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BRAIN TUMOR CLASSIFICATION USING DEEP LEARNING

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Abstract - The early detection of the tumor plays an important role in the recovery of the patient. In our proposed model, we have collected MRI scans as it helps with the information about the blood supply inside the brain. Thus, for the recognition of anomaly, for examining the increasing of the ailment, and for the diagnosis, we prepared a data set consisting of various MRI images. We then focused on removing unwanted noise and image enhancement. The image characteristics can be enhanced by using image pre-processing techniques. The image enhancement depends upon different factors like computational time, computational cost, quality of the uncorrupted image, and the techniques used for noise elimination. We have made use of various filters for the image pre-processing. In our next step, image segmentation, an image is divided into several regions. We have implemented different types of segmentation techniques including active contours snakes, fuzzy C means, and region-derived triple thresholding. We have further implemented two hybrid segmentation models and used computer-aided detection techniques. Post-processing of the data is done using artificial bee colony optimization and watershed filtering and extraction. We then classify two images into tumor and non-tumor category using the VGG-16 CNN model. The features of the segmented images were further classified into various types of tumors, including Glioma tumor, Meningioma tumor, Pituitary tumor, and no tumor using one-hot encoding. This approach was further validated using synthetic and real MR image dataset from Kaggle (name of data set), to detect and classify different types of tumor.

I. INTRODUCTION

A brain tumor is an aggregation of unusual self in the brain tissue. Brain tumors are classified as malignant and benign.

Malignant tumors are cancerous which can be further categorized as primary and secondary tumors. Primary tumors have starting points within the brain and secondary tumors can extend from a location to another location. benign tumors are non-cancerous and can also be categorized as adenomas and fibromas, benign tumors and malignant tumors are also known as low-grade and high-grade tumors. The detection of brain tumors is done by analyzing x-rays MIRs and ultrasound etc. The most common type of primary brain tumor seen in adults is gliomas. Pituitary tumors are considered benign and develop in the pituitary gland. They Are less likely to be sprayed but can cause serious health hazards because they are present in sensitive areas of the brain. Meningioma tumors arise from meninges, which are layers of tissues that protect the spinal cord and the brain. These tumors are considered benign because they have a slow growth and are also less likely to spread.

Image processing and deep learning algorithms are mainly used to analyze medical images and to identify and classify the brain tumor into subcategories, and help professionals with the diagnoses.

In this paper we present a six-step model to classify and detect brain tumors with high efficiency, in the first stage we have made use of various filters for the image pre-processing. In our next step, image segmentation, an image is divided into several regions. We have implemented different types of segmentation techniques including active contours snakes, fuzzy C means, and region-derived triple thresholding. We have further implemented two hybrid segmentation models and used computer-aided detection techniques. Post-processing of the data is done using artificial bee colony optimization and watershed filtering and extraction. We then classify two images into tumor and non-tumor category using the VGG-16 CNN model. The features of the segmented images were further classified into various types of tumors, including Glioma tumor, Meningioma tumor, Pituitary tumor, and no tumor using one-hot encoding. Further, this approach was validated



using synthetic and real MR image dataset from Kaggle (name of data set), to detect and classify different types of tumor.

This paper is divided into 6 sections. Section 2 gives us a literature survey conducted on different methods for a better understanding of the project. Section 3 describes the methods utilized in this paper. Section 4 provides the experimental results over MR images. The conclusions are given in section 5. Section 6 gives details about the future scope of the paper.

Section 2: Methodology

II. DATA PREPARATION AND PRE-PROCESSING

Data preparation is a data mining technique that involves the transformation of raw data to a format that is more interpretable and makes the images more suitable for further processing. While preparing the images, we implemented the technique of crop normalization on MRI images. This is a technique to find the extreme points in contours. We determined the extreme contours in the input image and outlined the skull. We removed the black redundant background, without damaging any pixel quality. The advantage of doing Crop Normalization is that we get a clear region of interest for further processing and we remove tags from the MRI without damaging any detail from the MRI.

The output was as follows:

We have used Tw1 and Tw2 mixed MRI images of brain tumour. The input dataset contains images with a different dimension and with different aspect ratios. Therefore, the images in the dataset are resized to a pre-set format, since the pre-trained models used require the images to be 200×200 dimensions.

FILTERS:

We have used a variety of filters to smooth out the MRI Images. To improve the contrast of the image, we used a Histogram Equalisation filter. An image can have values confined in a specific range. A brighter image may have all pixels confined to high values and a dull image may have all pixels confined to low values. However, a good image will have pixels from all regions of the image. Hence through adjustment, the intensities can be better distributed on the histogram. This method spreads out the most frequent intensity values, resulting in areas associated with lower contrast to gain a higher contrast. Histogram equalization normally improves the contrast of the image

Histogram equalization is responsible for increasing the global contrast of the image but is more effective only in images that have close contrast values.

