Brain Tumor Detection Through Image Processing

by

Tahaziba Azmim
17301019
Azizul Hakim chy.Shumon
18301300
Maksud Alam
16201033
Saurav Ahmed Mishu
16201022
Nuhash Ahmed Chowdhury
16301037

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Declaration

It is hereby declared that

1. The thesis submitted is my/our own original work while completing degree at Brac University.
2. The thesis does not contain material previously published or written by a third party, except where this is appropriately cited through full and accurate referencing.
3. The thesis does not contain material which has been accepted, or submitted, for any other degree or diploma at a university or other institution.
4. We have acknowledged all main sources of help.

Student's Full Name & Signature:

Tahaziba Azmin
17301019

Azizul Hakim chy.Shumon
18301300

Maksud Alam
16201033

Saurav Ahmed Mishu
16201022

Nuhash Ahmed Chowdhury
16301037

Approval

The thesis/project titled "Brain Tumor Detection Through Image" submitted by

1. Tahaziba Azmin (17301019)
2. Azizul Hakim chy.Shumon (18301300)
3. Maksud Alam (11201009)
4. Saurav Ahmed Mishu (16201022)
5. Nuhash Ahmed Chowdhury (16301037)

Of Fall, 2020 has been accepted as satisfactory in partial fulfillment of the requirement for the degree of B.Sc. in Computer Science on January 08, 2020.

Examining Committee:

Supervisor:
(Member)

Mostafijur Rahman Akhond
Lecturer
Department of Computer Science and Engineering
Brac University

Program Coordinator:
(Member)

Md.Golam Rabiul Alam
Program Coordinator
Department of Computer Science and Engineering
Brac University

Head of Department:
(Chair)

Mahbub Alam Majumdar
Head of Department
Department of Computer Science and Engineering
Brac University

Abstract

Start with image processing for brain tumor detection technologies. i.e. (Tumor/cancer cell detection from brain images are largely dependent on image processing techniques, as these images are complicated and having multiple levels of changes human eyes are not suitable to read the changed cells). There are various kinds of devices which help to detect brain tumor such as MRI scans, CT scans, etc. MRI (Magnetic Resonance Imaging), is the device that can detect any organ and brain problem. Cell multiplication on segmentation is an essential method to analyze the brain tumor images. The segmentation or cell multiplication can figure the tumor along with its around-compartments and also nearby tissues but, it is challenging enough for fixation and shaping the morphological changes which are caused by the tumor. Though there have a lot of existing works on the topic. Many approaches were used to develop image processing such as, template-based K means algorithm, fuzzy logic algorithms, threshold segmentation, etc. but, the accuracy of success rate is still not up to the mark. So, we are planning to improve the accuracy by using our approaches like machine learning, deep learning, deep neural network, and neural network algorithms. Our main objective is to compare multiple machine learning algorithms where we may find better accuracy for tumor detection. Moreover, we will use the statistical approach to find out the most probable locations of tumor starting cells. Though this affair is improving day by day, it will be more favorable to implement for future improvement.

Keywords: Data Mining;Image Processing; Cell multiplication; Tumor detection ; Template-based K means algorithm; Fuzzy logic algorithms; Threshold segmentation; Machine learning; Deep learning; Deep neural network; neural network algorithms; Accuracy; Statistical approach.

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Nomenclature

The next list describes several symbols & abbreviation that will be later used within the body of the document

ϵ Epsilon

υ Upsilon

IPL Indian Premier League

LBW Leg before Wicket

MR Runs scored by Home team

MRN Home Team Run Rate

ODI One day International

OR Runs scored by the opponent team

ORN Opponent Team Run Rate

$T20$ Twenty Twenty

Chapter 1

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.[**2**] 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[**1**]. 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 [**3**]. 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 technic 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 newish 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.

Chapter 2

Research Methodology

As indicated on the top this portion of our research paper includes the research methodology of our thesis paper. We tried to outline the research strategy, the research method, the research approach, the methods of data collection, the selection of the sample, the research process, the type of data analysis, the ethical consideration and the research limitations of the project.

2.1 Research strategy

The research held concerning this dissertation was an applied one but not new. Rather numerous pieces of previous academic research exist regarding tumor detection using MRI and brain image analysis. Our team researched some of the modern strategies that took place in recent times such as Morphological operations, Threshold segmentation, K means, Fuzzy C means clustering and U-net based networks. In our proposal we would like to use the concept of neural network and deep learning methods. The neural network is trained by adjusting neuron input weights based in the network's weights contributing performance on example inputs. If the network classifies an image correctly, weights contributing to the correct answer are increased while other weights are decreased. The procedure allowed early neural networks to learn in a way that superficially resembled the behavior of the human nervous system.

2.2 Why machine learning

First of all from our literature review, where we reviewed the existing methods for brain image analysis and choose machine learning and deep learning as our base for this project. At a very basic level, deep learning is a machine learning technique. It teaches a computer to filter inputs through layers to learn how to predict and classify information. Observation can be in the form of image, text or sound. The inspiration for deep learning is the way that the human brain filters information. This technique is ideal for brain tumor detection as well as our proposal. Though machine learning has been extensively used for brain image analysis but still can be used for this project and produce the expected result.

2.3 Research method – Qualitative versus Quantitative techniques

To satisfy the objective of the dissertation qualitative research was held. The main characteristics of qualitative research are that it is most appropriate for small samples, while its outcomes are not measurable and quantifiable (Table attached below). Its basic advantage, which also constitutes its basic difference with quantitative research, is that it offers a complete description and analysis of a research subject, without limiting the scope of the research and the nature of participant's responses (Collis and Hussey, 2003). However, the effectiveness of qualitative research is heavily based on the skills and abilities of researchers, while the outcomes may not be perceived as reliable because they mostly come from the researcher's judgments and interpretations. Because it is more appropriate for small samples, it is also risky for the results of qualitative research to be perceived as reflecting the opinions of a wider population (Bell, 2005).

2.4 Table: Features of Qualitative and Quantitative Research

[11]
Qualitative research
1) The aim is a complete, detailed description.
2) Researchers may only know roughly in advance what he/she is looking for.
3) Recommended during earlier phases of research projects.
4) The design emerges as the study unfolds.
5) The researcher is the data gathering instrument.
6) Data is in the form of words, pictures or objects.
7) Subjective – An individual's interpretation of events is important,e.g., uses participant observation, in-depth interviews, etc.
8) Qualitative data is more 'rich', time-consuming, and less able to be generalized.
9) The researcher tends to become subjectively immersed in the subject matter.

