

# Brain Tumor Detection Using a Convolutional Neural Network

## About the Brain MRI Images dataset:

The dataset contains 2 folders: yes and no which contains 253 Brain MRI Images. The folder yes contains 155 Brain MRI Images that are tumorous and the folder no contains 98 Brain MRI Images that are non-tumorous. You can find it [here](#).

## Import Necessary Modules

```
In [1]: import tensorflow as tf
from tensorflow.keras.layers import Conv2D, Input, ZeroPadding2D, BatchNormalization
from tensorflow.keras.models import Model, load_model
from tensorflow.keras.callbacks import TensorBoard, ModelCheckpoint
from sklearn.model_selection import train_test_split
from sklearn.metrics import f1_score
from sklearn.utils import shuffle
import cv2
import imutils
import numpy as np
import matplotlib.pyplot as plt
import time
from os import listdir

%matplotlib inline
```

## Data Preparation & Preprocessing

In order to crop the part that contains only the brain of the image, I used a cropping technique to find the extreme top, bottom, left and right points of the brain. You can read more about it here [Finding extreme points in contours with OpenCV](#).

```
In [2]: def crop_brain_contour(image, plot=False):

    #import imutils
    #import cv2
    #from matplotlib import pyplot as plt

    # Convert the image to grayscale, and blur it slightly
    gray = cv2.cvtColor(image, cv2.COLOR_BGR2GRAY)
    gray = cv2.GaussianBlur(gray, (5, 5), 0)

    # Threshold the image, then perform a series of erosions +
    # dilations to remove any small regions of noise
    thresh = cv2.threshold(gray, 45, 255, cv2.THRESH_BINARY)[1]
    thresh = cv2.erode(thresh, None, iterations=2)
    thresh = cv2.dilate(thresh, None, iterations=2)

    # Find contours in thresholded image, then grab the largest one
    cnts = cv2.findContours(thresh.copy(), cv2.RETR_EXTERNAL, cv2.CHAIN_APPROX_SIMPLE)
    cnts = imutils.grab_contours(cnts)
    c = max(cnts, key=cv2.contourArea)
```

```

# Find the extreme points
extLeft = tuple(c[c[:, :, 0].argmin()][0])
extRight = tuple(c[c[:, :, 0].argmax()][0])
extTop = tuple(c[c[:, :, 1].argmin()][0])
extBot = tuple(c[c[:, :, 1].argmax()][0])

# crop new image out of the original image using the four extreme points (left,
new_image = image[extTop[1]:extBot[1], extLeft[0]:extRight[0]]

if plot:
    plt.figure()

    plt.subplot(1, 2, 1)
    plt.imshow(image)

    plt.tick_params(axis='both', which='both',
                    top=False, bottom=False, left=False, right=False,
                    labelbottom=False, labeltop=False, labelleft=False, labelright=False)

    plt.title('Original Image')

    plt.subplot(1, 2, 2)
    plt.imshow(new_image)

    plt.tick_params(axis='both', which='both',
                    top=False, bottom=False, left=False, right=False,
                    labelbottom=False, labeltop=False, labelleft=False, labelright=False)

    plt.title('Cropped Image')

    plt.show()

return new_image

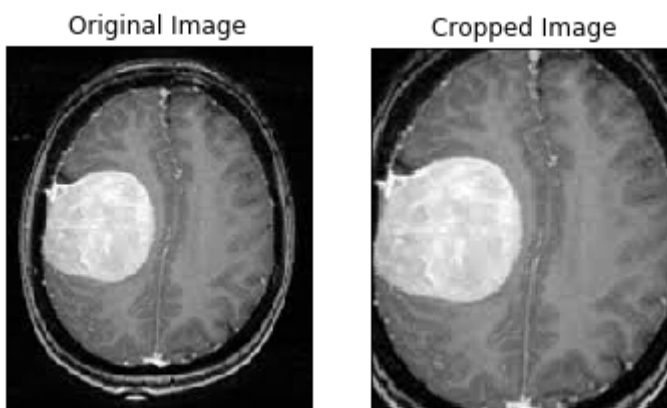
```

