Brain Tumor Detection
Through Image Processing

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Abstract—Begin with image processing for technology to detect brain tumors. I.e. (The identification of tumor/cancer cells from brain images is primarily based on image recognition methods, since these images are complex and human eyes are not ideal for interpreting the transformed cells with several degrees of changes). There are different types of instruments to help diagnose brain tumors, such as MRI scans, CT scans, etc. The device that can detect any organ and brain problem is MRI (Magnetic Resonance Imaging). Segmentation cell multiplication is an important strategy for processing brain tumor images. The segmentation or multiplication of cells will recognize the tumor along with its neighboring compartments and nearby tissues, but it is difficult enough to repair and shape the morphological changes caused by the tumor. Even though there are a number of current works on the subject. Many methods, such as template-based K means algorithm, fuzzy logic algorithms, threshold segmentation, etc., have been used to establish image processing, but the precision of the performance rate is still not up to the mark. In our proposed methodology our main purpose is to get a more clear image form MRI. We would try to use CNN algorithm which is more flexible and convenient. That will detect the position of the tumor automatically. This proposed methodology will be more efficient and faster to identify the tumor region and also it will be more effective and accurate for brain tumor detection and segmentation. Our main concentration is on the techniques which use image segmentation to detect brain tumor.

Index Terms—Convolutional neural network,MRI,Image Segmentation,CT scan , CNN Algorithm

I. INTRODUCTION

Computer plays a vast role in today's world. In today's world, we use computers in various ways such as, for communication, for animation, for making games, for doing various kinds of experiments, for running algorithms and most uses for medical science. Image processing is mostly used in medical science. There are two types of methods of image processing. One is analog image processing and another one is digital image processing. Digital image processing techniques help in the manipulation of the images by using the computer. So, by using digital image processing we can improve biological sciences. For example, many kinds of detection such as, tumor detection, cancer detection. Moreover, by using digital image processing we can do classification, testing and also can examine the critical parts of the human body. In today's medical science, brain tumor detection plays a conspicuous role. Therefore, the brain is the most important part and the most complex organ in the human body. It is the central organ of the human nervous system. Emotions, memory, behavior, thought, etc. are controlled by the brain as well as breathing and heart beating. The brain contains almost 50-100 billion neurons. Moreover, with large numbers of cells, the brain is manufactured though the damaged cells or the old cells die whenever the new natural cells grow and then the new cells take their place into the old one's or damaged cells place but, sometimes the damaged cells or old cells do not die and

the new cells procreate when the body does not necessarily of them. So, when the damaged cells do not die and grow of the new cells which are useless for the body, then the extra cells build up with a mass collection of tissues which is called a tumor. It is so chancy to treat the tumor because of its spreading capability and location. There are two general groups of brain tumors. One is primary brain tumors and another one is secondary brain tumors. The primary brain tumor starts in brain tissue and they take place there, on the other hand, secondary brain tumors are a most common issue where cancers start from somewhere else in the body and go to the brain, kidney, colon, skin, etc. that causes cancer and that can spread to the brain. Some brain tumors contain cancer cells and some don't contain. One is benign brain tumors and another one is malignant brain tumors. The benign brain tumors do not contain cancer cells moreover they generate so slowly, can be removed and its too rare to spread around the brain. On the other hand, malignant brain tumors have cancer cells whose growth rate is so fast. The tumor can be grown and spread so fast. In the beginning the tumors are going to look normal and will grow slowly then in 2nd grade the cells look abnormal and now this time the tumor can be spread to the nearby tissue. In the end, the tumor cells will look like most abnormal and it will grow so fast and spread quickly.

It is a common disease nowadays. For this reason, the mortality rate among adults and young people is increasing. In 2012, the age-specific incidence and mortality rate (ASR) of brain cancer in developed countries were 5.9 and 4 in men, and 4.4 and 0.4 in women, respectively. These rates were 3.3 and 2.6 in men and 2.7 and 9.1 in women, respectively in developing countries. (KHODAMORADI, GHONCHEH, PAKZAD, GANDOMANI, and SALEHINIYA, 2017) This year, an estimated 23,890 adults (13,590 men and 10,300 women) in the United States will be diagnosed with primary cancerous tumors of the brain and spinal cord [6]. A person's likelihood of developing this type of tumor in their lifetime is less than 1%. Brain tumors account for 85% to 90% of all primary central nervous system (CNS) tumors. Brain and other nervous system cancer are the 10th leading cause of death for men and women. It is estimated that 18,020 adults (10,190 men and 7,830 women) will die from primary cancerous brain and CNS tumors this year. In today's health care system, imaging plays a consequential role in medical science [5]. By the segmentation and partition of the image, doctors can easily find out the exact problem. But it is quite hard to do. There are some challenges to do imaging such as, medical image management, image data mining, bio-imaging, virtual reality in medical visualization and neuro imaging. At an early age, it was quite hard to detect the tumor but today, it becomes easy to detect the tumor at the exact location by using computers through digital image processing. By detection of brain tumors, we can identify not only the affected part of the brain but also the size, boundary, shape and position of the tumor. There are different kinds of imaging technologies such as computed tomography (CT), magnetic resonance image (MRI), etc. and these technologies are used for brain imaging

[7].

