

Configuration Manual

MSc Research Project
MSc. Data Analytics

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MSc Project Submission Sheet
School of Computing



Student Name: Nehal Sawant.....

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Programme:Msc Data Analytics..... **Year:** 2021-2022...

Module:Msc Research Project.....

Lecturer:31/01/2022.....

Submission

Due Date:

Project Title: ...Brain Tumor Detection using Deep Learning Models...

Word Count: **Page Count:**8.....

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Configuration Manual

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1 Introduction

Using VGG16, InceptionV3, and ResNet as Deep Learning Tools for Brain Tumour Detection, this manual explains the setup of the research system, software specifications, hardware platforms, and processes for implementing the research project: Deep Learning for Brain Tumour Detection using VGG16, InceptionV3, and ResNet.

2 System Configuration

Programming Language and Tools	Python version 3 and Google Collaboratory, Overleaf Latex and Excel
Web Browser	Google Chrome
Email	Access to Gmail Account

Fig 1: Software Configuration

OS	Windows 10
RAM	Minimum 8GB
Hard Disk Space	Minimum 100 GB

Fig 2: Hardware Configuration

3 Working with Google Colab

The benchmark was run on a Colab system with a 100 GB hard drive, 13.52 GB of RAM, and a 47.89 GB GPU. The more layers in an algorithm, the longer it takes to operate on a wider picture. The Keras and TensorFlow libraries are used to train algorithms. Google Collaboratory Notebook uses Python. Google Drive is where the information is stored. In order to normalize, argue, crop, Numpy and Keras libraries are utilized. You will need your Gmail account to access Google Colab.

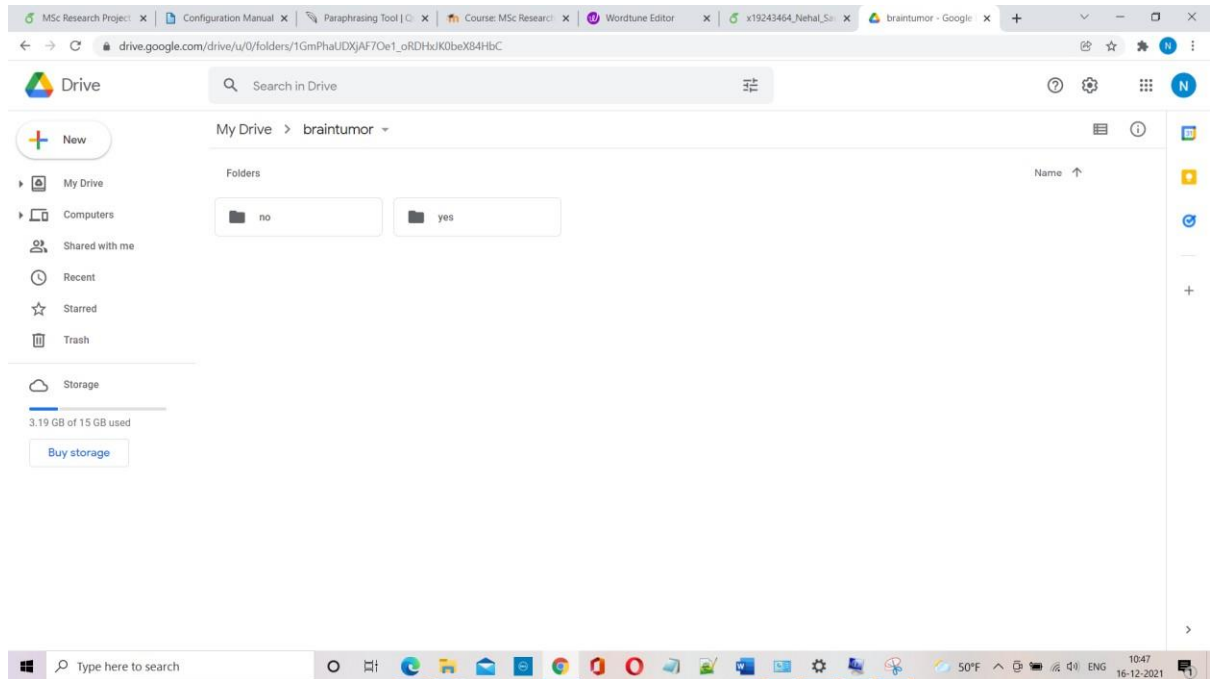
4 Project Development

4.1 Colab Environment Setup

The experiments are performed using the Google Colab environment. A valid Gmail account is required to access Google Colaboratory via Google Drive.