Histogram is not confined to a particular region, so we can lose information due to over brightness. Therefore, to solve this problem, adaptive histogram equalization is used. The image is divided into small 8x8 size blocks and each

block is individually equalized. So in a small area, a histogram would confine to a small region.

However, there are chances of noises being amplified. To avoid this problem, we apply contrast limiting. The pixel values above the specified contrast limit are clipped and then uniformly distributed to other bins before filtering.

An image contains a lot of features like edges, brightness or contrast, and color. Blurring is a method to process this image. An image looks more sharp and detailed if we can perceive all the objects and their shapes correctly. In blurring, we reduce the content of the edges to transition from one color to another color very smoothly.

Gaussian filters are fast processing and more effective while smoothing is applied on the images. It might not preserve image brightness and not particularly effective at removing salt and pepper noise. On the other hand, Median Filters maintain the sharpness of the picture boundaries and effective in non-linear smoothing. However median filter lacks in distinguish fine details from the noise. In Bilateral filtering, most of the fine texture is filtered away, and yet all contours are as crisp as in the original image.

III. IMAGE SEGMENTATION

Classically, image segmentation is defined as the partitioning of an image into non-overlapping regions, which are homogeneous with respect to some characteristics such as intensity or texture. We have used the following techniques for segmentation of the tumor from the MRI images:

A. Active Contours Snakes

Active Contours Snakes is a segmentation using curves and not pixels. Users can define a curve, which will then evolve.

The evolution of the curve should satisfy two aspects. It should adapt to image edges and it has to be smoothly varying.

To satisfy this evolution we need to have a measure. This is parameterized by the energy of the curve. The objective to satisfy the two aspects is measured by minimizing an energy parameter $E(c)$, where c represents the curve under evolution.

$$E(c) = E_{\text{internal}}(c) + E_{\text{external}}(c)$$

The curve has two aspects. The first is internal to the curve which corresponds to the smoothly varying aspect of the curve. This parameter regularizes the curve and makes it smooth. It depends on the shape of the curve as we want to minimize the distortions. The second is the external to the curve that looks for edges. This parameter refers to the direction towards which the curve should evolve. External parameter depends on the image intensity.

Internal Energy:

$$E_{\text{internal}}(c) = \int_0^1 (\alpha \|c'(s)\|^2 + \beta \|c''(s)\|^2) ds$$

$c'(s)$ and $c''(s)$ are the first and the second derivative of the curve respectively.

α and β are the two hyper parameters which we have taken as 0.06 and 0.6 respectively. These values refer to the weights we want to locate to the first and second-order derivatives of the curve.

ds indicates that the curve is divided into small segments. The limit 0 to 1 means we are converting the entire segment of the curve.

We define a region of interest i.e. the tumor outlining. As it is a discrete system, the curve is divided into various segments. We define a starting point. 0 to 1 integral limits traverse the curve from the start to the endpoint. The small separation is ds . Each of the location division has an x and y coordinate which is represented by s .

The first-order derivative is to keep the curve not too 'stretchy'. If the two-division points selected are far apart, then c' value will be very high. Higher value means less smoothness. Hence, to make it smoother the points chosen should be closer. Low c' means we are taking closer samples.

The second-order derivative ensures that the curve is not too 'bendy'. If there are irregularities or oscillations in the curve, then the c'' value will be high. Hence low second-order derivative prevents points of the curve from oscillating.

We want to minimize the internal energy to as low as possible and to achieve that we should ensure a curve that is smooth with no oscillations.

The first-order derivative is anisotropic, and the second-order derivative is isotropic.

$$E_{\text{external}}(c) = \int_0^1 -\|\nabla I(c(s))\|^2 ds = \int_0^1 -\left[\left(\frac{\partial I(x(s), y(s))}{\partial x}\right)^2 + \left(\frac{\partial I(x(s), y(s))}{\partial y}\right)^2\right] ds$$

Here, I represents the intensity at locations of $x(s)$ and $y(s)$.

It is obvious that when we have a large edge the intensity difference is also high. Applying a negative sign to a high

