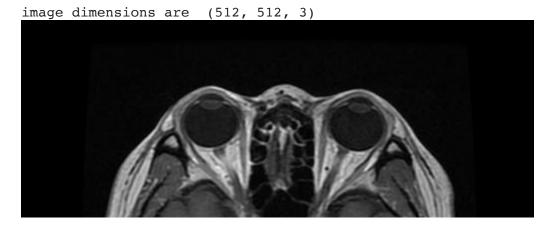
```
#mount the drive
from google.colab import drive
drive.mount('/content/drive')
    Mounted at /content/drive
#extract the dataset from zip
#!unzip /content/drive/MyDrive/brain_tumor_classification/archive.zip -d /content/driv
#import the required libraries
import matplotlib.pyplot as plt
from tensorflow.keras.preprocessing.image import ImageDataGenerator
import tensorflow as tf
import numpy as np
import cv2
from google.colab.patches import cv2 imshow
import os
import random
from tensorflow.keras.layers import *
#display a sample image
image path = '/content/drive/MyDrive/brain tumor classification/Training/pituitary tur
image_for_visualization = cv2.imread(image_path)
print('image dimensions are ', image for visualization.shape)
cv2 imshow(image for visualization)
```



Defining the model architecture

Let's defined the model, to check the how it would work on our defined model. For our model:

dense_model.summary()

Model: "sequential"

Layer (type)	Output Shape	Param #
dense (Dense)	(None, 256, 256, 32)	128
dense_1 (Dense)	(None, 256, 256, 16)	528
flatten (Flatten)	(None, 1048576)	0
dense_2 (Dense)	(None, 4)	4194308

Total params: 4,194,964

Trainable params: 4,194,964 Non-trainable params: 0

#dense model

dense model with dropout.summary()

Model: "sequential_1"

Layer (type)	Output Shape	Param #
dense_3 (Dense)	(None, 256, 256, 32)	128
dense_4 (Dense)	(None, 256, 256, 16)	528
dropout (Dropout)	(None, 256, 256, 16)	0
flatten_1 (Flatten)	(None, 1048576)	0
dense_5 (Dense)	(None, 4)	4194308

Total params: 4,194,964
Trainable params: 4,194,964
Non-trainable params: 0

VGG16 example (off the shelf implementation)

model_vgg16.summary()

Model: "vgg16"

Layer (type)	Output Shape	Param #
input_3 (InputLayer)		
block1_conv1 (Conv2D)	(None, 256, 256, 64)	1792
block1_conv2 (Conv2D)	(None, 256, 256, 64)	36928
block1_pool (MaxPooling2D)	(None, 128, 128, 64)	0
block2_conv1 (Conv2D)	(None, 128, 128, 128)	73856
block2_conv2 (Conv2D)	(None, 128, 128, 128)	147584
block2_pool (MaxPooling2D)	(None, 64, 64, 128)	0
block3_conv1 (Conv2D)	(None, 64, 64, 256)	295168
block3_conv2 (Conv2D)	(None, 64, 64, 256)	590080
block3_conv3 (Conv2D)	(None, 64, 64, 256)	590080
block3_pool (MaxPooling2D)	(None, 32, 32, 256)	0
block4_conv1 (Conv2D)	(None, 32, 32, 512)	1180160
block4_conv2 (Conv2D)	(None, 32, 32, 512)	2359808
block4_conv3 (Conv2D)	(None, 32, 32, 512)	2359808
block4_pool (MaxPooling2D)	(None, 16, 16, 512)	0
block5_conv1 (Conv2D)	(None, 16, 16, 512)	2359808
block5_conv2 (Conv2D)	(None, 16, 16, 512)	2359808
block5_conv3 (Conv2D)	(None, 16, 16, 512)	2359808
block5_pool (MaxPooling2D)	(None, 8, 8, 512)	0
flatten (Flatten)	(None, 32768)	0
fc1 (Dense)	(None, 4096)	134221824
fc2 (Dense)	(None, 4096)	16781312
predictions (Dense)	(None, 4)	16388

```
Total params: 165,734,212
Trainable params: 165,734,212
Non-trainable params: 0
```