Quantitative Research
1)The aim is to classify features, count them, and construct statistical models in an attempt to explain what is observed.
2)The researcher knows clearly in advance what he/she is looking for. 3)Recommended during the latter phases of research projects. All aspects of the study are carefully designed before data is collected.
4)The researcher uses tools, such as questionnaires or equipment to collect numerical data.
5)Data is in the form of numbers and statistics.
6)Objective: seeks precise measurement and analysis of target concepts, e.g., uses surveys, questionnaires, etc.
7)Quantitative data is more efficient, able to test hypotheses but may miss contextual detail.
8)The researcher tends to remain objectively separated from the subject matter.

2.5 Research approach

The research approach that was followed for this research was the inductive one. According to this approach, we begin with specific observations, which are used to produce generalized theories and conclusions drawn from the research. The reason for occupying the inductive approach was that it takes into account the context where research effort is active, while it is also most appropriate for small samples that produce qualitative data. However, the main weakness of the inductive approach is that it produces generalized theories and conclusions based only on a small number of observations, thereby the reliability of research results being under question (Denzin and Lincoln, 2005).

A. Experimental Dataset For Performance Evaluation of our proposed model, we used the benchmark dataset in the field of Brain Tumor Segmentation, and that is BRATS dataset, consisting two classes'— class-0 and class-1 represents the Non-Tumor and Tumor MRI images. 187 and 30 MRI Images containing tumor and non-tumor respectively classified as class-1 and class-0. All the images are MRI images from different modalities like- T1, T2, and FLAIR. For traditional machine learning classifiers, we obtained the superlative result splitting the dataset by 70 to 30 in terms of training to testing images, and for CNN, we divided the dataset in both 70 to 30 and 80 to 20 formation and compared the outcomes.

B. Segmentation using Image processing techniques Based on our proposed methodology, we segmented the tumor without loss of any subtle information. We removed the skull because for tumor segmentation the role of skull is approximately null and ambiguous in this process. From the dataset, a 2D MRI was taken as an input image, Skull stripping technique is performed on the input image (Fig. b) followed by image enhancement (Fig. c) for understanding the features of the MRI properly. After that, Gaussian filter (Fig. d) is used for noise removal and finally simulating the FCM segmentation technique (Fig. e) followed by tumor contouring (Fig. f) to find out the ROI which is the tumor for Brain MRI. After the segmentation of the tumor, we classified the tumor based on different traditional Machine learning Algorithms.

Chapter 3

Literature Review

3.1 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[**13**]:
• 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

3.2 Causes and Classification of Brain Tumor

The reason for most brain and spinal cord tumors is not completely perceived[**12**], 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[**14**]

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[**16**]. Examples of benign tumors include skin moles, lipomas, hepatic adenomas[**15**].

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.

3.3 Recurrent neural networks (RNN)

Recurrent neural networks also know in its abbreviated form as RNN's are neural networks with one or more layers of neurons or nodes especially one or more hidden layers therefore fall under the category of multilayer perceptrons or MLP's[**19**] for short.
Sk=f(Sk-1*Wrec+Xk*Wx) [**20**]
Where Sk is the state at time k, Xk an exogenous input at time k, Wrec and Wx are parameters like the weights parameters in feedforward nets. Note that the RNN can be viewed as a state model with a feedback loop. The state evolves over time due to the recurrence relation, and the feedback is fed back into the state with a delay of one timestep. This delayed feedback loop gives the model memory because it can remember information between timesteps in the states.[**21**] The final output of the network Yk at a certain timestep k is typically computed from one or more states Sk-i....Sk+j.[**22**]
Outputs in an RNN are based on previous input. Therefore it is able to accesses past input known as sequential data which is a series of data that can be used to create a pattern. Unlike the state machine the RNN is able to retain memory of past inputs known as sequential memory. To create a Neural Network that's strong for Sequential data, we include an inside state to our feed forward neural network that gives us with internal memory or in nutshell, Recurrent Neural Network may be a generalization of a feed forward neural network that has inner memory. RNN executes the theoretical concept of sequential memory, that makes a difference by providing the past encounter and in this way permitting it to anticipate superior on successive information. RNN proves it recurrent nature by performing the same function for every input, while the output of current input depends upon the past input.
Simple RNN Cells follow this pattern: [**21**] Given the following data:
input data: X
weights: wx
recursive weights: wRec
Initialize initial hidden state to 0
For each state, one by one:
Update new hidden state as:
(Input data * weights) + (Hidden state + recursive weights)

3.4 Deep Neural Networks (DNN)

Deep Neural Networks (DNN) are a type of Artificial Neural Network (ANN) which specificity is to contain more than one covered up layer of neurons between the input layer and the yield layer. DNNs are made and trained to grant precise comes about for the particular purpose they were made for. In the event that you need to utilize a DNN for another purpose, you'll better off be making another one and prepare it for that other reason. The preparing handle is called profound learning. Basically, data is to begin with encouraged to the input neurons. This data will at that point stream through different layers of neurons called hidden layers. Neurons in these hidden layers will send a high or low value to all the neurons within the following layer depending on the degree of significance (weight) of the connection between the primary said neurons and the ones within the previous layer. Finally the output neurons, values, from which we'll choose the highest to represent the result given by our neural network. That's for the forward pass. To train the DNN, the output values are compared to the expected value to calculate the total error, or total cost, of the neural network. We then back propagate the error back through the entire links of the network, with respect to the weights of those links. By doing so, we get the amount of error for which that weight participates towards the total cost. And therefore, how much we should make a change to that weight so that the output of our DNN gets closer to the expected output.

Algorithm for Forward Pass:-
• Sigmoid Function:
$S(x) = 1 + /e^{-}x$
returns a value between 0 and 1
FUNCTION sigmoid(x)
Return $1/(1 + exp^{-}x)$
END FUNCTION
/*
*
*/
PROCEDURE forwardPass()
// HIDDEN LAYERS
FOR each hiddenLayers
FOR each hiddenLayer's neurons
Set weightedSum to 0
FOR each neuron's links
Multiply link's weight with associated previousLayer's neuron's value
Add result to weightedSum
END FOR
Call sigmoid(weightedSum)
Set neuron's value to result
END FOR
END FOR
// OUTPUT LAYER
FOR each outputLayer's neurons
Set weightedSum to 0
FOR each neuron's links

