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Implementation of Crossbred Algorithm for Brain Tumor Detection in MRI

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ABSTRACT: In the field of medical image diagnosis advancements in technologies which can process images for a particular cause have undergone massive developments. Machine learning which has directly attributed to increase in the early positive case detections. In this paper we go through a model which can ensemble algorithms and pinpoint the location of a brain tumor with nearly 96provide many other capabilities in diagnosing Brain Tumor. This is an Ensemble Algorithm which can produce better results for the detection in the medical field.

Keywords: CAD, Otsu's method, support vector machine, image process.

Contents

1. Introduction

Researches made in medical image processing have made image processing algorithms essential components of MRI device software. These algorithms perform various tasks, including basic operations like contrast control and edge detection, as well as more complex functions like image segmentation, classification, and brain image diagnosis [2]. The malignancy in brain is regarded as the most perilous and prevalent forms of neoplasia. As a result, investigations have concentrated on enhancing the non-invasive visualization of brain structures through magnetic resonance imaging (MRI). MRI relies on the excitation of protons in water molecules within the human body using radio waves, with subsequent generation of radio energy as a response to this excitation by the protons [1].

In present years, significant studies have been conducted in this field. For instance, a 2019 study used watershed segmentation and K-nearest neighbor (KNN) classification algorithm to detect and classify brain tumors, achieving an accuracy of 89study in 2020 utilized wavelet transformation for feature extraction, applied principal component analysis (PCA) to reduce feature numbers [5], and designed a graphical user interface (GUI) to display processing results. However, this study lacked accuracy calculation and displayed feature values that were not meaningful to end-users. Another study extracted GLCM features using watershed segmentation technique. This got a result of almost 93was that 6 SVM classifiers were used to compare the classification. Though the accuracy was high in this study, the study only utilized thirty six images for training.

The driving force behind our research was the immense volume of medical images that pose challenges for clinicians in identifying all suspicious areas in a timely manner. Our research endeavors aimed to surpass the gold standard set by previous studies through the application of a novel hybrid algorithm incorporating multiple algorithms, resulting in higher accuracy. Our approach relied on a database of 150 cross-sectional MRI images of the brain.

Our methodology encompassed two pivotal stages:

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- Once the data we have is preprocessed, we perform some segmentation after the preprocessed data is enhanced. With the new data being easy for feature extraction, we apply our hybrid classification onto this dataset which has a foundation in three classifiers. This helps us decide on the presence of a tumor.
- Using a novel GUI to help physicians diagnose swiftly because this helps them view tumors which would rather have been missed by the naked eye.

We could accomplish 96.9% accuracy with the above-mentioned method. MATLAB 2018a was used to create the above-mentioned GUI. An additional application of the graphical user interface is that it can be used in teaching new or learning physicians on performing image diagnosis.

2. Methodology

Dataset:

The study analyzed a commonly used dataset, which can be accessed online via Kaggle. The dataset is divided into two subfolders, labeled ”YES” and ”NO,” containing 193 and 157 brain images with tumors and healthy brain images, respectively. To ensure impartiality, the dataset was randomly split into 120 training images, constituting 80representing the remaining 20

Work stages:

The workflow commences with pre-processing and enhancing the images, subsequently followed by isolating the region of interest. From this region we further move on to extracting features. With this step done, we can move on to performing classification. Finally, the GUI we mentioned is deployed to exhibit the outcomes. Fig. 1 illustrates the process in a flowchart.

Preprocessing:

To account for variations in all the images of the dataset like sizes or the clarity, certain preprocessing is required to optimize subsequent processing. The steps involved are:

- The image is converted to grayscale.
- All the images in the dataset are resized to 300 × 300 pixels.
- Subsequently, the black background in an MRI occupies a significant portion of the image but lacks information which can be considered for this study. Therefore, a vertical and horizontal projection-based approach is employed to crop out the non-relevant regions of the image, retaining only the rectangle containing the pertinent information.

This preprocessing helps make sure that the time taken to process these images in the further steps is quite uniform and the removal of the black background prevents unnecessary overhead.