Creating the data generator

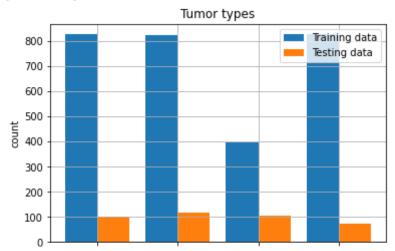
Defining the training, validation and test data generators

```
# path to the training directory
   train dir = '/content/drive/MyDrive/brain tumor classification/Training/'
   test_dir = '/content/drive/MyDrive/brain_tumor_classification/Testing/'
   # data augmentation to be applied in train_datagen [augmentation only applied on the t
   train datagen = ImageDataGenerator(rescale=1/255.,
                                        shear range=0.20,
                                        zoom range=0.20,
                                        horizontal flip=True,
                                        vertical_flip=True,
                                        validation split=0.25)
   test datagen = ImageDataGenerator(rescale=1/255.)
   # creating datagenerator for the training and validation data
   train generator = train datagen.flow from directory(train dir, # This is the source (
                                                          target size=(256, 256),
                                                          classes = ['glioma tumor', 'mening
                                                          class mode='categorical',
                                                          subset='training')
   validation generator = train datagen.flow from directory(train dir, # same directory &
                                                               target size=(256, 256),
                                                               class mode='categorical',
                                                               subset='validation') # set as
   test generator = test datagen.flow from directory(test dir,
                                                        target_size=(256, 256),
                                                        classes = ['glioma tumor', 'meningic']
                                                        class mode='categorical')
        Found 2155 images belonging to 4 classes.
        Found 715 images belonging to 4 classes.
        Found 394 images belonging to 4 classes.
   # visualization for training and testing data
   def visualizing data(list of image path, directory path):
https://colab.research.google.com/drive/1OYMYC4yueYYa3Z6yH8Jb3b3uOLzWd8RI#scrollTo=K70hrykhwyqh&printMode=true
                                                                                           5/16
```

```
index = 0
    count = 1
    plt.figure(figsize=(25, 8))
    for image in list of image path:
        path = directory path + image
        1 = os.listdir(path)
        img = l[index]
        img for visualization = cv2.imread(path+'/'+img)
        resized img for visualization = cv2.resize(img for visualization, (256, 256))
        #print('image selected to be visualized ', path+'/'+img)
        plt.subplot(1,4,count)
        plt.imshow(resized_img_for_visualization)
        plt.title(image)
        count += 1
    plt.tight_layout()
training_dir = '/content/drive/MyDrive/brain_tumor_classification/Training/'
testing dir = '/content/drive/MyDrive/brain tumor classification/Testing/'
train_tumor_types = os.listdir(training_dir)
testing_tumor_types = os.listdir(testing_dir)
visualizing data(train tumor types, training dir)
visualizing data(testing tumor types, testing dir)
```

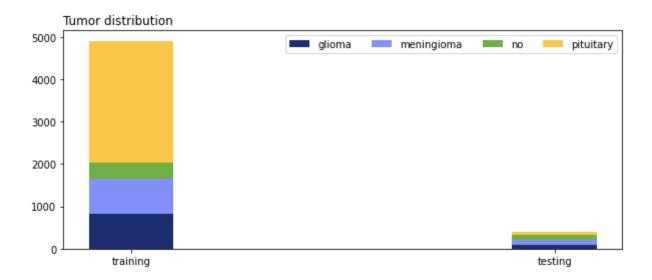
```
# plot the bar chart
list_of_training_classes = os.listdir(train_dir)
list_of_testing_classes = os.listdir(test_dir)
count_of_number_of_images_training = []
count_of_number_of_images_testing = []
for images in list of training classes:
    path = train_dir + '/' + images
    count of number of images training.append(len(os.listdir(path)))
for images in list of testing classes:
    path = test dir + '/' + images
    count of number of images testing.append(len(os.listdir(path)))
names of tumors = list of training classes
X axis = np.arange(len(names of tumors))
print(X axis)
plt.bar(X axis - 0.2, count of number of images training, 0.4, label = 'Training data'
plt.bar(X axis + 0.2, count of number of images testing, 0.4, label = 'Testing data')
plt.xticks(X axis, names_of_tumors, rotation=45)
plt.xlabel("names of tumors")
plt.ylabel("count")
plt.title("Tumor types")
plt.legend()
plt.grid()
plt.show()
```