Multiply link's weight with associated
previousLayer's neuron's value
Add result to weightedSum
END FOR
Call sigmoid(weightedSum)
Set neuron's value to result
END FOR
END PROCEDURE
Algorithm for Total Error(Total cost of the Network):-
• For E01 and E02 being the output errors of O1 and O2 respectively:- $E01 = (t1 - O1)^2, E02 = (t2 - O2)^2$
• Total Error of network= E01+E02
• Equation for Process = $n1/2(target_n - Output_n)^2$ n=Number of Output Neurons
PROCEDURE calculateTotalError()
Set totalError to 0
FOR each outputLayer's neurons
IF neuron EQUALS expected output neuron
Set neuron's expectedValue to 1
ELSE
Set neuron's expectedValue to 0
END IF
// /! don't forget the power of 2
Do (1 / 2) * (neuron's expectedValue - neuron's value)**2**
Add result to totalError
END FOR
END PROCEDURE
Combined Algorithm for Backpropogation and Hidden layers:-
FUNCTION sigmoidDerivative(x)
Return sigmoid(x) * (1 - sigmoid(x))
END FUNCTION
/*
*
*/
FUNCTION chainRuleOutput(neuron, link)
Do neuron's value - neuron's expectedValue
Set x to result
Call sigmoidDerivative(neuron's value)
Set y to result
Set z to previousLayer's linkedNeuron's value
Save x and y in link
Return x * y * z
END FUNCTION
/*
*
*/
FUNCTION chainRuleHidden(layer, neuron, link)
Set x to 0
FOR each nextLayer's linkedNeuron's links

```
Do linkedNeuron's link's x * linkedNeuron's link's y * linkedNeuron's link's weight
Add result to x
END FOR
Call sigmoidDerivative(nextLayer's linkedNeuron's value)
Set y to result
Set z to previousLayer's linkedNeuron's value
Save x and y in link
Return x * y * z
END FUNCTION
/*
*
*/
PROCEDURE updateWeights()
// HIDDEN LAYERS
FOR each hiddenLayers
FOR each hiddenLayer's neurons
FOR each neuron's links
Set link's weight to link's newWeight
END FOR
END FOR
END FOR
// OUTPUT LAYER
FOR each outputLayer's neurons
FOR each neuron's links
Set link's weight to link's newWeight
END FOR
END FOR
END PROCEDURE
/*
*
*/
PROCEDURE backpropagation()
Call calculateTotalError()
// OUTPUT LAYER
FOR each outputLayer's neurons
FOR each neuron's links
Call chainRuleOutput(neuron, link)
Set gradient to result
Do link's weight - (learningRate * gradient)
// do not overwrite link's weight (weight =/= newWeight)
Set link's newWeight to result
END FOR
END FOR
// HIDDEN LAYERS
FOR each hiddenLayers
FOR each hiddenLayer's neurons
FOR each neuron's links
Call chainRuleHidden(layer, neuron, link)
```

Set gradient to result
Do link's weight - (learningRate * gradient)
// do not overwrite link's weight (weight =/= newWeight)
Set link's newWeight to result
END FOR
END FOR
END FOR
Call updateWeights()
END PROCEDURE

3.5 U-net and Convolutional Neural Network

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.

ILLUSTRATION OF U-NET ARCHITECTURE

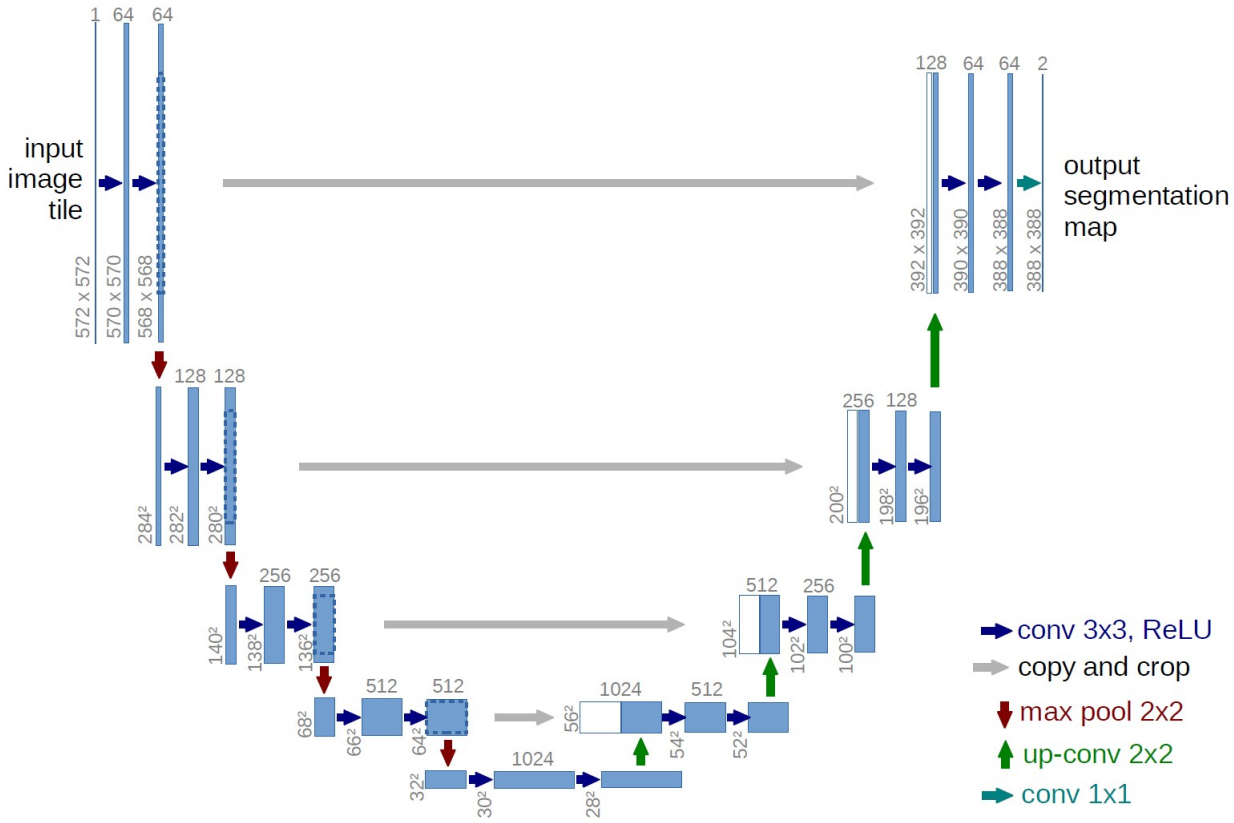

Figure 3.1: U-net Architecture.