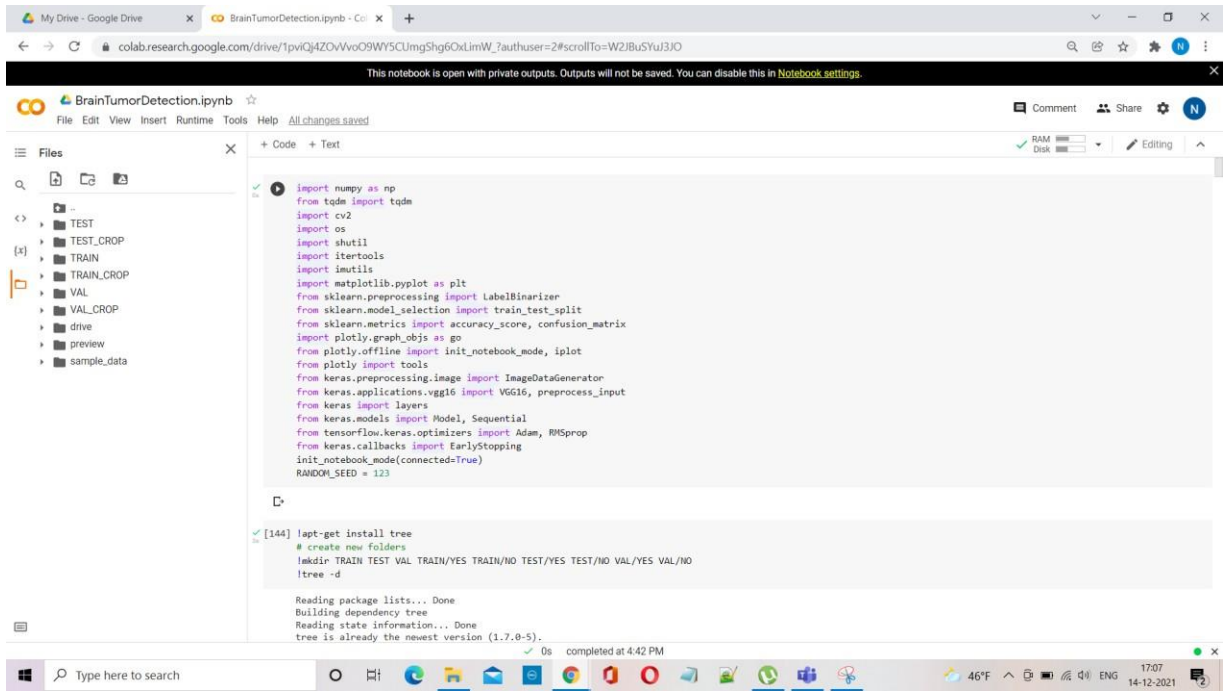
4.2 Data Handling

Step 1: Uploading data set on Google Drive

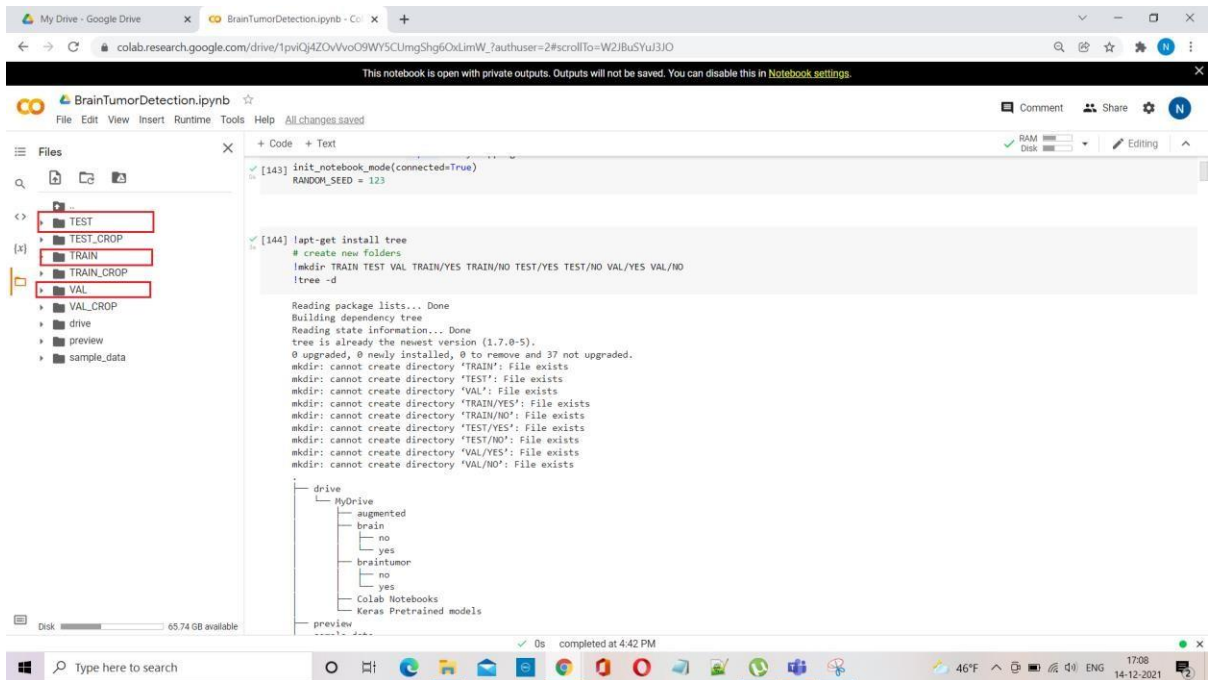


In this step, the downloaded data should be stored on