



BRAIN TUMOR CLASSIFICATION USING CNN

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ABSTRACT - Brain tumor is one of the most fatal diseases that can occur to the human beings. Detecting and treating a tumor almost concedes most of the doctor's time. Tumor which could occur in a brain may lead to death without any proper medications. And it is incurable. In today's modern world science has evolved along with the technology. In normally tumor can be detected as (Benign) which has slow death rate and 50% chance of survival. And the other one is (Malignant) which has higher chance of death rate. Here we are proposing the system in which is used to classifying the Three main grades of the tumor (Pituitary, Meningioma, Gliomas) with the help of the MRI (Magnetic Resonance Imaging). Here we are using CONVOLUTION NEURAL NETWORK to classify the grades of tumor. The ground work starts from collecting datasets which contains images of the mentioned three types of tumor.

KEYWORDS: Computer vision, Data Augmentation, Convolution neural network, classifying grades of tumor.

I. INTRODUCTION

We are developing a model which is using convolution neural networks (Deep Learning). CNN contains three specified layers combined with the Artificial Neural Networks. The challenging task was to collect a perfect datasets for our model. It's because collecting a datasets especially when it comes to images, it's not a quite easy task. The datasets which are used to build this model were taken from Kaggle. Our datasets contains four specified folders namely Pituitary, Meningioma, Gliomas and No Tumor containing MRI images. TENSORFLOW2.0 were used. Jupyter notebook is used to develop and compile these CNN model. Unlike machine learning, Deep learning model works well with huge amount of data, especially when it comes to image Recognition or Detection. The more the data we feed, higher accuracy we gains. Sometimes the images which we feed our model may not be sufficient. So that we are using a technique called Data Augmentation. In this method, we used to create a copies of the original images by flipping it horizontal, adjusting a shear range, height and width range and so on. By using this we end up with the more number of images to feed our model. There is also a parameter called target_size which is used to resize the images into same format. MRI images are a Greyscale images. So the pixel color will either be white or black. And then we comes into convolution part. While working with the images, convolution takes big part of it. The whole step of convolution is making an image smaller and faster. It's because images would have high size of length and width, so it is not an easy job to compute these high pixel value images even if we use GPU or TPU it would take lot more time to compute. In order to avoid these we are using convolution (CONV2D) layer. In convolution we feed an image with resized shape and there (FEATURE DETECTOR) alias Filters are used to smaller the image size and reserve its pixel values into a newly created (Feature map). Filters are defined by adjusting parameters. If we defined the filter values by 32. Each filter will focus on certain features from the input image And the resulted feature map will be in the stack form. After, the feature map (image) goes into the next layer which is called as (MaxPooling2D). Maxpooling layer is used to take the maximum pixel value in the feature map and form a Pooled Feature. It prevents the model from not to get stuck with overfitting. Pool size and strides parameters are tuned. Flatten layer is to align the output from the Maxpooling layer into a single column. So that it can be inputted into a Dense layer and in activation.

II-LITERATURE SURVEY:-

SI NO:	AUTHOR	YEAR	METHOD	ADVANTAGE	ACCURACY %	SENSITIVITY
1	V.ANITHA S.MURUGAVALI	2016	Preprocessing by non-local mean filter segmentation by k means algorithm, categorization-2 tier feature extraction by	Superior to SVM based classification. Computation time almost half. Real time application possible	84%	100

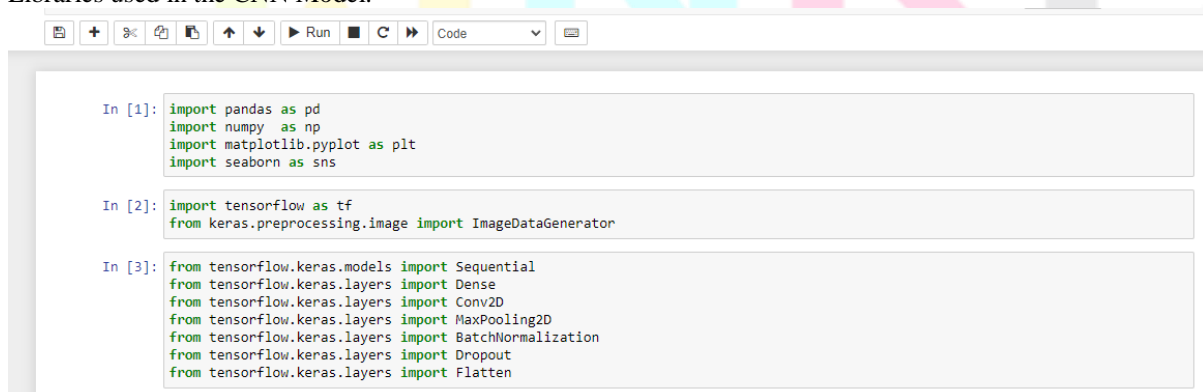
			DWT, filtering the basis of KNN.			
2	MUNDENDRA SINGH,ASHISH VERMA, NEERAJ SHARMA	2018	The optimum enrichment of MRI data through MSSR-MOALAO based hybridized algorithm.	Very good image clarity	76.1	Undefined
3	CHAO MA,GONGNING LUO ,KUANQUAN WANG	2018	Based on feature scheme learning, segmentation is made and it is then formulated as hybrid problem of voxel classification and boundary contour evaluation of tissue. Afterward both models are fused employing ccRFs to create highly precise soft segmentation mapping.	Good overall result on all major parameters such as accuracy sensitivity etc.	Up to 89%	Up to 85%
4	LAMIA SALLEMI ,INES NJEH ,AND STEPHANE LEHERICY	2015	Convivial algorithm for glioblastoma modelization. tumor region is extracted using fast distribution matching based global pixel wise data.	Very fast computation speed. Less than 0.5 sec/image.	----	-----

