

DAYANANDA SAGAR UNIVERSITY
KUDLU GATE, BANGALORE – 560068



**Bachelor of Technology
in
COMPUTER SCIENCE AND ENGINEERING**

Major Project Phase-II Report

**“Brain Tumor Diagnosis and Classification based on AutoML and
Traditional Analysis”**

By

Sathvik N G	ENG18CS0248
Siva Prakash Anupam Gollapalli	ENG18CS0277
Subhramanya N Sadhwani	ENG18CS0286
Vaishaali Kondapalli	ENG18CS0305
Vaishnavi A Punagin	ENG18CS0307

Under the supervision of

**Dr. Sindhu P Menon
Professor, Department of Computer Science and Engineering**

**DEPARTMENT OF COMPUTER SCIENCE & ENGINEERING,
SCHOOL OF ENGINEERING
DAYANANDA SAGAR UNIVERSITY,
BANGALORE**

(2021-2022)



DAYANANDA SAGAR UNIVERSITY

School of Engineering Department of Computer Science & Engineering

Kudlu Gate, Bangalore – 560068
Karnataka, India

CERTIFICATE

This is to certify that the Major project work titled "**Brain Tumor Diagnosis and Classification based on AutoML and Traditional Analysis**" is carried out by **Sathvik N G (ENG18CS0248), Siva Prakash Anupam Gollapalli (ENG18CS0277), Subhramanya N Sadhwani (ENG18CS0286), Vaishaali Kondapalli (ENG18CS0305), Vaishnavi A Punagin (ENG18CS0307)** of Team 16 bonafide students of Bachelor of Technology in Computer Science and Engineering at the School of Engineering, Dayananda Sagar University, Bangalore in partial fulfillment for the award of degree in Bachelor of Technology in Computer Science and Engineering, during the year **2021-2022**.

Dr. Sindhu P Menon	Dr. Girisha G S	Dr. A Srinivas
Professor, Dept. of CSE, School of Engineering Dayananda Sagar University	Chairman, Dept. of CSE, School of Engineering Dayananda Sagar University	Dean, School of Engineering Dayananda Sagar University
Date:	Date:	Date:

Name of the Examiner

Signature of Examiner

1.

2.

DECLARATION

We, **Sathvik N G (ENG18CS0248)**, **Siva Prakash Anupam Gollapalli (ENG18CS0277)**, **Subhramanya N Sadhwani (ENG18CS0286)**, **Vaishaali Kondapalli (ENG18CS0305)**, **Vaishnavi A Punagin (ENG18CS0307)** are students of eighth semester B.Tech in **Computer Science and Engineering**, at School of Engineering, **Dayananda Sagar University**, hereby declare that the Phase-II project titled "**Brain Tumor Diagnosis and Classification based on AutoML and Traditional Analysis**" has been carried out by us and submitted in partial fulfillment for the award of degree in **Bachelor of Technology in Computer Science and Engineering** during the academic year **2021-2022**.

Student	Signature
Name 1: Sathvik N G USN: ENG18CS0248	
Name 2: Siva Prakash Anupam Gollapalli USN: ENG18CS0277	
Name 3: Subhramanya N Sadhwani USN: ENG18CS0286	
Name 4: Vaishaali Kondapalli USN: ENG18CS0305	
Name 5: Vaishnavi A Punagin USN: ENG18CS0307	
Place : Bengaluru Date :	

ACKNOWLEDGEMENT

It is a great pleasure for us to acknowledge the assistance and support of many individuals who have been responsible for the successful completion of this project work.

First, we take this opportunity to express our sincere gratitude to the School of Engineering & Technology, Dayananda Sagar University for providing us with a great opportunity to pursue our Bachelor's degree in this institution.

*We would like to thank **Dr. A Srinivas. Dean, School of Engineering & Technology, Dayananda Sagar University** for his constant encouragement and expert advice.*

*It is a matter of immense pleasure to express our sincere thanks to **Dr. Girisha G S, Department Chairman, Computer Science and Engineering, Dayananda Sagar University**, for providing the right academic guidance that made our task possible.*

*We would like to thank our guide **Dr. Sindhu P Menon, Professor, Dept. of Computer Science and Engineering, Dayananda Sagar University**, for sparing her valuable time to extend help in every step of our project work, which paved the way for smooth progress and fruitful culmination of the project.*

*We would like to thank our Project Coordinators **Dr. Meenakshi Malhotra** and **Dr. Bharanidharan N**, and all the staff members of Computer Science and Engineering for their support.*

We are also grateful to our family and friends who provided us with every requirement throughout the course.

We would like to thank one and all who directly or indirectly helped us in the Project work.

Signature of Students

Sathvik N G

Siva Prakash Anupam Gollapalli

Subhramanya N Sadhwani

Vaishaali Kondapalli

Vaishnavi A Punagin

TABLE OF CONTENTS

	Page
NOMENCLATURE USED.....	i
LIST OF ABBREVIATIONS	ii
LIST OF FIGURES.....	iii
LIST OF TABLES.....	iv
ABSTRACT.....	v
CHAPTER 1 INTRODUCTION.....	1
1.1. INTRODUCTION.....	2
1.2. PURPOSE.....	9
1.3. INTENDED AUDIENCE.....	9
1.4. INTENDED USE.....	9
1.5. PRODUCT SCOPE.....	9
1.6. DEFINITIONS AND ACRONYMS.....	9
1.7. SCOPE.....	10
CHAPTER 2 PROBLEM DEFINITION	11
CHAPTER 3 LITERATURE SURVEY.....	14
CHAPTER 4 PROJECT DESCRIPTION.....	24
4.1. PROPOSED DESIGN	25
4.2 MODULE WISE DESIGN.....	26
4.2.1 PREPROCESSING MODULE.....	26
4.2.2 ALGORITHMS MODULE.....	29
4.2.3 TECHNIQUES USED.....	30
4.3 ASSUMPTIONS AND DEPENDENCIES.....	34
CHAPTER 5 REQUIREMENTS.....	35
5.1. EXTERNAL INTERFACE REQUIREMENTS.....	36
5.1.1 HARDWARE INTERFACE REQUIREMENTS.....	36
5.1.2 SOFTWARE INTERFACE REQUIREMENTS.....	36
5.2. FUNCTIONAL AND NONFUNCTIONAL REQUIREMENTS.....	37
5.2.1 FUNCTIONAL REQUIREMENTS.....	37
5.2.2 NON FUNCTIONAL REQUIREMENTS.....	37
CHAPTER 6 METHODOLOGY.....	38
6.1. SPLITTING THE DATASET.....	39

6.2. PREPROCESSING.....	40
6.2.1 OTSU, INVERSE-OTSU AND MULTI-OTSU.....	41
6.2.2 HSV.....	41
6.2.3 DWT.....	42
6.3 FEATURE EXTRACTION.....	43
6.3.1 BRIEF- Binary Robust Independent Elementary Features.....	43
6.3.2 STAR(CenSurE) in OpenCV.....	44
6.4. MODELS IMPLEMENTED.....	45
6.4.1 MACHINE LEARNING MODELS.....	45
6.4.2 CONVOLUTIONAL NEURAL NETWORK.....	49
6.4.3 TRANSFER LEARNING MODELS.....	51
6.4.4 AUTOML MODEL.....	53
CHAPTER 7 EXPERIMENTATION.....	56
CHAPTER 8 TESTING AND RESULTS.....	59
CHAPTER 9 CONCLUSION AND FUTURE SCOPE.....	68
REFERENCES.....	70
APPENDIX	73
FUNDING AND PUBLISHING PAPER DETAILS.....	74

NOMENCLATURE USED

ML	Machine Learning
DL	Deep Learning
MRI	Magnetic Resonance Imaging
KNN	K-Nearest Neighbors
CNN	Convolutional Neural Network
SVM	Support Vector Machine

LIST OF ABBREVIATIONS

1. **MRI:** Magnetic Resonance Imaging(MRI) is a medical imaging technique used in radiology to form pictures of the anatomy and the physiological processes of the body.
2. **KNNs:** K-Nearest Neighbors is a machine learning technique and algorithm that can be used for both regression and classification tasks. K-Nearest Neighbors examines the labels of a chosen number of data points surrounding a target data point, in order to make a prediction about the class that the data point falls into.KNN is a conceptually simple yet very powerful algorithm, and for those reasons, it's one of the most popular machine learning algorithms.
3. **CNNs:** A convolutional neural network (CNN) is a specific type of artificial neural network that uses perceptrons, a machine learning unit algorithm, for supervised learning, to analyze data. CNNs apply to image processing, natural language processing and other kinds of cognitive tasks.A convolutional neural network is also known as a ConvNet.
4. **SVMs:** 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.

LIST OF FIGURES

Fig. No.	Description of the figure	Page No.
1.1	Basic Structure of normal Human Brain	3
4.1	Proposed Design for the Project	25
4.2	HSV image processing method	26
4.3	DWT Image Preprocessing	27
4.4	OTSU Image Preprocessing	28
4.5	CNN Model	30
4.6	VGG Model	31
4.7	RESNET Model	32
4.8	Ensemble Model Stacking CV Classifier	33
4.9	AutoML Model Flowchart	34
6.1	Haar Wavelet function	43
6.2	CNN Model Architecture	50
6.3	VGG-16 Model Architecture	52
6.4	Google Cloud platform after creating the project	54
6.5	Defining and setting the model to run for 20 node hours.	54
6.6	AutoML evaluation results	55
8.1	Results with Preprocessing	60
8.2	Results Drawn Out from the BRIEF Feature Extractor	60
8.3	Logistic Regression Model Confusion Matrix	62

8.5	KNN Model Confusion Matrix	62
8.5	SVM Model Confusion Matrix	63
8.6	Ensemble Model Confusion Matrix	63
8.7	VGG16 Model Confusion Matrix	64
8.8	CNN Model Confusion Matrix	65
8.9	Comparison of All Models Accuracies	65
8.10	Precision vs Recall and Confidence Matrix of AutoML Model	66
8.11	AutoML Confusion Matrix	66

LIST OF TABLES

Table No.	Description of the Table	Page No.
6.1	Dataset Split for ML Models	39
6.2	Dataset Split for TL and DL models	40
6.3	Dataset Split for AutoML model	40
8.1	Validation Results of All the Models	61
8.2	AutoML Individual Class Accuracies	67

ABSTRACT

Brain tumor is a disease caused due to the growth of abnormal and uncontrolled growth of cells in the brain. There are two main categories of brain tumor, they are non-cancerous (benign) brain tumors and cancerous (malignant) brain tumors. Survival rate of a tumor prone patient is difficult to predict because brain tumors are uncommon and are of different types. Treatment for brain tumor depends on various factors like: the type of tumor, how abnormal the cells are and where it is in the brain. Magnetic Resonance Imaging (MRI) is an imaging technique used to diagnose brain tumors. The normal MRI images are not that suitable for fine analysis, so preprocessing and feature extraction are important processes which are required for efficiently analyzing the tumor images. The MRI images are diagnosed by the physician and later based on the results; the treatments are started. This procedure can be a little time consuming. With the growth of Artificial Intelligence, Machine Learning Models and Deep Learning Models can be used to diagnose the brain tumor by taking the images of MRI. Also, recent changes in automation by using tools like Automated Machine Learning (AutoML) have created significant room for research. The datasets containing the MRI scans have had various preprocessing techniques experimented on them along with feature extraction. The validation accuracies of each of the models implemented, taking into account the preprocessing techniques tested on these models along with the feature extraction implemented, will be compared to showcase the results obtained from using AutoML. This will assist in discerning the most optimal classification method along with the corresponding preprocessing technique used along with feature extraction, in detecting the presence of brain tumors in the given MRI scans.

Keywords— AutoML, VGG, Otsu, RESNET, KNN, SVM

CHAPTER 1

INTRODUCTION

CHAPTER 1 INTRODUCTION

1.1 INTRODUCTION

Tumor and Formation of Brain Tumor

Tumor is an abnormal mass of tissue that forms when cells grow and divide more than they should or do not die when they should. Tumors may be benign (non cancerous) or malignant (cancerous). Benign tumors may grow large but do not spread into, or invade, nearby tissues or other parts of the body. Malignant tumors can spread into, or invade, nearby tissues. They can also spread to other parts of the body through the blood and lymph systems.

Cancer is a disease in which some of the human body's cells grow uncontrollably and spread to the other parts of the body. Cancer could start almost anywhere in the body, which is made up of trillions of cells. Usually, human cells grow and multiply through cell division for formation of new cells as the body needs them. When cells grow old or become damaged, they die, and then new cells take their place.

Sometimes this orderly process breaks down, and abnormal or damaged cells grow and multiply when they shouldn't. These cells may form tumors, which are lumps of tissue. Tumors can be cancerous or non - cancerous.

The brain is a complex organ that controls thought, memory, emotion, touch, motor skills, vision, breathing, temperature, hunger and every process that regulates our body. Together, the brain and spinal cord that extends from it make up the central nervous system, or CNS. Weighing about 3 pounds in the average adult, the brain is about 60% fat. The remaining 40% is a combination of water, protein, carbohydrates and salts. The brain itself is not a muscle. It contains blood vessels and nerves, including neurons and glial cells.

According to John Hopkins Medical Journal there are over 120 brain tumor types, based on the brain tissues they affect. Not all brain tumors are brain cancer, but even benign tumors can be dangerous because of their size or location. A brain tumor is a growth of abnormal cells in the brain. The anatomy of the brain is very complex, with different parts responsible for different nervous system functions. Brain tumors can develop in any part of the brain or skull, including its protective lining, the underside of the brain (skull base), the brainstem, the sinuses and the nasal cavity, and many other areas.

Brain tumors are dangerous because they can put pressure on healthy or unaffected regions of the brain by spreading into those areas. They can cause problems if they block the

flow of fluid around the brain, which can lead to an increase in pressure inside the skull. Some of them can even spread through the spinal fluid to distant areas of the brain or the spine.

Primary brain tumors are tumors that start in the brain. Examples of tumors that most often originate in the brain include meningioma and glioma. Very rarely, these tumors can break away and spread to other parts of the brain and spinal cord. More commonly, tumors spread to the brain from other parts of the body.

Metastatic brain tumors, also called secondary brain tumors, are malignant tumors that originate as cancer elsewhere in the body and then metastasize (spread) to the brain. Metastatic brain tumors are about four times more common than primary brain tumors. They can grow rapidly, crowding or invading nearby brain tissue.

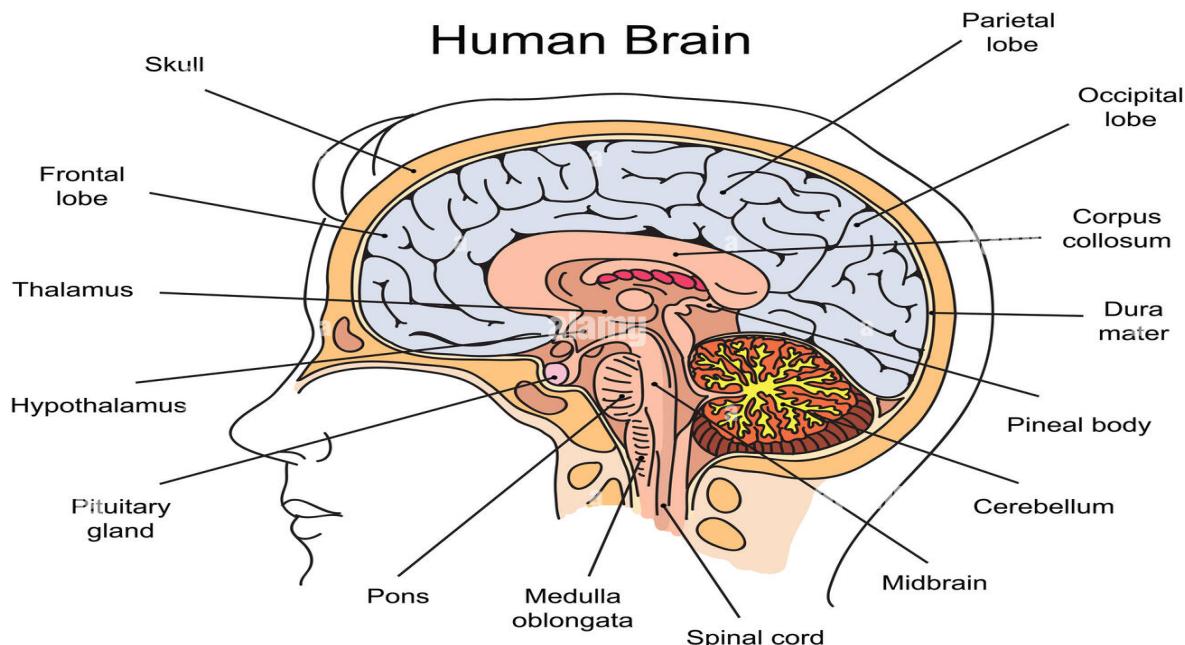


Fig. 1.1 Basic Structure of normal Human Brain

Brain tumors can form in any part of the brain as shown in Fig. 1.1, but there are certain regions where specific tumors form:

1. Meningiomas form in the meninges, the protective lining of the brain.
2. Pituitary tumors develop in the pituitary gland.
3. Medulloblastoma tumors arise from the cerebellum or brainstem.
4. Skull base tumors grow on the underside of the brain, called the skull base.

Causes of Brain Tumor

Usually one can never tell why some cells begin to form into tumor cells. It may have something to do with the environment, the food an individual consumes or sometimes can even be genetic. So some brain tumor causes and tumor causes and risk factors may include:

1. Cancers that spread from other parts of the body
2. Exposure to certain chemicals or radiations emitted by radioactive substances.
3. Genetics that could result in the formation of tumor like Lynch syndrome or Cowden syndrome.

Different Types of Brain Tumor

There are three types of tumors classified in this project: Glioma, Meningioma and the Pituitary tumors.

i. **Gliomas** are one of the most common types of primary brain tumors. About 33% of all the brain tumors are gliomas, they originate within the glial cells which surround and support the neurons in the brain. Gliomas are also called intra-axial brain tumors as they grow within the substance of the brain and often mix along with the normal brain's tissue. A glioma can affect the brain function and it can also be life-threatening depending on its location and its rate of growth. Gliomas are mostly common in older adults (over the age of 65) and children (under the age of 12). The grade of a brain tumor defines how serious it is. Using the biopsy sample, a pathologist will examine the tumor under a microscope to determine its grade. Brain tumor grading is a category system that describes the brain tumor cells and indicates how likely the tumor is to grow and spread. There are four grades of glioma, and each has different types of cells present and different treatment strategies. A glioblastoma is a grade IV glioma, which is the most aggressive form. This means that all glioblastomas are gliomas, but not all gliomas are glioblastomas.

1. Grade I

Grade I gliomas i.e, pilocytic astrocytomas are rare in adults and they usually occur in pediatric patients i.e, in children. As these tumors are grade I, they are least aggressive and will generally grow very slowly. Grade I tumors are relatively benign, but they might also put pressure on an area of the brain, leading to symptoms.

2. Grade II

Also known as the low-grade glioma, grade II tumors are the most benign glioma usually found in adults. If your glioma is classified as grade II, then that

means it's growing slowly. However, it could still lead to the symptoms by impacting some areas of the brain, and there is the potential that it may transform into grade III and grade IV tumors if not treated. This is why, in spite of the "low-grade" label, it is still important to work with the doctor to develop an appropriate treatment, and/or monitoring plan.

3. Grade III

A grade III glioma i.e, a malignant glioma, is a tumor made of anaplastic cells, which means they no longer look or function like the healthy version of the cells they are derived from. These tumors are very aggressive and require immediate treatment to prevent growth and/or transformation into a grade IV glioma.

4. Grade IV

Glioblastoma multiforme, a grade IV glioma, is very aggressive and has the potential to spread very rapidly. This is the most common form of primary brain tumor, but it is also the most destructive. Glioblastomas should be treated as quickly as possible because they grow so rapidly.

ii. A **meningioma** is a tumor that forms on membranes that cover the brain and the spinal cord right inside the skull, and therefore push the brain away rather than growing from within it. Specifically, the tumor formation takes place on three layers of membranes that are called meninges — the membranes that surround the brain and spinal cord. These tumors are usually slow-growing with low potential to spread, they often grow over many years without causing symptoms. As many as 90% are benign i.e, non - cancerous tumors. Most of the meningiomas occur in the brain but they can also grow on parts of the spinal cord too. Meningiomas represent about 20 percent of all tumors originating in the head and 10 percent of tumors of the spine. Meningioma tumors can become quite large. Diameters of 2 inches (5 cm)

Often, meningiomas cause no symptoms and require no immediate treatment. But the growth of benign meningiomas can cause serious problems. In some cases, such growth can lead to death. Meningiomas are the most common type of tumor that originates within the central nervous system. They occur more often in women rather than in men, and are often discovered at older ages, but they may occur at any age.

Some meningiomas are classified as atypical. These are not considered as either benign(non- cancerous) or malignant (cancerous). But they may become malignant later. A

small number of the meningiomas are cancerous. They do tend to grow quickly. They can also spread to various other parts of the brain and beyond, often to the lungs.

iii. The pituitary is a small gland in the brain. It is located behind the back of the nose. It's only about the size of a pea, but your pituitary gland controls a lot of important necessary functions, like your growth, heart rate, and ability to have kids. It's sometimes also known as the master gland because it tells the other glands when they should make more hormones. Those hormones then move throughout the human body and tell your organs what they need to do to keep everything in working order.

A **pituitary** gland tumor is a cluster of atypical cells that grows out of control in your pituitary gland. Most of the pituitary tumors are not cancerous. Pituitary cancer is very rare. Still, the tumors can cause serious problems, either because of the size (large tumors) or because they make extra hormones that your body doesn't need (functioning tumors). Most of the pituitary tumors also press against the nearby optic nerves. This can cause vision problems.

Most pituitary tumors don't cause symptoms. As a result, they are not diagnosed. Or they are found only during a routine brain imaging test. About 25% of people may have small pituitary tumors without knowing it.

Brain Tumor Identification and Cure

Brain tumors cause certain symptoms in the individual suffering. Brain tumors produce neurological deficits by destroying brain tissue, leaching nutrients from the non-cancerous brain cells, or exerting pressure in the brain. This can cause a gradual loss of movement or sensation in an arm or leg, unsteadiness, vision or hearing loss, or the gradual onset of speech difficulties. A growing brain tumor may produce pressure within the bones that form the skull or block the fluid in the brain (cerebrospinal fluid). This condition is called hydrocephalus. Abnormal nerve cell electrical activity can trigger seizures, and may signal a brain tumor.

Detecting brain tumors usually requires a combination of diagnostic procedures. Procedures such as neurological exams, Magnetic Resonance Imaging and recording of electrical activity in the brain (through a procedure known as electroencephalogram). MRI scans produce pictures of the brain and help medical experts in detecting metabolic activity in the brain tumor cells and hence discerning the severity of the brain tumor.

Doctors may also choose to perform biopsy i.e tissue sample collection and analysis. In a Biopsy they will diagnose the brain tumor and plan the treatment based on other test results by

classifying the grade of the tumor. Biopsy is mainly used to give a personalized treatment to the patients.

The most common treatment for brain tumors is surgery. For some tumors, surgical removal and continued monitoring may be the only treatment needed. Common surgical approaches to brain tumor removal include craniotomy, neuroendoscopy, laser ablation and laser interstitial thermal therapy.

Chemotherapy and radiation therapy can be used to treat brain cancer by helping shrink the tumor, slowing down its growth and/or preventing it from coming back. External beam radiation therapy, stereotactic radiosurgery and proton therapy are some of the radiation treatments for brain tumors.

What is Machine Learning, Transfer Learning and Cloud AutoML

Machine learning is an important component of the growing field of data science. Through the use of statistical methods, algorithms are trained to make classifications or predictions, uncovering key insights within data related projects. These insights subsequently drive decision making within applications and businesses, ideally impacting key growth metrics.

Machine learning classifiers fall into three primary categories: supervised, unsupervised and semi-supervised learning methods. In this project, there has been use of supervised machine learning algorithms.

Supervised learning, also known as supervised machine learning, is defined by its use of labeled datasets for training algorithms to classify data or predict outcomes accurately. As input data is fed into the model, it adjusts its weights until the model has been fitted appropriately. This occurs as part of the cross validation process to ensure that the model avoids overfitting or underfitting. Supervised learning helps organizations solve a variety of real-world problems at scale. Some methods used in supervised learning include neural networks, naïve bayes, linear regression, logistic regression, random forest, support vector machine (SVM), and more.

Deep learning is a subset of machine learning that achieves recognition accuracy at higher levels than ever before. This helps consumer electronics meet user expectations, and it is crucial for safety-critical applications. Recent advances in deep learning have improved to the point where deep learning outperforms humans in some tasks like classifying objects in images.

While deep learning was first theorized in the 1980s, there are two main reasons it has only recently become useful:

1. Deep learning requires large amounts of labeled data. For example, driverless car development requires millions of images and thousands of hours of video.
2. Deep learning requires substantial computing power. High-performance GPUs have a parallel architecture that is efficient for deep learning. When combined with clusters or cloud computing, this enables development teams to reduce training time for a deep learning network from weeks to hours or less.

Transfer learning involves the use of past knowledge gained while solving a problem, in solving another related problem. A pre-trained model is started with, and then the transferred knowledge can be used to be applied in another domain. The key to transfer learning is the generality of features within the learning model. The features exposed by the deep learning network feed the output layer for a classification. The ability to reuse these features means that the trained network can in some form be repurposed for a new problem.

In the case of our project we have used some pretrained models like VGG-16, ResNet-18, ResNet-50, etc. which are trained on a large ImageNet dataset. The ImageNet project is a large visual database designed for use in visual object recognition software research.

Automated Machine Learning(AutoML) is a cloud-based machine learning model builder that automates the process of Machine Learning for the purpose of image recognition. AutoML is based on Neural Architecture Search(NAS). NAS involves automating the design of neural networks. NAS aims to discern the best architecture for a neural network given the specific prerequisites for it. A large number of architectures are tested and evaluated across a search space. The best architecture is selected based on the given prerequisites and whether the objective is met in the most optimal method possible. Presently, a significant number of manual architectures and procedures have been replaced by architectures made by NAS. These procedures include image classification and so on.

In case of our project we have made use of Google Cloud AutoML Vision API to detect and classify the different types of brain tumors that are present.

1.2.PURPOSE

The aim is to find the tumorous region and detect the type of tumor based on an MRI scan of the patient's brain. High-resolution MRI plays a central part in the diagnosis. Once we find out if the tumor exists or not and then classify the type of tumor if it exists, the health care professionals can directly look into it and start with the diagnosis after performing the required tests.

1.3.INTENDED AUDIENCE

This Project is intended to benefit people in the field of medicine and healthcare industry, when an individual comes for an examination of brain tumor

1.4.INTENDED USE

Healthcare professionals are expected to use this project to test the MRI images that they obtain from the scanners and be able to predict the presence of any cancer cells in them by uploading the scanned images.

1.5.PRODUCT SCOPE

The scope of our project is:

To create a convenient and easy-to-use method of detection.

1. We hope to provide one of the fastest ways to detect the patient's tumorous areas in the brain based on an MRI scan of their brain.
2. Machine learning could make screening for tumorous areas more cost effective and efficient.
3. An Automated system could help scale screening and bridge the workforce gap.

1.6.DEFINITIONS AND ACRONYMS

1. **Benign tumor:** A growth that is not cancer. It does not invade nearby tissue or spread to other parts of the body.
2. **Malignant tumor:** Malignant tumors have cells that grow uncontrollably and spread locally and/or to distant sites. Malignant tumors are cancerous (ie, they invade other sites).
3. **Pituitary tumor:** A pituitary tumor is a tumor that forms in the pituitary gland near the brain that can cause changes in hormone levels in the body. Pituitary tumors are abnormal growths that develop in your pituitary gland.

1.7.SCOPE

The brain tumor classifier, on higher validation accuracies, can aid in reducing misclassification regarding whether a tumor is present or not.

In the dataset that has been used for this project, we have images only for glioma, meningioma and pituitary tumors. So, if data is obtained successfully for more tumor types then this project work can be extended to classify more classes than what has been presented in this work.

This project work can be extended to classifying tumors in other regions of the body like, lungs, pancreas, etc. provided labeled datasets are used to train the models.

CHAPTER 2

PROBLEM DEFINITION

CHAPTER 2 PROBLEM DEFINITION

MOTIVATION

The manual segmentation and analysis of a structural MRI of a brain requires strenuous effort and is a time consuming task, which thus far can only be accomplished accurately by professional neuro-radiologists; which also in certain cases is prone to human error. The symptoms which are common between the different types of tumors are the main cause of misclassification. Such misclassifications can lead to wrong interpretation by the doctors and radiologists. Which may lead to misdiagnosis that can be dangerous to the patient. These issues motivated us to come up with a system where the entire process of detecting the tumor as well as classifying it can be less time consuming and accurate. By the use of such a system, doctors and radiologists can spend more time on decision making rather than on screening based on the reports. This system is also intended to provide lesser misclassifications with high accuracy, which helps in providing the patient with better treatment at the right time and prolongs valuable human life. An accurate diagnosis can largely increase the chances of the patient's recovery after treatment.

PROBLEM STATEMENT

Hence the problem statement “Brain Tumor Diagnosis and Classification based on AutoML and Traditional Analysis” is proposed.

OBJECTIVES

The aim is to detect if there is a tumor or not and if a tumor is present then the type of tumor is classified based on an MRI scan of the patient's brain. High-resolution MRI plays a central part in the diagnosis. Once we find out the region and severity of the tumor, the health care professionals can use the automatically generated results and start with the diagnosis.

The objectives of the proposed system are given below:

1. To obtain MRI images of the brain.
2. To pre-process the MRI images by using various pre-processing methods so as to improve the overall accuracy and obtain correct classifications, and apply the suitable feature extraction method for marking the tumorous regions in the MRIs.

3. To detect the presence of a tumor in the brain MRI image, and to classify the tumor as meningioma, pituitary or glioma.
4. To produce a comparative analysis of the several models implemented to determine the method that results in the least mis-classifications and the highest accuracy.
5. To aid in accurate diagnosis, boosting the likelihood of a patient's recovery following therapy.

CHAPTER 3

LITERATURE REVIEW

CHAPTER 3 LITERATURE REVIEW

Prof.Kavitha Bathe et. al.[1] According to this paper there are two types of separable convolutions i.e spatial separable & depthwise convolution. In their paper they have worked on Brain Tumor Detection Using Deep Learning Technique which is Depthwise Separable CNN and classified the MRI image as Healthy or Tumorous. They have also worked on Simple Convolution Network, SVM and Adaboost algorithms. Out of these algorithms Depthwise Separable CNN has given the best Validation accuracy of 92%. In this technique MobileNet model is saved as a base model & on that base model global average 2D pooling layer is applied. Global average 2D pooling layer minimizes overfitting by reducing the total number of parameters in the model. AdaGrad and RMSProp algorithms provide an optimization algorithm that can handle sparse gradients on noisy problems. The limitation of this paper is that they are not able to detect specifically all the classes of brain tumor that are present.

Tahia Tazin et. al.[2] have compared different pre-trained CNN models i.e VGG19, InceptionV3, MobileNetV2 with minor modifications to obtain the classification report for the presence or absence of tumor. They have made use of the CNN architecture because it introduces hidden layers using neural networks and they execute a range of neural transformations and Deep Transfer Learning's base layer is the Convolutional Layer responsible for deciding the design characteristics and filter. The pooling layer was used to perform down sampling. Transfer learning models were used to analyze and categorize big data by avoiding expensive computations and time-consuming processes in a traditional algorithm implementation. On implementation MobileNetV2 outperformed all other networks with an accuracy of 92% and minimal loss. The precision, recall and F1 scores were also computed for all the models. The limitation of this paper is that ImageNet weights are used and there are no preprocessing techniques that are implemented before running the models. Only the presence or absence of tumor is explored

Tessy George et. al.[3] have performed analysis of Image Segmentation, Morphological Operations and Feature extraction, which are some of the image processing methods used for the Brain Tumor detection in MRI images. For performing image Segmentation they have made use of Morphological-based Fuzzy-C-Means (M-FCM) using the intensity of gray-levels present in the image. In their Methodology they have made use of Gaussian noise filtering in preprocessing to perform smoothening of the image. They have

segmented the image into four clusters i.e the brain region, skull region, background and the cancer region based on the texture. For morphological based segmentation, the image and the number of clusters are given as the input. For comparative analysis, they have made use of M-FCM and K-means for which M-FCM gave an accuracy of 97.89%. The limitation of this paper is that after localizing the tumor region, the area is not being calculated and as a result the grade cannot be identified, what type of tumor is being segmented is also unclear.

Sneha Grampurohit et. al.[4] have tried to detect the presence and absence of tumors using CNN and its VGG16 Transfer Learning model which is an extension of the CNN model. They Performed data preprocessing by converting images to grayscale, removal of noise, smoothen images, and finding extreme contours. Compared CNN and VGG16 models validation, test accuracies, over 25 epochs. The number of images used was 2065 with a split of 1445, 310, 310 for training, testing and validation. The highest accuracy achieved was in the VGG-16 model with a Test set accuracy of 91.9%. The limitation of this paper is again that the specific brain tumor classes haven't been classified.

A. Hussain and A. Khunteta [5] took gray scale MRI images of Brain Tumor and performed Semantic Segmentation and SVM Classification using (Gray Level Co-occurrence Matrix) GLCM Features. In their methodology the given MRI images are converted into jpg format and Median Filter is applied, Skull Stripping is performed, Watershed segmentation is applied and then the GLCM features are extracted. This has been implemented using MATLAB. After preprocessing, classification of the images is done using the different types of (all 6)SVM classifiers such as Linear, Quadratic, Cubic, Fine-Gaussian, MediumGaussian, and Coarse-Gaussian. Out of all the SVM classifiers, Linear and Quadratic SVM classifier gave the highest classification accuracy as 97.2% to tumorous or non-tumorous types. The limitation of this project is that only 2 classes of tumor i.e Tumorous or Non-Tumorous are classified and multiple other Machine Learning models with the preprocessing techniques are not tested in the work.

M.Anto Bennet et. al.[6] have worked on Identification and Detection of Brain Tumor Segmentation using Fuzzy and Neural Networks. They have approached their problem in a very different way, i.t first they have taken a 3D video and several frames of the video are considered for preprocessing and running the algorithms on the images. The DTCWT(Dual Tree advanced ripple Transform) is employed to get the important and unreal components. The GLCM (Gray Level Co-occurrence Matrix)which is being employed to

extract the options Associate in Nursing textures of the given input from the previous step so input is processed by Neural Network classifier that has an characteristic am fond of it won't perform the particular task and it'll conjointly tries to get information from given input. It will classify whether or not the given brain is stricken by tumor (Normal/Abnormal) and it'll predict the stage-benign or malignant. The tumor half is clustered by victimization spatial Fuzzy C-Means clump (SFCM) and also the output is displayed. The limitations are again that it is restricted only for 2 classes i.e tumorous or non tumorous. The scale against which the segmentation is performed is also not present.

S.Somasundaram and R.Gobinath [7] took the MRI, preprocessed, segmented and classified using the image processing techniques. Classification is done using deep convolutional neural networks and the deep belief neural network. The brain tumor is identified, located and the size of the tumor is found. The performance metrics used are recall, precision, sensitivity, accuracy and specificity. In the preprocessing of the input images, the MRI is changed from grayscale to rgb format and 3 level DWT is applied and this image is given to a median filter to remove noise from the image. Later IDWT is applied to reconstruct the image back to original. Fast Fuzzy segmentation is used and given to the CNN for feature extraction. Then the classification is done using DBCNN with metric scores of 97.5%, 100%, 94.20% and 99.57%.. Limitations to this paper: 4 level DWT can be used instead of 3 level DWT.

Tonmoy Hossain et. al.[8], took a 2D MRI and segmented using Fuzzy C Means clustering algorithm followed by traditional classifiers and CNN for classification of tumor. The traditional classifiers include SVM, KNN, Multi Layer perceptron, logistic regression, naive bayes and random forest using scikit learn. A comparative study was performed using the above mentioned models out of which SVM performed the best with an accuracy of 92.42%. A CNN was also employed to get an accuracy of 97.87% using a data split of 80:20 i.e. 80% of training data and 20% of testing data. CNN consists of five layers that are convolution layer, max pooling layer, flattened and two dense layers. Activation function was relu, adam optimizer and loss function was binary cross entropy. Limitations of this paper: this method can't be applied to 3D MRI and the segmentation method employed is not that efficient.

M. Kurnar et. al.[9] were involved in calculating the area of the brain tumor from the MRI image. The pre-processing of the tumor images was done using the median filter

pre-processing technique in order to remove the Salt & Pepper noise that is present in the MRI image. The image segmentation is performed using the K-means clustering algorithm. The image is segmented into 3 segments having different gray levels. The type of morphological operations used are the erosion and dilation operations. These morphological operations extract the tumor from the gray-scale input MRI image. For calculation of the tumor area in the MRI image, the binarization method is used. However, the validation accuracy of the tumor detection is not specified. Hence, the efficiency of the tumor detection is unclear and this serves as a limitation. The number of brain MRI images in the training dataset is also not specified. Hence it is unclear how efficient the system really is.

Mr. T. Sathies Kumar et. al.[10] detected brain tumors from the input MRI images using the SVM classifier. The MRI images are obtained from various sources like health-care centers, hospitals and so on. In order to remove noise that may be present in the input images, pre-processing techniques are made use of. These pre-processing techniques include converting the MRI images from RGB to gray-level images. After this, the edges are detected using the Canny edge detector, and smoothed using a Gaussian filter. After the pre-processing on the images are done, the dataset of the image along with its extracted features are trained using the neural network, and the performance of the training operation is validated. After this, the morphological, clustering and segmentation operations are performed on the MRI images. A “Classification Learner” app is used for comparison between various classifiers such as K-NN, SVM, and Trees. A limitation of this paper is that the number of images in the training dataset is not specified. Also the overall validation accuracies for the different classifiers such as the Linear SVM and the Medium KNN classifiers are not specified. Hence, the efficiency of the entire system of brain tumor detection is unclear. Moreover, the security mechanism is not specified for the “Classification Learner App” that had been brought about in the paper. Security mechanisms include authentication of users(or medical professionals in this case) by the use of passwords or any other authentication mechanism.

Mariam Saii and Zaid Kraitem, [11] used techniques such as Anisotropic Diffusion Filter and SVM to detect and enclose the boundary of the brain tumor, i.e. to perform segmentation. Anisotropic Diffusion Filter is a pre-processing technique which aids in enhancing the brain MRI images. Anisotropic Diffusion Filter reduces the image noise and enhances the image contours. The diffusion coefficient is also adapted in order to be

negligible. All this ensures that the precise boundary of the brain tumor is found out. After the Anisotropic Diffusion Filter is used, the head region is cropped and a mask image is created (using cumulative frame differencing to calculate the differences between the sub-images) in order to aid the SVM classifier in detection of the tumor. The overall validation accuracy achieved is 95.5% depending on the dice coefficient. A limitation regarding this paper is that there are only forty brain MRI images in the testing dataset. The overall validation accuracy is calculated only for those forty MRI images.

Garima Singh and Dr.M.A.Anvari [12] did a Comparative analysis of image denoising filters is done in terms of the peak signal to noise ratio (PSNR) and Mean Squared Error(MSE), the filters include: Median filter, Adaptive Filter, Averaging Filter, Gaussian Filter, Unsharp Masking Filter. Out of all the filters, with respect to PSNR, Median filter performed the best with PSNR value of 78.7316 and with respect to MSE, Averaging Filter performed the best with MSE value of 0.0038. The histogram of the preprocessed image is normalized, The MRI is converted to a grayscale image. Then the obtained histogram is normalized so that the sum of all probabilities must be equal to 1. Classification of MRI: Naive Bayes classifier and Support Vector Machine are used for classification. Where SVM performed better compared to the other with an efficiency of 91.49%. Segmentation of MRI images using K means algorithm to identify the location of the tumor. Which is implemented using Matlab. Limitations of the paper: In some tumor images, the results were not satisfactory and the detection of tumors was not accurate. Finding out the precise boundary of the tumor region was not done.

Anupurba Nandi [13] performed the detection of tumors using MRI. Preprocessing methods include Thresholding: used to convert gray scale images to binary images based on a particular intensity level. Watershed Transformation: on a plain surface with places having few ditches, if water spilt in it then we can easily understand that it will fill the deeper gradient first then the lighter gradient. So, for a grayscale image black is considered to be the deepest gradient and lighter gradients are considered as we move through gray shades toward white. K means clustering is used for segmentation where it segregates the different intensity pixels having similar characteristics and Morphological operators where it refers to deforming of the shape of an object. Morphological operations are applied on binary images. Noise detection and filtering techniques include high pass and median filter. Finally the output image shows the detected tumor. Limitations of the paper is that the detection of

tumors is not done based on malignancy level. And other classification algorithms can perform better at the task such as perceptron, SVC and correlation clustering.

Swapnil R Telrandhe et. al.[14] aimed at developing an automated system for detecting and identifying the tumor from the MRI. The preprocessing contains applying median filter and skull masking. The MRI is converted to gray scale after which a median filter of size 3X3 is applied on the MRI, then the obtained image is passed through a high pass filter to detect edges. Skull Masking is performed by calculating the centroid in the image. Then the skull stripping is performed. Segmentation method used is K means segmentation which is performed on preprocessed images. Object labeling is performed to get detailed information about the tumor. Three scales of patch size are used for computingHOG and LBP. This helps in better coverage of different scales and makes the features more invariant to scale changes. SVM is used for pattern mapping and pattern matching. Limitations of the paper is that the tumor size and stage is not found.

Kailash Sinha and G.R.Sinha [15] presented a comparative study of three segmentation methods - k-means clustering with watershed algorithm, optimized k-means clustering with genetic algorithm, and optimized c-means clustering with genetic algorithm, implemented for tumor detection. They worked on a real-time collected dataset of 50 images only. In k-means clustering with watershed algorithm, MR images were collected and converted to gray-scale and an intensity level histogram of the image is obtained. In Optimized k-means with genetic algorithms, Genetic Algorithms are used to prevent and overcome over segmentation and sensitivity to false edges. In optimized c-means clustering method, clustering method is applied to cluster N objects based on a resemblance function and homogeneity inside clusters and heterogeneity between clusters. The implementation of genetic algorithms begins with an initial population of chromosomes which are randomly selected. The end result here was the extraction of the tumor from the MR image and the determination of the exact shape and position. Their comparison parameters for the segmentation algorithms were time taken for the search and area of the tumor. The conclusion arrived at was that the time required is lesser in the optimized c-means clustering method as compared to the k-means method, and thus the c-means clustering method is considered more efficient. The major limitation in their approach in this method of brain tumor segmentation is the size of the dataset that is worked on, the size of the dataset used is

only 50 images and only three different methods of segmentation of tumors were worked with. We use a larger dataset and several more methods of detection of brain tumors.

Y. Sharma and Y. K. Meghrajani [16] describes an experimental approach to extract tumors from a labeled brain MRI based on mathematical morphological reconstruction. Their input to their system is an MRI image with impulse noise. Global thresholding is applied as a pre-processing method to convert images to grayscale and then to binary images to employ binary mathematical morphological operations. Hole filling and Opening by reconstruction is applied on this binary image to segment tumor regions as well as to remove label or film artifacts and salt noise. To remove the pepper noise that was leftover from the previous step, Morphological closing with a square based structuring element of size 3 is performed. Application of certain mathematical multiplication operations on this morphological resultant image generates and presents the tumor region. For purposes of testing and validation simulation, salt and pepper noise density of 0.015 was added to the images and the generated experimental value for threshold was 0.6. The Peak Signal to Noise Ratio (PSNR) is calculated to present an objective mathematical analysis of the method. PSNR is used to measure the quality difference between the original and the reconstructed image. The method proposed by them performed well if the width of the tumor is greater than the radius of the squared error. They present a comparison of the proposed algorithm against only one k-means method of tumor detection. The other limitations of this approach are that a smaller set of MR images are used and only a method for detection of tumor is proposed, there is no way of classifying and detecting the type of tumor.

H. S. Abdulbaqi et. al.[17] presents a method for brain tumor detection using a hybridized approach based on Hidden Markov Random Fields (HRMF) that provides good initial classification and Threshold methods that provide the final segmentation. Raw MRI images are converted to mathematical formulas using MATLAB. To work with the HRMF-EM algorithm, k-means clustering and a gray level histogram method is used to generate an initial segmentation to provide labels to the MAP algorithm and initial parameters to the EM algorithm. This method wasn't smooth enough and did not preserve the Canny edges. Hence, HRMF labels overcome this, and it is a type of a graphical probability model within which the states are estimated indirectly using an observational field instead of observing the actual true states. Final thresholding segmentation is applied using MATLAB. The limitations of this approach and study is that only 3 different patient data images have

been used, and have three cases of brain cancer of the type of Glioma only. They conclude that the result obtained gives the possibility and serves as a base for calculating the size of the tumor in the future.

Minakshi Sharma and Dr. Sourabh Mukharjee [18] present an image segmentation technique to locate a certain type of brain tumor named Astrocytoma. MRI image databases containing Grade I to IV Astrocytoma scans are gathered from an MRI simulator, and preprocessed using Histogram Equalization to present the gray level frequencies using inbuilt functions from MATLAB and Binarization to convert grayscale images into binary based on an auto generated threshold value and Morphological operations such as dilation, erosion, opening, and closing to sharpen regions. Feature Extraction is performed on the pre-processed images using Gray Level Co-occurrence Matrix (GLCM - gray level spatial dependence matrix), Feature Selection, and Feature Segmentation is performed. An inbuilt function, greycomatrix, from MATLAB was used to calculate and look at 20 features that were listed in proposed methodology. Selecting a subset of a feature using a hybrid Genetic Algorithm + fuzzy rough set improved the accuracies that were achieved. This research produced a comparative analysis of ANFIS, neural network, Fuzzy, FCM (Fuzzy C-Means), K-NN (K-Nearest Neighbor), DWT+SOM (Discrete Wavelet Transform + Self Organizing Map), DWT+PCA+KNN (Discrete Wavelet Transform + Principle Component Analysis + K-Nearest Neighbor), Texture combined+ANN (Artificial Neural Network), Texture Combined+SVM (Support Vector Machine) in terms of sensitivity, specificity, and accuracy. Texture combined+SVM model presented with the highest accuracy of 97.9%. The limitations observed to this comparative analysis is that the dataset of images used is only of a single certain type of tumor called Astrocytoma even though multiple models and algorithms were implemented.

I. Maiti and M. Chakraborty [19] developed a new method of detection of a brain tumor where they've used the watershed method along with edge detection operations run on MATLAB and used only 20 .jpg images. The general morphological operation, the watershed method, is used to find the ‘watershed lines’ in an image to isolate and separate distinct regions, and often has the issue of over segmentation. Images are preprocessed using Gradient magnitude wherein pixels along the object edges are of high values and the rest is considered to be a low value. Modification of the watershed and gradient technique is done using the application of markers, internal and external, using the MATLAB toolbox. This

method of tumor detection uses colored images in the HSV model, input RGB images are converted to the 3 regions of the HSV color space i.e. Hue, Saturation and Value. Initially, histogram equalization is done to modify and enhance the dynamic range and contrast of the hue region followed by which the marker based watershed algorithm is applied. The edge is then obtained by applying the canny edge detection operation. This process is repeated for Saturation and Value regions of the image. Output images from all 3 are combined and converted to the RGB color model. Hence the tumor region is detected effectively. The limitation of this approach and method is that only the tumor region is identified, we further this by detecting and then classifying the type of tumor if detected, and a set of only 20 images are used.

CHAPTER 4

PROJECT DESCRIPTION

CHAPTER 4 PROJECT DESCRIPTION

This chapter throws light on the various preprocessing techniques and the algorithms that we have implemented in our project. The different preprocessing techniques that were used in our project are DWT, Otsu and HSV along with other normal preprocessing options such as resizing the image and flipping the images horizontally or vertically. We have also applied feature extraction on the DWT preprocessed images to assess if it will aid the models in the tumor type classification. The techniques used in the project are also discussed in detail in the further sections of this chapter.

4.1. PROPOSED DESIGN

Fig. 4.1 shows the proposed system of the project. The MRI images are passed as input to perform preprocessing and the training tasks

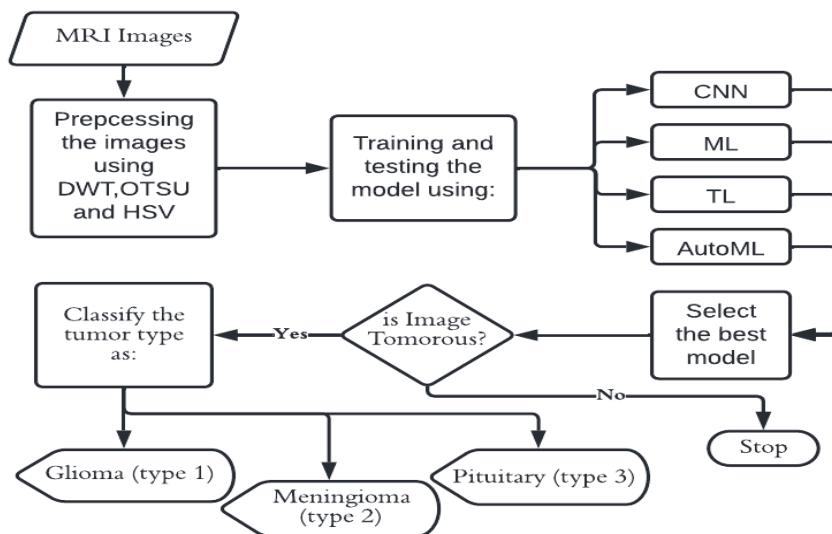


Fig. 4.1 Proposed Design for the Project

We propose the following steps to achieve the solution for the problem statement:

1. Collecting MRI scans images as the input data.
2. The images are preprocessed using DWT, Otsu, Inverse-Otsu, Multi-Otsu and HSV.
3. The best model is selected after training and testing different ML models.
4. The MRI scan image is fed, to check if it is tumorous or not.
5. The image is classified as glioma_tumor/meningioma_tumor/no_tumor/pituitary_tumor.

4.2. MODULE WISE DESIGN

4.2.1 Preprocessing Module

4.2.1.1 HSV

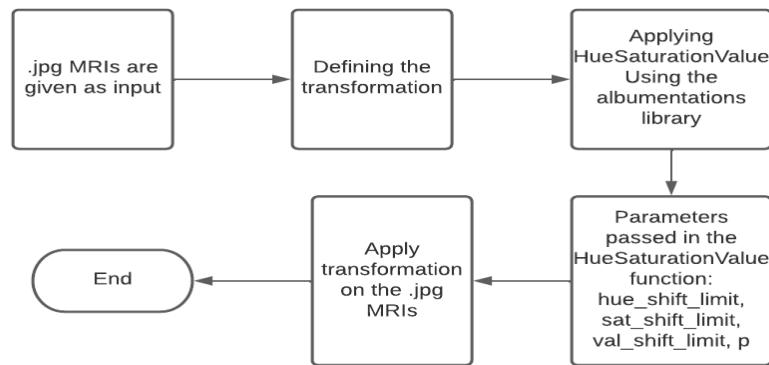


Fig. 4.2 HSV Image Processing Method

Fig. 4.2 depicts the implementation of Hue Saturation Value(HSV) pre-processing method on the input MRI images.

1. In this project we have made use of the albummentations library.
2. There are four parameters which have been made use of for successfully implementing HSV on the original MRIs, namely, hue_shift_limit, sat_shift_limit, val_shift_limit and ‘p’ i.e, the probability of the transformation getting applied on the original dataset.
3. Hue, saturation, and value are the main color properties that allow us to distinguish between different colors.
4. Hues are the three primary colors (red, blue, and yellow) and the three secondary colors (orange, green, and violet) that appear in the color wheel or color circle.
5. Hue refers to ‘pure color’, or the visible spectrum of basic colors that can be seen on a rainbow.
6. Color saturation is the purity and intensity of a color as displayed in an image. The higher the saturation of a color, the more vivid and intense it is. The lower a color’s saturation, or chroma, the closer it is to pure gray on the grayscale.
7. Color value refers to the relative lightness or darkness of a color. We perceive color value based on the quantity of light reflected off of a surface and absorbed by the human eye. We refer to the intensity of the light that reaches the eye as “luminance.”

8. For detecting brain tumors in the MRI images, it would be beneficial to separate color components(black, white and gray levels in this case) from the intensity of colors for reasons such as robustness to lighting changes and so on. As this value is separated, a histogram or thresholding rules can be constructed using only saturation and hue. This robustness to lighting changes can be advantageous for the model, and can help in improving the validation accuracy obtained by the model used for brain tumor detection. This is the advantage when using the HSV pre-processing method.

4.2.1.2 DWT

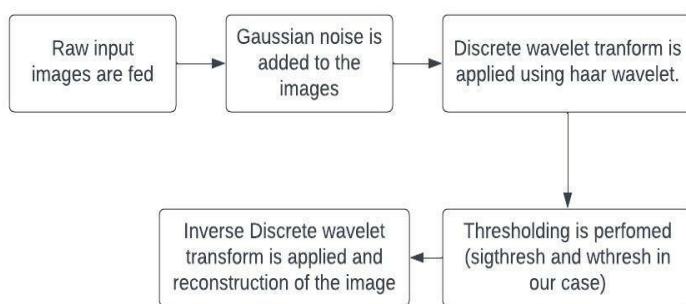


Fig. 4.3 DWT Image Preprocessing

1. In the DWT pre-processing method, as shown in Fig. 4.3, feeds the raw input images and gaussian noise with a variance of 0.01 is added to the images.
2. With the help of imnoise function in matlab, the Haar wavelet variant of discrete wavelet transform is applied.
3. The input image is decomposed into multiple levels and thresholding is performed, each level consisting of a high pass and low pass filter.
4. Multilevel decomposition is done in order to obtain the approximation coefficients. After obtaining the approximation coefficients, an inverse discrete wavelet transform is applied and the image is reconstructed to original dimensions.
5. Haar wavelets are used to enhance the quality of the brain MRI images. These wavelets are used in image processing to detect and filter Gaussian noise since they have a high contrast between them and the pixel intensity values in the adjacent pixels. This is how Haar wavelets enhance the input images.

4.2.1.3 OTSU

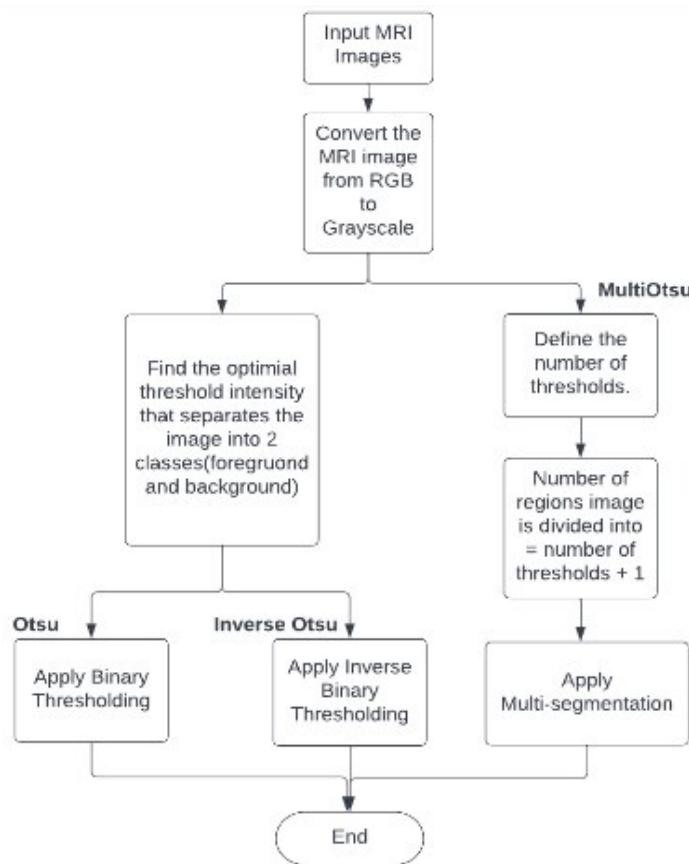


Fig. 4.4 Otsu Image Preprocessing

Thresholding is one of the most common segmentation techniques in object detection (we detect the brain tumor in our case). Basically, thresholding is the binarization of an image. As shown in Fig. 4.4, the Inverse-Otsu and Multi-Otsu are the other two variants used along with the Otsu thresholding. In general, we seek to convert a grayscale image to a binary image, where the pixels are either 0 or 255.

1. The main idea for Otsu thresholding is to separate the foreground, i.e. the brain tumor that we are interested in, from the background, i.e. the remaining portion of the MRI image of the brain. Converting the input MRI image into a simpler “black and white” image aids in easier analysis and segmentation of the MRI image. This is the main advantage for using the Otsu and Inverse Otsu thresholding methods.
2. For every pixel in the input MRI image, a threshold value is applied. In Otsu thresholding, this threshold value is automatically computed such that the threshold value is the most optimal based on the input MRI image.

3. Otsu's method makes the assumption that the grayscale histogram of our pixel intensities of our image is bi-modal, which simply means that the histogram is two peaks. Otsu's method has no prior knowledge of what pixels belong to the foreground and which pixels belong to the background; it's simply trying to optimally separate the peaks of the histogram.
4. Based on the grayscale histogram, Otsu's method then computes an optimal threshold value T for the entire image such that the variance between the background and foreground peaks is minimal.
5. The Otsu method automatically computes the threshold value T , and sets all pixel intensities below T to 255, and all pixel intensities greater than T are set to 0.
6. Inverse Otsu thresholding, on the other hand, involves the use of inverse thresholding along with Otsu thresholding. This implies that all pixel intensities below T are set to 0, and all pixel intensities greater than T are set to 255.
7. In Multi-Otsu thresholding, the pixels of the input MRI image are separated into more than two different classes.
8. These classes are separated according to the intensity of the gray levels within the image. For the in-built Multi-Otsu function in the scikit-image library, the number of thresholds are determined by the specified number of classes in the function parameter. By default there will be three classes. Multi-Otsu is a more efficient version of Otsu thresholding. In Multi-Otsu, the required number of classes can be defined as a parameter. Also, Multi-Otsu requires less computation and takes less time compared to Otsu thresholding.

4.2.2 Feature Extraction Module

4.2.2.1 BRIEF(*Binary Robust Independent Elementary Features*)

BRIEF stands for Binary Robust Independent Elementary Features. It uses binary strings as a descriptor(which is a vector representing the size of the features/ keypoints). In other words, instead of the 128-bin vector in the SIFT, we will use binary strings in BRIEF. The neighbors around the keypoint are called patches. Thus, the major function of BRIEF is to identify the patches around the keypoint and convert them into a binary vector, so that they can represent an object. Thus, each key point will be described with the help of the binary 1's and 0's. One major consideration about the BRIEF is that it is very noise sensitive as it deals closely with

pixel-level images. Thus, smoothening is very important to reduce the noise from the image. Gaussian Kernels smoothes the BRIEF descriptor.

4.2.3 Techniques Used

4.2.3.1 CNN

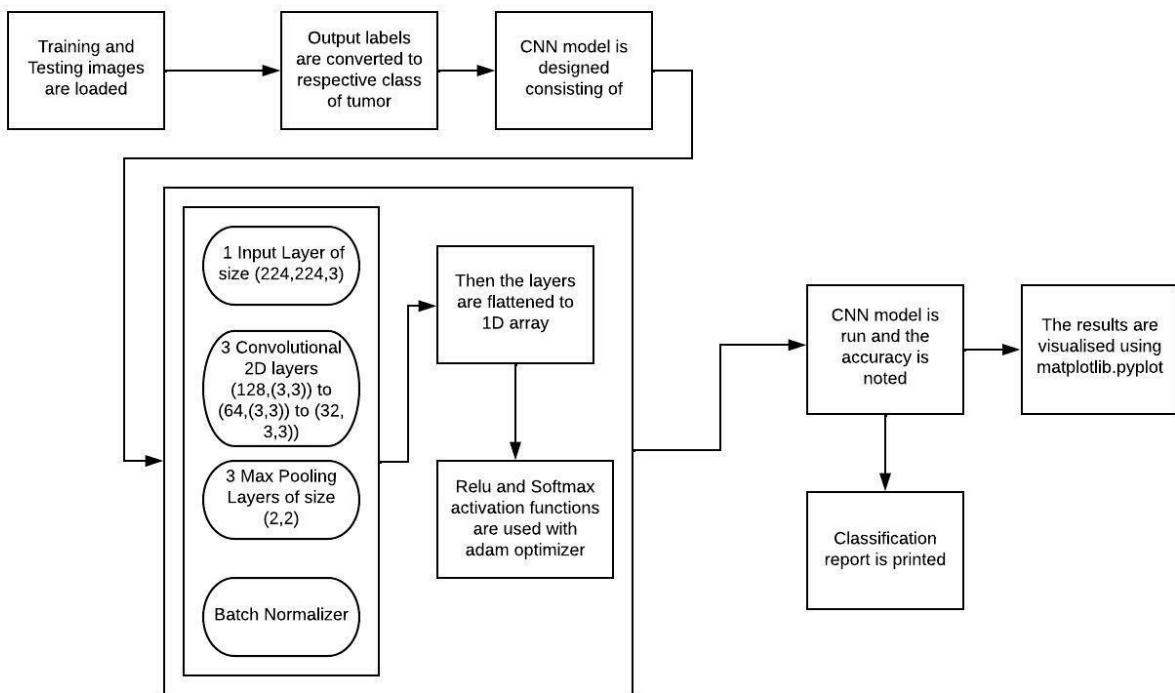


Fig. 4.5 CNN Model

As shown in Fig. 4.5,

1. In the beginning input convolutional kernel is generated to produce the tensor of the input images using homogeneous 128, 64, 32 layers of 3×3 filters and winding.
2. Down sampling of the tensor is performed using a pooling layer by changing the stride of the convolution across the image.
3. Then a BatchNormalization layer is applied to the intermediate tensors of the image to normalize the outputs of the previous layer by applying an activation scale.
4. Three fully connected layers named Dense, Dense1 and Dense2 are utilized and put into operation to apply a level of processing to the Neural Network.
5. The activation function from the dense layer is in charge of signal transmission from one layer to the next.

6. RELU and the sigmoid activation functions are employed to hasten the training period of the neural network.

4.2.3.2 VGG

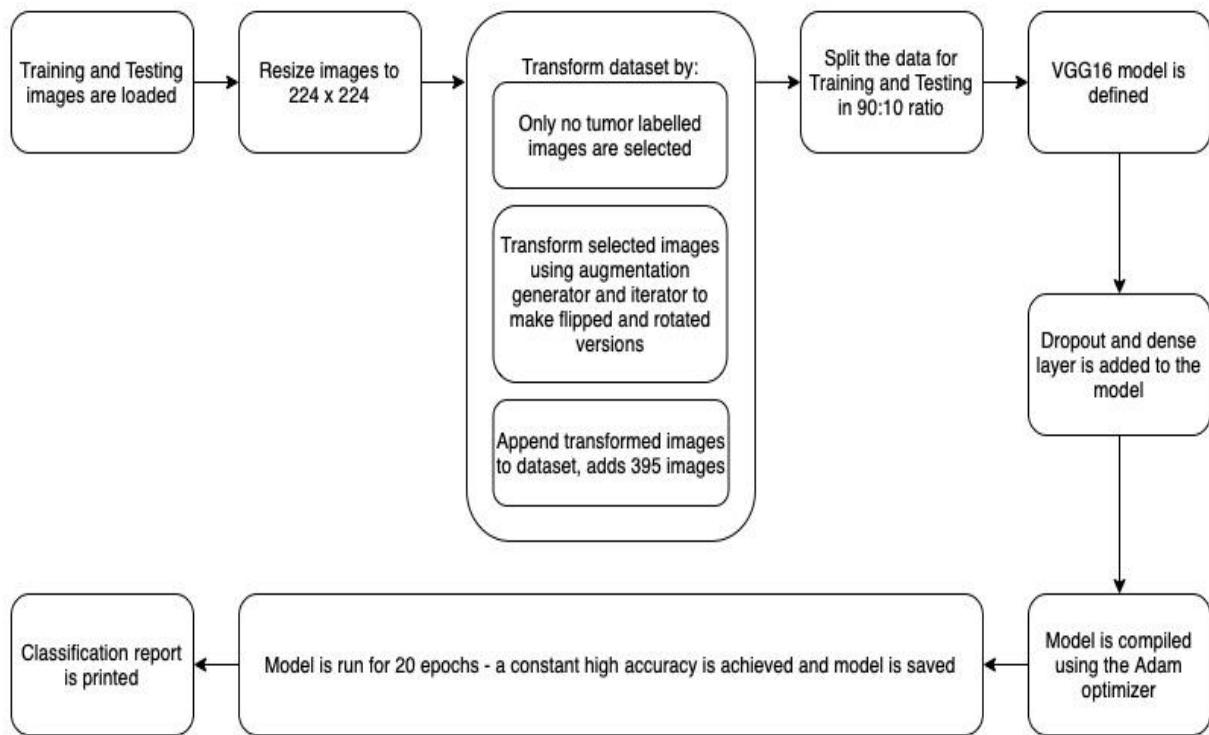


Fig. 4.6 VGG Model

- As shown in Fig. 4.6 VGG16 model is a 16 layers deep CNN learning model, and it has an image input of RGB 224-by-224 fixed size.
- The received input image is made to go through a series of several convolutional layers where filters with a lower receptive field of (3*3) are used.
- Amongst the Conv. layers, there also are five MaxPooling layers that help perform spatial pooling which is performed over a 2x2 pooling window with stride 1.
- These are followed by 3 Fully Connected layers of varied depths, 4096 channels each within the first two, and the third one has 1000-channels to perform the ILSVRC based classification on the given data passed to the model.
- The last and final layer in this model is a Soft-max layer. Lesser time and resources are consumed in the application of this model as pretrained weights are used.
- The model has been trained for 20 epochs because the validation accuracies remain the same after 20 epochs.

4.2.3.3 RESNET

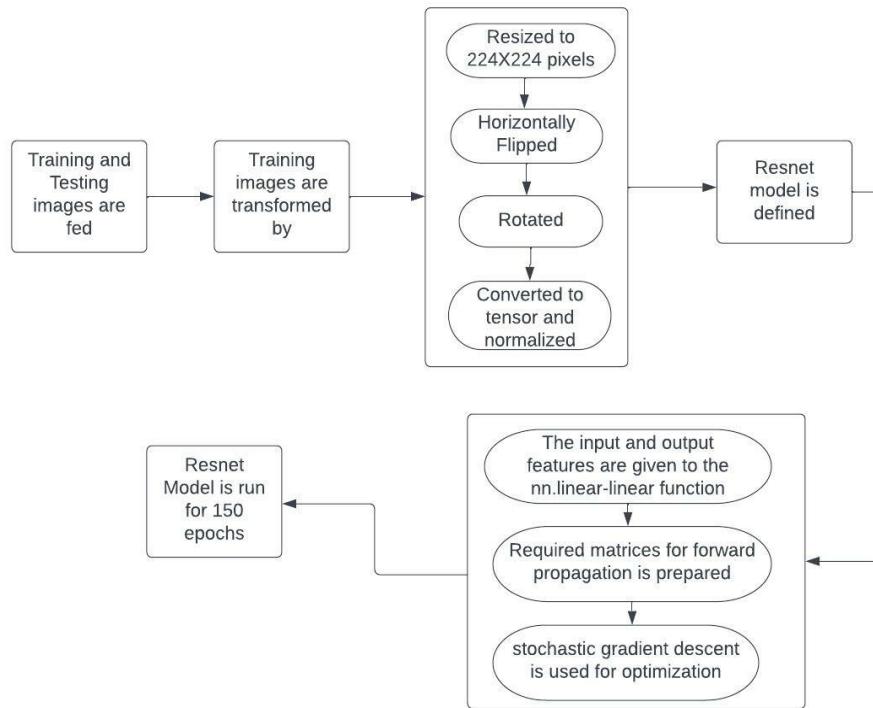


Fig 4.7 RESNET Model

1. As shown in Fig. 4.7, for Resnet, initially, Training and testing images are split.
2. The training images undergo transformation where the images are resized to 224X224 pixels and then horizontally flipped.
3. After flipping, the images are rotated and converted to tensors and normalized.
4. The resnet model is defined in which the input and output features are given to the nn.linear function and then the required matrices for forward propagation are prepared.
5. Here, stochastic gradient is used for optimisation and the model is run for 150 epochs.

4.2.3.4 ENSEMBLE MODEL

1. In this project, there are four machine learning models whose performance has been compared. Logistic Regression, SVM, KNN and the ensemble model - StackingCV classifier.
2. Stacking is an ensemble learning technique to combine multiple classification models via a meta-classifier.
3. The StackingCVClassifier extends the standard stacking algorithm using cross-validation to prepare the input data for the level-2 classifier. In the standard stacking procedure, the

first-level classifiers are fit to the same training set that is used to prepare the inputs for the second-level classifier, which may lead to overfitting.

4. The StackingCVClassifier, however, uses the concept of cross-validation: as shown in Fig. 4.8 the dataset is split into k folds, and in k successive rounds, k-1 folds are used to fit the first level classifier; in each round, the first-level classifiers are then applied to the remaining 1 subset that was not used for model fitting in each iteration.

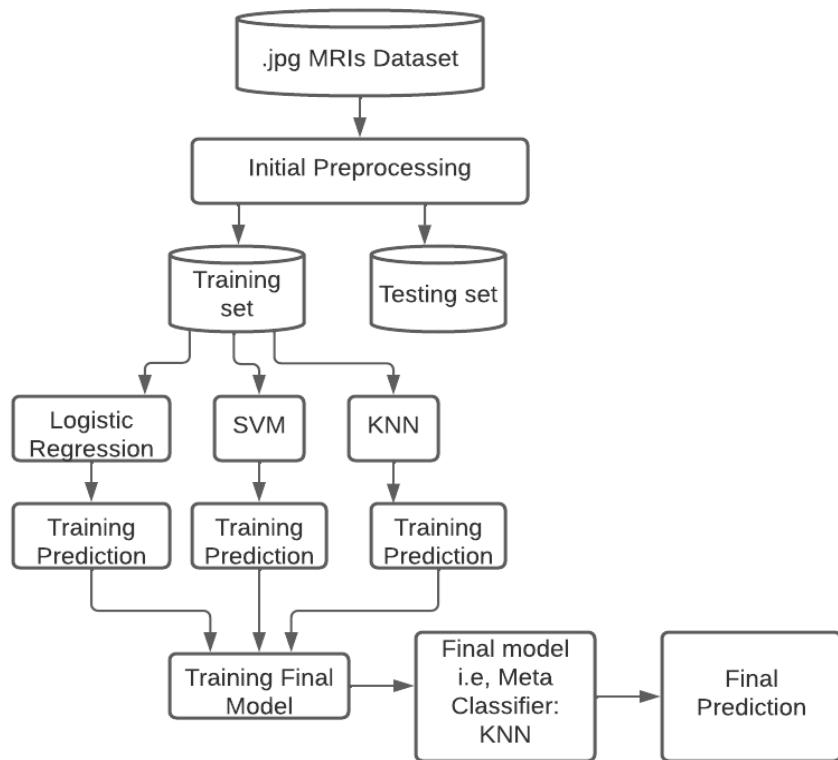


Fig. 4.8 Ensemble Model Stacking CV Classifier

5. The resulting predictions are then stacked and provided as input data to the second-level classifier. After the training of the StackingCVClassifier, the first-level classifiers are fit to the entire dataset.
6. Since KNN has outperformed Logistic Regression and SVM, it has been used as the meta classifier to take the final decision of which class a given test MRI belongs to.

4.2.3.5 AUTOML

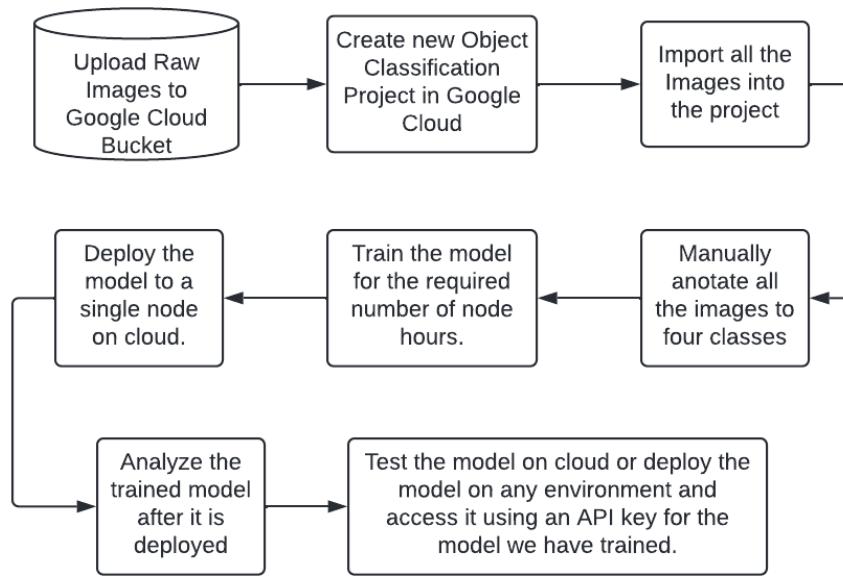


Fig. 4.9 AutoML Model Flowchart

1. In AutoML as shown in Fig. 4.9, the images are uploaded into Google Cloud Storage Bucket.
2. A new project of type Image classification is created and all the images are imported from Google Cloud Storage Bucket into the newly created project on Google Cloud Vision API.
3. The images are now manually labeled as the different types of tumor classes that are present and trained in Google Cloud for 20 node hours.
4. The trained model is deployed to a single node with which the model is tested and evaluated.

4.3. ASSUMPTIONS AND DEPENDENCIES

We are assuming the dataset and data from the source has not been tampered with.

CHAPTER 5

REQUIREMENTS

CHAPTER 5 REQUIREMENTS

A System Requirements Specification (SRS) (also known as a Software Requirements Specification) is a document or set of documentation that describes the features and behavior of a system or software application. It includes a variety of elements that attempt to define the intended functionality required by the customer to satisfy their different users. In addition to specifying how the system should behave, the specification also defines at a high-level the main business processes that will be supported, what simplifying assumptions have been made and what key performance parameters will need to be met by the system.

5.1 EXTERNAL INTERFACE REQUIREMENTS

5.1.1. Hardware Interface Requirements

There are hardware requirements, also known as system requirements, for every OS we are going to use. These requirements include the minimum processor speed, memory, and disk space required to install Windows. In almost all cases, you will want to make sure that your hardware exceeds these requirements to provide adequate performance for the services and applications running on the server. The table below outlines the minimum hardware requirements to execute this project

1. Processor: Intel core i3 and above series.
2. RAM: 4GB and above.
3. Graphics: At Least 2GB graphics

5.1.2. Software Interface Requirements

The software requirements are descriptions of features and functionalities of the target system. Requirements convey the expectations of users from the software product. The requirements can be obvious or hidden, known or unknown, expected or unexpected from the client's point of view.

It defines how the intended software will interact with hardware, external interfaces, speed of operation, response time of system, portability of software across various platforms, maintainability, speed of recovery after crashing, Security, Quality, Limitations etc.

1. Operating System: Windows/Ubuntu/MacOS
2. User interfaces: Jupyter notebook or matlab, depending on the models used in the project.
3. Dataset: Every patient's MRI scan is in the format of .jpg image files.

5.2. FUNCTIONAL & NON-FUNCTIONAL REQUIREMENTS

5.2.1. Functional Requirements

The project will be used by healthcare professionals to predict whether the patient has developed a brain tumor or not.

1. The MRI images of the patient's brain will be given as input.
2. The model will make the necessary predictions and conclude if there is a tumorous region present.
3. Based on the predictions made by the model, accurate diagnosis can be given.

5.2.2. Non-Functional Requirements

- 1. Performance:** High-resolution MRI plays a central part in the diagnosis. The system will be able to generate the results quickly as long as the system requirements are met.
- 2. Maintenance and Scalability:** The system(model) requires minimal maintenance, and can be scaled to detect tumorous regions in multiple patients.
- 3. Security:** The predictions done should be highly accurate so that there are minimal chances that the patient will be misdiagnosed. Health care professionals have to ensure correct diagnosis by taking into consideration the symptoms of the patient and by taking the prediction from the model.
- 4. Reliability:** The model is reliable in detecting the tumorous region. Once the region and the severity of the tumor is found out, health care professionals can directly look into it and start the diagnosis after performing the required tests.

CHAPTER 6

METHODOLOGY

CHAPTER 6 METHODOLOGY

The purpose of this project is to identify the tumorous region (if present) in the MRIs. According to the prediction made by the model, diagnosis of the tumor shall be performed by the health care experts, and shall be used for treating the cancer patient.

Initially the data is split into testing and training. The preprocessing techniques such as DWT, Otsu, Inverse-Otsu, Multi-Otsu and HSV are applied to the original images and then BRIEF feature extraction has been applied on the DWT preprocessed images. All the preprocessed images are run on different algorithms / models, i.e, KNN, SVM & Logistic Regression, Ensemble model, under Machine Learning(ML) models, ResNet50 and VGG16, transfer learning models and the CNN deep learning model too. The best model is then chosen manually and considered for evaluation of the results to find out the presence of tumor. Once the presence of tumor is confirmed, it is further classified as to what type of tumor is present i.e Glioma or Meningioma or Pituitary tumor.

6.1 SPLITTING DATASET

The dataset used for training and testing purposes was employed from [20]. The dataset contains MRI data. For the ML models that have been run, the dataset images used have been split into two parts in the 90:10 ratio for Training and Testing respectively.

Table 6.1 Dataset Split for ML models

Dataset Division	Tumorous Images			Non-Tumorous Images
	Glioma	Meningioma	Pituitary	
Training Data	752	735	736	360
Testing Data	74	87	91	35

For the ML models as shown in Table 6.1, the total number of images used for training is 2583, and the total number of classes is 4, namely, glioma_tumor, meningioma_tumor, no_tumor and pituitary_tumor.

For the TL and DL models as shown in Table 6.2, the total number of images for training are 826, 822, 827 and 395 images for Glioma, Meningioma, Pituitary and No Tumor respectively.

The total number of images for the data set used to run the AutoML Model is 1751 MRIs. The total number of images for training are 394, 380, 392 & 395 images for Glioma as

shown in Table 6.3 , Meningioma, Pituitary and No Tumor respectively. The split into validation and testing is done automatically depending on the size of the dataset for a particular class by the inbuilt controller that AutoML has. This is why there are only 7 images for testing under Glioma but on the other hand there are 49, 49 & 34 images for Meningioma, Pituitary and No-Tumor class.

Table 6.2 Dataset Split for TL and DL models

Dataset Division	Tumorous Images			Non– Tumorous Images
	Glioma	Meningioma	Pituitary	
Training Data	826	822	827	395
Testing Data	100	115	74	105

Table 6.3 Dataset Split for AutoML model

Dataset Division	Tumorous Images			Non– Tumorous Images
	Glioma	Meningioma	Pituitary	
Training Data	394	380	392	395
Validation Data	49	47	49	33
Testing Data	7	49	49	34

6.2 PREPROCESSING

Preprocessing of the input MRIs is essential in making these input images more suitable for the machine learning, deep learning and the transfer learning models to run predictions. This in turn improves the overall validation accuracies and the efficiencies of these models, and thereby reduces the number of misclassifications that may occur. Preprocessing techniques used in this project include thresholding, color segmentation and wavelet transform.

6.2.1 Otsu, Inverse-Otsu and Multi-Otsu

Otsu thresholding applies thresholding values automatically to the input images. The implementation of Otsu thresholding comprises Binary thresholding along with Otsu thresholding.

Implementation for Otsu:

```
res1,Otsu = cv2.threshold(gray,0,255,cv2.THRESH_BINARY+cv2.THRESH_OTSU)
```

Here, the variable ‘gray’ refers to the input image converted to grayscale. Other variants of Otsu thresholding are Inverse-Otsu and Multi-Otsu thresholding. Multi-Otsu segregates the input image pixels into different classes based on the intensity of gray levels within the image. The “threshold_multotsu” function from the skimage.filters library is used for the implementation of Multi-Otsu thresholding.

Implementation for Multi-Otsu:

```
new_image=threshold_multotsu(gray, classes=5)
```

InverseOtsu comprises both Inverse Binary Thresholding with Otsu thresholding.

```
res2,Otsu_inv = cv2.threshold(gray,0,255,cv2.THRESH_BINARY+cv2.THRESH_OTSU)
```

It is observed that on applying any of the three types of Otsu thresholding(viz. Otsu, Multi-Otsu and Inverse-Otsu) on the input images, results in worse validation accuracies compared to applying no pre-processing at all, for all the models that have been implemented. It is also to be noted that the RESNET50 model gives a significantly lower validation accuracy when any of these pre-processing techniques are applied to the input MRIs.

6.2.2 HSV

HSV color segmentation is used to isolate specific areas of the MRI image of the patient’s brain which have similar HSV levels. For the implementation, the albumentations library is used to perform the image pre-processing.

Implementation for HSV:

```
transform=albumentations.Compose([ albumentations.HueSaturationValue() ])
```

It is observed that on applying HSV, the validation accuracy improves for the VGG16 model compared to the validation accuracy for VGG16 without pre-processing. However, there is no improvement observed in the other models that were implemented. However, there is no improvement observed in the other models that were implemented. A significant

decrease in the validation_accuracy for the RESNET50 model is observed when HSV color segmentation is applied to the input MRI images.

6.2.3 DWT

Discrete Wavelet Transform(DWT) is a variant of wavelet transform wherein the wavelets are discretely sampled. DWT is essential in denoising and compressing images. This includes performing a multilevel wavelet decomposition, identifying and implementing a thresholding technique, and reconstructing the resultant image. Hence, this aids in dividing the number of coefficients of the input image, which in turn enables better image analysis. Implementation of DWT on an input image includes performing multilevel wavelet decomposition and detail coefficients. Suitable thresholding techniques are then used which are sigthresh and wthresh in this case. Subsequent to this, the ‘imnoise’ function is used to add gaussian white noise to the input image. DWT implementations include Haar wavelets, Daubechies wavelets, and the dual-tree complex wavelet transform. In this case, the Haar wavelet is made use of. The Haar wavelet, mathematically, is a sequence of rescaled "square-shaped" functions which together form a wavelet family or basis.

The Discrete Wavelet Transform for the input images is implemented using MATLAB.

The ‘imnoise’ function in matlab adds gaussian white noise to the input image. The dwt2 function computes the single-level 2-D wavelet decomposition, which is done with respect to the haar wavelet.

In Equation(6.1) ‘ $\Psi(t)$ ’ is the scaling function and ‘t’ is the time period. t is 1 if it lies between 0 to 0.5, -1 if it lies between 0.5 to 1 and 0 otherwise.

It is observed that applying DWT to the input MRIs results in a higher validation accuracy for VGG16, SVM, Logistic Regression and the Ensemble model. There was no significant change in validation accuracy for the K Nearest Neighbors model. However, there is a drastic decrease in the RESNET50 and CNN when DWT is applied to the input images. Overall, input MRIs for which DWT was applied, resulted in the highest improvement for the SVM, Logistic Regression and Ensemble models.

As shown in Fig. 6.1, the haar wavelet function gives a value of 1 if the time period lies between 0 and 0.5. The value is -1 if the time period lies in the range of 0.5 to 1 and 0 otherwise.

```
J = imnoise(input_image, 'gaussian');  
[cA1, cH1, cV1, cD1] = dwt2(J, 'haar')
```

The Haar wavelet's mother wavelet function:

$$\psi(t) = \begin{cases} 1 & 0 \leq t < \frac{1}{2}, \\ -1 & \frac{1}{2} \leq t < 1, \\ 0 & \text{otherwise.} \end{cases} \quad \dots\dots\dots(6.1)$$

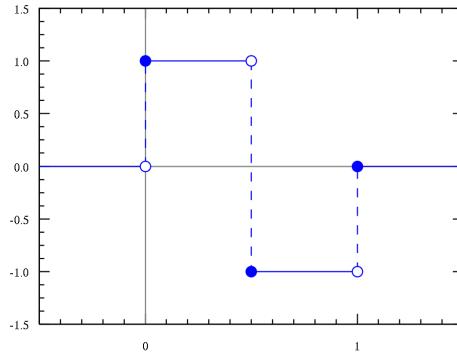


Fig. 6.1 Haar wavelet function

6.3 FEATURE EXTRACTION

Feature extraction refers to the process of transforming raw data into features that can be processed while preserving the information in the original data set.

6.3.1 BRIEF- Binary Robust Independent Elementary Features

SIFT uses a 128-dim vector for descriptors. Since it is using floating point numbers, it takes basically 512 bytes. Similarly SURF also takes a minimum of 256 bytes (for 64-dim). Creating such a vector for thousands of features takes a lot of memory which is not feasible for resource-constraint applications especially for embedded systems. Larger the memory, longer the time it takes for matching.

But all these dimensions may not be needed for actual matching. We can compress it using several methods like PCA, LDA etc. Even other methods like hashing using LSH (Locality Sensitive Hashing) is used to convert these SIFT descriptors in floating point numbers to binary strings. These binary strings are used to match features using Hamming distance. This provides better speed-up because finding hamming distance is just applying XOR and bit count, which are very fast in modern CPUs with SSE instructions. But here, we need to find the descriptors first, then only we can apply hashing, which doesn't solve our initial problem with memory.

BRIEF comes into picture at this moment. It provides a shortcut to find the binary strings directly without finding descriptors. It takes a smoothed image patch and selects a set of nd (x,y) location pairs in an unique way. Then some pixel intensity comparisons are done on these location pairs. For eg, let first location pairs be p and q . If $I(p) < I(q)$, then its result is 1, else it is 0. This is applied for all the nd location pairs to get a nd -dimensional bitstring. This nd can be 128, 256 or 512. OpenCV supports all of these, but by default, it would be 256 (OpenCV represents it in bytes. So the values will be 16, 32 and 64).

6.3.2 STAR(CenSurE) in OpenCV

STAR is a feature detector derived from CenSurE. Unlike CenSurE however, which uses polygons like squares, hexagons and octagons to approach a circle, Star emulates a circle with 2 overlapping squares: one upright and one 45-degree rotated. These polygons are bi-level. They can be seen as polygons with thick borders. The borders and the enclosed area have weights of opposing signs. This has better computational characteristics than other scale-space detectors and it is capable of real-time implementation. In contrast to SIFT and SURF, which find extrema at sub-sampled pixels that compromises accuracy at larger scales, CenSurE creates a feature vector using full spatial resolution at all scales in the pyramid.

Below code shows the computation of BRIEF descriptors with the help of CenSurE detector.

```
img = cv2.imread('image path',0)
# Initiate FAST detector
star = cv2.xfeatures2d.StarDetector_create()
# Initiate BRIEF extractor
brief = cv2.xfeatures2d.BriefDescriptorExtractor_create()
# find the key points with STAR
kp = star.detect(img,None)
#drawing the key points
kp_image = cv2.drawKeypoints(img, kp, None, color=(0, 255, 0), flags=0)
```

6.4 MODELS IMPLEMENTED

All models that were employed and worked on were coded in python and run on Google Collaboratory. Google Collaboratory is a cloud-hosted Jupyter notebook service environment majorly used for Python language - based programming applications.

6.4.1 Machine Learning Models:

Scikit Learn which is also called the sklearn is a python library that can be employed to work on implementing several statistical and machine learning models. The scikit-learn library is used to fabricate several kinds of machine learning models to perform predictions based on regression methods, classification, clustering applications and it also delivers a variety of statistical tools and metrics to evaluate these models. Some of the in library functions that are extremely useful are dimensionality reduction, pre existing datasets, feature selection and feature extraction methods, ensemble model based approaches that have been incorporated.

6.4.1.1 Logistic Regression:

Logistic Regression Models, even though the name suggests otherwise, are classifiers and are used to categorize and classify a dependent variable based on a set of independent features and inputs. In terms of this project, the set of independent features and inputs given to the model is the data set and the output that is predicted is to be one of the classes of tumors or being detected as non-tumorous. The multinomial Logistic Regression is employed to classify MRIs into one of 4 classes.

Mathematically speaking, For Linear Regression, if $y(w,x)$ is the predicted value, it is intended to be a linear combination of features or independent variables and their weights which can be represented as:

$$y^{(w,x)} = w_0 + w_1 x_1 + \dots + w_p x_p \quad \dots \quad (6.2)$$

In the case of Logistic Regression, y , the predicted output variable is supposed to be either 0 or 1 crudely speaking, to obtain that the linear equation above is divided throughout by $(1 - y)$.

$$y^{(w,x)} / (1 - y) \dots \quad (6.3)$$

To limit the range to between $-\infty$ to $+\infty$ a log function is applied to the equation and it will act as the mathematical equation of the general Logistic Regression Classification model.

$$\log[y^{(w,x)} / (1 - y)] = w_0 + w_1 x_1 + \dots + w_p x_p \dots \quad (6.4)$$

Where x_1, x_2, \dots, x_p are distinct independent predictor values, the distinct features that the Linear Model looks at, and the w_0, w_1, \dots, w_p is designated as $w = \{w_0, w_1, \dots, w_p\}$; a vector which is known as the coefficient and w_0 as the intercept.

The model definition and fitting it to the training set:

```
lg=LogisticRegression()
```

```
lg.fit(pca_train,ytrain)
```

Here, we apply linear dimensionality reduction by using the singular value decomposition of the data to project it to a lower dimensional space. To apply PCA on the training set, the n_components value that has been used is 0.98,

pca=PCA(.98)

and ‘y_train’ is the target/label vector of the training set.

Logistic Regression is one of the most efficient techniques for solving classification problems. Some of the advantages of using Logistic regression are as mentioned below.

- Logistic regression is easier to implement, interpret, and very efficient to train. It is very fast at classifying unknown records.
 - It performs well when the dataset is linearly separable.
 - It can interpret model coefficients as indicators of feature importance.

6.4.1.2 K - Nearest Neighbors:

The underlying principle governing the nearest neighbor method works on choosing a training sample point from a set of predefined training sets, that is at the closest distance from the new data point. The label for this current data point is then predicted from the class label points that are the closest.

The method where a constant user defined number is taken to be as the number of set of samples is called the K-Nearest Neighbor learning method, that has been implemented in this project for classifying if there is a tumor or not and to classify the type of tumor if a tumor exists on the MRI.

This classification method is a type of instance -based learning which is also known as a non-generalizing learning. The label or class for the data point is determined by taking into account a majority of votes on the nearest data point neighbors of each point in the set.

The chosen value of k is to indicate the total number of training samples that are needed to classify the test sample. In this case k=3.

The model definition and fitting it to the training set:

```
knn=KNeighborsClassifier(n_neighbors=3)  
knn.fit(pca_train,ytrain)
```

Here, we apply linear dimensionality reduction by using the singular value decomposition of the data to project it to a lower dimensional space. To apply PCA on the training set, the n_components value that has been used is 0.98,

```
pca=PCA(.98)
```

and ‘y_train’ is the target/label vector of the training set.

The KNN algorithm is a simple, coherent yet versatile supervised learning algorithm that can be used to solve the classification problem. It can essentially be considered as an algorithm that makes predictions based on the nature of other data points in the dataset which are present close to it in the training set.

6.4.1.3 Support Vector Machine Classifier:

The basic idea behind a Support Vector Machine is to generate an algorithm for pattern recognition and it is useful in applications like this project where one of the major objectives is tumor type classification. The SVM classifier is a supervised learning algorithm.

With the SVM we aim to generate an optimal hyperplane to separate and classify four classes; and we used the RBF(Radial Bias Function) kernel to add extra dimensionality and map the linear data into a higher dimension. The decision points that lie closest to the hyperplane in the passed set of input dataset are called the support vectors, the support vectors positions along with the hyperplane’s position are used to classify the test data points. The SVC tries to generate a widest margin to separate classes.

The Support Vector Machine Classifier (SVC) from scikit learn's library is used, and is trained on the training data and outputs are predicted on the testing data that is passed to the supervised learning model. The “one-versus-all” method is used for classification.

The model definition and fitting it to the training set:

```
sv=SVC()  
sv.fit(pca_train,ytrain)
```

Here, we apply linear dimensionality reduction by using the singular value decomposition of the data to project it to a lower dimensional space. To apply PCA on the training set, the n_components value that has been used is 0.98,

```
pca=PCA(.98)
```

and 'y_train' is the target/label vector of the training set.

SVM draws a decision boundary which is a hyperplane between any two classes in order to separate them or classify them. It uses a technique called the kernel trick to transform your data and then based on these transformations it finds an optimal boundary between the possible outputs.

6.4.1.4 Ensemble model - StackingCV Classifier:

The StackingCV classifier makes use of a technique called Stacking. By using stacking, the combination of multiple classification models performances, namely, logistic regression, KNN and the SVM have been used to make this ensemble model.

The StackingCV classifier makes use of cross validation where the dataset is split into 'k' folds. In the following rounds, 'k-1' folds are used for fitting the first level classifier. In every round, first level classifiers are applied to the left over one subset that has not been used for model fitting in every iteration. Then the final resulting predictions are stacked and given as the input to the second level classifier i.e, the meta classifier. The meta classifier is what takes in all of the predicted values by LG(logistic regression), KNN(k-nearest neighbors), SVM(support vector machine) and takes the final call of deciding which class a given data point falls into. The meta classifier used is the KNN as it has outperformed the other two machine learning models in terms of overall performance.

The model definition and fitting it to the training set:

```
scv=StackingCVClassifier(classifiers = [lg,knn,sv], meta_classifier=knn)  
scv.fit(xtrain,ytrain)
```

Here, 'xtrain' is what carries the float feature matrix i.e, the design matrix of the training data, and 'y_train' is the target/label vector of the training set.

There are two main reasons to use an ensemble over a single model, and they are related; they are: Performance: An ensemble can make better predictions and achieve better

performance than any single contributing model like SVM, KNN and Logistic Regression. Robustness: An ensemble reduces the spread or dispersion of the predictions and model performance.

6.4.2 Convolution Neural Network:

The CNN model has been used by several researchers over several years to increase the efficacy and efficiency of a robust and significant task of detection, classification, and segmentation of a brain tumor. A convolution is elementally just sliding a filter atop the input layer. As an alternative to going through the entirety of the image at once, we look at a smaller part of the image to locate certain features.

For tumor detection, a Six-Layered CNN model has been worked on and implemented. Every layer in the CNN model associates with a distinct batch of filters and then aggregates the conclusions before sending it as an output to the next consequent layers in the network. A kernel may be thought of as a tiny matrix that sweeps over a huge picture from the left to the right and then from the top to the bottom. The image's neighborhood is calculated for each pixel in the input given.

Brief narration: A beginning input convolutional kernel is generated to produce the tensor of the input images using homogeneous 128, 64, 32 layers of 3*3 filters and winding. Down sampling of the tensor is performed using a pooling layer by changing the stride of the convolution across the image. Then a BatchNormalization layer is applied to the intermediate tensors of the image to normalize the outputs of the previous layer by applying an activation scale. Three fully connected layers named Dense, Dense1 and Dense2 are utilized and put into operation to apply a level of processing to the Neural Network.

The activation function from the dense layer is in charge of signal transmission from one layer to the next. RELU and the sigmoid activation functions are employed to hasten the training period of the neural network.

```
r1=model_cnn.fit(train_x,train_data.label,validation_split=0.1,epochs=20,callbacks=[reduce LR])
```

Here, ‘train_x’ is what carries the float feature matrix i.e, the design matrix of the training data, and ‘train.data_label’ is the target/label vector of the training set. The model has been trained for 20 epochs because the validation accuracies remain the same after 20 epochs.

All the layers of a CNN have multiple convolutional filters working and scanning the complete feature matrix and carry out the dimensionality reduction. This enables CNN to be a very apt and fit network for image classifications and processing.

The model definition for CNN is as shown in Fig. 6.2.

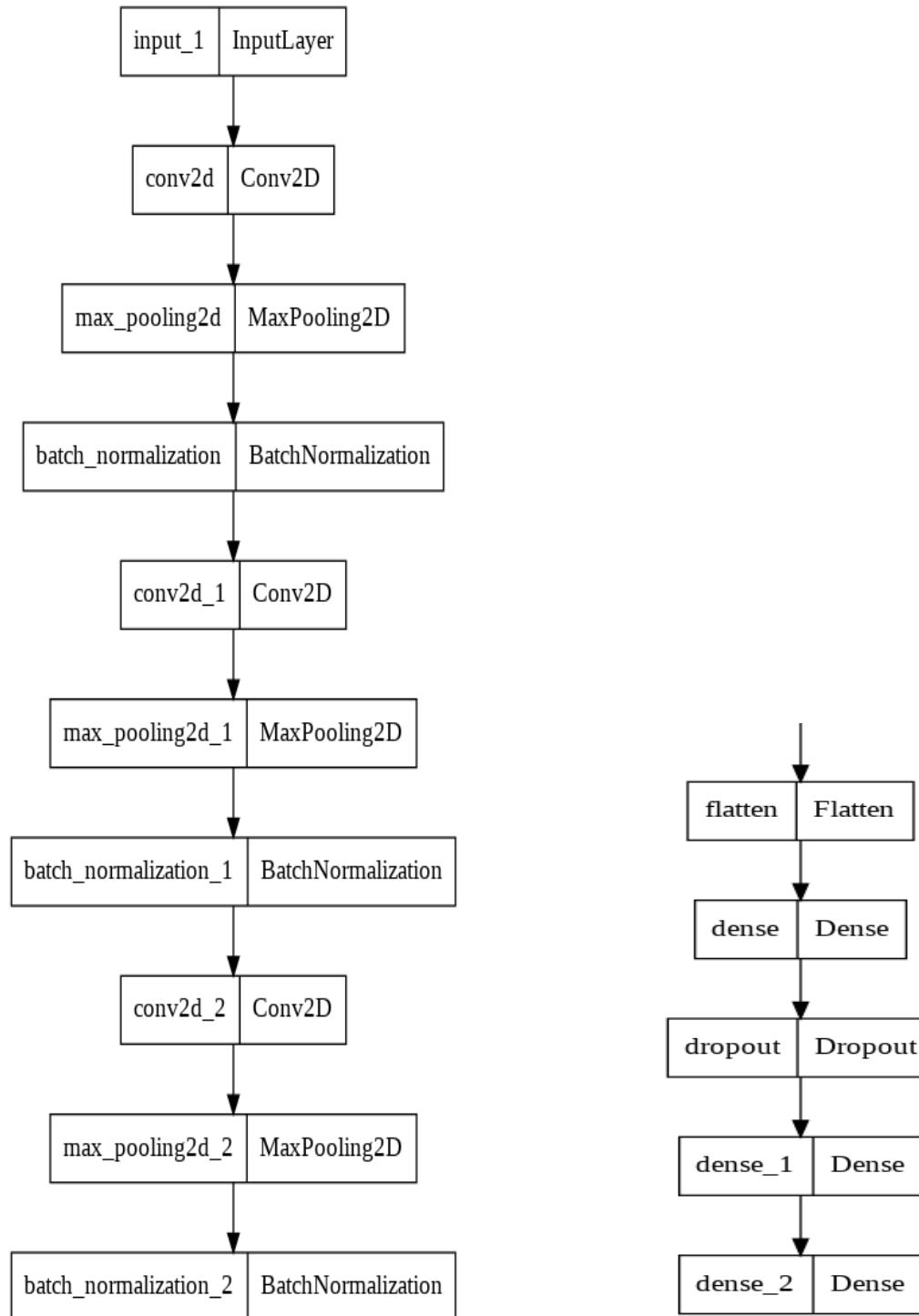


Fig. 6.2 CNN Model Architecture

6.4.3 Transfer Learning Models:

Transfer Learning is a Machine Learning Approach where a model that has been created and trained for one task is now utilized and repurposed as a basis for a different task. The main aim of this method is to focus on storing and applying the information obtained while addressing the older problem to a separate but related topic.

The most common approaches are: Developed Model Approach, and the Pretrained Model Approach. We use pretrained models trained on the ImageNet database which are majorly used for image processing applications. The ImageNet project is a vast visual database that was created to aid in the development of visual object identification software.

6.3.2.1 ResNet50

ResNet50 is a 50 layered Convolutional Neural Network. It is a distinct type of the ResNet model within which 48 layers are convolutional layers and the others are 1 MaxPool layer and 1 AvgPool layer. A pretrained variation of the model that has been trained on over greater than a million images from the Imagenet database is to be imported; The ImageNet project is a vast visual database that was created to aid in the development of visual object identification software. Once the model is imported, a set split on data is applied to train the model after which the model is run on the test data sequentially.

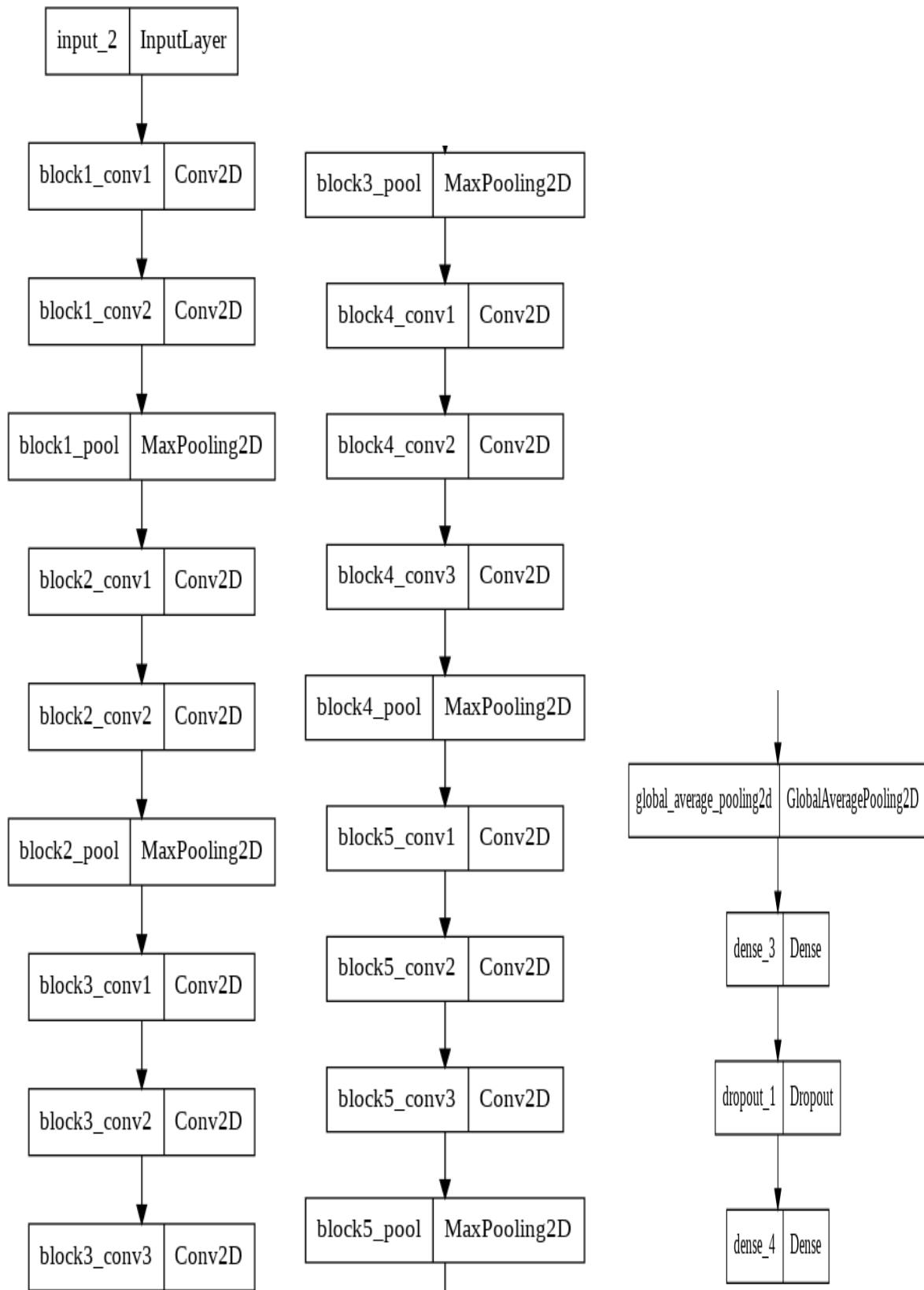
The weights which have been used for executing the ResNet50 model are from pre - trained imagenet models.

```
base_model = ResNet50(include_top=False, weights = 'imagenet')
```

All the layers of a ResNet50 have multiple convolutional filters working and scanning the complete feature matrix and carry out the dimensionality reduction. This enables CNN to be a very apt and fit network for image classifications and processing.

6.3.2.2 VGG16

VGG is an abbreviation for Visual Geometry Group, it's also known as OxfordNet and is a Convolutional Neural Network widely used for ImageNet. This model was the winner of the ImageNet Large Scale Visual Recognition Challenge (ILSVRC) hosted in 2014. A VGG16 model is a 16 layers deep CNN learning model, and it has an image input of RGB 224-by-224 fixed size. The received input image is made to go through a series of several convolutional layers where filters with a lower receptive field of (3*3) are used.

**Fig. 6.3 VGG-16 Model Architecture**

Amongst the Conv. layers, there also are five MaxPooling layers that help perform spatial pooling which is performed over a 2x2 pooling window with stride 1. These are followed by 3 Fully Connected layers of varied depths, 4096 channels each within the first two, and the third one has 1000-channels to perform the ILSVRC based classification on the given data passed to the model.

The last and final layer in this model is a Soft-max layer. Lesser time and resources are consumed in the application of this model as pretrained weights are used.

```
r2=model2.fit(train_x,train_data.label,validation_split=0.1,epochs=20,callbacks=[early_stop,reduceLR])
```

Here, ‘train_x’ is what carries the float feature matrix i.e, the design matrix of the training data, and ‘train.data_label’ is the target/label vector of the training set. The model has been trained for 20 epochs because the validation accuracies remain the same after 20 epochs.

All the layers of a VGG16 have multiple convolutional filters working and scanning the complete feature matrix and carry out the dimensionality reduction. This enables CNN to be a very apt and fit network for image classifications and processing.

The VGG-16 Model Architecture is shown in Fig. 6.3.

6.4.4 AutoML:

Automated Machine Learning(AutoML) is a cloud-based machine learning model builder that automates the process of Machine Learning for the purpose of image recognition. AutoML is based on Neural Architecture Search(NAS). NAS involves automating the design of neural networks. NAS aims to discern the best architecture for a neural network given the specific prerequisites for it. A large number of architectures are tested and evaluated across a search space. The best architecture is selected based on the given prerequisites and whether the objective is met in the most optimal method possible. Presently, a significant number of manual architectures and procedures have been replaced by architectures made by NAS. These procedures include image classification and so on.

One of our main objectives is to reduce the misclassifications, a robust model like AutoML aids in doing so by resulting in a significantly higher validation accuracy compared to the machine learning and deep learning models implemented. The images are uploaded into Google Cloud Storage Bucket. A new project of type Image classification is created and all

the images are imported from Google Cloud Storage Bucket into the newly created project on Google Cloud Vision API as shown in Fig. 6.4. The description and the split of the images for all the classes can also be seen in Fig. 6.4.

The screenshot shows the Google Cloud Platform interface for the 'kaggle' project under the 'Vision' category. The left sidebar has 'Dashboard' selected. The main area shows a message: 'You have enough images to start training'. Below it is a table of labeled images:

Labels	Images	Train	Validation	Test
glioma	450	394	49	7
meningioma	476	380	47	49
no_tumor	835	268	33	34
pituitary_tumor	490	392	49	49

At the bottom left is a 'START TRAINING' button. On the right, a 'Train new model' panel is open, showing step 1: 'Define your model' with a checked 'Cloud hosted' radio button and a 'Model name' field containing 'kaggle_20210917053159'. Step 2: 'Set a node hour budget' is partially visible. Buttons for 'START TRAINING' and 'CANCEL' are at the bottom.

Fig. 6.4 Google Cloud Platform after Creating the Project.

The images are now manually labeled as the different types of tumor classes that are present and trained in Google Cloud for 20 node hours as shown in Fig. 6.5.

The 'Train new model' dialog box is shown. Step 1: 'Define your model' is completed with a checked 'Cloud hosted' radio button and a 'Model name' field containing 'kaggle_20210917053159'. Step 2: 'Set a node hour budget' is active. It prompts the user to enter the maximum number of node hours for training. A note for beta users states: 'AutoML Vision has updated its pricing for node hours.' A 'Set your budget' input field shows '20' node hours. Below it, an estimated completion date is listed as 'Sep 17, 2021 8 PM GMT+5'. A checked checkbox 'Deploy model to 1 node after training' is present. Buttons for 'START TRAINING' and 'CANCEL' are at the bottom.

Fig. 6.5 Defining and Setting the Model to Run for 20 Node Hours.

The trained model is deployed to a single node with which the model is tested and evaluated. The evaluation results of the Google Cloud AutoML model are shown in Fig. 6.6

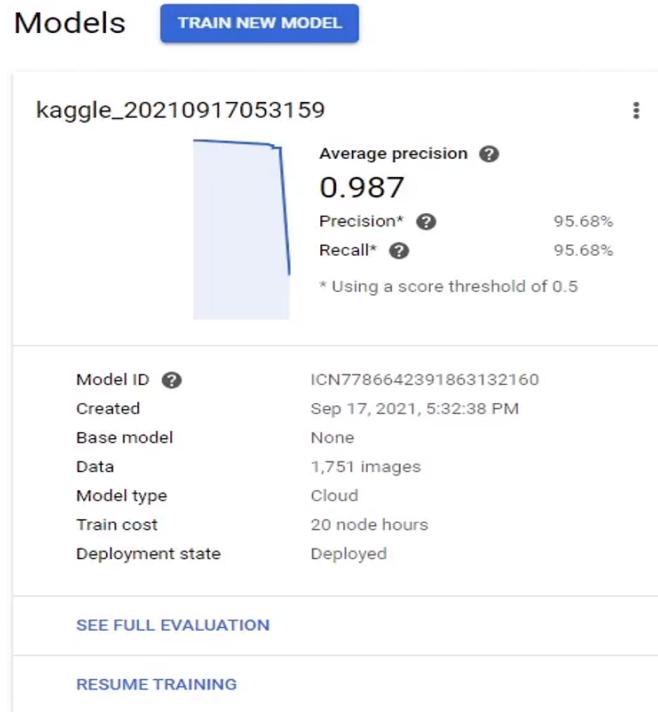


Fig. 6.6 Evaluation Results of AutoML Model

CHAPTER 7

EXPERIMENTATION

CHAPTER 7 EXPERIMENTATION

The following points state the experimentation we have indulged in so far with our project:

1. We wanted to convert the raw data to a format through which we can draw out significant results and information more easily, and that is why we have applied five pre-processing techniques on the original images, namely:
 - a. Otsu (including Inverse-Otsu & Multi-Otsu)
 - b. HSV
 - c. DWT
2. By experimenting with various pre-processing methods, we wanted to make the dataset more suitable for the models, which will lead to an increase in the accuracy and efficiency of the models performance.
3. After thorough experimentation we now know which pre-processing methods do and do not aid in increasing the models performance.
4. Gray Level Co-Occurrence Matrix (GLCM) was taken into consideration to perform feature extraction onto the images for location and classification of tumors. GLCM ideally could be used to extract textural feature data such as Contrast, Homogeneity, Energy, Correlation, Dissimilarity, and Entropy of marked pixels to the neighboring pixel area from the image; while the areas of the tumors are to be predefined. It was not possible to define the area of the tumors on every image in a vast dataset like ours where we have images of different types of tumors and different orientations. Hence the application of GLCM to perform feature extraction and classification of the tumors was futile and not possible.
5. In this project we have also experimented with the BRIEF feature extraction algorithm, unlike glcm, it is a method that we can apply on any MRI for extracting significant features from it without having to pass in any area coordinates for the algorithm to provide the result successfully.
6. We have tested various train-test data splits. Namely, 50-50,60-40,70-30,80-20 and 90-10.
7. The ensemble model has got two classifiers: the first level classifier and the meta classifier. For deciding the meta classifier we have experimented with logistic regression, KNN and SVM MODELS.

8. In this project, we have experimented with tweaking various parameters in the deep learning, transfer learning and machine learning models to try and increase the models' accuracy.
9. We have tweaked parameters like the learning rate, number of epochs we're training the deep learning and transfer learning models for.
10. In the deep learning, transfer learning models definitions we have added and removed dense layers, dropout layers.
11. For all deep learning and transfer learning models, we have also experimented with various activation functions, optimizers, and the loss functions too.
12. By observing the performance results of various machine learning, deep learning and transfer learning models we have executed, we have drawn out a clear understanding of which models do and do not do a good job at classifying an MRI into one of the four classes.

CHAPTER 8

TESTING AND RESULTS

CHAPTER 8 TESTING AND RESULTS

Fig. 8.1 shows some examples of the MRI images used in the project with no pre - processing and varied pre - processing techniques applied:

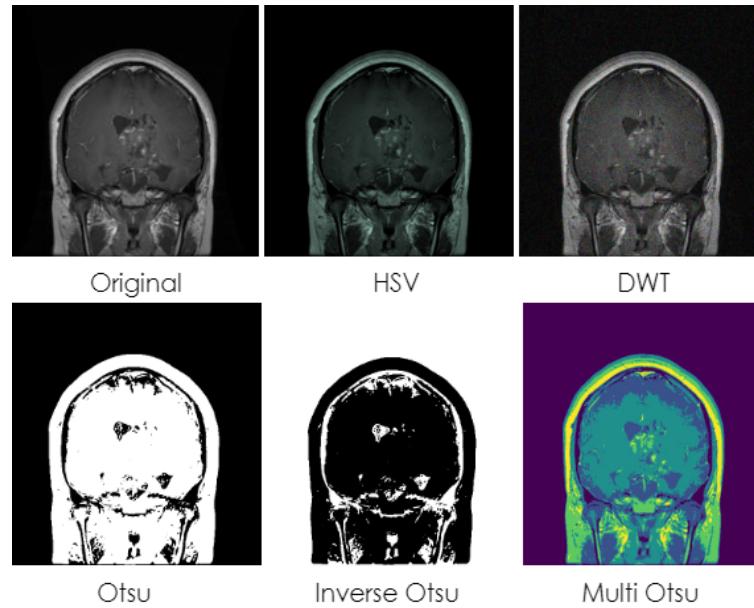


Fig. 8.1 Results with Preprocessing.

The results drawn out after passing the DWT preprocessed image to the BRIEF feature extractor are as shown below in Fig. 8.2

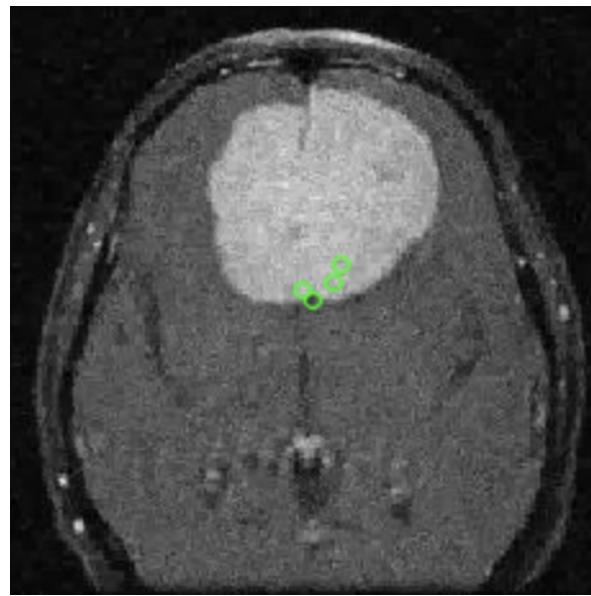


Fig. 8.2 Results Drawn Out from the BRIEF Feature Extractor.

The accuracies drawn out from the models are presented in Table 8.1.

Table 8.1 Validation Results of All the Models

Preprocessing Technique →	No Pre-processing	Multi-Otsu	HSV	Otsu	DWT	DWT-BRIEF	Inverse-Otsu
Algorithm Implemented ↓							
KNN	86.75	84.08	79.09	85.36	86.39	78.04	83.62
SVM	82.57	73.01	81.18	78.39	87.5	73.17	79.44
Logistic Regression	77.7	71.62	76.3	77.35	86.02	82.92	75.95
Ensemble model	87.45	74.04	83.27	86.06	89.33	85.36	84.66
CNN	90.59	88.93	87.11	12.54	30.51	-	86.06
Resnet50	83.91	57.96	58.6	36.71	71.79	-	36.94
VGG16	90.59	87.54	92.68	80.14	91.54	-	81.88

Significant observations drawn out are as follows:

1. Out of all the machine learning models, the ensemble model outperforms the accuracies achieved by logistic regression, KNN and SVM.
2. DWT pre - processing technique aids all models in performing better and makes a positive impact on their accuracy. This is one of the major reasons due to which we have made use of the DWT preprocessed images for feature extraction. One major drawback that has been noticed after implementation of the DWT pre - processing technique on original images is that it does not get applied on all original images due to resolution conflict. Due to this reason, the number of DWT pre- processed images is lesser than the total number of original images.
3. Multi-Otsu and Inverse-Otsu can be good noise to impose on raw images depending on the model we're working with.
4. In the ensemble model, KNN is used as the meta classifier as it gives a better performance compared to using SVM or Logistic Regression as the meta classifiers.
5. CNN and VGG16, these models notably have much higher validation accuracies compared to the machine learning models.

6. Even though the ensemble model outperformed the machine learning models, it has underperformed compared to the CNN and VGG16 deep learning models.
 7. By observing the accuracies drawn out from the deep learning models and transfer learning models, it is notable that Multi-Otsu made more of a positive impact on the models' performances compared to Otsu and Inverse-Otsu.
- I. Fig. 8.3 shows confusion matrix drawn out from the Logistic Regression model to which DWT pre-processed images have been fed:

Confusion Matrix (Logistic Regression)					
True Label	Glioma	53	13	0	1
	Meningioma	12	59	6	4
	No Tumor	0	0	37	0
	Pituitary	1	1	0	85
	Glioma	53	13	0	1
Predicted Label					

Fig. 8.3 Logistic Regression Model Confusion Matrix

- II. Fig. 8.4 shows the confusion matrix drawn out from the K-Nearest Neighbors model to which the original images have been fed:

Confusion Matrix (KNN)					
True Label	Glioma	69	4	4	0
	Meningioma	11	67	6	3
	No Tumor	6	1	25	3
	Pituitary	2	0	1	88
	Glioma	69	4	4	0
Predicted Label					

Fig. 8.4 KNN Model Confusion Matrix

- III. Fig. 8.5 shows the confusion matrix drawn out from the Support Vector Machine model to which DWT pre-processed images have been fed:

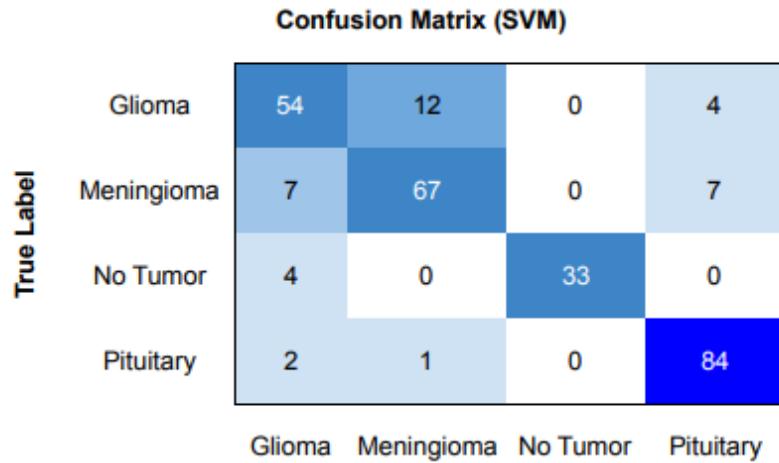


Fig. 8.5 SVM Model Confusion Matrix.

- IV. Fig. 8.6 shows the confusion matrix drawn out from the StackingCV Classifier ensemble model to which DWT pre-processed images have been fed:

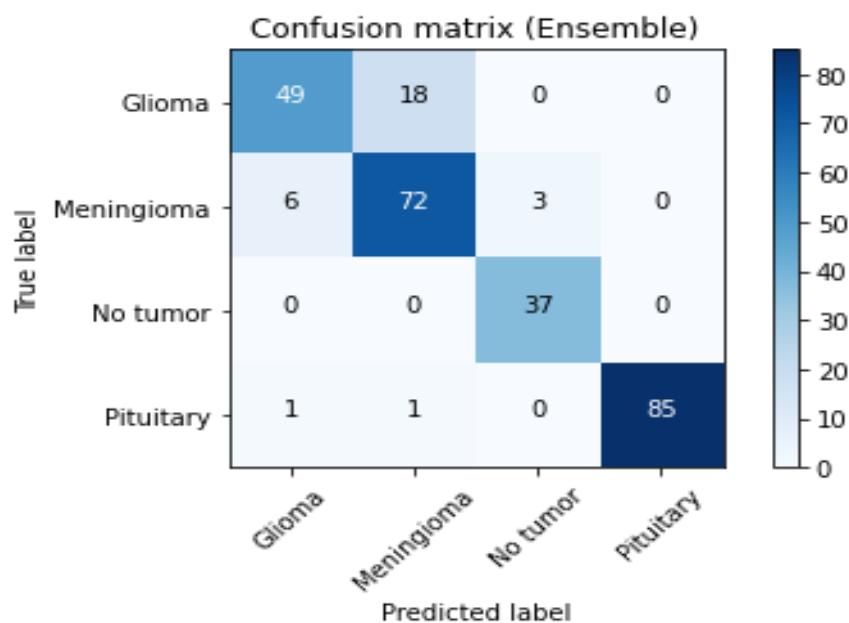


Fig. 8.6 Ensemble Model Confusion Matrix.

- V. In Fig. 8.6, Even though the CNN and VGG16 deep learning models have given the highest accuracies, on drawing out their confusion matrices, they provide more misclassifications compared to the ensemble model's results. As the deep

- learning models interpretability is less, this places more hurdles in our way to analyze and make more observations regarding their performance.
- VI. Since, in most cases, validation accuracies for deep learning models cannot be discerned beforehand, it may not be feasible to expect satisfactory results every time by using them. On the other hand, machine learning models are much more interpretable, they have an easy-to-tweak-parameters structure and their results are less volatile.
- VII. Fig. 8.7 shows the confusion matrix drawn out from the VGG16 model to which the original images have been fed:

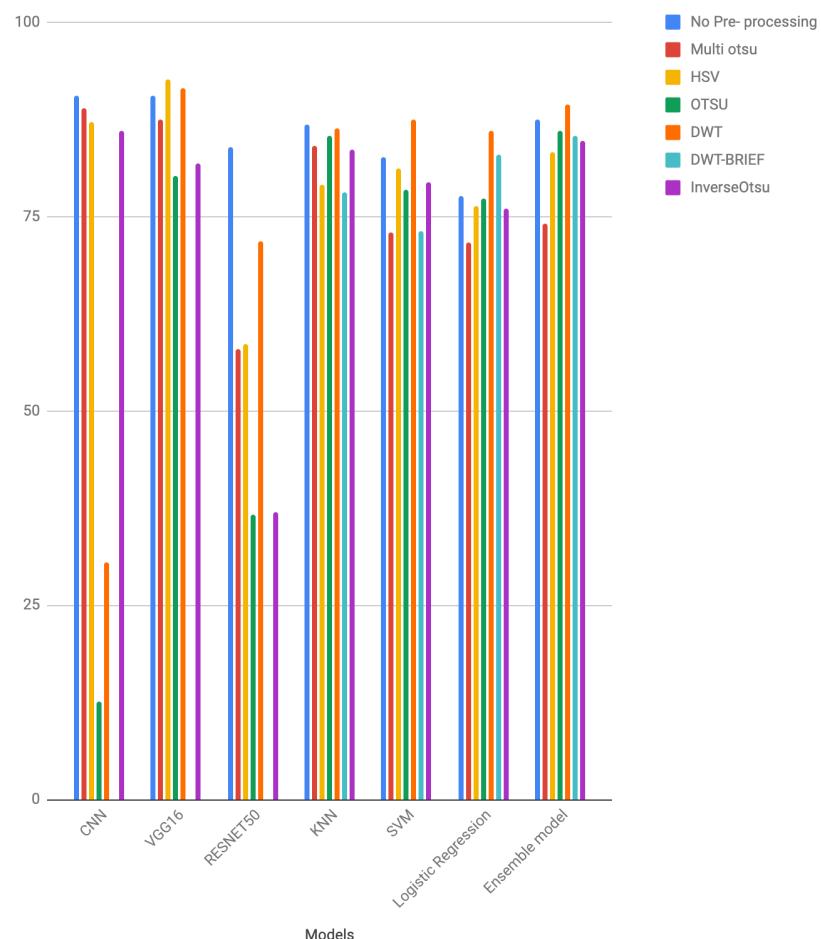
Confusion Matrix (VGG16)					
True Label	Glioma	4	17	14	
	No Tumor	82	0	3	
	Meningioma	33	15	18	
	Pituitary	4	3	2	
		Glioma	No Tumor	Meningioma	Pituitary
		Predicted Label			

Fig. 8.7 VGG16 Model Confusion Matrix.

- VIII. Fig. 8.8 shows the confusion matrix drawn out from the CNN model to which the original images have been fed.
- IX. The graph in Fig. 8.9 portrayed below represents the accuracies of the four machine learning models: KNN, SVM, Logistic Regression, ensemble model - StackingCV classifier, two transfer learning models: RestNet50, VGG16 and the CNN deep learning model, with and without the pre - processing techniques along with the results drawn out through DWT-BRIEF implementation which was performed on the original images.

Confusion Matrix (CNN Without Preprocessing)				
True Label	Pituitary	Glioma	Meningioma	No Tumor
	59	4	11	0
Glioma	7	33	3	21
Meningioma	2	1	112	0
No Tumor	1	100	3	1

Predicted Label

Fig. 8.8 CNN Model Confusion Matrix.**Fig. 8.9 Comparison of All Models Accuracies**

- X. AutoML, as known, is a subfield of Neural Architecture Search (NAS). It uses a controller that selects the neural network internally and produces highly accurate results for even less than half the size of dataset used for running Machine Learning and Deep learning Models.
- XI. In Fig. 8.10, The misclassification rate for AutoML models is close to zero. The average precision obtained for the AutoML cloud model is 98.67% and a Recall of 95.68% (Fig. 8.9) with an average validation accuracy of 98.702% at a score threshold value of 0.5 when trained for a total of 20 node hours using the Vision API.

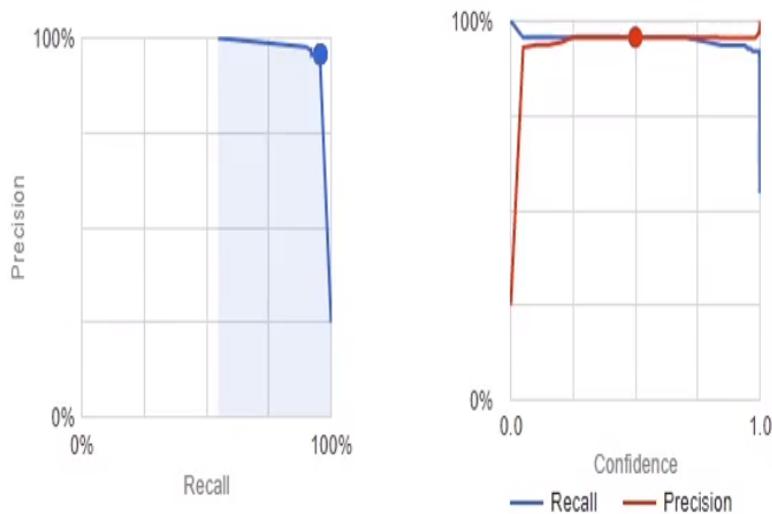


Fig. 8.10. Precision vs Recall and Confidence Matrix of AutoML Model

True Label	Predicted Label				
	glioma	no_tumor	pituitary_tumor	meningioma	-
glioma	86%	-	-	14%	
no_tumor	3%	97%	-	-	
pituitary_tumor	4%	-	96%	-	
meningioma	4%	-	-	96%	

Fig. 8.11 AutoML Confusion Matrix

- XII. The Confusion matrix as displayed above in Fig. 8.11 shows how often the model classified each label correctly (in blue), and which labels were most often confused for that label. While testing the model the misclassification rate was close to 0 for all the four classes. The main advantage here is that even without preprocessed images the model has outperformed all the Machine Learning models that were tested. The individual class prediction made by AutoML is also shown in Table 8.2 below.

Table 8.2 AutoML Individual Class Accuracies

AutoML	
Types of Tumor	Accuracy
Glioma	89.23%
Meningioma	99.39%
No Tumor	100%
Pituitary	99.69%

CHAPTER 9

CONCLUSION AND FUTURE SCOPE

CHAPTER 9 CONCLUSION AND FUTURE SCOPE

The aim of this project was to detect if there is a tumor or not and if there is a tumor present then the type of tumor is classified based on an MRI scan of the patient's brain. High-resolution MRI plays a central part in diagnosing the type of tumor.

The objectives of the proposed system have been met as given below:

- The MRIs of the brain tumors have been collected.
- Pre-processing was performed on the MRIs by using various pre-processing methods so as to improve the overall accuracy and obtain correct classifications, application of suitable feature extraction method has been performed for marking the tumorous regions in the MRIs.
- The presence of the tumor was detected in the brain MRIs, and the tumor type has been classified as being meningioma or pituitary or glioma.
- A comparative analysis was produced for the several models implemented in order to determine the method that results in the least number of mis-classifications and the highest accuracy.

The future scope of this project is as follows:

The brain tumor classifier, on higher validation accuracies, can aid in reducing misclassification regarding whether a tumor is present or not.

In the dataset that has been used for this project, we have images only for glioma, meningioma and pituitary tumors. So, if data is obtained successfully for more tumor types then this project work can be extended to classify more classes than what has been presented in this work, such as: Medulloblastoma, Oligodendrogioma, Schwannoma and so on. Moreover, this project can also be extended to classify tumors in other regions of the body like lungs, pancreas, and so on, provided labeled datasets are used to train the models.

Medical imaging has various unique challenges associated with the scarcity of labeled data. Moreover, unless corroborated by biopsy, there may exist a large variability in labeling from various radiologists. In this regard, weakly supervised approaches such as MIL(Multiple Instance Learning) can be worth exploring. Active learning can be another solution to alleviate the difficulty in labeling. Unsupervised learning approaches are also surely worth exploring to address multiple unique medical imaging challenges.

REFERENCES

- [1] Bathe, Kavita and Rana, Varun and Singh, Sanjay and Singh, Vijay, Brain Tumor Detection Using Deep Learning Techniques (MAY 7, 2021). Proceedings of the 4th International Conference on Advances in Science & Technology (ICAST2021), Available at SSRN: <https://ssrn.com/abstract=3867216> or <http://dx.doi.org/10.2139/ssrn.3867216>
- [2] Tahia Tazin, Sraboni Sarker, Punit Gupta, Fozayel Ibn Ayaz, Sumaia Islam, Mohammad Moniruzzaman Khan, Sami Bourouis, Sahar Ahmed Idris, Hammam Alshazly, "A Robust and Novel Approach for Brain Tumor Classification Using Convolutional Neural Network", Computational Intelligence and Neuroscience, vol. 2021, Article ID 2392395, 11 pages, 2021. <https://doi.org/10.1155/2021/2392395>
- [3] Tessy George, T. Ramakrishnan, "A Professional Estimate on the Segmentation of Brain Cancer in MR Images using M-FCM", International Journal of Recent Technology and Engineering (IJRTE) issn: 2277-3878, volume-9 Issue-1, May 2020.
- [4] S. Grampurohit, V. Shalavadi, V. R. Dhotargavi, M. Kudari and S. Jolad, "Brain Tumor Detection Using Deep Learning Models," 2020 IEEE India Council International Subsections Conference (INDISCON), 2020, pp. 129-134, doi: 10.1109/INDISCON50162.2020.00037.
- [5] A. Hussain and A. Khunteta, "Semantic Segmentation of Brain Tumor from MRI Images and SVM Classification using GLCM Features," 2020 Second International Conference on Inventive Research in Computing Applications (ICIRCA), 2020, pp. 38-43, doi: 10.1109/ICIRCA48905.2020.9183385.
- [6] M.Anto Bennet, D.Haritha, P.Karthika, K.Mahalakshmi, B.Pavithra, "Identification and Detection of Brain Tumor Segmentation using Fuzzy and Neural Network", International Journal of Recent Technology and Engineering (IJRTE), issn: 2277-3878, volume-7, Issue-6S3, Apr. 2019.

- [7] S.Somasundaram, R.Gobinath, "A Hybrid Convolutional Neural Network and Deep Belief Network for Brain Tumor Detection in MR Images", International Journal of Recent Technology and Engineering (IJRTE) issn: 2277-3878, volume-8 Issue-2S4, July 2019.
- [8] T. Hossain, F. S. Shishir, M. Ashraf, M. A. Al Nasim and F. Muhammad Shah, "Brain Tumor Detection Using Convolutional Neural Network," 2019 1st International Conference on Advances in Science, Engineering and Robotics Technology (ICASERT), 2019, pp. 1-6, doi: 10.1109/ICASERT.2019.8934561.
- [9] M. Kurnar, A. Sinha and N. V. Bansode, "Detection of Brain Tumor in MRI Images by Applying Segmentation and Area Calculation Method Using SCILAB," 2018 Fourth International Conference on Computing Communication Control and Automation (ICCUBEA), 2018, pp. 1-5, doi: 10.1109/ICCUBEA.2018.8697713.
- [10] T. S. Kumar, K. Rashmi, S. Ramadoss, L. K. Sandhya and T. J. Sangeetha, "Brain tumor detection using SVM classifier," 2017 Third International Conference on Sensing, Signal Processing and Security (ICSSS), 2017, pp. 318-323, doi: 10.1109/SSPS.2017.8071613.
- [11] Mariam Saii, Zaid Kraitem, "Automatic Brain Tumor Detection in MRI Using Image Processing Techniques", Biomedical Statistics and Informatics. Vol. 2, No. 2, 2017, pp. 73-76. doi: 10.11648/j.bsi.20170202.16
- [12] G. Singh and M. A. Ansari, "Efficient detection of brain tumor from MRIs using K-means segmentation and normalized histogram," 2016 1st India International Conference on Information Processing (IICIP), 2016, pp. 1-6, doi: 10.1109/IICIP.2016.7975365.
- [13] A. Nandi, "Detection of human brain tumor using MRI image segmentation and morphological operators," 2015 IEEE International Conference on Computer Graphics, Vision and Information Security (CGVIS), 2015, pp. 55-60, doi: 10.1109/CGVIS.2015.7449892.

- [14] S. R. Telrandhe, A. Pimpalkar and A. Kendhe, "Detection of brain tumor from MRI images by using segmentation & SVM," 2016 World Conference on Futuristic Trends in Research and Innovation for Social Welfare (Startup Conclave), 2016, pp. 1-6, doi: 10.1109/STARTUP.2016.7583949.
- [15] K. Sinha and G. R. Sinha, "Efficient segmentation methods for tumor detection in MRI images," 2014 IEEE Students' Conference on Electrical, Electronics and Computer Science, 2014, pp. 1-6, doi: 10.1109/SCEECS.2014.6804437.
- [16] Y. Sharma and Y. K. Meghrajani, "Brain tumor extraction from MRI image using mathematical morphological reconstruction," 2014 2nd International Conference on Emerging Technology Trends in Electronics, Communication and Networking, 2014, pp. 1-4, doi: 10.1109/ET2ECN.2014.7044982.
- [17] H. S. Abdulbaqi, M. Zubir Mat, A. F. Omar, I. S. Bin Mustafa and L. K. Aboot, "Detecting brain tumor in Magnetic Resonance Images using Hidden Markov Random Fields and Threshold techniques," 2014 IEEE Student Conference on Research and Development, 2014, pp. 1-5, doi: 10.1109/SCORED.2014.7072963.
- [18] Sharma, Mukharjee. "Brain Tumor Segmentation Using Hybrid Genetic Algorithm and Artificial Neural Network Fuzzy Inference System (ANFIS)." International Journal of Fuzzy Logic Systems, vol. 2, no. 4, 31 Oct. 2012, pp. 31–42, 10.5121/ijfls.2012.2403
- [19] I. Maiti and M. Chakraborty, "A new method for brain tumor segmentation based on watershed and edge detection algorithms in HSV color model," 2012 National Conference on Computing and Communication Systems, 2012, pp. 1-5, doi: 10.1109/NCCCS.2012.6413020.

The Github repository link for the project is:

<https://github.com/vaishaalik/Brain-Tumor-Diagnosis-And-Classification-Based-On-AutoML-And-Traditional-Analysis>

APPENDIX

1. **Benign tumor:** A growth that is not cancer. It does not invade nearby tissue or spread to other parts of the body.
2. **Malignant tumor:** Malignant tumors have cells that grow uncontrollably and spread locally and/or to distant sites. Malignant tumors are cancerous (ie, they invade other sites).
3. **Pituitary tumor:** A pituitary tumor is a tumor that forms in the pituitary gland near the brain that can cause changes in hormone levels in the body. Pituitary tumors are abnormal growths that develop in your pituitary gland.
4. **MRI:** Magnetic Resonance Imaging(MRI) is a medical imaging technique used in radiology to form pictures of the anatomy and the physiological processes of the body.
5. **KNNs:** K-Nearest Neighbors is a machine learning technique and algorithm that can be used for both regression and classification tasks. K-Nearest Neighbors examines the labels of a chosen number of data points surrounding a target data point, in order to make a prediction about the class that the data point falls into.KNN is a conceptually simple yet very powerful algorithm, and for those reasons, it's one of the most popular machine learning algorithms.
6. **CNNs:** A convolutional neural network (CNN) is a specific type of artificial neural network that uses perceptrons, a machine learning unit algorithm, for supervised learning, to analyze data. CNNs apply to image processing, natural language processing and other kinds of cognitive tasks.A convolutional neural network is also known as a ConvNet.
7. **SVMs:** 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.

FUNDING AND PUBLISHING PAPER DETAILS

From: Lech M. Grzesiak <ijece@iaescore.com>

Date: Thu, Apr 21, 2022 at 9:54 AM

Subject: [IJECE] Submission Acknowledgement "Comparative Study of Cloud AutoML and Traditional Techniques to Detect and Classify Brain Tumors"

To: Dr Sindhu P Menon <sindhu33in@gmail.com>

The following message is being delivered on behalf of International Journal of Electrical and Computer Engineering (IJECE).

-- IJECE for writing format and style: <https://iaescore.com/gfa/ijece.docx>

-- Research paper: min 25 references primarily to journal papers

-- Review paper: min 50 references primarily to journal papers

-- Similarity score of your manuscript must be less than 25%

Dear Prof/Dr/Mr/Mrs: Dr Sindhu P Menon,

Thank you for submitting the manuscript, "Comparative Study of Cloud AutoML and Traditional Techniques to Detect and Classify Brain Tumors" to International Journal of Electrical and Computer Engineering (IJECE), an open access and Scopus indexed; CiteScore: 1.63; SNIP: 1.144; SJR (ScimagoJR): 0.32, Q2. With the online journal management system that we are using, you will be able to track its progress through the editorial process by logging in to the journal web site:

Manuscript URL:

<http://ijece.iaescore.com/index.php/IJECE/author/submission/28205>

Username: sindhu33in

A high quality paper should has:

- (1) a clear statement of the problem the paper is addressing;
- (2) the proposed solution(s); and
- (3) results achieved. It describes clearly what has been done before on the problem, and what is NEW.

Original/Research paper should be presented with IMRaD style/model:

1. Introduction
2. The Proposed Method/Algorithm/Procedure specifically designed (optional).

Authors may present complex proofs of theorems or non-obvious proofs of correctness of algorithms after introduction section (obvious theorems & straightforward proofs of existing theorems are NOT needed).

3. Research Method
4. Results and Discussion
5. Conclusion.

For original research paper, there are four (4) types of novel technical results: 1) An algorithm; 2) A system construct: such as hardware design, software system, protocol, etc.; 3) A performance evaluation: obtained through analyses, simulation or measurements; or 4) A theory: consisting of a collection of theorems. Number of minimum references for original research paper is 25 references (and minimum 20 recently journal articles).

For review paper, the paper should present a critical, constructive analysis of the literature in a specific field through summary, classification, analysis and comparison. The function and goal of the review paper is: 1) to organize literature; 2) to evaluate literature; 3) to identify patterns and trends in the literature; 4) to synthesize literature; or 5) to identify research gaps and recommend new research areas. The structure includes:

1. Title – in this case does not indicate that it is a review article.
2. Abstract – includes a description of subjects covered.
3. Introduction includes a description of context (paragraph 1 – 3), motivation for review (paragraph 4, sentence 1) and defines the focus (paragraph 4, sentences 2 – 3)
4. Body – structured by headings and subheadings
5. Conclusion – states the implications of the findings and an identifies possible new research fields
6. References (“Literature Review”) – organised by number in the order they were cited in the text.

Number of minimum references for review paper is 50 references (and minimum 40 recently journal articles).

Before review process, please re-upload your revised paper as "author version" as soon as possible for avoiding delay on review process. If you have any questions, please contact me. Thank you for considering this journal as a venue for your work.

Best Regards,
Lech M. Grzesiak

International Journal of Electrical and Computer Engineering (IJECE)

NOTE:

-- Your paper ID number is "NUMBER" on the

<http://ijece.iaescore.com/index.php/IJECE/author/submission/28205>

-- A single author is NOT preferred in this journal, except come from qualified researcher
(min WoS/Scopus h-index:

15). We would like to publish high quality papers of a research group.

-- Paper with single author normally will be REJECTED

OUR FREE OF CHARGE JOURNALS:

<http://ijaas.iaescore.com>

<http://ijict.iaescore.com>

<http://ijra.iaescore.com>

<http://ijape.iaescore.com>

<http://iaesprime.com/index.php/csit>

Kindly forward this email to other interested parties

::: Checklist for preparing your paper for publication :::

1. Is your manuscript written in IAES format (<https://iaescore.com/gfa/ijece.docx>)? At this stage, it is essential that you follow every detail of IAES format. Please try to follow the format as closely as possible.
2. Is your title adequate and is your abstract correctly written? The title of paper is max 10 words, without Acronym or abbreviation. The Abstract (MAX 200 WORDS) should be informative and completely self-explanatory (no citation in abstract), provide a clear statement of the problem, the proposed approach or solution, and point out major findings and conclusions.
3. Authors are suggested to present their articles in the sections structure: Introduction - The Proposed Method/Algorithm/Procedure specifically designed (optional) - Research Method - Results and Discussion – Conclusion. Authors may present complex proofs of theorems or non-obvious proofs of correctness of algorithms after introduction section (obvious theorems & straightforward proofs of existing theorems are NOT needed).

4. Introduction section: explain the context of the study and state the precise objective. An Introduction should contain the following three parts (within 3-7 paragraphs):
 - Background: Authors have to make clear what the context is. Ideally, authors should give an idea of the state-of-the art of the field the report is about.
 - The Problem: If there was no problem, there would be no reason for writing a manuscript, and definitely no reason for reading it. So, please tell readers why they should proceed reading. Experience shows that for this part a few lines are often sufficient.
 - The Proposed Solution: Now and only now! - authors may outline the contribution of the manuscript. Here authors have to make sure readers point out what are the novel aspects of authors work. Authors should place the paper in proper context by citing relevant papers. At least, 15 references (recently journal articles) are used in this section.
5. Method section: the presentation of the experimental methods should be clear and complete in every detail facilitating reproducibility by other scientists.
6. Results and discussion section: The presentation of results should be simple and straightforward in style. This section reports the most important findings, including results of statistical analyses as appropriate and comparisons to other research results. Results given in figures should not be repeated in tables. This is where the author(s) should explain in words what he/she/they discovered in the research. It should be clearly laid out and in a logical sequence. This section should be supported with suitable references.
7. Conclusion section: Summarize sentences the primary outcomes of the study in a paragraph. Are the claims in this section supported by the results, do they seem reasonable? Have the authors indicated how the results relate to expectations and to earlier research? Does the article support or contradict previous theories? Does the conclusion explain how the research has moved the body of scientific knowledge forward?
8. Language. If an article is poorly written due to grammatical errors, while it may make it more difficult to understand the science.
9. Please be sure that the manuscript is up to date. It is expected that 10 to 20% of references are to recent papers.
10. Is the manuscript clearly written? Is the article exciting? Does the content flow well from one section to another? Please try to keep your manuscript on the proper level. It should be easy to understand by well qualified professionals, but at the same time please avoid describing well known facts (use proper references instead). Often manuscripts receive negative reviews because reviewers are not able to understand the manuscript and this is authors' (not reviewers') fault. Notice, that if reviewers have difficulties, then other readers will face the same problem and there is no reason to publish the manuscript.

11. Do you have enough references? We will usually expect a minimum of 25 references primarily to journal papers, depending on the length of the paper. Citations of textbooks should be used very rarely and citations to web pages should be avoided. All cited papers should be referenced within the text of the manuscript.

12. Figures and Tables. Relation of Tables or Figures and Text: Because tables and figures supplement the text, all tables and figures should be referenced in the text. Authors also must explain what the reader should look for when using the table or figure. Focus only on the important point the reader should draw from them, and leave the details for the reader to examine on her own. Figures: a. All figures appearing in article must be numbered in the order that they appear in the text. b. Each figure must have a caption fully explaining the content c. Figure captions are presented as a paragraph starting with the figure number i.e. Figure 1, Figure 2, etc. d. Figure captions appear below the figure e. Each figure must be fully cited if taken from another article f. all figures must be referred to in the body of the article Tables: a. Material that is tabular in nature must appear in a numbered captioned table. b. All tables appearing in article must be numbered in the order that they appear in the text. c. Each table must have a caption fully explaining the content with the table number i.e. Table 1, Table 2, etc. d. Each column must have a clear and concise heading e. Tables are to be presented with single horizontal line under: the table caption, the column headings and at the end of the table. f. All tables must be referred to in the body of the article g. Each table must be fully cited if taken from another article 13. Each citation should be written in the order of appearance in the text in square brackets. For example, the first citation [1], the second citation [2], and the third and fourth citations [3,4]. When citing multiple sources at once, the preferred method is to list each number separately, in its own brackets, using a comma or dash between numbers, as such: [1], [3], [5] or [4-8]. It is not necessary to mention an author's name, pages used, or date of publication in the in-text citation. Instead, refer to the source with a number in a square bracket, e.g. [9], that will then correspond to the full citation in your reference list. Examples of in-text citations: This theory was first put forward in 1970 [9]." Sutikno [10] has argued that...

Several recent studies [7], [9], [11-15] have suggested that....

...end of the line for our research [16].

14. Please be aware that for the final submission of regular paper you will be asked to tailor your paper so the last page is not half empty.