Google Drive so that we can import the dataset in google colab by mounting the Google Drive.

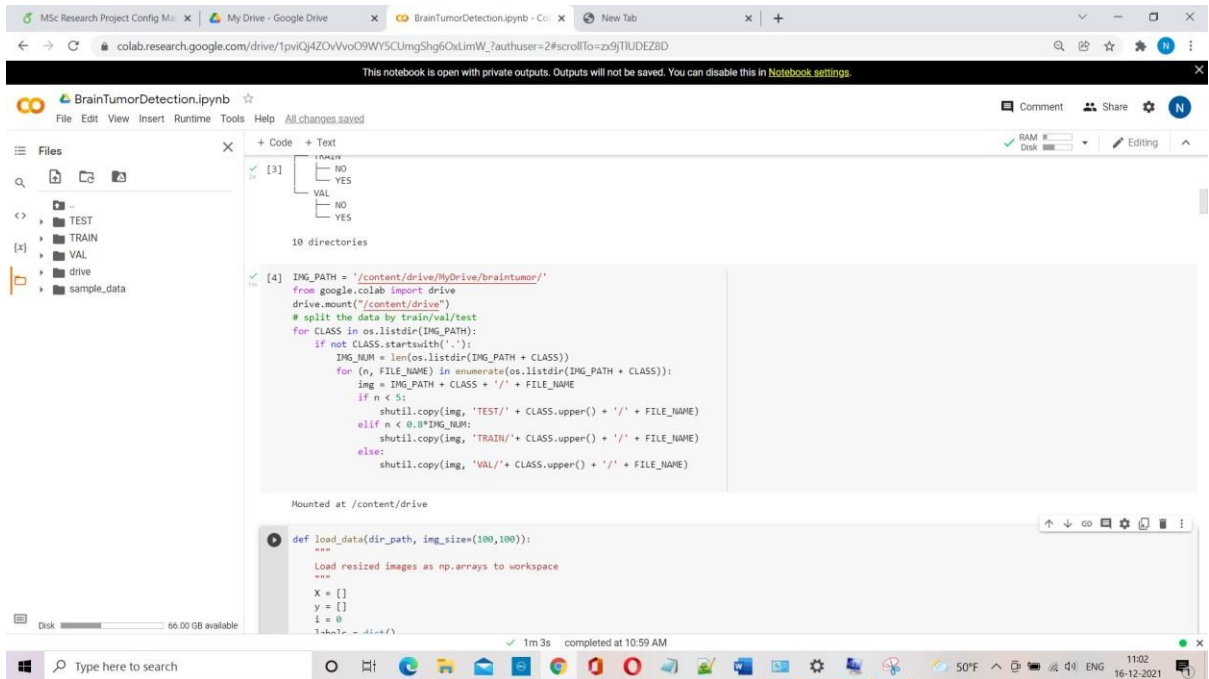
Step 2: Importing all of the necessary packages and libraries