Enhancement

Enhancement of the image occurs in two steps by applying two independent filters to the preprocessed images. They solve two problems:

- Elimination of noise: We utilize the median filter to solve this problem so that it can smoothen out the image [7].
- Enhance detail: To get more detail in the image we use the unsharp masking [8].

Segmentation

The objective of this phase is to identify the area of focus, specifically the region affected by the tumor, in order to extract relevant attributes for subsequent classification. This was accomplished through a two-step process; they are Skull stripping and tumor area segmentation.

The first step in this process is called Skull stripping. The procedure for skull stripping involves the following stages:

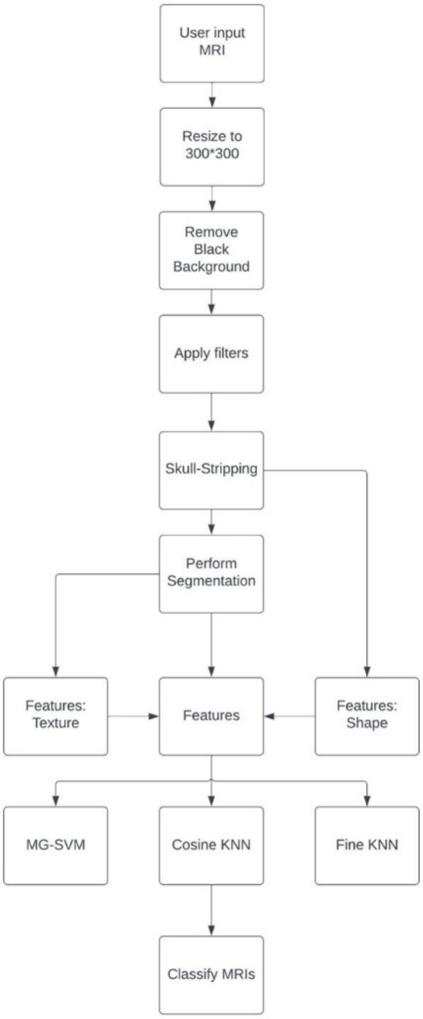


Figure 1: Flow chart of the work flow

- Utilizing a method called gray-level value method.

  This step is primarily used for thresholding [7,8].
- Retaining only the most sizable element, which corresponds to the tissue of the brain [8].

  We use an algorithm called the Connected components algorithm to achieve this.
- Conducting a closing operation on the image to bridge any gaps [7,8].
- Finally, restoring the original pixel values

The second step of tumor area segmentation also is a multi-staged process. This particular stage is among the more intricate aspects, as the tumor region often intersects with the brain tissue. We define all the stages below:

- Enhancement of contrast: We apply gamma corrections to solve this issue and to compensate for the nonlinear behavior of electronic displays and human visual perception [8].

- Convert the gamma image to binary: We utilize Otsu's method to achieve this step [9].
- Remove undesired components: Application of morphological operations will achieve this step and also bridge any gaps.
- Restore: Restoration of the pixel values back to original is the final step.

Extraction of features

Upon obtaining the tumor region from the image, various components need to be represented as a feature set for classification and diagnosis purposes. These features can be divided into two classifications, one of texture [10,11] which include all the ten features of LBP, and the other basic ones like mean, variance, and standard deviation. These also include some more features like entropy, RMS, GLCM, smoothness, skewness, and the kurtosis. The other classification is regarding the shape, which include solidity, the perimeter, and the major axis length.

Classification

We will be using the following algorithms: Cosine KNN, Fine KNN and MG-SVM models to categorize an MRI as either having a tumor or not in this stage. What sparked the idea of creating a hybrid algorithm that combines all three classifiers is the divergence in misclassifications among classifiers. For example, Fine KNN may incorrectly classify an image that the other two classifiers get right. So, we created this approach in which, each image is classified by all three classifiers, and the final classification is determined by the majority opinion. Since it's improbable that all or most of the classifiers will make the same mistake, this approach increases accuracy. For example, if Fine KNN classifies an image as "NO", while the other two categorize it as a tumor, then the final result is going to be a tumor.

