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Presented by:

- **LalmiAhmmedNidhal**
- **Chihi Oussama**

THEME

**Artificial Intelligence Neuropathologist for Glioma
Classification using Deep Learning**

Supervisor :
Dr. KHOLLADI NedjouaHouda

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Dedications

**I dedicate this work to all my friends, to the staff of
Exact Sciences Faculty of HammaLakhdar University, and
my family members one by one.**

Acknowledge

**I wish to express my deep gratitude to
Dr.KholladiNedjouaHouda, the supervisor of this thesis,
who provided valuable comments suggestions, and
guidance that enhanced the merit of this study**

Abstract

AI-driven solutions for auto contouring brain tumors. Based on contrast-enhanced imaging, it computes multiregional segmentations and/or multi-class classification of glioma tumors. The most difficult issue in /the realm of MRI/ scan is medical image diagnosis or medical image prognosis. Medical image analysis is used in oncology to decide the characteristics of cancer, plan treatment, and monitor the disease's progression. Glioma is a type of malignant brain tumor that has serious effects on cognitive functions and lowered the quality of patients' lives. The neurotic identification of glioma subtypes is essential for planning and anticipating therapies. Neuropathologists use postoperative hematoxylin and eosin-stained slides to localize glioma in the standard histological manner. The purpose of this research field is to establish a deep learning model used for glioma segmentation and classification to detect different lesions.

Computer-aided systems for detection are now commonly employed for the accurate and explicit detection of brain abnormalities. To assist the interpretation of radiological and pathological images, CAD utilizes a multidisciplinary approach combining together different techniques of artificial intelligence and computer vision based on image processing methods.

There are currently few methods for addressing glioma multiple classes challenges since they are mostly based on single-task approaches without taking the correlation between them into account. Here, for simultaneous glioma classification-based segmentation, we propose a fully automated multimodal MRI-based multi-task learning framework.

Keywords: Image processing, Deep Learning, Convolutional Neural Network, ResUnet, SVM, Computer Aide Diagnostic, Brain tumor.

ملخص

يعد تشخيص الصور الطبية من أكثر المشكلات تحديًا في مجال البحث لتحليل فحص التصوير بالرنين المغناطيسي. يعد الاكتشاف العصبي للأنواع الفرعية للورم الدبقي أمرًا أساسيًا لترتيب العلاج والتنبؤ به. يعتمد التحديد النسيجي القياسي للورم الدبقي على شرائح الهيماتوكسيلين المصبوغة بعد العملية الجراحية والأیوزین بواسطة أطباء الأمراض العصبية. مع التقدم في التفكير من صنع الإنسان (AI) ، كان الهدف من هذه المراجعة هو تحديد ما إذا كان يمكن تطبيق التعلم العميق على مجموعات الورم الدبقي.

في مجال التصوير الطبي والتشخيص بمساعدة الكمبيوتر ، تتم مناقشة جميع النظريات والمفاهيم المرتبطة بمعالجة الصور والتعلم الآلي وطرق التحسين.

تُستخدم أنظمة الكشف بمساعدة الكمبيوتر الآن بشكل شائع للكشف الدقيق والصريح عن تشوهات الدماغ. CAD هي تقنية متعددة التخصصات تجمع بين عناصر الذكاء الاصطناعي ورؤية الكمبيوتر مع معالجة الصور للصور الإشعاعية وعلم الأمراض لمساعدة الأطباء في تفسير الصور الطبية.

ينصب تركيز هذا العمل أولاً على عملية تعتمد على دمج مجموعة من الأساليب:

عملية التجزئة: تم تصميم النظام المقترح على بنية ResU-Net وهي عبارة عن CNNs بالكامل ، والتي حققت تنفيذًا من الدرجة الأولى لتجزئة الصور الطبية تلقائيًا.

خطوة استخراج الميزات: تُستخدم لاستخراج الخصائص المحددة للصورة ، والتي يتم من خلالها إنشاء ناقل سمة مميز ويمكن تصنيف الصور. يلعب دور الداعم للمصنفات.

عملية التصنيف: استخدمنا خوارزمية SVM لتصنيف جميع الميزات المستخرجة.

الكلمات المفتاحية: معالجة الصور ، التعلم العميق ، الشبكة العصبية التلافيفية ، ResUnet ، SVM ، التشخيص بمساعدة الكمبيوتر ، ورم الدماغ.

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GLOSSARY

AI: Artificial Intelligence.

ML: Machine Learning.

DL: Deep Learning.

CNN: Convolutional Neural Network.

NN: Neural Network.

ANN:Artificial neural network

ResUNet: Residual Neural Network

MRI:Magnetic Resonance Imaging.

CT: Computerized Tomography.

CV: Computer Vision.

SVM: support vector machine.

KNN: K-Nearest Neighbor.

CSV: Comma-separated values.

HGG: High-grade Glioma

LGG:Low-grade Glioma

General Introduction

GENERAL INTRODUCTION

Cancer is one of the leading causes of death in the world, and brain cancer is the worst type. Accurate segmentation of the brain tumor region on multimodal MR images prior to surgery is a critical part of the surgical removal process, as it is the only clinical option for treating brain tumors.

Magnetic resonance imaging (MRI) is a crucial tool used to determine the best course of treatment for those who have been diagnosed with tumors at the appropriate time. detects changes in tissue's induced magnetic properties for a very long time, this method has been the gold standard for producing anatomically accurate pictures of the human brain at very high resolution. In the past decade, it has become a standard tool for researchers interested in understanding how the human brain works. The most active regions of the brain can be pinpointed with the use of MRI, which analyzes variations in regional blood flow.(MRI) segmentation is a way operated in the domain of diagnosis and detection of lesions, tumors, or other abnormalities.

Brain tumor MRI image analysis is a laborious process that requires the identification, categorization, detection, and segmentation of contaminated areas. One method for doing so is called "object recognition," and it involves using various metrics, such as likelihood, loss, accuracy, etc., to determine which classes of classification labels should be applied to an image. In addition to its dual role in object localization and picture classification, object detection algorithms also perform well when presented with objects that occur in several classes. Using a pixel-by-pixel filter designed specifically for each object in the image, we can then detect the presence of the object using the segmentation method of further extrusion. This method is more precise than object detection's bounding box since it determines each object's actual shape. This data will be used to select the most effective treatment option from among radiation, surgery, and chemotherapy. Therefore, an infected patient has a far better chance of surviving if the tumor is diagnosed at an early stage.

In this paper, we will discuss the various methods used for segmenting and classifying brain tumors from MR images and highlight some intriguing proposed solutions from the literature review.

The objective of this dissertation is to propose an architecture of machine learning with employing different stages from preprocessing to classification passing through the features extraction that combined region of interests with edges of interests, also the use of segmentation algorithms.

The following is the outline for this research project:

- Chapter 01: INTRODUCTION

This work has presented a brief overview of knowledge and information in machine learning, deep learning, classification algorithms.

- Chapter 02: LITTERATURE REVIEW AND BACKGROUND

This dissertation has highlighted image processing, segmentation approaches, and classification approaches, then a detailed overview of the related works.

- Chapter 03: PROPOSED METHODOLOGY

Here, it has tackled the proposed conception for the proposed methodology, the proposed pipeline, and the proposed architecture for the used DL models, and metrics for evaluating the performance of classification algorithms.

- Chapter 04: RESULTS AND EXPERIMENTAL TESTS

At the final stage, several Results and experimental tests of the proposed model on several known datasets {Kaggle, Brats18}, the results have outperformed the execution of the proposed model compared to the literature models, a multiple metrics have illustrated the efficiency of the proposed model by computing statistical scores that have evaluated the performance of the model in terms of accuracy, precision and different types of graphs have explicitly shown the efficiency of the proposed model by many comparisons of the existed models.

Chapter I

Introduction

1.Introduction

within the recent years. Deep Learning (DL), a type of AI that is increasingly in use today, has the potential to transform the way that healthcare is provided in the future.

Computer-aided detection (CAD) has emerged as one of the most crucial methods for quickly diagnosing any diseases as a result of artificial intelligence algorithms. It involves the use of deep learning techniques in the field of image processing to improve the diagnosis of CAD. As a result, we cover the fundamentals of machine learning, Deep Learning, image classification techniques, medical imaging, and how to assess the system's effectiveness in this chapter.

2.Neuronal Network and Deep Learning Algorithms

2.1.Machine learning

Machine learning (ML) is a type of artificial intelligence (AI) that allows software applications to become more accurate at predicting outcomes without being explicitly programmed to do so. Machine learning algorithms use historical data as input to predict new output values. [1]

2.2.Field of machine learning

Machine learning is a widely used term in several industries, including healthcare, e-commerce, finance, and transportation

. there are a lot of applications of these algorithms in different fields: [2]

Table 1: Field of machine learning

Field	Applications
Computer vision	Face Recognition, Object Recognition, Robotics, Self-Driving cars, etc...
Medical	Drug Development, Biomedical Data Analysis, Neurosciences, etc.
Finance and E-commerce	Analytics, Insurance, Fraud detection, Financial Forecasting, Spam Email, etc.
Geography	Earthquake Detection, Weather Detection (Google weather), etc.
Signal	language NLP, Speech Processing, etc.

2.3.The different types of machine learning

The way in which a prediction-making algorithm learns to improve its accuracy is a common way to classify traditional machine learning. There are four fundamental strategies: reinforcement learning, semi-supervised learning, unsupervised learning, and supervised learning. The kind of data that data scientists wish to predict determines the kind of algorithm they use.

2.3.1.Supervised learning

In this type of machine learning, data scientists supply algorithms with labeled training data and define the variables they want the algorithm to assess for correlations. Both the input and the output of the algorithm is specified. [1]

List of common algorithms

- Decision Trees
- Linear Regression
- Logistic Regression
- Support Vector Machines (SVM)
- Neural Networks

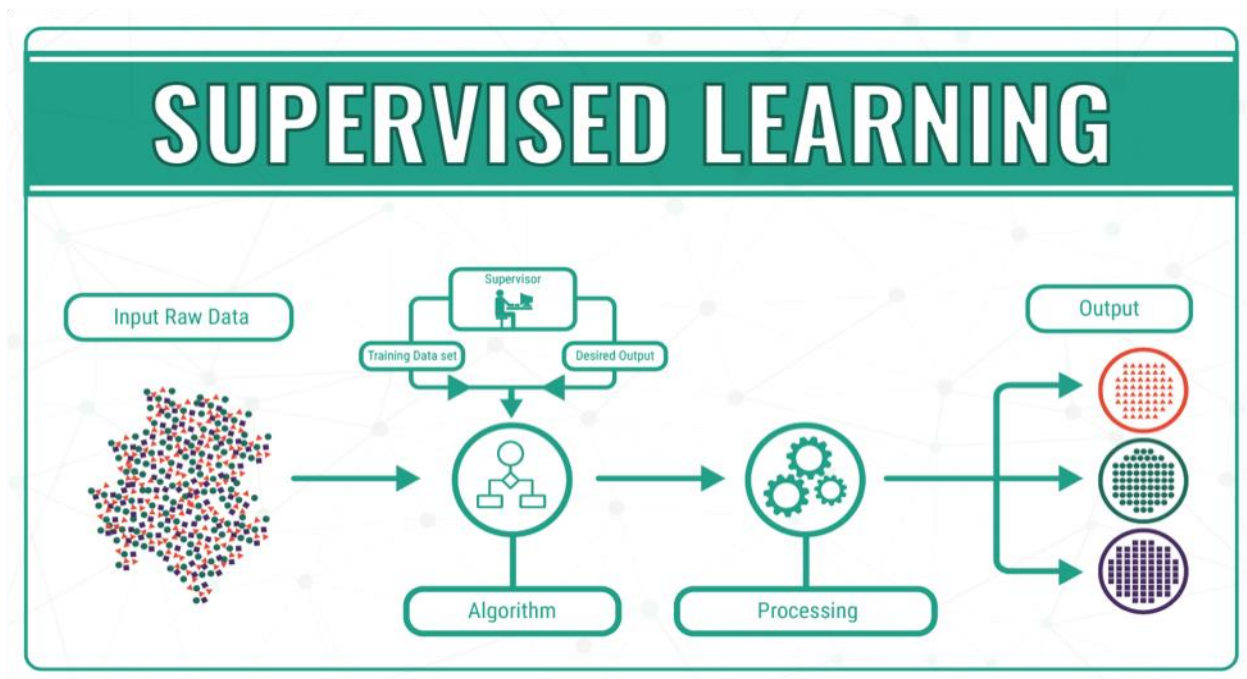


figure 1: supervised learning algorithm

2.3.2. Unsupervised Learning

This type of machine learning involves algorithms that train on unlabeled data. The algorithm scans through data sets looking for any meaningful connection. The data that algorithms train on as well as the predictions or recommendations they output are predetermined. [1]

List of common algorithms

- ✓ Clustering
 - k-Means.
 - Hierarchical Cluster Analysis(HCA).
 - Expectation Maximization.
- ✓ Visualization and dimensionality reduction
 - Principal Component Analysis(PCA).
 - Kernel PCA.
 - Locally-Linear Embedding(LLE).
 - t-distributed Stochastic Neighbor Embedding (t-SNE).
- ✓ Association rule learning
 - Apriori.
- ✓ Eclat.

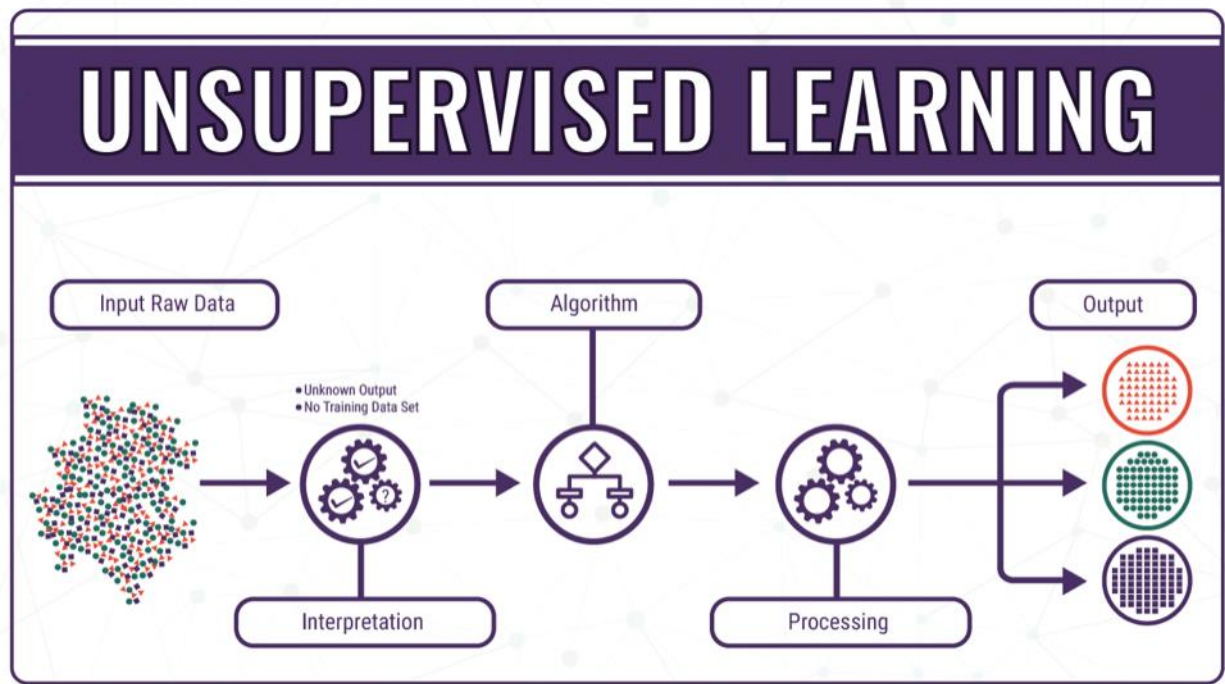


figure 2: unsupervised learningalgorithm

2.3.3.Semi-supervisedLearning

This approach to machine learning involves a mix of the two preceding types. Data scientists may feed an algorithm mostly labeled training data, but the model is free to explore the data on its own and develop its own understanding of the data set. [1]