In order to better understand what it's doing, let's grab an image from the dataset and apply this cropping function to see the result:

```

In [3]: ex_img = cv2.imread('yes/Y1.jpg')
        ex_new_img = crop_brain_contour(ex_img, True)

```



## Load up the data:

The following function takes two arguments, the first one is a list of directory paths for the folders 'yes' and 'no' that contain the image data and the second argument is the image size, and for every image in both directories and does the following:

1. Read the image.
2. Crop the part of the image representing only the brain.
3. Resize the image (because the images in the dataset come in different sizes (meaning width, height and # of channels). So, we want all of our images to be (240, 240, 3) to feed it as an input to the neural network.
4. Apply normalization because we want pixel values to be scaled to the range 0-1.
5. Append the image to  $X$  and its label to  $y$ .

After that, Shuffle  $X$  and  $y$ , because the data is ordered (meaning the arrays contains the first part belonging to one class and the second part belonging to the other class, and we don't want that).

Finally, Return  $X$  and  $y$ .

```
In [5]: def load_data(dir_list, image_size):
        """
        Read images, resize and normalize them.
        Arguments:
            dir_list: list of strings representing file directories.
        Returns:
            X: A numpy array with shape = (#_examples, image_width, image_height, #_channels)
            y: A numpy array with shape = (#_examples, 1)
        """

        # Load all images in a directory
        X = []
        y = []
        image_width, image_height = image_size

        for directory in dir_list:
            for filename in listdir(directory):
                # Load the image
                image = cv2.imread(directory + '\\' + filename)
                # crop the brain and ignore the unnecessary rest part of the image
                image = crop_brain_contour(image, plot=False)
                # resize image
                image = cv2.resize(image, dsize=(image_width, image_height), interpolation=cv2.INTER_LINEAR)
                # normalize values
                image = image / 255.
                # convert image to numpy array and append it to X
                X.append(image)
                # append a value of 1 to the target array if the image
                # is in the folder named 'yes', otherwise append 0.
                if directory[-3:] == 'yes':
                    y.append([1])
                else:
                    y.append([0])

        X = np.array(X)
        y = np.array(y)

        # Shuffle the data
        X, y = shuffle(X, y)

        print(f'Number of examples is: {len(X)}')
        print(f'X shape is: {X.shape}')
        print(f'y shape is: {y.shape}')

        return X, y
```

Load up the data that we augmented earlier in the Data Augmentation notebook.

**Note:** the augmented data directory contains not only the new generated images but also the original images.

```
In [6]: augmented_path = 'augmented data/'

# augmented data (yes and no) contains both the original and the new generated examples
augmented_yes = augmented_path + 'yes'
augmented_no = augmented_path + 'no'

IMG_WIDTH, IMG_HEIGHT = (240, 240)

X, y = load_data([augmented_yes, augmented_no], (IMG_WIDTH, IMG_HEIGHT))

Number of examples is: 2065
X shape is: (2065, 240, 240, 3)
y shape is: (2065, 1)
```

As we see, we have 2065 images. Each images has a shape of **(240, 240, 3)=(image\_width, image\_height, number\_of\_channels)**