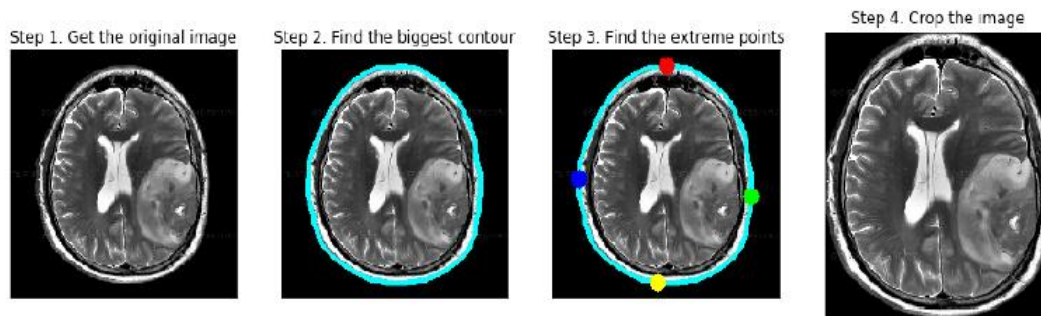


Fig. 1. Output of crop normalization

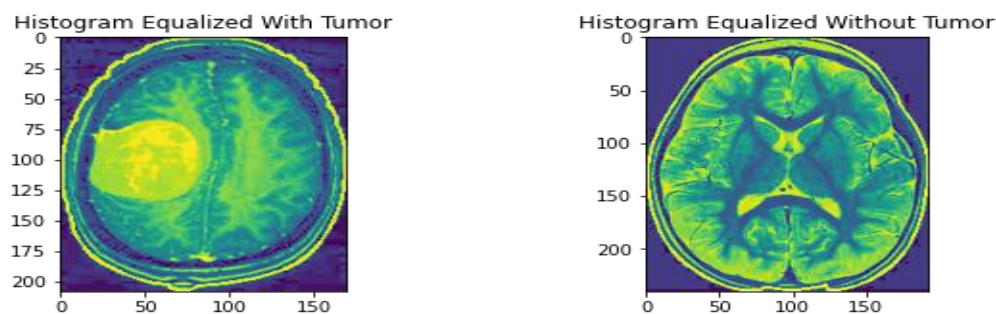


Fig. 2.

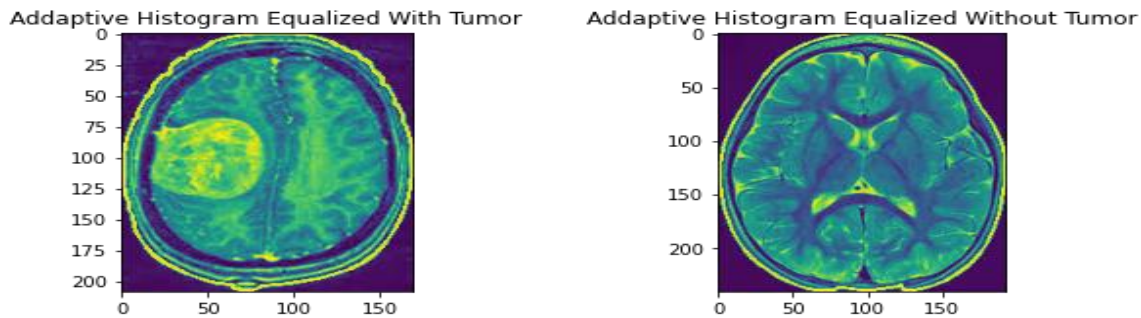


Fig. 3.

magnitude will ensure that the energy is minimum. As the snake moves towards lower energies, it will be attracted towards the large edges.

B. Fuzzy C means

There exists a set $S = \{x_1, x_2, \dots, x_n\}$ and any chosen point x_i either belongs or does not belong to this set.

It is an indicator function to determine this possibility. If I_s is 0, then x_i does not belong to S and if I_s is 1, then x_i does belong to S . The set is divided into n number of data points, k number of clusters, and m number of numerical attributes.

Fuzzy set mainly deals with 1's and 0's and all the values in between them. Fuzzy is unlike crisp sets where membership values can only take values 0 and 1.

In our project, we have initialized four clusters and chosen a fuzziness factor of 2.

Cluster center initialization is done randomly. Any four points will be randomly selected and be chosen as the center of the four clusters we have defined. The Euclidean distance from each sample point to the center of the cluster is calculated using the formula:

$$D_{i,j} = \sum_{l=1}^m (x_{i,l} - c_{j,l})^2, 1 \leq i \leq n, 1 \leq j \leq k$$

Here i and j refer to the sample point and the center cluster respectively.

Membership function can be defined as the degree to which a sample point belongs to a particular cluster. Thus points nearer to the cluster center will have a higher degree of membership than those towards the edges or further. Membership function can be calculated using the following equation:

$$U_{i,j} = 1 / (\sum_{l=1}^k (D_{i,l} / D_{i,j})^{2/(m-1)}); 1 \leq i \leq n, 1 \leq j \leq k$$

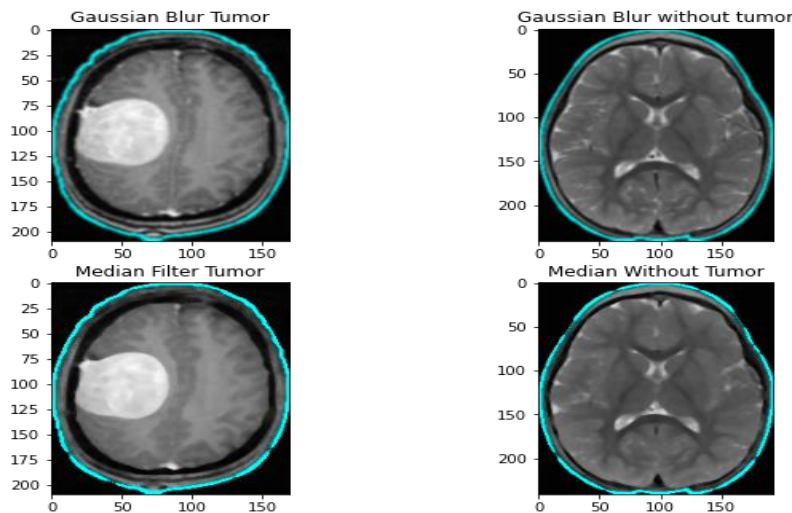


Fig. 4.