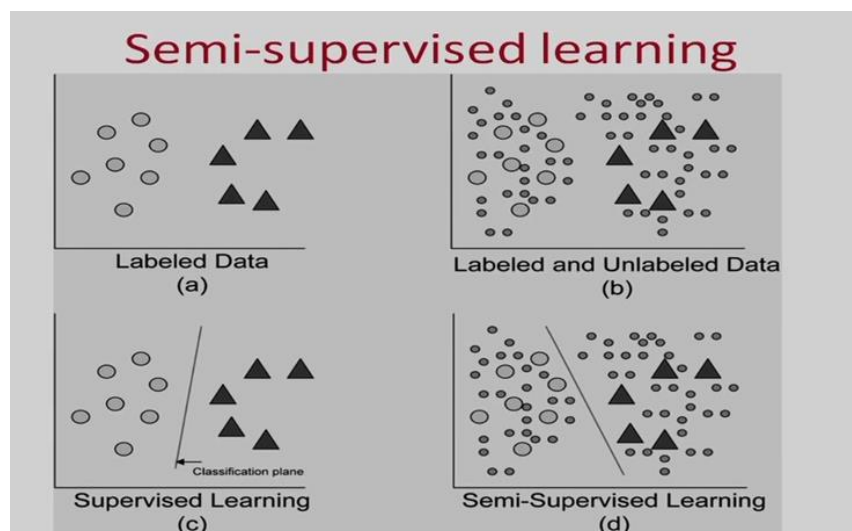


figure 3: semi-supervised learningalgorithm

2.3.4. Reinforcement learning

Data scientists typically use reinforcement learning to teach a machine to complete a multi-step process for which there are clearly defined rules. Data scientists program an algorithm to complete a task and give it positive or negative cues as it works out how to complete a task. But for the most part, the algorithm decides on its own what steps to take along the way. [2]

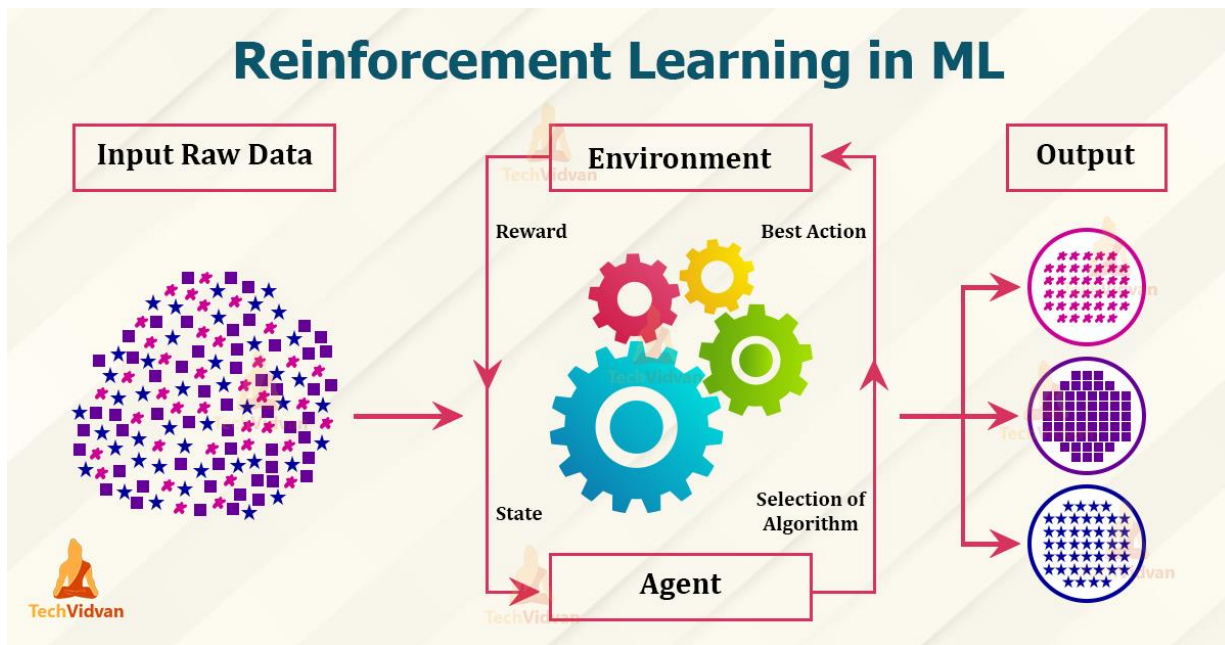


figure 4: reinforcement learning algorithm

3. Deep Learning

Deep learning is a class of machine learning which performs much better on unstructured data. Deep learning techniques are outperforming current machine learning techniques. It enables computational models to learn features progressively from data at multiple levels. The popularity of deep learning amplified as the amount of data available increased as well as the advancement of hardware that provides powerful computers. [3]

Deep Learning is a subfield of machine learning concerned with algorithms inspired by the structure and function of the brain called artificial neural networks.

3.1. Neural Networks

Neural networks, also known as artificial neural networks (ANNs) or simulated neural networks (SNNs), are a subset of machine learning and are at the heart of deep learning algorithms. Their name and structure are inspired by the human brain, mimicking the way that biological neurons

signal to one another.

Artificial neural networks (ANNs) are comprised of a node layers, containing an input layer, one or more hidden layers, and an output layer. Each node, or artificial neuron, connects to another and has an associated weight and threshold. If the output of any individual node is above the specified threshold value, that node is activated, sending data to the next layer of the network. Otherwise, no data is passed along to the next layer of the network. [4]

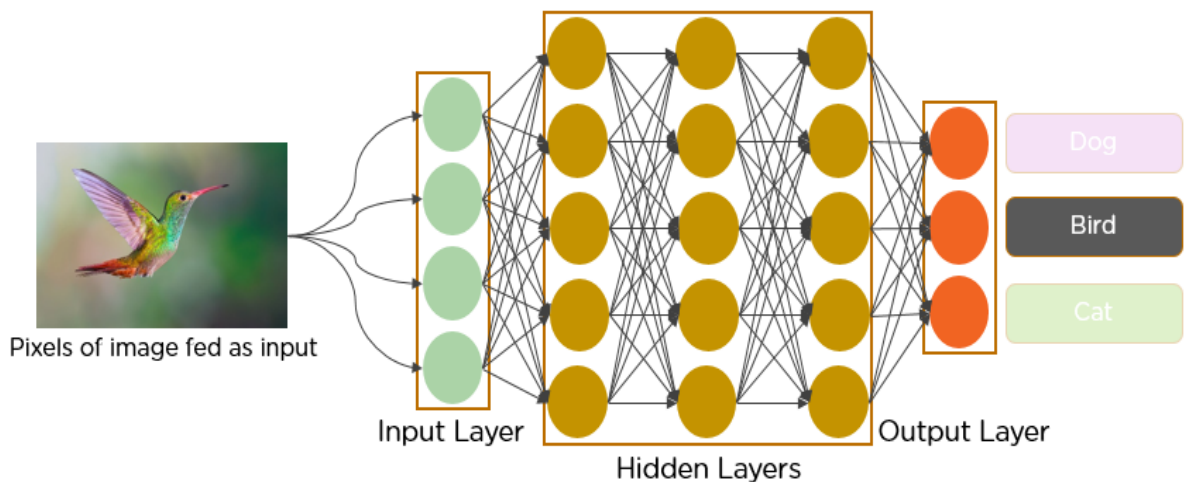


figure 5: example of artificial neural networks

There exist some types of architectures for neural networks:

- The multilayer perceptrons, that are the oldest and simplest ones
- the Convolutional Neural Networks (CNN), particularly adapted for image processing
- The recurrent neural networks, used for sequential data such as text or times series

3.2.Convolutional Neural Network

In deep learning, a convolutional neural network (CNN/ConvNet) is a class of deep neural networks, most commonly applied to analyze visual imagery. Now when we think of a neural network we think about matrix multiplications but that is not the case with ConvNet. It uses a special technique called Convolution. Now in mathematics convolution is a mathematical operation on two functions that produces a third function that expresses how the shape of one is modified by the other. Bottom line is that the role of the ConvNet is to reduce the images into a form that is easier to process, without losing features that are critical for getting a good prediction.

A CNN is an algorithm used to recognize patterns in data. CNN is a specialized type of DNN

(deep neural network) model designed for working with two or more-dimensional image data.

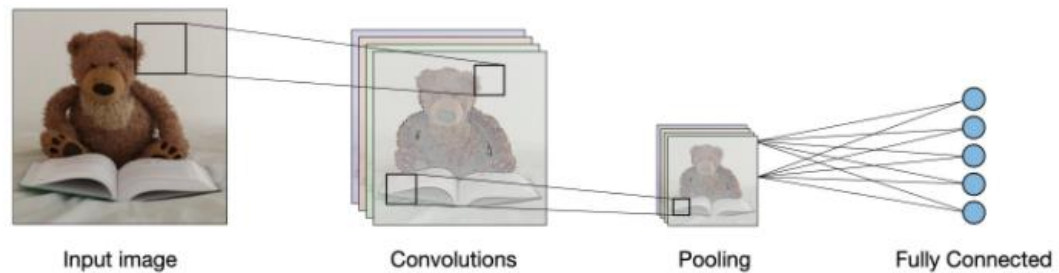


figure 6: CNN Model

3.3. Building blocks of CNN architecture

The CNN architecture includes several building blocks, such as convolution layers, pooling layers, and fully connected layers. A typical architecture consists of repetitions of a stack of several convolution layers and a pooling layer, followed by one or more fully connected layers. The step where input data are transformed into output through these layers is called forward propagation. [5]

3.3.1. Convolution Layer

A convolutional layer involves the multiplication of a set of weights with the input, like traditional neural network but for CNNs, we have twodimensional input. The multiplication is performed between an array of input data and a two dimensional array of weights, called a filter or a kernel.

This filter or kernel is always smaller than input, and moves all over the image matrix. It multiply its values by the original pixel values, and all these multiplications are summed up to one number at the end. This filter moves to the right and down in n (can vary) steps. Result matrix is (should be) smaller than the input matrix. [5]

3.3.2. Pooling Layer

Its functions are used to reduce the spatial size of the representation to reduce the amount of parameters, and computation in the network, and also control overfitting. There are two main types of pooling layers. They are max pooling, and average pooling:

Max Pooling — Calculate the maximum value for each patch of the feature map.

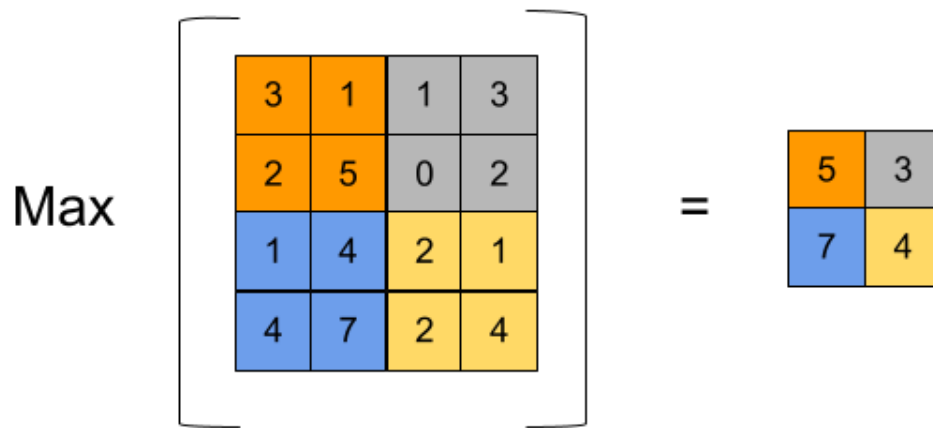


figure 7: Max pooling exemple

Average Pooling — Calculate the average value for each patch on the feature map.

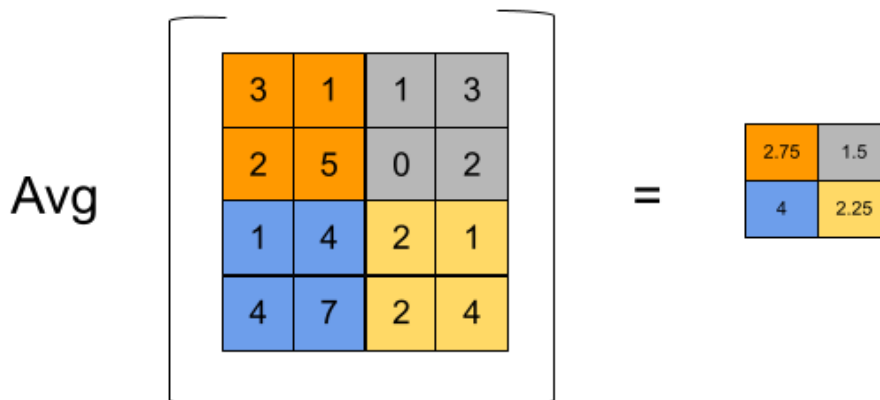


figure 8: Average pooling exemple

3.3.3.Fully-Connected Layer

Neurons in a fully connected layer have full connections to all activations in the previous layer and are seen in regular neural networks. The input of the fully-connected layer is the output from the final layer, pooling or convolutional layer, which is flattened, and then fed into the fully connected layer. This layer converts a three-dimensional layer into a one-dimensional vector to fit the input of a fully-connected layer. [5]

3.3.4.Last layer activation function

Activation functions are functions used in neural networks to calculate the weighted sum of input and biases, it is used to decide if a neuron can be released or not. It manipulates the presented data through some gradient processing usually gradient descent and afterwards produce an output for the neural network, that contains the parameters in the data.

The activation function applied to the last fully connected layer is usually different from the

others. An appropriate activation function needs to be selected according to each task. An activation function applied to the multiclass classification task is a softmax function which normalizes output real values from the last fully connected layer to target class probabilities, where each value ranges between 0 and 1 and all values sum to 1. [5]

Table 2: different last layer activation function

Problem Type	Output Type	Final Activation Function	Loss Function
Regression	Numerical value	Linear	Mean Squared Error (MSE)
Classification	Binary outcome	Sigmoid	Binary Cross Entropy
Classification	Single label, multiple classes	Softmax	Cross Entropy
Classification	Multiple labels, multiple classes	Sigmoid	Binary Cross Entropy

4. Brain tumor

The brain is a vital organ in the human body and responsible for control and decision making. As the managing center of nervous systems, this part is very essential to be protected from any harm and illness. The term “brain tumor” refers to a collection of neoplasms, each with its own biology, prognosis, and treatment; these tumors are better identified as intracranial neoplasms. Tumors are the predominant infections caused by abnormal growth of cells that damages the Brain. Meningioma, Glioma, and Pituitary are brain tumors as opposed to the other types. [6]

Brain tumors can be benign or malignant:

- **Benign Brain Tumor:** The least aggressive type of brain tumor is often called a benign brain tumor. They originate from cells within or surrounding the brain, do not contain cancer cells, grow slowly, and typically have clear borders that do not spread into other tissue. They may become quite large before causing any symptoms. If these tumors can be removed entirely, they tend not to return. Still, they can cause significant neurological symptoms depending on their size, and location near other structures in the brain. Some benign tumors can progress to become malignant.

Malignant Brain Tumor: Malignant brain tumors contain cancer cells and often do not have clear borders. They are considered to be life-threatening because they grow rapidly and invade surrounding brain tissue. Although malignant brain tumors very rarely spread to other areas of the body, they can spread throughout the brain or to the spine. These tumors can be treated with surgery, chemotherapy and radiation, but they may recur after treatment.