## Plot sample images:

```
In [6]: def plot_sample_images(X, y, n=50):
        """
        Plots n sample images for both values of y (labels).
        Arguments:
            X: A numpy array with shape = (#_examples, image_width, image_height, #_channels)
            y: A numpy array with shape = (#_examples, 1)
        """

        for label in [0,1]:
            # grab the first n images with the corresponding y values equal to label
            images = X[np.argwhere(y == label)]
            n_images = images[:n]

            columns_n = 10
            rows_n = int(n/ columns_n)

            plt.figure(figsize=(20, 10))

            i = 1 # current plot
            for image in n_images:
                plt.subplot(rows_n, columns_n, i)
                plt.imshow(image[0])

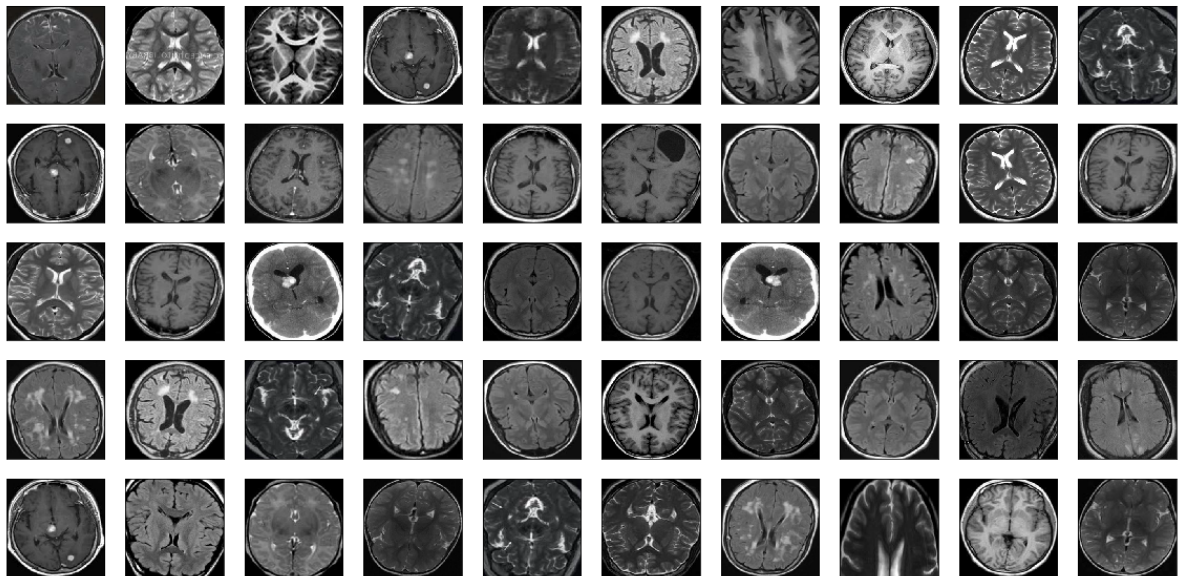
                # remove ticks
                plt.tick_params(axis='both', which='both',
                                top=False, bottom=False, left=False, right=False,
                                labelbottom=False, labeltop=False, labelleft=False, labelright=False)

                i += 1

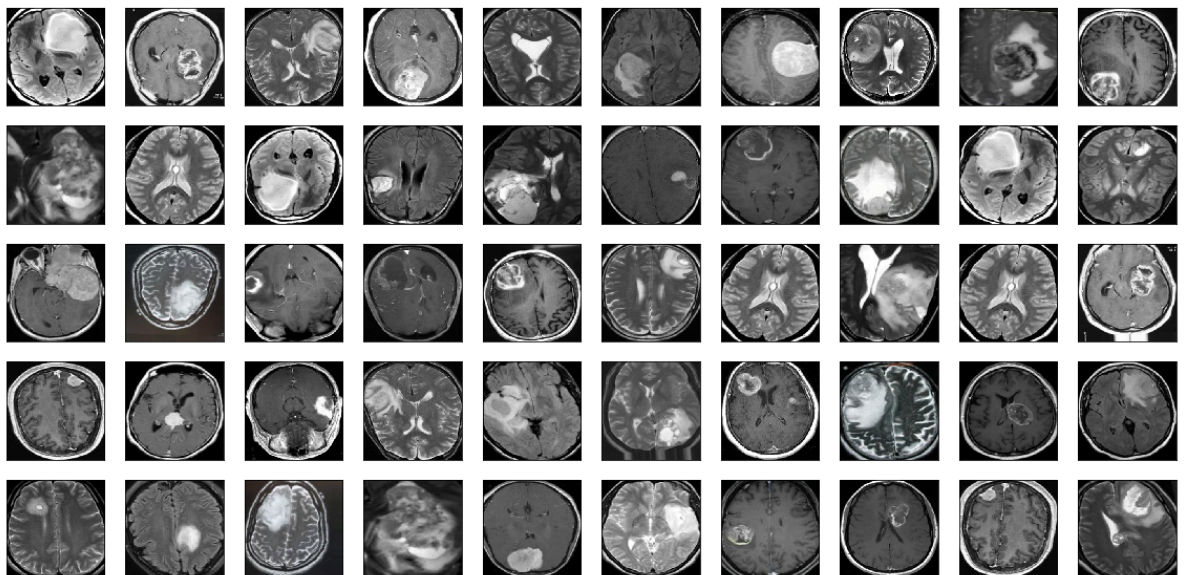
            label_to_str = lambda label: "Yes" if label == 1 else "No"
            plt.suptitle(f"Brain Tumor: {label_to_str(label)}")
            plt.show()
```

```
In [7]: plot_sample_images(X, y)
```