Fig-3.1 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:

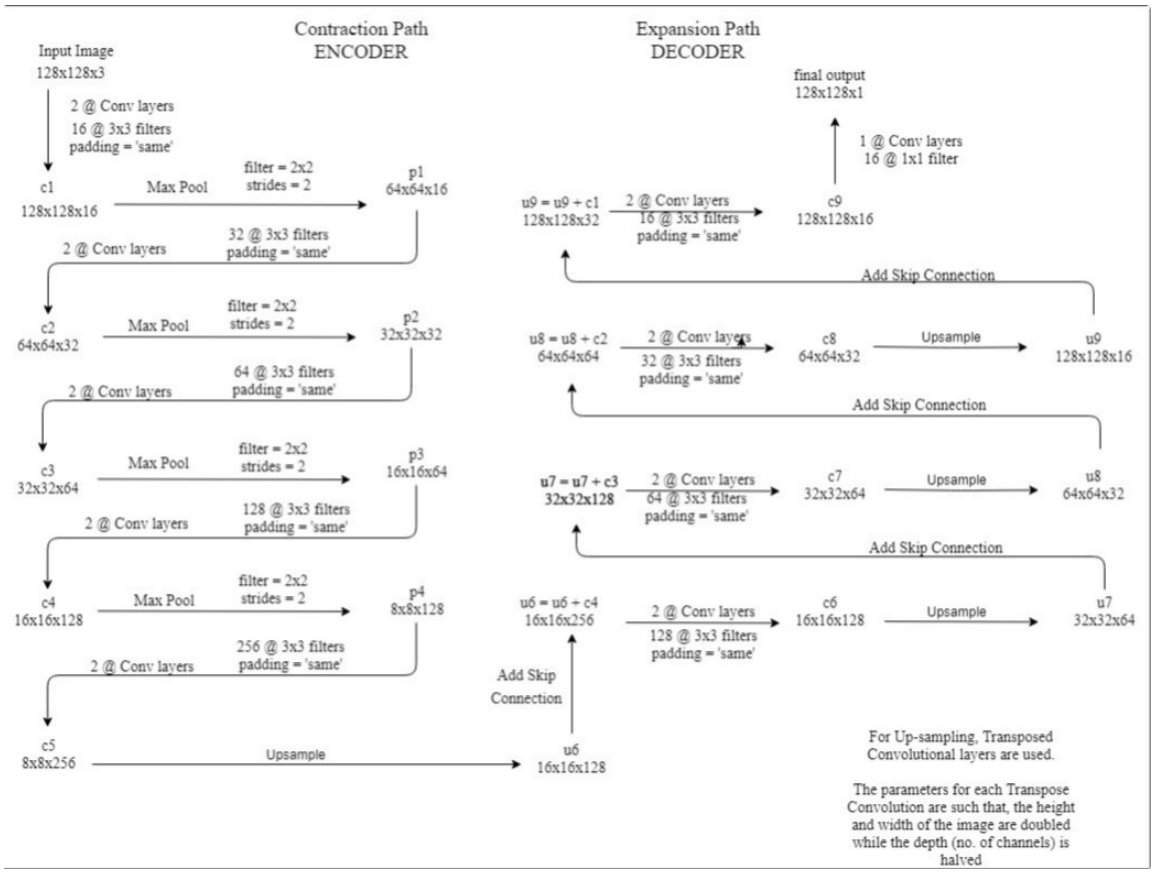

Figure 3.2: Detailed U-net Architectur

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 up-sampling
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)

3.6 Convolutional Neural Network

Convolutional Neural Network is broadly used in the field of medical image processing. A Five-Layer Convolutional Neural Network is introduced and implemented for tumor detection. Using convolutional layer as the beginner layer, an input shape of the MRI images is generated which is 64*64*3 converting all the images into a homogeneous dimension. After accumulating all the images in the same aspect, we created a convolutional kernel that is convoluted with the input layer — administering with 32 convolutional filters of size 3*3 each with the support of 3 channels tensors. ReLU is used as an activation function so that it's not corroborating with the output.
For spatial data which substantiate with our input image, we use MaxPooling2D for the model. This convolutional layer runs on 31*31*32 dimension. Because of divide the input images in both spatial dimensions, the pool size is (2, 2) which means a tuple of two integers by which to downscale by vertically and horizontally.
After the pooling layer, a pooled feature map is obtained. Flattening is one of the essential layers after the pooling because we've to transformed the whole matrix representing the input images into a single column vector and it's imperative for processing. It is then fed to the Neural Network for the processing
Two fully connected layers were employed Dense-1 and Dense-2 represented the dense layer. The dense function is applied in Keras for the processing of the Neural Network, and the obtained vector is work as an input for this layer. There are 128 nodes in the hidden layer. Because the number of dimension or nodes proportional with the computing resources we need to fit our model we kept it as moderate as possible and for this perspective 128 nodes gives the most substantial result. ReLU is used as the activation function because of showing better convergence performance. After the first dense layer, the second fully connected layer was used as the final layer of the model. In this layer, we used sigmoid function as activation function where the total number of the node is one because we need to lower the uses of computing resources so that a more significant amount assuages the execution time. Though there is a chance of hampering the learning in deep networks for using of the sigmoid as the activation function, we scale the sigmoid function, and the number of the nodes is much lesser and easy to handle for this deep network. In a summary, Fig. 1 shown the working flow of the proposed CNN model. [**7**]

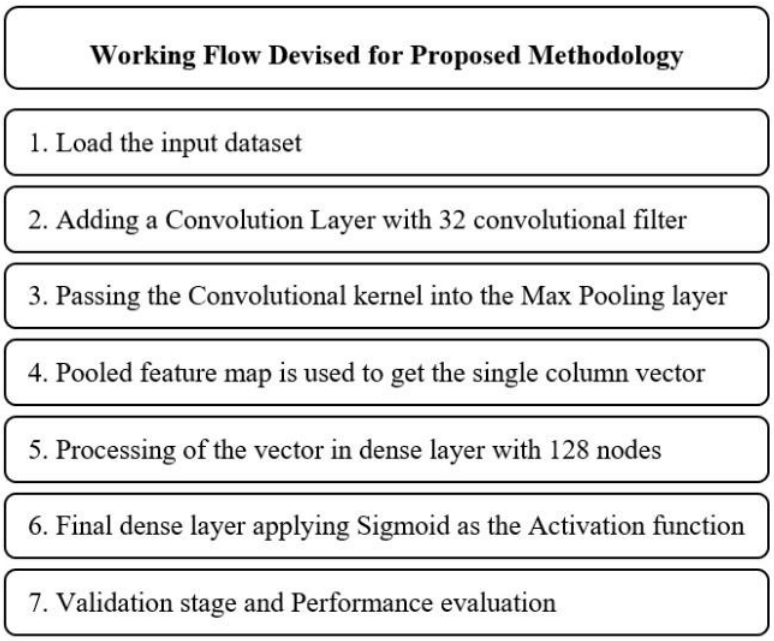

Figure 3.3: CNN Methodology

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

3.7 Image Segmentation and Technology used for Brain Tumor Detection

Image segmentation is the process where many mathematical algorithms are applied for segment-specific parts of the image. Nowadays this process is used in the medical sector for early diagnosis. Brain tumor image is one of the sectors of medical image analysis. Early diagnosis will increase the survival rate of patients. Brain tumor cells are abnormal cells that the brain produces in an uncontrolled way various kinds of brain tumors exist. But there are two types of brain tumors, one is benign and the other is malignant. In the past ten years, the number of brain tumor affected people

has been increasing day by day, it has been reduced by early diagnosis. Researchers are now trying to make a new algorithm for detecting the brain tumor and segment the tumor cell which can help the doctor for making decisions. Researchers are using MRI images for brain tumor image analysis. Four standard MRI modalities for brain tumor diagnosis which are T1 weighted MRI (T1), T2 weighted MRI (T2), T1 weighted MRI with contrast enhancement and Fluid attenuated inversion recovery. During the MR1 acquisition although it can vary from device to device, around one hundred and fifty slices of 20 Images are produced to represent the 3D brain volume. (Soltaninejad, Zhang, Lambrou, Allinson, and Ye, 2017)