III- PROPOSED METHOD

In this project, we have described our objective in two parts, the first half deals with detection of brain tumour that is the presence of the tumor in the provided MRI. The second part here describes the grade of the tumour and also states the estimated treatment period and the estimated cost. Here, we will analyse the MRI images which will conclude the Grade of the tumor as (Pituitary, Meningioma, Gliomas). In general the diagram for our process. The input images will undergo various stages

1. MRI images
2. Pre-processing
3. Building a CNN model
4. Compiling a Model
5. Accuracy Metrics

Libraries used in the CNN Model:



```

In [1]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

In [2]: import tensorflow as tf
from keras.preprocessing.image import ImageDataGenerator

In [3]: from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Dense
from tensorflow.keras.layers import Conv2D
from tensorflow.keras.layers import MaxPooling2D
from tensorflow.keras.layers import BatchNormalization
from tensorflow.keras.layers import Dropout
from tensorflow.keras.layers import Flatten
  
```

Figure 1: Libraries used in the CNN Model

1. MRI IMAGES:

This is the first step of our proposed model. In this the data is been provided with the MRI (Magnetic Resonance Imaging) that has been collected from the open source Kaggle. The images are in Greyscale Format. Here the Greyscale Images are inputted into the system. There will be four different types of folders containing MRI images [No_tumor, pituitary, meningioma, gliomas].

2. PRE-PROCESSING

2.1 Data Augmentation:

Data augmentation is a technique which is used to increase the amount of data by slightly modified copies of already existed data or newly created synthetic data from existing data. It acts as regularize and helps to avoid overfitting when training a machine learning model.

For this model, we used data augmentation on the images to create a more copies of it just to feed to our model. So that it can be precise at finding patterns and wont stuck with overfitting.

CODE:

```
from keras.preprocessing.image import ImageDataGenerator
```

3. BUILDING A CNN MODEL:

STEP1: Convolution

The whole step of convolution is to making an image smaller and faster in order to compute. Convolution done on the input image in order to transform a original function into form to obtain more information. Convolution layer performs various operations on input images such as enhance, edge, sharpen and emboss. These operations are performed by filters which we used to extract the useful features from it. We do convolutions

A convolution is nothing but a element wise matrix multiplication. Where one of the matrices is the image, and the other is the filter or kernel that turns the image into new form. The output of this convolution is called as feature map. Filters are defined in the CNN. The filter which ends up with the higher information gain will be learned by our model during training. CNN filters would perform better on images than the human designed filters

Conv2D:

```
from tensorflow.keras.layers import Conv2D
Conv2D (filters=32, kernel_size=3, input_shape=[64,64,2],activation='relu')
```

STEP 2:Maxpooling2D:

In this layer we formally use Matrix (Pool_size) to obtain the maximum values from the resulted feature map from the convolution layer. We can set the strides to move along the feature map. By doing this we just end up with smaller minimized matrix, so that our model won't stuck with overfitting.

```
from tensorflow.keras.layers import MaxPooling2D
MaxPooling2D(Pool_size=2,strides=2))
```

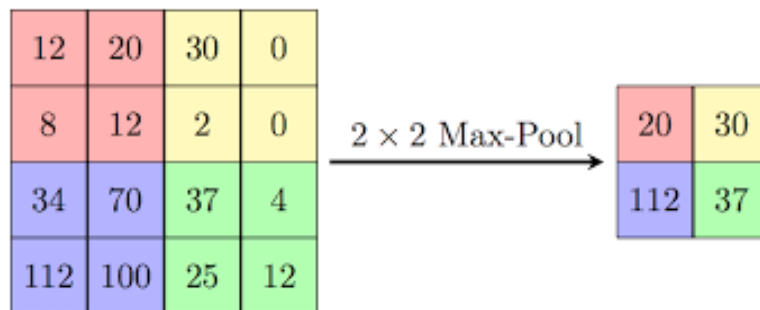


Figure 2: Maxpooling2D

STEP3:Flattening:

After convolution and pooling process, we end up with Pooled feature map. In flatten layer is used to transform a resulted matrix(Pooled Feature) into a single column, in order to pass it as input to the next fully connected layer (ANN).