Brain Tumor: No



Brain Tumor: Yes



## Split the data:

Split  $X$  and  $y$  into training, validation (development) and validation sets.

```
In [8]: def split_data(X, y, test_size=0.2):

        """
        Splits data into training, development and test sets.
        Arguments:
            X: A numpy array with shape = (#_examples, image_width, image_height, #_channels)
            y: A numpy array with shape = (#_examples, 1)
        Returns:
            X_train: A numpy array with shape = (#_train_examples, image_width, image_height, #_channels)
            y_train: A numpy array with shape = (#_train_examples, 1)
            X_val: A numpy array with shape = (#_val_examples, image_width, image_height, #_channels)
            y_val: A numpy array with shape = (#_val_examples, 1)
            X_test: A numpy array with shape = (#_test_examples, image_width, image_height, #_channels)
            y_test: A numpy array with shape = (#_test_examples, 1)
        """
```

```
X_train, X_test_val, y_train, y_test_val = train_test_split(X, y, test_size=test_size)
X_test, X_val, y_test, y_val = train_test_split(X_test_val, y_test_val, test_size=test_size)

return X_train, y_train, X_val, y_val, X_test, y_test
```

Let's use the following way to split:

1. 70% of the data for training.
2. 15% of the data for validation.
3. 15% of the data for testing.

```
In [9]: X_train, y_train, X_val, y_val, X_test, y_test = split_data(X, y, test_size=0.3)
```

```
In [10]: print ("number of training examples = " + str(X_train.shape[0]))
print ("number of development examples = " + str(X_val.shape[0]))
print ("number of test examples = " + str(X_test.shape[0]))
print ("X_train shape: " + str(X_train.shape))
print ("Y_train shape: " + str(y_train.shape))
print ("X_val (dev) shape: " + str(X_val.shape))
print ("Y_val (dev) shape: " + str(y_val.shape))
print ("X_test shape: " + str(X_test.shape))
print ("Y_test shape: " + str(y_test.shape))
```

```
number of training examples = 1445
number of development examples = 310
number of test examples = 310
X_train shape: (1445, 240, 240, 3)
Y_train shape: (1445, 1)
X_val (dev) shape: (310, 240, 240, 3)
Y_val (dev) shape: (310, 1)
X_test shape: (310, 240, 240, 3)
Y_test shape: (310, 1)
```

Some helper functions:

```
In [11]: # Nicely formatted time string
def hms_string(sec_elapsed):
    h = int(sec_elapsed / (60 * 60))
    m = int((sec_elapsed % (60 * 60)) / 60)
    s = sec_elapsed % 60
    return f"{h}:{m}:{round(s,1)}"
```

```
In [12]: def compute_f1_score(y_true, prob):
# convert the vector of probabilities to a target vector
y_pred = np.where(prob > 0.5, 1, 0)

score = f1_score(y_true, y_pred)

return score
```