3.8 Papers Based on Brain Tumor Detection

In the paper "A Noble Approach for Brain Tumor Detection Using MRI Images" describes

Based on modern technology MRI is the most used technology of detecting brain tumors. Where wave used MRI to find out the high-quality image from all over the body tissues. MRI can detect the smallest abnormality in the body, it has the great ability to identify the differences in tissue structure. It is more appropriate than the computed tomography for identifying tumor size. A more versatile approach is thresholding which divides an image into two regions and forms a binarized image for segmentation. It gives a better result because the thresholding value depends on the inner cluster variance[**6**]. And the morphological operation is broad image processing operation that process image based on shapes in this operation each pixel is adjusted based on the value of another neighborhood pixel. The morphological filter works on the binarized images and provides output through operations like erosion and dilation. In this paper they used threshold segmentation based on the morphological operation. This two-approach improve significantly the threshold segmentation, detection and extraction of the tumor zone based on the morphological operation. In their proposed methodology firstly they collected the image from the MRI database and then they send the image for pre-processing and enhancement. Where it removes the noise and high-frequency artifact and also removes the patient's details. For pre-processing they used median filter and histogram equalization for image enhancement. Here threshold segmentation is done by taking the binary image from gray-level ones by turning all pixels below the threshold to and all pixels above that threshold to one. And in the case of morphological operation it identifies and extracts relevant information by using the properties of the shape in the image using binary opening and binary closing with the help of an equation. This approach based on morphological operation detects the tumor area in MRI brain images, it also detects tumor image alone and also the morphological operation image. (Abd and Shuai, 2016)

In the paper "Brain Tumor MRI Images Detection and Segmentation Using Genetic Algorithm" describes

Genetic Algorithm (GA) is a naturally inspired Metaheuristic algorithm. Where each solution is represented as chromosome and each chromosome is built up from genes. In this paper they proposed to find out the position and edge of the tumor automatically. This research was carried out on real pictures. Segmentation of MRI images is challenging due to poor image contrast and artifacts that result in missing or diffuse tissue boundaries. This paper proposed a discrete wavelet-based Genetic

Algorithm to detect MR brain images. In their proposed methodology they firstly the MR images are enhanced using discrete wavelet description and then the genetic algorithms are applied to detect the tumor pixels. For the execution of genetic algorithms it needs to go through four steps. The first step is the genotype, whereby using k-means segmentation result of an image SI is considered as an individual described by the class of each pixel. The second step is the initial population, where a set of individuals characterized by their genotype. It is composed of the segmentation results to combine. The third step is fitness function, this function enables us to quantify the fitness of an individual to the environment by considering its genotype. In the fitness function there are two phases and these two phases run from the formation of cluster till the encoded in the chromosome by the mean points of the respective cluster. After completing all the four phases they gone through the two processes which are a selection of individuals and mutation and cross-over of individuals, for going to the next process of implementation which is termination criterion. After that we can get the final result. Their result shows that their algorithm is flexible and convenient. (Joseph, 2018)

In the paper "Automatic Human Brain Tumor Detection in MRI Image Using Template-Based K Means and Improved Fuzzy C Means Clustering Algorithm" describes

In late decades, human cerebrum tumor discovery has gotten one of the most testing issues in clinical science. Right now, propose a model that incorporates the layout based K implies, what's more, improved fluffy C implies (TKFCM) calculation for recognizing human cerebrum tumors in an attractive reverberation imaging (X-ray) picture. Right now, initially, the format based K-implies calculation is utilized to introduce division fundamentally through the ideal determination of a layout, in light of dark level force of picture; also, the refreshed participation is controlled by the good ways from group centroid to bunch information focuses utilizing the fluffy C-implies (FCM) [**1**] calculation while it contacts its best outcome, lastly, the improved FCM bunching calculation is utilized for identifying tumor position by refreshing participation work that is acquired dependent on the various highlights of tumor picture including Complexity, Vitality, Difference, Homogeneity, Entropy, and Relationship. Reenactment results show that the proposed calculation accomplishes better recognition of irregular and typical tissues in the human mind under the little separation of dark level power. Also, this calculation distinguishes human mind tumors inside a brief timeframe—in seconds contrasted with minutes with different calculations. Effective identification and evaluation of brain tumors are important. Computer-aided diagnostic (CAD) devices are generally usually used to diagnose systemic and serious brain abnormalities.

A brain tumor is the abnormal tissue development or central spine that can disrupt proper brain function. From the National Statistics Institute on Cancer (NCIS) study. There are some issues, such as it takes a long time, and the segmentation of the MR picture by various experts can vary considerably. Besides, the result of tumor detection can vary by the same physician under various conditions, and the brightness and contrast of the display screen can vary the segmentation outcomes. That is why the automatic identification of tumors in the brain are becoming big. Automatic brain tumor detection can improve a tumor's chances of survival. There is no specific procedure for brain-tumor diagnosis which can be established in the medical field. A variety of research works are attempting to automatically identify

brain tumors with enhanced precision, precision, and computational speed by reducing manual effort. Detection of brain tumors involves not only recognizing the affected part of the brain but also the form, scale, boundary and location of the tumor. For brain imaging, various imaging techniques such as magnetic resonance imaging (MRI), computed tomography (CT), positron emission tomography (PET), etc. are used. The pathology of the brain tumor will most frequently be examined with an MRI scan or CT scan. Nevertheless, the CT scan produces radiation that is harmful to the human body, while the MRI provides a detailed representation of the anatomical structure of brain tissues.

Propositions on the paper are as follows:-

• We propose the TKFCM algorithm that will detect brain tumors with more accuracy, even if the tumor to be detected is very tiny.

• The proposed algorithm works more accurately and efficiently than others with an MR image even if it is a noisy MR image.

• The performance of the proposed algorithm is better than others such as thresholding, region growing, region splitting and merging, artificial neural network (ANN), TK-means, FCM algorithms, etc. for sensing and specifying brain tumors in an MR image.

• The required execution time of the proposed algorithm is very much lower—40–50 s, compared with conventional algorithms such as ANN, which require 7–15 min to execute the output results.

