```
In [58]: # Importing the necessary Libraries
         import numpy as np
         import pandas as pdi
         import matplotlib.pyplot as plt
         import seaborn as sns
         import tensorflow as tf
         import cv2
         import os
         import sklearn
         from tensorflow.keras.preprocessing.image import load_img
         from PIL import Image
         from keras.preprocessing import image
         from tqdm import tqdm
         from sklearn.utils import shuffle
         from sklearn.preprocessing import LabelEncoder
         from sklearn.metrics import classification report, confusion matrix
         from tensorflow.keras.callbacks import EarlyStopping, ModelCheckpoint, TensorBoard, Re
         from tensorflow.keras import models, layers
         from tensorflow.keras.applications import EfficientNetB0
         from sklearn.model_selection import train_test_split
```

Dataset: We managed to find a dataset on Kaggle which already divided the tumor images into four different categories, which are glioma tumor, meningioma tumor, pituitary tumor, and no tumor. Further, the images are already split in to Training and Testing Folders.

Dataset Link: https://www.kaggle.com/datasets/sartajbhuvaji/brain-tumor-classification-mri

The first part of this project involves detecting the presence or absence of brain tumors if a tumor is present classify the tumor into one of the three categories mentioned above.

- Meningioma is the most common type of brain tumor. Most Meningiomas are classified as benign tumors meaning it is a mass of cells that grows slowly and remains localized (does not spread to other parts of the brain.)
- Gliomas are also common in adults and be either benign or malignant with malignant
 meaning that it is a mass of cells that grows uncontrollably and has the ability to spread to
 other nearby tissues in the brain. The further classification of gliomas depend on the
 specific types of glioma and it's aggressiveness which can range from Grade I IV (grade IV
 being the most aggressive).
- Pituitary Tumors is the least common among the three and are typically classified as benign.

1. Loading the Dataset

```
In [2]: # Loading the Training Dataset directory

# Define the path
train_dir = './Dataset/Training/'

# Creating a dictionary to associate the name of each class (tumor type - key) with th
```

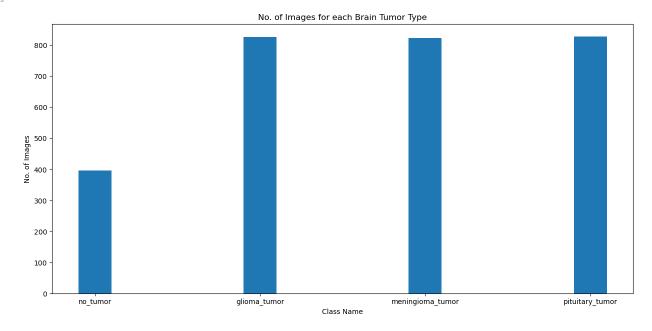
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2. Data Exploration (Exploratory Analysis)

```
In [4]: # Creating a class frequency bar-plot

plt.subplots(figsize=(15, 7))
plt.bar(number_classes.keys(), number_classes.values(), width = .2)
plt.xlabel('Class Name')
plt.ylabel('No. of Images')
plt.title('No. of Images for each Brain Tumor Type')
```

Out[4]: Text(0.5, 1.0, 'No. of Images for each Brain Tumor Type')



```
In [5]: # Loading the images...

def get_images(base_dir, path, extension = ".jpg"):
    return [ fn for fn in os.listdir(f'{base_dir}{path}') if fn.endswith(extension)]

no_tumor_images = get_images(train_dir, "no_tumor")
glioma_images = get_images(train_dir, "glioma_tumor")
meningioma_images = get_images(train_dir, "meningioma_tumor")
pituitary_images = get_images(train_dir, "pituitary_tumor")
```

```
In [7]: #glioma_images
In [8]: # Randomly selecting 5 images from each class

def select_random_image(image):
```

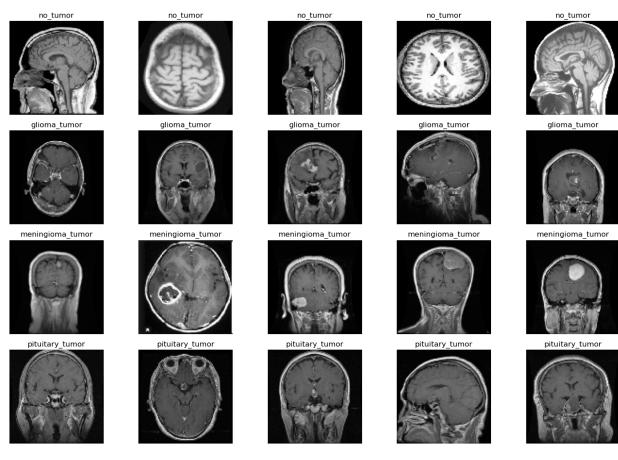
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plt.tight_layout()