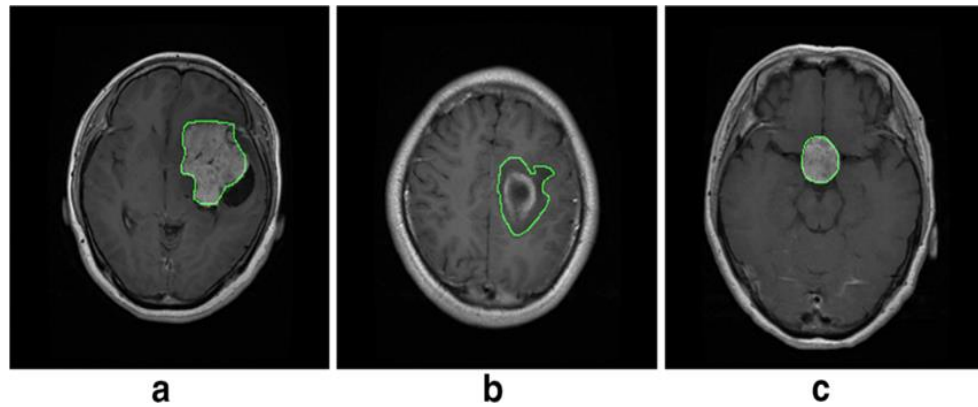


figure 9: Common tumor types. a Meningioma. b Glioma. c Pituitary

4.1.Meningioma

Tumors that develop in the membranes that cover and protect the brain and spinal cord are called meningiomas. Even though it is not a true brain tumor, it is included here because of the risk of compression or squeezing that it poses to the surrounding brain, nerves, and vessels. meningioma is the most common type of tumor that forms in the head. [41]

4.2.Pituitary

The pituitary gland is a pea-sized endocrine gland that is situated in the middle of the skull base and kept protected within a body cavity called the sella turcica. It plays an essential role in regulating the functions of various other endocrine glands and maintaining overall hormone levels in the blood. [42]

4.3.Gliomas

Glioma is a common type of tumor originating in the brain. About 33 percent of all brain tumors are gliomas, which form in the glial cells that surround and support neurons in the brain, including astrocytes, oligodendrocytes, and ependymal cells. [7]

glioma can be Low or High -grade:

4.3.1.Low-grade Glioma

Tumors of the brain's glial cells, which provide insulation and nutrition to neurons, are called low-grade gliomas. Gliomas, which are tumors of the nervous system, are classified into four different stages based on the microscopic characteristics of their tumor cells. About two-thirds of all tumors in children and adolescents are gliomas, the majority of which are grades 1 and 2. Low-grade gliomas are subdivided not only by their stage but also by their location and the type of glial cell (astrocytes, oligodendrocytes, or ependymocytes) from which they originate. Most cases of low-grade glioma are easily diagnosable and respond well to treatment. The cure rate for pilocytic

astrocytoma, the most common type of low-grade glioma, is over 90%. [8]

4.3.2.High-grade Glioma

High-grade gliomas are tumors of the glial cells, cells found in the brain and spinal cord. They are called “high-grade” because the tumors are fast-growing and they spread quickly through brain tissue, which makes them hard to treat. High-grade gliomas are rare and account for 8-12% of brain tumors. High-grade gliomas are classified by their location and by how they appear when examined under a microscope. Classifying the tumor helps determine how the disease will progress, and helps identify the best treatment for it. Although the outlook for high-grade gliomas is generally poor. [9]

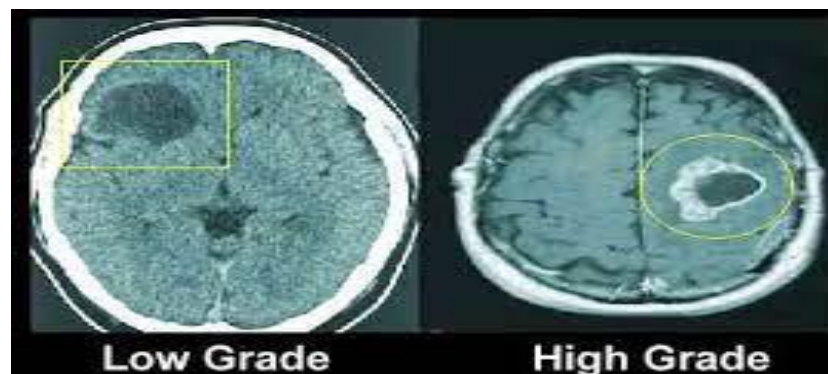


figure 10: low grade glioma vs high grade glioma

5. Medical imaging in neuro-oncology

One of the best-known acquisition modalities is magnetic resonance imaging (MRI), which is used widely in the analysis of brain tumors by means of acquisition protocols (conventional and advanced). Due to the wide variation in the shape, location, and appearance of tumors, automated segmentation in MRI is a difficult task. Although many studies have been conducted, automated segmentation is difficult, and work to improve the accuracy of tumor segmentation is still ongoing. Imaging plays several key roles in managing brain tumors, including diagnosis, prognosis, and treatment response assessment. Ongoing challenges remain as new therapies emerge and there are urgent need to find accurate and clinically feasible methods to noninvasively evaluate brain tumors before and after treatment. [25]

6. Modalities for Medical Image Acquisition

The laboratory tests are considered by MIT's medical community to be one of the most common medical tests (blood and specimen tests). In the past decade, more precise and less invasive imaging tools have rapidly emerged, ushering in a new era in medical diagnostics [36]. Figure 11 depicts the

fundamental principle behind a medical imaging system, which consists of a sensor or source of energy that can penetrate the human body, the energy passing through the body, and being absorbed or attenuated to varying degrees by the different tissues according to their density and atomic number, thus producing signals. Special detectors that are compatible with the energy source pick up these signals, which are then mathematically manipulated to form an image.

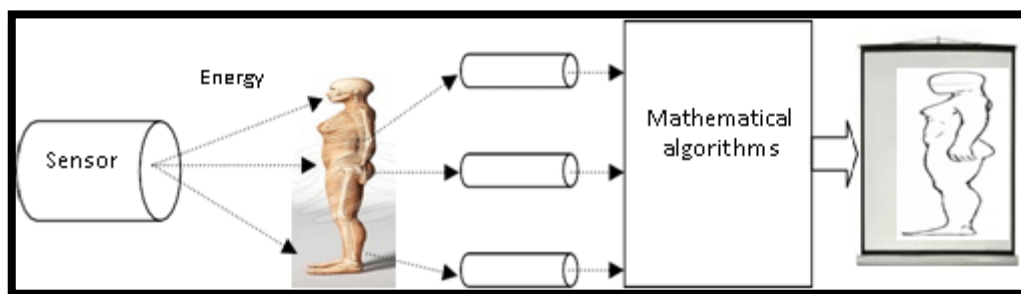


figure 11: medical imaging

The ever-expanding gamut of medical imaging techniques provides the clinician with an increasingly multifaceted view of brain function and anatomy. The information provided by the various imaging modalities is often complementary and synergistic. For example, X-ray computed tomography (CT) and magnetic resonance (MR) imaging exquisitely demonstrate brain anatomy but provide little functional information. Positron emission tomography (PET) and single photon emission computed tomography (SPECT) scans display aspects of brain function and allow metabolic measurements but poorly delineate anatomy. Furthermore, CT and MR images describe complementary morphologic features. [12]

7.Magnetic resonance imaging (MRI)

Magnetic resonance imaging (MRI) is a method that has evolved continuously during the past 20 years, yielding MR systems with stronger static magnetic fields, faster and stronger gradient magnetic fields, and more powerful radiofrequency transmission coils. MRI is a medical imaging technique that uses a magnetic field and computer-generated radio waves to create detailed images of the organs and tissues in body.

MRI is radiation-free and thus a safer imaging fashion than CT and provides finer details of the brain, spinal cord, and vascular deconstruction due to its good discrepancy. Axial, sagittal, and coronal are the introductory airplanes of MRI to fantasize the brains. The most generally used MRI sequences for brain analysis are T1- ladened, T2- ladened, and Faculty. T1- ladened checkup provides argentine and white matter discrepancy. T2- ladened is sensitive to water content and thus well suited to conditions where the water accumulates inside brain napkins. T1-and T2-weighted

images are also used to separate cerebrospinal fluid (CSF). The CSF is tintless and planted in the brain and spinal cord. It looks dark in T1- ladened imaging and bright on T2- ladened imaging. The third sequence is fluid downgraded inversion recovery (Faculty) which is analogous to T2- a ladened image except for its accession protocol. [11]

7.1-Comparison between Medical Imaging Modalities

Here are a few examples of imaging modalities, along with some key features of each: [37]

Table 3: Comparison between Medical Imaging Modalities

Modalities	Main characteristics	Application	cost	Radiation sourceand type
X-Rays	A photograph or image obtainedthroughtheuseofx- rays.	Anatomical	Low cost	X-rays (ionizing)
CT	A method of examining body organs by scanning them with X rays andusing a computer to construct a series of cross-sectional im- ages	Anatomical Functional	Intermediate cost	X-rays (ionizing)
MRI	A method which uses magneticsignalstocreateimage "slices" of the humanbody	Anatomical Functional	Intermediate cost	Electric and Magnetic fields (Non-ionizing)
Ultrasound	Amethodwhichuseofhigh frequency sound to make imageinternalstructuresby signals from differentdensi- tiestissues.	Anatomical Functional	Low cost	Sound waves (Non-ionizing)

PET	PET is a type of nuclear medicine technique in which tracers are used for diagnosing disease	Functional Metabolism	High cost	Positron (ionizing)
SPECT	A non-invasive technique for constructing cross-sectional images of radiotracer distribution inside the body	Functional	High cost	Photons (ionizing)

8.T1-weighted sequence

This type of MRI sequence is generated by using short TE and TR times. The T1 properties of tissue identify the brightness of the image such that the cerebrospinal fluid (CSF) appears dark in this type of MRI image. In the T1-weighted image, the contrast depends mainly on the differences in the T1 times between tissues like water or fat. [13]

9.T2-weighted

As compared with T1-weighted images, T2-weighted images are created by using long time TE and TR and the CSF region appears brighter. In the T2-weighted image, the contrast depends mainly on the differences in the T2 times between tissues like water or fat. The amount of T2 decay that can occur before the signal is received is adjusted by the TE time. [13]

10.Fluid Attenuated Inversion Recovery

Fluid Attenuated Inversion Recovery (FLAIR) is a pulse sequence magnetic resonance imaging technique, and it can be used as two-dimensional imaging (2D FLAIR) or as three-dimensional imaging (3D FLAIR). FLAIR images can show a better detection of small hyper-intense lesions. In the FLAIR sequence image, TE and TR are very long, and CSF appears darker as compared to the T1-weighted image. This type of MRI sequence can distinguish between abnormal. [14]

11.T1-weighted with contrast-enhanced (T1-contrast enhanced)

This MRI sequence is produced by injecting a non-toxic agent called ‘Gadolinium’ while

scanning the T1-weighted image. Gadolinium is beneficial in recognizing the barrier between blood and brain (like tumors, multiple sclerosis, etc.) due to its ability to make the T1 time shorter and then affect the intensity of the image.

12.Problematic

Brain Tumors are complex, they are considered one of the most aggressive diseases, among children and adults. There are a lot of abnormalities in the sizes and location of the brain tumor(s). This makes it really difficult to completely understand the nature of the tumor. Also, a professional Neurosurgeon is required for MRI analysis. Oftentimes in developing countries, the lack of skillful doctors and lack of knowledge about tumors makes it really challenging and time-consuming to generate reports from MRI. So, an automated system in Cloud can solve this problem.

13.The Aim of the Research

The main aims of this work are:

- ✓ Detect if Glioma exists or not
- ✓ Segmentation of brain tumors
- ✓ Proposing an algorithm for classification of a brain tumor in MRI slices
- ✓ Designing and implementing a classifier model for status of glioma
- ✓ Comparing the performance of this algorithm with other works in this field

Chapter II

Literature Review and Background

1.Introduction

Due to the high volume of diagnostic requests or the complexity of the diagnosis itself, scientists discovered numerous issues with identifying medical photos. We must process photos in order to enhance their quality or extract various attributes in order to do the proper diagnosis.

2.Computer-aided Diagnosis,DetectionSystem for Brain Tumor Analysis

To attain a more reliable and accurate diagnosis, recently, varieties of computer-aided detection (CAD) and diagnosis (CADX) approaches have been developed to assist in the interpretation of medical images.CAD is a technology that includes multiple elements like concepts of artificial intelligence (AI), computer vision, and medical image processing. The main application of the CAD system is finding abnormalities in the human body. Among all these, the detection of tumors is the typical application because if it misses in basic screening, it leads to cancer. [15]

2.1Objectives of the CAD system

The main goal of CAD systems is to identify abnormal signs at the earliest that a human professional fails to find. In mammography, identification of small lumps in dense tissue, finding architectural distortion, and prediction of mass type as benign or malignant by its shape, size, etc.

2.2Applications of CAD system

CAD is used in the diagnosis of breast cancer, lung cancer, colon cancer, prostate cancer, bone metastases, coronary artery disease, congenital heart defect, pathological brain detection, Alzheimer's disease, and diabetic retinopathy.

3.Brain TumorsApproaches

A brain tumor, known as an intracranial tumor, is an abnormal mass of tissue in which cells grow and multiply uncontrollably, seemingly unchecked by the mechanisms that control normal cells. More than 150 different brain tumors have been documented, but the two main groups of brain tumors are termed primary and metastatic. Primary brain tumors include tumors that originate from the tissues of the brain or the brain's immediate surroundings.

Primary tumors are categorized as glial (composed of glial cells) or non-glial (developed on or in the structures of the brain, including nerves, blood vessels, and glands) and benign or malignant.The World Health Organization (WHO) has developed a grading system to indicate a tumor's malignancy or benignity based on its histological features under a microscope: Most

malignant, Rapid growth, aggressive, Widely infiltrative, Rapid recurrence, and Necrosis prone. [16]

Based on a tumor's histological characteristics as seen under a microscope, the World Health Organization (WHO) has created a grading system to reflect a tumor's malignancy or benignity. most harmful rapid expansion, combative Widely infiltrative, recurrent quickly, and prone to necrosis. [16]

Grade	Characteristics	Tumor Types
Low Grade	<ul style="list-style-type: none"> • Least malignant (benign) • Possibly curable via surgery alone • Non-infiltrative • Long-term survival • Slow growing 	<ul style="list-style-type: none"> • Pilocytic astrocytoma • Craniopharyngioma • Gangliocytoma • Ganglioglioma
	<ul style="list-style-type: none"> • Relatively slow growing • Somewhat infiltrative • May recur as higher grade 	<ul style="list-style-type: none"> • "Diffuse" Astrocytoma • Pineocytoma • Pure oligodendroglioma
High Grade	<ul style="list-style-type: none"> • Malignant • Infiltrative • Tend to recur as higher grade 	<ul style="list-style-type: none"> • Anaplastic astrocytoma • Anaplastic ependymoma • Anaplastic oligodendroglioma
	<ul style="list-style-type: none"> • Most malignant • Rapid growth, aggressive • Widely infiltrative • Rapid recurrence 	<ul style="list-style-type: none"> • Glioblastoma multiforme (GBM) • Pineoblastoma • Medulloblastoma • Ependyoblastoma

Table 4: Brain tumors approaches

4.Segmentation Approaches

Image segmentation is defined as the method of segregating the image into mutually exclusive and exhaustive sectors being uniform and corresponding to some predefined standard.