In clustering procedures, K implies clustering calculation, FCM clustering calculation and expectation maximization (EM) calculation are the most broadly utilized brain tumor discovery strategies. Clustering is a procedure of dividing a set of information into a particular number of bunches. K-means clustering algorithm is an unsupervised calculation that isolates objects on the premise of traits/ highlights into k bunches (k could be a positive number). It is an exceptionally basic clustering calculation, points to deliver close-fitting cluster and works well for moo dimensional information. It performs quicker than various leveled clustering when the number of factors are huge. In any case, the cons of this calculation are, it is exceptionally difficult to predict K-value and does not perform well with a worldwide cluster. Besides, with distinctive estimates and density, the execution of this algorithm is poor. Fuzzy C-means may be a delicate clustering method where each pixel may have a place to two or more clusters with a changing degree of individuals. Network or Feed-Backward neural Network (FBNN). ANN technique provides a robust parallel ability and fast computing. However, it may take a very long period for training input images and partial information should be acquainted beforehand (Sharma, Kaur, Gujral, 2014) (Pereira, Pinto, Alves, Silva, 2016) (Matta, 2014). Kmeans algorithm is an iterative algorithm that tries to partition the dataset into Kpre-defined distinct non-overlapping subgroups (clusters) where each data point belongs to only one group. It tries to make the inter-cluster data points as similar as possible while also keeping the clusters as different (far) as possible. It assigns data points to a cluster such that the sum of the squared distance between the data points and the cluster's centroid (arithmetic mean of all the data points that belong to that cluster) is at the minimum. The less variation we have within clusters, the more homogeneous (similar) the data points are within the same cluster. The entire methodology has been introduced for the detection of tumors in the human brain. MR image utilizing temper based K-means and improved fuzzy C-means clustering

algorithm are represented by the subsequent flowchart shown in Figure 2. At first, the acquisition of the human brain MR image is done and the input image is pre-processed and enhancement of the MR image is also carried out. Furthermore, the template base window is selected and the output of the window has been segmented with the temper based K-means clustering segmentation. After that, the required features are extracted. Finally, the tumor is acquired by detecting with a red line marked by the improved fuzzy C-means algorithm with the updated membership. This is committed through the clustered image which is automatically chosen from the image features.

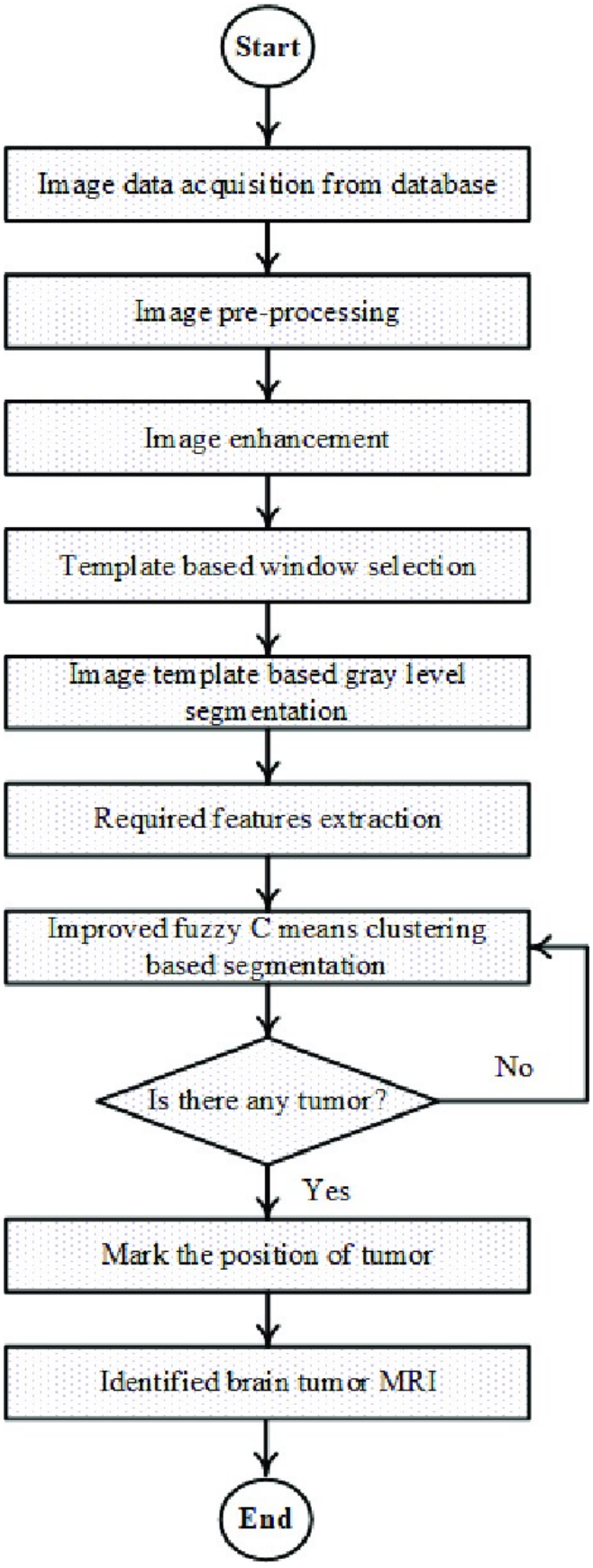

Figure 3.4: Flowchart of the proposed TKFCM algorithm

MR picture pre-processing is exceptionally noteworthy to enhance the visual impact of the picture for further preparation. More often than not the collected pictures within the dataset are so destitute in quality that requires filtering clamor and honing the picture. In the pre-processing step, the procured picture within the dataset is converted into a two-dimensional lattice and the picture is changed over into RGB image to grayscale image. To kill the commotion within the picture, a middle channel is utilized. At that point, the upgrade of the image is done by performing a balanced operation, histogram-based operation and versatile histogram based operation. For the most part, the upgrade of a picture implies making strides in the differentiation of the picture. After that different highlights are at first extricated implicitly. After that, distinctive highlights are at first extricated verifiably. Each parcel of the brain tumor must be chosen indeed a little parcel of the brain tumor is not dodged. At first, the input image is prepared through a few channels that are portrayed in the paper. At that point, there's initial segmentation of the picture utilizing format based K-means (TK) which is portioned on the premise of there gray level concentrated and mood of color where k = 8. After that the tumor is sifted by the median filter once more. At that point, the tumor is identified and checked as a ruddy line utilizing progressed FCM algorithm based on the Euclidean remove from cluster middle to each information point which essentially depends on the different features. This may be critical to get a handle on the significance of this changed and incorporated technique. The enhanced FCM is performed for 13 clusters according to the gray level strength. The clustered image is characterized as the image with its lowest gray level, and separated by its successive color intensity from each other. The performance of the proposed TKFCM algorithm obtained better precision compared to the conventional schemes. Moreover, this algorithm has shown that it has an optimum over the standard schemes. 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% over the standard thresholding, Region growing, 'Second-order + ANN', 'Texture Combined + ANN', FCM and TK mean algorithms, respectively. additionally, 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, Region growing, 'Second-order + ANN', 'Texture Combined + ANN', FCM and TK mean algorithms, respectively. Moreover, 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, Region growing, 'Second-order + ANN', 'Texture Combined + ANN', FCM and TK mean algorithms, respectively. However, the time required to detect neoplasm with the proposed TKFCM algorithm is very short compared to the conventional algorithms. (Alam, et al., 2019)

