

Effective classification of medical images using image segmentation and machine learning

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Abstract

Because of an increase in the frequency of encephalon tumors in each age group, the mortality rate has grown in recent years. In medical imaging, tumors are hard to see because of their complicated structure and noise, which makes it hard and time-consuming for specialists to find them. It is very important to find and pinpoint the tumor's location at an early stage, so this is very important. Medical scans can be used to look for and predict cancerous spots at different levels. These scans can be combined with segmentation and relegation methods to help doctors make an early diagnosis, which can save a lot of time. Physical tumor identification has become a challenging and time-consuming process for medical practitioners due to the intricate structure of tumors and the involution of noise in magnetic resonance (MR) imaging data. As a result, detecting and pinpointing the site of the tumour at an early stage is critical. Medical scans can be used in conjunction with segmentation and relegation procedures to deliver an accurate diagnosis at an early stage in cancer tumour locations at various levels. This research offers a system based on machine learning for segmenting and classifying MRI images for brain tumor identification. The K* classifier, Additive Regression, Bagging, Input Mapped Classifier, and Decision Table algorithms are used in this framework for image preprocessing, image segmentation, feature extraction, and classification..

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1 Introduction

Due to the increase of encephaloma tumor's throughout all age groups, the mortality rate has increased. Conventional knowledge says that unchecked growth in the encephalon classifies tumors as either benign or malignant. Cells that are cancerous have multiplied in tumors labeled "malignant" because of their "non-uniform" growth pattern. Regularly arranged and non-malignant cells make up benign tumors, according to the American Society of Clinical Pathology. In medical imaging, tumors are difficult to physically identify because to their complicated structure and inherent noise, which makes it difficult and time-consuming for specialists. Detecting and pinpointing the tumor's

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location at an early stage is thus very important. It is possible to follow and predict cancerous spots at various levels by employing medical scans, which may be combined with segmentation and reclassification methods to offer an early diagnosis. [17, 6]

Identification of brain tumor tissues requires the time-consuming and challenging job of segmenting an MRI image. With the help of segmentation, it is possible to identify and diagnose clinically the structures that are often muddled in medical images. With more photographs, the radiologist's manual examination of the tumor might lead to an inaccurate tumor diagnosis. To eliminate the chance of human mistake, an automated approach was necessary for the analysis and reclassification of medical pictures. [16]

A wide range of subjects are included in the study of digital image processing, including medicine, microscopy, astronomy, computer vision, and geology, to name just a few. There are several steps to the process of scientific and medical research. Medical imaging is a critical step since it enables the automated segmentation of medical images and the creation of computer-aided designs. Through the use of human-machine interaction, they help in particular to enhance surgical treatment planning and precision. Developing imaging devices and implementing a treatment plan are two parts of this method that aim to give useful diagnostic tools in the medical field. Segment pictures of the human anatomy were created using a variety of medical instruments. MRI and computed tomography (CT) are the two most often utilized noninvasive imaging modalities for capturing images of the human body. [15, 2]

To develop a brain tumor, aberrant tissues must pile up over time. While normal tissue formation, growth, and death are disrupted by these aberrant tissue types, these abnormal tissue types cause the tissue to grow and proliferate at an uncontrolled pace. Medical Imaging (MR) modalities, including CT and MRI, are used to detect brain tumors, and CT is the most often employed. When it comes to diagnosing and identifying brain tumors, CT and MRI are the two most often employed procedures, respectively. There are three-dimensional (3D) pictures that physicians and radiologists use to identify a brain tumor in MRI/CT scans. If the analysis is done by a computer, for example, the computer detects the features of a brain tumor and defines it in the 3D picture, which reduces the time spent by the expert and provides more consistent findings. There are several advantages to using this kind of automated/ semi-automated tumor segmentation, which helps human professionals plan patient care while they concentrate on other activities [21]. Various steps involved in MRI image processing are shown below in Figure 1.