Segmentation in the light of brain tumor comprises of distinguishing the abnormal tissues from normal tissues of brain. [17]

Segmentation techniques are generally divided into the following categories [18]:

- Thresholding techniques
- Region growing techniques
- Edge-based techniques
- Clustering techniques
- Watershed technique
- Deformable model-based techniques

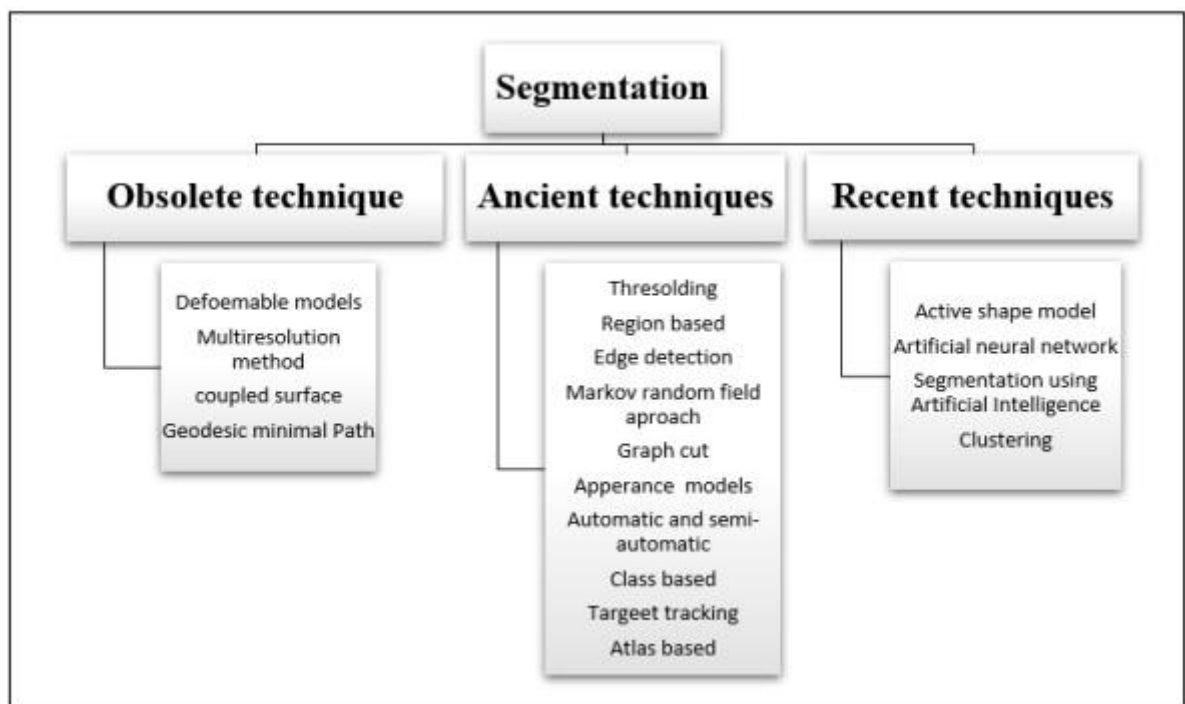


figure 12: Segmentation techniques

5. Classification Approaches

There is a lot of classification methods, we chose some of them:

Table:5 Classification methods

Classification method	Description	Characteristics
Logistic Regression	Logistic Regression is a classification and not a regression algorithm. It estimates discrete values (Binary values like 0/1, yes/no, true/false) based on a given set of the independent variable(s). Simply put, it basically, predicts the probability of occurrence of an event by fitting data to a logit function. Hence, it is also known as logit regression. The values obtained would always lie within 0 and 1 since it predicts the probability. [30]	Particularly in epidemiologic research, logistic regression is an effective tool because it enables simultaneous analysis of several explanatory variables while minimizing the impact of confounding variables.
Artificial Neural network	Artificial neural networks are a technology based on studies of the brain and nervous system. These networks emulate a biological neural network but they use a reduced set of concepts from biological neural systems. Specifically, ANN models simulate the electrical activity of the brain and nervous system. Processing elements (also known as either a neurode or perceptron) are connected to other processing elements. [19]	It uses Nonpara- the metric approach. Performance and accuracy depend upon the network structure and number of inputs

Decision tree	<p>A decision tree is a type of supervised machine learning used to categorize or make predictions based on how a previous set of questions were answered. A model is a form of supervised learning, meaning that the model is trained and tested on a set of data that contains the desired categorization.</p> <p>Decision trees imitate human thinking, so it's generally easy for data scientists to understand and interpret the results. [20]</p>	<p>DT are based on hierarchical rule based method and use Nonparametric approach.</p>
Support Vector Machine	<p>A support vector machine (SVM) is a supervised machine learning model that uses classification algorithms for two-group classification problems. After giving an SVM model sets of labeled training data for each category, they're able to categorize new text.</p>	<p>SVM uses Non-parametric with binary classifier approach and can handle more input data very efficiently. Performance and accuracy depends upon the hyper- plane selection and kernel parameter.</p>
Random Forest	<p>A random forest is a supervised machine learning algorithm that is constructed from decision tree algorithms. This algorithm is applied in various industries such as banking and e-commerce to predict behavior and outcomes. [21]</p>	<p>It's more accurate than the decision tree algorithm. It provides an effective way of handling missing data. It can produce a reasonable prediction without hyper-parameter tuning.</p>

6.ObjectRecognitionApproaches

Object recognition is a general term to describe a collection of related computer vision tasks that involve identifying objects in digital photographs. [22]

Image classification involves predicting the class of one object in an image. Object localization refers to identifying the location of one or more objects in an image and drawing an abounding box around their extent. Object detection combines these two tasks and localizes and classifies one or more objects in an image.

Image Classification: Predict the type or class of an object in an image.

Object Localization: Locate the presence of objects in an image and indicate their location with a bounding box.

Object Detection: Locate the presence of objects with a bounding box and types or classes of the located objects in an image.

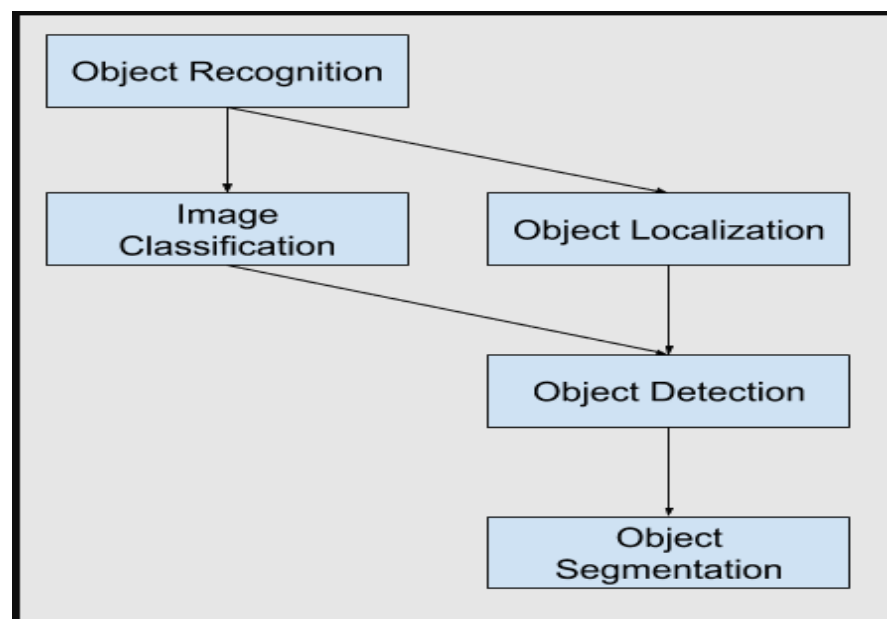


figure 13: Object Recognition Approaches

These are the six most prevalent object detection techniques.

Histogram of Oriented Gradients (HOG) Feature Descriptor / Region-based Convolutional Neural Networks (R-CNN) / Region-based Fully Convolutional Network (R-FCN) / Single Shot Detector (SSD) / Spatial Pyramid Pooling (SPP-net) / YOLO (You Only Look Once

7.Semantic Segmentation Approaches

Semantic segmentation is a natural step in the progression from coarse to fine inference: The origin could be located at classification, which consists of making a prediction for a whole input. The next step is localization/detection, which provides not only the classes but also additional information regarding the spatial location of those classes. Finally, semantic segmentation achieves fine-grained inference by making dense predictions inferring labels for every pixel so that each pixel is labeled with the class of its enclosing object or region. [27]

A general semantic segmentation architecture can be broadly thought of as an encoder network followed by a decoder network:

The encoder is usually a pre-trained classification network like VGG/ResNet followed by a decoder network.

The task of the decoder is to semantically project the discriminative features (lower resolution) learned by the encoder onto the pixel space (higher resolution) to get a dense classification.

the existing Semantic Segmentation approaches:

- 1—Region-Based Semantic Segmentation
- 2—Fully Convolutional Network-Based Semantic Segmentation (FCN)
- 3—Weakly Supervised Semantic Segmentation

8.Related WorkusingDeep Learning for Glioma Tumor Analysis

Neurologists benefit from computer-aided diagnosis systems in several ways, we can cite such points as:

Detecting tumors in an early stage helps for better diagnosis and also will reduce human intervention

By using a physician as a second opinion, the final decision can be made with confidence. In order to diagnose a brain tumor, it is crucial to classify it. As a result, researchers are motivated to develop a system for detecting brain pathology. By detecting abnormalities in the brain image, the pathology detection system classifies it as normal or abnormal.

Nayak et al. [44], the technique for detecting pathological brains is based on fast curvelet

entropy features. Siyuan et al [50], in order to detect pathological brains, they have developed a pre-trained AlexNet that has incorporated a transfer learning method. Mallick et al. [51], the authors have proposed a deep neural network-based deep wavelet autoencoder for brain cancer detection.

Kaur et al. [52] have implemented an optimizer DL model based on Fisher criteria and parameter-free BAT. Hemanth et al. [53] have designed brain abnormality detection based on a genetic algorithm.

Table 6: Related Work using Deep Learning for Glioma Tumor

Authors	Publication Year	The proposed Approach	datasets	Accuracy
Sajjad et al. [65]	2018	VGG19 + Extensive Data Augmentation	Radiopaedia [66] The brain tumor dataset[67]	94.58
Gumaei et al.[68]	2019	Regularized Extreme Learning Machine	Brain tumor dataset provided in[69][70]	94.23
Anarki et al. [71]	2019	CNN + Genetic Algorithm	IXI Dataset[72] TCIA[73] REMBRANDT[74] TCGA-GBM[75] TCGA-LGG[76] Brain tumor dataset	94.20
Swati et al. [77]	2019	VGG19 + Fine Tuning	CE-MRI dataset[26]	94.82
Deepak et al. [78]	2019	GoogleNet + Transfer Learning	CE-MRI dataset	97.10
Kumar, R. L. [79]	2021	ResNet-50 and Global Average Pooling	CE-MRI dataset	97.08
Kumar, R. L.	2021	ResNet-50 and Global Average Pooling	CE-MRI dataset	97.48

8.1 Brain tumor segmentation and grading of lower-grade glioma using transfer learning

The varied grades of glioma tumors aid in assessing the patient's chances of survival. To partition the tumors in this work [23], they combined CNN based on the U-Net. With Vgg16 as the foundation model, they employed a transfer learning-based methodology. In this study, T1 flare

pictures from 110 individuals with lower-grade gliomas were employed (LGG). With a classification accuracy of 26 of 89% for MRI images and 95% for patients, the model divided LGG into grades II and III. The outcomes of this study demonstrated that transfer learning can be employed for tumor classification and segmentation. While in our work transfer learning was used to categorize various tumor kinds, in this study it was utilized to categorize glioma tumors into various grades. Since the Grades of the tumor is mostly reliant on the shape of the tumor, segmentation and classification were also used in this study.

8.2 Combining statistical features using GLCM algorithm and recurrent neural network for tumor detection

A variety of analyses were performed in order to identify the relevant features for the prediction, classification, segmentation, and classification [45]. Analysis of texture is based on obtaining the specific patterns of hidden characteristics, simplifying and presenting them in a unique way. Based on the spatial relationship between pixels, Grey Level Cooccurrence Matrix (GLCM) has been identified as a promising statistical technique for examining the texture of an image [46]. A gray level correlation matrix (GLCM) is identified by a square matrix that sums neighboring gray levels of pixels within an image based on the number of gray levels (n) in the image (I) along several angles orientation 0° , 45° , 90° , and 135° . The GLCM matrix calculation is shown in equation 1; GLCM identifies the joint probability occurrence of the pixel pairs having x and y grey level for δ_v and δ_s specific spatial offset between the pixel pairs, knowing that I represent the 2D image map within $n \times n$ (number of grey levels) dimensions [47][48].

$$L\delta_v, \delta_s(x, y) = \sum_{x, y} \begin{cases} 1, & \text{if } I(s, v) = x \text{ and } I(s + \delta_{s,v} + \delta_v) = y \\ 0, & \text{Otherwise} \end{cases}$$

This study developed a method based on clinical neuroimaging that utilizes Magnetic Resonance Imaging (MRI), which measures water diffusion within tissues using Diffusion-weighted Imaging (DWI). In this work, they propose a robust Machine Learning (ML) model to predict glioma aggressiveness based on psychometric data, higher-order moments, and grey level co-occurrence matrix (GLCM) texture features. As a result of the f-test, three features (patient gender, GLCM energy, and correlation) were excluded from the ML model, which was able to predict tumor categories with an accuracy of 88.14% over the test set, indicating a high level of prediction accuracy for glioma grades which illustrated in [49].

8.3 Segmentation of brain tumors from MRI images based on deep learning using Res-UNet

Due to their ability to learn complex features from data, Deep Learning techniques have shown

promising results for brain tumor segmentation [54]. It has been demonstrated that segmentation tasks can be accomplished using Convolutional Neural Networks (CNNs) and Fully Convolutional Networks (FCNs), such as SegNet [55], Deep Neural Networks [56], U-Net [57], QuickNAT [58], and DenseNet [59] and variants of these models [1,15,20,31].

In Deep Learning, Res-UNet is widely used as a base model for many architectures due to its superior performance and effectiveness in feature extraction[60]. Kermi et al. improved segmentation accuracy by combining a weighted cross entropy and generalized dice loss function with a modified U-Net architecture[61]. In contrast, these methods pass all extracted features to the decoder stage via the skip connection.

To suppress irrelevant activations and focus primarily on features relevant to the specific task, attention gates were introduced [62]. Zhang et al. developed the attention gates on Res-UNet for brain tumor segmentation and have exposed its efficiency over the Res-UNet [63]

In this study [64], a generator architecture is proposed that is capable of explicitly guiding each decoder layer's learning process. Each decoder layer has an individual loss function that supervises the learning process so that better feature maps can be generated. Instead of allowing all information to pass through the skip connections in the Res-UNet, the attention gates in the generator activate relevant information. The performance of the proposed model was better than the baseline models such as UNet, Res-UNet, and Res-UNet. A proposed model has been validated using unseen data from high-grade glioma test cases and achieved Dice score values of 0.911, 0.876, and 0.801 as well as mean IoU values of 0.838, 0.781, and 0.668 respectively.

8.4.A framework for Brain Tumor segmentation and classification using Deep Learning

Feature extraction is essential, but deciding which machine learning classifiers to use is equally important. For binary classification of Glioma into low grade or high grade, and sometimes multiclass classification, researchers use classifiers like SVM, KNN, NB, Tree, and MLP. SVM has reached best performance according to other classifiers [28].

In this study [29], As a result, CAD systems using a combined deep learning-based brain tumor segmentation and classification algorithms are broadly utilized. In the deep learning-based brain tumor segmentation and classification technique, the CNN model has an excellent brain segmentation and classification effect. In this project, an incorporated and hybrid approach based on deep convolutional neural network and machine learning classifiers is proposed for the accurate segmentation and classification of brain MRI tumor. Two steps are proposed for this model

In the first step, A CNN is implemented for learning the tumor marker region represented in feature map from image space of brain MRI. A faster region-based CNN is designed in the second step, for the localization of tumor region followed by region proposal network (RPN). The proposed classification model that is based on the proposed deep CNN and SVM-RBF classifier. The performance evaluated the experimental results and validated by assessing metrics which achieved an accuracy of 98.3% and a dice similarity coefficient (DSC) of 97.8%.

Authors	Publication Year	Modalities	Segmentation Process	Classification Process	datasts	Performance metrics
Xiao et al. [80]	2019	T1, T1c, T2, and FLAIR MRI	(ROIs): 956 Radiomics feature from the regions of interest + VGG-16 pre-trained network is used to extract 512 deep features RFE for feature selection	SVM, LR and LDA Low- or High-grade Glioma	Dataset consist of 210 cases of HGG and 75 cases of LGG MRI taken from the BRATS 2018 challenge	SVM ACC=94.2%
Li J.,&al. [81]	2020	T2 FLAIR	Manual segmentation and histogram based features, GLCM, Haralick and GLRLM methods	Prediction of the four immunohistochemical Biomarkers like Ki-67, S-100, vimentin and CD34 of glioma	Local dataset consist of T2 Flair MRI sequences of 51 glioma patients	ACC=80.11%
Zhang et al. [82]	2020	DTI	Structural and texture based deep convolutional features, GLCM based texture features, Intensity histogram and uniformity features, Wavelet texture features, 2D and 3D shapebased features	SVM Low- or High-grade Glioma and Grade III or Grade IV	Local dataset consist of DTI sequences of 43 LGG and 65 HGG patients	Acc=94% (Low vs. high grade classification) and ACC= 98% (Grade III vs. Grade IV classification)

Table 7: Related framework for Brain Tumor segmentation and classification using svm

9. Conclusion

According to the published studies, physical therapy can enhance glioma patients' functional prognosis and quality of life. Future research should focus more on the therapeutic benefits of rehabilitation for glioma patients.

