Assignment 6

Medical Devices and Robotics

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In case of X-ray, CT scan, Ultrasound and MRI, describe the image segmentation processes for disease/ tumor detection. Using a basic neural network model train the uploaded images for tumor detection. Choose any 10 images from each class. Builtin commands are allowed. Submit a report for the assignment.

Medical Image Modalities And Segmentations Process:

1. **X-Ray:**

- X-rays are a form of electromagnetic radiation, similar to visible light. Unlike light, however, x-rays have higher energy and can pass through most objects, including the body. Medical x-rays are used to generate images of tissues and structures inside the body. If x-rays travelling through the body also pass through an x-ray detector on the other side of the patient, an image will be formed that represents the “shadows” formed by the objects inside the body.

2. **CT Scan:**

- CT machine consists of a circular arrangement of x-ray emitters and detectors in which progressive scans through the brain can be taken. A 2-dimensional image of horizontal sections can then be produced. This technique is used mainly to diagnose neurological conditions such as tumors, blood clots, degenerative disease and the location of strokes.
- Image slices can either be displayed individually or stacked together by the computer to generate a 3D image of the patient that shows the skeleton, organs, and tissues as well as any abnormalities the physician is trying to identify.

3. **MRI:**

- An MRI machine uses a powerful magnetic field to align the magnetization of some atoms in the body, radio frequency fields systematically alter the alignment of this magnetization. This causes the nuclei to produce a rotating magnetic field detectable by the scanner. This information is recorded to construct an image of the body.
- It is a form of medical imaging that uses no Ionizing radiation

4. **Ultrasound:**

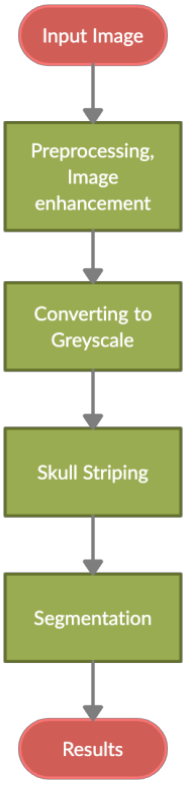
- Ultrasound uses high-frequency sound waves to produce images of organs and structures within the body.
- It is a form of medical imaging that uses no Ionizing radiation

Medical Image Segmentation

Processing a medical image involves two main steps. The first is the pre-processing of the image. This involves performing operations like noise reduction and filtering so that the image is suitable for the next step. The second step is to perform segmentation and morphological operations. These determine the size and the location of the tumor. The steps are as follows:

1. **Image Pre-Processing:**

The first step is to processing our image to remove any kind of unwanted data, noise, artifacts etc. General Pre-processing involves processes like conversion to greyscale, noise reduction, noise removal, image reconstruction, image enhancement, improving signal to noise ratio, and bone/skull removal from a medical image scan.



2. **Skull stripping**

Skull stripping is an important part in the medical image analysis and it involves removing all non tissue material from the image. It is also possible to remove other tissues such as fat, skin etc. Skull stripping can be performed using image contour, histogram analysis or a threshold value.