The physiology of the brain tumor can be tested by a CT scan or MRI. MRI (magnetic resonance imaging) is a type of scan that uses strong magnetic fields and radio waves to produce high- quality images of the inside of the body and body parts such as the brain, bones, joints, heart, blood vessels and internal organs. Through the high quality or resolution of the image we can derive the corporal tidings and can easily apprehend the abnormalities of tumors. Moreover, that technique can easily detect the varieties in tissues and structure of the tissues. But, the main goal of our tumor detection by image processing is going to solve by multiple machine learning algorithms. Machine learning is an application of artificial intelligence that provides systems the ability to automatically learn and improve from experience without being explicitly programmed furthermore, it is the concept that a computer program can learn and accommodate to new data without human trespass. Machine learning mainly focuses on the development of computer programs that can access data and use it to learn for themselves moreover, it enables the exploration of voluminous quantities of data. Moreover, machine learning algorithms are classified as supervised or unsupervised. Supervised machine learning algorithms can be applied where what has been learned already in the past to new data using labeled examples to predict future thoughts. On the other hand, when the information is not classified or labeled then unsupervised machine learning algorithms are being used. So, we will use machine learning for our image processing. suppose, training the machine to do something (here, image processing) by providing a set of training data. Machine Learning has models/architectures, loss functions and several approaches that can be used to determine which would provide better image processing.Also, it depends on the type of image processing that we intend to do as certain loss functions perform better than others due to their inherent properties for example there's a high possibility that cross-entropy loss function could perform better than other loss function to give a better image processing.

A. Causes of Tumor Development

In general, tumors occur when cells divide and grow unreasonably in the body. Normally, the body controls cell growth and division. New cells are created to supplant older ones or to perform new functions. Cells that are damaged or no longer needed die to make room for healthy replacements. If the balance of cell growth and death is disturbed, a tumor may form. Problems with the body's immune system can lead to tumors. Tobacco causes more deaths from cancer than any other

environmental substance.

The risk factors are [17]:
• Benzene and other chemicals and toxins
• Drinking too much alcohol
• Environmental toxins, such as certain poisonous mushrooms and a type of poison that can grow on peanut plants (aflatoxins) • Excessive sunlight exposure

- Genetic problems
- Obesity
- Radiation exposure
- Viruses

B. Causes and Classification of Brain Tumor

The reason for most brain and spinal cord tumors is not completely perceived, and there are not many settled danger factors. In any case, scientists have discovered a portion of the progressions that happen in typical synapses that may lead them to shape brain tumors. There are three types of Tumor: 1)Benign 2)Pre malignant 3) Malignant [18]

Benign Benign tumors are abnormal growths that are no longer under normal regulation .They are not cancerous .They develop gradually, take after typical cells, and are not harmful .They grow only in one place and cannot spread or attack different parts of the body. They can anyway get unsafe on the off chance that they push on essential organs.They do not generally return after being removed [20]. Examples of benign tumors include skin moles, lipomas, hepatic adenomas [19]. 8 **Pre malignant** In these tumors, the cells are not yet cancerous, but they have the potential to become malignant. i.e. developing the properties of cancer.

Malignant These tumors are composed of embryonic, primitive, or poorly differentiated cells. They grow in a rapid, disorganized manner that is harmful to the body. They can also invade surrounding tissues and are become metastatic, initiating the growth of similar tumors in distant organs.

C. Literature Review of Paper "A Noble Approach for Brain Tumor Detection Using MRI Images"

[2]

Based on modern technology, the most commonly used brain tumor detection technology is MRI. Where wave used MRI from all over the body tissues to find out the high-quality image. The smallest abnormality in the body can be identified by MRI, which has the great ability to recognise the variations in tissue structure. It is more suitable for tumor size detection than computed tomography. Thresholding, which splits an image into two regions and forms a binary image for segmentation, is a more flexible technique. It offers a better outcome since the threshold value depends on the variance of the inner cluster [10]. And the morphological operation is a large image processing operation in which each pixel is modified based on the value of another neighborhood pixel to process images based on shapes in this operation. out On the binary images, the morphological filter works and output through operations like erosion and dilation. They used threshold segmentation based on the morphological operation in this paper. Based on the morphological operation, this two-approach greatly improves the threshold segmentation, identification and extraction of the tumor region , They first retrieved the image from the MRI database in their suggested technique and then submitted the image to be pre-processing and enhancement. Where the noise and high-frequency device are removed and the patient's data are also removed. The

median filter and histogram equalization for image enhancement were used for pre-processing. Threshold segmentation is achieved here by turning all pixels below the threshold to one and all pixels above the threshold to one by taking the binary picture from gray-level ones. And it defines and extracts relevant information in the case of morphological operation by using the properties of the shape in the image using binary opening and binary closing with the assistance of an equation. This morphological method detects the tumor region in MRI brain images, and also detects the tumor image alone and also the picture of the morphological operation.(2016 Abd and Shuai)