Chapter III

Proposed Methodology

1.Introduction

The best categorization is the product of a number of steps, including enhancing the image's quality and correctly extracting characteristics. The process of extracting the proper characteristics that would improve the classification result involves multiple processes, including brain detection and segmentation, which are the two primary ones. In this chapter, we provide our suggested solution and go over all the significant actions we took during our research.

2.Proposed Pipeline

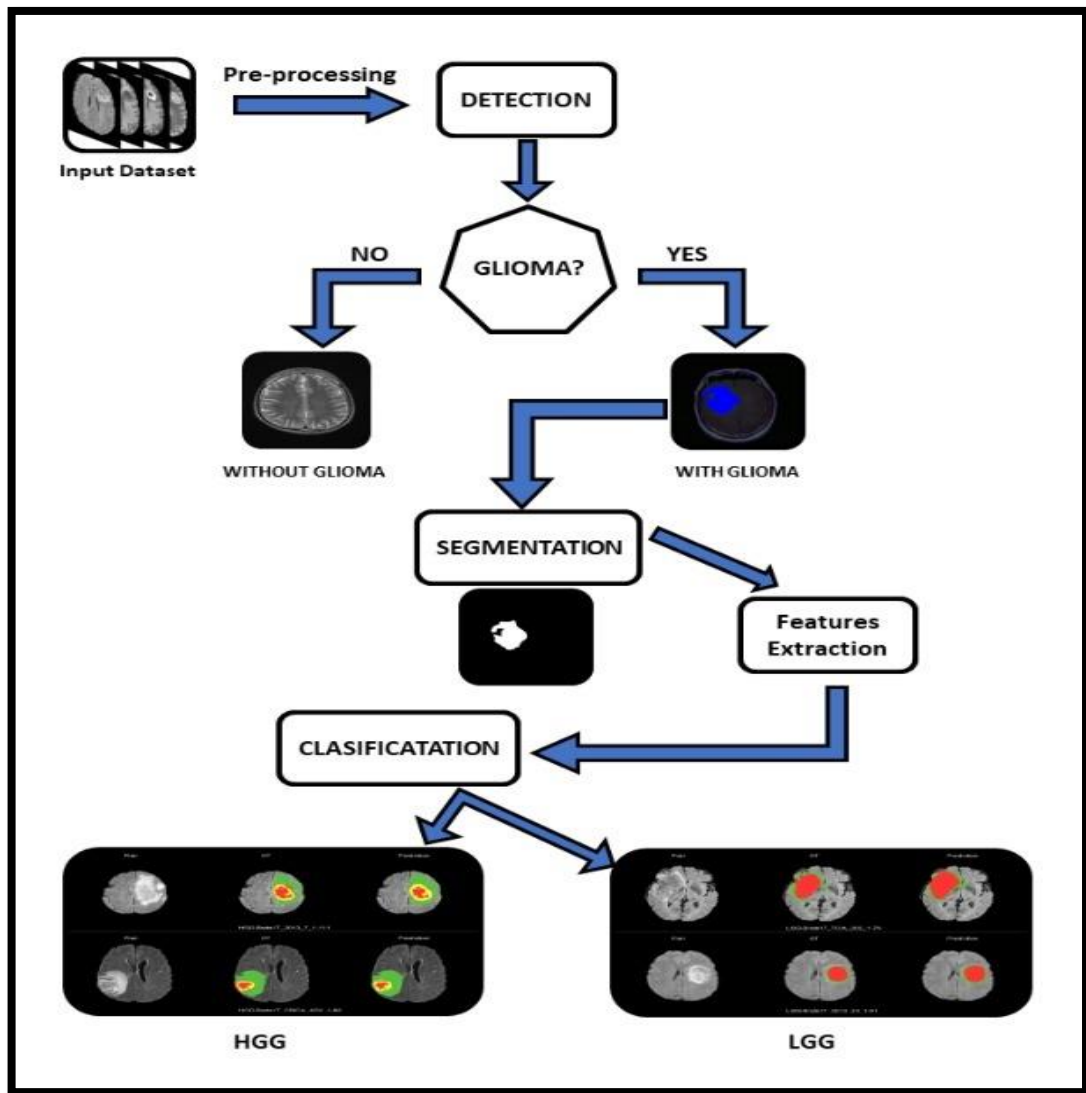


figure 14: The pipeline of the proposed glioma classification scheme

The pipeline of the proposed scheme is shown in Figure. It uses four modalities of MRIs as the inputs (T1, T1e, T2, and FLAIR). In the proposed scheme, 2D image slices are extracted from 3D volume scans in four modalities, and they are partitioned into the training, validation, and testing subsets.

Based on the above plan, we will first load all of the MRI Images we got from the dataset.

The second process is preprocessing, which is a step in the data mining and data analysis process that takes raw data and transforms it into a format that can be understood and easily parsed by the machine.

The next step is to detect if a glioma tumor exists or not. if the tumor does not exist, we consider the situation normal, else We segment and localize the tumor.

For our Support Vector Classifier, we will be extracting statistical features that detail certain physical characteristics of the tumor, such as the volume, surface area, and roughness. These elements determine the state of the tumor (high or low-grade glioma).

3.Pre-Processing

In this phase of the CAD system, the images are pre-processed to enhance image quality and remove noise. The main goal of the pre-processing process is to prevent misleading results that can occur in segmentation and classification processes.

3.1Image Enhancement

Enhancements are used to optimize for specific feature measurement methods, rather than fix problems. Familiar image processing enhancements include sharpening and color balancing. Here are some general examples of image enhancement:

3.1.1Image Cropping

:ImageCropping is an important action to reach a high recognition rate. the crop is useful for preprocessing in the case that the position of the object has a large variance. So, we crop the input image and make batch data.

3.1.2Image Resizing:

images in the training dataset had different sizes, therefore images had to be resized before being used as input to the model. Square images were resized to the shape of 256×256 pixels. Rectangular images were resized to 256 pixels on their shortest side, then the middle 256×256 square was cropped from the image

3.1.3.Image filtering and de-noising (Noise Reduction):

Image filtering and de-noising:By default,images haveGaussian noise because of the variations in illumination.Pixel-based filtering such as a low pass filter can be used to de-noise images.

3.1.4 Image Normalisation:

Also referred to as data re-scaling, it is the process of projecting image data pixels (intensity) to a predefined range (usually (0,1) or (-1, 1)). This is commonly used on different data formats.

4-Processing

4.1. Glioma Detection

This phase is considered an important phase in our project. It is a crucial phase for building a proper model. we present model-based learning for brain tumor detection from multimodal MRI protocols. The model uses ResNet50 -based fully convolutional networks.

In this process, we create a classifier model to detect if tumor exists or not.

The objectives of this phase are:

Reduction of the number of treated images

Minimization of time lost

Increase system efficiency

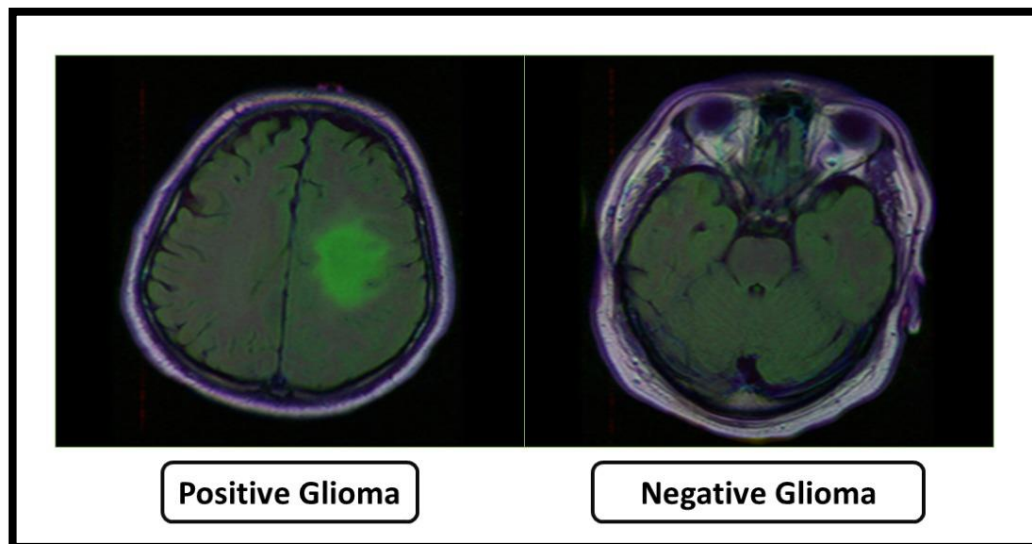


figure 15: Glioma Detection

4.1.1. Model description

ResNet (Residual Network) is a convolutional neural network that democratized the concepts of residual learning and skips connections. This enables us to train much deeper models.

4.1.2. ResNet50 model architecture

ResNet50 is a 50-layer Residual Network with 26M parameters. The residual network is a deep

convolutional neural network model that is introduced by Microsoft in 2015[39]. In Residual network rather than learning features, we learn from residuals that are subtraction of features learned from the layer's inputs. ResNet used the skip connection to propagate information across layers. ResNet connects n th layer input directly to some $(n+x)$ th layer which enables additional layers to be stacked and a to establish a deep network. We used a pre-trained ResNet50 model in our experiment and fine-tuned it. In Figure 16, the architecture of ResNet50 is shown

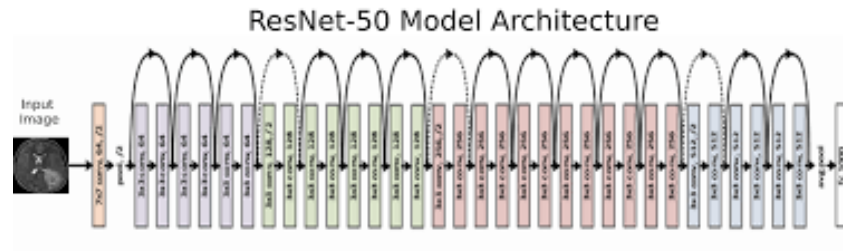


figure 16: ResNet50 architecture

4.2 Segmentation Process

In an image classification task, the network assigns a label (or class) to each input image. However, suppose you want to know the shape of that object, which pixel belongs to which object, etc. In this case, you need to assign a class to each pixel of the image—this task is known as segmentation.

In this process, we will create the segmentation model, called ResU-Net to tumor localize

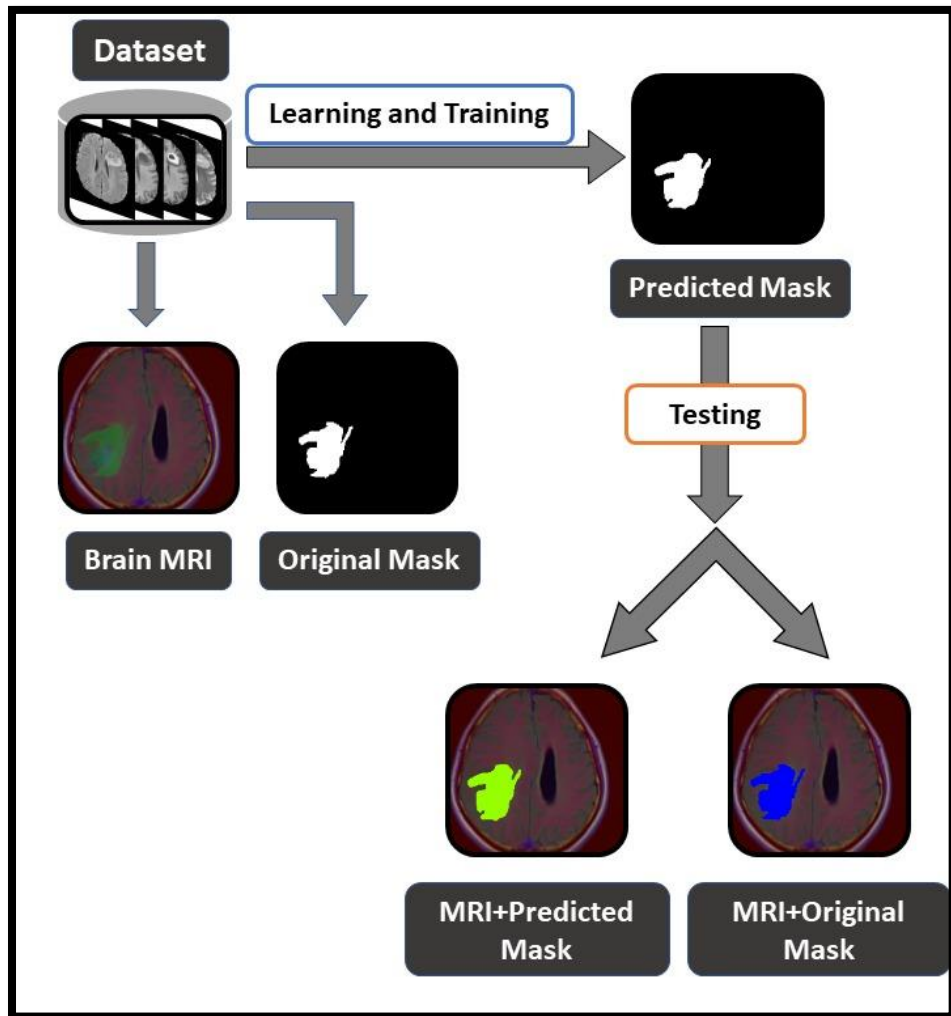


figure 17: Segmentation Process

4.2.1. ResUnet model architecture

ResUNet architecture combines UNet backbone architecture with residual blocks to overcome the vanishing gradients problem present in deep architectures.

Unet architecture is based on Fully Convolutional Networks and modified in a way that it performs well on segmentation tasks.

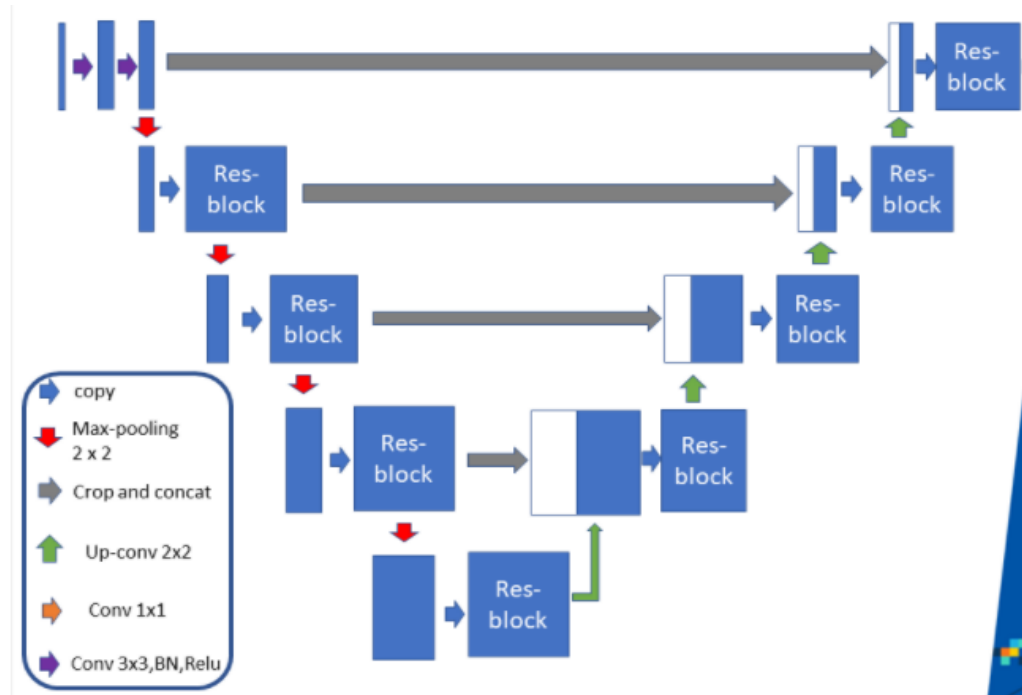


figure 18: ResUnet model architecture

As shown in the previous figure. ResUNet consists of three parts:

Encoder: The contraction path consist of several contraction blocks, each block takes an input that passes through res-blocks followed by 2x2 max pooling. Feature maps after each block doubles, which helps the model learn complex features effectively.