In the paper "Automatic Brain Tumor Detection and Segmentation Using U-Net Based Fully Convolutional Networks" describes

A huge part of brain tumor treatment is the detection, quantitative evaluation and determination of the tumor extent. Magnetic Resonance Imaging(MRI) has been revolutionary in providing us with the aforementioned capabilities and is also healthier than the previous techniques with similar capabilities such as Ionizing radiation! Ionizing radiation has been known to make cells in human bodies react in one of three ways – cell dies, the cell repairs itself or it mutates incorrectly and becomes cancerous! This further emphasizes the advent of MRI which not only has enhanced capabilities but is also free form such health hazards. Central to the MRI is segmen-

tation; Manual segmentation is the first and the most common form of segmentation but due its time consuming and human error-prone nature fully automatic segmentation has been the way to go. Less human interference and more algorithm-based image processing and segmentation can be a more accurate and efficient way of tumor detection. Multimodal Brain Tumor Image Segmentation (BRATS) an image segmentation benchmark rater that uses both recent and a great variety of data sets to compare the modern automated segmentation techniques will be used to compare our discussed segmentation techniques[**8**]. There are two kinds of Brain tumor High-grade glioblastoma (HGG) and Low-grade Gliomas (LGG). According to a study from (Smoll, N.R., Schaller, K., Gautschi,2013) at the Long-term survival of patients with glioblastoma multiforme (GBM). J. Clinic of Neuroscience high-grade glioblastoma and metastasis, are still considered untreatable with a 2.5-year cumulative relative survival rate of 8%and 2% at 10 years[**9**]. Whereas a study from (Ramakrishna, R., Hebb, A., Barber, J., Rostomily, R., Silbergeld,2015) Outcomes in Reoperated Low-Grade Gliomas Neurosurgery there are variable prognosis results for patients with low-grade gliomas (LGG) with an overall 10-year survival rate about 57%[**10**].

MRI protocols use vascularity, cellularity and blood-brain barrier integrity to evaluate the brain tumor. The contrasts produced by these different protocols during the imaging is what produces an image with all of the brain's physical complexities, therefore, providing important visual information which could ultimately allow the diagnosis of successfully identifying the tumor. Usual MRI protocols use T1 weighted T2 weighted Fluid-Attenuated Inversion Recovery or FLAIR and gadolinium-enhanced T1-weighted imaging sequences. The segmented brain tumor extent can separate structures from other brain tissues and can, therefore, provide a more accurate classification of brain tumor types. Also the Segmentation of longitudinal MRI scans can efficiently monitor brain tumor recurrence, both growth, and shrinkage. But even this still requires some manual delineation from human operators thus leaving room for error and subjective decision making; which is what we are trying to reduce if not eliminate. Studies on brain tumor segmentation can be divided into two parts supervised and unsupervised learning.

Unsupervised learning has been successfully used for clustering methods. Especially fuzzy clustering which grouped with region-growing for brain tumor cases scanned by T1-weighted and T2-weighted sequences and achieved a segmentation accuracy of 73A study (Juan-Albarracín, J., Fuster-Garcia, E., Manjón, J. V, Robles, M., Aparici, F., Martí-Bonmatí, L., García-Gómez,2015) has been carried out to evaluate different clustering algorithms for glioblastoma segmentation, and results showed that Gaussian hidden Markov random field outperformed k-means, fuzzy k-means and Gaussian mixture model for this task. However, the best performing algorithm described in this study still only achieved 77

Supervised learning on the other hand requires training data so that it can learn classification models on which new instances can be classified and then segmented. One such supervised learning method is deep convolutional neural networks (CNN). Compared to conventional supervised machine learning methods, these deep learning-based methods are not dependent on hand-crafted features, but automatically learn a hierarchy of increasingly complex features directly from data. They also rank at the top of the BARTS benchmarking system for image processing. The basic idea behind a fully convolutional network is that it is "fully convolutional", that is, all

of its layers are convolutional layers.
FCNs(Fully convolutional Networks) don't have any of the fully-connected layers at the end, which are typically used for classification. Instead, FCNs(Fully convolutional networks) use convolutional layers to classify each pixel in the image. So the final output layer will be the same height and width as the input image, but the number of channels will be equal to the number of classes. If we're classifying each pixel as one of fifteen different classes, then the final output layer will be height x width x 15 classes. Using a softmax probability function, we can find the most likely class for each pixel.
Biomedical images can often have detailed patterns of the imaged objects. A study by Fully convolutional networks for semantic segmentation (Long, J., Shelhamer, E., Darrell,2015) has proposed the use of skip-architecture that combined the high-level representation from deep decoding layers with the appearance representation from shallow encoding layers to produce detailed segmentation to overcome the detailed image patterns. Ronnenberger (Ronneberger, O., Fischer, P., Brox,2015) introduced U-net to biomedical imaging which was initially employed for its skip architecture as a solution to cell tracking. This proposed supervised learning method has been validated using datasets acquired for both LGG and HGG patients. Compared with manually delineated ground truth, our fully automatic method has obtained promising results. Also compared to other state-of-the-art methods, we have achieved comparable results for delineating the complete tumor regions, and superior segmentation for the core tumor regions. (Dong, 2017)

Chapter 4

Problem Statement / Definition

According to the biological study, the tumor is also known as a neoplasm, which means abnormal expansion of tissue where the cell divides more then they need[**17**]. Unregulated by the mechanism that controls cells. In this recent technology we used magnetic resonance image (MRI) for detecting any kind of brain tumor or abnormality in tissues. In our proposed methodology our main purpose is to get a more clear image form MRI. We would try to use an algorithm that 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.

Chapter 5

Research objectives

As we are planning to use machine learning algorithms such as, deep learning algorithms, neural networks and deep neural networks to detect brain tumors by image processing. Though, so many researchers already researched brain tumor detection by using MRI where they used many algorithms such as template-based K means algorithm, fuzzy logic algorithm, threshold algorithm, FCM, TKFCM and TK means algorithm, etc. and by using these algorithms they tried to bring more accuracy rate. K-means clustering is the most used clustering algorithms
due to its simplicity that tries to partition the dataset into K pre-defined distinct non- overlapping subgroups where each data point belongs to only one group. Furthermore, the FCM
algorithm is a method of clustering that allows one piece of data to belong to two or more clusters. That method is used frequently for pattern visualization. On the contrary, the smooth method of image segmentation is a thresholding method. Moreover, the thresholding method can be used for creating binary images from the grayscale image.