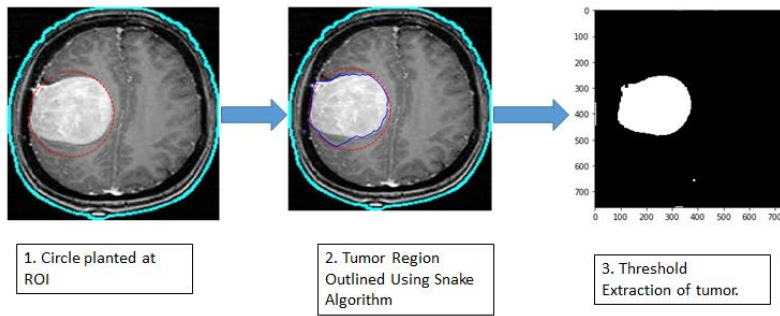


Fig. 5.

The fraction distance from any point to the cluster center is raised to the inverse fuzziness parameter, making a fuzzy measurement. This is divided by the sum of all fraction distances to ensure that the sum of all memberships is 1. The centroid for each cluster is further recomputed. This is done by taking the mean of all the sample points in the cluster and taking this value as the new centroid and is represented by the equation:

$$C_{i,j} = (\sum_{i=1}^n (u_{i,j})^m x_{i,j}) / (\sum_{i=1}^n (u_{i,j})^m) ; 1 \leq j \leq k, 1 \leq i \leq n$$

The objective function is the product of summation of square of Euclidean distance and membership function raised to the power of a user-defined exponent value.

The main objective is to minimize objective function given by the equation:

$$J_a(X,C,U) = \sum_{j=1}^k \sum_{i=1}^n (u_{i,j})^a D_{i,j} ; 1 \leq a < \infty$$

C. Region Derived Triple Thresholding

In the region-based segmentation, the image is segmented by grouping pixels into distinct regions based on some common characteristics like texture, contour, intensity level, etc. Thresholding is a method of region-based image segmentation, where the grouping of pixels is done based on the difference between the pixel intensities and the threshold intensity, due to its

simplicity and computational speed Thresholding occupies a central position in image segmentation. In Region Derived Triple Thresholding, pixels are clustered into four regions based on their intensities. It uses the process of thresholding, with two local thresholds and one global threshold. There is automatic generation of three thresholds based on intrinsic characteristics of the image. The global threshold is obtained through neighborhood comparison of localized regions spanning through the image. The global threshold forms two sets of pixels, from which the local thresholds are obtained. In our project, we have modified this approach by fashioning it with Contrast Limited Adaptive Histogram Equalization. At first, we run the image through CLAHE filters, and then from the output of the image, we calculate one global and two local thresholds. Regions of size 5x5 were considered over the entire image which was shifted by one pixel horizontally. Expectation value of pixel intensities for each region calculated: weighted average of all possible results is calculated by taking each potential variable and multiplying it by its probability of occurrence in that region. This is done till the whole image is covered.

Later we calculate the Average of maximum expectation and minimum expectation value, which gives the global threshold value of the image. Global threshold t divides all the pixels into

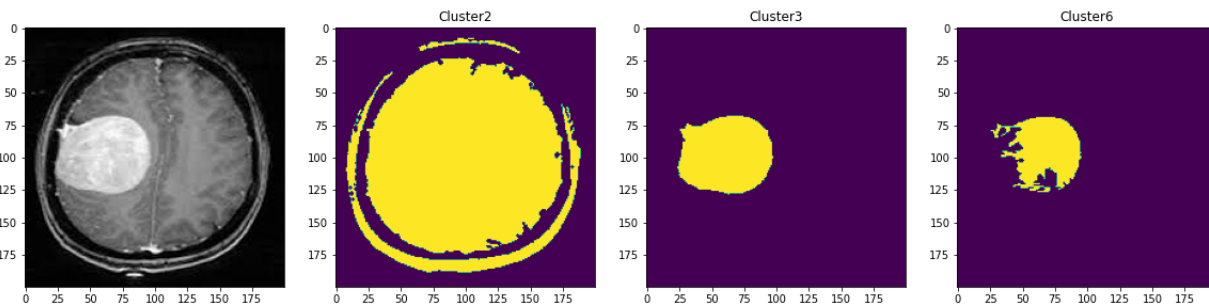


Fig. 6.

two sets- S1 with pixel intensities less than or equal to t and S2 consists of all pixel intensities that are more than t . Mean of both sets computed: two local threshold values obtained.