GUI

The "App Designer", a built-in tool in MATLAB 2020, was used to develop a graphical user interface (GUI) which works in a plug-and-play fashion. Once the user passes an MRI as the input, they get to view the presence of any tumor along with the contrasts and the brightness. Since we have multiple decisions by the independent classifiers, we allow the user to view each of these outputs too.

Evaluation

We evaluate our model based on the following values:

- Accuracy: Accuracy measures the effectiveness of a classifier in correctly categorizing images. It is calculated by dividing the number of accurately classified images by the total number of images [14].

  It is represented as:

  Sum of True Negatives and True Positives /Total images

- Specificity: It gauges the classifier's capability to discern non-tumor images. It is determined by dividing the number of non-tumor images correctly classified as healthy by the total number of non-tumor images [12].

  It is represented as:

  True Negatives/(Sum of True Negatives and False Positives)

- Negative Predicated Value: It quantifies the number of images correctly classified as not having a tumor, divided by the total number of images categorized as not having a tumor [13].

  It is represented as:

  True Negatives/(Sum of True Negatives and False Negatives)

- Positive Predicated Value: We define this by taking the ratio of the number of MRIs which actually have a tumor and the number of images outputted by our model to have a tumor [13].

  It is represented as:

  True Positives/(Sum of True Positive and False Positives)

- Sensitivity: The classifier's capacity to differentiate between states is assessed by determining the proportion of images which have a tumor that were correctly identified as such, out of the total number of damaged images [12].

  It is represented as:

  True Positives/(Sum of True Positive and False Negatives)

In all the above representations we classify [12]:

- A True Positive as an MRI that accurately detects a tumor
- A True Negative as an MRI that accurately detects an image with no tumor in it
- A False Negative is when we have an inaccurate detection of a tumor
- A False Positive is when we have an inaccurate detection of a brain with no tumor

The values that we have deducted above come from the confusion matrix that was created for the three classifiers we have used. This is done post classification to test the accuracy of the model we have created.

3. Results

Following the application of each stage of the algorithm to an image from the database, we will assess the resulting images.

- In Fig. 2, an original image from the database is displayed.

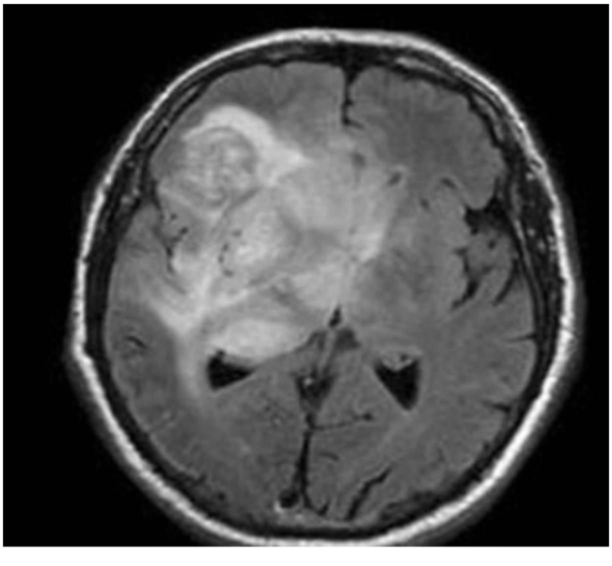


Figure 2: The MRI in original form

- Fig. 3 showcases the outcome of the first two steps in our novel model. As a refresher, in these two stages combined we are cleaning the image and segmenting it so that the classification can be done more accurately and uniformly.

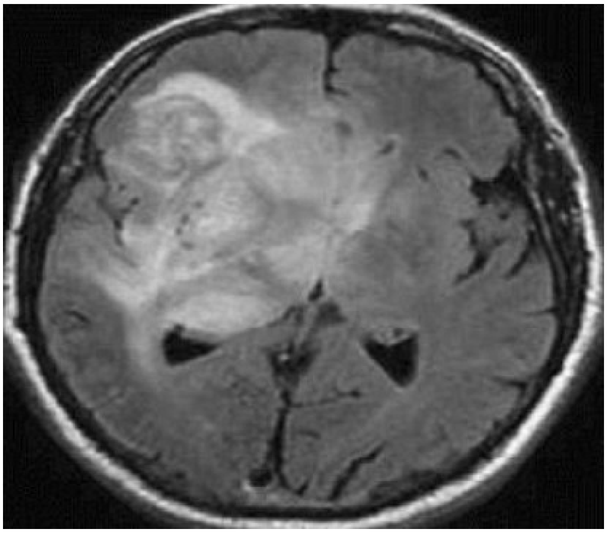


Figure 3: First two stages output

- The significance of the skull-stripping process can be observed in Figure 4, as it mitigates errors arising from the similarity in gray levels between the skull and the tumor. This step involves cropping the skull pixels.