Because of noise, non-brain tissues, bias field, and other factors, complete MRI pictures are not ready for processing right away. Different pre-processing strategies are available to us to deal with this particular problem. Pre-processing is a time-consuming process that involves removing all of the unneeded components from the photos after they have been successfully processed. Image pre-processing [15] is the first stage in the process of achieving this. Pre-processing includes operations such as image conversion to grayscale, noise removal, and image reconstruction, among others. A popular pre-processing technique is to convert an image into grayscale [17], which is the most prevalent pre-processing technique. After the image has been converted to grayscale, the excess noise is eliminated with the use of several filtering methods. After collecting the photos from the database in order to achieve an effective outcome, the process of removing the noise becomes critical. When it comes to reducing noise from current methods, there are severe flaws.

Segmentation: Large images were produced throughout the scanning process, and it is expected that clinical professionals will be able to manually identify these photos in a fair amount of time. It is an important step. It plays a vital role in clinical diagnosis, and it is also used in pre-surgical planning and computer-assisted surgery procedures.

Feature Extraction: This method is known as feature extraction, and it involves representing each and every character with a feature vector, which is then likely to become its identity. Its goals are to extract the features that optimize the recognition rate with the fewest amount of components while also creating the same feature set for several instances of the same symbol, both of which are difficult to achieve. For further diagnosis, current feature extraction systems were unable to choose the most important features for future investigation.

Classification: It categorizes each and every item in a batch of data into one of a preset set of classes or groupings of items. A common application for this approach is to discriminate between normal and malignant brain pictures. The basic goal of classification is to accurately anticipate the target class for each case in the data. To accomplish this, it divides brain pictures into two categories: tumors and non-tumors. Because present approaches do not place a strong emphasis on effective categorization of MRI images, our proposed effort will place a strong emphasis on this phase.

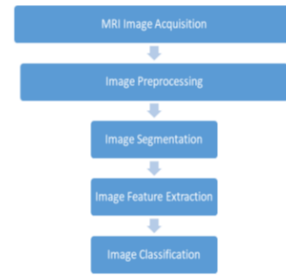


Figure 1: Steps Involved in MRI Image Processing

2 Literature Review

2.1 Preprocessing Techniques

Brain pictures may be analyzed via image processing. Doctors use Magnetic Resonance Imaging (MRI) in a variety of diagnostic and therapeutic procedures. Pre-processing a picture entails the following steps: An improvement in noise reduction and removal of artifacts. This image should make it simple to locate tumors'. For astrocytoma-related MRI brain images, the Suryavamsi et al. [22] team proposed three methods: "Histogram Equalization," "Adaptive Histogram Equalization," and "Brightness-Preserving Dynamic Fuzzy Histogram Equalization." These three methods have been verified and their results computed using performance metrics. MSE), PSNR, RMSE.

Background noise must be eliminated from MRI data before the required signal can be retrieved. A number of pre-processing processes rely on the usage of nuisance regression and independent component analysis. De Blasi and her colleagues eliminate non-BO LD signals from healthy people and patients with temporal lobe epilepsy using a variety of LD cleaning processes. All preprocessing processes evaluated enhanced temporal characteristics, such as SNR and power spectrum density in the resting-state frequency range, relative to data that was simply preprocessed (0.01-0.1 Hz). As part of the pre-ICA procedure, the pre-processing pipeline was inspected in order to locate the DMN. Compared to other pipelines and groups, these pipelines and groups were able to better characterize the posterior region of the cingulate cortex.

Poornachandra and Naveena's enhanced pre-processing methods can efficiently segregate glioma tumors' [20]. Tumors in the brain Medical Imaging has just recently been produced using cutting-edge Deep Learning techniques. Thanks to superior segmentation results, researchers with a greater understanding of brain tumors are better able to detect the ailment and give treatment options to patients who have been diagnosed with it.

The use of a brain MR imaging to detect and segment the tumor's anatomy has sparked a lot of debate. Image segmentation is difficult because of the image's consistency. Setyawan Widyarto et al. [24] improved the Region Scalable Fitting technique for image segmentation to include pre-processing before a region-based active contour model. In certain locations, models using intensity data are used. Preprocessing enforces the 2D-sigmoid function at the tumor boundary. In the pre-processing steps of the brain MRI picture, an extra 2D-sigmoid function increased the contrasts.