D. Literature Review of Paper " "Brain Tumor MRI Images Detection and Segmentation Using Genetic Algorithm"

[4]

A naturally-inspired meta heuristic algorithm is the Genetic Algorithm (GA). Where each solution is represented as a chromosome, each chromosome is constructed from genes. They proposed automatically finding out the position and edge of the tumor in this paper. This analysis was carried out on real images. Due to poor image contrast and artifacts that result in missing or diffuse tissue borders, segmentation of MRI images is challenging. In order to detect MR brain images, this paper proposed a discrete wavelet-based Genetic Algorithm. First, the MR images are enhanced with discrete wavelet description in their proposed methodology and then the genetic algorithms are applied to detect the tumor pixels. It needs to go through four phases to execute genetic algorithms. The first step is the genotype, whereby the result of an image SI segmentation using k-means is regarded as an individual described by the class of each pixel. The second step is the initial population, where the genotype characterizes a set of individuals. It consists of a combination of the outcomes of segmentation. The third step is the function of fitness, which allows us to quantify an individual's fitness to the environment by considering its genotype. There are two phases in the fitness function and these two phases run from the formation of the cluster until the chromosome is encoded. By the mean points of the respective cluster. They went through the two processes, which are a selection of people and mutation and cross-over of people, after completing all four phases, to go to the next implementation process, which is the termination criterion. We'll get the final outcome after that. Their outcome demonstrates that their algorithm is flexible and simple. (2018, Joseph)

E. Literautre Review of Paper "Automatic Human Brain Tumor Detection in MRI Image Using Template-Based K Means and Improved Fuzzy C Means Clustering Algorithm"

[1]

This paper proposes a Template based K-means and modified Fuzzy C-means clustering algorithm also known as TK-FCM to propose a model that identifies or detects brain tumor from MRI images. In this model, the template is selected based on the convolution between the intensity of the grey level in

the small portion of the brain image and the image of the brain tumor. K-means algorithm accentuates the initial segmentation by the selection of the template. The paper calls the C means integration as a mathematical improvement to the K means model as its clustering method of identifying different features can add to important information that can help to identify the tumor in an MRI image better as opposed to just a single cluster centroid using a mean calculation of the data points in a K means model. The paper claims that the results for this model shows a better distinction between irregular and regular brain tissues. It also claims that the calculation for this model in identifying distinctions in brain tissues are faster than that of other models. The paper proposes that their TKFCM model has such high accuracy that even very tiny irregularities in Brain tissues! They also propose the algorithm to work more effectively and accurately than other algorithms for noisy images. In clustering, K implies clustering calculation, the most widely used brain tumor discovery strategies are the calculation of FCM clustering computations and the maximization of expectations (EM). Clustering is a process by which information is divided into certain bunches. In K-means clustering algorithm the calculation is not supervised, that raw data are isolated into k bunches where k could be a positive number. It is a very basic calculation of clusters, provides clusters and works well for multi dimension information. When the number of factors is huge, it works faster than different level clustering. The paper however admits to the poor performance of the algorithm to large datasets and yet proposes its higher execution time as opposed to Artificial Neural Network as a major advantage for their preference. The paper then describes how the K means model and algorithm utilizes the dataset into K pre-defined separate, non-overlapping subgroups (clusters), where only one group is part of each point. It attempts to keep the inter cluster data points as similar as possible and the clusters as distinct (far). It allots data points to a cluster, so that all data points belonging to that cluster are at a minimum amount of the squared distance between data points and the arithmetical mean of the cluster's centroid. The less change in clusters, the more homogenous the data points are in the same cluster. The entire tumor detection methodology in the human brain has been introduced. It then describes how the C means algorithm is integrated by the model by feeding this pre processed image which has gone through the K means model to the fuzzy C means algorithm which then separates the features using its multiple clusters groups on the single cluster group of the K means processed image. This is shown in Figure 1 below.

