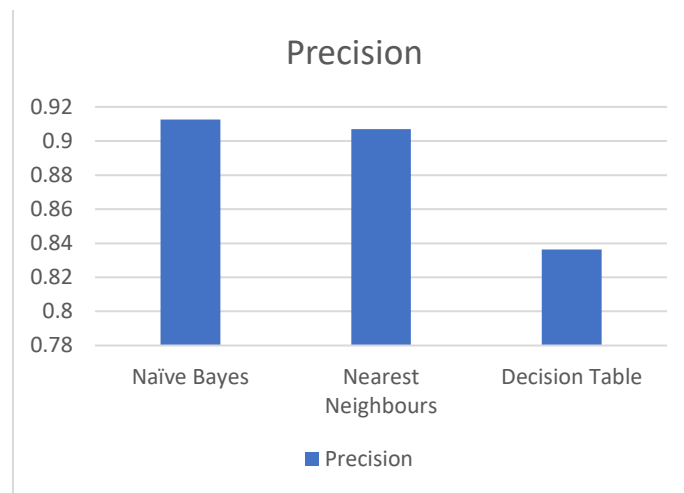


Figure 7 Precision of Naïve Bayes, Nearest Neighbours, and decision tree.

V. CONCLUSION

The fatality rate from encephaloma has risen as the number of tumors has increased across all age ranges. Physical tumor detection is difficult and time consuming for clinicians because to the tumors complexity and the involution of noise in MR imaging data. Therefore, it is essential to find the tumor and pinpoint its location as soon as possible. Utilizing segmentation and relegation methods, medical imaging can be used for the early detection of malignant tumors at varying stages. When it comes to detecting brain tumors,

our approach employs machine learning to analyse MRI scans and label suspicious areas. The pre-processing, segmentation, feature extraction, and classification of images are all handled by the Naive Bayes, Nearest Neighbours, and Decision Table algorithms included in this framework. According to our experiments, the Naive Bayes classifier is the most effective method for analysing our dataset. During the identification phase, morphological analysis techniques are done to clean up the image and highlight key details (image intensity, shape, texture, and color). The authors hope to deepen their investigation into this topic by investigating an additional approach to medical image classification in the future.

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