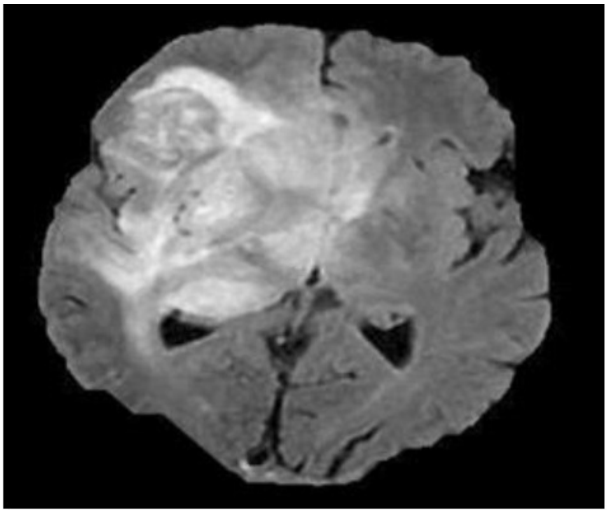


Figure 4: After Skull-stripping

- We can observe the effects of thresholding performed in Fig 5.

  In Fig. 6 and Fig. 7, the designed graphical user interface is displayed. The figures show how we allow to view the iterative results. Since we have three algorithms being used, we want the user to also see the output of each of these. Finally, the most important result of the MRI according to our model is shown.

  Some supplementary features like control for the contrast can be seen which is also available for the brightness. Another supplementary observation can be made in the form of circling the tumor.

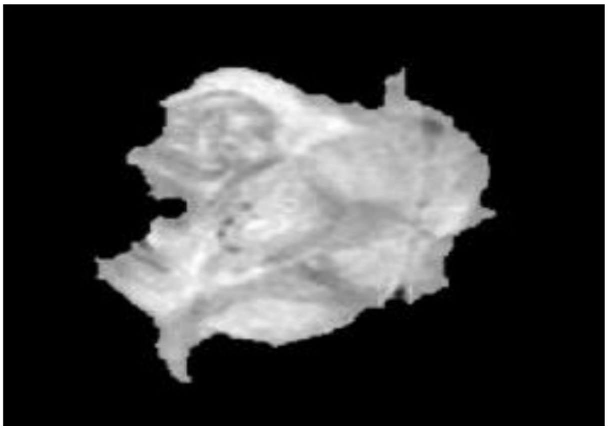
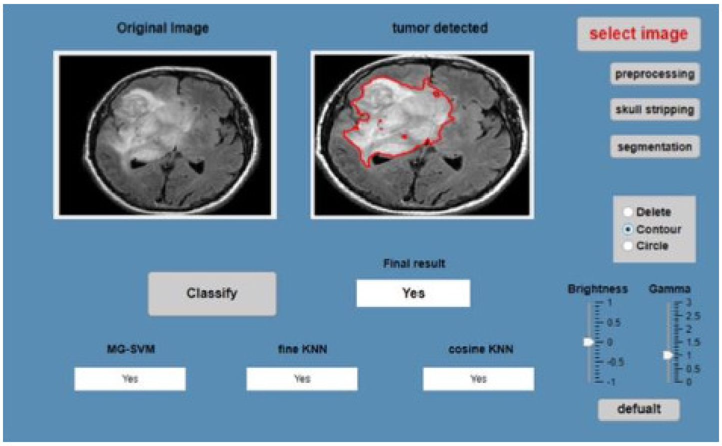