The images collected in the data set are most often so deprived of the quality that filters clamor and forms the image. The image obtained is converted into a two-dimensional gate in the pre-processing step and is converted in the RGB image to a gray image. A middle channel is used to kill the concussion in the picture. At that point, the image is upgraded by a balanced operation based on the histogram. The initial fragmentation using a format K-means (TK) is based on the premise that concentrates gray level and color mood where k =
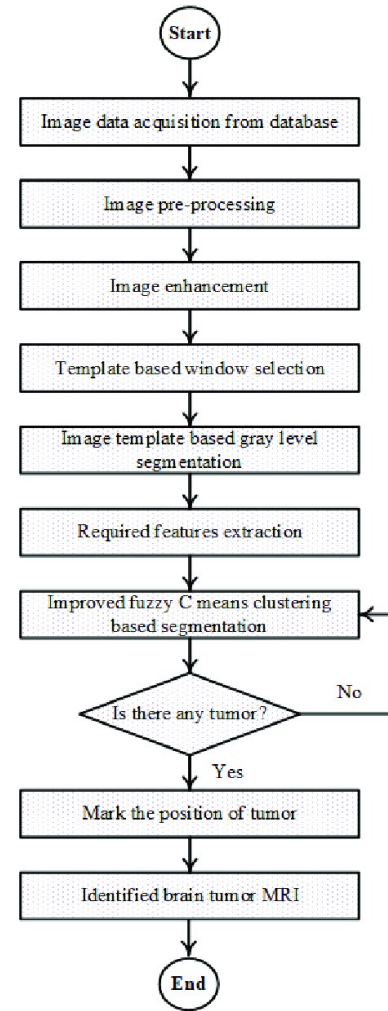

Fig. 1. Flowchart of the proposed TKFCM algorithm.

8 is concentrated at that level. Once again, the tumor is sifted by the median filter. At that point, the tumor is identified and checked as a rugged line using the advanced FCM algorithm based on the Euclidean removal from the cluster center to each information point, which is essentially dependent on the different features. This may be critical if we are to get a grip on the significance of this modified and incorporated technique. The enhanced FCM is performed for 13 clusters on the basis of the gray level strength. The clustered images are then separated factoring the lowest grey level and differences colour intensity. And therefore the paper proposes that TKFCM has a better precision than the other models! The results presented in the paper are as follows :-

- In detecting human neoplasm, the sensitivity of the proposed TKFCM algorithm is 27.07%, 4.75%, 1.98%, 2.03%, 15.11% and 17.89%.
- The specificity of the proposed TKFCM algorithm is 27.04%, 16.07%, 11.2%, 5.56%, 9.1% and 20.00% over the standard thresholding. [10]
- The accuracy of the proposed TKFCM algorithm is

25.64%, 7.692%, 5.12%, 2.56%, 12.82% and 17.94% over the standard thresholding.

F. Literature Review of Paper "Automatic Brain Tumor Detection and Segmentation Using U-Net Based Fully Convolutional Networks"

[3]

This paper proposes U-Net Based Fully Convolutional Networks for Brain tumor detection and segmentation. This paper begins by analyzing the different medical imaging methods for brain tumor segmentation from Ionizing radiation techniques to Magnetic resonance imaging (MRI). The paper then goes onto explain the inefficiency of manual segmentation for MRI imaging due to its time consuming and human error prone nature, which is why much faster and human error p less technology powered algorithms have taken over. The paper then sets up high grade glioblastoma (HGG) and low grade gilomas (LGG) as the tumors that are going to be the major targets for identification using these U Net Based Fully CNN's using the BRATS datasets [12]. The paper then describes the challenges as contrasts generated during imaging by these various protocols create an image with all the physical complexities in the brain and thus provide valuable visual information that can eventually diagnose the tumor successfully. Usual MRI protocols use fluid-attenuated reverse retrieval, weighted T1 and T2 or FLAIR and gadolinium-enhanced T1 images. The segmented extent of the brain tumor can separate structures from other tissues of the brain and thus allow a more accurate classification of brain tumor types. Segmentation of longitudinal MRI scans can also accurately track the recurrence of brain tumors, both growth and shrinkage. But even in this case, operators have to manually delineate the method to allow space for mistakes and subjective decision-making which is what the paper wants to eliminate using its model. The paper then informs us of the supervised learning that the BRATS dataset will be put through as opposed to the unsupervised learning because deep learning requires a hierarchy of increasingly complex features directly from the data.The fundamental idea behind a totally convolutionary network is that all its layers in other words are fully - connected layers.The paper then describes how fully connected layers use convolutional layers to classify each pixel in the image. Therefore, the final layer of output is the same height and width as the image, but the number of channels is equal to the number of classes. The final output layer will be height x width x 15 classes if we classify each pixel as a class of fifteen. We can find the most likely class for every pixel with a soft max probability function. The proposed supervised learning approach was validated with both LGG and HGG patients' data obtained [14]. Our fully automatic method obtained promising results compared to manually defined ground truth. Compared to other state-of-the-art methods, comparable results have been achieved for the delineation of the complete tumor regions and higher segmentation for the core tumor regions.