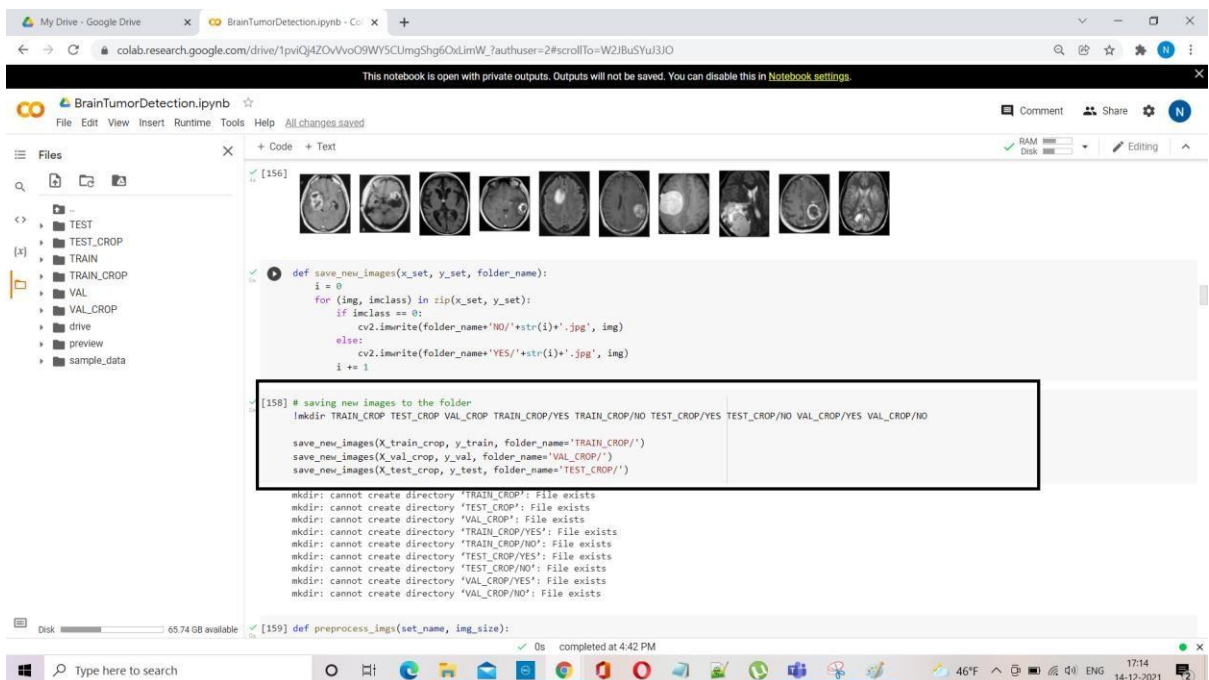
Step3: Creating 3 different directories to store data



Step 4: Mounting Google Drive



Step 5: Create Crop Folder



Step 6: Perform Augmentation on crop folders

BrainTumorDetection.ipynb

```

TRAIN_DIR = 'TRAIN_CROP/'
VAL_DIR = 'VAL_CROP/'

train_datagen = ImageDataGenerator(
    rotation_range=15,
    width_shift_range=0.1,
    height_shift_range=0.1,
    shear_range=0.1,
    brightness_range=[0.5, 1.5],
    horizontal_flip=True,
    vertical_flip=True,
    preprocessing_function=preprocess_input
)

test_datagen = ImageDataGenerator(
    preprocessing_function=preprocess_input
)

train_generator = train_datagen.flow_from_directory(
    TRAIN_DIR,
    color_mode='rgb',
    target_size=IMG_SIZE,
    batch_size=32,
    class_mode='binary',
    seed=RANDOM_SEED
)

test_generator = test_datagen.flow_from_directory(
    TEST_DIR,
    color_mode='rgb',
    target_size=IMG_SIZE,
    batch_size=16,
    class_mode='binary',
    seed=RANDOM_SEED
)

```

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Step 7: VGG16 Model

BrainTumorDetection.ipynb

```

[166] base_model = VGG16(
    weights='imagenet',
    include_top=False,
    input_shape=IMG_SIZE + (3,)
)

[167] NUM_CLASSES = 1

model1 = Sequential()
model1.add(base_model)
model1.add(layers.Flatten())
model1.add(layers.Dropout(0.5))
model1.add(layers.Dense(NUM_CLASSES, activation='sigmoid'))

model1.layers[0].trainable = False

model1.compile(
    loss='binary_crossentropy',
    optimizer=RMSprop(lr=1e-4),
    metrics=['accuracy']
)

model1.summary()