[0 1 2 3]



```
count_of_number_of_images_training = [826, 822, 395, 827]
count_of_number_of_images_testing = [100, 115, 105, 74]
names_of_tumors = ['glioma', 'meningioma', 'no tumor', 'pituitary']
x_ticks = ['training', 'testing']
# define figure
plt.figure(figsize=(10, 4))
# numerical x
x = np.arange(0, len(x ticks))
# plot bars
plt.bar(x[0], count of number of images training[0], width=0.2, color='#1D2F6F')
plt.bar(x[0], count of number of images training[1], bottom=826, width=0.2, color='#83
plt.bar(x[0], 826+822+count of number of images training[2], bottom=826+822, width=0.2
plt.bar(x[0], 826+822+395+count of number of images training[3], bottom=822+826+395, v
plt.bar(x[1], count of number of images testing[0], width=0.2, color='#1D2F6F')
plt.bar(x[1], count of number of images testing[1], bottom=100, width=0.2, color='#839
plt.bar(x[1], count_of_number_of_images_testing[2], bottom=100+115, width=0.2, color='
plt.bar(x[1], count of number of images testing[3], bottom=100+115+105, width=0.2, col
plt.bar(x[0], count of number of images training[0], width=0.2)
plt.bar(x[0], count of number of images training[1], bottom=826, width=0.2)
plt.bar(x[0], 826+822+count of number of images training[2], bottom=826+822, width=0.2
plt.bar(x[0], 826+822+395+count of number of images training[3], bottom=822+826+395, v
plt.bar(x[1], count of number of images testing[0], width=0.2)
plt.bar(x[1], count of number of images testing[1], bottom=100, width=0.2)
plt.bar(x[1], count_of_number_of_images_testing[2], bottom=100+115, width=0.2)
plt.bar(x[1], count of number of images testing[3], bottom=100+115+105, width=0.2)
plt.xticks(x, x ticks)
```

```
# title and legend
plt.title('Tumor distribution', loc ='left')
plt.legend(['glioma', 'meningioma', 'no', 'pituitary'], ncol = 4)
plt.show()
```



Training the model

Here our model is being trained, and we are saving the model as "user_defined_model.h5"

```
dense model.compile(optimizer = tf.optimizers.Adam(),
                                                        # optimizer for the learning p
                    loss = 'categorical crossentropy', # categorical : because one ho
                    metrics=['accuracy'])
dense model with dropout.compile(optimizer = tf.optimizers.Adam(),
                                                                     # optimizer for t
                    loss = 'categorical crossentropy', # categorical : because one ho
                    metrics=['accuracy'])
model vgg16.compile(optimizer = tf.optimizers.Adam(),
                                                        # optimizer for the learning p
                    loss = 'categorical crossentropy', # categorical : because one ho
                    metrics=['accuracy'])
history dense model = dense model.fit generator(train generator,
                                                steps per epoch = train generator.samp
                                                validation data = validation generator
                                                validation steps = validation generate
                                                epochs = epochs)
# to save the trained model in .h5 file
dense model.save('/content/dense model.h5')
    /usr/local/lib/python3.7/dist-packages/ipykernel launcher.py:5: UserWarning: `Moo
```

Epoch 1/15

```
Epoch 2/15
 67/67 [============] - 58s 873ms/step - loss: 1.0775 - accuracy
 Epoch 3/15
 Epoch 4/15
 Epoch 5/15
 Epoch 6/15
 67/67 [============== ] - 59s 875ms/step - loss: 0.9383 - accurac
 Epoch 7/15
 Epoch 8/15
 67/67 [============== ] - 58s 872ms/step - loss: 0.9195 - accurac
 Epoch 9/15
 Epoch 10/15
 Epoch 11/15
 67/67 [============== ] - 58s 867ms/step - loss: 0.8330 - accurac
 Epoch 12/15
 Epoch 13/15
 Epoch 14/15
 67/67 [============= ] - 58s 870ms/step - loss: 0.8291 - accuracy
 Epoch 15/15
 history dense model with dropout = dense model with dropout.fit generator(train generator)
                             steps per er
                             validation (
                             validation :
                             epochs = epo
# to save the trained model in .h5 file
dense model with dropout.save('/content/dense model with dropout.h5')
 /usr/local/lib/python3.7/dist-packages/ipykernel launcher.py:5: UserWarning: `Moo
 Epoch 1/15
 Epoch 2/15
 Epoch 3/15
 Epoch 4/15
 Epoch 5/15
 Epoch 6/15
```

