#### NeuroScan - Detecting Brain Tumors with CNNpowered MRI Analysis



#### **About the Dataset:**

The dataset consists of 253 files containing Brain MRI (Magnetic Resonance Imaging) scans. MRI is a non-invasive medical imaging technique that provides detailed images of the brain's internal structures. These images are captured using strong magnetic fields and radio waves, allowing for the visualization of various tissues within the brain.

The dataset is labeled with two distinct classes:

- **No Tumor:** This class represents brain MRI scans from individuals who do not have any detectable brain tumors. These scans serve as the baseline for comparison against scans with tumors.
- **Tumor:** This class includes brain MRI scans from individuals who have been diagnosed with brain tumors. Tumors in the brain can vary in size, location, and type, which makes their accurate detection and classification a challenging task.

Each MRI scan file in the dataset likely contains a 3D array of pixel intensity values that represent different tissue types and structures within the brain. These arrays can be used as input data for various machine learning algorithms, such as Convolutional Neural Networks (CNNs), to learn patterns associated with the presence or absence of brain tumors.

#### **Objective:**

The primary objective of this project is to develop a machine learning model, specifically a Convolutional Neural Network (CNN) using the Keras framework, to accurately detect the presence of brain tumors in MRI scans. The CNN architecture is chosen due to its effectiveness in processing image data and capturing intricate patterns. The successful implementation of this project can contribute to medical diagnosis and treatment planning for patients with brain tumors.

## Importing Essential Libraries and Tools

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt

import tensorflow as tf
from tensorflow import keras
from tensorflow.keras import layers
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Conv2D, MaxPooling2D, Dense, Flatten
from tensorflow.keras.metrics import BinaryAccuracy, Precision, Recall
import warnings
warnings.filterwarnings("ignore")
tf.keras.backend.clear_session()
```

#### **Loading the Data**

We load the data by making use of the tool image\_dataset\_from directory. It helps us fetch the data from the relevant directory, automatically does labeling, shuffles the data, batches the data (in this case as 32) and resizes images into 256 by 256.

```
In [316]: data = keras.utils.image_dataset_from_directory("../input/brain-mri-images-for-brain-
Found 253 files belonging to 2 classes.
```

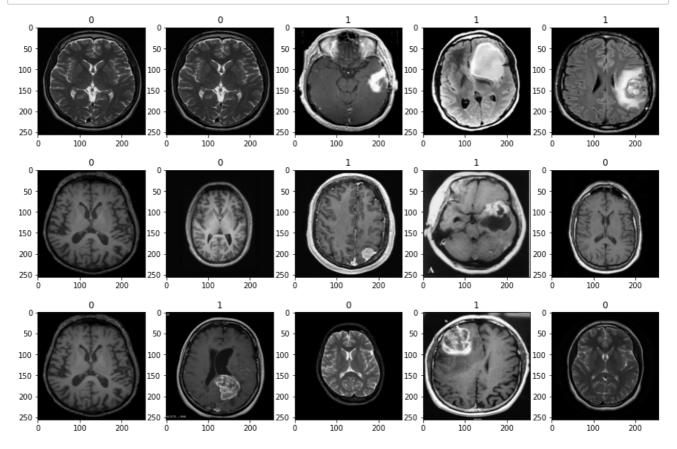
## Plotting a few Example Images

If a brain has tumor it is labeled as 1, if no it is labeled as 0.

```
In [317]: batch = data.as_numpy_iterator().next()

Cleanup called...
```

```
In [318]: fig, ax = plt.subplots(3, 5, figsize=(15,10))
    ax = ax.flatten()
    for idx, img in enumerate(batch[0][:15]):
        ax[idx].imshow(img.astype(int))
        ax[idx].title.set_text(batch[1][idx])
```



## **Data Scaling**

Maximum value of the scaled data: 1.0

Since our data consists of images and images consist of pixels, we divide all the pixel values by 255—each pixel can have a value in [0, 255]— so that all the pixel values are on the same scale i.e. [0, 1].

#### **Train-Validation-Test Split**

```
In [322]: print("There are", len(data), "batches in our data")
```

There are 8 batches in our data

Now, we have to divide the whole data into 3 separate sets: Train set for training the model, Validation set for adjusting the hyperparameters of our model and Test set for evaluating our model on the set that our model has not seen before. As it can be seen, we have 8 batches in our data. I preferred allocating 4 batches for Train set, 2 batches for Validation set and 2 batches for Test set.

```
In [323]: train_size = int(len(data)*0.6)
    val_size = int(len(data)*0.2)+1
    test_size = int(len(data)*0.2)+1

In [324]: print("Train Size:", train_size)
    print("Validation Size:", val_size)
    print("Test Size:", test_size)

    print("Sum of Train, Validation and Test sizes is equal to:", train_size + val_size +

    Train Size: 4
    Validation Size: 2
    Test Size: 2
    Sum of Train, Validation and Test sizes is equal to: 8