```

Model: "sequential_7"

Layer (type)	Output Shape	Param #
vgg16 (Functional)	(None, 7, 7, 512)	14714688
flatten_7 (Flatten)	(None, 25088)	0
dropout_18 (Dropout)	(None, 25088)	0
dense_16 (Dense)	(None, 1)	25089

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Model: "sequential_1"

Layer (type)	Output Shape	Param #
vgg16 (Functional)	(None, 7, 7, 512)	14714688
flatten_1 (Flatten)	(None, 25088)	0
dropout_1 (Dropout)	(None, 25088)	0
dense_1 (Dense)	(None, 1)	25089

Total params: 14,739,777
Trainable params: 25,089
Non-trainable params: 14,714,688

Step 8: InceptionV3

The screenshot shows a Google Colab notebook titled "BrainTumorDetection.ipynb". The notebook is open to a cell containing the following code:

```
[182] inception_model.add(Dense(1,activation='sigmoid'))  
[183] inception_model.summary()
```

The output of the summary function is displayed as follows:

```
Model: "sequential_9"  
Layer (type) Output Shape Param #  
-----  
inception_v3 (Functional) (None, 5, 5, 2048) 21802784  
dropout_23 (Dropout) (None, 5, 5, 2048) 0  
flatten_9 (Flatten) (None, 51200) 0  
batch_normalization_200 (Batch Normalization) (None, 51200) 204800  
dense_19 (Dense) (None, 1024) 52429824  
batch_normalization_201 (Batch Normalization) (None, 1024) 4096  
activation_196 (Activation) (None, 1024) 0  
dropout_24 (Dropout) (None, 1024) 0  
dense_20 (Dense) (None, 1024) 1049600  
batch_normalization_202 (Batch Normalization) (None, 1024) 4096  
activation_197 (Activation) (None, 1024) 0  
dropout_25 (Dropout) (None, 1024) 0  
dense_21 (Dense) (None, 1) 1025
```

The notebook interface includes a file explorer on the left showing folders like TEST, TRAIN, VAL, and sample_data. The bottom status bar indicates the notebook is completed at 4:42 PM.

My Drive - Google Drive | BrainTumorDetection.ipynb - Co | +

colab.research.google.com/drive/1pviQj4ZovVvoO9WY5CUimgShg6OxLimW_?authuser=2#scrollTo=rVzpvZ9qG3QP

This notebook is open with private outputs. Outputs will not be saved. You can disable this in [Notebook settings](#).

BrainTumorDetection.ipynb

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Files

- TEST
- TEST_CROP
- TRAIN
- TRAIN_CROP
- VAL
- VAL_CROP
- drive
- preview
- sample_data

```
[184] #OPT = tensorflow.keras.optimizers.Adam(lr=0.0001)
base_learning_rate = 0.0001
import tensorflow as tf

inception_model.compile(loss='binary_crossentropy',
                        metrics=['accuracy'],
                        optimizer=tf.keras.optimizers.Adam(learning_rate=base_learning_rate))

[185] initial_epochs = 10

[186] inception_model_history=inception_model.fit(train_generator,
                                                validation_data=test_generator,
                                                epochs = initial_epochs)

Epoch 1/10
7/7 [=====] - 59s 7s/step - loss: 0.9869 - accuracy: 0.4922 - val_loss: 17.5713 - val_accuracy: 0.5000
Epoch 2/10
7/7 [=====] - 35s 5s/step - loss: 0.6626 - accuracy: 0.6373 - val_loss: 14.0169 - val_accuracy: 0.5000
Epoch 3/10
7/7 [=====] - 35s 5s/step - loss: 0.6991 - accuracy: 0.6891 - val_loss: 8.5592 - val_accuracy: 0.5417
Epoch 4/10
7/7 [=====] - 35s 5s/step - loss: 0.6415 - accuracy: 0.6891 - val_loss: 8.0737 - val_accuracy: 0.5167
Epoch 5/10
7/7 [=====] - 36s 5s/step - loss: 0.6015 - accuracy: 0.7306 - val_loss: 4.9471 - val_accuracy: 0.5417
Epoch 6/10
7/7 [=====] - 35s 5s/step - loss: 0.6040 - accuracy: 0.7254 - val_loss: 3.7254 - val_accuracy: 0.5590
Epoch 7/10
7/7 [=====] - 35s 5s/step - loss: 0.5465 - accuracy: 0.7489 - val_loss: 2.7256 - val_accuracy: 0.5417
Epoch 8/10
7/7 [=====] - 35s 5s/step - loss: 0.5781 - accuracy: 0.7358 - val_loss: 2.7610 - val_accuracy: 0.5417
Epoch 9/10
7/7 [=====] - 35s 5s/step - loss: 0.5675 - accuracy: 0.7254 - val_loss: 3.2385 - val_accuracy: 0.5250
Epoch 10/10
7/7 [=====] - 35s 5s/step - loss: 0.5480 - accuracy: 0.7306 - val_loss: 2.7250 - val_accuracy: 0.5417
```