II. PROPOSED METHODOLOGY

This section describes the process of brain tumor segmentation approach of our U-NET based Convolutional Neural Network in detail including CNN methodology, Algorithm, Reason behind using CNN, U-NET architecture.

A. Brief description of U-net Architecture:

The UNET for Bio Medical Image Segmentation was designed by Olaf Ronneberger et al. There are two approaches to this architecture. The first path is the path of contraction (also called the encoder) that is used in the image to capture the context. The encoder is just a conventional stack of layers of convolutional and max pooling. The second path is the symmetrical expanding path (also referred to as the decoder) that uses transposed convolutions to allow precise localization. It is therefore a fully convolutional end-to-end (FCN) network, i.e. it only contains convolutional layers and does not contain any dense layer that enables it to accept images of any size.
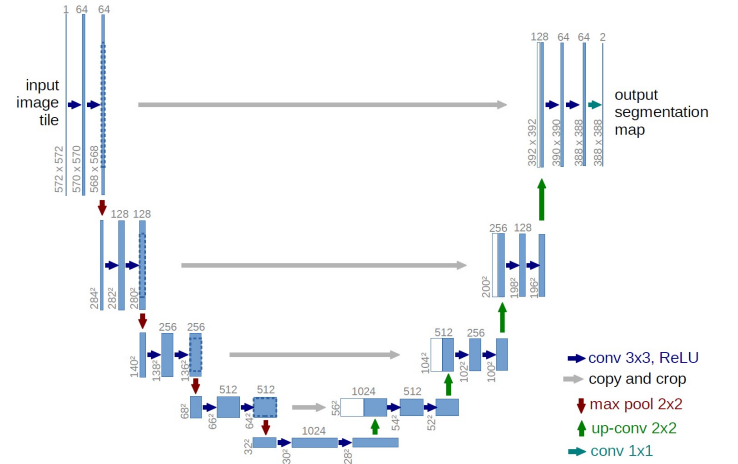
B. ILLUSTRATION OF U-NET ARCHITECTURE:

Fig. 2. U-net Architecture

Fig 2:U-net Architecture (Example for the lowest resolution of 32*32 pixels). Each blue box corresponds to a multi-channel feature map. On the top of the box, the number of channels is denoted. At the lower left edge of the box, the x-y size is given. White boxes represent copied feature maps. The arrows denote the distinct operation.
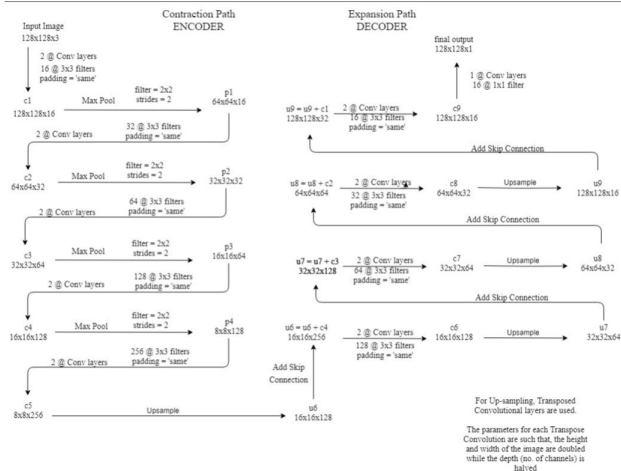
The extensive description of the architecture is below:

Fig. 3. Detailed U-net Architecture

Points that are to be mentioned:

o 2@Conv layers suggest that the application of two consecutive Convolution Layers

o c1, c2, ... c9 are the output tensors of Convolutional Layers

o The output tensors of Max Pooling Layers p1, p2, p3 and p4 are

o The output tensors of up-sampling (transposed convolutional) layers are u6, u7, u8 and u9

o The left hand side is the contraction path (Encoder) where we apply regular convolutions and max pooling layers.

o The right side is the direction of expansion (Decoder) where transposed convolutions are added along with standard convolutions.

o In the Encoder, the size of the image gradually reduces while the depth gradually increases. Starting from 128x128x3 to 8x8x256

o This simply means that the network knows the "WHAT" data in the image, but it has ignored the "WHERE" data in the image.

o In the decoder, the size of the image gradually increases and the depth gradually decreases. Starting from 8x8x256 to 128x128x1 o Intuitively, the Decoder recovers the "WHERE" information (precise localization) by gradually applying upsampling

o To get better precise locations, at every step of the decoder we use skip connections by concatenating the output of the transposed convolution layers with the feature maps from the Encoder at the same level:

u6 = u6 + c4

u7 = u7 + c3

u8 = u8 + c2

u9 = u9 + c1

After every concatenation we again apply two consecutive regular convolutions so that the model can learn to assemble a more precise output

o This is what gives the architecture a symmetric U-shape, hence the name UNET

o On a high level, we have the following relationship:

o Input (128x128x1) =¿ Encoder =¿(8x8x256) =¿ Decoder =¿Ouput (128x128x1)