plt.show()

```
return np.random.choice(image, 5, replace = False)
         select_no_tumor = select_random_image(no_tumor_images)
         select_glioma = select_random_image(glioma_images)
         select_meningioma = select_random_image(meningioma_images)
         select_pituitary = select_random_image(pituitary_images)
In [9]: select_no_tumor
         array(['image(160).jpg', 'image(124).jpg', 'image(207).jpg',
Out[9]:
                'image(143).jpg', 'image(200).jpg'], dtype='<U14')
In [10]: # Plotting a matrix of images selected
         # Function to plot images
         def plot_images(image_array, class_name, start_index, rows, cols):
             for i in range(len(image_array)):
                 fp = f'{train_dir}{class_name}/{image_array[i]}'
                 ax = fig.add_subplot(rows, cols, start_index + i)
                 fn = load_img(fp, target_size=(100, 100), color_mode='grayscale')
                 plt.imshow(fn, cmap="Greys_r")
                 plt.title(class_name)
                 plt.axis('off')
         # Create a figure
         fig = plt.figure(figsize=(15, 10))
         # Plotting no tumor images
         plot_images(select_no_tumor, "no_tumor", 1, 4, 5)
         # Plotting glioma images
         plot_images(select_glioma, "glioma_tumor", 6, 4, 5)
         # Plotting meningioma images
         plot_images(select_meningioma, "meningioma_tumor", 11, 4, 5)
         # Plotting pituitary images
         plot_images(select_pituitary, "pituitary_tumor", 16, 4, 5)
```

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Flattening the images into a 1D vector and creating a 2D array of the entire images, In [11]: # array representing an image. def img2mat(path, filename, size=(64,64)): for fn in filename: fp = path + fncurrent_image = image.load_img(fp, target_size = size, color_mode = 'grayscale') # Convert the image into a matrix img_vector = image.img_to_array(current_image) # Turn current_image into a vector img_vector = [img_vector.ravel()] try: # Concatenate different images full_mat = np.concatenate((full_mat, img_vector)) # If full matrix is not defined during the first ireration, create one. full_mat = img_vector return full_mat # Run the function on our folders no_tumor_images = img2mat(f'{train_dir}no_tumor/', no_tumor_images) glioma_images = img2mat(f'{train_dir}glioma_tumor/', glioma_images) meningioma_images = img2mat(f'{train_dir}meningioma_tumor/', meningioma_images) pituitary_images = img2mat(f'{train_dir}pituitary_tumor/', pituitary_images)

```
def mean_of_images(full_mat, title, size = (64, 64)):
    # Calculate the average
```

In [12]: # Creating a function that will take the average for each category.

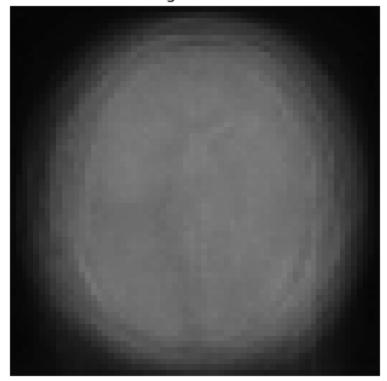
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```
avg_image = np.mean(full_mat, axis = 0)
# Reshape it back into a matrix
avg_image = avg_image.reshape(size)
plt.imshow(avg_image, vmin=0, vmax=255, cmap='Greys_r')
plt.title(f'Average {title}')
plt.axis('off')
plt.show()
return avg_image

# Running the function on our 4 matrices

no_tumor_mean = mean_of_images(no_tumor_images, 'No Tumor')
glioma_mean = mean_of_images(glioma_images, 'Glioma Tumor')
meningioma_mean = mean_of_images(meningioma_images, 'Meningioma Tumor')
pituitary_mean = mean_of_images(pituitary_images, 'Pituitary Tumor')
```

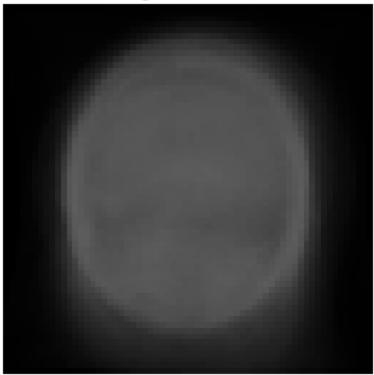
Average No Tumor



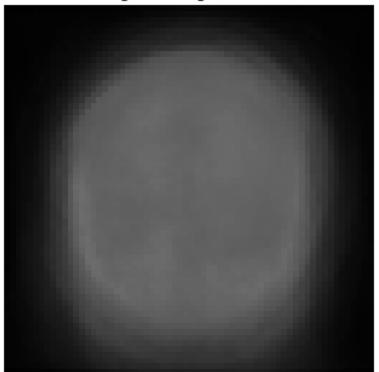
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2/29/24, 10:55 PM Brain-Tumor-Detection

Average Glioma Tumor

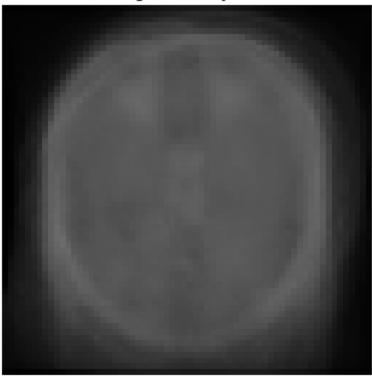


Average Meningioma Tumor



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Average Pituitary Tumor



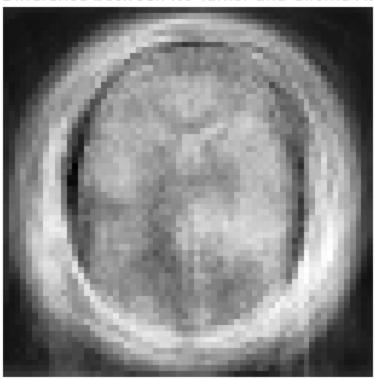
This is essentially the average image for each of the 4 categories in the dataset. Now, I will compare the average of no_tumor images with each of the other three categories and plot an image for the same... this helps visualize and analyze the typical characteristics of each tumor type.