Saving notebook without code cell output... [Notebook settings](#)

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Step 9: ResNet50

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colab.research.google.com/drive/1pviQj4ZovVvoO9WY5CUimgShg6OxLimW_?authuser=2#scrollTo=rVzpvZ9qG3QP

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BrainTumorDetection.ipynb

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Files

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- TRAIN
- TRAIN_CROP
- VAL
- VAL_CROP
- drive
- preview
- sample_data

```
[192] from tensorflow.keras.applications.resnet50 import ResNet50

[193] base_model1 = ResNet50(input_shape=(224,224,3),
                           include_top=False,
                           weights='imagenet')

[194] base_model.trainable = False

base_model1.summary()

conv5_block2_1_conv (Conv2D) (None, 7, 7, 512) 1049088 ['conv5_block1_out[0][0]']
conv5_block2_1_bn (BatchNormal (None, 7, 7, 512) 2048 ['conv5_block2_1_conv[0][0]']
ization)
conv5_block2_1_relu (Activatio (None, 7, 7, 512) 0 ['conv5_block2_1_bn[0][0]']
n)
conv5_block2_2_conv (Conv2D) (None, 7, 7, 512) 2359088 ['conv5_block2_1_relu[0][0]']
conv5_block2_2_bn (BatchNormal (None, 7, 7, 512) 2048 ['conv5_block2_2_conv[0][0]']
ization)
conv5_block2_2_relu (Activatio (None, 7, 7, 512) 0 ['conv5_block2_2_bn[0][0]']
n)
conv5_block2_3_conv (Conv2D) (None, 7, 7, 2048) 1050624 ['conv5_block2_2_relu[0][0]']
conv5_block2_3_bn (BatchNormal (None, 7, 7, 2048) 8192 ['conv5_block2_3_conv[0][0]']
ization)
conv5_block2_add (Add) (None, 7, 7, 2048) 0 ['conv5_block1_out[0][0]',
'conv5_block2_3_bn[0][0]']
```

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colab.research.google.com/drive/1pviQJ4Z0vVvoO9WYSCLimgShg6OxLimW_?authuser=2#scrollTo=rVzPvZ9qG3QP

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BrainTumorDetection.ipynb

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RAM Disk Editing

Files

- TEST
- TEST_CROP
- TRAIN
- TRAIN_CROP
- VAL
- VAL_CROP
- drive
- preview
- sample_data

```

[194] conv5_block3_add (Add) (None, 7, 7, 2048) 0 ['conv5_block2_out[0][0]',
['conv5_block3_bn[0][0]']

conv5_block3_out (Activation) (None, 7, 7, 2048) 0 ['conv5_block3_add[0][0]']

Total params: 23,587,712
Trainable params: 23,534,592
Non-trainable params: 53,120
-----

[195] resnet_model=Sequential()
resnet_model.add(base_model1)
resnet_model.add(Dropout(0.2))
resnet_model.add(Flatten())
resnet_model.add(BatchNormalization())
resnet_model.add(Dense(1024, kernel_initializer='he_uniform'))
resnet_model.add(BatchNormalization())
resnet_model.add(Activation('relu'))
resnet_model.add(Dropout(0.2))
resnet_model.add(Dense(1024, kernel_initializer='he_uniform'))
resnet_model.add(BatchNormalization())
resnet_model.add(Activation('relu'))
resnet_model.add(Dropout(0.2))
resnet_model.add(Dense(1, activation='sigmoid'))

[196] resnet_model.summary()

Model: "sequential_10"
-----
Layer (type) Output Shape Param #
-----
resnet50 (Functional) (None, 7, 7, 2048) 23587712
dropout_26 (Dropout) (None, 7, 7, 2048) 0

```

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