C. Convolutional Neural Network

Convolutional Neural Network: In the medical image processing field, the Convolutional Neural Network is widely used. For tumor identification, a Five-Layer Convolution Neural Network has been introduced and implemented. An input form of the MRI images is created using the convolutional layer as the beginner layer, which is 64 * 64 * 3, transforming all the images into a homogeneous dimension. We generated a convolutional kernel that is convoluted with the input layer after accumulating all the images in the same aspect, administering 32 convolutional filters of size 3 * 3 each with the help of 3 channel tensors. ReLU is used as an activation function, such that the output does not corroborate.

For spatial data that is supported by our input map, we use MaxPooling2D for the model. This convolutional layer resides on a scale of 31*31*32. The pool size is (2, 2) since the input images are divided into all spatial dimensions, indicating a tuple of two integers that can be down scaled vertically and horizontally.

A pooled features map is obtained after the pooling layer. After the pooling, flattening is one of the essential layers since we have to turn the whole matrix representing the input images into a single column vector, and for processing it is imperative. For computation, it is then fed to the Neural Network.

Two entirely connected layers were used and Dense-1 and Dense-2 represented the dense layer. For the operation of the Neural Network, the dense function is used in Keras, and the vector obtained acts as an input for this layer. In the secret layer, there are 128 nodes. Since we held it as mild as possible because of the amount of dimension or nodes equal to the computational capital we need to fit our model, and 128 nodes provide the most important outcome for this perspective. To demonstrate better convergence efficiency, ReLU is used as the activation function. The second fully-connected layer was used as the final layer of the model after the first thick layer. [4]

Using Adam optimizer and binary cross-entropy as a loss function, we compiled the model and find the accuracy of detecting the tumor. An algorithm is depicted below where we evaluated the performance of the model.

Algorithm : Evaluation process of CNN model

loadImage();

dataAugmentation();

splitData();

loadModel();

for each epoch in epochNumber do

for each batch inbatchSize do

y = model (features);

loss = crossEntropy(y, y);

optimization(loss);

Working Flow Devised for Proposed Methodology

1. Load the input dataset

2. Adding a Convolution Layer with 32 convolutional filter

3. Passing the Convolutional kernel into the Max Pooling layer

4. Pooled feature map is used to get the single column vector

5. Processing of the vector in dense layer with 128 nodes

6. Final dense layer applying Sigmoid as the Activation function

7. Validation stage and Performance evaluation

Fig. 4. CNN Methodology

```
accuracy();
bestAccuracy = max(bestAcuuracy, accuracy);
return
```

D. Reason behind choosing CNN:

Assume we have a standard neural feed-forward network, and as an input, giving it the word "neuron" and process the word character by character. "It has already forgotten about "n," "e" and "u" by the time it hits the character "r," which makes it almost difficult for this form of neural network to determine which character will come next. However, because of its internal memory, a recurrent neural network is capable of recalling certain characters. This creates output, copies it and loops it back into the network. Simply stated, recurrent neural networks add the present to the recent past. Therefore, two inputs are required for an RNN: the current and the recent past. This is important because the data sequence provides vital details on what is coming next, which is why other algorithms can not do things an RNN can.

The state of the art sequential data algorithm, Recurrent Neural Networks (RNN), is used by Apple's Siri and Google's voice scan. Because of an intrinsic memory, it is the first algorithm that remembers its input, which makes it ideally suited for machine learning problems involving sequential data. It is one of the algorithms behind the scenes of the incredible successes over the past few years seen in deep learning.

III. DATA AND RESULT ANALYSIS

In this study, it had been identified distinct genomic subtypes of low-grade gliomas could potentially be used to guide the treatment of patients. The aim of this study is to determine whether there is an association between the genomics of low-grade glioma tumors and patient outcomes using computational measurements of tumor morphology in magnetic resonance imaging (MRI) [8]. Preoperative imaging and genomic data had been used from 110 patients from 5 facilities with inferior gliomas from the Cancer Genome Atlas. To analyze the imaging data, computer algorithms were applied and given five quantitative tumor shape measurements in two dimensions. Based on IDH mutation and 1p/19q co-deletion, DNA methylation, gene expression, DNA copy number, and microRNA expression, the genomic data for the examined patient cohort consisted of previously identified genomic clusters. Tumors associated with much worse results in the IDH wild type cluster and R2 RNASeq cluster typically had higher ASD indicating a more irregular form. The images were obtained from the archive of cancer imaging. The image dataset contains 110 patients with a total of 4456 brain images where we used 1056 images for test. Here we used 70% images for training and 30% images for testing. Each image contained an original size of 128 x 128 x 1 in pixels [9].