## Build the model

Let's build a convolutional neural network model:



```
In [13]: def build_model(input_shape):
"""
```



```

Arugments:
    input_shape: A tuple representing the shape of the input of the model. shape
Returns:
    model: A Model object.
"""
# Define the input placeholder as a tensor with shape input_shape.
X_input = Input(input_shape) # shape=(?, 240, 240, 3)

# Zero-Padding: pads the border of X_input with zeroes
X = ZeroPadding2D((2, 2))(X_input) # shape=(?, 244, 244, 3)

# CONV -> BN -> RELU Block applied to X
X = Conv2D(32, (7, 7), strides = (1, 1), name = 'conv0')(X)
X = BatchNormalization(axis = 3, name = 'bn0')(X)
X = Activation('relu')(X) # shape=(?, 238, 238, 32)

# MAXPOOL
X = MaxPooling2D((4, 4), name='max_pool0')(X) # shape=(?, 59, 59, 32)

# MAXPOOL
X = MaxPooling2D((4, 4), name='max_pool1')(X) # shape=(?, 14, 14, 32)

# FLATTEN X
X = Flatten()(X) # shape=(?, 6272)
# FULLYCONNECTED
X = Dense(1, activation='sigmoid', name='fc')(X) # shape=(?, 1)

# Create model. This creates your Keras model instance, you'll use this instance
model = Model(inputs = X_input, outputs = X, name='BrainDetectionModel')

return model

```

Define the image shape:

```
In [14]: IMG_SHAPE = (IMG_WIDTH, IMG_HEIGHT, 3)
```

```
In [15]: model = build_model(IMG_SHAPE)
```

```
In [16]: model.summary()
```

Layer (type)	Output Shape	Param #
input_1 (InputLayer)	(None, 240, 240, 3)	0
zero_padding2d (ZeroPadding2D)	(None, 244, 244, 3)	0
conv0 (Conv2D)	(None, 238, 238, 32)	4736
bn0 (BatchNormalization)	(None, 238, 238, 32)	128
activation (Activation)	(None, 238, 238, 32)	0
max_pool0 (MaxPooling2D)	(None, 59, 59, 32)	0
max_pool1 (MaxPooling2D)	(None, 14, 14, 32)	0
flatten (Flatten)	(None, 6272)	0
fc (Dense)	(None, 1)	6273
Total params: 11,137		
Trainable params: 11,073		
Non-trainable params: 64		

Compile the model:

```
In [17]: model.compile(optimizer='adam', loss='binary_crossentropy', metrics=['accuracy'])
```

```
In [18]: # tensorboard
log_file_name = f'brain_tumor_detection_cnn_{int(time.time())}'
tensorboard = TensorBoard(log_dir=f'logs/{log_file_name}')
```

```
In [19]: # checkpoint
# unique file name that will include the epoch and the validation (development) accuracy
filepath="cnn-parameters-improvement-{epoch:02d}-{val_acc:.2f}"
# save the model with the best validation (development) accuracy till now
checkpoint = ModelCheckpoint("models/{}.model".format(filepath, monitor='val_acc',
```

## Train the model

```
In [20]: start_time = time.time()

model.fit(x=X_train, y=y_train, batch_size=32, epochs=10, validation_data=(X_val, y_val))

end_time = time.time()
execution_time = (end_time - start_time)
print(f"Elapsed time: {hms_string(execution_time)}")
```



Train on 1445 samples, validate on 310 samples

Epoch 1/10

1445/1445 [=====] - 434s 300ms/step - loss: 0.8331 - acc: 0.5945 - val\_loss: 0.6829 - val\_acc: 0.4968

Epoch 2/10

1445/1445 [=====] - 463s 320ms/step - loss: 0.4817 - acc: 0.7668 - val\_loss: 0.6342 - val\_acc: 0.6742

Epoch 3/10

1445/1445 [=====] - 471s 326ms/step - loss: 0.4361 - acc: 0.8069 - val\_loss: 0.5294 - val\_acc: 0.8065

Epoch 4/10

1445/1445 [=====] - 465s 322ms/step - loss: 0.3641 - acc: 0.8574 - val\_loss: 0.6092 - val\_acc: 0.6323

Epoch 5/10

1445/1445 [=====] - 457s 316ms/step - loss: 0.3940 - acc: 0.8339 - val\_loss: 0.4689 - val\_acc: 0.7742