```
In [13]: # 1. Glioma Tumor VS No Tumor
    difference_mean = no_tumor_mean - glioma_mean
    plt.imshow(difference_mean, cmap='Greys_r')
    plt.title(f'Mean Difference between No Tumor and Glioma Average')
    plt.axis('off')
    plt.show()
```

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2/29/24, 10:55 PM Brain-Tumor-Detection

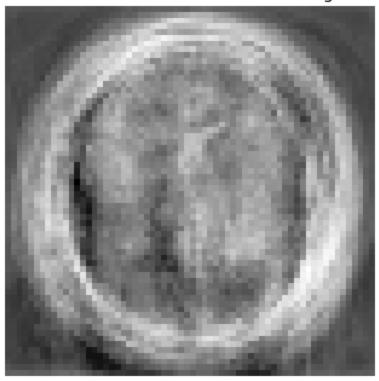
Mean Difference between No Tumor and Glioma Average



```
In [14]: # 2. Meningioma Tumor VS No Tumor

difference_mean = no_tumor_mean - meningioma_mean
plt.imshow(difference_mean, cmap='Greys_r')
plt.title(f'Mean Difference between No Tumor and Meningioma Average')
plt.axis('off')
plt.show()
```

Mean Difference between No Tumor and Meningioma Average

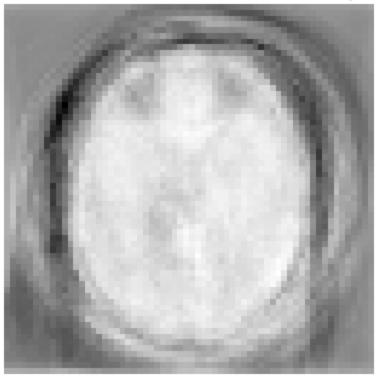


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```
In [15]: # 3. Pituitary Tumor vs No Tumor

difference_mean = no_tumor_mean - pituitary_mean
   plt.imshow(difference_mean, cmap='Greys_r')
   plt.title(f'Mean Difference between No Tumor and Pituitary Average')
   plt.axis('off')
   plt.show()
```

Mean Difference between No Tumor and Pituitary Average



3. Data Preparation

```
In [33]: # Train and Test Sets : I have created a function here which will generate the training
         def train_test_set(size, labels):
             X_train, X_test, y_train, y_test = [], [], [], []
             # Training Set
             for label in labels:
                 fp = os.path.join('./Dataset/', 'Training/', label)
                 # To display the progress
                 for unique in tqdm(os.listdir(fp)):
                     # Read the images
                     image = cv2.imread(os.path.join(fp, unique))
                     # Set the image size the the defined size...
                     image = cv2.resize(image, (size, size))
                     # Append the image to the X_train set
                     X_train.append(image)
                     # Append the corresponding label to the y_train set
                     y_train.append(label)
               # Testing Set
             for label in labels:
```

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```
fp = os.path.join('./Dataset/', 'Testing/', label)
# To display the progress
for unique in tqdm(os.listdir(fp)):
    # Read the images
    image = cv2.imread(os.path.join(fp, unique))
    # Set the image size the the defined size...
    image = cv2.resize(image, (size, size))
    # Append the image to the X_test set
    X_train.append(image)
    # Append the corresponding label to the y_test set
    y_train.append(label)
return X_train, y_train
```

```
In [34]: # Train and Test Sets : created a function here which will generate the training and t
         def train test set 2(size, labels):
             X_train, X_test, y_train, y_test = [], [], [], []
             # Training Set
             for label in labels:
                 fp = os.path.join('./Dataset/', 'Training/', label)
                 # To display the progress
                 for unique in tqdm(os.listdir(fp)):
                     # Read the images
                     image = cv2.imread(os.path.join(fp, unique))
                     # Set the image size the the defined size...
                     image = cv2.resize(image, (size, size))
                     # Append the image to the X_train set
                     X_train.append(image)
                     # Append the corresponding label to the y_train set
                     y_train.append(label)
               # Testing Set
             for label in labels:
                 fp = os.path.join('./Dataset/', 'Testing/', label)
                 # To display the progress
                 for unique in tqdm(os.listdir(fp)):
                     # Read the images
                     image = cv2.imread(os.path.join(fp, unique))
                     # Set the image size the the defined size...
                     image = cv2.resize(image, (size, size))
                     # Append the image to the X_test set
                     X_test.append(image)
                     # Append the corresponding label to the y test set
                     y_test.append(label)
             return X_train, X_test, y_train, y_test
```