Then the Image is segmented into 4 sets using the three thresholds obtained.

$$g(x,y) = \begin{cases} a, & \text{when } 0 \leq f(x,y) \leq m1 \\ =b, & \text{when } m1 < f(x,y) \leq \text{thres1} \\ =c, & \text{when } \text{thres1} < f(x,y) \leq m2 \\ =d, & \text{when } f(x,y) > m2 \end{cases}$$

It is seen that even though the proposed algorithm clusters pixels into four regions only, it successfully detects all of the regions of interest (ROI) specified in the images. By selecting appropriate values of the intensity levels a, b, c, and d, different areas of the image can be highlighted and object identification can be done. It can be inferred that region-based triple thresholding fused with CLAHE is a simple yet efficient thresholding method for the segmentation of grayscale images.

IV. FEATURE EXTRACTION

A. Hybrid Segmentation

Automatic segmentation of the abnormality from the MR imaging modalities is a huge concern for the radiologist. In the past various distinguished approaches and methods have been proposed based on different approaches like edge detection, region growing, fuzzy logics, and clustering for fast and effective segmentation. Edge-based snakes used for the extraction of the tumor region from brain MR image gives satisfactory results but due to weak gradient magnitude, the algorithm works effectively well only for high contrast images and degrades performance with low contrast images. The various clustering-based segmentation approaches like k-means, fuzzy clustering works well for the extraction of tumors but as the algorithm was based on randomness so whenever the algorithm runs gives different outputs. To overcome we suggest using Hybrid Segmentation, a Technique integrating two or more techniques which is efficiently giving better results than the segmentation algorithms working alone. A combination of both thresholding and fuzzy clustering techniques will be considered because thresholding finds out the uniform regions for fuzzy clustering, which makes the clustering performance better. In this article, we have proposed two Hybrid Segmentation techniques for user-defined and automated segmentation.

B. Hybrid Snake's-Enhanced FCM Method

The hybrid Snake's-Enhanced FCM is Edge Based Snakes segmentation normalized Enhanced FCM (EnFCM) feature extraction which combines Snake's Tumor Segmentation method with EnFCM clustering which is an improved version of traditional Fuzzy C-Means introduced by Szilagy et al. with a filter introduced inside the cyclical optimization problem, which led to better image quality.

C. Hybrid Triple Thresholding- Modified FCM Method

The hybrid triple thresholding-Modified FCM or bias-corrected FCM is Region Derived Triple Thresholding normalized Modified FCM(MFCM) feature extraction which combines Triple Thresholding Segmentation into four regions based on intrinsic image characteristics with MFCM clustering which is modified object function of standard Fuzzy C-Means algorithm introduced by Ahmed et al. This compensates for intensity inhomogeneities and the labelling of a pixel takes the labels in its immediate neighborhood into account. This regularisation results in piecewise-homogeneous labelling.

D. Computer-Aided Detection:

Features of the brain tumor have been extracted to further improve the efficiency of the classification algorithms in detecting the type of tumor. The more processing of MRI images along with feature extraction is done, the higher accuracy will be shown by the classification models. To detect & extract features of brain tumors, a model is constructed by combining Convolutional Neural Networks with MRI detection technology using Computer-aided detection technology. The main function of this model is to segment and recognize brain tumors and use a convolutional layer to perform convolution operations for improving recognition efficiency & rate and combine artificially selected features with machine learning features. Also, feature fusion is used by this mechanism to further improve the diagnostic results.

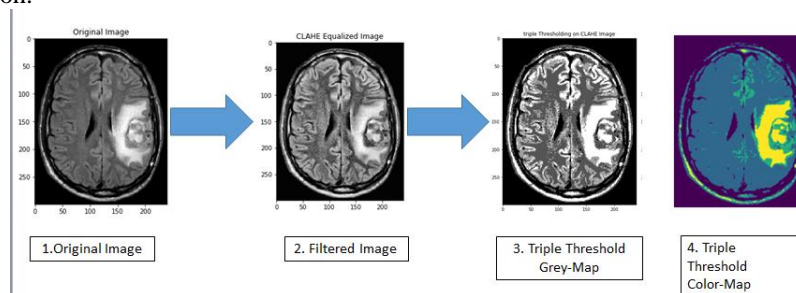


Fig. 7.

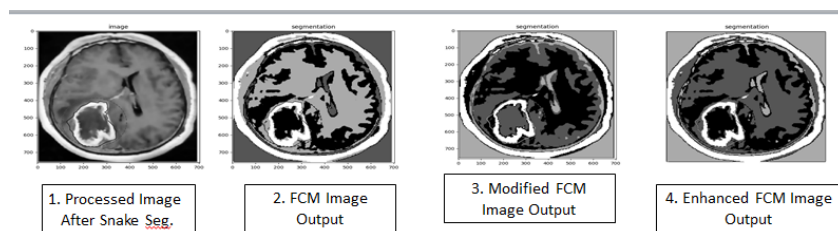


Fig. 8.