Epoch 6/10

1445/1445 [=====] - 452s 313ms/step - loss: 0.3154 - acc: 0.8692 - val\_loss: 0.4448 - val\_acc: 0.7806

Epoch 7/10

1445/1445 [=====] - 465s 322ms/step - loss: 0.2776 - acc: 0.8872 - val\_loss: 0.4747 - val\_acc: 0.7323

Epoch 8/10

1445/1445 [=====] - 439s 304ms/step - loss: 0.3271 - acc: 0.8519 - val\_loss: 0.3655 - val\_acc: 0.8516

Epoch 9/10

1445/1445 [=====] - 435s 301ms/step - loss: 0.2182 - acc: 0.9190 - val\_loss: 0.4557 - val\_acc: 0.8129

Epoch 10/10

1445/1445 [=====] - 438s 303ms/step - loss: 0.2054 - acc: 0.9225 - val\_loss: 0.4038 - val\_acc: 0.8129

Elapsed time: 1:15:23.8

Let's train for a few more epochs:

```
In [36]: start_time = time.time()

model.fit(x=X_train, y=y_train, batch_size=32, epochs=3, validation_data=(X_val, y_val))

end_time = time.time()
execution_time = (end_time - start_time)
print(f"Elapsed time: {hms_string(execution_time)}")
```

Train on 1445 samples, validate on 310 samples

Epoch 1/3

1445/1445 [=====] - 431s 299ms/step - loss: 0.2065 - acc: 0.9239 - val\_loss: 0.3357 - val\_acc: 0.8871

Epoch 2/3

1445/1445 [=====] - 432s 299ms/step - loss: 0.1811 - acc: 0.9363 - val\_loss: 0.3529 - val\_acc: 0.8516

Epoch 3/3

1445/1445 [=====] - 425s 294ms/step - loss: 0.1827 - acc: 0.9287 - val\_loss: 0.4038 - val\_acc: 0.8323

Elapsed time: 0:21:29.4

```
In [37]: start_time = time.time()

model.fit(x=X_train, y=y_train, batch_size=32, epochs=3, validation_data=(X_val, y_val))

end_time = time.time()
execution_time = (end_time - start_time)
print(f"Elapsed time: {hms_string(execution_time)}")
```

Train on 1445 samples, validate on 310 samples

Epoch 1/3

1445/1445 [=====] - 438s 303ms/step - loss: 0.1471 - acc: 0.9612 - val\_loss: 0.3190 - val\_acc: 0.8903

Epoch 2/3

1445/1445 [=====] - 432s 299ms/step - loss: 0.1384 - acc: 0.9564 - val\_loss: 0.3509 - val\_acc: 0.8613

Epoch 3/3

1445/1445 [=====] - 429s 297ms/step - loss: 0.1240 - acc: 0.9647 - val\_loss: 0.3358 - val\_acc: 0.8710

Elapsed time: 0:21:38.5

```
In [38]: start_time = time.time()

model.fit(x=X_train, y=y_train, batch_size=32, epochs=3, validation_data=(X_val, y_val))

end_time = time.time()
execution_time = (end_time - start_time)
print(f"Elapsed time: {hms_string(execution_time)}")
```

Train on 1445 samples, validate on 310 samples

Epoch 1/3

1445/1445 [=====] - 536s 371ms/step - loss: 0.1586 - acc: 0.9453 - val\_loss: 0.4005 - val\_acc: 0.8548

Epoch 2/3

1445/1445 [=====] - 427s 296ms/step - loss: 0.1244 - acc: 0.9647 - val\_loss: 0.3149 - val\_acc: 0.9000

Epoch 3/3

1445/1445 [=====] - 429s 297ms/step - loss: 0.1074 - acc: 0.9668 - val\_loss: 0.3118 - val\_acc: 0.8935

Elapsed time: 0:23:11.9

```
In [39]: start_time = time.time()

model.fit(x=X_train, y=y_train, batch_size=32, epochs=5, validation_data=(X_val, y_val))

end_time = time.time()
execution_time = (end_time - start_time)
print(f"Elapsed time: {hms_string(execution_time)}")
```