```
In [35]: # Image folder labels
labels = ['glioma_tumor', 'meningioma_tumor', 'no_tumor', 'pituitary_tumor']
# Calling the function..
X_train, y_train = train_test_set(150, labels)
```

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```
100%
                          826/826 [00:01<00:00, 500.19it/s]
                          822/822 [00:01<00:00, 518.72it/s]
         100%
                          395/395 [00:00<00:00, 707.15it/s]
         100%
         100%
                          827/827 [00:02<00:00, 411.47it/s]
         100%
                          100/100 [00:00<00:00, 647.60it/s]
         100%
                          115/115 [00:00<00:00, 802.41it/s]
         100%
                          105/105 [00:00<00:00, 1521.93it/s]
         100%
                          74/74 [00:00<00:00, 252.67it/s]
        # Two Sets
In [36]:
         X2_train, X2_test, y2_train, y2_test = train_test_set_2(150, labels)
         100%
                          826/826 [00:01<00:00, 463.68it/s]
         100%
                          822/822 [00:01<00:00, 513.36it/s]
                          395/395 [00:00<00:00, 653.04it/s]
         100%
                          827/827 [00:01<00:00, 433.34it/s]
         100%
         100%
                          100/100 [00:00<00:00, 636.04it/s]
                          115/115 [00:00<00:00, 794.98it/s]
         100%
         100%
                          105/105 [00:00<00:00, 1707.94it/s]
         100%
                          74/74 [00:00<00:00, 212.61it/s]
        # Converting into numpy arrays
In [37]:
         X_train = np.array(X_train)
         y_train = np.array(y_train)
         X2_train = np.array(X2_train)
         y2_train = np.array(y2_train)
         X2_test = np.array(X2_test)
         y2_test = np.array(y2_test)
        # Let's check the shapes now...
In [38]:
         print('Shapes of the sets')
         print(f'{"-"*30}\n')
         print('First Set:')
         print(f'X_train: {X_train.shape}')
         print(f'y_train: {y_train.shape}')
         print('Second Set:')
         print(f'X_train: {X2_train.shape}')
         print(f'y_train: {y2_train.shape}')
         print(f'X_test: {X2_test.shape}')
         print(f'y_test: {y2_test.shape}')
         Shapes of the sets
         First Set:
         X_train: (3264, 150, 150, 3)
         y_train: (3264,)
         Second Set:
         X_train: (2870, 150, 150, 3)
         y_train: (2870,)
         X_test: (394, 150, 150, 3)
         y_test: (394,)
```

The sets have 3 channels which indicates that they are in RGB format.

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4. Shuffling and the Encoding the Training and Testing Sets

```
In [39]: # First Set
         X_train, y_train = shuffle(X_train, y_train, random_state = 0)
         # Train-test-split
         X_train, X_test, y_train, y_test = train_test_split(X_train, y_train, test_size = 0.1,
In [40]: # Second Set
         # Shuffling the dataset to randomize the order
         X2_train, y2_train = shuffle(X2_train, y2_train, random_state = 0)
         X2_test, y2_test = shuffle(X2_test, y2_test, random_state = 0)
In [41]: # Encoding...
         # Label encoding...
         y1_train = LabelEncoder().fit_transform(y_train)
         y1_test = LabelEncoder().fit_transform(y_test)
         y2_train = LabelEncoder().fit_transform(y2_train)
         y2_test = LabelEncoder().fit_transform(y2_test)
In [42]: # One hot Encoding..
         y_train_new = []
         for i in y_train:
             y_train_new.append(labels.index(i))
         y_train = y_train_new
         y3_train = tf.keras.utils.to_categorical(y_train)
         y_test_new = []
         for i in y_test:
             y_test_new.append(labels.index(i))
         y_test = y_test_new
         y3_test = tf.keras.utils.to_categorical(y_test)
```