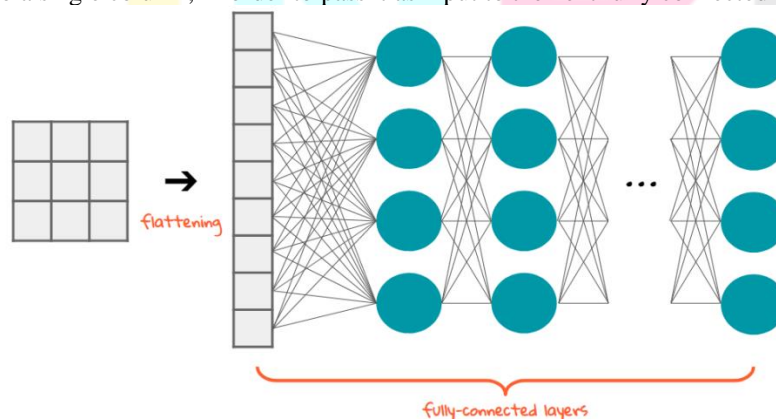


Figure 3: Flattening

4. COMPILING THE CNN:

Here, we are going to compile the model to get trained by the MRI Images containing in four different folders. An optimizer is used to optimize the model. There are different types of optimizers that are used in CNN model. Adam optimizer is used to optimize the model. SGD looks for global minimum rather than the local minimum. As we are developing a multi-class classification model, Categorical_crossentropy is used as a loss function for the model. On the contrary, Binary_crossentropy is used as loss function for binary conditions.

```

In [8]: model = Sequential()

In [9]: model.add(Conv2D(filters=32, kernel_size=3, activation='relu', input_shape=[64,64,3]))
model.add(MaxPooling2D(pool_size=2, strides=2))

In [ ]: model.add(Conv2D(filters=32, kernel_size=3, activation='relu'))
model.add(MaxPooling2D(pool_size=2, strides=2))

In [10]: model.add(Flatten())

Fully Connected Neural Network

In [13]: model.add(Dense(units=64,activation='relu'))
model.add(Dense(num_classes,activation='softmax'))

In [14]: model.compile(optimizer='adam', loss='categorical_crossentropy', metrics=['Accuracy'])

```

Figure 4: Compiling the CNN

5. ACCURACY METRICS:

```

In [70]: history = model.fit(training_set,
steps_per_epoch= training_set.n//training_set.batch_size,
epochs=5,
validation_data=testing_set)

Epoch 1/5
268/268 [=====] - 74s 273ms/step - loss: 0.6950 - Accuracy: 0.7234 - val_loss: 0.8839 - val_Accuracy:
0.7777
Epoch 2/5
268/268 [=====] - 75s 278ms/step - loss: 0.3083 - Accuracy: 0.8916 - val_loss: 0.6587 - val_Accuracy:
0.8516
Epoch 3/5
268/268 [=====] - 74s 276ms/step - loss: 0.1810 - Accuracy: 0.9395 - val_loss: 0.8620 - val_Accuracy:
0.8657
Epoch 4/5
268/268 [=====] - 79s 294ms/step - loss: 0.1133 - Accuracy: 0.9627 - val_loss: 0.9330 - val_Accuracy:
0.8839
Epoch 5/5
268/268 [=====] - 75s 278ms/step - loss: 0.0702 - Accuracy: 0.9801 - val_loss: 0.9340 - val_Accuracy:
0.8933

```

Figure 5: Accuracy Metrics

Prediction:

After we fit the model with the training data and validation data, now it time to make prediction with the new unseen MRI Images.