A. Comparison of different functions:

We tried to show the difference in our result when we use different combination of Activation function and Optimizer function.

ReLU: The rectified linear activation function or ReLU for short is a piecewise linear function that will output the input directly if it is positive, otherwise, it will output zero. ... The rectified linear activation function overcomes the vanishing gradient problem, allowing models to learn faster and perform better.

Adam: Adam is an optimization algorithm that can be used instead of the classical stochastic gradient descent procedure to update network weights iterative based in training data.

ELU: Exponential Linear Unit or its widely known name ELU is a function that tend to converge cost to zero faster and produce more accurate results.

RmsProp optimizer: RmsProp is an optimizer that utilizes the magnitude of recent gradients to normalize the gradients. We always keep a moving average over the root mean squared (hence Rms) gradients, by which we divide the current gradient.

B. Result and discussion

Convolutional neural network method has been used to analysis the performance for the algorithm. Different kinds of activation functions and optimizer has been used to find the accuracy level. First of all, the combination of activation function 'elu' and optimizer 'ADAM' has shown 90.40%, 98.64%, 99.23%, 99.27%, 99.35%, respectively. moreover, , the combination of activation function 'elu' and optimizer 'RMSPROP' has shown 90.28%, 98.48%, 99.17%, 99.27%, 99.33%, respectively. Furthermore, , the combination of activation function 'ReLU' and optimizer 'RMSPROP'

has shown 90.28%, 98.96%, 99.23%, 99.35%, 99.41%, respectively. However, the combination of activation function 'ReLU' and optimizer 'ADAM' has shown 96.19%, 99.20%, 99.32%, 99.39%, 99.45%, respectively. From the comparison, it is observed that the activation function 'ReLU' and the optimizer 'ADAM' performs better than others.

```
up8 = concatenate([Conv2DTranspose(128, (2, 2), strides=(2, 2), padding='same')(bn7), conv2], axis=3)
conv8 = Conv2D(128, (3, 3), padding='same')(up8)
bn8 = Activation('relu')(conv8)
conv8 = Conv2D(128, (3, 3), padding='same')(bn8)
bn8 = BatchNormalization(axis=3)(conv8)
bn8 = Activation('relu')(bn8)

up9 = concatenate([Conv2DTranspose(64, (2, 2), strides=(2, 2), padding='same')(bn8), conv1], axis=3)
conv9 = Conv2D(64, (3, 3), padding='same')(up9)
bn9 = Activation('relu')(conv9)
conv9 = Conv2D(64, (3, 3), padding='same')(bn9)
bn9 = BatchNormalization(axis=3)(conv9)
bn9 = Activation('relu')(bn9)

conv10 = Conv2D(1, (1, 1), activation='sigmoid')(bn9)

model =Model(inputs=[inputs], outputs=[conv10])
model.compile(loss=dice_coef_loss,
              optimizer="ADAM",
              metrics = ['accuracy',dice_coef])

return model
```

Fig. 5. ReLU and ADAM(Attributes)

In the above figure5: ReLU has been used for activation function and ADAM has been used for optimizer. By using this combination, we found the better accuracy.
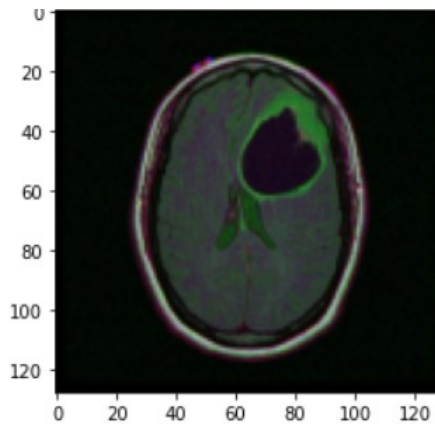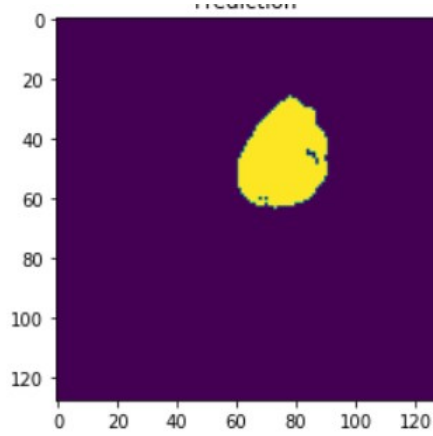

Fig. 6. Input image

Fig. 7. Output image.

Fig. 8. Maximum accuracy (01)

From the above figure of accuracy level01, here it has been shown top five epochs where the accuracy are 96.19%, 99.20%, 99.32%, 99.39%, 99.45%.

Fig. 9. Maximum accuracy (02)

From the above figure of accuracy level02, here it has been shown the next epochs where the accuracy are 99.49%, 99.50%, 99.53%, 99.54%, 99.57% respectively.