5. CNN Models...

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```
In [43]: # Function to generate line plots based on the history of the model to evaluate it.
         def generate_plot(hist):
             fig, ax = plt.subplots(figsize = (10, 5))
             plt.plot(hist.history['accuracy'], label='Accuracy')
             plt.plot(hist.history['val_accuracy'], label = 'val_accuracy')
             plt.xlabel('Epoch')
             plt.ylabel('Accuracy')
             plt.ylim([0.5, 1])
             plt.legend(loc = 'upper right')
             plt.show()
In [44]: def model_1(shape, labels, X_train, X_test, y_train, y_test, loss = 'categorical_cross'
             # Define the model
             model = models.Sequential()
             model.add(layers.Conv2D(32, (3,3), activation = 'relu', kernel_initializer = 'he_u
             model.add(layers.MaxPooling2D((2,2)))
             model.add(layers.Conv2D(64, (3,3), activation = 'relu'))
             model.add(layers.MaxPooling2D((2,2)))
             model.add(layers.Conv2D(64, (3,3), activation = 'relu'))
             model.add(layers.MaxPooling2D((2,2)))
             model.add(layers.Flatten())
             model.add(layers.Dense(64, activation = 'relu'))
             model.add(layers.Dropout(0.5))
             model.add(layers.Dense(len(labels), activation = 'softmax'))
             print('CNN Layer Model Summary \n')
             print(model.summary())
             # Compile the model
             model.compile(optimizer = 'adam', loss = loss, metrics = ['accuracy'])
             # Fit the model
             history = model.fit(X_train, y_train, epochs = 15, validation_data = (X_test, y_te
             # Plotting the train and validation accuracy line plots
             generate_plot(history)
             print()
             print()
             print()
             # Accuracy
             print('\n Model Accuracy and Loss \n')
             test_loss, test_acc = model.evaluate(X_test, y_test)
             print(f'Test Accuracy: {test_acc}')
             print(f'Test Loss: {test loss}')
             print()
             print()
             print()
             # Prediction
             pred = np.argmax(model.predict(X_test), axis = 1)
             y_test_new = np.argmax(y_test, axis = 1)
             # Classification report
             print('\n Classification report \n')
             report = classification_report(y_test_new, pred)
             print(report)
```

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```
print()
    print()
    print()
    # Heatmap
    fig, ax = plt.subplots(figsize = (10, 8))
    sns.heatmap(confusion_matrix(y_test_new, pred), xticklabels = labels, yticklabels
    plt.title('Heatmap', y=1.05)

In [45]: shape = X_train.shape[1:]
    shape
Out[45]: (150, 150, 3)
In [46]: model_1(shape, labels, X_train, X_test, y3_train, y3_test, loss = 'categorical_crosser')
```

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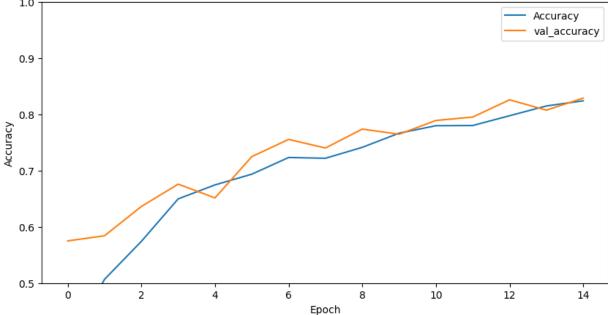
CNN Layer Model Summary

Model: "sequential_1"

				_
Layer (type)		Shape ========	Param #	=
conv2d_3 (Conv2D)		148, 148, 32)		-
<pre>max_pooling2d_3 (MaxPoolin g2D)</pre>	(None,	74, 74, 32)	0	
conv2d_4 (Conv2D)	(None,	72, 72, 64)	18496	
<pre>max_pooling2d_4 (MaxPoolin g2D)</pre>	(None,	36, 36, 64)	0	
conv2d_5 (Conv2D)	(None,	34, 34, 64)	36928	
<pre>max_pooling2d_5 (MaxPoolin g2D)</pre>	(None,	17, 17, 64)	0	
flatten_1 (Flatten)	(None,	18496)	0	
dense_2 (Dense)	(None,	64)	1183808	
dropout_1 (Dropout)	(None,	64)	0	
dense_3 (Dense)	(None,	4)	260	
None Epoch 1/15 92/92 [====================================	val_acc ====== l_accur ====== l_accur ======	uracy: 0.5749 ==] - 20s 215ms/ste acy: 0.5841 ==] - 21s 227ms/ste acy: 0.6361 ==] - 21s 229ms/ste	ep - loss: :	1.1167 - accuracy: 0. 0.9599 - accuracy: 0.
Epoch 5/15 92/92 [====================================	- ====== 1_accur ======	==] - 21s 226ms/ste acy: 0.6514 ==] - 21s 228ms/ste		,
Epoch 7/15 92/92 [====================================	1_accur ======	acy: 0.7554 ==] - 21s 227ms/ste		