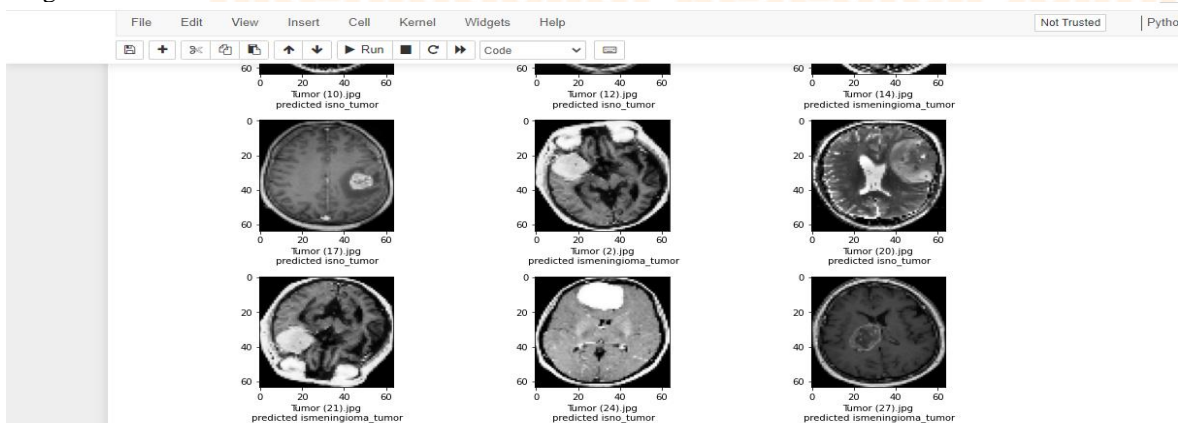


Figure 6: stages of the tumor

Here stages of the tumor is predicted.

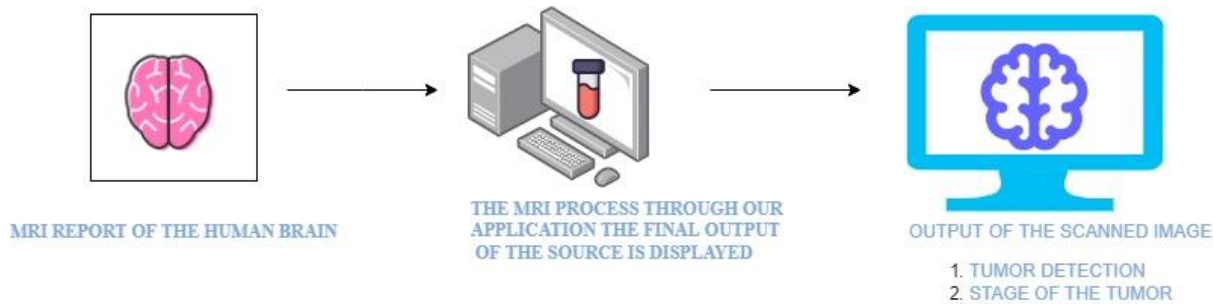


Figure 7: Data Flow of System

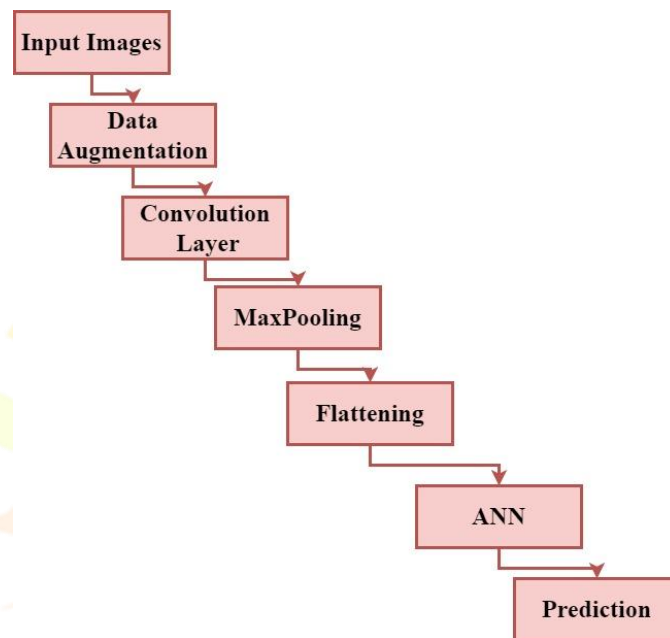


Figure 8: Flowchart of the System

V- MAIN THREE STAGES:

- **PITUITARY TUMOR** (95% survival rates depends upon the individual)
- **MENINGIOMA TUMOR** (60% survival rates depends upon the individual)
- **GLIOMA TUMOR** (22% survival rates depends upon the individual)

VI- CONCLUSION

Nowadays the artificial intelligence is a revolutionary thing it plays a vital role for treating and detecting various diseases. By using this system, along with the human expertise it will be easier to identify the tumor for treating the patient. Tensorflow2.0 library is used to develop the model .We are using Data Augmentation order to obtain a higher accuracy while testing MRI (Magnetic Resonance Imaging) images. In this proposed paper we are using the CNN model to predict the grade of tumor and also state the estimated treatment period and also the estimated cost. By using this waiting period and also the errors made can be overcome. We notched up with 90% accuracy on testing a MRI images. Finally the MRI image is processed and the (tumor detection/ grade of the tumor) is detected.

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