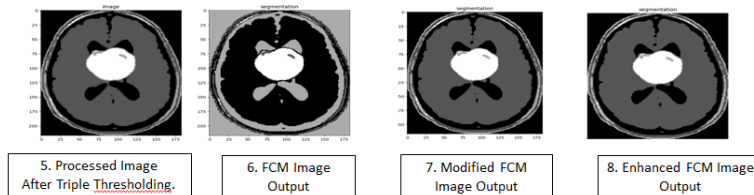


Fig. 9.



Fig. 10.

V. POST-PROCESSING

We propose a Post-Processing Stage which consists of Artificial Bee Colony Optimization [4] and Watershed [5] of the image is retrieved to extract the tumor. MRI images always contain a significant amount of noise caused by the operator, equipment, and the environment. This leads to serious inaccuracies in the segmentation as any changes in pixels' intensity such as noise, significantly affect the clustering results. One way to improve the accuracy of the results is to use the optimization method. Optimization is a technique used to seek values for a set of parameters that maximize or minimize objective functions subject to certain constraints. Artificial Bee Colony algorithm is a novel optimization algorithm inspired by the natural behavior of honey bees in their search process for the best food sources. Inspired by Karaboga's algorithm we implemented

Artificial Bee Colony and its output is provided to the watershed algorithm. The term watershed refers to a ridge that divides areas drained by different river systems. A catchment basin is the geographical area draining into a river or reservoir. Watershed Algorithm causes averse segmentation but due to our novel approach of Hybrid Segmentation of Triple Thresholding and modified FCM with Artificial Bee Colony [6] we get better output at the end of post-processing, with help of spatial domain filtering we calculate a gradient image to mark borders of skull region and tumor region, then we calculate marker image and finally develop a tumor developed image which highlights tumor region and is then feed to classifiers. Post Processing removes noise from filtering, operations, and clustering is done on image and therefore increases output efficiency. Now the extracted image is sent to the classifier.

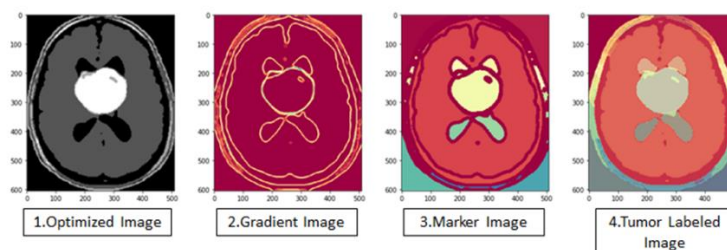


Fig. 11.



VI. CLASSIFICATION

VGG16 is a convolution neural network (CNN) architecture that was used to win The ImageNet Large Scale Visual Recognition Challenge. It is considered to be one of the most excellent vision model architecture to date. A unique thing about the VGG16 is that instead of having a large number of hyper-parameters they focused on having convolution layers of 3x3 filter with a stride 1 and used the same padding and max-pool layers of 2x2 filter of stride 2. It follows this arrangement of convolution and max pool layers consistently throughout the whole architecture. In the end, it has 2 fully connected layers followed by a SoftMax for output. The 16 in VGG16 refers to it has 16 layers that have weights. This network is pretty large and it has about 138 million parameters.

In our project, we have used the model for brain tumor image classification. The input dimensions of the model are (224,224,3) which is the size of the image that is 224x224. A total of 204 images were used to train the model which may seem less but are more than enough for achieving great accuracy. To attain better metrics and compensate for the loss we reduced the epochs to 25 from 50 and trained them each for 5 steps instead of 8. The results were significantly better than the previous model. The training accuracy is 97.14% while the testing accuracy is 80.85%. The epoch vs accuracy graph depicts that it is an optimal model which neither overfits nor underfits.

One Hot Encoding

Categorical data consists of information that is classified as groups. It is used to group information with similar characteristics, which may not have a defined logical order. The parameters in a categorical dataset are labelled according to their features & characteristics. To make categorical data more expressive, the approach of One Hot Encoding has been used. Both, the input & output variables which are categories, are converted to numbers.

This approach is termed as One Hot Encoding because, in its representation, each row has only one feature with a value of 1 and the rest of the features have a value of 0. To convert the categorical data to binary values, the categorical values need to be mapped to integer values. Following this, each integer value is represented as a binary vector which consists of all 0 values except the index of the integer, which is marked with value 1.

The categories are first converted into numbers. This is done by Integer encoding. A mapping of all possible input values is created from labelled values to integer values. This mapping is then used to encode the input categorical data. The integer encoding is then converted to One Hot Encoding. Encoding is done one integer character at a time. Next, the index of a specific character is marked with value 1 while the rest are marked with value 0. This has been done by locating the index of in the binary vector with the largest

value using the NumPy argmax() function and then using the integer value in a reverse lookup table of character values to integers.

While classifying the brain tumor, four different classes were made for predicting the exact type of tumor. The tumors are labelled as glioma, meningioma, pituitary & no tumor. Integer coding was used for converting these labels to integers.