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```
Brain-Tumor-Detection
7412 - val_loss: 0.6756 - val_accuracy: 0.7737
Epoch 10/15
92/92 [===========] - 21s 226ms/step - loss: 0.5357 - accuracy: 0.
7664 - val_loss: 0.6674 - val_accuracy: 0.7645
Epoch 11/15
92/92 [===========] - 21s 227ms/step - loss: 0.4870 - accuracy: 0.
7797 - val_loss: 0.7407 - val_accuracy: 0.7890
Epoch 12/15
7800 - val_loss: 0.6221 - val_accuracy: 0.7951
Epoch 13/15
7974 - val_loss: 0.5969 - val_accuracy: 0.8257
Epoch 14/15
8148 - val_loss: 0.7659 - val_accuracy: 0.8073
Epoch 15/15
8240 - val_loss: 0.6095 - val_accuracy: 0.8287
 1.0
                                          Accuracy
                                          val_accuracy
 0.9
```



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Model Accuracy and Loss

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Test Accuracy: 0.8287461996078491 Test Loss: 0.609499990940094

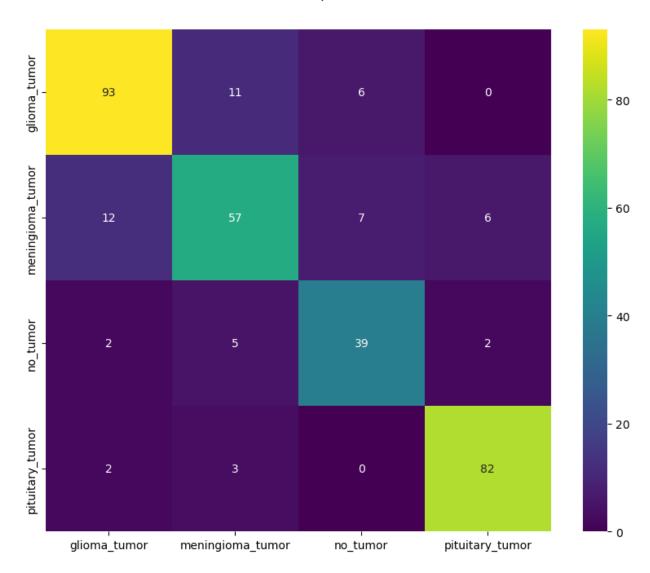
11/11 [======] - 1s 66ms/step

Classification report

	precision	recall	f1-score	support	
0	0.85	0.85	0.85	110	
1	0.75	0.70	0.72	82	
2	0.75	0.81	0.78	48	
3	0.91	0.94	0.93	87	
accuracy			0.83	327	
macro avg	0.82	0.82	0.82	327	
weighted avg	0.83	0.83	0.83	327	

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Heatmap



Second Presentation

Using Transfer Learning to improve the performance of the Model.

Will try to use EfficientNetB0 as this keras application has a good trade-off between accuracy and time(ms) per inference step for both CPU and GPU. More about this at: https://keras.io/api/applications/

```
In [53]: # Defining the model

def transfer_learning_performance(shape, labels, X_train, X_test, y_train_one_hot_enco

# Loading the Pre-trained model
    efficient_net_b0 = EfficientNetB0(input_shape = shape, weights='imagenet', include

# Model Definition
    model = efficient_net_b0.output
    model = tf.keras.layers.GlobalAveragePooling2D()(model)
    model = tf.keras.layers.Dropout(rate=0.5)(model)
```

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```
model = tf.keras.layers.Dense(4, activation='softmax')(model)
model = tf.keras.models.Model(inputs=efficient_net_b0.input, outputs = model)
#Compiling the Model
model.compile(loss = 'categorical_crossentropy', optimizer = 'Adam', metrics = ['&
# Fitting the Model on the dataset
history = model.fit(X_train, y_train_one_hot_encoded, validation_data = (X_test, y
print('\nModel Evaluation\n')
generate_plot(history)
print()
# Accuracy
print('\nModel Accuracy and Loss\n')
test loss, test acc = model.evaluate(X test, y3 test)
print(f'Test Accuracy: {test_acc}')
print(f'Test Loss: {test_loss}')
print()
# Prediction
pred = model.predict(X test)
pred = np.argmax(pred, axis=1)
y_test_new = np.argmax(y3_test, axis=1)
# Classification Report
print('\nClassification Report\n')
report = classification_report(y_test_new, pred)
print(report)
print()
# Heatmap
fig,ax = plt.subplots(figsize = (10, 8))
sns.heatmap(confusion_matrix(y_test_new, pred), xticklabels=labels, yticklabels=la
           cmap = 'viridis', fmt = 'g')
plt.title('Heatmap', y = 1.05)
```

```
# Saving the model and a tflite model
In [59]:
         def save transfer_learning_model(shape, X_train, X_test, y_train, y_test):
             # Transfer Learning Model
             efficient_net_b0 = EfficientNetB0(input_shape = shape, weights='imagenet', include
             # Model Definition
             model = efficient net b0.output
             model = tf.keras.layers.GlobalAveragePooling2D()(model)
             # Overfitting Reduction
             model = tf.keras.layers.Dropout(rate=0.5)(model)
             model = tf.keras.layers.Dense(4, activation='softmax')(model)
             model = tf.keras.models.Model(inputs=efficient_net_b0.input, outputs = model)
             # Compiling the Model
             model.compile(loss='categorical_crossentropy', optimizer = 'Adam', metrics=['accur
             # Saving the model
             checkpoint = ModelCheckpoint('efficient_net_b0.h5', monitor='val_accuracy', save_t
             #Reduce Learning rate once it saturates
             reduce_lr = ReduceLROnPlateau(monitor = 'val_accuracy', factor = 0.3, patience = 2
```