Decoder: In the decoder, each block takes in the up-sampled input from the previous layer and concatenates it with the corresponding output features from the res-block in the contraction path. this is then passed through the res-block followed by 2x2 upsampling convolution layers this helps to ensure that features learned while contracting are used while reconstructing the image.

Bottleneck: The bottleneck block, serves as a connection between the contraction path and expansion path. The block takes the input and then passes through a res-block followed by 2 x 2 up-sampling convolution layers.

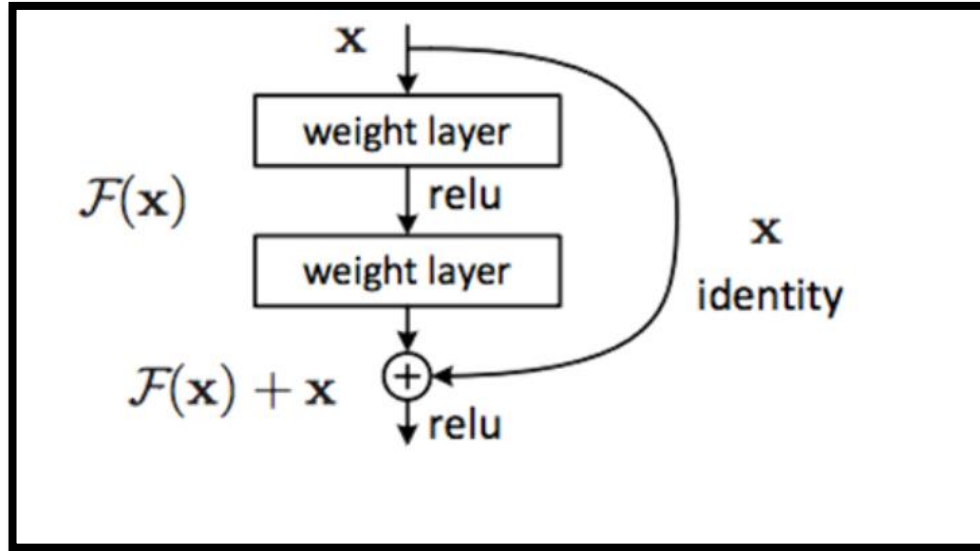


Figure 19: basic transformation in the residual block

In deep CNN networks, the vanishing gradient problem arises during the training process. The gradient norm of earlier layers decreased to zero as the training proceeded. To resolve this problem, the Residual Network learning method is used. In ResNet, the yield of each residual layer is convolved with its input to be the input of the next layer. Let, represents the residual mapping to build a residual learning block as shown in Fig 19.

4.3.Features Extraction

Feature extraction is an important step in the construction of any pattern classification and aims at the extraction of the relevant information that characterizes each class. It becomes easier for the classifier to classify between different classes by looking at these features. The features can be divided into four types: Geometric features, Statistical features, Texture features, and Color features. In our proposed system, we use an application of gray level co-occurrence matrix (GLCM) to extract second order statistical texture features for motion estimation of images.

4.3.1.GLCM

GLCM is calculated for a selected pair of distance and angle. The relative frequencies of pair of each reference pixel and its neighboring pixel at a certain distance and angle are calculated for finding its GLCM matrix. The matrix thus obtained is divided by sum of all the frequencies in order to get normalized matrix[83]. Fig. +++++ shows how GLCM is calculated from greycomatrix of 4-by-5 image I for $D=1$ and $\Theta=0^\circ$.

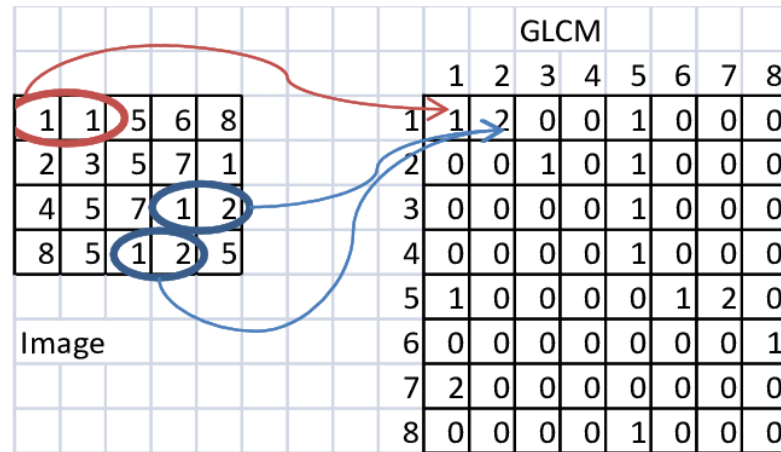


figure 20: GLCM calculation from greycomatrix of 4-by-5 image

4.4 Classification Using Support Vector Machine (SVM)

4.4.1. Description of algorithm

In the SVM algorithm, we plot each data item as a point in n-dimensional space (where n is the number of features we have), with each feature's value being the value of a certain coordinate.

SVM chooses the extreme points/vectors that help in creating the hyper-plane. These extreme cases are called as support vectors, and hence algorithm is termed as Support Vector Machine. Consider the below diagram in which there are two different categories that are classified using a decision boundary or hyper-plane:

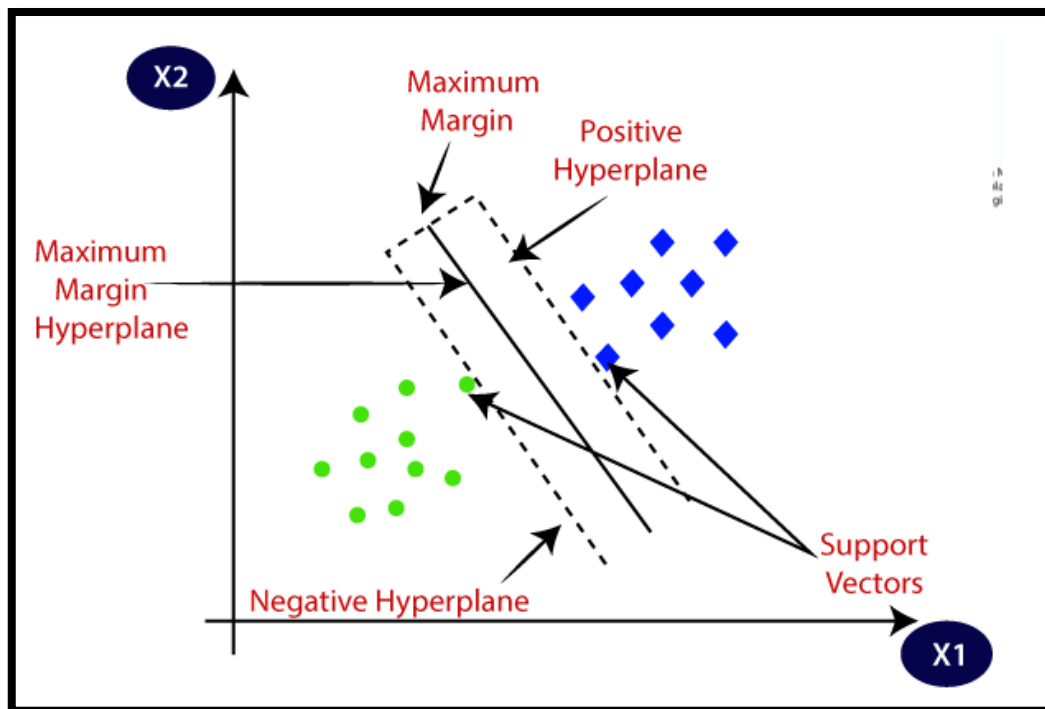


Figure 21: SVM algorithm

SVM comes in two varieties:

Linear SVM: Linear SVM is used for data that can be divided into two classes using a single straight line. This type of data is called linearly separable data, and the classifier employed is known as a Linear SVM classifier.

Non-linear SVM: Non-Linear SVM is used for non-linearly separated data. If a dataset cannot be classified using a straight line, it is considered non-linear data, and the classifier employed is referred to as a Non-linear SVM classifier.

By presenting an example, the SVM algorithm's operation can be better understood. Consider a dataset with two tags (green and blue), two features (x_1 and x_2), and two tags. We need a classifier that can identify whether the pair of coordinates (x_1 , x_2) is blue or green. Think on the picture below:

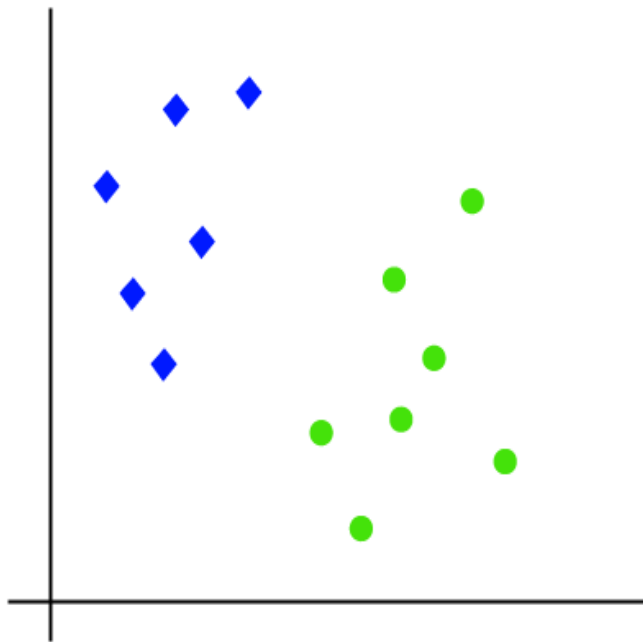


Figure 22: SVM with two tags

Since it is a two-dimensional space, we may easily distinguish between these two classes by utilizing merely a straight line. But these classes may be divided by more than one line:

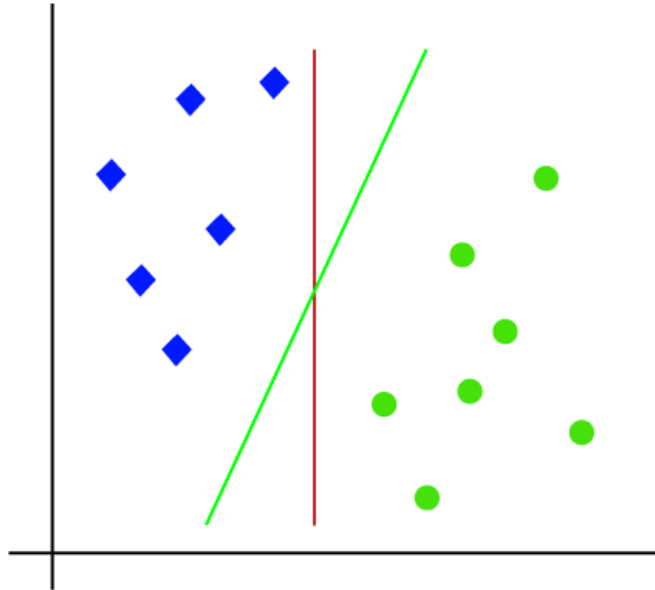


Figure 23: classes by utilizing merely a straight line

As a result, the SVM method aids in identifying the ideal decision boundary or region, often known as a hyperplane. The SVM algorithm determines which line from each class is closest to the other. Support vectors are the names for these points. Margin is the distance between the hyperplane and the vectors. Maximizing this margin is the aim of SVM. The ideal hyperplane is the one with the largest margin.

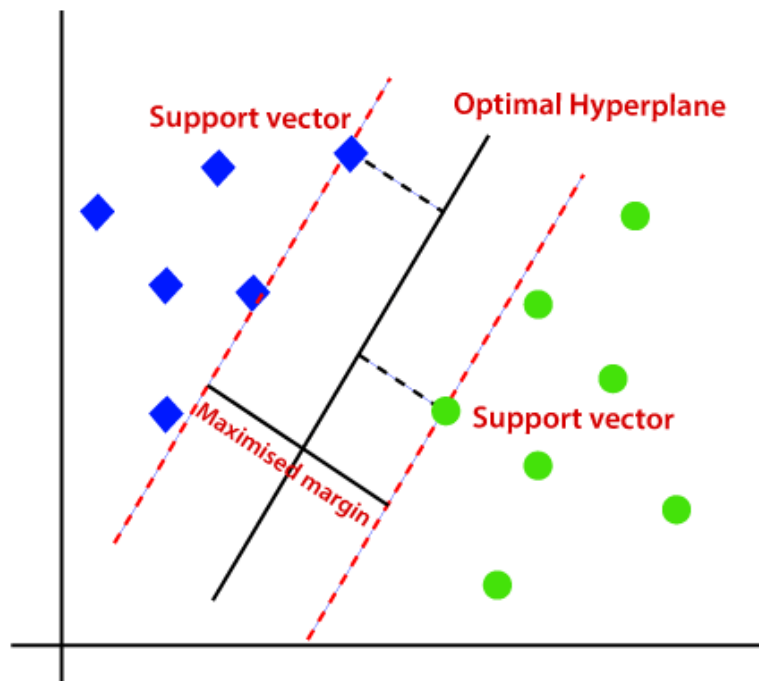


Figure 24: The margin between the hyperplane and the vectors

After extracting all the features from the segmented image and storing it as csv file. the the SVM classifier began the training on two classes of gliomagrade (HGG, LGG).

5. Performance and Evaluation

Once the model has been implemented and some results in the form of a class or probability have been obtained, the next step is to use the test datasets to detect the model's efficiency using a number of different metrics. Various Machine Learning Algorithms are fine-tuned using a set of performance metrics. Selecting an appropriate metric is crucial because it affects how well the machine learning technique works.

5.1. Confusion Matrix

The confusion matrix, also known as the error matrix, is depicted as a matrix describing the performance of a classification model on a set of test data (Fig 25). [40]

		Actual Values	
		Positive(1)	Negative(0)
Predicted Values	Positive(1)	TP	FP
	Negative(0)	FN	TN

Figure 25: Confusion Matrix

The terms used in defining a confusion matrix are:

True positive (**TP**): Observation is predicted positive and is actually positive.

False positive (**FP**): Observation is predicted positive and is actually negative.

True negative (**TN**): Observation is predicted negative and is actually negative.

False negative (**FN**): Observation is predicted negative and is actually positive.

5.1.1.Accuracy

Accuracy gives the proportion of the total number of predictions that were correct. used if the ratio of patients with the disease (true positive, false negative) and patients without the disease (true negative, false positive) reflects the prevalence of the illness.

$$Accuracy = (TP + TN)/(TP + TN + FP + FN)$$

5.1.2.Precision

Precision or the positive predictive value is the fraction of positive values out of the total predicted positive instances. In other words, precision is the proportion of positive values that were correctly identified:

$$Precision = TP / (TP + FP)$$

5.1.3.Sensitivity

sensitivity, recall, or the TP rate (TPR) is the fraction of positive values out of the total actual positive instances (the proportion of actual positive cases that are correctly identified):

$$Sensitivity = TP / (TP + FN)$$

5.1.4.F1 score

The F1 score, F score, or F measure is the harmonic mean of precision and sensitivity it gives importance to both factors:

$$F1\ score = 2 * (Precision * Sensitivity) / (Precision + Sensitivity)$$

6.conclusion

Previously we have presented the proposed solution, provided the overall structure of the solution organized in several phases, and presented each phase in detail. We will evaluate and discuss the obtained results by our proposed solution in the next chapter.

Chapter VI

Results and

Experimental Tests

1.Introduction

As was explained in the previous chapter our model has five steps. Thus, in this chapter, we will explain the last one, explain the used tools and the programming code for each step. In the end, we will discuss the obtained results.

2.Dataset

2.1.Dataset used in[34]:

Mateusz Buda, Ashirbani Saha, Maciej A. Mazurowski "Association of genomic subtypes of grade gliomas with shape features automatically extracted by a deep learning algorithm." Computers in Biology and Medicine, 2019.

And Maciej A. Mazurowski, Kal Clark, Nicholas M. Czarnek, Parisa Shamsesfandabadi, Katherine B. Peters, Ashirbani Saha "Radiogenomics of lower-grade glioma: algorithmically-assessed tumor shape is associated with tumor genomic subtypes and patient outcomes in a multi-institutional study with The Cancer Genome Atlas data." Journal of Neuro-Oncology, 2017.