The kind of tumor that gets recognized is marked with value 1, while the rest three columns are marked with zero.

In a dataset, if the images uploaded are {Pituitary, Glioma, Meningioma, Meningioma, Pituitary, Meningioma, Glioma, No tumor}, then the following would be the One Hot Encoding representation: (Table 2)

On running the code for training the dataset containing MRI images of the 4 types of tumors using Keras, it was observed that the most common primary brain malignancies are gliomas. Our aim was to diagnosis the type of tumor efficiently using deep learning methods for predicting the survival rate and, the most suitable treatment planning & identification of risk factors if any, for the patients in time. To fulfil this aim, accurate & robust tumor segmentation & classification was required.

Gliomas are categorized into glioblastoma & lower-grade glioma, the former being the most fatal type. Gliomas contain various heterogeneous histological sub-regions, including peritumoral edema, a necrotic core, an enhancing & a non-enhancing tumor core. Magnetic resonance imaging (MRI) is used in radiology very often to portray the phenotype and intrinsic heterogeneity of gliomas, since multimodal MRI scans, such as T1-weighted, contrast-enhanced T1-weighted, T2-weighted, and FLAIR images, provide complementary profiles for different sub-regions of gliomas.

Meningioma tumors are often quite vascular without a blood-brain barrier, whereas gliomas have varying degrees of vascularity and blood-brain barrier disruption depending on grade & characteristics.

A pituitary tumor is an abnormal growth of cells in the pituitary gland, which is the main hormone-producing gland in the body. About the size of a pea, the pituitary gland is located in the center of the brain behind the nose and eyes. A tumor in the pituitary gland may affect the balance of hormones in the body and affect a person's overall health.

A good fit curve was obtained for the model loss graph, thus showing that the learning algorithm was efficient as it neither overfit nor underfit the model. The training & validation loss decreased to a point of stability with a certain minimal generalization gap value between the two final loss values.

To test the algorithm on a random MRI image, an image from the given data set was uploaded on the model. The classification algorithm worked well on the MRI image, as the accuracy

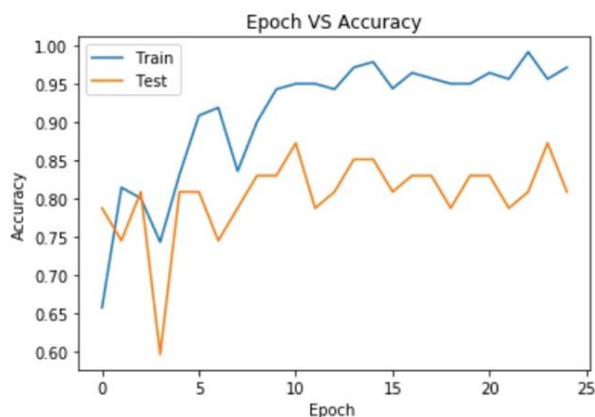


Fig. 12. Epoch VS Accuracy Graph of VGG 16 Model

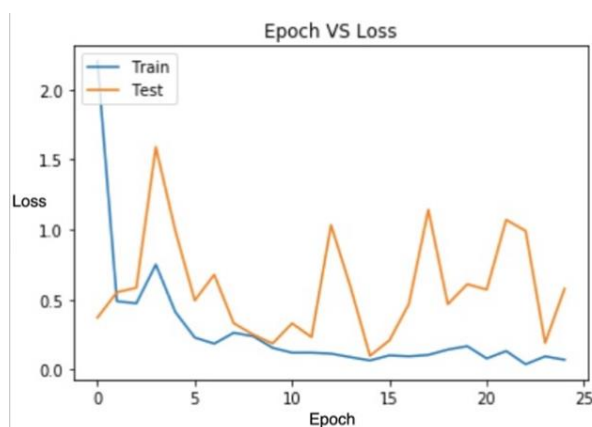


Fig. 13. Epoch VS Loss Graph of VGG 16 Model

TABLE I
CASE VALUES FOR VARIOUS TYPES OF TUMORS

Tumour type	Class
Glioma tumour	1
Meningioma	2
Pituitary tumour	3
No tumour	4

TABLE II
BINARY OUTPUTS FOR VARIOUS TYPES OF TUMORS MENTIONED IN THE EXAMPLE SET

Glioma (1)	Meningioma (2)	Pituitary (3)	No Tumour (4)
0	0	1	0
1	0	0	0
0	1	0	0
0	1	0	0
0	0	1	0
0	1	0	0
1	0	0	0
0	0	0	1

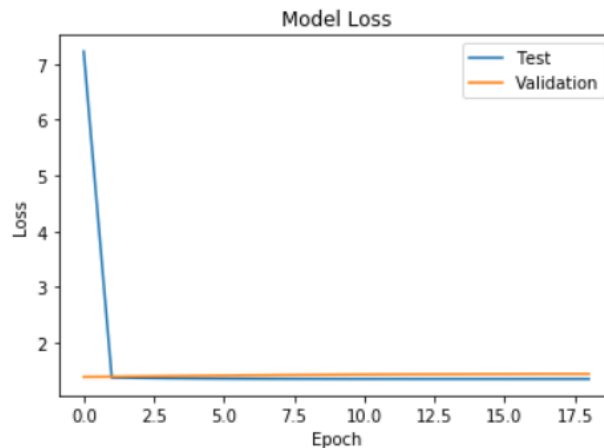


Fig. 14. One hot encoding: Model loss graph for Epoch VS Loss Perfect fit observed for epoch: 19 and batch size: 32

obtained for prediction of the tumour was 99.959%. The type of the tumour was Pituitary.