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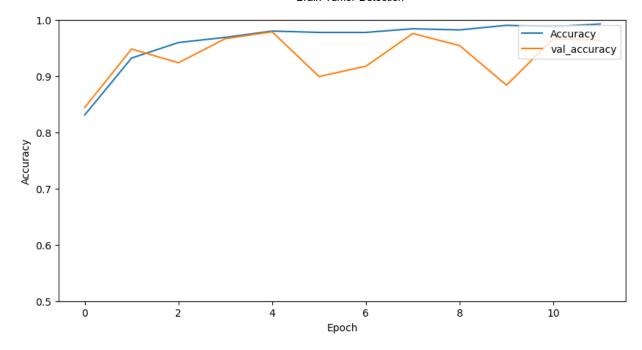
```
# Fitting the Model
        model.fit(X_train, y3_train, validation_data = (X_test, y3_test), epochs = 12, ver
        converter = tf.lite.TFLiteConverter.from_keras_model(model)
        # Converting the model to a tflite model
        tflite_model = converter.convert()
        # Saving the tflite model
        with open('model.tflite' , 'wb') as f:
           f.write(tflite model)
In [54]: | transfer_learning_performance(shape, labels, X_train, X_test, y3_train, y3_test)
     Epoch 1/12
     08 - val_loss: 0.6392 - val_accuracy: 0.8440
      Epoch 2/12
     19 - val loss: 0.1818 - val accuracy: 0.9480
     Epoch 3/12
     92/92 [==========] - 148s 2s/step - loss: 0.1185 - accuracy: 0.95
     95 - val_loss: 0.2019 - val_accuracy: 0.9235
      Epoch 4/12
     92/92 [============= - - 149s 2s/step - loss: 0.1074 - accuracy: 0.96
     87 - val_loss: 0.1143 - val_accuracy: 0.9664
     Epoch 5/12
     99 - val_loss: 0.0586 - val_accuracy: 0.9786
     Epoch 6/12
     75 - val_loss: 0.4282 - val_accuracy: 0.8991
     Epoch 7/12
     92/92 [==========] - 152s 2s/step - loss: 0.0663 - accuracy: 0.97
     75 - val_loss: 0.3304 - val_accuracy: 0.9174
      Epoch 8/12
     40 - val_loss: 0.1232 - val_accuracy: 0.9755
     Epoch 9/12
     20 - val_loss: 0.1510 - val_accuracy: 0.9541
     Epoch 10/12
     01 - val_loss: 0.4921 - val_accuracy: 0.8838
      Epoch 11/12
     9877 - val_loss: 0.1445 - val_accuracy: 0.9664
```

Model Evaluation

25 - val_loss: 0.1314 - val_accuracy: 0.9633

Epoch 12/12

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Model Accuracy and Loss

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Test Accuracy: 0.963302731513977 Test Loss: 0.13140340149402618

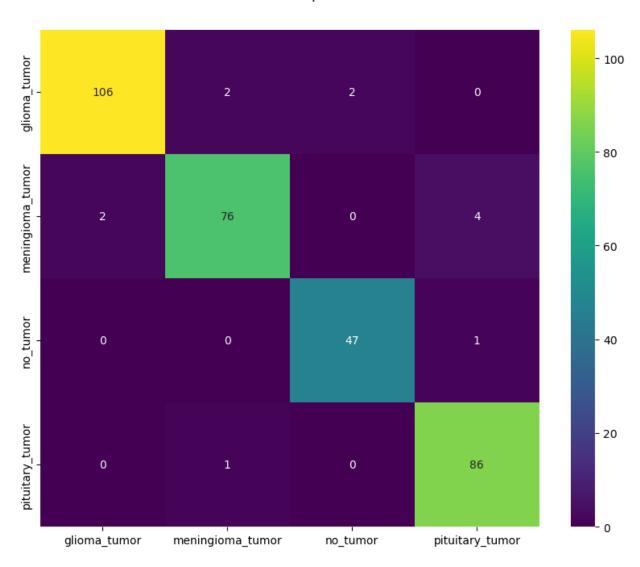
11/11 [========] - 4s 246ms/step

Classification Report

	precision	recall	f1-score	support	
0	0.98 0.96	0.96 0.93	0.97 0.94	110 82	
2	0.96	0.98	0.97	48	
3	0.95	0.99	0.97	87	
accuracy			0.96	327	
macro avg	0.96	0.96	0.96	327	
weighted avg	0.96	0.96	0.96	327	

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Heatmap



Some Observations from this model

1. The model accuracy becomes stable, achieving a high-value of 94-96%. Instances of misclassification are low as well. In order to rectify the occasional

misclassification, more images can be used to train the model.