Brain MR images with manual-created FLAIR abnormality segmentation masks are included in this dataset. These photos came from the Cancer Imaging Archive (TCIA). These numbers correspond to 110 patients with at least FLAIR sequence and genomic cluster data from The Cancer Genome Atlas (TCGA) dataset. The data.csv file contains clusters of tumor genomics and patient information.

2.2 Dataset used in[43]:

In our classification work, we made use of the widely-used BraTS-2018 dataset from the medical field. Nineteen different locations employ a wide variety of MRI systems scanners for the BraTS dataset. which provides multimodal 3D brain MRIs and ground truth brain tumor segmentations annotated by physicians.

BraTS-2018 has 285 instances in its training dataset, with 210 being High-Grade Glioblastomas (HGG) and 75 being Low-Grade Gliomas (LGG). Each MR image is of size $240 \times 240 \times 155$, with four 3D MRI modalities (Fluid Attenuated Inversion Recovery (FLAIR), T1, T1c, T2), rigidly aligned, skull stripped, and resampled to $1 \times 1 \times 1$ mm isotropic resolution.

3.Dataset implementation

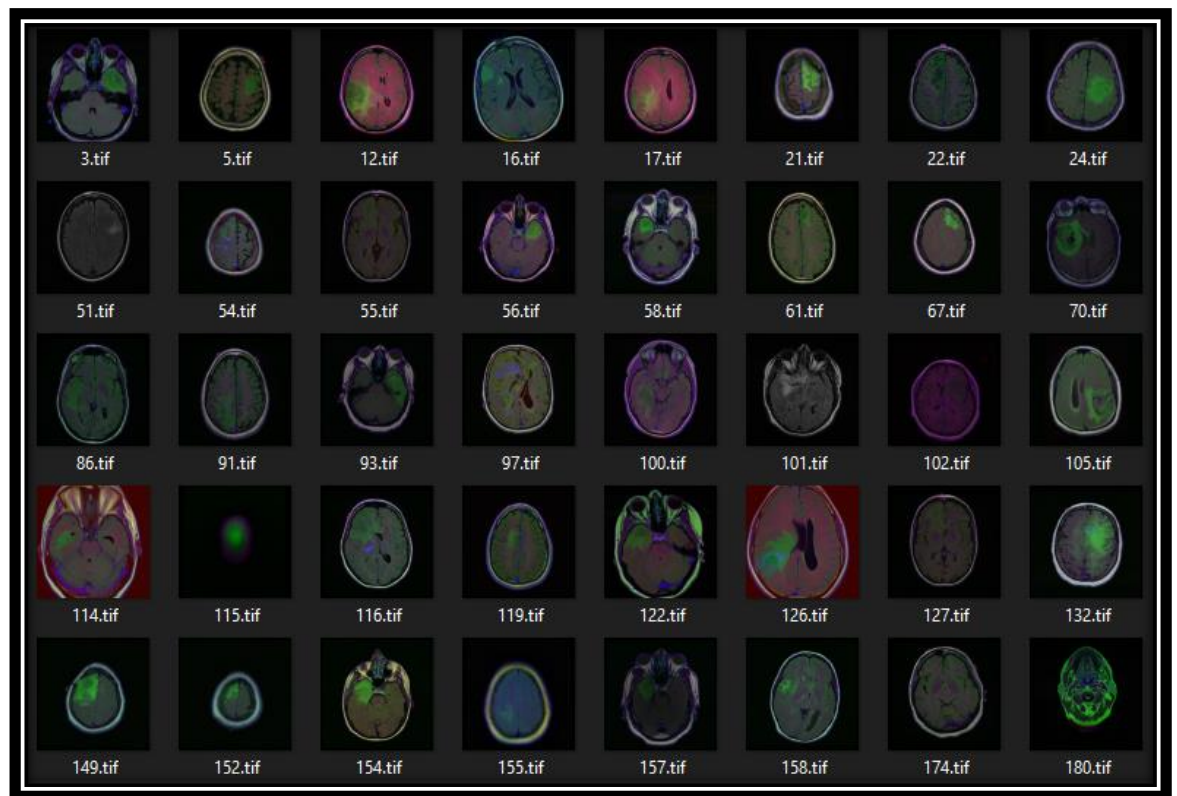


figure 26: Total Original MRI images : 3929

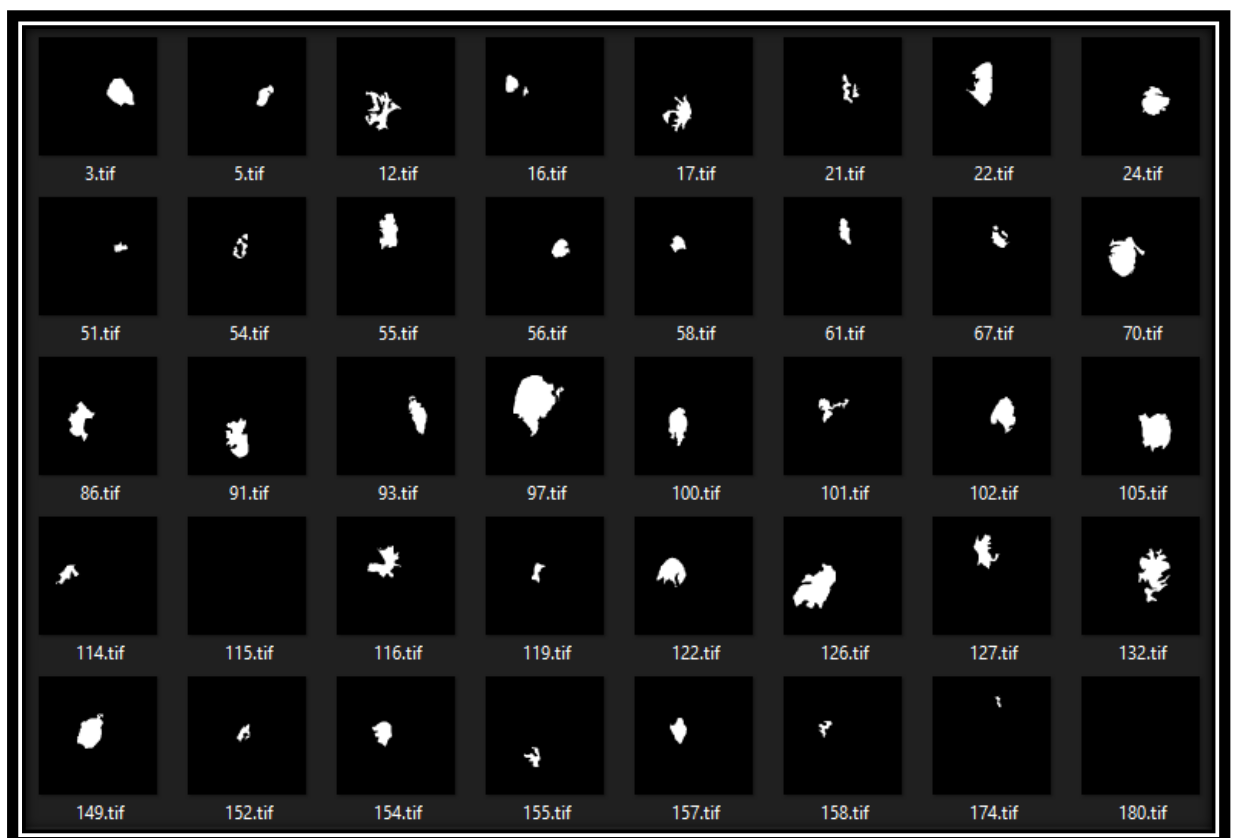


figure 27: Total Original Mask images : 3929

4. Software and Hardware Settings

4.1. Hardware Settings

Our pc: AMD Ryzen 5 5600G with Radeon Graphics 3.90 GHz

RAM 8.00 GB, GPU: NVIDIA GeForce GTX 980

Kaggle: RAM 13GB , Disk 73.1 GB GPU Memory 15.9GB

4.2 Software Settings

4.2.1. Python Language

Python is a high-level, interpreted, object-oriented language which has dynamic semantics. Because of its high-level, in-built data structures, dynamic typing, and dynamic binding, this language is perfect for Rapid Application Development and may also be used as a scripting or glue language to connect disparate components. Python's easy-to-learn syntax places an emphasis on readability, which helps keep maintenance costs down. Python's module and package system facilitates both modularity and code reuse in applications. The Python programming language and its comprehensive standard library are open-source and freely distributable in source or binary form for all major platforms. [10]

4.2.2. Numpy

For those working in the realm of scientific computing in Python, the NumPy library is essential. As a Python library, it supports a multidimensional array object, as well as a number of derived objects (including masked arrays and matrices), and a wide range of routines for performing fast operations on arrays, such as mathematical operations, logical operations, shape manipulation, sorting, selecting, I/O, discrete Fourier transforms, elementary linear algebra, elementary statistical operations, random simulation, and many more. [31]

4.2.3. Pandas

pandas is an open source, BSD-licensed library providing high-performance, easy-to-use data structures and data analysis tools for the Python programming language. [32]

4.2.4. Matplotlib

Matplotlib is an all-inclusive Python package for making every kind of visualization, from still images to dynamic Animations to interactive 3D models. Matplotlib creates figures fit for publication in a number of print and interactive media formats. Python scripts, the Python and IPython shell, web application servers, and graphical user interface development tools are all places where Matplotlib can be put to use.

4.2.5.Tensorflow

TensorFlow is an end-to-end open source platform for machine learning. Created by the Google Brain team that makes DL and ML faster and easier. It has a comprehensive, flexible ecosystem of tools, libraries and community resources that lets researchers push the state-of-the-art in ML and developers easily build and deploy ML powered applications[33]. It provides stable Python and C++ APIs, as well as non-guaranteed backward compatible API for other languages.

4.2.6.OpenCV

OpenCV, short for "Open-Source Computer Vision Library," is a massive open-source repository of computer vision and ML tools.

OpenCV was created to standardize the development of computer vision programs and hasten the application of machine perception into goods and services. OpenCV's BSD license makes it simple for enterprises to adopt and customize the software. [35]

4.2.7.Kaggle

Kaggle is an online community platform for data scientists and machine learning enthusiasts. Kaggle allows users to collaborate with other users, find and publish datasets, use GPU-integrated notebooks, and compete with other data scientists to solve data science challenges. The aim of this online platform (founded in 2010 by Anthony Goldbloom and Jeremy Howard and acquired by Google in 2017) is to help professionals and learners reach their goals in their data science journey with the powerful tools and resources it provides.[24]

4.2.8.WhyKaggle

Kaggle includes several benefits. These are the reasons we use this website:

There are several datasets for use on Kaggle

Code is plentiful on Kaggle. If you want to see countless examples of code from other Kaggle users, you can easily search Notebooks that include code

Like Medium, GitHub, Stack Overflow, and LinkedIn, Kaggle serves as a community where data analysts, data scientists, and machine learning engineers can come to learn, grow, and network

Kaggle competitions

Courses

4.2.9. Visual Studio Code

Visual Studio Code is a lightweight but powerful source code editor which runs on your desktop and is available for Windows, macOS, and Linux. It comes with built-in support for JavaScript, TypeScript, and Node.js and has a rich ecosystem of extensions for other languages and runtimes (such as C++, C#, Java, Python, PHP, Go, .NET). [\[38\]](#)

5. Baseline Setting

In this project, there are three sets of the globally used dataset: Training, Validation, and Test, which are 70%, 15%, and 15%, respectively. Also, several metrics are calculated to measure the performance of the proposed model in each step: Accuracy, precision, recall, f1-score, and Loss function for the final accuracy. The final accuracy of the final step of this project is compared to previous works that used only the classification model.

6.Results and Discussion

6.1.Glioma Detection

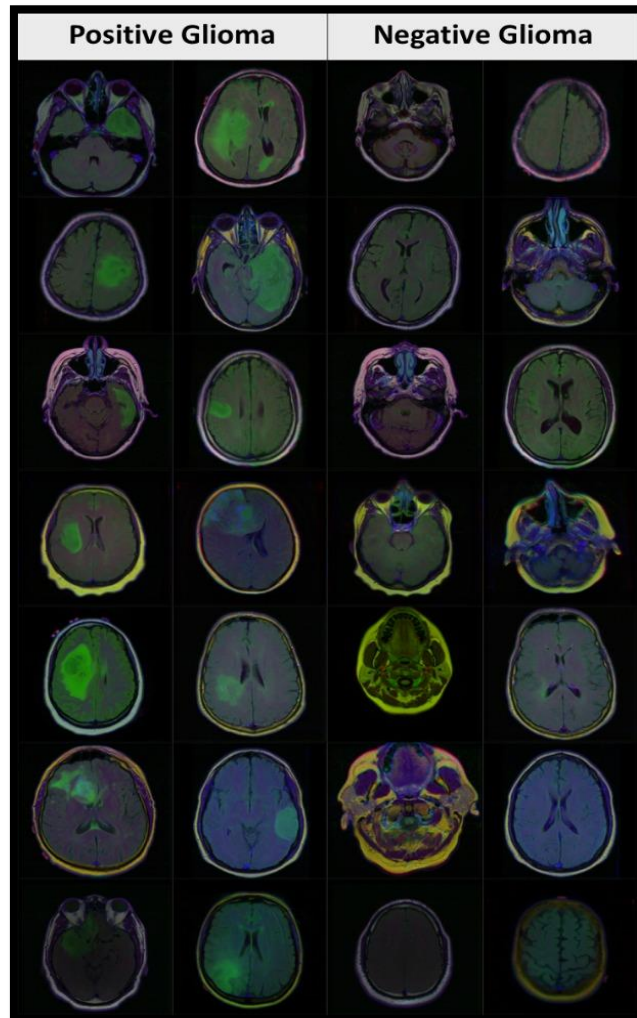


Figure 28: some results glioma detection

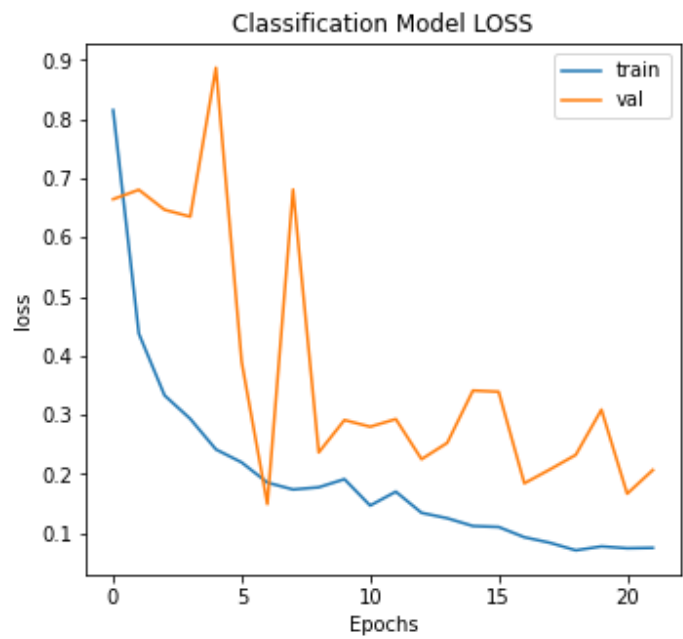


Figure 29:Classification Model Loss Function over Epoch

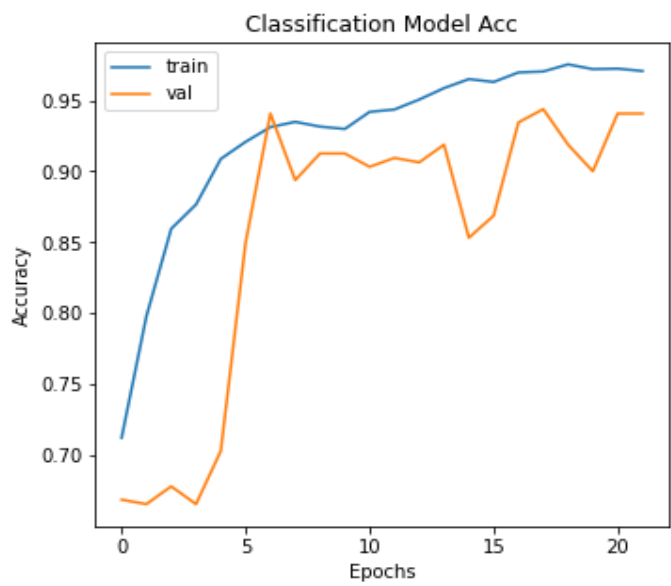


Figure 30: Classification Model Accuracy Function over Epoch

	precision	recall	f1-score	support
0	0.93	0.99	0.96	383
1	0.98	0.86	0.91	207
micro avg	0.94	0.94	0.94	590
macro avg	0.96	0.92	0.94	590
weighted avg	0.95	0.94	0.94	590