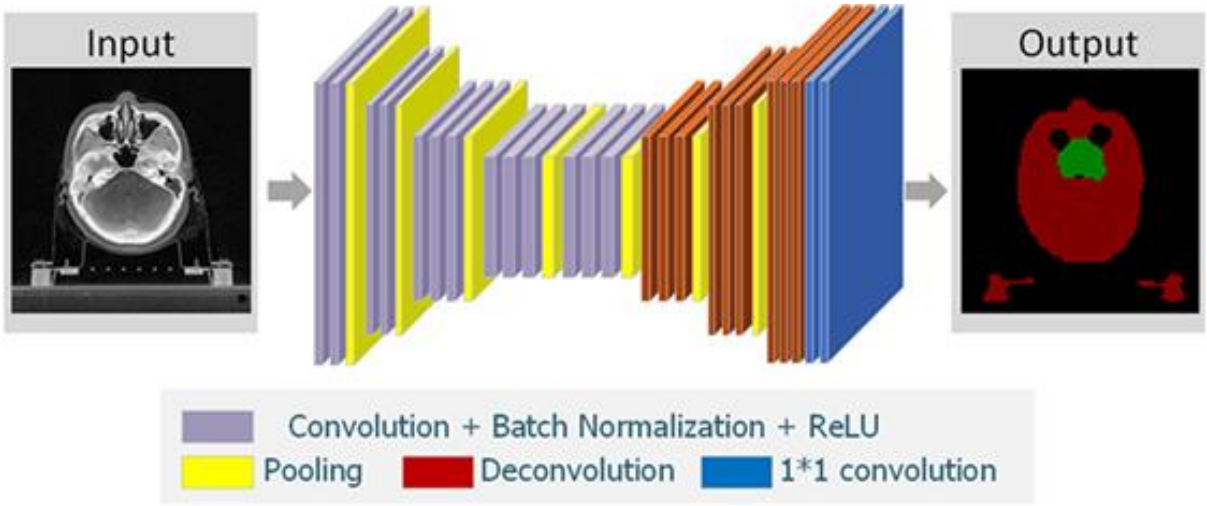
3. **Segmentation**

Segmentation is the process of labeling each pixel in an image such that they share the same characteristics. The process results in pixels sharing a common property. There are various algorithms that can be used to perform medical image segmentation. Traditionally computer vision method include: thresholding, Otsu thresholding, clustering techniques etc.

Thresholding is also a very popular and straightforward segmentation technique. It creates a binary segmented image from a greyscale image. All it does is replace the pixel with a black pixel at a certain point if the intensity at that point is less than a certain intensity or replace it a with a white pixel if the intensity is more than that.

Now a days, deep learning based segmentation methods are used for tumor segmentation. Some of the common architecture include:

- ParseNet
- U-Net
- Feature Pyramid Network (FPN)
- Pyramid Scene Parsing Network (PSPNet)
- Mask R-CNN
- DeepLab, DeepLabv3 and DeepLabv3+
- Path Aggregation Network (PANet)
- Context Encoding Network (EncNet)



Post-Processing:
Successful segmentation of the image is followed by the post-processing of the image. Post Processing of the image involves steps to judge the size of the tumor and its type. Post processing may also involve various optimization techniques to further improve the result.

References:

- Nilesh Bhaskarrao Bahadure, Arun Kumar Ray, Har Pal Thethi, "**Image Analysis for MRI Based Brain Tumor Detection and Feature Extraction Using Biologically Inspired BWT and SVM**", International Journal of Biomedical Imaging, vol. 2017, Article ID 9749108, 12 pages, 2017. https://doi.org/10.1155/2017/9749108
- J.selvakumar, A.Lakshmi and T.Arivoli, "**Brain Tumor Segmentation and Its AreaCalculation in Brain MR Images using K-Mean Clustering and Fuzzy C-Mean Algorithm**" 2012 IEEE-International Conference On Advances In Engineering, Science And Management (ICAESM -2012) March 30, 31, 2012
- L. Kapoor and S. Thakur, "**A survey on brain tumor detection using image processing techniques**," 2017 7th International Conference on Cloud Computing, Data Science & Engineering - Confluence, Noida, 2017, pp. 582-585, doi: 10.1109/CONFLUENCE.2017.7943218.
- Garg A., Bajaj A., Lal R. (2020) **Brain Tumor Detection Using Image Processing Based on Anisotropic Filtration Techniques**. In: Sharma D., Balas V., Son L., Sharma R., Cengiz K. (eds) Micro-Electronics and Telecommunication Engineering. Lecture Notes in Networks and Systems, vol 106. Springer, Singapore. https://doi.org/10.1007/978-981-15-2329-8_37
- Mezgar R., Mahjoub M.A., Salem R., Mtibaa A. (2012) **Brain MRI Image Segmentation in View of Tumor Detection: Application to Multiple Sclerosis**. In: Elmoataz A., Mammass D., Lezoray O., Nouboud F., Aboutajdine D. (eds) Image and Signal Processing. ICISP 2012. Lecture Notes in Computer Science, vol 7340. Springer, Berlin, Heidelberg. https://doi.org/10.1007/978-3-642-31254-0_43
- https://blog.radiology.virginia.edu/different-imaging-tests-explained
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Using a Convolutional Neural Network (CNN, ResNet) for brain tumor classification