2. This model has the better performance than the previous model and therefore will be used to implement the solution to this problem.

```
In [60]: # Saving the original model, as well ad the tflite model
save_transfer_learning_model(shape, X_train, X_test, y3_train, y3_test)
```

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C:\Users\rachitsainii\AppData\Local\anaconda3\Lib\site-packages\keras\src\engine\trai
ning.py:3103: UserWarning: You are saving your model as an HDF5 file via `model.save
()`. This file format is considered legacy. We recommend using instead the native Ker
as format, e.g. `model.save('my_model.keras')`.
 saving_api.save_model(

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```
92/92 [============== ] - 164s 2s/step - loss: 0.4609 - accuracy: 0.82
74 - val loss: 0.5291 - val accuracy: 0.8532 - lr: 0.0010
Epoch 2/12
Epoch 2: val_accuracy did not improve from 0.85321
92/92 [======================= ] - 624s 7s/step - loss: 0.1542 - accuracy: 0.94
82 - val_loss: 0.8208 - val_accuracy: 0.8349 - lr: 0.0010
Epoch 3/12
Epoch 3: val_accuracy improved from 0.85321 to 0.92661, saving model to efficient_net
b0.h5
92/92 [============== - 146s 2s/step - loss: 0.1084 - accuracy: 0.96
08 - val_loss: 0.2715 - val_accuracy: 0.9266 - lr: 0.0010
Epoch 4/12
Epoch 4: val accuracy did not improve from 0.92661
22 - val_loss: 0.2815 - val_accuracy: 0.8991 - lr: 0.0010
Epoch 5/12
Epoch 5: val accuracy did not improve from 0.92661
Epoch 5: ReduceLROnPlateau reducing learning rate to 0.0003000000142492354.
92/92 [=======================] - 149s 2s/step - loss: 0.0868 - accuracy: 0.97
04 - val_loss: 0.2467 - val_accuracy: 0.9235 - lr: 0.0010
Epoch 6/12
Epoch 6: val_accuracy improved from 0.92661 to 0.98471, saving model to efficient_net
92/92 [============= - - 147s 2s/step - loss: 0.0273 - accuracy: 0.99
22 - val_loss: 0.0612 - val_accuracy: 0.9847 - lr: 3.0000e-04
Epoch 7/12
Epoch 7: val accuracy did not improve from 0.98471
92/92 [============= - - 149s 2s/step - loss: 0.0136 - accuracy: 0.99
56 - val_loss: 0.0834 - val_accuracy: 0.9817 - lr: 3.0000e-04
Epoch 8/12
Epoch 8: val_accuracy did not improve from 0.98471
Epoch 8: ReduceLROnPlateau reducing learning rate to 9.000000427477062e-05.
69 - val loss: 0.0834 - val accuracy: 0.9847 - lr: 3.0000e-04
Epoch 9/12
Epoch 9: val_accuracy did not improve from 0.98471
80 - val_loss: 0.0908 - val_accuracy: 0.9817 - lr: 9.0000e-05
Epoch 10/12
Epoch 10: val_accuracy did not improve from 0.98471
Epoch 10: ReduceLROnPlateau reducing learning rate to 2.700000040931627e-05.
80 - val_loss: 0.0870 - val_accuracy: 0.9755 - lr: 9.0000e-05
Epoch 11/12
Epoch 11: val_accuracy did not improve from 0.98471
83 - val_loss: 0.0847 - val_accuracy: 0.9755 - lr: 2.7000e-05
```

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```
92/92 [=============] - ETA: 0s - loss: 0.0063 - accuracy: 0.9983

Epoch 12: val_accuracy did not improve from 0.98471

Epoch 12: ReduceLROnPlateau reducing learning rate to 8.100000013655517e-06.

92/92 [============] - 152s 2s/step - loss: 0.0063 - accuracy: 0.99

83 - val_loss: 0.0852 - val_accuracy: 0.9755 - lr: 2.7000e-05

INFO:tensorflow:Assets written to: C:\Users\RACHIT~1\AppData\Local\Temp\tmpvks7zs1c\assets

INFO:tensorflow:Assets written to: C:\Users\RACHIT~1\AppData\Local\Temp\tmpvks7zs1c\a
```

The EfficientNetB0 model will be deployed in a User Interface for Brain Tumor Detection

Performance Summary:

Epoch 12/12

ssets

- 1. Manually Trained Model (One-Hot Encoded label)
- Accuracy: 82%
- High Model bias towards the pituitary tumour class. (Other classes have an F1 score lower than 0.9, while the latter has an F1 score of 0.94)
- The precision of each class is below 95%, these values are inadequate, as the detection and classification of brain tumors is a sensitive matter, and false predictions won't be tolerated.
- 1. Model fitting on pre-trained model (EfficientNetB0)
- Accuracy: 96%
- A great improvement from the previous model. Furthermore, the model has a more stable and reliable performance.
- All the classes have an F1 score >= 97%, greatly reducing the bias previously seen in the preceding model.
- THe model attains high class precison values >=95%. Therefore, there are very few instances of false detections and classifications.

In []:

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