TABLE I
DATA ANALYSIS TABLE(A)

Activation function	Optimizer function	Epoch	Loss	Accuracy	Dice coefficient Accuracy	Val Loss	Val accuracy	Val dice coefficient
ReLU	Adam	1/30	-0.3195	0.9619	0.3209	-0.0131	0.1741	0.0127
ReLU	Adam	2/30	-0.6365	0.9920	0.6368	-0.0155	0.3056	0.0150
ReLU	Adam	3/30	-0.6747	0.9932	0.7050	-0.4079	0.9952	0.4094
ReLU	Adam	4/30	-0.7441	0.9939	0.7438	-0.3829	0.9956	0.3857
ReLU	Adam	5/30	-0.7720	0.9945	0.7725	-0.4561	0.9949	0.4648

TABLE II
DATA ANALYSIS TABLE(B)

Activation function	Optimizer function	Epoch	Loss	Accuracy	Dice coefficient Accuracy	Val Loss	Val accuracy	Val dice coefficient
Elu	Adam	1/30	-0.1831	0.9040	0.1825	-0.0112	0.0315	0.0109
Elu	Adam	2/30	-0.5218	0.9864	0.5206	-0.0139	.02285	0.0135
Elu	Adam	3/30	-0.6697	0.9923	0.6690	-0.4213	0.9956	0.4252
Elu	Adam	4/30	-0.6888	0.9987	0.6894	-0.4545	0.9948	0.4665
Elu	Adam	5/30	-0.72.59	0.9935	0.7262	-0.4574	0.9952	0.4675

TABLE III
DATA ANALYSIS TABLE(C)

Activation function	Optimizer function	Epoch	Loss	Accuracy	Dice coefficient Accuracy	Val Loss	Val accuracy	Val dice coefficient
ReLU	RMSProp	1/30	-0.1325	0.9028	0.1332	-0.0114	0.9941	0.0112
ReLU	RMSProp	2/30	-0.4936	0.9896	0.4932	-0.1867	0.9926	0.1817
ReLU	RMSProp	3/30	-0.6624	0.9923	0.6622	-0.3157	0.9945	0.3349
ReLU	RMSProp	4/30	-0.7224	0.9935	0.7227	-0.4678	0.9952	0.4842
ReLU	RMSProp	5/30	-0.7577	0.9941	0.7581	-0.5223	0.9958	0.5362

TABLE IV
DATA ANALYSIS TABLE(D)

Activation function	Optimizer function	Epoch	Loss	Accuracy	Dice coefficient Accuracy	Val Loss	Val accuracy	Val dice coefficient
ELu	RMSProp	1/30	-0.1719	0.9028	0.1735	-0.0114	0.0541	0.1387
ELu	RMSProp	2/30	-0.4606	0.9848	0.4625	-0.1412	0.9755	0.1387
ELu	RMSProp	3/30	-0.6492	0.9917	0.6480	-0.4126	0.9957	0.4195
ELu	RMSProp	4/30	-0.6894	0.9927	0.6902	-0.3519	0.9942	0.3602
ELu	RMSProp	5/30	-0.7238	0.9933	0.7234	-0.1520	0.9940	0.1697

IV. CONCLUSION AND FUTURE WORK

We plan to use a convolutional neural network which is a part of machine learning algorithm in image processing for the detection of brain tumors. This article is a draft of stuff that we are going to deal with. We have explored all the recent common segmentation techniques in this paper that have shown good efficiency and accuracy and tried to reduce if not eliminate human delineation in such matters, thus eliminating human error. The paper describes the segmentation techniques and the algorithms such as template-based K means algorithm, fuzzy logic algorithm, convolutional neural network, FCM, TKFCM and TK means algorithm but we used convolutional neural network (CNN) for our work. We also briefly describe the methodology we will follow in the future for our thesis. Through our methodology and research objective we move forward. There are many fields to function or grow but we have chosen image processing because nowadays, the brain tumor is an important medical issue. Although there are lots of researchers behind the subject working in different ways, the rate of accuracy still leaves a lot to be desired. We want to improve this field so it can be useful for medical research in the future.In addition to the use of machine learning in medical imaging, we agree that attention in the medical world can also be leveraged to improve the general computational attitude of

medical researchers and practitioners, integrating the field of computational medicine Once the everyday workflow in the clinic has sufficient high-impact software systems based on mathematics, computer science, physics and engineering, the acceptance of other such systems would likely expand. Access to biosensors and (edge) computing on wearable disease or lifestyle tracking systems, plus a machine learning environment and other computational medicine-based innovations, would likely accelerate the transition to a new predictive, preventive, personalized and participatory medical paradigm, P4 medicine. Therefore, we want to increase the precision rate by using advanced machine learning techniques.

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