In [325]: train = data.take(train_size)
    val = data.skip(train_size).take(val_size)
    test = data.skip(train_size + val_size).take(test_size)
```

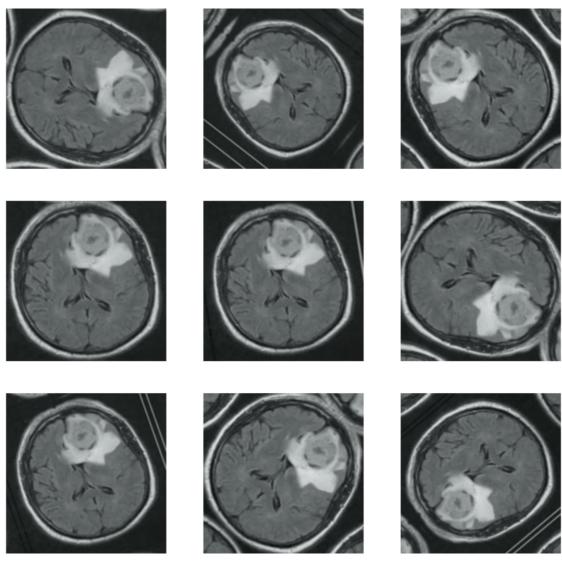
## **Data Augmentation**

Because our Train set has relatively small number of images, we can apply data augmentation which is reproducing the images by applying some changes such as random rotating, random flipping, random zoom and random contrast. This may possibly increase the accuracy score of the model. Since we will be applying the data augmentation in the beginning of the neural network architecture, we should pass the input shape.

Note: Data augmentation will be inactive when testing the data. Input images will be augmented during calls to model.fit (not model.evaluate or model.predict). If you want to learn more about data augmentation in Tensorflow, you can check the official documentation.

```
In [326]: batch = data.as_numpy_iterator().next()

Cleanup called...
```



**Building Deep Learning Model** 

In [329]: model.compile(optimizer="adam", loss=keras.losses.BinaryCrossentropy(), metrics=["acc

#### In [330]: model.summary()

Model: "sequential\_1"

Layer (type)	Output Shape	Param #
sequential (Sequential)	(None, 256, 256, 3)	0
conv2d (Conv2D)	(None, 256, 256, 16)	448
conv2d_1 (Conv2D)	(None, 256, 256, 16)	2320
max_pooling2d (MaxPooling2D)	(None, 128, 128, 16)	0
conv2d_2 (Conv2D)	(None, 128, 128, 32)	12832
conv2d_3 (Conv2D)	(None, 128, 128, 32)	25632
max_pooling2d_1 (MaxPooling2	(None, 64, 64, 32)	0
conv2d_4 (Conv2D)	(None, 64, 64, 16)	4624
conv2d_5 (Conv2D)	(None, 64, 64, 16)	2320
max_pooling2d_2 (MaxPooling2	(None, 32, 32, 16)	0
flatten (Flatten)	(None, 16384)	0
dense (Dense)	(None, 128)	2097280
	(None, 1)	129

Total params: 2,145,585 Trainable params: 2,145,585 Non-trainable params: 0

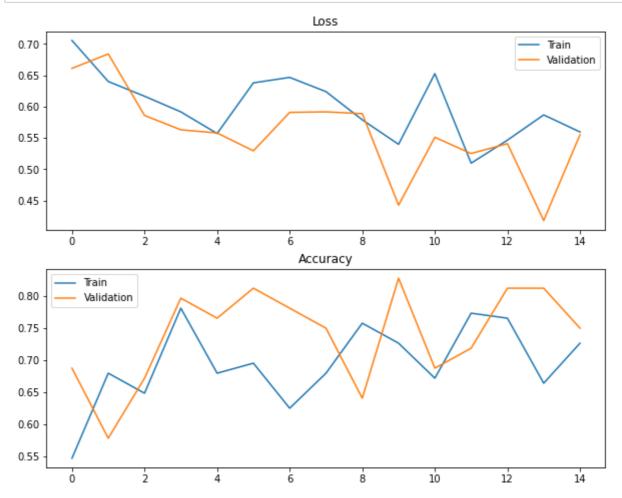
```
In [331]: history = model.fit(train, epochs=15, validation_data=val)
        Epoch 1/15
        Cleanup called...
        Cleanup called...
```

# **Plotting the Performance**

```
In [332]: fig, ax = plt.subplots(2, 1, figsize=(10,8))

ax[0].plot(history.history["loss"], label="Train")
ax[0].plot(history.history["val_loss"], label="Validation")
ax[0].title.set_text("Loss")
ax[0].legend()

ax[1].plot(history.history["accuracy"], label="Train")
ax[1].plot(history.history["val_accuracy"], label="Validation")
ax[1].title.set_text("Accuracy")
ax[1].legend()
```



#### **Results**

```
In [333]:
          bin acc = BinaryAccuracy()
          recall = Recall()
          precision = Precision()
          for batch in test.as_numpy_iterator():
              X, y = batch
              yhat = model.predict(X)
              bin_acc.update_state(y, yhat)
              recall.update_state(y, yhat)
              precision.update_state(y, yhat)
          print("Accuracy:", bin_acc.result().numpy(), "\nRecall:", recall.result().numpy(),
          Cleanup called...
          Accuracy: 0.78394395
          Recall: 0.75757575
          Precision: 0.8333333
```

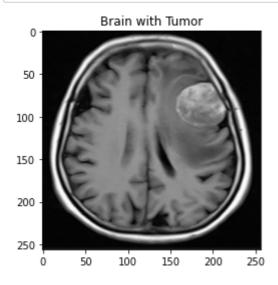
## **Manual Testing**

We have already evaluated our model using various metrics and visualizations but it is always a good practice to test the model by hand to make sure everything is working well. In the code below, I randomly chose an image and plotted it with its true label on title so let's see if our model is going to classify this example correctly.

```
In [334]: batch = test.as_numpy_iterator().next()

Cleanup called...
```

```
In [335]: img, label = batch[0][15], batch[1][15]
    plt.imshow(img)
    if label==1:
        plt.title("Brain with Tumor")
    else:
        plt.title("Brain with No Tumor")
    plt.show()
```



```
In [336]: y_hat = model.predict(np.expand_dims(img, 0))
```

We are able to see the probability of this brain's having tumor below. I opted to determine the classification threshold as 0.5. Meaning that, if it is below 0.5 this will be classified as Brain Having No Tumor otherwise it is going to be classified as Brain Having Tumor.

Tumor detected

Here we can see that our model predicted its class correctly.