Epoch 7/15

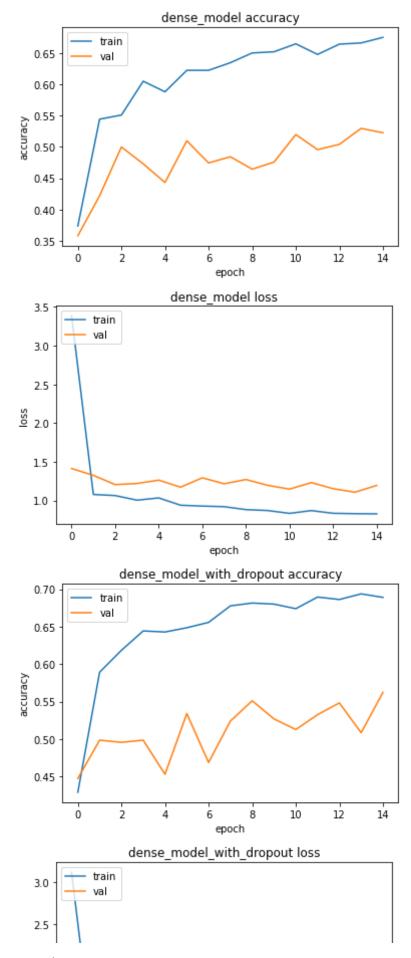
```
Epoch 8/15
 67/67 [============] - 58s 873ms/step - loss: 0.8298 - accuracy
 Epoch 9/15
 Epoch 10/15
 67/67 [============== ] - 58s 868ms/step - loss: 0.8020 - accurac
 Epoch 11/15
 Epoch 12/15
 67/67 [============== ] - 58s 862ms/step - loss: 0.7968 - accurac
 Epoch 13/15
 67/67 [============== ] - 58s 863ms/step - loss: 0.7837 - accurac
 Epoch 14/15
 67/67 [============== ] - 58s 860ms/step - loss: 0.7561 - accurac
 Epoch 15/15
 history model_vgg16 = model_vgg16.fit_generator(train_generator,
                   steps_per_epoch = train_generator.sam;
                   validation_data = validation_generator
                   validation steps = validation generato
                   epochs = epochs)
# to save the trained model in .h5 file
model vgg16.save('/content/model vgg16.h5')
 /usr/local/lib/python3.7/dist-packages/ipykernel launcher.py:5: UserWarning: `Moo
 Epoch 1/15
 Epoch 2/15
 Epoch 3/15
 Epoch 4/15
 Epoch 5/15
 Epoch 6/15
 Epoch 7/15
 Epoch 8/15
 Epoch 9/15
 Epoch 10/15
 Epoch 11/15
 Epoch 12/15
```

```
Epoch 13/15
    Epoch 14/15
    Epoch 15/15
    # plotting the performance of the model from the history object obtained after training
plt.plot(history dense model.history['accuracy'])
plt.plot(history_dense_model.history['val_accuracy'])
plt.title('dense model accuracy')
plt.ylabel('accuracy')
plt.xlabel('epoch')
plt.legend(['train', 'val'], loc='upper left')
plt.show()
plt.plot(history_dense_model.history['loss'])
plt.plot(history dense model.history['val loss'])
plt.title('dense model loss')
plt.ylabel('loss')
plt.xlabel('epoch')
plt.legend(['train', 'val'], loc='upper left')
plt.show()
# plotting the performance of the model from the history object obtained after training
plt.plot(history dense model with dropout.history['accuracy'])
plt.plot(history dense model with dropout.history['val accuracy'])
plt.title('dense model with dropout accuracy')
plt.ylabel('accuracy')
plt.xlabel('epoch')
plt.legend(['train', 'val'], loc='upper left')
plt.show()
plt.plot(history dense model with dropout.history['loss'])
plt.plot(history dense model with dropout.history['val loss'])
plt.title('dense_model_with_dropout loss')
plt.ylabel('loss')
plt.xlabel('epoch')
plt.legend(['train', 'val'], loc='upper left')
plt.show()
# plotting the performance of the model from the history object obtained after training
plt.plot(history model vgg16.history['accuracy'])
plt.plot(history model vgg16.history['val accuracy'])
plt.title('model vgg16 accuracy')
plt.ylabel('accuracy')
```

```
plt.xlabel('epoch')
plt.legend(['train', 'val'], loc='upper left')
plt.show()

plt.plot(history_model_vgg16.history['loss'])
plt.plot(history_model_vgg16.history['val_loss'])
plt.title('model_vgg16 loss')
plt.ylabel('loss')
plt.xlabel('epoch')
plt.legend(['train', 'val'], loc='upper left')
plt.show()
```





evaluation code

References:

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