Train on 1445 samples, validate on 310 samples

Epoch 1/5

1445/1445 [=====] - 427s 296ms/step - loss: 0.0899 - acc: 0.9785 - val\_loss: 0.3310 - val\_acc: 0.8935

Epoch 2/5

1445/1445 [=====] - 426s 295ms/step - loss: 0.1343 - acc: 0.9509 - val\_loss: 0.5169 - val\_acc: 0.8258

Epoch 3/5

1445/1445 [=====] - 425s 294ms/step - loss: 0.1137 - acc: 0.9626 - val\_loss: 0.6945 - val\_acc: 0.7516

Epoch 4/5

1445/1445 [=====] - 430s 298ms/step - loss: 0.1018 - acc: 0.9640 - val\_loss: 0.3210 - val\_acc: 0.9065

Epoch 5/5

1445/1445 [=====] - 434s 300ms/step - loss: 0.0949 - acc: 0.9689 - val\_loss: 0.4250 - val\_acc: 0.8484

Elapsed time: 0:35:41.9

```
In [21]: history = model.history.history
```

```
In [22]: for key in history.keys():
          print(key)
```

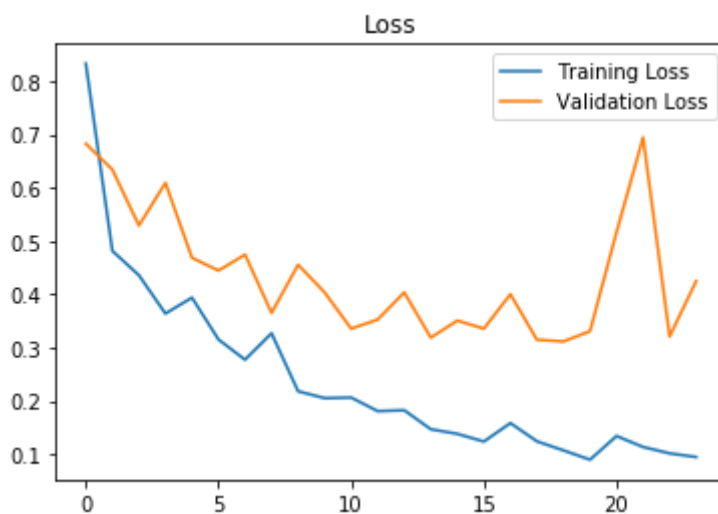
```
val_loss  
val_acc  
loss  
acc
```

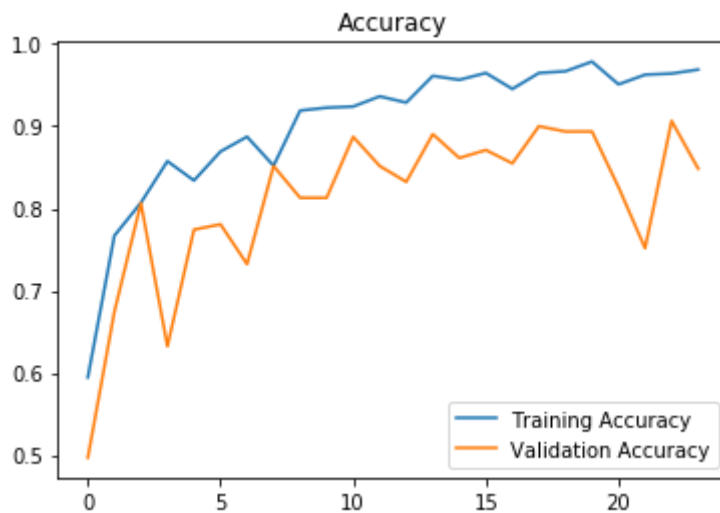
## Plot Loss & Accuracy

```
In [23]: def plot_metrics(history):  
  
    train_loss = history['loss']  
    val_loss = history['val_loss']  
    train_acc = history['acc']  
    val_acc = history['val_acc']  
  
    # Loss  
    plt.figure()  
    plt.plot(train_loss, label='Training Loss')  
    plt.plot(val_loss, label='Validation Loss')  
    plt.title('Loss')  
    plt.legend()  
    plt.show()  
  
    # Accuracy  
    plt.figure()  
    plt.plot(train_acc, label='Training Accuracy')  
    plt.plot(val_acc, label='Validation Accuracy')  
    plt.title('Accuracy')  
    plt.legend()  
    plt.show()
```