January 11, 2021

0.1 Imoprting Libraries

We will start with importing necessary libraries

[1]:
```
# Importing different libraries for processing
import math
import os

import itertools

# For graph plotting
import matplotlib.pyplot as plt
import pandas as pd
import scipy

import cv2 #Library for image processing functions
from PIL import Image # PIL is another python image library (PIL)
import numpy as np # For dealing with multi dimensional arrays

# Importing Keras libarary for deep learning
from keras import layers
from keras.applications import ResNet50 # Importing pre-trained ResNet model
from keras.utils.np_utils import to_categorical # For one hot encoding of label␣
 ↪vector
from keras.models import Sequential
from keras.optimizers import Adam # Adam is a type of gradient descent optimizer
from sklearn.model_selection import train_test_split # For splitting the␣
 ↪dataset into training and testing sets
from sklearn.metrics import accuracy_score # Importing some accuracy metrics
from tqdm import tqdm # Library for showing progress bar when loading images,␣
 ↪https://pypi.org/project/tqdm/
from keras import backend as K
import tensorflow as tf # Importing tensorflow as well

device_name = tf.test.gpu_device_name() # Selecting GPU for model training
```

```
if device_name != '/device:GPU:0':
  raise SystemError('GPU device not found')
print('Found GPU at: {}'.format(device_name))

%matplotlib inline
```

```
Found GPU at: /device:GPU:0
```

0.2 Importing the dataset

0.2.1 Accessing the dataset on google drive

The dataset was upload on Google drive and was processed in Google Colab.

[2]:
```
#Mounting the google drive so that the dataset uploaded on it can be accessed␣
 ↪in Colab

from google.colab import drive

drive.mount("/content/gdrive")

!ls "/content/gdrive/My Drive/brain_tumor_dataset"
```

```
Drive already mounted at /content/gdrive; to attempt to forcibly remount, call
drive.mount("/content/gdrive", force_remount=True).
no  yes
```

0.2.2 Loading the dataset

[4]:
```
# A function to load set of images from a directory
def Dataset_loader(DIR, RESIZE):
    IMG = [] # A list in which we will add/append the images of the dataset

    for IMAGE_NAME in tqdm(os.listdir(DIR)): #Loop through the all of the␣
 ↪filenames present in the DIR, tqdm is for showing the progress bar
        PATH = os.path.join(DIR,IMAGE_NAME) #IMAGE_NAME contains the name of␣
 ↪one image file for the for loop iteration, we will joing the filename with␣
 ↪the directory path
        _, ftype = os.path.splitext(PATH) # to get the file type of the loaded␣
 ↪file (file type such as .png, .doc)
        if ftype == ".jpg": # to process only .JPG file type
            img = np.asarray(Image.open(PATH).convert("RGB")) # Open the image,␣
 ↪convert it to a RGB, 3 channel numpy array
            img = cv2.resize(img, (RESIZE,RESIZE)) # resize the image
```

```
            IMG.append(np.array(img)) # append the loaded list to the list IMD␣
 ↪defined outside the loop

    return IMG # return the IMG list containg the arrays of images loaded␣
 ↪through the for loop

path = "/content/gdrive/My Drive/brain_tumor_dataset/" # Path where the dataset␣
 ↪is stored
benign_data = np.array(Dataset_loader(path+'no',IMAGE_RESIZE))
malign_data = np.array(Dataset_loader(path+'yes',IMAGE_RESIZE))

# Print our the number of images in each dataset
print("Total images in the benign dataset: ", len(benign_data))
print("Total images in the malign dataset: ", len(malign_data))
```

```
100%|      | 98/98 [00:00<00:00, 337.94it/s]
100%|      | 155/155 [00:00<00:00, 329.24it/s]

Total images in the benign dataset:  85
Total images in the malign dataset:  86
```

0.3 Hyper parameters

The hyper parameters are defined here

[3]:
```
# All hyper parameters
IMAGE_RESIZE = 224 #224 is the input to various CNN archs (Transfer Learning)
num_classes= 2
BATCH_SIZE = 16 # batch size tell us the no of images process at once through␣
 ↪our model when training
lr=1e-4 #Learning rate used in Adam (Gradient Descent) optimizer
epochs=10 # total number of epochs
```

0.4 Creating Label

Now, we will create lables for the loaded images. Since, this is a binary classification problem (tumor is present or not), we will create two binary labels.

After the label creation, the two datasets (malign data and benign data) are merged, and then shuffled. After that, the label vector is one hot encoded.

[5]:
```
# Skin Cancer: Malignant vs. Benign

# Create labels
benign_data_label = np.zeros(len(benign_data)) #Using 0 for BENIGN
```

```
malign_data_label = np.ones(len(malign_data)) # Using 1 for MALIGN

# Merging data
X_data = np.concatenate((benign_data, malign_data), axis = 0)
Y_data = np.concatenate((benign_data_label, malign_data_label), axis = 0)

# Shuffling data
s = np.arange(X_data.shape[0])
np.random.shuffle(s)
X_data = X_data[s]
Y_data = Y_data[s]

# One hot encoding the label vector
Y_data = to_categorical(Y_data, num_classes)
```

0.5 Train and Testing split

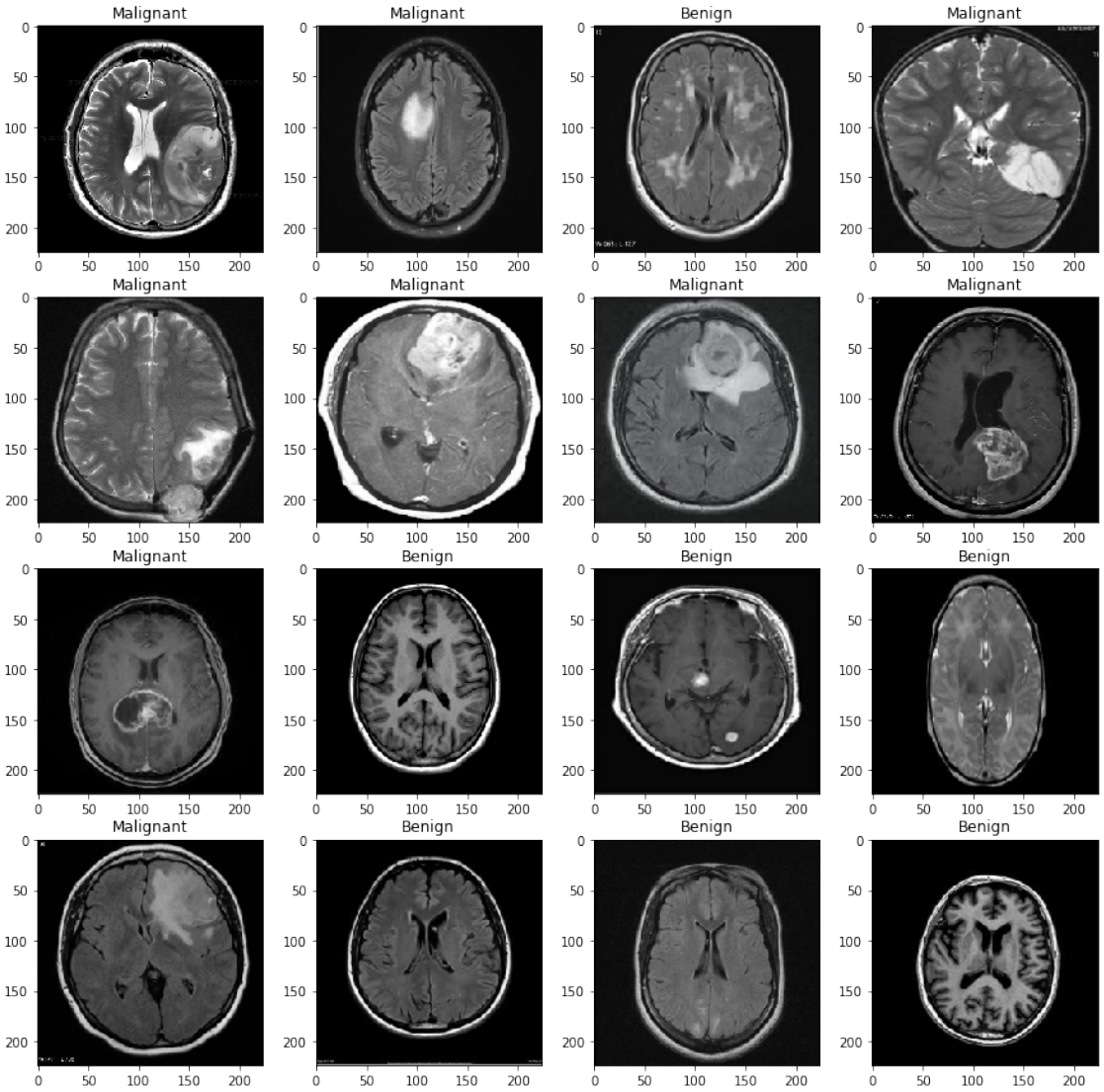
Now, it is time to split our dataset to training and testing set. The test size is 20% while for the traning set, the size is 80%.

[6]:
```
x_train, x_test, y_train, y_test = train_test_split(
    X_data, Y_data,
    test_size=0.2,
    random_state=11
)
```

0.6 Displaying Tumor Images

Here, lets display some images from the dataset with their label as well.

[7]:
```
w=60
h=40
fig=plt.figure(figsize=(15, 15))
columns = 4
rows = 4

for i in range(1, columns*rows +1):
    ax = fig.add_subplot(rows, columns, i)
    if np.argmax(y_train[i]) == 0:
        ax.title.set_text('Benign')
    else:
        ax.title.set_text('Malignant')
    plt.imshow(x_train[i], interpolation='nearest')
plt.show()
```



0.7 CNN Model

Here, I am using pretrained ResNet Architecture trained on imagenet data (Transfer Learning). The last layers of ResNet are removed and custom trainable layers are added. The model is compiled and the summary is printed as well.

[8]:
```
K.clear_session() # Clearning the session i.e. any previously pre defined␣
↪variables

model = Sequential() # Defining a sequntial model

densenet = ResNet50( # Defninng our model
```

```
    weights='imagenet', #using the pretrained weights of image net competition
    include_top=False, #not including the outer layer of imported model
    input_shape=(224,224,3) # input image shape of model
)

model.add(densenet) # adding the 'backbone' model as the first layer
model.add(layers.GlobalAveragePooling2D()) # global average pooling layer
model.add(layers.Dropout(0.5)) # Adding 50% dropout rate
model.add(layers.BatchNormalization()) # Batch normalization
model.add(layers.Dense(2, activation='softmax')) # Output layer, using softmax␣
 ↪activations

model.compile( # compiling the model
        loss='binary_crossentropy', # Using the cross entropy loss,
        optimizer=Adam(lr=lr), # using adam optimizer
        metrics=['accuracy'] # using the accuracy metric
    )

model.summary() # printing out all the layers info
```

```
Model: "sequential"
_________________________________________________________________
Layer (type)                 Output Shape              Param #
=================================================================
resnet50 (Functional)        (None, 7, 7, 2048)        23587712
_________________________________________________________________
global_average_pooling2d (Gl (None, 2048)              0
_________________________________________________________________
dropout (Dropout)            (None, 2048)              0
_________________________________________________________________
batch_normalization (BatchNo (None, 2048)              8192
_________________________________________________________________
dense (Dense)                (None, 2)                 4098
=================================================================
Total params: 23,600,002
Trainable params: 23,542,786
Non-trainable params: 57,216
_________________________________________________________________
```

0.7.1 Model Training

Now, the model is trained on the training set as follows:

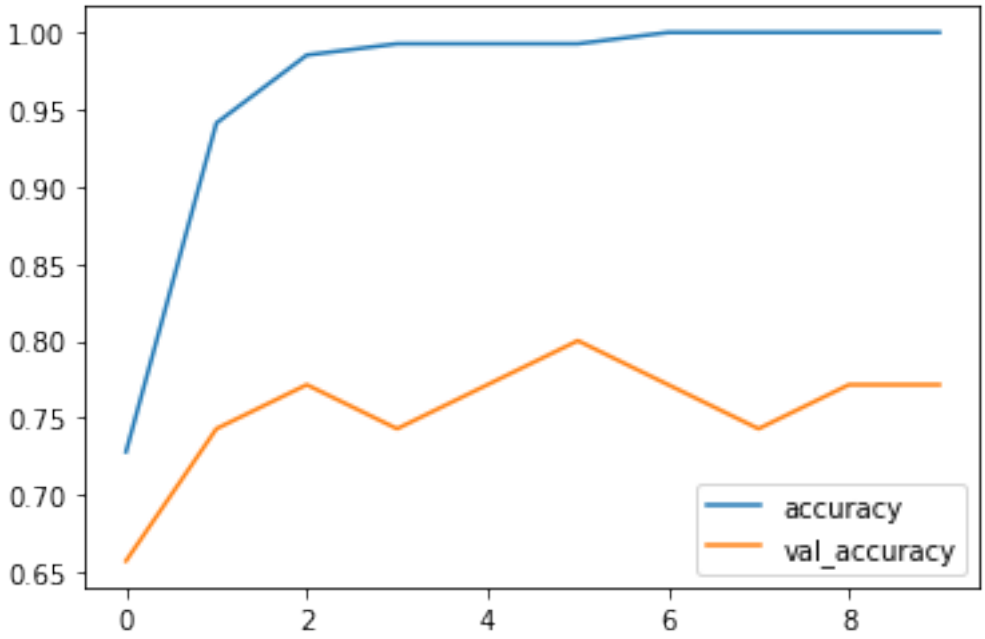
[9]:
```
# Fitting the model to the trainig set
history = model.fit(x_train, y_train, batch_size=BATCH_SIZE,␣
 ↪validation_data=(x_test, y_test), epochs=epochs)
```

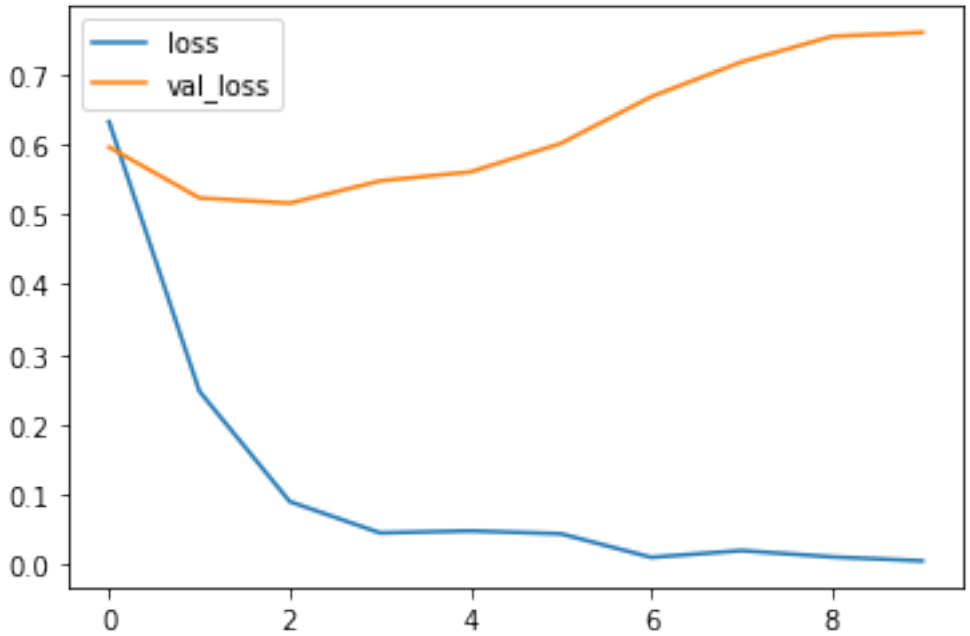
```
Epoch 1/10
9/9 [==============================] - 11s 484ms/step - loss: 0.6875 - accuracy:
0.6951 - val_loss: 0.5953 - val_accuracy: 0.6571
Epoch 2/10
9/9 [==============================] - 2s 236ms/step - loss: 0.2805 - accuracy:
0.9375 - val_loss: 0.5229 - val_accuracy: 0.7429
Epoch 3/10
9/9 [==============================] - 2s 237ms/step - loss: 0.0907 - accuracy:
0.9887 - val_loss: 0.5156 - val_accuracy: 0.7714
Epoch 4/10
9/9 [==============================] - 2s 238ms/step - loss: 0.0572 - accuracy:
0.9878 - val_loss: 0.5473 - val_accuracy: 0.7429
Epoch 5/10
9/9 [==============================] - 2s 237ms/step - loss: 0.0279 - accuracy:
0.9985 - val_loss: 0.5601 - val_accuracy: 0.7714
Epoch 6/10
9/9 [==============================] - 2s 237ms/step - loss: 0.0361 - accuracy:
0.9958 - val_loss: 0.6006 - val_accuracy: 0.8000
Epoch 7/10
9/9 [==============================] - 2s 237ms/step - loss: 0.0165 - accuracy:
1.0000 - val_loss: 0.6673 - val_accuracy: 0.7714
Epoch 8/10
9/9 [==============================] - 2s 237ms/step - loss: 0.0180 - accuracy:
1.0000 - val_loss: 0.7168 - val_accuracy: 0.7429
Epoch 9/10
9/9 [==============================] - 2s 237ms/step - loss: 0.0113 - accuracy:
1.0000 - val_loss: 0.7532 - val_accuracy: 0.7714
Epoch 10/10
9/9 [==============================] - 2s 237ms/step - loss: 0.0056 - accuracy:
1.0000 - val_loss: 0.7588 - val_accuracy: 0.7714
```

0.7.2 Plotting accuracy curves

[10]:
```
# Converting the 'history' list to a python pandas dataframe
history_df = pd.DataFrame(history.history)

# Plotting the accuracy curve

history_df[['accuracy', 'val_accuracy']].plot()

# Plotting the loss curve

history_df[['loss', 'val_loss']].plot()
```

[10]:
```
<matplotlib.axes._subplots.AxesSubplot at 0x7ff2ce212c50>
```





0.7.3 Model Evaluation

The model is evaluated on the test set and the achieved accuracy is as follows:

[11]:
```
# Predicting the label/classes of x_test dataset using the trainined model
Y_pred = model.predict(x_test)
```

[12]:
```
# Getting the test accuract by comparing the original label and the predicted␣
↪label
acc = accuracy_score(np.argmax(y_test, axis=1), np.argmax(Y_pred, axis=1))

print("Test Accuracy (%) : ", acc*100)
```

```
Test Accuracy (%) :  77.14285714285715
```

0.7.4 Classification Report

The classification metrics (Precision, recall, f1-score) are as follows:

[15]:
```
#Printing the classification report,

from sklearn.metrics import classification_report
print(classification_report( np.argmax(y_test, axis=1), np.argmax(Y_pred,␣
↪axis=1), target_names = ["BENIGN TUMOR", "MALIGN TUMOR"]))
```

```
              precision    recall  f1-score   support

BENIGN TUMOR       0.70      0.88      0.78        16
MALIGN TUMOR       0.87      0.68      0.76        19

    accuracy                           0.77        35
   macro avg       0.78      0.78      0.77        35
weighted avg       0.79      0.77      0.77        35
```

0.8 Conclusion

We can see that our model was able to successfully classify tumor images into benign and malign categories. The f1 score for benign tumor was 0.78 and for malign tumor, it was 0.76. Also, the testing accuracy was 77.14%