Test Accuracy	Test Loss
94.57 %	19.95%

6.2.Glioma Segmentation

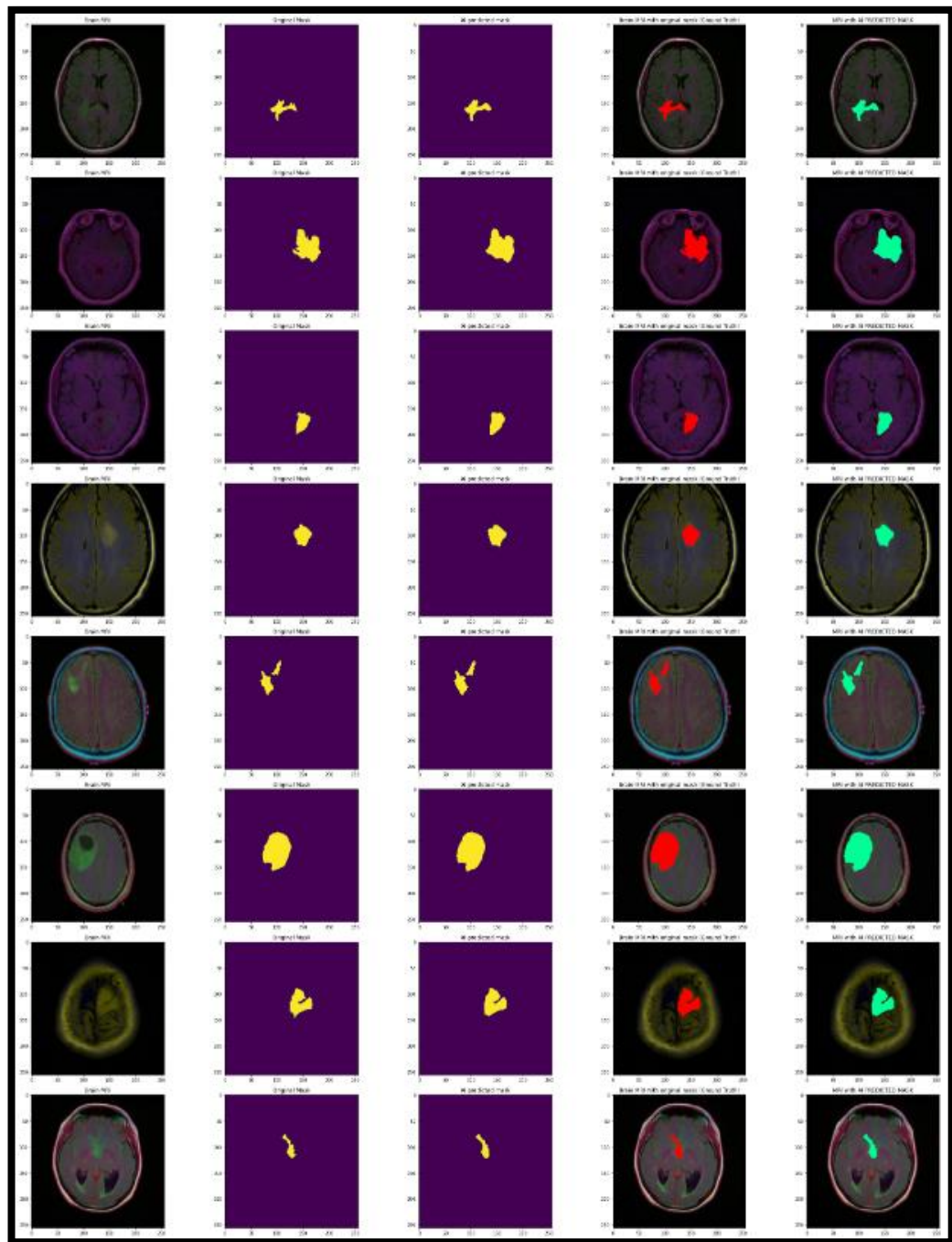


figure 31: Figure represents some results glioma detection segmentation

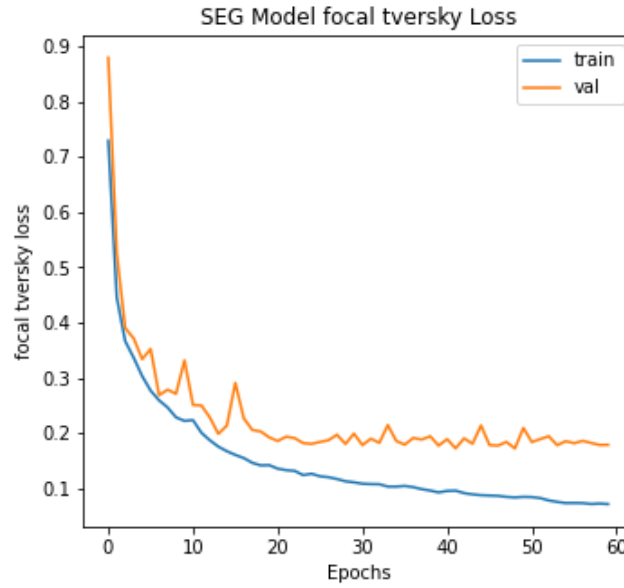


figure 32: Figure represents Segmentation Model Loss Function over Epoch

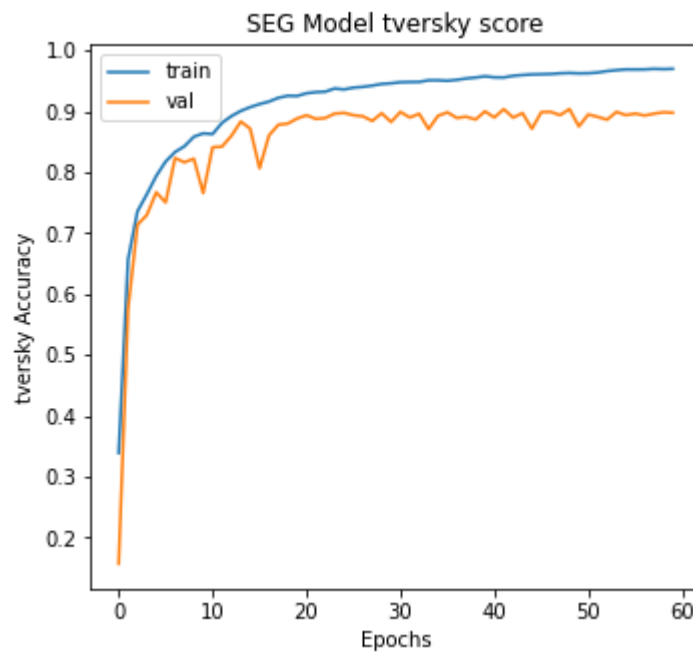


Figure 33: Figure represents Segmentation Model Accuracy Function over Epoch

	precision	recall	f1-score	support
0	0.94	0.99	0.96	383
1	0.98	0.88	0.93	207
micro avg	0.95	0.95	0.95	590
macro avg	0.96	0.94	0.95	590
weighted avg	0.95	0.95	0.95	590

Test Accuracy	Test Loss
89.13%	18.86%

6.3.Features Extraction

Following the segmentation of tumor regions, it is necessary to identify whether the tumor is high or low grade. Although the decision is made with the help of classifiers, some identifying features of the tumor help the decision process. Therefore, tumor features on MR images that will present the characteristics of high or low-grade tumors should be extracted.

6.3.1-Standard features

In the data.csv file, we have statistical features that detail about description of patient:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
1	Patient	RNASeqCl	Methylati	miRNAClu	CNCluster	RPPAClus	Oncosign	COCCLuste	histologic	neoplasm	tumor_tis	laterality	tumor_loc	gender	age_at_in	race	ethnicity	death01
2	TCGA_CS_4941	2	4	2	2		3	2	1	2	1	3	2	2	67	3	2	1
3	TCGA_CS_4942	1	5	2	1	1	2	1	1	2	1	3	2	1	44	2		1
4	TCGA_CS_4943	1	5	2	1	2	2	1	1	2	1	1	2	2	37	3		0
5	TCGA_CS_4944		5	2	1	2	1	1	1	1	1	3	6	2	50	3		0
6	TCGA_CS_5393	4	5	2	1	2	3	1	1	2	1	1	6	2	39	3		0
7	TCGA_CS_5395	2	4	2	2		3	2	3	1	1	3	5	2	43	2		1
8	TCGA_CS_5396	3	3	2	3	2	2	3	3	2	1	3	2	1	53	3	2	0
9	TCGA_CS_5397		4	1	2	3	3	2	1	2	1	1	6	1	54	3	2	1
10	TCGA_CS_6186	2	4	1	2	1	3	2	2	2	1	3	2	2	58	3	2	1
11	TCGA_CS_6188	2	4	3	2	3	3	2	1	2	1	3	6	2	48	3	2	0
12	TCGA_CS_6290	1	5	2	1		2	1	1	2	1	1	6	2	31			0
13	TCGA_CS_6665	2	5	1	1	1	2	1	1	2	1	3	6	1	51	3	2	0

figure 34: Standard features

6.3.2.Specific features

we will extract statistical features that detail certain physical characteristics of the tumor, such as the volume, surface area, and roughness. We will be extracting the following features:

```

patient_id = []
elongation = []
flatness = []
major_axis_length = []
minor_axis_length = []
max_3D_diameter = []
sphericity = []
surface_area = []
energy = []
entrop = []
kurtosis = []
mean = []
skewness = []
contrast = []
correlation = []
inverse_diff_moment = []
coarseness = []
complexity = []
strength = []
y_labels = []

```

7.Code Explaining

```
import os
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import zipfile
import cv2
from skimage import io

import tensorflow as tf
from tensorflow.python.keras import Sequential
from tensorflow.keras import layers, optimizers
from tensorflow.keras.layers import *
from tensorflow.keras.models import Model
from tensorflow.keras.initializers import glorot_uniform
from tensorflow.keras.utils import plot_model
from tensorflow.keras.callbacks import ReduceLROnPlateau, EarlyStopping, ModelCheckpoint, LearningRateScheduler
import tensorflow.keras.backend as K

import random
import glob
from sklearn.preprocessing import StandardScaler, normalize
from IPython.display import display
```

figure 35: Import necessary libraries

```
count = 0
i = 0
fig,axs = plt.subplots(12,3, figsize=(20,50))
for mask in brain_df['mask']:
    if (mask==1):
        img = io.imread(brain_df.image_path[i])
        axs[count][0].title.set_text("Brain MRI")
        axs[count][0].imshow(img)

        mask = io.imread(brain_df.mask_path[i])
        axs[count][1].title.set_text("Mask")
        axs[count][1].imshow(mask, cmap='gray')

        img[mask==255] = (0,255,150) # change pixel color at the position of mask
        axs[count][2].title.set_text("MRI with Mask")
        axs[count][2].imshow(img)
        count +=1
    i += 1
    if (count==12):
        break

fig.tight_layout()
```

figure 36: Data Visualization : Visualize MRI with Mask

```
from sklearn.model_selection import train_test_split

train, test = train_test_split(brain_df_train, test_size=0.15)
```

figure 37: Create and split data into train test and Set

```
from keras_preprocessing.image import ImageDataGenerator

datagen = ImageDataGenerator(rescale=1./255., validation_split=0.1)

train_generator = datagen.flow_from_dataframe(train,
                                              directory='.',
                                              x_col='image_path',
                                              y_col='mask',
                                              subset='training',
                                              class_mode='categorical',
                                              batch_size=16,
                                              shuffle=True,
                                              target_size=(256,256)
                                              )

valid_generator = datagen.flow_from_dataframe(train,
                                              directory='.',
                                              x_col='image_path',
                                              y_col='mask',
                                              subset='validation',
                                              class_mode='categorical',
                                              batch_size=16,
                                              shuffle=True,
                                              target_size=(256,256)
                                              )

test_datagen = ImageDataGenerator(rescale=1./255.)
test_generator = test_datagen.flow_from_dataframe(test,
                                                  directory='.',
                                                  x_col='image_path',
                                                  y_col='mask',
                                                  class_mode='categorical',
                                                  batch_size=16,
                                                  shuffle=False,
                                                  target_size=(256,256)
                                                  )
```

```
# saving model achitecture in json file
model_json = model.to_json()
with open("clf-resnet-model.json", "w") as json_file:
    json_file.write(model_json)
```

figure 38: Saving our model

```
prediction = model.predict(test_generator)

pred = np.argmax(prediction, axis=1)
#pred = np.asarray(pred).astype('str')
original = np.asarray(test['mask']).astype('int')

from sklearn.metrics import accuracy_score, confusion_matrix, classification_report
accuracy = accuracy_score(original, pred)
print(accuracy)

cm = confusion_matrix(original, pred)

report = classification_report(original, pred, labels = [0,1])
print(report)
plt.figure(figsize = (5,5))
sns.heatmap(cm, annot=True);
```

Figure 39: Classification model evaluation

```

def resblock(X, f):
    ...

    function for creating res block
    ...

    X_copy = X #copy of input

    # main path
    X = Conv2D(f, kernel_size=(1,1), kernel_initializer='he_normal')(X)
    X = BatchNormalization()(X)
    X = Activation('relu')(X)

    X = Conv2D(f, kernel_size=(3,3), padding='same', kernel_initializer='he_normal')(X)
    X = BatchNormalization()(X)

    # shortcut path
    X_copy = Conv2D(f, kernel_size=(1,1), kernel_initializer='he_normal')(X_copy)
    X_copy = BatchNormalization()(X_copy)

    # Adding the output from main path and short path together
    X = Add()([X, X_copy])
    X = Activation('relu')(X)

    return X

def upsample_concat(x, skip):
    ...

    function for upsampling image
    ...

    X = UpSampling2D((2,2))(x)
    merge = Concatenate()([X, skip])

    return merge

```

figure 40: Building a segmentation model to localize tumor

```
plt.figure(figsize=(12,5))
plt.subplot(1,2,1)
plt.plot(h.history['loss']);
plt.plot(h.history['val_loss']);
plt.title("SEG Model focal tversky Loss");
plt.ylabel("focal tversky loss");
plt.xlabel("Epochs");
plt.legend(['train', 'val']);

plt.subplot(1,2,2)
plt.plot(h.history['tversky']);
plt.plot(h.history['val_tversky']);
plt.title("SEG Model tversky score");
plt.ylabel("tversky Accuracy");
plt.xlabel("Epochs");
plt.legend(['train', 'val']);
```

figure 41: Segmentation model evaluation

8. conclusion

After we explained the concepts, in the previous chapters, Through the results and curves that we obtained in the detection and segment stage, and using the resnet50 and res-unet algorithms

Also, using SVM gives us the best choice in the classification stage hgg/lgg. We conclude that the model learns gradually and correctly with acceptable results in the two stages.

GENERAL CONCLUSION

In oncology, medical image analysis is used to identify the features of cancer, formulate a treatment strategy, and track the course of the illness. Malignant brain tumors of the glioma variety seriously impair cognitive abilities while also shortening patients' lives. Planning and expecting therapeutics requires the anxious identification of glioma subtypes.

The diagnosis of brain tumors, if made in error, can lead to errors in medical intervention and can therefore reduce the patient's chances of survival.

Indeed, it is a tedious and time-consuming task to manually segment brain tumors from a large number of MRI images. Therefore, brain tumor classification remains too complicated for radiologists and clinicians.

In this sense, computer-aided techniques have been used to support decisions and accurate diagnoses, especially, deep learning models.

The purpose of this research field is to establish a deep learning model used for glioma segmentation and classification to detect different lesions to easier to detect, segment, and classification of brain tumors.

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