**Note:** Since we trained the model using more than model.fit() function call, this made the history only contain the metric values of the epochs for the last call (which was for 5 epochs), so to plot the metric values across the whole process of training the model from the beginning, I had to grab the rest of the values.

```
In [68]: plot_metrics(history)
```





## Results

Let's experiment with the best model (the one with the best validation accuracy):

Concretely, the model at the 23rd iteration with validation accuracy of 91%

### Load the best model

```
In [71]: best_model = load_model(filepath='models/cnn-parameters-improvement-23-0.91.model')
```

```
In [72]: best_model.metrics_names
```

```
Out[72]: ['loss', 'acc']
```

Evaluate the best model on the testing data:

```
In [73]: loss, acc = best_model.evaluate(x=X_test, y=y_test)
```

```
310/310 [=====] - 18s 57ms/step
```

### Accuracy of the best model on the testing data:

```
In [74]: print (f"Test Loss = {loss}")
print (f"Test Accuracy = {acc}")
```

```
Test Loss = 0.33390871454631127
Test Accuracy = 0.8870967741935484
```

### F1 score for the best model on the testing data:

```
In [75]: y_test_prob = best_model.predict(X_test)
```

```
In [76]: f1score = compute_f1_score(y_test, y_test_prob)
print(f"F1 score: {f1score}")
```

```
F1 score: 0.8829431438127091
```

Let's also find the f1 score on the validation data:

```
In [83]: y_val_prob = best_model.predict(X_val)
```

```
In [85]: f1score_val = compute_f1_score(y_val, y_val_prob)
print(f"F1 score: {f1score_val}")
```

F1 score: 0.9123867069486403

## Results Interpretation

Let's remember the percentage of positive and negative examples:

```
In [77]: def data_percentage(y):

    m=len(y)
    n_positive = np.sum(y)
    n_negative = m - n_positive

    pos_prec = (n_positive* 100.0)/ m
    neg_prec = (n_negative* 100.0)/ m

    print(f"Number of examples: {m}")
    print(f"Percentage of positive examples: {pos_prec}%, number of pos examples: ")
    print(f"Percentage of negative examples: {neg_prec}%, number of neg examples: ")
```

```
In [81]: # the whole data
data_percentage(y)
```

Number of examples: 2065  
 Percentage of positive examples: 52.54237288135593%, number of pos examples: 1085  
 Percentage of negative examples: 47.45762711864407%, number of neg examples: 980

```
In [79]: print("Training Data:")
data_percentage(y_train)
print("Validation Data:")
data_percentage(y_val)
print("Testing Data:")
data_percentage(y_test)
```

Training Data:  
 Number of examples: 1445  
 Percentage of positive examples: 52.8719723183391%, number of pos examples: 764  
 Percentage of negative examples: 47.1280276816609%, number of neg examples: 681  
 Validation Data:  
 Number of examples: 310  
 Percentage of positive examples: 54.83870967741935%, number of pos examples: 170  
 Percentage of negative examples: 45.16129032258065%, number of neg examples: 140  
 Testing Data:  
 Number of examples: 310  
 Percentage of positive examples: 48.70967741935484%, number of pos examples: 151  
 Percentage of negative examples: 51.29032258064516%, number of neg examples: 159

As expected, the percentage of positive examples are around 50%.

## Conclusion:

Now, the model detects brain tumor with:

**88.7%** accuracy on the **test set**.

**0.88** f1 score on the **test set**.

These results are very good considering that the data is balanced.

**Performance Table:**

	Validation set	Test set
Accuracy	91%	89%
F1 score	0.91	0.88

Hooray!

In [ ]: