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A project report submitted to

# Dr. BHARADWAJA KUMAR SCHOOL OF COMPUTER SCIENCE & ENGINEERING

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## **CSE 1015 – MACHINE LEARNING ESSENTIALS**

in

## B.Tech. COMPUTER SCIENCE & ARTIFICIAL INTELLIGENCE ENGINEERING

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We thank our parents, family, and friends for bearing with us throughout the course of our project and for the opportunity they provided us in undergoing this course in such a prestigious institution.

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## **ABSTRACT**

A tumor is a solid mass of tissue that forms when abnormal cells group together. A cancerous or non-cancerous mass or growth of abnormal cells in the brain. Tumors can start in the brain, or cancer elsewhere in the body can spread to the brain.

Many tumors are not cancer. A brain tumor is a cluster of abnormal cells that grows out of control in your brain. Some brain tumors are benign, which means the cells aren't cancer. Brain tumors are called primary tumors if they started in your brain. They're considered secondary if they started somewhere else in your body and spread to your brain.

Symptoms of brain tumors vary according to the type of tumor and the location. Because different areas of the brain control different functions of the body, where the tumor lies affects the symptoms you get. So you cannot predict the tumour type by examine the type of symptoms you are getting

This project aims to use the MRI Images of the brain and classifies it as to three main tumor types i.e Meningioma, Glioma and Pituitary Tumor. The Classification of the MRI Images helps the patient to proceed with a pre doctor aid as well as the doctor to go with the treatment of the patient without any further confusion.

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#### **CHAPTER 1: INTRODUCTION AND BACKGROUND STUDY**

A tumor is a solid mass of tissue that forms when abnormal cells group together. A cancerous or non-cancerous mass or growth of abnormal cells in the brain. Tumors can start in the brain, or cancer elsewhere in the body can spread to the brain.

Many tumors are not cancer. A brain tumor is a cluster of abnormal cells that grows out of control in your brain. Some brain tumors are benign, which means the cells aren't cancer. Brain tumors are called primary tumors if they started in your brain. They're considered secondary if they started somewhere else in your body and spread to your brain.

Symptoms of brain tumors vary according to the type of tumor and the location. Because different areas of the brain control different functions of the body, where the tumor lies affects the symptoms you get.

- Headaches, which may not get better with the standard migraine cures. You might see you're getting them on a more regular basis or they're more regrettable than expected
- Seizures, particularly in a person who doesn't have a history of seizures
- Changes in speech or hearing
- Changes in vision
- Balance problems
- Problems with walking

#### **Background study**

#### **MENINGIOMA:**

Meningioma is the most common type of primary brain tumor, accounting for approximately 30 percent of all brain tumors.

- About 85% of meningiomas are noncancerous, slow-growing tumors
- Meningioma originates from the meningeal layers of either the brain or the spinal cord
- Machine learning analyses can differentiate meningioma grade by features on magnetic resonance imaging
- While magnetic resonance imaging (MRI), is the standard radiologic technique for provisional diagnosis and surveillance of meningioma

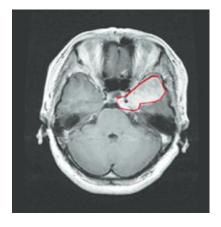
#### **GLIOMA:**

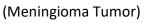
- Gliomas are brain tumours that start in glial cells. These are the supporting cells of the brain and the spinal cord
- Machine learning has been applied to the analysis of MRI data in glioma research and has the potential to change clinical practice and improve patient outcomes.

- This systematic review synthesizes and analyzes the current state of machine learning applications to glioma MRI data and explores the use of machine learning for systematic review automation
- To truly profit from the power of machine learning in glioma imaging, larger amounts of well-annotated data are required to achieve good generalization across datasets. Data sharing in medical research is being actively pursued in an effort to raise the integrity and accelerate the pace of research
- MR images and histopathology are the most important indicators in the determination of whether it is gliomas or other abnormalities. Machine learning methods have good performance at pattern recognition of images.

#### **PITUITARY TUMOR**

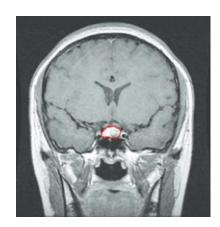
- Pituitary tumors are abnormal growths that develop in your pituitary gland. Some
  pituitary tumors result in too much of the hormones that regulate important functions
  of your body
- Pituitary tumors are abnormal growths that develop in your pituitary gland. Some pituitary tumors result in too much of the hormones that regulate important functions of your body
- Machine learning (ML) have garnered increasing attention to quantitatively analyze complex medical data to improve individualized care for patients with Pituitary tumors
- ML can be used to design andtrain software algorithms to learn from and act on data.
- The type of PA cannot be clearly recognized by preoperative MRIbut can be classified by immunohistochemical staining of resected tumor samples after surgery
- MR imaging could potentially serve as a novel approach to preoperatively predict visual recovery and allow personalized counseling for individual pituitary adenoma patients.
- Machine learning algorithms was proposed with the feasible predictive performance for postoperative visual recovery, allowing personalized counseling for pituitary adenoma patients.







(Glioma Tumor)



(Pituitary Tumor)

#### **CHAPTER 2: PROPOSED METHODOLOGY**

Our Project aims to do the comparison study between the three famous Image Classification Algorithms that is VGG 16, Resnet 50 and Efficient Net B series Algorithms.

This project aims to use the MRI Images of the brain and classifies it as to three main tumor types i.e Meningioma, Glioma and Pituitary Tumor. The Classification of the MRI Images helps the patient to proceed with a pre doctor aid as well as the doctor to go with the treatment of the patient without any further confusion.

#### **VGG Algorithm:**

Visual Geometry Group is an acronym for Visual Geometry Group (a group of researchers at Oxford who developed this architecture). The VGG architecture is divided into blocks, each of which is made up of 2D Convolution and Max Pooling layers. VGGNet is available in two varieties: VGG16 and VGG19, which differ in the number of layers they contain.

The ability of a Convolutional Neural Network (CNN) to fit more complex functions increases as the number of layers increases. As a result, having more layers is always preferable (not to be confused with an artificial neural network which does not necessarily give a significantly better performance with increase in number of hidden layers).

The backpropagation algorithm is used to update the weights of a neural network. The backpropagation algorithm makes a tiny adjustment to each weight in order to reduce the model's loss. What causes this to happen? It refreshes each weight in such a way that the loss progresses in the right direction. This direction is nothing more than the weight's gradient (with respect to the loss).

We can find this gradient for each weight using the chain rule. It's the same as (local gradient) x. (gradient flowing from ahead)

This is where the issue arises. This value keeps getting multiplied by each local gradient as this gradient flows backward to the initial layers. As a result, the gradient gets smaller and smaller, making the updates more difficult.

VGG 16 was proposed by Karen Simonyan and Andrew Zisserman of the Visual Geometry Group Lab of Oxford University in 2014 in the paper "VERY DEEP CONVOLUTIONAL NETWORKS FOR LARGE-SCALE IMAGE RECOGNITION". CNN is a deep learning algorithm which takes input image, assigns weights according to the features in the image and be able to differentiate one from another. CNN is used for image recognition, object classification and face recognition.

#### **Resnet Algorithm:**

ResNet-50 is a residual network. A residual network is a type of DAG network that has residual (or shortcut) connections that bypass the main network layers.

Residual connections enable the parameter gradients to propagate more easily from the output layer to the earlier layers of the network, which makes it possible to train deeper networks. This increased network depth can result in higher accuracies on more difficult tasks.

ResNet50 is a variant of ResNet model which has 48 Convolution layers along with 1 MaxPool and 1 Average Pool layer. It has 3.8 x 10^9 Floating points operations.

ResNet50 is a variant of ResNet model which has 48 Convolution layers along with 1 MaxPool and 1 Average Pool layer. It has 3.8 x 10^9 Floating points operations

The ResNets were initially applied to the image recognition task but as it is mentioned in the paper that the framework can also be used for non computer vision tasks also to achieve better accuracy.

This architecture can be used on computer vision tasks such as image classification, object localisation, object detection and this framework can also be applied to non computer vision tasks to give them the benefit of depth and to reduce the computational expense also.