Chapter 6

DATA ANALYSIS

6.1 DATA 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)[**4**]. 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.[**5**]

6.2 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.

Tables of Data Analysis

Table:01

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 6.1: Data Analysis Table(a)

Table:02

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 6.2: Data Analysis Table(b)

Table:03

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 6.3: Data Analysis Table(c)

Table:04

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

Table 6.4: Data Analysis Table(d)

Chapter 7

Result

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
```

Figure 7.1: ReLU and ADAM(Attributes)

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

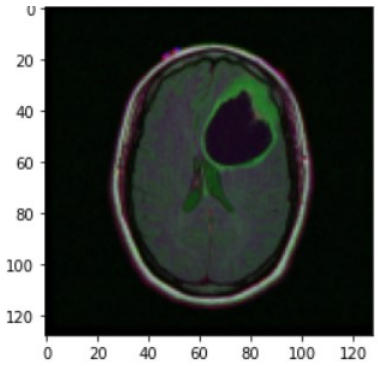

Figure 7.2: Sample test image

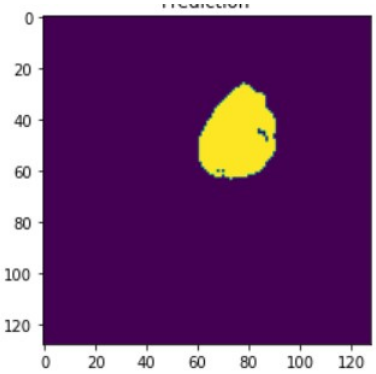

Figure 7.3: Sample predicted image

```
Epoch 1/30
107/107 [==============================] - 44s 409ms/step - loss: -0.3195 - accuracy: 0.9619 - dice_coef: 0.3209 - val_loss: -0.0131 -
val_accuracy: 0.1741 - val_dice_coef: 0.0127
Epoch 2/30
107/107 [==============================] - 41s 385ms/step - loss: -0.6365 - accuracy: 0.9920 - dice_coef: 0.6368 - val_loss: -0.0155 -
val_accuracy: 0.3056 - val_dice_coef: 0.0150
Epoch 3/30
107/107 [==============================] - 41s 385ms/step - loss: -0.7047 - accuracy: 0.9932 - dice_coef: 0.7050 - val_loss: -0.4079 -
val_accuracy: 0.9952 - val_dice_coef: 0.4094
Epoch 4/30
107/107 [==============================] - 41s 385ms/step - loss: -0.7441 - accuracy: 0.9939 - dice_coef: 0.7438 - val_loss: -0.3829 -
val_accuracy: 0.9956 - val_dice_coef: 0.3857
Epoch 5/30
107/107 [==============================] - 41s 383ms/step - loss: -0.7720 - accuracy: 0.9945 - dice_coef: 0.7725 - val_loss: -0.4561 -
val_accuracy: 0.9949 - val_dice_coef: 0.4648
```

Figure 7.4: 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%.

Figure 7.5: 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.

Chapter 8

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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...

How to install LaTeX

Windows OS

TeXLive package - full version

1. Download the TeXLive ISO (2.2GB) from
   https://www.tug.org/texlive/

2. Download WinCDEmu (if you don't have a virtual drive) from
   http://wincdemu.sysprogs.org/download/

3. To install Windows CD Emulator follow the instructions at
   http://wincdemu.sysprogs.org/tutorials/install/

4. Right click the iso and mount it using the WinCDEmu as shown in
   http://wincdemu.sysprogs.org/tutorials/mount/

5. Open your virtual drive and run setup.pl

or

Basic MikTeX - TeX distribution

1. Download Basic-MiKTeX(32bit or 64bit) from
   http://miktex.org/download

2. Run the installer

3. To add a new package go to Start ¿¿ All Programs ¿¿ MikTex ¿¿ Maintenance (Admin) and choose Package Manager

4. Select or search for packages to install

TexStudio - TeX editor

1. Download TexStudio from
   http://texstudio.sourceforge.net/#downloads

2. Run the installer

Mac OS X

MacTeX - TEX distribution

1. Download the file from
   https://www.tug.org/mactex/
2. Extract and double click to run the installer. It does the entire configuration, sit back and relax.

TexStudio - TEX editor

1. Download TexStudio from
   http://texstudio.sourceforge.net/#downloads
2. Extract and Start

Unix/Linux

TeXLive - TEX distribution

Getting the distribution:

1. TexLive can be downloaded from
   http://www.tug.org/texlive/acquire-netinstall.html.
2. TexLive is provided by most operating system you can use (rpm,apt-get or yum) to get TexLive distributions

Installation

1. Mount the ISO file in the mnt directory

   ```
   mount -t iso9660 -o ro,loop,noauto /your/texlive####.iso /mnt
   ```

2. Install wget on your OS (use rpm, apt-get or yum install)
3. Run the installer script install-tl.

   ```
   cd /your/download/directory
   ./install-tl
   ```

4. Enter command 'i' for installation
5. Post-Installation configuration:
   http://www.tug.org/texlive/doc/texlive-en/texlive-en.html#x1-320003.4.1
6. Set the path for the directory of TexLive binaries in your .bashrc file

For 32bit OS

For Bourne-compatible shells such as bash, and using Intel x86 GNU/Linux and a default directory setup as an example, the file to edit might be

```
edit $~/.bashrc file and add following lines
PATH=/usr/local/texlive/2011/bin/i386-linux:$PATH;
export PATH
MANPATH=/usr/local/texlive/2011/texmf/doc/man:$MANPATH;
export MANPATH
INFOPATH=/usr/local/texlive/2011/texmf/doc/info:$INFOPATH;
export INFOPATH
```

For 64bit OS

```
edit $~/.bashrc file and add following lines
PATH=/usr/local/texlive/2011/bin/x86_64-linux:$PATH;
export PATH
MANPATH=/usr/local/texlive/2011/texmf/doc/man:$MANPATH;
export MANPATH
INFOPATH=/usr/local/texlive/2011/texmf/doc/info:$INFOPATH;
export INFOPATH
```

Fedora/RedHat/CentOS:

```
sudo yum install texlive
sudo yum install psutils
```

SUSE:

```
sudo zypper install texlive
```

Debian/Ubuntu:

```
sudo apt-get install texlive texlive-latex-extra
sudo apt-get install psutils
```

Overleaf: GitHub for LaTeX projects

This Project was developed using Overleaf(https://www.overleaf.com/), an online LaTeX editor that allows real-time collaboration and online compiling of projects to PDF format. In comparison to other LaTeX editors, Overleaf is a server-based application, which is accessed through a web browser.