Figure 5: Post-segmentation



○ Delete
● Contour
○ Circle

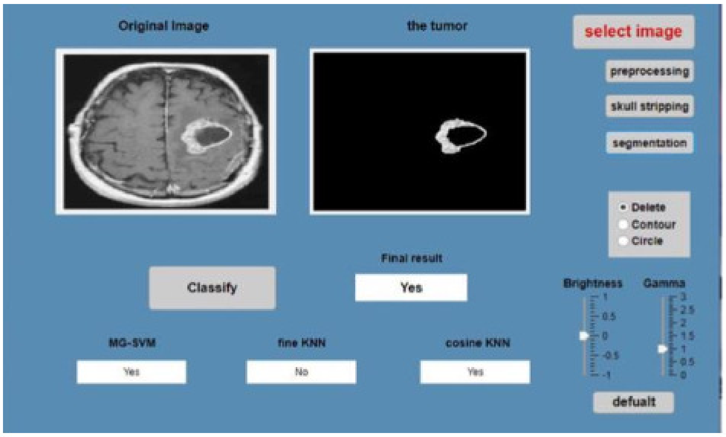
Final result: Yes

MG-SVM: Yes

fine KNN: Yes

cosine KNN: Yes

Figure 6: Implementation of GUI



● Delete
○ Contour
○ Circle

Final result: Yes

MG-SVM: Yes

fine KNN: No

cosine KNN: Yes

Figure 7: Final results

4. Discussion

Upon the culmination of every stage of work, it became imperative to assess the precision of the outcomes acquired. Thus, we proceeded to compute the testing and training accuracy for each model individually. The ensuing findings are training accuracies of 92.3% for both MG-SVM and Fine KNN, while Cosine KNN had only 88.5%. Whereas the testing accuracies were recorded higher at 90% for both Cosine KNN and Fine KNN. MG-SVM performed better with 93.3%. These were the results of individual models, but out novel model which takes the majority of the decision of these models gave a whopping accuracy of 96.7% with the testing dataset. The Confusion Matrix of each classifier was utilized to generate the necessary parameters for result evaluation, in which we can see that the hybrid classifier demonstrates a superior accuracy compared to the individual classifiers as depicted in Fig 8 and Table 1.

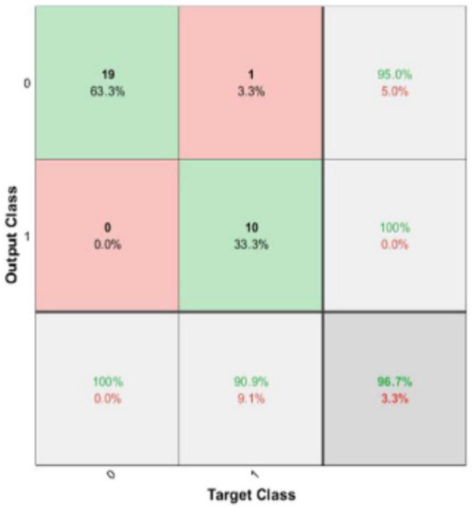


Figure 8: Confusion Matrix

Significance of the success of us pioneering hybrid approach and its substantial enhancement can be observed in Table 1 which presents the extracted values from the Confusion Matrix for each classifier individually, as well as for the hybrid classifier.

Table 1: Evaluation values

Model	**Accuracy**	**Specificity**	**Positive Predicate Value**	**Negative Predicate Value**	**Sensitivity**
MG- SVM	93.3%	100%	100%	83.3%	90%
Fine KNN	90%	90%	94.7%	81.8%	90%
Cosine KNN	90%	70%	87%	100%	100%
Novel model	96.7%	90.9%	95%	100%	100%

5. Conclusions

As the field of image processing is vast, there is constant potential for advancement and enhancements like refinement for tumor type diagnosis. As such, our efforts will not be halted at this juncture.

Despite the challenges faced, we are optimistic that we have achieved favorable results and developed a novel ensemble model. We shall endeavor to refine and expand upon this work with ideas such as training additional classifiers. Other direction which can be explored involves exploring superior techniques for segmentation.

We hope this serves as a stepping stone towards further accomplishments and breakthroughs in the future.

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