2.2 Feature extraction techniques

One of the most critical steps in tumor segmentation systems is the extraction of important properties. [7] To improve brain tumor segmentation accuracy, Jui et al. developed an upgraded feature extraction component that takes into account the link between intracranial structural deformation and compression as a consequence of brain tumor expansion. Non-rigid registration and deformation modeling are used to distort 3D volumetric pictures in the LaV region of the brain. LaV deformation feature data on brain tumor segmentation may be confirmed and enforced using frequently utilized classification methods, such as k-means in a quantitative and qualitative examination of the proposed component, the author found positive results.

Nonlinear registration or tissue segmentation are not required in the application stage of the extraction approach developed by Jun Zhang landmark-based feature for AD diagnosis using longitudinal structural MR images. For testing pictures, we employ a rapid landmark detection approach that does not need any nonlinear registration or tissue segmentation to discover the landmarks quickly and reliably. Based on these landmarks, we next define the brai's structural absorption in spatial terms using high-level statistical characteristics and contextual longitudinal

variables. 88.30% classification accuracy for Alzheimer's disease and MCI was found in the Alzheimer's Disease Neuroimaging Initiative database using our proposed approach, which is superior in performance and efficiency. [26]

This is a comprehensive, automated breast CAD system developed by Gabriele Piantadosi and his colleagues to aid in the detection of breast cancer. In a design given by Michael Osadebey and his colleagues, the modules for breast segmentation, motion artifact attenuation, lesions localization, and classification based on their malignancy are included. In order to provide a fair comparison, 42 individuals with proven histological lesions were chosen for cross-validation. There is no need for any human intervention in any of the processing stages of the BLADeS system's breast lesion diagnosis, according to the findings of the studies. [18]

Parallelization of feature extraction using the Gray-Level Co-Occurrence Matrix (GLCM) has been proposed by Hsin-Yi Tsai et al. [23]. Instead of being built and optimized on a single computer, this solution uses a number of GPUs to run the code. When testing on Geforce GTX 1080s with single-precision MR brain pictures and double-precision MR brain images, the proposed approach is more than 25-105 times quicker than its serial equivalent, depending on the size of the ROIs.

2.3 Segmentation techniques

Sérgio Pereira et al. [23] suggested an automatic segmentation approach based on Convolution Neural Networks (CNN) that examines the small 3 x 3 kernels. In addition to helping to prevent over fitting, the fewer weights in the network allow for the creation of a more complex architecture. Despite the fact that this pre-processing step is not typical in CNN-based segmentation approaches, it showed to be quite effective for brain tumor segmentation in MRI images when paired with data augmentation.

Jinyoung Kim et al. [19] introduced a semi-automatic segmentation technique that takes use of the better picture quality provided by ultrahigh field (7 T) MRI. In this method, the complementary edge information from the multiple structural MRI modalities was used. It connects susceptibility-weighted, T2-weighted, and diffusion MRI, and introduces a customized new edge indicator function from these three modalities. Geometric active surfaces are aided in their evolution by prior knowledge of the sub cortical structures' shape and layout. Iteratively, neighboring structures were segmented, imposing a non-overlapping penalty on over-segmentation at their borders.

It has been suggested by Antonios Makropoulos et al. [14] that the early preterm period through term-equivalent age should be divided into 50 distinct brain regions. Here, a unique segmentation approach is used to model intensity over the entire brain by bringing the structural hierarchy and anatomical restrictions into account. This approach differs from traditional atlas-based strategies in that it improves label overlaps in terms of manual reference segmentations. Experiment findings show that the suggested method is very reliable throughout a large range of gestational ages, from 24 weeks gestational age to term-equivalent age.

3 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.