The ResNet architecture (seen below) should now make perfect sense in terms of how it prevents the vanishing gradient problem. ResNet is an abbreviation for Residual Network.

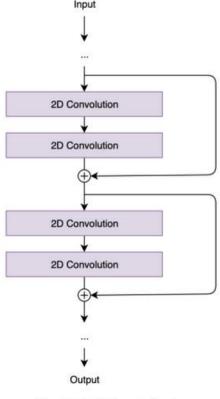
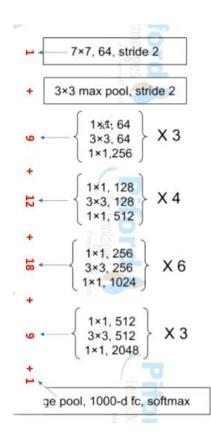


Fig. 4 ResNet architecture



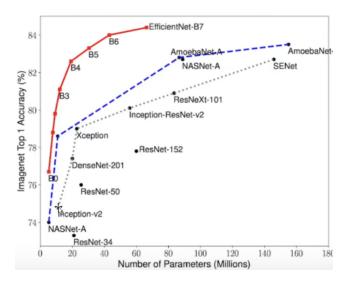
#### **Efficient Net B series Algorithm:**

All EfficientNet models are scaled from our baseline EfficientNet-B0 using different compound coefficients, resulting in EfficientNet performance results on ImageNet. The EfficientNet-B0 architecture was created by the neural network itself, not by engineers. They used a multi-objective neural architecture search to create this model, which maximises both accuracy and floating-point operations. Accepting B0 as a benchmark model, the developers developed a series of EfficientNets ranging from B1 to B7 that achieved cutting-edge precision on ImageNet while outperforming its competition. EfficientB0 has 230 layers and 7 MBConv blocks, and it has a thick block structure with four tightly linked layers and a development rate of four.

Stage	Operator	Resolution	#Channels	#Layers
i	$ \mathcal{F}_i $	$\hat{H}_i  imes \hat{W}_i$	$\hat{C}_i$	$ L_i $
1	Conv3x3	$224 \times 224$	32	1
2	MBConv1, k3x3	$112 \times 112$	16	1
3	MBConv6, k3x3	$112 \times 112$	24	2
4	MBConv6, k5x5	$56 \times 56$	40	2
5	MBConv6, k3x3	$28 \times 28$	80 3	
6	MBConv6, k5x5	$14 \times 14$	112	3
7	MBConv6, k5x5	$14 \times 14$	192	4
8	MBConv6, k3x3	$7 \times 7$	320	1
9	Conv1x1 & Pooling & FC	$7 \times 7$	1280	1

Same in B0 to B7

Resolution, Channels, Layers change



## **CHAPTER 3: IMPLEMENTATION OF THE MODEL**

## **Link of the ipynb notebook:**

https://colab.research.google.com/drive/1VvcXMfhhtDgO9SF8T327h8dZzfkIs6w8?usp=sharing

```
Dataset Labeling and setting
   [ ] import numpy as np
import tensorflow as tf
                import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import os
   what kinds of classes are in this dataset
   dataset_path = os.listdir('/content/dataset')
print (dataset_path)
print("Types of classes labels found: ", len(dataset_path))
   (a) ['3', '2', '1']
Types of classes labels found: 3
                  for item in dataset_path:
all_classes = os.listdir('dataset' + '/' +item)
print(all_classes)
                  for room in all classes:
    class_labels.append((item, str('dataset_path' + '/' +item) + '/' + room))
    print(class_labels[:5])
 0
            # Build a dataframe

df = pd.Dataframe(data=class_labels, columns=['tabels', 'image'])

print(df.tail())

print(df.tail())
         •

    VGG Implementation on the Dataset

 [] from _future__ import print_function
import numpy as np
import tampings
from keras.nedels import Model
from keras.layers import Elatten
from keras.layers import Elatten
from keras.layers import Enput
from keras.layers import Input
from keras.layers import MaxPooling2D
from keras.layers import MaxPooling2D
from keras.layers import GlobalMaxPooling2D
from keras.layers import Section Layer utils
from keras.utils import layer utils
from keras.applications.imagenet_utils import decode_predictions
from keras.applications.imagenet_utils import decode_predictions
from keras.applications.imagenet_utils import preprocess_input
                          img_rows, img_cols = 224, 224  # by default size is 224,224
img_channels = 3
```

```
VGGupdated(input_tensor=None,classes=3):
                  img_rows, img_cols = 224, 224 --# by default-size is 224,224
img_channels = 3
                  img_dim = (img_rows, img_cols, img_channels)
                  img_input = Input(shape=img_dim)
                  ##Block1
x = Conv2D(64, (3, 3), activation='relu', padding='same', name='block1_conv1')(img_input)
x = Conv2D(64, (3, 3), activation='relu', padding='same', name='block1_conv2')(x)
x = MaxPooling2D((2, 2), strides=(2, 2), name='block1_pool')(x)
                  x = Conv2D(128, (3, 3), activation='relu', padding='same', name='block2_conv1')(x)
x = Conv2D(128, (3, 3), activation='relu', padding='same', name='block2_conv2')(x)
x = MaxPoolingD((2, 2), strides=(2, 2), name='block2_pool')(x)
                  # Block:3
x = Conv2D(256, (3, 3), activation='relu', padding='same', name='block3_conv1')(x)
x = Conv2D(256, (3, 3), activation='relu', padding='same', name-'block3_conv2')(x)
x = Conv2D(256, (3, 3), activation='relu', padding='same', name-'block3_conv3')(x)
x = MaxPooling2D((2, 2), strides=(2, 2), name-'block3_pool')(x)
                  ### Block 4

**E-Conv2D(512, (3, 3), activation='nelu', padding='same', name='blockd_conv1')(x)

**x = Conv2D(512, (3, 3), activation='relu', padding='same', name='blockd_conv2')(x)

**x = Conv2D(512, (3, 3), activation='relu', padding='same', name='blockd_conv3')(x)

**x = Conv2D(512, (3, 3), activation='relu', padding='same', name='blockd_conv3')(x)

**x = Conv2D(512, (3, 3), activation='relu', padding='same', name='blockd_conv3')(x)
                  # Block 5
x = conv2D(512, (3, 3), activation='relu', padding='same', name='block5_conv1')(x)
x = conv2D(512, (3, 3), activation='relu', padding='same', name='block5_conv2')(x)
x = conv2D(512, (3, 3), activation='relu', padding='same', name='block5_conv3')(x)
x = MavDonline2D(/2 2) ctridec=(2 2) name='block5_conv1')(x)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ↑↓⊝目‡ॄ [ i :
                           # Classification block
x = Flatten(name-'flatten')(x)
x = Dense(4096, activation-'nelu', name-'fc1')(x)
x = Dense(4096, activation-'nelu', name-'fc2')(x)
x = Dense(classes, activation-'softmax', name-'predictions')(x)
         0
                            model = Model(inputs = img_input, outputs = x, name='VGGdemo')
return model
       [] model = VGGupdated(classes = 3) # Meningioma, Glioma and Pituitary are our types model.compile(optimizer='adam', loss='categorical_crossentropy', metrics=['accuracy'])
        [ ] import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import os
       [ ] dataset_path = os.listdir('dataset')
                    tumor_types = os.listdir('dataset')
print (tumor_types)  #what kinds of tumor are in our dataset
             all_tumor = os.listdir('dataset' + '/' +item)
#print(all_shoes)
            # Add them to the list
for tumor in all tumor:
tumor.apend(item, str('dataset' + '/' *item) + '/' + tumor))
print(tumor)
         # Bullding a dataframe
tumor_df - pd.Dataframe(data-tumor, columns-['tumor type', 'image'])
print(tumor_df.tail())
print(tumor_df.tail())
0
             room type image
3 dataset/3/2237.png
3 dataset/3/1708.png
3 dataset/3/1708.png
3 dataset/3/1716.png
3 dataset/3/1716.png
 [] # Let's check how many samples for each category are present
print("Total number of tumor in the dataset: ", len(tumor_df))
tumor_count = tumor_df("tumor type'].value_counts()
print("tumor in each category: ")
print(tumor_count)
         Total number of rooms in the dataset: 3064 rooms in each category: 2 1426 3 939 1 708 Name: room type, dtype: int64
           images = []
labels = []
           for i in tumor_types:
    data_path = path + str(i)
    filenames = [i for i in os.listdir(data_path)]
 [ ] images = np.array(images)
            images = images.astype('float32') / 255.0
images.shape
           (3064, 224, 224, 3)
 from sklearn.preprocessing import LabelEncoder , OneHotEncoder y=tumor_df['tumor type'].values
#print(y[:5])
```

```
or on skinarm.untils deport shuffle
from skinarm.anded_selection import train_test_split

images, Y = shuffle(images, Y, random_state=1)

train_x, test_x, train_y, test_y = train_test_split(images, Y, test_size=0.65, random_state=415)

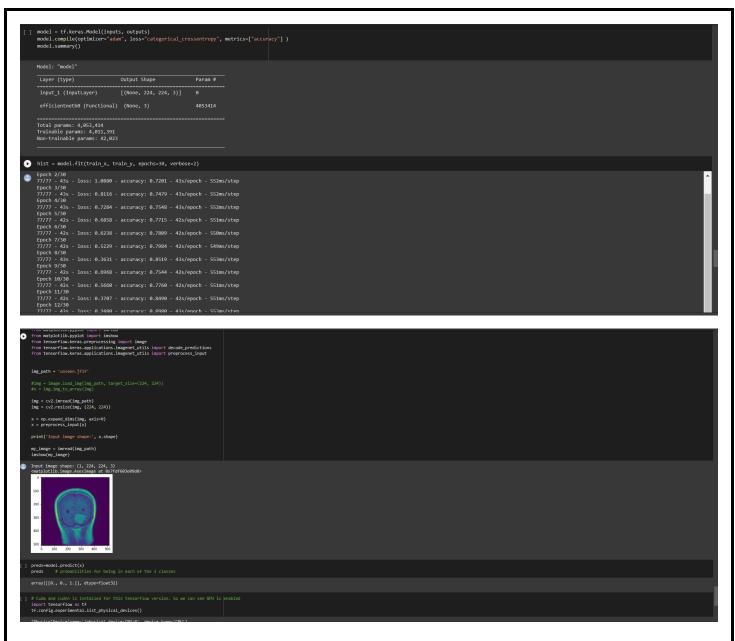
#import the shape of the training and testing.

#print(train_x, shape)

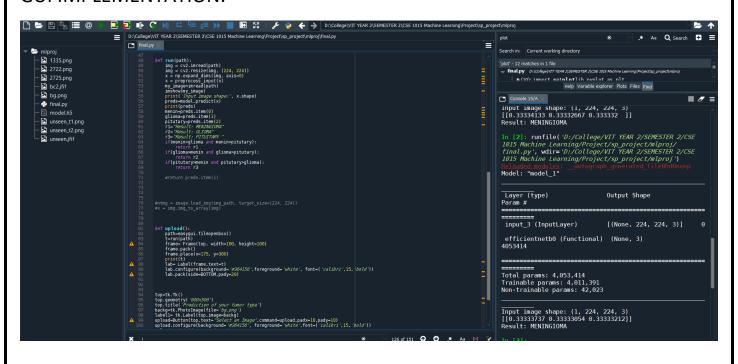
print(train_y, shape)

print(train_
```

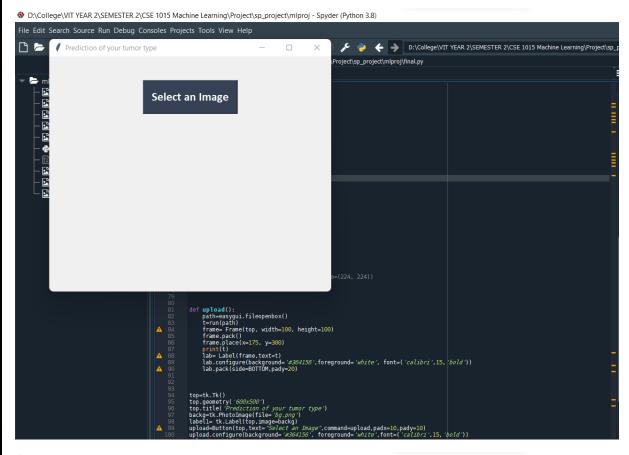
//

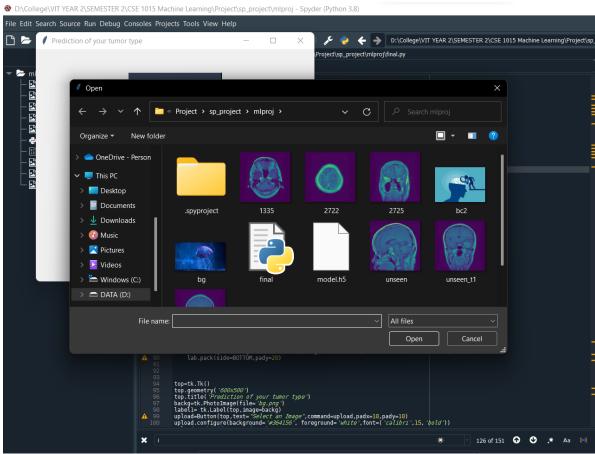


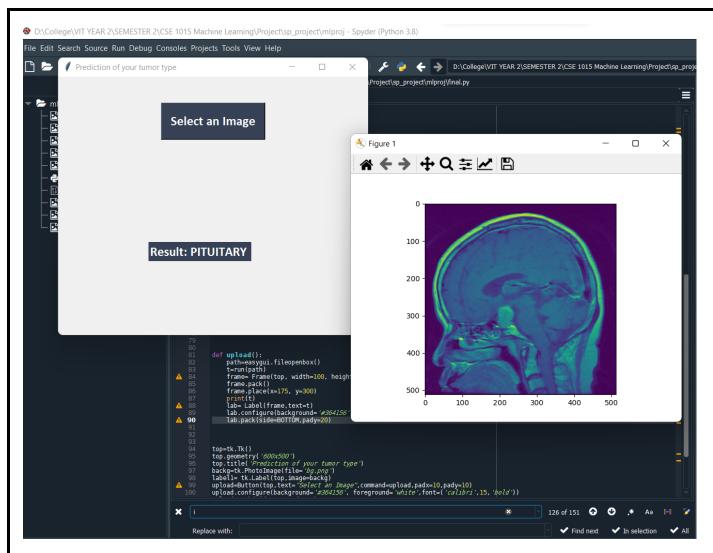
#### **GUI IMPLEMENTATION:**



#### **CHAPTER 4: RESULTS DISCUSSION, CONCLUSION AND FUTURE WORKS**







Among the three models i.e VGG16, Resnet50 and Efficient net B0, the model Efficient net B0 gives the highest accuracy then comes the Resnet50 model and then VGG16 model.

So we have implemented the weights which we got by implementing the Efficientnet B0 model in our GUI.

When a user inserted the MRI image of the Brain, the model predicts and generates the probability of the MRI image falling in the 3 different tumor classes, later based on the highest probability the model prints the type of tumor the MRI image belongs to.

Future works: For getting even more better accuracy we can implement the Efficientnet B7 Algorithm by scaling the image size and we can update the weights and further modify the GUI of the model by giving some more additional features. We can also work on a different dataset and increase the types of Brain Tumors.

REFERENCES:
Link of the Notebook:
https://colab.research.google.com/drive/1VvcXMfhhtDgO9SF8T327h8dZzfkIs6w8?usp=sharing
Link of GUI:
https://drive.google.com/drive/folders/16p3_rlEsVCTfmhA0VC6UhpjWtC56XZTB?usp=sharing
Reference Links: <a href="https://www.topbots.com/important-cnn-architectures/">https://www.topbots.com/important-cnn-architectures/</a>
https://ai.googleblog.com/2019/05/efficientnet-improving-accuracy-and.html
https://www.researchgate.net/figure/Illustrations-of-three-typical-brain-tumors-a-meningioma-b-glioma-and-c_fig1_307649824
https://dl.acm.org/doi/abs/10.1145/2222444.2222467
https://ieeexplore.ieee.org/abstract/document/8964846
https://ieeexplore.ieee.org/abstract/document/6020885