The loss of the model is lower on the training dataset than the testing dataset.

As a good fit was obtained for the model, if the training was continued then the model would have overfitted.

VII. CONCLUSION

Pre-processing, segmentation and Post Processing Stage plays a vital role in increasing efficiency of detecting and classifying tumor at deployment of CNN classifier. Artificial Bee Colony Optimization solves the Fuzzy Clustering Problem and therefore its application in Bio-Medical Projects is very crucial as it helps in increasing efficiency. Hybrid Segmentation is better than using a single segmentation technique as it's a combination of the pros of two techniques, giving better segmentation results and eases work at the extraction stage. Our proposed algorithm reduces manual segmentation and improves classification. The loss of the model is lower on the training dataset than the testing dataset.

As a good fit was obtained for the model, if the training was continued then the model would have overfitted.

VIII. FUTURE SCOPE

As it is known, brain tumor is a very common disease and millions of people succumb to it every year. The earlier it is diagnosed, the higher are the chances for the patients to survive. This research primarily deals with the fast diagnosis of a large number of patients suffering from brain tumor. The deep learning algorithms used in this research deal with quick diagnosis of the brain tumor and its type for thousands of patients at a time, so that medical professionals can provide speedy treatment more efficiently to all the

patients suffering from various kinds of brain tumor to cure maximum cases.

A web application can be deployed for implementing the entire deep learning model so that the dataset containing MRI images of the patients can be processed in a sophisticated way to get the required results following the pipelined algorithm of MRI image Pre-processing-Segmentation- Feature Extraction- Classification.

Once designed & deployed with all the required features, the web application can be used by the medical professionals in healthcare institutes for coming to conclusion about the tumor & its type and treating several patients at a time.

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99.95991587638855% Accuracy This Is pituitary_tumor

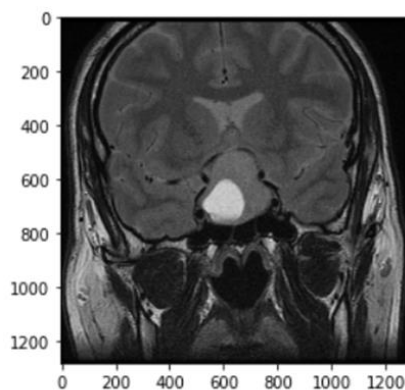


Fig. 15. Output for an MRI image tested with the One Hot Encoding model

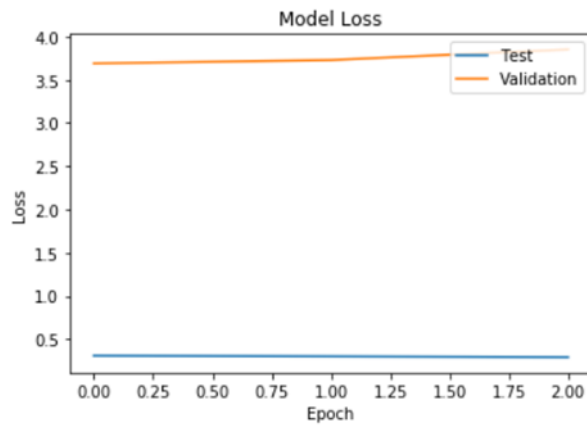


Fig. 16. One hot encoding: Model loss graph for Epoch VS Loss. Underfit curve observed for epoch: 4 and batch size 32

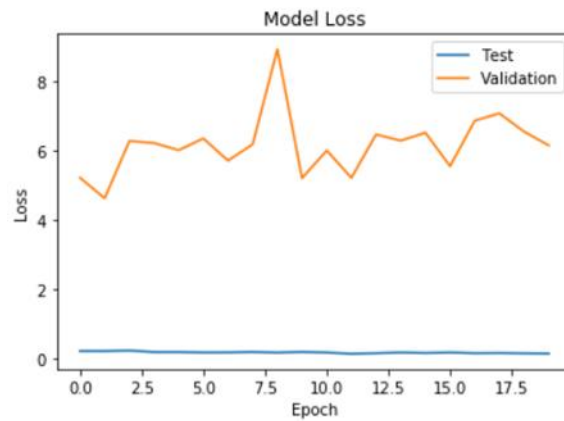


Fig. 17. One hot encoding: Model loss graph for Epoch VS Loss. Overfit curve observed for epoch: 30 and batch size: 25

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