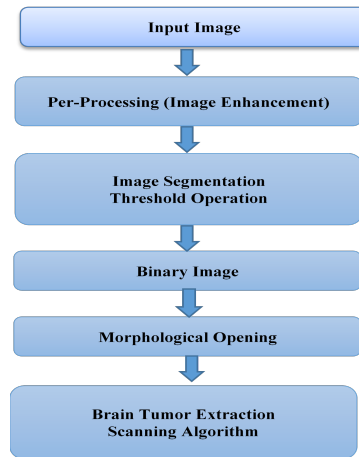


Figure 2: Flowchart of proposed method

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 [3, 12, 10, 1, 25]. 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 [11, 13, 5, 4, 8, 9]. 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 feature set of 22 features is created and is considered as an input to the classification systems.

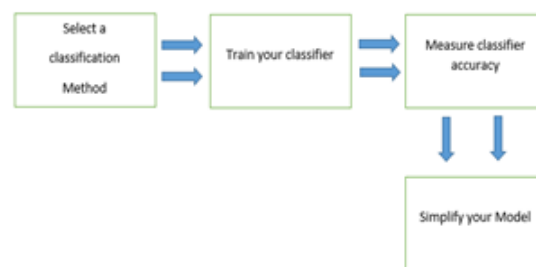


Figure 3: The block diagram of the classification process

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 [8]. The classification technique is a systematic approach to design classification models from an input data set. In this paper, the focus will be on K^* classifier, Additive Regression, Bagging, Input Mapped Classifier, 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.

4 Result Analysis

"Dataset-160 and Data-255" from Harvard's clinical college of "architecture" have been analyzed by our team. As part of our analysis, we looked at datasets 160, 255, and 35, which included "Normal-20" and "Abnormal-140" MR256x256 axial aeroplane encephalon pictures, respectively. The "Dataset-255" Irregular Encephalon Magnetic Resonance metaphors represent eleven distinct symptoms and link to the "Dataset-160" by linking the seven distinct syndromes. "Dataset-160" includes cases of agnosia, glioma, meningioma, Pick's infection, and sarcoma in addition to Huntington's syndrome, Alzheimer's infection, and Alzheimer's sickness. Herpes encephalitis, chronic subdural hematoma, and various forms of sclerosis are among the four novel conditions documented in "Dataset-255". "Dataset-255".

Mean Absolute Error (MAE) is a statistical fault measurement that computes the average of the distances between each pair of real data (Z_t) and fitted predicted data (Z'_t) points. The average of the absolute errors is used to calculate MAE, which is most appropriate when the cost of forecast errors is proportional to the absolute size of the forecast errors. The Root Mean Square Deviation (RMSD) (also known as the Root Mean Square Error (RMSE)) is used to calculate the differences between values predicted by a model and values observed from the real model. These single deviations are referred to as residuals, and the RMSD works to aggregate them all into a single measure of predictive power. RMSD values can be used to distinguish between model performances during a calibration period, followed by a validation period to compare individual model performance to predictive model performance. The square root of the average of each squared error yields the RMSD. The relative absolute error (RAE) is the difference in degrees between the prediction model's absolute deviation and the one obtained by directly speculating the training sample. It varies inversely with prediction accuracy. The RRSE (Root Relative Squared Error) is also inversely proportional to prediction accuracy. The lower the RRSE, the higher the prediction accuracy. The performance comparison of different classifiers is shown in Figure 4 – Figure 8. Five parameters Root Relative Squared error, Root mean square deviation, Correlation coefficient, mean absolute error; Relative absolute error are used for comparative study. Based on the figures presented above the K^* is achieved best result. The second best is additive regression the bagging.

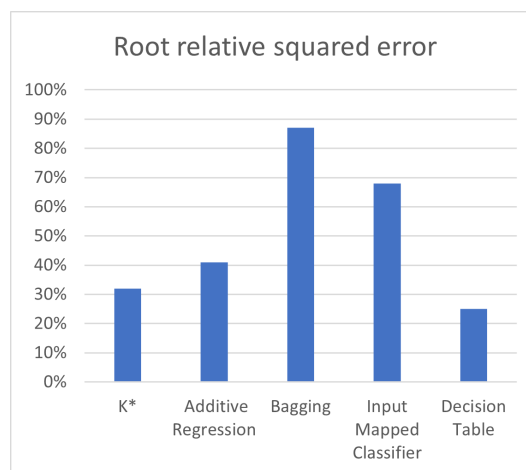


Figure 4: Root relative Squared error

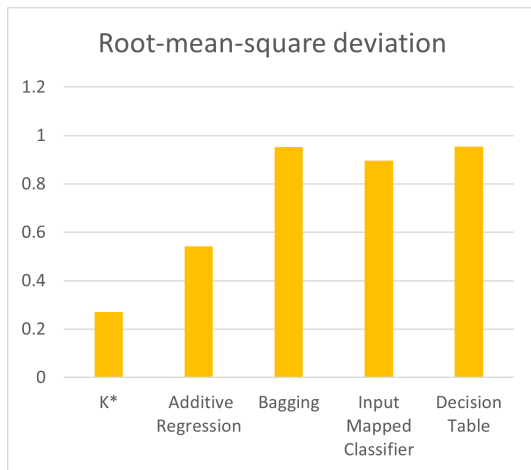


Figure 5: Root mean square deviation

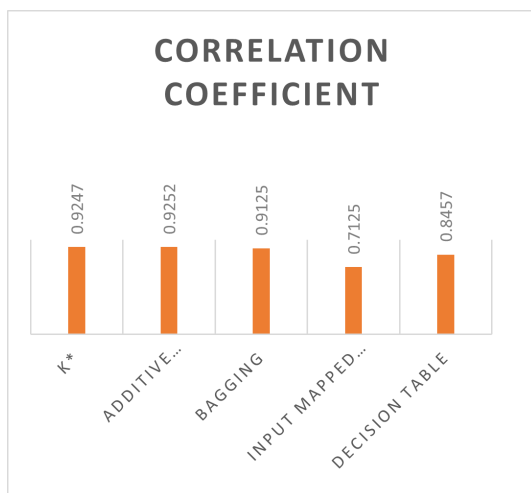


Figure 6: Correlation coefficient

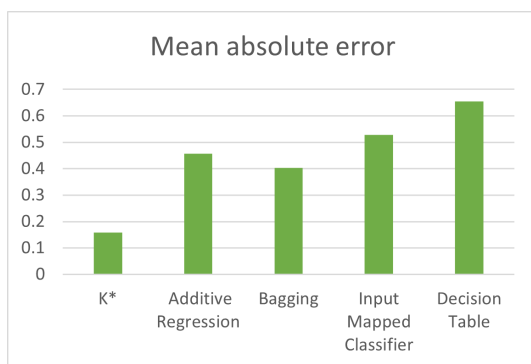


Figure 7: Mean absolute error

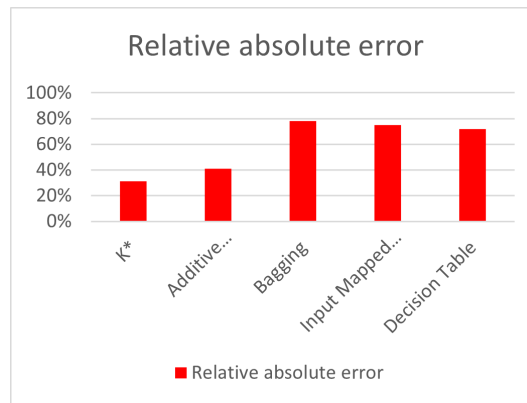


Figure 8: Relative absolute error

5 Conclusion

A rise in the number of encephaloma tumors in each age group has increased the fatality rate. The complex nature of tumors and the involution of noise in MR imaging data make physical tumor detection challenging and time consuming for doctors. As a result, early detection and localization of the tumor is critical. Medical scans can be used in conjunction with segmentation and relegation techniques to enable an early detection of cancer tumors at various levels. Our system uses machine learning to segment and classify MRI images for brain tumor identification. This framework comprises K*, Additive Regression, Bagging, input Mapped Classifier, and Decision Table algorithms for image preprocessing, segmentation, feature extraction, and classification. The experimental findings demonstrate that the K* classifier outperforms all others on our dataset. Morphological analysis operations are used during the identification process to reduce image corrodes and improve important features (image intensity, shape, texture, and color). In the future, the authors plan to expand this research to look into another method of medical image classification.

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